**Online Supporting Information S2.** The benchmark dataset S2 includes 7,329 proteins from 1070 super-families and 1824 families (see Ref. 12).

>d1dlwa\_ a.1.1.1 (A:) Truncated hemoglobin {Ciliate (Paramecium caudatum)}

SLFEQLGGQAAVQAVTAQFYANIQADATVATFFNGIDMPNQTNKTAAFLCAALGGPNAWTGRNLKEVHANMGVSNAQFTTVIGHLRSALTGAGVAAALVEQTVAVAETVRGDVVTV

>d1dlya\_ a.1.1.1 (A:) Truncated hemoglobin {Green alga (Chlamydomonas eugametos)}

SLFAKLGGREAVEAAVDKFYNKIVADPTVSTYFSNTDMKVQRSKQFAFLAYALGGASEWKGKDMRTAHKDLVPHLSDVHFQAVARHLSDTLTELGVPPEDITDAMAVVASTRTEVLNMPQQ

>d1idra\_ a.1.1.1 (A:) Truncated hemoglobin {Mycobacterium tuberculosis}

GLLSRLRKREPISIYDKIGGHEAIEVVVEDFYVRVLADDQLSAFFSGTNMSRLKGKQVEFFAAALGGPEPYTGAPMKQVHQGRGITMHHFSLVAGHLADALTAAGVPSETITEILGVIAPLAVDVTS

>d1scta\_ a.1.1.2 (A:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}

VDAAVAKVCGSEAIKANLRRSWGVLSADIEATGLMLMSNLFTLRPDTKTYFTRLGDVQKGKANSKLRGHAITLTYALNNFVDSLDDPSRLKCVVEKFAVNHINRKISGDAFGAIVEPMKETLKARMGNYYSDDVAGAWAALVGVVQAAL

>d1sctb\_ a.1.1.2 (B:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}

KVAELANAVVSNADQKDLLRMSWGVLSVDMEGTGLMLMANLFKTSPSAKGKFARLGDVSAGKDNSKLRGHSITLMYALQNFVDALDDVERLKCVVEKFAVNHINRQISADEFGEIVGPLRQTLKARMGNYFDEDTVAAWASLVAVVQASL

>d3sdha\_ a.1.1.2 (A:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}

SVYDAAAQLTADVKKDLRDSWKVIGSDKKGNGVALMTTLFADNQETIGYFKRLGNVSQGMANDKLRGHSITLMYALQNFIDQLDNPDDLVCVVEKFAVNHITRKISAAEFGKINGPIKKVLASKNFGDKYANAWAKLVAVVQAAL

>d1b0b\_\_ a.1.1.2 (-) Hemoglobin I {Clam (Lucina pectinata)}

SLSAAQKDNVKSSWAKASAAWGTAGPEFFMALFDAHDDVFAKFSGLFSGAAKGTVKNTPEMAAQAQSFKGLVSNWVDNLDNAGALEGQCKTFAANHKARGISAGQLEAAFKVLAGFMKSYGGDEGAWTAVAGALMGMIRPDM

>d1h97a\_ a.1.1.2 (A:) Trematode hemoglobin/myoglobin {Paramphistomum epiclitum}

TLTKHEQDILLKELGPHVDTPAHIVETGLGAYHALFTAHPQYISHFSRLEGHTIENVMQSEGIKHYARTLTEAIVHMLKEISNDAEVKKIAAQYGKDHTSRKVTKDEFMSGEPIFTKYFQNLVKDAEGKAAVEKFLKHVFPMMAAEI

>d1vrea\_ a.1.1.2 (A:) Glycera globin {Marine bloodworm (Glycera dibranchiata)}

GLSAAQRQVVASTWKDIAGSDNGAGVGKECFTKFLSAHHDMAAVFGFSGASDPGVADLGAKVLAQIGVAVSHLGDEGKMVAEMKAVGVRHKGYGNKHIKAEYFEPLGASLLSAMEHRIGGKMNAAAKDAWAAAYADISGALISGLQS

>d2hbg\_\_ a.1.1.2 (-) Glycera globin {Marine bloodworm (Glycera dibranchiata)}

GLSAAQRQVIAATWKDIAGADNGAGVGKKCLIKFLSAHPQMAAVFGFSGASDPGVAALGAKVLAQIGVAVSHLGDEGKMVAQMKAVGVRHKGYGNKHIKAQYFEPLGASLLSAMEHRIGGKMNAAAKDAWAAAYADISGALISGLQS

>d1a6m\_\_ a.1.1.2 (-) Myoglobin {Sperm whale (Physeter catodon)}

VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDLKKHGVTVLTALGAILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGADAQGAMNKALELFRKDIAAKYKELGY

>d1mba\_\_ a.1.1.2 (-) Myoglobin {Sea hare (Aplysia limacina)}

SLSAAEADLAGKSWAPVFANKNANGLDFLVALFEKFPDSANFFADFKGKSVADIKASPKLRDVSSRIFTRLNEFVNNAANAGKMSAMLSQFAKEHVGFGVGSAQFENVRSMFPGFVASVAAPPAGADAAWTKLFGLIIDALKAAGA

>d1mbs\_\_ a.1.1.2 (-) Myoglobin {Common seal (Phoca vitulina)}

GLSDGEWHLVLNVWGKVETDLAGHGQEVLIRLFKSHPETLEKFDKFKHLKSEDDMRRSEDLRKHGNTVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSKHPAEFGADAQAAMKKALELFRNDIAAKYKELGFHG

>d1mwca\_ a.1.1.2 (A:) Myoglobin {Pig (Sus scrofa)}

GLSDGEWQLVLNVWGKVEADVAGHGQEVLIRLFKGHPETLEKFDKFKHLKSEDEMKASEDLKKHGNTVLTALGGILKKKGHHEAELTPLAQSHATKHKIPVKYLEFISEAIIQVLQSKHPGDFGADAQGAMSKALELFRNDMAAKYKELGFQG

>d1dwta\_ a.1.1.2 (A:) Myoglobin {Horse (Equus caballus)}

GLSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFTGHPETLEKFDKFKHLKTEAEMKASEDLKKHGTVVLTALGGILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISDAIIHVLHSKHPGDFGADAQGAMTKALELFRNDIAAKYKELGFQ

>d2mm1\_\_ a.1.1.2 (-) Myoglobin {Human (Homo sapiens)}

GLSDGEWQLVLNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDRFKHLKSEDEMKASEDLKKHGATVLTALGGILKKKGHHEAEIKPLAQSHATKHKIPVKYLEFISEAIIQVLQSKHPGDFGADAQGAMNKALELFRKDMASNYKELGFQG

>d1emy\_\_ a.1.1.2 (-) Myoglobin {Asian elephant (Elephas maximus)}

GLSDGEWELVLKTWGKVEADIPGHGETVFVRLFTGHPETLEKFDKFKHLKTEGEMKASEDLKKQGVTVLTALGGILKKKGHHEAEIQPLAQSHATKHKIPIKYLEFISDAIIHVLQSKHPAEFGADAQGAMKKALELFRNDIAAKYKELGFQG

>d1lht\_\_ a.1.1.2 (-) Myoglobin {Loggerhead sea turtle (Caretta caretta)}

GLSDDEWNHVLGIWAKVEPDLSAHGQEVIIRLFQLHPETQERFAKFKNLTTIDALKSSEEVKKHGTTVLTALGRILKQKNNHEQELKPLAESHATKHKIPVKYLEFICEIIVKVIAEKHPSDFGADSQAAMKKALELFRNDMASKYKEFGFQG

>d1myt\_\_ a.1.1.2 (-) Myoglobin {Yellowfin tuna (Thunnus albacares)}

ADFDAVLKCWGPVEADYTTMGGLVLTRLFKEHPETQKLFPKFAGIAQADIAGNAAISAHGATVLKKLGELLKAKGSHAAILKPLANSHATKHKIPINNFKLISEVLVKVMHEKAGLDAGGQTALRNVMGIIIADLEANYKELGFSG

>d1eco\_\_ a.1.1.2 (-) Erythrocruorin {Midge (Chironomus thummi thummi), fraction III}

LSADQISTVQASFDKVKGDPVGILYAVFKADPSIMAKFTQFAGKDLESIKGTAPFETHANRIVGFFSKIIGELPNIEADVNTFVASHKPRGVTHDQLNNFRAGFVSYMKAHTDFAGAEAAWGATLDTFFGMIFSKM

>d2gdm\_\_ a.1.1.2 (-) Leghemoglobin {Yellow lupin (Lupinus luteus)}

GALTESQAALVKSSWEEFNANIPKHTHRFFILVLEIAPAAKDLFSFLKGTSEVPQNNPELQAHAGKVFKLVYEAAIQLEVTGVVVTDATLKNLGSVHVSKGVADAHFPVVKEAILKTIKEVVGAKWSEELNSAWTIAYDELAIVIKKEMDDAA

>d1fsla\_ a.1.1.2 (A:) Leghemoglobin {Soybean (Glycine max), isoform A}

VAFTEKQDALVSSSFEAFKANIPQYSVVFYTSILEKAPAAKDLFSFLANGVDPTNPKLTGHAEKLFALVRDSAGQLKASGTVVADAALGSVHAQKAVTDPQFVVVKEALLKTIKAAVGDKWSDELSRAWEVAYDELAAAIKKA

>d1d8ua\_ a.1.1.2 (A:) Non-symbiotic plant hemoglobin {Rice (Oryza sativa)}

ALVEDNNAVAVSFSEEQEALVLKSWAILKKDSANIALRFFLKIFEVAPSASQMFSFLRNSDVPLEKNPKLKTHAMSVFVMTCEAAAQLRKAGKVTVRDTTLKRLGATHLKYGVGDAHFEVVKFALLDTIKEEVPADMWSPAMKSAWSEAYDHLVAAIKQEMKPAE

>d1i3da\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (Homo sapiens)}

GHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVYPWTQRFFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDDLKGTFAQLSELHCDKLHVDPENFKLLGNVLVTVLAIHFGKEFTPEVQASWQKMVTAVASALSSRYH

>d1irda\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (Homo sapiens)}

VLSPADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADALTNAVAHVDDMPNALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR

>d1jeba\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (Homo sapiens), zeta isoform}

SLTKTERTIIVSMWAKISTQADTIGTETLERLFLSHPQTKTYFPHFDLHPGSAQLRAHGSKVVAAVGDAVKSIDDIGGALSKLSELHAYILRVDPVNFKLLSHCLLVTLAARFPADFTAEAHAAWDKFLSVVSSVLTEKYR

>d1ibea\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Horse (Equus caballus)}

VLSAADKTNVKAAWSKVGGHAGEFGAEALERMFLGFPTTKTYFPHFDLSHGSAQVKAHGKKVGDALTLAVGHLDDLPGALSDLSNLHAHKLRVDPVNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLSSVSTVLTSKYR

>d1hdsa\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Deer (Odocoileus virginianus)}

VLSAANKSNVKAAWGKVGGNAPAYGAQALQRMFLSFPTTKTYFPHFDLSHGSAQQKAHGQKVANALTKAQGHLNDLPGTLSNLSNLHAHKLRVNPVNFKLLSHSLLVTLASHLPTNFTPAVHANLNKFLANDSTVLTSKYR

>d1g08a\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Cow (Bos taurus)}

VLSAADKGNVKAAWGKVGGHAAEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGAKVAAALTKAVEHLDDLPGALSELSDLHAHKLRVDPVNFKLLSHSLLVTLASHLPSDFTPAVHASLDKFLANVSTVLTSKYR

>d1qpwa\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Pig (Sus scrofa)}

VLSAADKANVKAAWGKVGGQAGAHGAEALERMFLGFPTTKTYFPHFNLSHGSDQVKAHGQKVADALTKAVGHLDDLPGALSALSDLHAHKLRVDPVNFKLLSHCLLVTLAAHHPDDFNPSVHASLDKFLANVSTVLTSKYR

>d1fhja\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Maned wolf (Chrysocyon brachyurus)}

VLSPADKTNIKSTWDKIGGHAGDYGGEALDRTFQSFPTTKTYFPHFDLSPGSAQVKAHGKKVADALTTAVAHLDDLPGALSALSDLHAYKLRVDPVNFKLLSHCLLVTLACHHPTEFTPAVHASLDKFFTAVSTVLTSKYR

>d1hbra\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Chicken (Gallus gallus)}

MLTAEDKKLIQQAWEKAASHQEEFGAEALTRMFTTYPQTKTYFPHFDLSPGSDQVRGHGKKVLGALGNAVKNVDNLSQAMAELSNLHAYNLRVDPVNFKLLSQCIQVVLAVHMGKDYTPEVHAAFDKFLSAVSAVLAEKYR

>d1a4fa\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Bar-headed goose (Anser indicus)}

VLSAADKTNVKGVFSKISGHAEEYGAETLERMFTAYPQTKTYFPHFDLQHGSAQIKAHGKKVVAALVEAVNHIDDIAGALSKLSDLHAQKLRVDPVNFKFLGHCFLVVVAIHHPSALTAEVHASLDKFLCAVGTVLTAKYR

>d1outa\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Trout (Oncorhynchus mykiss)}

SLTAKDKSVVKAFWGKISGKADVVGAEALGRMLTAYPQTKTYFSHWADLSPGSGPVKKHGGIIMGAIGKAVGLMDDLVGGMSALSDLHAFKLRVDPGNFKILSHNILVTLAIHFPSDFTPEVHIAVDKFLAAVSAALADKYR

>d1cg5a\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Cartilaginous fish akaei (Dasyatis akajei)}

VLSSQNKKAIEELGNLIKANAEAWGADALARLFELHPQTKTYFSKFSGFEACNEQVKKHGKRVMNALADATHHLDNLHLHLEDLARKHGENLLVDPHNFHLFADCIVVTLAVNLQAFTPVTHCAVDKFLELVAYELSSCYR

>d1t1na\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Fish (Trematomus newnesi)}

SLSDKDKAAVRALWSKIGKSSDAIGNDALSRMIVVYPQTKIYFSHWPDVTPGSPNIKAHGKKVMGGIALAVSKIDDLKTGLMELSEQHAYKLRVDPSNFKILNHCILVVISTMFPKEFTPEAHVSLDKFLSGVALALAERYR

>d1spga\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Teleost fish (Leiostomus xanthurus)}

SLSATDKARVKALWDKIEGKSAELGAEALGRMLVSFPQTKIYFSEWGQDLGPQTPQVRNHGAVIMAAVGKAVKSIDNLVGGLSQLSELHAFKLRVDPANFKILAHNIILVISMYFPGDFTPEVHLSVDKFLACLALALSEKYR

>d1gcva\_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Houndshark (Mustelus griseus)}

AFTACEKQTIGKIAQVLAKSPEAYGAECLARLFVTHPGSKSYFEYKDYSAAGAKVQVHGGKVIRAVVKAAEHVDDLHSHLETLALTHGKKLLVDPQNFPMLSECIIVTLATHLTEFSPDTHCAVDKLLSAICQELSSRYR

>d1irdb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Human (Homo sapiens)}

VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPPVQAAYQKVVAGVANALAHKYH

>d1a9we\_ a.1.1.2 (E:) Hemoglobin, beta-chain {Human (Homo sapiens), embryonic gower II}

VHFTAEEKAAVTSLWSKMNVEEAGGEALGRLLVVYPWTQRFFDSFGNLSSPSAILGNPKVKAHGKKVLTSFGDAIKNMDNLKPAFAKLSELHCDKLHVDPENFKLLGNVMVIILATHFGKEFTPEVQAAWQKLVSAVAIALAHKY

>d1ibeb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Horse (Equus caballus)}

VQLSGEEKAAVLALWDKVNEEEVGGEALGRLLVVYPWTQRFFDSFGDLSNPGAVMGNPKVKAHGKKVLHSFGEGVHHLDNLKGTFAALSELHCDKLHVDPENFRLLGNVLVVVLARHFGKDFTPELQASYQKVVAGVANALAHKYH

>d1hdsb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Deer (Odocoileus virginianus)}

MLTAEEKAAVTGFWGKVDVDVVGAQALGRLLVVYPWTQRFFQHFGNLSSAGAVMNNPKVKAHGKRVLDAFTQGLKHLDDLKGAFAQLSGLHCNKLHVNPQNFRLLGNVLALVVARNFGGQFTPNVQALFQKVVAGVANALAHKYH

>d1g08b\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Cow (Bos taurus)}

MLTAEEKAAVTAFWGKVKVDEVGGEALGRLLVVYPWTQRFFESFGDLSTADAVMNNPKVKAHGKKVLDSFSNGMKHLDDLKGTFAALSELHCDKLHVDPENFKLLGNVLVVVLARNFGKEFTPVLQADFQKVVAGVANALAHRYH

>d1qpwb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Pig (Sus scrofa)}

VHLSAEEKEAVLGLWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSNADAVMGNPKVKAHGKKVLQSFSDGLKHLDNLKGTFAKLSELHCDQLHVDPENFRLLGNVIVVVLARRLGHDFNPDVQAAFQKVVAGVANALAHKYH

>d1fhjb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Maned wolf (Chrysocyon brachyurus)}

VHLTAEEKSLVSGLWGKVNVDEVGGEALGRLLIVYPWTQRFFDSFGDLSTPDAVMSNAKVKAHGKKVLNSFSDGLKNLDNLKGTFAKLSELHCDKLHVDPENFKLLGNVLVCVLAHHFGKEFTPQVQAAYQKVVAGVANALAHKYH

>d1jebb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Mouse (Mus musculus)}

VHLTDAEKAAVSGLWGKVNADEVGGEALGRLLVVYPWTQRYFDSFGDLSSASAIMGNAKVKAHGKKVITAFNDGLNHLDSLKGTFASLSELHCDKLHVDPENFRLLGNMIVIVLGHHLGKDFTPAAQAAFQKVVAGVAAALAH

>d1hbrb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Chicken (Gallus gallus)}

VHWTAEEKQLITGLWGKVNVAECGAEALARLLIVYPWTQRFFASFGNLSSPTAILGNPMVRAHGKKVLTSFGDAVKNLDNIKNTFSQLSELHCDKLHVDPENFRLLGDILIIVLAAHFSKDFTPECQAAWQKLVRVVAHALARK

>d1a4fb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Bar-headed goose (Anser indicus)}

VHWSAEEKQLITGLWGKVNVADCGAEALARLLIVYPWTQRFFSSFGNLSSPTAILGNPMVRAHGKKVLTSFGDAVKNLDNIKNTFAQLSELHCDKLHVDPENFRLLGDILIIVLAAHFAKEFTPDCQAAWQKLVRVVAHALARKYH

>d1outb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Trout (Oncorhynchus mykiss)}

VEWTDAEKSTISAVWGKVNIDEIGPLALARVLIVYPWTQRYFGSFGNVSTPAAIMGNPKVAAHGKVVCGALDKAVKNMGNILATYKSLSETHANKLFVDPDNFRVLADVLTIVIAAKFGASFTPEIQATWQKFMKVVVAAMGSRYF

>d1pbxb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Antarctic fish (Pagothenia bernacchii)}

VEWTDKERSIISDIFSHMDYDDIGPKALSRCLIVYPWTQRHFSGFGNLYNAEAIIGNANVAAHGIKVLHGLDRGVKNMDNIAATYADLSTLHSEKLHVDPDNFKLLSDCITIVLAAKMGHAFTAETQGAFQKFLAVVVSALGKQYH

>d1cg5b\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Cartilaginous fish akaei (Dasyatis akajei)}

VKLSEDQEHYIKGVWKDVDHKQITAKALERVFVVYPWTTRLFSKLQGLFSANDIGVQQHADKVQRALGEAIDDLKKVEINFQNLSGKHQEIGVDTQNFKLLGQTFMVELALHYKKTFRPKEHAAAYKFFRLVAEALSSNYH

>d1t1nb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Fish (Trematomus newnesi)}

VEWTDKERSIISDIFSHMDYDDIGPKALSRCLVVYPWTQRYFSGFGNLYNAEGIMSNANVAAHGIKVLHGLDRGMKNMDNIADAYTDLSTLHSEKLHVDPDNFKLLSDCITIVLAAKMGHAFTAETQGAFQKFLAAVVSALGKQYH

>d1spgb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Teleost fish (Leiostomus xanthurus)}

VDWTDAERAAIKALWGKIDVGEIGPQALSRLLIVYPWTQRHFKGFGNISTNAAILGNAKVAEHGKTVMGGLDRAVQNMDNIKNVYKQLSIKHSEKIHVDPDNFRLLGEIITMCVGAKFGPSAFTPEIHEAWQKFLAVVVSALGRQYH

>d1gcvb\_ a.1.1.2 (B:) Hemoglobin, beta-chain {Houndshark (Mustelus griseus)}

VHWTQEERDEISKTFQGTDMKTVVTQALDRMFKVYPWTNRYFQKRTDFRSSIHAGIVVGALQDAVKHMDDVKTLFKDLSKKHADDLHVDPGSFHLLTDCIIVELAYLRKDCFTPHIQGIWDKFFEVVIDAISKQYH

>d1ch4a\_ a.1.1.2 (A:) Chimeric hemoglobin beta-alpha {Synthetic, based on Homo sapiens sequence}

VHLTPEEKSAVTALWGKVNVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLRVDPVNFKLLSHCLLVTLAAHLPAEFTPAVHASLDKVLASVSTVLTSKYR

>d1it2a\_ a.1.1.2 (A:) Hagfish hemoglobin {Inshore hagfish (Eptatretus burgeri)}

PIIDQGPLPTLTDGDKKAINKIWPKIYKEYEQYSLNILLRFLKCFPQAQASFPKFSTKKSNLEQDPEVKHQAVVIFNKVNEIINSMDNQEEIIKSLKDLSQKHKTVFKVDSIWFKELSSIFVSTIDGGAEFEKLFSIICILLRSAY

>d2lhb\_\_ a.1.1.2 (-) Lamprey globin {Sea lamprey (Petromyzon marinus)}

PIVDTGSVAPLSAAEKTKIRSAWAPVYSTYETSGVDILVKFFTSTPAAQEFFPKFKGLTTADELKKSADVRWHAERIINAVDDAVASMDDTEKMSMKLRNLSGKHAKSFQVDPEYFKVLAAVIADTVAAGDAGFEKLMSMICILLRSAY

>d1ash\_\_ a.1.1.2 (-) Ascaris hemoglobin, domain 1 {Pig roundworm (Ascaris suum)}

ANKTRELCMKSLEHAKVDTSNEARQDGIDLYKHMFENYPPLRKYFKSREEYTAEDVQNDPFFAKQGQKILLACHVLCATYDDRETFNAYTRELLDRHARDHVHMPPEVWTDFWKLFEEYLGKKTTLDEPTKQAWHEIGREFAKEINK

>d1itha\_ a.1.1.2 (A:) Hemoglobin {Innkeeper worm (Urechis caupo)}

GLTAAQIKAIQDHWFLNIKGCLQAAADSIFFKYLTAYPGDLAFFHKFSSVPLYGLRSNPAYKAQTLTVINYLDKVVDALGGNAGALMKAKVPSHDAMGITPKHFGQLLKLVGGVFQEEFSADPTTVAAWGDAAGVLVAAMK

>d1hlb\_\_ a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (Caudina (Molpadia) arenicola)}

GGTLAIQAQGDLTLAQKKIVRKTWHQLMRNKTSFVTDVFIRIFAYDPSAQNKFPQMAGMSASQLRSSRQMQAHAIRVSSIMSEYVEELDSDILPELLATLARTHDLNKVGADHYNLFAKVLMEALQAELGSDFNEKTRDAWAKAFSVVQAVLLVKHG

>d1hlm\_\_ a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (Caudina (Molpadia) arenicola)}

GATQSFQSVGDLTPAEKDLIRSTWDQLMTHRTGFVADVFIRIFHNDPTAQRKFPQMAGLSPAELRTSRQMHAHAIRVSALMTTYIDEMDTEVLPELLATLTRTHDKNHVGKKNYDLFGKVLMEAIKAELGVGFTKQVHDAWAKTFAIVQGVLITKHAS

>d1vhba\_ a.1.1.2 (A:) Bacterial dimeric hemoglobin {Vitreoscilla stercoraria}

LDQQTINIIKATVPVLKEHGVTITTTFYKNLFAKHPEVRPLFDMGRQESLEQPKALAMTVLAAAQNIENLPAILPAVKKIAVKHCQAGVAAAHYPIVGQELLGAIKEVLGDAATDDILDAWGKAYGVIADVFIQVEADLYAQAV

>d1cqxa1 a.1.1.2 (A:1-150) Flavohemoglobin, N-terminal domain {Alcaligenes eutrophus}

MLTQKTKDIVKATAPVLAEHGYDIIKCFYQRMFEAHPELKNVFNMAHQEQGQQQQALARAVYAYAENIEDPNSLMAVLKNIANKHASLGVKPEQYPIVGEHLLAAIKEVLGNAATDDIISAWAQAYGNLADVLMGMESELYERSAEQPGG

>d1ew6a\_ a.1.1.2 (A:) Dehaloperoxidase {Marine worm (Amphitrite ornata)}

GFKQDIATIRGDLRTYAQDIFLAFLNKYPDERRYFKNYVGKSDQELKSMAKFGDHTEKVFNLMMEVADRATDCVPLASDANTLVQMKQHSSLTTGNFEKLFVALVEYMRASGQSFDSQSWDRFGKNLVSALSSAGMK

>d1phna\_ a.1.1.3 (A:) Phycocyanin {Red alga (Cyanidium caldarium)}

MKTPITEAIAAADNQGRFLSNTELQAVNGRYQRAAASLEAARSLTSNAERLINGAAQAVYSKFPYTSQMPGPQYASSAVGKAKCARDIGYYLRMVTYCLVVGGTGPMDEYLIAGLEEINRTFDLSPSWYVEALNYIKANHGLSGQAANEANTYIDYAINALS

>d1phnb\_ a.1.1.3 (B:) Phycocyanin {Red alga (Cyanidium caldarium)}

MLDAFAKVVAQADARGEFLSNTQLDALSKMVSEGNKRLDVVNRITSNASAIVTNAARALFSEQPQLIQPGGNAYTNRRMAACLRDMEIILRYVSYAIIAGDSSILDDRCLNGLRETYQALGVPGASVAVGIEKMKDSAIAIANDPSGITTGDCSALMAEVGTYFDRAATAVQ

>d1f99a\_ a.1.1.3 (A:) Phycocyanin {Red alga (Polysiphonia urceolata)}

MKTPLTEAIAAADSQGRFLSNTELQVVNGRYNRATSSLEAAKALTANADRLISGAANAVYSKFPYTTQMPGPNYSSTAIGKAKCARDIGYYLRMVTYCLVVGGTGPMDDYLVAGLEEINRTFELSPSWYIEALKYIKNNHGLSGDVANEANTYIDYAINTLS

>d1f99b\_ a.1.1.3 (B:) Phycocyanin {Red alga (Polysiphonia urceolata)}

MLDAFAKVVAQADARGEFLSNTQIDALLAIVSEGNKRLDVVNKITNNASAIVTNAARALFAEQPQLISPGGNAYTSRRMAACLRDMEIVLRYVSYAMIAGDASVLDDRCLNGLRETYQALGTPGASVAVAIQKMKDAALALVNDTTGTPAGDCASLVAEIATYFDRAAAAVA

>d1cpca\_ a.1.1.3 (A:) Phycocyanin {Cyanobacterium (Fremyella diplosiphon)}

MKTPLTEAVAAADSQGRFLSSTEIQTAFGRFRQASASLAAAKALTEKASSLASGAANAVYSKFPYTTSQNGPNFASTQTGKDKCVRDIGYYLRMVTYCLVVGGTGPLDDYLIGGIAEINRTFDLSPSWYVEALKYIKANHGLSGDPAVEANSYIDYAINALS

>d1cpcb\_ a.1.1.3 (B:) Phycocyanin {Cyanobacterium (Fremyella diplosiphon)}

MLDAFAKVVSQADARGEYLSGSQIDALSALVADGNKRMDVVNRITGNSSTIVANAARSLFAEQPQLIAPGGNAYTSRRMAACLRDMEIILRYVTYAIFAGDASVLDDRCLNGLKETYLALGTPGSSVAVGVQKMKDAALAIAGDTNGITRGDCASLMAEVASYFDKAASAVA

>d1i7ya\_ a.1.1.3 (A:) Phycocyanin {Synechococcus vulcanus}

MKTPITEAIAAADTQGRFLSNTELQAVDGRFKRAVASMEAARALTNNAQSLIDGAAQAVYQKFPYTTTMQGSQYASTPEGKAKCARDIGYYLRMITYCLVAGGTGPMDEYLIAGLSEINSTFDLSPSWYIEALKYIKANHGLTGQAAVEANAYIDYAINALS

>d1i7yb\_ a.1.1.3 (B:) Phycocyanin {Synechococcus vulcanus}

MLDAFAKVVAQADARGEFLTNAQFDALSNLVKEGNKRLDAVNRITSNASTIVANAARALFAEQPQLIQPGGNAYTNRRMAACLRDMEIILRYVTYAILAGDSSVLDDRCLNGLRETYQALGTPGSSVAVAIQKMKDAAIAIANDPNGITPGDCSALMSEIAGYFDRAAAAVA

>d1gh0a\_ a.1.1.3 (A:) Phycocyanin {Spirulina platensis}

MKTPLTEAVSVADSQGRFLSSTEIQVAFGRFRQAKAGLEAAKALTSKADSLISGAAQAVYNKFPYTTQMQGPNYAADQRGKDKCARDIGYYLRMVTYCLIAGGTGPMDEYLIAGIDEINRTFELSPSWYIEALKYIKANHGLSGDAAVEANSYLDYAINALS

>d1gh0b\_ a.1.1.3 (B:) Phycocyanin {Spirulina platensis}

MFDAFTKVVSQADTRGEMLSTAQIDALSQMVAESNKRLDVVNRITSNASTIVSNAARSLFAEQPQLIAPGGNAYTSRRMAACLRDMEIILRYVTYAVFAGDASVLEDRCLNGLRETYLALGTPGSSVAVGVGKMKEAALAIVNDPAGITPGDCSALASEIAGYFDRAAAAVS

>d1alla\_ a.1.1.3 (A:) Allophycocyanin {Spirulina platensis}

SIVTKSIVNADAEARYLSPGELDRIKSFVTSGERRVRIAETMTGARERIIKQAGDQLFGKRPDVVSPGGNAYGADMTATCLRDLDYYLRLITYGIVAGDVTPIEEIGVVGVREMYKSLGTPIEAIAEGVRAMKSVATSLLSGADAAEAGSYFDYLIGAMS

>d1allb\_ a.1.1.3 (B:) Allophycocyanin {Spirulina platensis}

MQDAITSVINSSDVQGKYLDASAIQKLKAYFATGELRVRAATTISANAANIVKEAVAKSLLYSDVTRPGGNMYTTRRYAACIRDLDYYLRYATYAMLAGDPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTAGLVGGGAGKEMGIYFDYICSGLS

>d1b33a\_ a.1.1.3 (A:) Allophycocyanin {Cyanobacterium (Mastigocladus laminosus)}

SIVTKSIVNADAEARYLSPGELDRIKSFVSSGEKRLRIAQILTDNRERIVKQAGDQLFQKRPDVVSPGGNAYGQEMTATCLRDLDYYLRLITYGIVAGDVTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVASSILSAEDAAEAGAYFDYVAGALA

>d1b33b\_ a.1.1.3 (B:) Allophycocyanin {Cyanobacterium (Mastigocladus laminosus)}

MQDAITAVINSSDVQGKYLDTAALEKLKSYFSTGELRVRAATTIAANAAAIVKEAVAKSLLYSDITRPGGNMYTTRRYAACIRDLDYYLRYATYAMLAGDPSILDERVLNGLKETYNSLGVPISATVQAIQAMKEVTASLVGPDAGKEMGVYFDYICSGLS

>d1liaa\_ a.1.1.3 (A:) Phycoerythrin {Red alga (Polysiphonia urceolata)}

MKSVITTTISAADAAGRYPSTSDLQSVQGNIQRAAARLEAAEKLGSNHEAVVKEAGDACFSKYGYNKNPGEAGENQEKINKCYRDIDHYMRLINYTLVVGGTGPLDEWGIAGAREVYRTLNLPSAAYIAAFVFTRDRLCIPRDMSAQAGVEFCTALDYLINSLS

>d1liab\_ a.1.1.3 (B:) Phycoerythrin {Red alga (Polysiphonia urceolata)}

MLDAFSRVVVNSDSKAAYVSGSDLQALKTFINDGNKRLDAVNYIVSNSSCIVSDAISGMICENPGLITPGGNCYTNRRMAACLRDGEIILRYVSYALLAGDASVLEDRCLNGLKETYIALGVPTNSTVRAVSIMKAAAVCFISNTASQRKVEVIEGDCSALASEVASYCDRVVAAVS

>d1b8da\_ a.1.1.3 (A:) Phycoerythrin {Red alga (Griffithsia monilis)}

MKSVITTTISAADAAGRFPSSSDLESIQGNIQRAAARLEAAQKLSGNHEAVVKEAGDACFAKYSYLKNAGEAGDSPEKINKCYRDIDHYMRLINYSLVVGGTGPVDEWGIAGSREVYRALNLPGSAYIAAFTFTRDRLCVPRDMSSQAGVEFTSALDYVINSLC

>d1b8db\_ a.1.1.3 (B:) Phycoerythrin {Red alga (Griffithsia monilis)}

MLDAFSRVVVTSDAKAAYVGGSDLQSLKSFINDGNKRLDAVNYIVSNASCIVSDAVSGMICENPGLIAPGGNCYTNRRMAACLRDGEIILRYVSYALLAGDSSVLDDRCLNGLKETYIALGVPTASSSRAVSIMKATATAFITNTASGRKVEVAAGDCQALQAEAASYFDKVGSSID

>d1eyxa\_ a.1.1.3 (A:) Phycoerythrin {Red algae (Gracilaria chilensis)}

MKSVITTVISAADSAGRFPSSSDLESVQGNIQRASARLEAAEKLASNHEAVVKEAGDACFGKYGYLKNPGEAGENQEKINKCYRDIDHYMRLVNYSLVIGGTGPLDEWGIAGAREVYRTLNLPTSAYIAAFAFTRDRLCGPRDMSAQAGVEYSTALDYIINSLS

>d1eyxb\_ a.1.1.3 (B:) Phycoerythrin {Red algae (Gracilaria chilensis)}

MLDAFSRVISNADAKAAYVGGSDLQALRTFISDGNKRLDAVNYIVSNSSCIVSDAISGMICENPGLITPGGNCYTNRRMAACLRDGEIILRYISYALLAGDSSVLEDRCLNGLKETYIALGVPTNSTVRAVSIMKAAVGAFISNTASQRKGEVIEGDCSALAAEIASYCDRISAAVS

>d1qgwc\_ a.1.1.3 (C:) Phycoerythrin {Cryptophite (Rhodomonas sp.), cs24}

DAFSRVVTNADSKAAYVGGADLQALKKFISEGNKRLDSVNSIVSNASCIVSDAVSGMICENPSLISPSGNCYTNRRMAACLRDGEIILRYVSYALLSGDASVLEDRCLNGLKETYSSLGVPANSNARAVSIMKACAVAFVNNTASQKKLSTPQGDCSGLASEVGGYFDKVTAAIS

>d1fumb1 a.1.2.1 (B:106-243) Fumarate reductase iron-sulfur protein, C-terminal domain {Escherichia coli}

MTHFIESLEAIKPYIIGNSRTADQGTNIQTPAQMAKYHQFSGCINCGLCYAACPQFGLNPEFIGPAAITLAHRYNEDSRDHGKKERMAQLNSQNGVWSCTFVGYCSEVCPKHVDPAAAIQQGKVESSKDFLIATLKPR

>d1qlab1 a.1.2.1 (B:107-239) Fumarate reductase iron-sulfur protein, C-terminal domain {Wolinella succinogenes}

TGNWFNGMSQRVESWIHAQKEHDISKLEERIEPEVAQEVFELDRCIECGCCIAACGTKIMREDFVGAAGLNRVVRFMIDPHDERTDEDYYELIGDDDGVFGCMTLLACHDVCPKNLPLQSKIAYLRRKMVSVN

>d1h7wa1 a.1.2.2 (A:2-183) Dihydropyrimidine dehydrogenase, N-terminal domain {Pig (Sus scrofa)}

APVLSKDVADIESILALNPRTQSHAALHSTLAKKLDKKHWKRNPDKNCFHCEKLENNFDDIKHTTLGERGALREAMRCLKCADAPCQKSCPTHLDIKSFITSISNKNYYGAAKMIFSDNPLGLTCGMVCPTSDLCVGGCNLYATEEGSINIGGLQQFASEVFKAMNIPQIRNPCLPSQEKMP

>d1grj\_1 a.2.1.1 (2-79) GreA transcript cleavage protein, N-terminal domain {Escherichia coli}

QAIPMTLRGAEKLREELDFLKSVRRPEIIAAIAEAREHGDLKENAEYHAAREQQGFCEGRIKDIEAKLSNAQVIDVTK

>d1jj2u\_ a.2.2.1 (U:) Ribosomal protein L29 (L29p) {Archaeon Haloarcula marismortui}

TVLHVQEIRDMTPAEREAELDDLKTELLNARAVQAAGGAPENPGRIKELRKAIARIKTIQGEEGD

>d1fpoa1 a.2.3.1 (A:1-76) HSC20 (HSCB), N-terminal (J) domain {Escherichia coli}

MDYFTLFGLPARYQLDTQALSLRFQDLQRQYHPDKFASGSQAEQLAAVQQSATINQAWQTLRHPLMRAEYLLSLHG

>d1hdj\_\_ a.2.3.1 (-) HSP40 {Human (Homo sapiens)}

MGKDYYQTLGLARGASDEEIKRAYRRQALRYHPDKNKEPGAEEKFKEIAEAYDVLSDPRKREIFDRYGEEGLKGSGC

>d1xbl\_\_ a.2.3.1 (-) DnaJ chaperone, N-terminal (J) domain {Escherichia coli}

AKQDYYEILGVSKTAEEREIRKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEAYEVLTDSQKRAAYDQYGHAAFEQ

>d1fafa\_ a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Murine polyomavirus}

MDRVLSRADKERLLELLKLPRQLWGDFGRMQQAYKQQSLLLHPDKGGSHALMQELNSLWGTFKTEVYNLRMNLGGTGFQ

>d1gh6a\_ a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Simian virus 40, Sv40}

SHMREESLQLMDLLGLERSAWGNIPLMRKAYLKKCKEFHPDKGGDEEKMKKMNTLYKKMEDGVKYAHQPDFGGFWDATEIPTYGTDEWEQWWNAFNEENLFCSEEMPSSDDEAT

>d1du2a\_ a.2.4.1 (A:) Theta subunit of DNA polymerase III {Escherichia coli}

MLKNLAKLDQTEMDKVNVDLAAAGVAFKERYNMPVIAEAVEREQPEHLRSWFRERLIAHRLASVNLSRLPYEPKLK

>d1fxkc\_ a.2.5.1 (C:) Prefoldin alpha subunit {Archaeon Methanobacterium thermoautotrophicum}

AALAEIVAQLNIYQSQVELIQQQMEAVRATISELEILEKTLSDIQGKDGSETLVPVGAGSFIKAELKDTSEVIMSVGAGVAIKKNFEDAMESIKSQKNELESTLQKMGENLRAITDIMMKLSPQAEELLAAVA

>d1fxka\_ a.2.5.1 (A:) Prefoldin beta subunit {Archaeon Methanobacterium thermoautotrophicum}

QNVQHQLAQFQQLQQQAQAISVQKQTVEMQINETQKALEELSRAADDAEVYKSSGNILIRVAKDELTEELQEKLETLQLREKTIERQEERVMKKLQEMQVNIQEAMK

>d1cxzb\_ a.2.6.1 (B:) Effector domain of the protein kinase pkn/prk1 {Human (Homo sapiens)}

WSLLEQLGLAGADLAAPGVQQQLELERERLRREIRKELKLKEGAENLRRATTDLGRSLGPVELLLRGSSRRLDLLHQQLQELHAHV

>d1seta1 a.2.7.1 (A:1-110) Seryl-tRNA synthetase (SerRS) {Thermus thermophilus, strain hb27}

MVDLKRLRQEPEVFHRAIREKGVALDLEALLALDREVQELKKRLQEVQTERNQVAKRVPKAPPEEKEALIARGKALGEEAKRLEEALREKEARLEALLLQVPLPPWPGAP

>d1eiya1 a.2.7.2 (A:6-84) Phenylalanyl-tRNA synthetase (PheRS) {Thermus thermophilus}

LAAIQNARDLEELKALKARYLGKKGLLTQEMKGLSALPLEERRKRGQELNAIKAALEAALEAREKALEEAALKEALERE

>d1a36a1 a.2.8.1 (A:641-712) Eukaryotic DNA topoisomerase I, dispensable insert domain {Human (Homo sapiens)}

EKSMMNLQTKIDAKKEQLADARRDLKSAKADAKVMKDAKTKKVVESKKKAVQRLEEQLMKLEVQATDREENK

>d1e52a\_ a.2.9.1 (A:) C-terminal, UvrC-binding domain of UvrB {Escherichia coli}

LEPDNVPMDMSPKALQQKIHELEGLMMQHAQNLEFEEAAQIRDQLHQLRELFIAAS

>d1qoja\_ a.2.9.1 (A:) C-terminal, UvrC-binding domain of UvrB {Escherichia coli}

SPKALQQKIHELEGLMMQHAQNLEFEEAAQIRDQLHQLRELFIAAS

>d1aqt\_1 a.2.10.1 (87-136) Epsilon subunit of F1F0-ATP synthase C-terminal domain {Escherichia coli}

QDLDEARAMEAKRKAEEHISSSHGDVDYAQASAELAKAIAQLRVIELTKK

>d1e79h1 a.2.10.1 (H:101-145) Epsilon subunit of F1F0-ATP synthase C-terminal domain {Cow (Bos taurus)}

DMLDLGAAKANLEKAQSELLGAADEATRAEIQIRIEANEALVKAL

>d1idsa1 a.2.11.1 (A:2-85) Fe superoxide dismutase (FeSOD) {Mycobacterium tuberculosis}

AEYTLPDLDWDYGALEPHISGQINELHHSKHHATYVKGANDAVAKLEEARAKEDHSAILLNEKNLAFNLAGHVNHTIWWKNLSP

>d1dt0a1 a.2.11.1 (A:1-83) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}

AFELPPLPYAHDALQPHISKETLEFHHDKHHNTYVVNLNNLVPGTEFEGKTLEEIVKTSSGGIFNNAAQVWNHTFYWNCLSPN

>d3sdpa1 a.2.11.1 (A:5-83) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}

PPLPYAHDALQPHISKETLEYHHDKHHNTYVVNLNNLVPGTPEFEGKTLEEIVKSSSGGIFNNAAQVWNHTFYWNCLSP

>d1isaa1 a.2.11.1 (A:1-82) Fe superoxide dismutase (FeSOD) {Escherichia coli}

SFELPALPYAKDALAPHISAETIEYHYGKHHQTYVTNLNNLIKGTAFEGKSLEEIIRSSEGGVFNNAAQVWNHTFYWNCLAP

>d1coja1 a.2.11.1 (A:2-90) Fe superoxide dismutase (FeSOD) {Aquifex pyrophilus}

VHKLEPKDHLKPQNLEGISNEQIEPHFEAHYKGYVAKYNEIQEKLADQNFADRSKANQNYSEYRELKVEETFNYMGVVLHELYFGMLTP

>d1sssa1 a.2.11.1 (A:4-92) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus solfataricus}

IQFKKYELPPLPYKIDALEPYISKDIIDVHYNGHHKGYVNGANSLLERLEKVVKGDLQTGQYDIQGIIRGLTFNINGHKLHALYWENMA

>d1b06a1 a.2.11.1 (A:3-92) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus acidocaldarius}

VIQLKRYEFPQLPYKVDALEPYISKDIIDVHYNGHHKGYVNGANSLLDRLEKLIKGDLPQGQYDLQGILRGLTFNINGHKLHAIYWNNMA

>d1ap6a1 a.2.11.1 (A:1-83) Mn superoxide dismutase (MnSOD) {Human (Homo sapiens)}

KHSLPDLPYDYGALEPHINAQIMQLHHSKHHAAFVNNLNVTEEKYQEALAKGDVTAQIALQPALKFNGGGHINHSIFWTNLSP

>d1kkca1 a.2.11.1 (A:14-97) Mn superoxide dismutase (MnSOD) {Aspergillus fumigatus}

QQYTLPPLPYPYDALQPYISQQIMELHHKKHHQTYVNGLNAALEAQKKAAEATDVPKLVSVQQAIKFNGGGHINHSLFWKNLAP

>d1i0ha1 a.2.11.1 (A:1-90) Mn superoxide dismutase (MnSOD) {Escherichia coli}

SYTLPSLPYAYDALEPHFDKQTMEIHHTKHHQTYVNNANAALESLPEFANLPVEELITKLDQLPADKKTVLRNNAGGHANHSLFWKGLKK

>d1mnga1 a.2.11.1 (A:1-92) Mn superoxide dismutase (MnSOD) {Thermus thermophilus}

PYPFKLPDLGYPYEALEPHIDAKTMEIHHQKHHGAYVTNLNAALEKYPYLHGVEVEVLLRHLAALPQDIQTAVRNNGGGHLNHSLFWRLLTP

>d1bsma1 a.2.11.1 (A:1-86) Cambialistic superoxide dismutase {Propionibacterium shermanii}

AVYTLPELPYDYSALEPYISGEIMELHHDKHHKAYVDGANTALDKLAEARDKADFGAINKLEKDLAFNLAGHVNHSVFWKNMAPKG

>d1qnna1 a.2.11.1 (A:1-84) Cambialistic superoxide dismutase {Porphyromonas gingivalis}

MTHELISLPYAVDALAPVISKETVEFHHGKHLKTYVDNLNKLIIGTEFENADLNTIVQKSEGGIFNNAGQTLNHNLYFTQFRPG

>d1dava\_ a.139.1.1 (A:) Cellulosome endoglucanase SS {Clostridium thermocellum}

MSTKLYGDVNDDGKVNSTDAVALKRYVLRSGISINTDNADLNEDGRVNSTDLGILKRYILKEIDTLPYKNG

>d1h9ea\_ a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}

PEFLEDPSVLTKDKLKSELVANNVTLPAGEQRKDVYVQLYLQHLTARNRPPLPAGT

>d1h9fa\_ a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}

RQEDKDDLDVTELTNEDLLDQLVKYGVNPGPIVGTTRKLYEKKLLKLREQGTESRSS

>d1jeia\_ a.140.1.1 (A:) Inner nuclear membrane protein emerin {Human (Homo sapiens)}

DNYADLSDTELTTLLRRYNIPHGPVVGSTRRLYEKKIFEYETQRRRLSPPSSS

>d1jeqa1 a.140.2.1 (A:559-609) DNA binding C-terminal domain of ku70 {Human (Homo sapiens)}

YSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSGLKKQELLEALTKHFQD

>d1kcfa1 a.140.2.1 (A:3-38) Mitochondrial resolvase ydc2 N-terminal domain {Fission yeast (Schizosaccharomyces pombe)}

TVKLSFLQHICKLTGLSRSGRKDELLRRIVDSPIYP

>d1a62\_1 a.140.3.1 (1-47) Rho termination factor, N-terminal domain {Escherichia coli}

MNLTELKNTPVSELITLGENMGLENLARMRKQDIIFAILKQHAKSGE

>d1e7la1 a.140.4.1 (A:104-157) Recombination endonuclease VII, C-terminal and dimerization domains {Bacteriophage T4}

IHPNFVGDKSKEFSRLGKEEMMAEMLQRGFEYNESDTKTQLIASFKKQLRKSLK

>d1c75a\_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Bacillus pasteurii}

VDAEAVVQQKCISCHGGDLTGASAPAIDKAGANYSEEEILDIILNGQGGMPGGIAKGAEAEAVAAWLAEKK

>d1ctj\_\_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Monoraphidium braunii}

EADLALGKAVFDGNCAACHAGGGNNVIPDHTLQKAAIEQFLDGGFNIEAIVYQIENGKGAMPAWDGRLDEDEIAGVAAYVYDQAAGNKW

>d1c53\_\_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Desulfovibrio vulgaris, different strains}

ADGAALYKSCVGCHGADGSKQAMGVGHAVKGQKADELFKKLKGYADGSYGGEKKAVMTNLVKRYSDEEMKAMADYMSKL

>d2dvh\_\_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Desulfovibrio desulfuricans}

ADGAALYKSCIGCHGADGSKAAMGSAKPVKGQGAEELYKKMKGYADGSYGGERKAMMTNAVKKASDEELKALADYMSKL

>d1cyi\_\_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Chlamydomonas reinhardtii}

ADLALGAQVFNGNCAACHMGGRNSVMPEKTLDKAALEQYLDGGFKVESIIYQVENGKGAMPAWADRLSEEEIQAVAEYVFKQATDAAWK

>d1c6s\_\_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Cyanobacterium (Synechococcus elongatus)}

ADLANGAKVFSGNCAACHMGGGNVVMANKTLKKEALEQFGMYSEDAIIYQVQHGKNAMPAFAGRLTDEQIQDVAAYVLDQAAKGWAG

>d1f1fa\_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Arthrospira maxima}

DVAAGASVFSANCAACHMGGRNVIVANKTLSKSDLAKYLKGFDDDAVAAVAYQVTNGKNAMPGFNGRLSPLQIEDVAAYVVDQAEKGW

>d1c6ra\_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Green alga (Scenedesmus obliquus)}

ADLALGKQTFEANCAACHAGGNNSVIPDHTLRKAAMEQFLQGGFNLEAITYQVENGKGAMPAWSGTLDDDEIAAVAAYVYDQASGDKW

>d1gdva\_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Red alga (Porphyra yezoensis)}

ADLDNGEKVFSANCAACHAGGNNAIMPDKTLKKDVLEANSMNTIDAITYQVQNGKNAMPAFGGRLVDEDIEDAANYVLSQSEKGW

>d1c52\_\_ a.3.1.1 (-) Cytochrome c552 {Thermus thermophilus}

QADGAKIYAQCAGCHQQNGQGIPGAFPPLAGHVAEILAKEGGREYLILVLLYGLQGQIEVKGMKYNGVMSSFAQLKDEEIAAVLNHIATAWGDAKKVKGFKPFTAEEVKKLRAKKLTPQQVLAERKKLGLK

>d1cnoa\_ a.3.1.1 (A:) Cytochrome c552 {Pseudomonas nautica}

AGDIEAGKAKAAVCAACHGQNGISQVPIYPNLAGQKEQYLVAALKAYKAGQRQGGQAPVMQGQATALSDADIANLAAYYASNPAAA

>d1ql3a\_ a.3.1.1 (A:) Cytochrome c552 {Paracoccus denitrificans}

ADPAAGEKVFGKCKACHKLDGNDGVGPHLNGVVGRTVAGVDGFNYSDPMKAHGGDWTPEALQEFLTNPKAVVKGTKMAFAGLPKIEDRANLIAYLEGQQ

>d1ayg\_\_ a.3.1.1 (-) Cytochrome c552 {Hydrogenobacter thermophilus}

NEQLAKQKGCMACHDLKAKKVGPAYADVAKKYAGRKDAVDYLAGKIKKGGSGVWGSVPMPPQNVTDAEAKQLAQWILSIK

>d1a56\_\_ a.3.1.1 (-) Cytochrome c552 {Nitrosomonas europaea}

DADLAKKNNCIACHQVETKVVGPALKDIAAKYADKDDAATYLAGKIKGGSSGVWGQIPMPPNVNVSDADAKALADWILTLK

>d1e29a\_ a.3.1.1 (A:) Photosystem II associated cytochrome c549 {Synechocystis sp., pcc 6803}

VELTESTRTIPLDEAGGTTTLTARQFTNGQKIFVDTCTQCHLQGKTKTNNNVSLGLADLAGAEPRRDNVLALVEFLKNPKSYDGEDDYSELHPNISRPDIYPEMRNYTEDDIFDVAGYTLIAPKLDERWGGTIYF

>d1f1ca\_ a.3.1.1 (A:) Photosystem II associated cytochrome c549 {Arthrospira maxima}

LTEELRTFPINAQGDTAVLSLKEIKKGQQVFNAACAQCHALGVTRTNPDVNLSPEALALATPPRDNIAALVDYIKNPTTYDGFVEISELHPSLKSSDIFPKMRNISEDDLYNVAGYILLQPKVRGEQWG

>d1ycc\_\_ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}

TEFKAGSAKKGATLFKTRCLQCHTVEKGGPHKVGPNLHGIFGRHSGQAEGYSYTDANIKKNVLWDENNMSEYLTNPKKYIPGTKMAFGGLKKEKDRNDLITYLKKACE

>d1yeb\_\_ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}

TEFKAGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTDANINKNVKWDEDSMSEYLTNPKKYIPGTKMAFGGLKKEKDRNDLITYLKKACE

>d1ytc\_\_ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}

AKESTGFKPGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTDAIINKNVKWDEDSMSEYLTNPKKYIPGTKMAFAGLKKEKDRNDLITYMTKAAK

>d1wejf\_ a.3.1.1 (F:) Mitochondrial cytochrome c {Horse (Equus caballus)}

GDVEKGKKIFVQKCAQCHTVEKGGKHKTGPNLHGLFGRKTGQAPGFTYTDANKNKGITWKEETLMEYLENPKKYIPGTKMIFAGIKKKTEREDLIAYLKKATNE

>d1ccr\_\_ a.3.1.1 (-) Mitochondrial cytochrome c {Rice embryos (Oryza sativa)}

ASFSEAPPGNPKAGEKIFKTKCAQCHTVDKGAGHKQGPNLNGLFGRQSGTTPGYSYSTADKNMAVIWEENTLYDYLLNPKKYIPGTKMVFPGLKKPQERADLISYLKEATS

>d5cytr\_ a.3.1.1 (R:) Mitochondrial cytochrome c {Tuna (Thunnus alalunga and Thunnus thynnus)}

GDVAKGKKTFVQKCAQCHTVENGGKHKVGPNLWGLFGRKTGQAEGYSYTDANKSKGIVWNNDTLMEYLENPKKYIPGTKMIFAGIKKKGERQDLVAYLKSATS

>d1qn2a\_ a.3.1.1 (A:) Cytochrome ch {Methylobacterium extorquens}

EGDAAAGEKAFAPCKACHNFEKNGVGPTLKGVVGAKAGEGADGYAFSDALKKSGLTWDQADLKQWLADPKKKVPGTKMVFPGISDPKKVDDIIAYLKTK

>d3c2c\_\_ a.3.1.1 (-) Cytochrome c2 {Rhodospirillum rubrum}

EGDAAAGEKVSKKCLACHTFDQGGANKVGPNLFGVFENTAAHKDNYAYSESYTEMKAKGLTWTEANLAAYVKNPKAFVLEKSGDPKAKSKMTFKLTKDDEIENVIAYLKTLK

>d1c2ra\_ a.3.1.1 (A:) Cytochrome c2 {Rhodobacter capsulatus}

GDAAKGEKEFNKCKTCHSIIAPDGTEIVKGAKTGPNLYGVVGRTAGTYPEFKYKDSIVALGASGFAWTEEDIATYVKDPGAFLKEKLDDKKAKTGMAFKLAKGGEDVAAYLASVVK

>d1cxc\_\_ a.3.1.1 (-) Cytochrome c2 {Rhodobacter sphaeroides}

QEGDPEAGAKAFNQCQTCHVIVDDSGTTIAGRNAKTGPNLYGVVGRTAGTQADFKGYGEGMKEAGAKGLAWDEEHFVQYVQDPTKFLKEYTGDAKAKGKMTFKLKKEADAHNIWAYLQQVAVRP

>d1co6a\_ a.3.1.1 (A:) Cytochrome c2 {Rhodopseudomonas viridis}

QDAASGEQVFKQCLVCHSIGPGAKNKVGPVLNGLFGRHSGTIEGFAYSDANKNSGITWTEEVFREYIRDPKAKIPGTKMIFAGVKDEQKVSDLIAYIKQFNADGSKK

>d1i8oa\_ a.3.1.1 (A:) Cytochrome c2 {Rhodopseudomonas palustris}

EDAKAGEAVFKQCMTCHRADKNMVGPALAGVVGRKAGTAAGFTYSPLNHNSGEAGLVWTADNIVPYLADPNAFLKKFLTEKGKADQAVGVTKMTFKLANEQQRKDVVAYLATLK

>d1hroa\_ a.3.1.1 (A:) Cytochrome c2 {Rhodopila globiformis}

SAPPGDPVEGKHLFHTICITCHTDIKGANKVGPSLYGVVGRHSGIEPGYNYSEANIKSGIVWTPDVLFKYIEHPQKIVPGTKMGYPGQPDPQKRADIIAYLETLK

>d155c\_\_ a.3.1.1 (-) Cytochrome c2 {Paracoccus denitrificans}

NEGDAAKGEKEFNKCKACHMIQAPDGTDIKGGKTGPNLYGVVGRKIASEEGFKYGEGILEVAEKNPDLTWTEANLIEYVTDPKPLVKKMTDDKGAKTKMTFKMGKNQADVVAFLAQDDPDAXXXXXXXXXXXXX

>d1cot\_\_ a.3.1.1 (-) Cytochrome c2 {Paracoccus denitrificans}

DGDAAKGEKEFNKCKACHMIQAPDGTDIIKGGKTGPNLYGVVGRKIASEEGFKYGEGILEVAEKNPDLTWTEADLIEYVTDPKPWLVKMTDDKGAKTKMTFKMGKNQADVVAFLAQNSPDA

>d1jdla\_ a.3.1.1 (A:) Cytochrome c2 {Rhodospirillum centenum}

GDPAKGEAVFKKCMACHRVGPDAKNLVGPALTGVIDRQAGTAPGFNYSAINHAAGEAGLHWTPENIIAYLPDPNAFLRKFLADAGHAEQAKGSTKMVFKLPDEQERKDVVAYLKQFSP

>d1cc5\_\_ a.3.1.1 (-) Cytochrome c5 {Azotobacter vinelandii}

GGGARSGDDVVAKYCNACHGTGLLNAPKVGDSAAWKTRADAKGGLDGLLAQSLSGLNAMPPKGTCADCSDDELKAAIGKMSGL

>d1kx2a\_ a.3.1.1 (A:) Mono-heme c-type cytochrome ScyA {Shewanella putrefaciens}

ADLQDAEAIYNKACTVCHSMGVAGAPKSHNTADWEPRLAKGVDNLVKSVKTGLNAMPPGGMCTDCTDEDYKAAIEFMSKAK

>d1cch\_\_ a.3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}

QDGEALFKSKPCAACHSVDTKMVGPALKEVAAKNAGVEGAADTLALHIKNGSQGVWGPIPMPPNPVTEEEAKILAEWVLSLK

>d1cor\_\_ a.3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}

EDGEALFKSKPCAACHSIDAKLVGPAFKEVAAKYAGQDGAADLLAGHIKNGSQGVWGPIPMPPNPVTEEEAKILAEWILSQK

>d1dvva\_ a.3.1.1 (A:) Cytochrome c551 {Pseudomonas aeruginosa}

EDPEVLAKNKGCMACHAIDTKMVGPAYKDVAAKYAGQAGAEAYLAQRIKNGSQGVWGPIPMPPNAVSDDEAQTLAKWILSQK

>d451c\_\_ a.3.1.1 (-) Cytochrome c551 {Pseudomonas aeruginosa}

EDPEVLFKNKGCVACHAIDTKMVGPAYKDVAAKFAGQAGAEAELAQRIKNGSQGVWGPIPMPPNAVSDDEAQTLAKWVLSQK

>d2mtac\_ a.3.1.1 (C:) Cytochrome c551 {Paracoccus denitrificans}

APQFFNIIDGSPLNFDDAMEEGRDTEAVKHFLETGENVYNEDPEILPEAEELYAGMCSGCHGHYAEGKIGPGLNDAYWTYPGNETDVGLFSTLYGGATGQMGPMWGSLTLDEMLRTMAWVRHLYTGDPKDASWLTDEQKAGFTPFQP

>d1gks\_\_ a.3.1.1 (-) Cytochrome c551 {Ectothiorhodospira halophila}

DGESIYINGTAPTCSSCHDRGVAGAPELNAPEDWADRPSSVDELVESTLAGKGAMPAYDGRADREDLVKAIEYMLSTL

>d05c1\_\_ a.3.1.1 (-) Cytochrome c555 {Chlorobium thiosulfatophilum}

YDAAAGKATYDASCAMCHKTGMMGAPKVGDKAAWAPHIAKGMNVMVANSIKGYKGTKGMMPAKGGNPKLTDAQVGNAVAYMVGQSK

>d1dw0a\_ a.3.1.1 (A:) SHP, an oxygen binding cytochrome c {Rhodobacter sphaeroides}

GDTSPAQLIAGYEAAAGAPADAERGRALFLSTQTGGKPDTPSCTTCHGADVTRAGQTRTGKEIAPLAPSATPDRFTDSARVEKWLGRNCNSVIGRDCTPGEKADLLAWLAAQ

>d1e8ea\_ a.3.1.1 (A:) Cytochrome c'' {Methylophilus methylotrophus, strain w3a1}

DVTNAEKLVYKYTNIAHSANPMYEAPSITDGKIFFNRKFKTPSGKEAACASCHTNNPANVGKNIVTGKEIPPLAPRVNTKRFTDIDKVEDEFTKHCNDILGADCSPSEKANFIAYLLTETKPTK

>d1diqc\_ a.3.1.1 (C:) p-Cresol methylhydroxylase, cytochrome c subunit {Pseudomonas putida}

SQWGSGKNLYDKVCGHCHKPEVGVGPVLEGRGLPEAYIKDIVRNGFRAMPAFPASYVDDESLTQVAEYLSSLPA

>d1dy7b1 a.3.1.2 (B:32-135) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase {Paracoccus pantotrophus}

LAQQDVAAPGAPEGVSALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGFDYLQSFITYGSPAGMPNWGTSGELSAEQVDLMANYLLLDPAAPP

>d1h9xa1 a.3.1.2 (A:42-133) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase {Paracoccus pantotrophus}

APEGVSALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGFDYLQSFITYGSPAGMPNWGTSGELSAEQVDLMANYLLLDPAA

>d1hj3a1 a.3.1.2 (A:17-133) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase {Paracoccus pantotrophus}

HKTRTDNRYEPSLDNLAQQDVAAPGAPEGVSALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGFDYLQSFITYGSPAGMPNWGTSGELSAEQVDLMANYLLLDPAA

>d1hzua1 a.3.1.2 (A:23-117) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase {Pseudomonas aeruginosa}

VRTNGAPDMSESEFNEAKQIYFQRCAGCHGVLRKGATGKPLTPDITQQRGQQYLEALITYGTPLGMPNWGSSGELSKEQITLMAKYIQHTPPQPP

>d1nira1 a.3.1.2 (A:6-117) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase {Pseudomonas aeruginosa}

AAEQYQGAASAVDPAHVVRTNGAPDMSESEFNEAKQIYFQRCAGCHGVLRKGATGKPLTPDITQQRGQQYLEALITYGTPLGMPNWGSSGELSKEQITLMAKYIQHTPPQPP

>d1e2rb1 a.3.1.2 (B:25-135) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase {Paracoccus denitrificans}

YEPSLDNLAQQDVAAPGAPEGVTALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGFDYLQSFITYASPAGMPNWGTSGELSAEQVDLMANYLLLDPAAPP

>d1qksa1 a.3.1.2 (A:9-135) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase {Paracoccus denitrificans}

DPAAALEDHKTRTDNRYEPSLDNLAQQDVAAPGAPEGVTALSDAQYNEANKIYFERCAGCHGVLRKGATGKALTPDLTRDLGFDYLQSFITYASPAGMPNWGTSGELSAEQVDLMANYLLLDPAAPP

>d1kb0a1 a.3.1.6 (A:579-675) Quinoprotein alcohol dehydrogenase, C-terminal domain {Comamonas testosteroni}

TGQLLQGVKYDPAKVEAGTMLYVANCVFCHGVPGVDRGGNIPNLGYMDASYIENLPNFVFKGPAMVRGMPDFTGKLSGDDVESLKAFIQGTADAIRP

>d1qcrd2 a.3.1.3 (D:167-195) Cytochrome bc1 domain {Cow (Bos taurus)}

EVLEFDDGTPATMSQVAKDVCTFLRWAAE

>d1bccd2 a.3.1.3 (D:1-195) Cytochrome bc1 domain {Chicken (Gallus gallus)}

SDLELHPPSYPWSHRGPLSSLDHTSIRRGFQVYKQVCSSCHSMDYVAYRHLVGVCYTEDEAKALAEEVEVQDGPNEDGEMFMRPGKLSDYFPKPYPNPEAARAANNGALPPDLSYIVRARHGGEDYVFSLLTGYCEPPTGVSVREGLYFNPYFPGQAIGMAPPIYNDVLEFDDGTPATMSQVAKDVCTFLRWAAE

>d1ezvd1 a.3.1.3 (D:62-260) Cytochrome bc1 domain {Baker's yeast (Saccharomyces cerevisiae)}

MTAAEHGLHAPAYAWSHNGPFETFDHASIRRGYQVYREVCAACHSLDRVAWRTLVGVSHTNEEVRNMAEEFEYDDEPDEQGNPKKRPGKLSDYIPGPYPNEQAARAANQGALPPDLSLIVKARHGGCDYIFSLLTGYPDEPPAGVALPPGSNYNPYFPGGSIAMARVLFDDMVEYEDGTPATTSQMAKDVTTFLNWCAE

>d1etpa1 a.3.1.4 (A:1-92) Cytochrome c4 {Pseudomonas stutzeri}

AGDAEAGQGKVAVCGACHGVDGNSPAPNFPKLAGQGERYLLKQLQDIKAGSTPGAPEGVGRKVLEMTGMLDPLSDQDLEDIAAYFSSQKGSV

>d1etpa2 a.3.1.4 (A:93-190) Cytochrome c4 {Pseudomonas stutzeri}

GYADPALAKQGEKLFRGGKLDQGMPACTGCHAPNGVGNDLAGFPKLGGQHAAYTAKQLTDFREGNRTNDGDTMIMRGVAAKLSNKDIEALSSYIQGLH

>d1fcdc1 a.3.1.4 (C:1-80) Flavocytochrome c sulfide dehydrogenase, FCSD, cytochrome subunit {Purple phototrophic bacterium (Chromatium vinosum)}

EPTAEMLTNNCAGCHGTHGNSVGPASPSIAQMDPMVFVEVMEGFKSGEIASTIMGRIAKGYSTADFEKMAGYFKQQTYQP

>d1fcdc2 a.3.1.4 (C:81-174) Flavocytochrome c sulfide dehydrogenase, FCSD, cytochrome subunit {Purple phototrophic bacterium (Chromatium vinosum)}

AKQSFDTALADTGAKLHDKYCEKCHVEGGKPLADEEDYHILAGQWTPYLQYAMSDFREERRPMEKKMASKLRELLKAEGDAGLDALFAFYASQQ

>d1eb7a1 a.3.1.5 (A:1-164) Di-haem cytochrome c peroxidase {Pseudomonas aeruginosa}

DALHDQASALFKPIPEQVTELRGQPISEQQRELGKKLFFDPRLSRSHVLSCNTCHNVGTGGADNVPTSVGHGWQKGPRNSPTVFNAVFNAAQFWDGRAKDLGEQAKGPIQNSVEMHSTPQLVEQTLGSIPEYVDAFRKAFPKAGKPVSFDNMALAIEAYEATLV

>d1eb7a2 a.3.1.5 (A:165-323) Di-haem cytochrome c peroxidase {Pseudomonas aeruginosa}

TPDSPFDLYLKGDDKALDAQQKKGLKAFMDSGCSACHNGINLGGQAYFPFGLVKKPDASVLPSGDKGRFAVTKTQSDEYVFRAAPLRNVALTAPYFHSGQVWELKDAVAIMGNAQLGKQLAPDDVENIVAFLHSLSGKQPRVEYPLLPASTETTPRPAE

>d1iqca1 a.3.1.5 (A:1-150) Di-haem cytochrome c peroxidase {Nitrosomonas europaea}

ANEPIQPIKAVTPENADMAELGKMLFFDPRLSKSGFISCNSCHNLSMGGTDNITTSIGHKWQQGPINAPTVLNSSMNLAQFWDGRAKDLKEQAAGPIANPKEMASTHEIAEKVVASMPQYRERFKKVFGSDEVTIDRITTAIAQFEETLV

>d1iqca2 a.3.1.5 (A:151-308) Di-haem cytochrome c peroxidase {Nitrosomonas europaea}

TPGSKFDKWLEGDKNALNQDELEGYNLFKGSGCVQCHNGPAVGGSSYQKMGVFKPYETKNPAAGRMDVTGNEADRNVFKVPTLRNIELTYPYFHDGGAATLEQAVETMGRIQLNREFNKDEVSKIVAFLKTLTGDQPDFKLPILPPSNNDTPRSQPYE

>d1jjua1 a.3.1.7 (A:1-85) Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2 {Paracoccus denitrificans}

VTGEEVLQNACAACHVQHEDGRWERIDAARKTPEGWDMTVTRMMRNHGVALEPEERAAIVRHLSDTRGLSLAETEERRYILEREP

>d1jjua2 a.3.1.7 (A:86-165) Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2 {Paracoccus denitrificans}

VAWDEGPDTSMTQTCGRCHSYARVALQRRTPEDWKHLVNFHLGQFPTLEYQALARDRDWWGIAQAEIIPFLARTYPLGEA

>d1jmxa1 a.3.1.7 (A:2-85) Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2 {Pseudomonas putida}

EQGPSLLQNKCMGCHIPEGNDTYSRISHQRKTPEGWLMSIARMQVMHGLQISDDDRRTLVKYLADKQGLAPSETDGVRYAMERR

>d1jmxa2 a.3.1.7 (A:86-162) Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2 {Pseudomonas putida}

LNTVEQFDTQLSETCGRCHSGARVALQRRPAKEWEHLVNFHLGQWPSLEYQAQARDRDWLPIALQQVVPDLAKRYPL

>d1enh\_\_ a.4.1.1 (-) Engrailed Homeodomain {Drosophila melanogaster}

RPRTAFSSEQLARLKREFNENRYLTERRRQQLSSELGLNEAQIKIWFQNKRAKI

>d2hdda\_ a.4.1.1 (A:) Engrailed Homeodomain {Drosophila melanogaster}

RTAFSSEQLARLKREFNENRYLTERRRQQLSSELGLNEAQIKIWFKNKRAKIKKS

>d1akha\_ a.4.1.1 (A:) Mating type protein A1 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}

ISPQARAFLEEVFRRKQSLNSKEKEEVAKKCGITPLQVRVWFINKRMRS

>d1f43a\_ a.4.1.1 (A:) Mating type protein A1 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}

KKEKSPKGKSSISPQARAFLEQVFRRKQSLNSKEKEEVAKKCGITPLQVRVWFINKRMRSK

>d1akhb\_ a.4.1.1 (B:) mat alpha2 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}

TKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKTITIAPELADLLSGEPL

>d1aplc\_ a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}

YRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKT

>d1mnmc\_ a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}

GLVFNVVTQDMINKSTKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKEKT

>d1lfb\_\_ a.4.1.1 (-) Transcription factor LFB1 {Rat (Rattus rattus)}

RFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGSNLVTEVRVYNWFANRRKEEAFRHK

>d2lfb\_\_ a.4.1.1 (-) Transcription factor LFB1 {Rat (Rattus rattus)}

MARIDPTKKGRRNRFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGSNLVTEVRVYNWFANRRKEEAFRHKLAMDTYKLN

>d1e3oc1 a.4.1.1 (C:104-160) Oct-1 POU Homeodomain {Human (Homo sapiens)}

KRTSIETNIRVALEKSFMENQKPTSEDITLIAEQLNMEKEVIRVWFSNRRQKEKRIN

>d1hf0a1 a.4.1.1 (A:102-159) Oct-1 POU Homeodomain {Human (Homo sapiens)}

RKKRTSIETNIRVALEKSFLENQKPTSEEITMIADQLNMEKEVIRVWFSNRRQKEKRI

>d1au7a1 a.4.1.1 (A:103-160) Pit-1 POU homeodomain {Rat (Rattus norvegicus)}

KRRTTISIAAKDALERHFGEHSKPSSQEIMRMAEELNLEKEVVRVWFCNRRQREKRVK

>d1ftt\_\_ a.4.1.1 (-) Thyroid transcription factor 1 homeodomain {Rat (Rattus norvegicus)}

MRRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLTPTQVKIWFQNHRYKMKRQAKDKAAQQ

>d1hdp\_\_ a.4.1.1 (-) Oct-2 POU Homeodomain {Human (Homo sapiens)}

RRKKRTSIETNVRFALEKSFLANQKPTSEEILLIAEQLHMEKEVIRVWFCNRRQKEKRINPCS

>d1ocp\_\_ a.4.1.1 (-) Oct-3 POU Homeodomain {Mouse (Mus musculus)}

METLVQARKRKRTSIENRVRWSLETMFLKCPKPSLQQITHIANQLGLEKDVVRVWFCNRRQKGKRSS

>d1b72a\_ a.4.1.1 (A:) Homeobox protein hox-b1 {Human (Homo sapiens)}

ARTFDWMKVKRNPPKTAKVSEPGLGSPSGLRTNFTTRQLTELEKEFHFNKYLSRARRVEIAATLELNETQVKIWFQNRRMKQKKRERE

>d1b72b\_ a.4.1.1 (B:) pbx1 {Human (Homo sapiens)}

RKRRNFNKQATEILNEYFYSHLSNPYPSEEAKEELAKKCGITVSQVSNWFGNKRIRYKKNIGKFQEEANIYAA

>d1du6a\_ a.4.1.1 (A:) pbx1 {Mouse (Mus musculus)}

SSGHIEGRHMNKQATEILNEYFYSHLSNPYPSEEAKEELAKKCGITVSQVSNWFGNKRIRYKKN

>d1bw5\_\_ a.4.1.1 (-) Insulin gene enhancer protein isl-1 {Rat (Rattus norvegicus)}

MKTTRVRTVLNEKQLHTLRTCYAANPRPDALMKEQLVEMTGLSPRVIRVWFQNKRCKDKKRSIMMK

>d1ig7a\_ a.4.1.1 (A:) Msx-1 homeodomain {Mouse (Mus musculus)}

RKPRTPFTTAQLLALERKFRQKQYLSIAERAEFSSSLSLTETQVKIWFQNRRAKAKRL

>d1ahdp\_ a.4.1.1 (P:) Antennapedia Homeodomain {Drosophila melanogaster}

MRKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRRMKWKKENKTKGEPG

>d1san\_\_ a.4.1.1 (-) Antennapedia Homeodomain {Drosophila melanogaster}

MTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRRMKWKKENKTKGEPG

>d9anta\_ a.4.1.1 (A:) Antennapedia Homeodomain {Drosophila melanogaster}

RQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRRMKWKKEN

>d1b8ia\_ a.4.1.1 (A:) Ultrabithorax (ubx) homeodomain {Drosophila melanogaster}

FYPWMAIAGTNGLRRRGRQTYTRYQTLELEKEFHTNHYLTRRRRIEMAHALSLTERQIKIWFQNRRMKLKKEI

>d1b8ib\_ a.4.1.1 (B:) Extradenticle (exd) homeodomain {Drosophila melanogaster}

RRNFSKQASEILNEYFYSHLSNPYPSEEAKEELARKCGITVSQVSNWFGNKRIRYKKN

>d1jgga\_ a.4.1.1 (A:) Even-skipped homeodomain {Fruit fly (Drosophila melanogaster)}

RYRTAFTRDQLGRLEKEFYKENYVSRPRRCELAAQLNLPESTIKVWFQNRRMKDKRQ

>d1ftz\_\_ a.4.1.1 (-) Fushi Tarazu protein {Fruit fly (Drosophila melanogaster)}

MDSKRTRQTYTRYQTLELEKEFHFNRYITRRRRIDIANALSLSERQIKIWFQNRRMKSKKDRTLDSSPEH

>d1nk3p\_ a.4.1.1 (P:) VND/NK-2 protein {Fruit fly (Drosophila melanogaster)}

KKRKRRVLFTKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKTKRAQNE

>d1vnd\_\_ a.4.1.1 (-) VND/NK-2 protein {Fruit fly (Drosophila melanogaster)}

ASDGLPNKKRKRRVLFTKAQTYELERRFRQQRYLSAPEREHLASLIRLTPTQVKIWFQNHRYKTKRAQNEKGYEGHP

>d1fjla\_ a.4.1.1 (A:) Paired protein {Fruit fly (Drosophila melanogaster)}

KQRRSRTTFSASQLDELERAFERTQYPDIYTREELAQRTNLTEARIQVWFQNRRARLRKQHTSVS

>d1fjlb\_ a.4.1.1 (B:) Paired protein {Fruit fly (Drosophila melanogaster)}

QRRSRTTFSASQLDELERAFERTQYPDIYTREELAQRTNLTEARIQVWFQNRRARLRK

>d1hcra\_ a.4.1.2 (A:) HIN recombinase (DNA-binding domain) {Synthetic}

GRPRAINKHEQEQISRLLEKGHPRQQLAIIFGIGVSTLYRYFPASSIKKRMN

>d1ijwc\_ a.4.1.2 (C:) HIN recombinase (DNA-binding domain) {Synthetic}

GRPRAINKHEQEQISRLLEKGHPRQQLAIIFGIGVSTLYRYFPASSI

>d1gdta1 a.4.1.2 (A:141-183) gamma,delta resolvase (C-terminal domain) {Escherichia coli}

GRKRKIDRDAVLNMWQQGLGASHISKTMNIARSTVYKVINESN

>d1tc3c\_ a.4.1.2 (C:) Transposase tc3a1-65 {Caenorhabditis elegans}

PRGSALSDTERAQLDVMKLLNVSLHEMSRKISRSRHCIRVYLKDPVSYGTS

>d2ezl\_\_ a.4.1.2 (-) Ibeta subdomain of the mu end DNA-binding domain of phage mu transposase {Bacteriophage mu}

MIARPTLEAHDYDREALWSKWDNASDSQRRLAEKWLPAVQAADEMLNQGISTKTAFATVAGHYQVSASTLRDKYYQVQKFAKPDWAAALVDGRGASRRN

>d2ezh\_\_ a.4.1.2 (-) Transposase {Bacteriophage mu}

SEFDEDAWQFLIADYLRPEKPAFRKCYERLELAAREHGWSIPSRATAFRRIQQLDEAMVVACREG

>d2ezi\_\_ a.4.1.2 (-) Transposase {Bacteriophage mu}

MNVHKSEFDEDAWQFLIADYLRPEKPAFRKCYERLELAAREHGWSIPSRATAFRRIQQLDEAMVVACREGEHALM

>d1h88c1 a.4.1.3 (C:39-88) c-Myb, DNA-binding domain {Mouse (Mus musculus)}

GKTRWTREEDEKLKKLVEQNGTDDWKVIANYLPNRTDVQCQHRWQKVLNP

>d1h88c2 a.4.1.3 (C:89-143) c-Myb, DNA-binding domain {Mouse (Mus musculus)}

ELIKGPWTKEEDQRVIKLVQKYGPKRWSVIAKHLKGRIGKQCRERWHNHLNPEVK

>d1idz\_\_ a.4.1.3 (-) c-Myb, DNA-binding domain {Mouse (Mus musculus)}

MEVKKTSWTEEEDRILYQAHKRLGNRWAEIAKLLPGRTDNAIKNHWNSTMRRKV

>d1a5j\_1 a.4.1.3 (1-55) b-Myb DNA binding domain {Chicken (Gallus gallus)}

GIPDLVKGPWTKEEDQKVIELVKKYGTKQWTLIAKHLKGRLGKQCRERWHNHLNP

>d1a5j\_2 a.4.1.3 (56-110) b-Myb DNA binding domain {Chicken (Gallus gallus)}

EVKKSSWTEEEDRIIFEAHKVLGNRWAEIAKLLPGRTDNAVKNHWNSTIKRKVDT

>d1h8ac1 a.4.1.3 (C:87-143) v-Myb {Avian myeloblastosis virus}

NPELNKGPWTKEEDQRVIEHVQKYGPKRWSDIAKHLKGRIGKQCRERWHNHLNPEVK

>d1h8ac2 a.4.1.3 (C:144-191) v-Myb {Avian myeloblastosis virus}

KTSWTEEEDRIIYQAHKRLGNRWAEIAKLLPGRTDNAVKNHWNSTMRR

>d1fexa\_ a.4.1.3 (A:) Rap1 {Human (Homo sapiens)}

GRIAFTDADDVAILTYVKENARSPSSVTGNALWKAMEKSSLTQHSWQSLKDRYLKHLRG

>d1ba5\_\_ a.4.1.4 (-) DNA-binding domain of human telomeric protein, htrf1 {Human (Homo sapiens)}

RKRQAWLWEEDKNLRSGVRKYGEGNWSKILLHYKFNNRTSVMLKDRWRTMKKL

>d1k78a1 a.4.1.5 (A:19-81) Pax-5 {Human (Homo sapiens)}

GVNQLGGVFVNGRPLPDVVRQRIVELAHQGVRPCDISRQLRVSHGCVSKILGRYYETGSIKPG

>d1k78a2 a.4.1.5 (A:82-142) Pax-5 {Human (Homo sapiens)}

VIGGSKPKVATPKVVEKIAEYKRQNPTMFAWEIRDRLLAERVCDNDTVPSVSSINRIIRTK

>d6paxa1 a.4.1.5 (A:1-68) Pax-6 {Human (Homo sapiens)}

SHSGVNQLGGVFVNGRPLPDSTRQRIVELAHSGARPCDISRILQVSNGCVSKILGRYYATGSIRPRAI

>d6paxa2 a.4.1.5 (A:69-133) Pax-6 {Human (Homo sapiens)}

GGSKPRVATPEVVSKIAQYKQECPSIFAWEIRDRLLSEGVCTNDNIPSVSSINRVLRNLASEKQQ

>d1pdnc\_ a.4.1.5 (C:) Paired protein (prd) {Fruit fly (Drosophila melanogaster)}

QGRVNQLGGVFINGRPLPNNIRLKIVEMAADGIRPCVISRQLRVSHGCVSKILNRYQETGSIRPGVIGGSKPRIATPEIENRIEEYKRSSPGMFSWEIREKLIREGVCDRSTAPSVSAISRLV

>d1igna1 a.4.1.6 (A:360-445) DNA-binding domain of rap1 {Baker's yeast (Saccharomyces cerevisiae)}

KASFTDEEDEFILDVVRKNPTRRTTHTLYDEISHYVPNHTGNSIRHRFRVYLSKRLEYVYEVDKFGKLVRDDDGNLIKTKVLPPSI

>d1igna2 a.4.1.6 (A:446-594) DNA-binding domain of rap1 {Baker's yeast (Saccharomyces cerevisiae)}

KRKFSADEDYTLAIAVKKQFYRDLFQIDPDTGRSLITDEDTPTAIARRNMTMDPNHVPGSEPNFAAYRTQSRRGPIAREFFKHFAEEHAAHTENAWRDRFRKFLLAYGIDDYISYYEAEKAQNREPEPMKNLTNRPKRPGVPTPGNYNS

>d1bw6a\_ a.4.1.7 (A:) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}

MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASE

>d1hlva1 a.4.1.7 (A:1-66) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}

MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTCR

>d1hlva2 a.4.1.7 (A:67-131) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}

KTNKLSPYDKLEGLLIAWFQQIRAAGLPVKGIILKEKALRIAEELGMDDFTASNGWLDRFRRRRS

>d1g2ha\_ a.4.1.10 (A:) Transcriptional regulator TyrR, C-terminal domain {Haemophilus influenzae}

SAVISLDEFENKTLDEIIGFYEAQVLKLFYAEYPSTRKLAQRLGVSHTAIANKLKQYGIGK

>d1bl0a1 a.4.1.8 (A:9-62) MarA {Escherichia coli}

DAITIHSILDWIEDNLESPLSLEKVSERSGYSKWHLQRMFKKETGHSLGQYIRS

>d1bl0a2 a.4.1.8 (A:63-124) MarA {Escherichia coli}

RKMTEIAQKLKESNEPILYLAERYGFESQQTLTRTFKNYFDVPPHKYRMTNMQGESRFLHPL

>d1d5ya1 a.4.1.8 (A:3-56) Rob transcription factor, N-terminal domain {Escherichia coli}

QAGIIRDLLIWLEGHLDQPLSLDNVAAKAGYSKWHLQRMFKDVTGHAIGAYIRA

>d1d5ya2 a.4.1.8 (A:57-121) Rob transcription factor, N-terminal domain {Escherichia coli}

RRLSKSAVALRLTARPILDIALQYRFDSQQTFTRAFKKQFAQTPALYRRSPEWSAFGIRPPLRLG

>d1a6i\_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}

SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAVEILARHHDYS

>d2tct\_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}

ARLNRESVIDAALELLNETGIDGLTTRKLAQKLGIEQPTLYWHVKNKRALLDALAVEILARHHDYS

>d1jt6a1 a.4.1.9 (A:2-72) Multidrug binding protein QacR {Staphylococcus aureus}

NLKDKILGVAKELFIKNGYNATTTGEIVKLSESSKGNLYYHFKTKENLFLEILNIEESKWQEQWKKEQIKA

>d1sfe\_1 a.4.2.1 (93-176) Ada DNA repair protein {Escherichia coli}

GTAFQQQVWQALRTIPCGETVSYQQLANAIGKPKAVRAVASACAANKLAIVIPCHRVVRGDGSLSGYRWGVSRKAQLLRREAEN

>d1qnta1 a.4.2.1 (A:92-176) O6-alkylguanine-DNA alkyltransferase {Human (Homo sapiens)}

ESFTRQVLWKLLKVVKFGEVISYQQLAALAGNPKAARAVGGAMRGNPVPILIPCHRVVCSSGAVGNYSGGLAVKEWLLAHEGHRL

>d1mgta1 a.4.2.1 (A:89-169) O6-alkylguanine-DNA alkyltransferase {Archaeon Pyrococcus kodakaraensis}

VTPFEKKVYEWLTKNVKRGSVITYGDLAKALNTSPRAVGGAMKRNPYPIVVPCHRVVAHDGIGYYSSGIEEKKFLLEIEGV

>d1c20a\_ a.4.3.1 (A:) DNA-binding domain from the dead ringer protein {Fruit fly (Drosophila melanogaster)}

GWSFEEQFKQVRQLYEINDDPKRKEFLDDLFSFMQKRGTPINRLPIMAKSVLDLYELYNLVIARGGLVDVINKKLWQEIIKGLHLPSSITSAAFTLRTQYMKYLYPYECEKKNLSTPAELQAAIDGNR

>d1ig6a\_ a.4.3.2 (A:) MRF-2 DNA-binding domain {Human (Homo sapiens)}

RADEQAFLVALYKYMKERKTPIERIPYLGFKQINLWTMFQAAQKLGGYETITARRQWKHIYDELGGNPGSTSAATCTRRHYERLILPYERFIKGEEDKPLPPIKPRK

>d1bia\_1 a.4.5.1 (1-63) Biotin repressor, N-terminal domain {Escherichia coli}

MKDNTVPLKLIALLANGEFHSGEQLGETLGMSRAAINKHIQTLRDWGVDVFTVPGKGYSLPEP

>d1jhfa1 a.4.5.2 (A:2-72) LexA repressor, N-terminal DNA-binding domain {Escherichia coli}

KALTARQQEVFDLIRDHISQTGMPPTRAEIAQRLGFRSPNAAEEHLKALARKGVIEIVSGASRGIRLLQEE

>d1aoy\_\_ a.4.5.3 (-) Arginine repressor (ArgR), N-terminal DNA-binding domain {Escherichia coli}

MRSSAKQEELVKAFKALLKEEKFSSQGEIVAALQEQGFDNINQSKVSRMLTKFGAVRTRNAKMEMVYCLPAELGVPTT

>d1b4aa1 a.4.5.3 (A:4-78) Arginine repressor (ArgR), N-terminal DNA-binding domain {Bacillus stearothermophilus}

GQRHIKIREIIMSNDIETQDELVDRLREAGFNVTQATVSRDIKEMQLVKVPMANGRYKYSLPSDQRFNPLQKLKR

>d1f9na1 a.4.5.3 (A:3-78) Arginine repressor (ArgR), N-terminal DNA-binding domain {Bacillus subtilis}

KGQRHIKIREIITSNEIETQDELVDMLKQDGYKVTQATVSRDIKELHLVKVPTNNGSYKYSLPADQRFNPLSKLKR

>d1hw5a1 a.4.5.4 (A:138-208) Catabolite gene activator protein (CAP), C-terminal domain {Escherichia coli}

DVTGRIAQTLLNLAKQPDAMTHPDGMQIKITRQEIGQIVGCSRETVGRILKMLEDQNLISAHGKTIVVYGT

>d1ft9a1 a.4.5.4 (A:134-213) CO-sensing protein CooA, C-terminal domain {Rhodospirillum rubrum}

DIKQRIAGFFIDHANTTGRQTQGGVIVSVDFTVEEIANLIGSSRQTTSTALNSLIKEGYISRQGRGHYTIPNLVRLKAAA

>d1i1ga1 a.4.5.32 (A:2-61) LprA {Archaeon Pyrococcus furiosus}

IDERDKIILEILEKDARTPFTEIAKKLGISETAVRKRVKALEEKGIIEGYTIKINPKKLG

>d1smta\_ a.4.5.5 (A:) SmtB repressor {Cyanobacteria (Synechococcus), pcc7942}

ELQAIAPEVAQSLAEFFAVLADPNRLRLLSLLARSELCVGDLAQAIGVSESAVSHQLRSLRNLRLVSYRKQGRHVYYQLQDHHIVALYQNALDHLQEC

>d1jgsa\_ a.4.5.28 (A:) Multiple antibiotic resistance repressor, MarR {Escherichia coli}

LFNEIIPLGRLIHMVNQKKDRLLNEYLSPLDITAAQFKVLCSIRCAACITPVELKKVLSVDLGALTRMLDRLVCKGWVERLPNPNDKRGVLVKLTTGGAAICEQCHQLVGQDLHQELTKNLTADEVATLEYLLKKVLP

>d1hsja1 a.4.5.28 (A:373-487) staphylococcal accessory regulator A homolog, SarR {Staphylococcus aureus}

MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDLKLLSKKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN

>d1fzpb\_ a.4.5.28 (B:) Pleiotropic regulator of virulence genes, SarA {Staphylococcus aureus}

AITKINDCFELLSMVTYADKLKSLIKKEFSISFEEFAVLTYISENKEKEYYLKDIINHLNYKQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNKRIT

>d1hw1a1 a.4.5.6 (A:5-78) Fatty acid responsive transcription factor FadR, N-terminal domain {Escherichia coli}

AQSPAGFAEEYIIESIWNNRFPPGTILPAERELSELIGVTRTTLREVLQRLARDGWLTIQHGKPTKVNNFWETS

>d1bm9a\_ a.4.5.7 (A:) Replication terminator protein (RTP) {Bacillus subtilis}

EEKRSSTGFLVKQRAFLKLYMITMTEQERLYGLKLLEVLRSEFKEIGFKPNHTEVYRSLHELLDDGILKQIKVKKEGAKLQEVVLYQFKDYEAAKLYKKQLKVELDRCKKLIEKALSDNF

>d1b9ma1 a.4.5.8 (A:-1-126) N-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}

HMQAEILLTLKLQQKLFADPRRISLLKHIALSGSISQGAKDAGISYKSAWDAINEMNQLSEHILVERATGGKGGGGAVLTRYGQRLIQLYDLLAQIQQKAFDVLSDDDALPLNSLLAAISRFSLQTS

>d1bjaa\_ a.4.5.9 (A:) Transcription factor MotA, activation domain {Bacteriophage T4}

SKVTYIIKASNDVLNEKTATILITIAKKDFITAAEVREVHPDLGNAVVNSNIGVLIKKGLVEKSGDGLIITGEAQDIISNAATLYAQENAPELLK

>d1repc1 a.4.5.10 (C:15-143) RepE54 {Escherichia coli, mini-F plasmid}

SPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIRKSDGTLQEHDGICEIHVAKYAEIFGLTSAEASKDIRQALKSFAGKEVVFYRPEEDAGDEKGYESFPWFIKPAHSPSRGLYSVHINPYLIPFFIGLQ

>d1repc2 a.4.5.10 (C:144-246) RepE54 {Escherichia coli, mini-F plasmid}

NRFTQFRLSETKEITNPYAMRLYESLCQYRKPDGSGIVSLKIDWIIERYQLPQSYQRMPDFRRRFLQVCVNEINSRTPMRLSYIEKKKGRQTTHIVFSFRDIT

>d1hqca1 a.4.5.11 (A:243-318) Holliday junction helicase RuvB {Thermus thermophilus}

LGLEKRDREILEVLILRFGGGPVGLATLATALSEDPGTLEEVHEPYLIRQGLLKRTPRGRVPTELAYRHLGYPPPV

>d1in4a1 a.4.5.11 (A:255-329) Holliday junction helicase RuvB {Thermotoga maritima}

EGLDEFDRKILKTIIEIYRGGPVGLNALAASLGVEADTLSEVYEPYLLQAGFLARTPRGRIVTEKAYKHLKYEVP

>d1fnna1 a.4.5.11 (A:277-388) CDC6, C-terminal domain {Archaeon Pyrobaculum aerophilum}

ISEEVLIGLPLHEKLFLLAIVRSLKISHTPYITFGDAEESYKIVCEEYGERPRVHSQLWSYLNDLREKGIVETRQNKRGEGVRGRTTLISIGTEPLDTLEAVITKLIKEELR

>d1foka3 a.4.5.12 (A:287-386) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}

VPKRVYWEMLATNLTDKEYVRTRRALILEILIKAGSLKIEQIQDNLKKLGFDEVIETIENDIKGLINTGIFIEIKGRFYQLKDHILQFVIPNRGVTKQLV

>d2foka1 a.4.5.12 (A:5-143) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}

IRTFGWVQNPGKFENLKRVVQVFDRNSKVHNEVKNIKIPTLVKESKIQKELVAIMNQHDLIYTYKELVGTGTSIRSEAPCDAIIQATIADQGNKKGYIDNWSSDGFLRWAHALGFIEYINKSDSFVITDVGLAYSKSAD

>d2foka2 a.4.5.12 (A:144-286) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}

GSAIEKEILIEAISSYPPAIRILTLLEDGQHLTKFDLGKNLGFSGESGFTSLPEGILLDTLANAMPKDKGEIRNNWEGSSDKYARMIGGWLDKLGLVKQGKKEFIIPTLGKPDNKEFISHAFKITGEGLKVLRRAKGSTKFTR

>d2foka3 a.4.5.12 (A:287-386) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}

VPKRVYWEMLATNLTDKEYVRTRRALILEILIKAGSLKIEQIQDNLKKLGFDEVIETIENDIKGLINTGIFIEIKGRFYQLKDHILQFVIPNRLGKPDLV

>d1f1za1 a.4.5.27 (A:169-267) TnsA endonuclease, C-terminal domain {Escherichia coli}

NPVVKENIEWLYSVKTEEVSAELLAQLSPLAHILQEKGDENIINVCKQVDIAYDLELGKTLSEIRALTANGFIKFNIYKSFRANKCADLCISQVVNMEE

>d1fp1d1 a.4.5.29 (D:19-128) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}

QTEDSACLSAMVLTTNLVYPAVLNAAIDLNLFEIIAKATPPGAFMSPSEIASKLPASTQHSDLPNRLDRMLRLLASYSVLTSTTRTIEDGGAERVYGLSMVGKYLVPDES

>d1fp2a1 a.4.5.29 (A:8-108) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}

RKPSEIFKAQALLYKHIYAFIDSMSLKWAVEMNIPNIIQNHGKPISLSNLVSILQVPSSKIGNVRRLMRYLAHNGFFEIITKEEESYALTVASELLVRGSD

>d1hsta\_ a.4.5.13 (A:) Histone H5, globular domain {Chicken (Gallus gallus)}

SHPTYSEMIAAAIRAEKSRGGSSRQSIQKYIKSHYKVGHNADLQIKLSIRRLLAAGVLKQTKGVGASGSFRLAK

>d1ghc\_\_ a.4.5.13 (-) Histone H1, globular domain {Chicken (Gallus gallus)}

MAGPSVTELITKAVSASKERKGLSLAALKKALAAGGYDVEKNNSRIKLGLKSLVSKGTLVQTKGTGASGSFRLSK

>d1e17a\_ a.4.5.14 (A:) Afx (Foxo4) {Human (Homo sapiens)}

SRRNAWGNQSYAELISQAIESAPEKRLTLAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKVHNEATGKSSWWMLNPEGG

>d1d5va\_ a.4.5.14 (A:) Adipocyte-transcription factor FREAC-11 (s12, fkh-14) {Human (Homo sapiens)}

MLVKPPYSYIALITMAIQNAPEKKITLNGIYQFIMDRFPFYRENKQGWQNSIRHNLSLNECFVKVPRDDKKPGKGSYWTLDPDSYNMFENGSFL

>d2hdca\_ a.4.5.14 (A:) Genesis {Rat (Rattus norvegicus)}

VKPPYSYIALITMAILQSPQKKLTLSGICEFISNRFPYYREKFPAWQNSIRHNLSLNDCFVKIPREPGNPGKGNYWTLDPQSEDMFDNGSFLRRRKR

>d1kq8a\_ a.4.5.14 (A:) HFH-1 (HNF-3 forkhead homolog-1) {Rat (Rattus norvegicus)}

YIALITMAIRDSAGGRLTLAEINEYLMGKFPFFRGSYTGWRNSVRHNLSLNDCFVKVLRDPSRPWGKDNYWMLNP

>d2bby\_\_ a.4.5.15 (-) DNA-binding domain from rap30 {Human (Homo sapiens)}

RARADKQHVLDMLFSAFEKHQYYNLKDLVDITKQPVVYLKEILKEIGVQNVKGIHKNTWELKPEYRHYQ

>d1i27a\_ a.4.5.30 (A:) C-terminal domain of the rap74 subunit of TFIIF {Human (Homo sapiens)}

GPLGSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKKTGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE

>d1dpua\_ a.4.5.16 (A:) C-terminal domain of RPA32 {Human (Homo sapiens)}

ANGLTVAQNQVLNLIKACPRPEGLNFQDLKNQLKHMSVSSIKQAVDFLSNEGHIYSTVDDDHFKSTDAE

>d1fsha\_ a.4.5.31 (A:) Segment polarity protein Dishevelled-1 {Mouse (Mus musculus)}

EAPLTVKSDMSAIVRVMQLPDSGLEIRDRMWLKITIANAVIGADVVDWLYTHVEGFKERREARKYASSMLKHGFLRHTVNKITFSEQCYYVFGD

>d1cf7a\_ a.4.5.17 (A:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}

SRHEKSLGLLTTKFVSLLQEAKDGVLDLKLAADTLAVRQKRRIYDITNVLEGIGLIEKKSKNSIQWK

>d1cf7b\_ a.4.5.17 (B:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}

GKGLRHFSMKVCEKVQRKGTTSYNEVADELVSEFTNSNNHLAADSAYDQKNIRRRVYDALNVLMAMNIISKEKKEIKWIGLP

>d1d8ja\_ a.4.5.18 (A:) The central core domain of TFIIE beta {Human (Homo sapiens)}

ALSGSSGYKFGVLAKIVNYMKTRHQRGDTHPLTLDEILDETQHLDIGLKQKQWLMTEALVNNPKIEVIDGKYAFKPKYNVR

>d1qbja\_ a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1 {Human (Homo sapiens)}

SIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKGKLQKEAGTPPLWKIA

>d1qgpa\_ a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1 {Human (Homo sapiens)}

LSSHFQELSIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKGKLQKEAGTPPLWKIAVSD

>d1j75a\_ a.4.5.19 (A:) Dlm-1 {Mouse (Mus musculus)}

NLEQKILQVLSDDGGPVKIGQLVKKCQVPKKTLNQVLYRLKKEDRVSSPEPATWSIG

>d1dp7p\_ a.4.5.20 (P:) MHC class II transcription factor RFX1 {Human (Homo sapiens)}

TVQWLLDNYETAEGVSLPRSTLYNHYLLHSQEQKLEPVNAASFGKLIRSVFMGLRTRRLGTRGNSKYHYYGLRIKA

>d1flia\_ a.4.5.21 (A:) Fli-1 {Human (Homo sapiens)}

PGSGQIQLWQFLLELLSDSANASCITWEGTNGEFKMTDPDEVARRWGERKSKPNMNYDKLSRALRYYYDKNIMTKVHGKRYAYKFDFHGIAQALQPHP

>d1k78b\_ a.4.5.21 (B:) ETS-1 transcription factor, residues 331-440 {Mouse (Mus musculus)}

IQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKTAGKRYVYRFVCDLQSLLGYTPEELHAMLDVK

>d2stta\_ a.4.5.21 (A:) ETS-1 transcription factor, residues 331-440 {Human (Homo sapiens)}

VIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNKPKMNYEKLSRGLRYYYDKNIIHKTAGKRYVYRFV

>d1puee\_ a.4.5.21 (E:) Transcription factor PU.1, residues 171-259 {Mouse (Mus musculus)}

KIRLYQFLLDLLRSGDMKDSIWWVDKDKGTFQFSSKHKEALAHRWGIQKGNRKKMTYEKMARALRNYGKTGEVKKVKKKLTYQFSGEV

>d1awca\_ a.4.5.21 (A:) GA binding protein (GABP) alpha {Mouse (Mus musculus)}

IQLWQFLLELLTDKDARDCISWVGDEGEFKLNQPELVAQKWGQRKNKPTMNYEKLSRALRYYYDGDMICKVQGKRFVYKFVCDLKTLIGYSAAELNRLVIECEQKKLARM

>d1bc8c\_ a.4.5.21 (C:) Serum responce factor accessory protein 1a, SAP-1 {Human (Homo sapiens)}

MDSAITLWQFLLQLLQKPQNKHMICWTSNDGQFKLLQAEEVARLWGIRKNKPNMNYDKLSRALRYYYVKNIIKKVNGQKFVYKFVSYPEILNM

>d1hbxg\_ a.4.5.21 (G:) Serum responce factor accessory protein 1a, SAP-1 {Human (Homo sapiens)}

DSAITLWQFLLQLLQKPQNKHMICWTSNDGQFKLLQAEEVARLWGIRKNKPNMNYDKLSRALRYYYVKNIIKKVNGQKFVYKFVSYPEILNMDPMTVGRIEGDCESLNFSEVSSSSKDVENGGKDKPPQPGAKTSSRNDYIHSGLYSSFTLNSLN

>d1duxc\_ a.4.5.21 (C:) Elk-1 {Human (Homo sapiens)}

VTLWQFLLQLLREQGNGHIISWTSRDGGEFKLVDAEEVARLWGLRKNKTNMNYDKLSRALRYYYDKNIIRKVSGQKFVYKFVSYPE

>d1hks\_\_ a.4.5.22 (-) Heat-shock transcription factor {Drosophila melanogaster}

GSGVPAFLAKLWRLVDDADTNRLICWTKDGQSFVIQNQAQFAKELLPLNYKHNNMASFIRQLNMYGFHKITSIDNGGLRFDRDEIEFSHPFFKRNSPFLLDQIKRK

>d1fbqa\_ a.4.5.22 (A:) Heat-shock transcription factor {Milk yeast (Kluyveromyces lactis)}

PAFVNKLWSMVNDKSNEKFIHWSTSGESIVVPNRERFVQEVLKKYFKHSNFASFVRQLNMYGWHKVQDVKSGSMLSNNDSRWEFENERH

>d2hts\_\_ a.4.5.22 (-) Heat-shock transcription factor {Milk yeast (Kluyveromyces lactis)}

ARPAFVNKLWSMVNDKSNEKFIHWSTSGESIVVPNRERFVQEVLPKYFKHSNFASFVRQLNMYGWHKVQDVKSGSNDSRWEFENERHA

>d1if1a\_ a.4.5.23 (A:) Interferon regulatory factor 1 (IRF-1) {Mouse (Mus musculus)}

RMRPWLEMQINSNQIPGLIWINKEEMIFQIPWKHAAKHGWDINKDACLFRSWAIHTGRYKAGEKEPDPKTWKANFRCAMNSLPDIEEVKDQSRNKGSSAVRVYRM

>d2irfg\_ a.4.5.23 (G:) Interferon regulatory factor-2, IRF-2 {Mouse (Mus musculus)}

RMRMRPWLEEQINSNTIPGLKWLNKEKKIFQIPWMHAARHGWDVEKDAPLFRNWAIHTGKHQPGIDKPDPKTWKANFRCAMNSLPDIEEVKDRSIKKGNNAFRVYRMLP

>d1g3sa1 a.4.5.24 (A:4-64) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}

LVDTTEMYLRTIYELEEEGVTPLRARIAERLEQSGPTVSQTVARMERDGLVVVASDRSLQM

>d1fx7a1 a.4.5.24 (A:1-64) Iron-dependent regulator IdeR {Mycobacterium tuberculosis}

MNELVDTTEMYLRTIYDLEEEGVTPLRARIAERLDQSGPTVSQTVSRMERDGLLRVAGDRHLEL

>d1xgsa1 a.4.5.25 (A:195-271) Methionine aminopeptidase, insert domain {Archaeon Pyrococcus furiosus}

GQVIEVPPTLIYMYVRDVPVRVAQARFLLAKIKREYGTLPFAYRWLQNDMPEGQLKLALKTLEKAGAIYGYPVLKEI

>d1b6a\_1 a.4.5.25 (375-448) Methionine aminopeptidase, insert domain {Human (Homo sapiens)}

HDDMECSHYMKNFDVGHVPIRLPRTKHLLNVINENFGTLAFCRRWLDRLGESKYLMALKNLCDLGIVDPYPPLC

>d1g4da\_ a.4.5.26 (A:) mu transposase, DNA-binding domain {Bacteriophage mu}

KSIWCSPQEIMAADGMPGSVAGVHYRANVQGWTKRKKEGVKGGKAVEYDVMSMPTKEREQVIAHLGLST

>d1tns\_\_ a.4.5.26 (-) mu transposase, DNA-binding domain {Bacteriophage mu}

MELWVSPKELANLPGLPKTSAGVIYVAKKQGWQNRTRAGVKGGKAIEYNANSLPVEAKAALLLRQGEIETSLGYFE

>d1opc\_\_ a.4.6.1 (-) OmpR {Escherichia coli}

VIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNLARGREYSAMERSIDVQISRLRRMVEEDPAHPRYIQTVWGLGYVFVPD

>d1kgsa1 a.4.6.1 (A:124-225) PhoB {Thermotoga maritima}

SKSTKLVCGDLILDTATKKAYRGSKEIDLTKKEYQILEYLVMNKNRVVTKEELQEHLWSFDDEVFSDVLRSHIKNLRKKVDKGFKKKIIHTVRGIGYVARDE

>d1qqia\_ a.4.6.1 (A:) PhoB {Escherichia coli}

MAVEEVIEMQGLSLDPTSHRVMAGEEPLEMGPTEFKLLHFFMTHPERVYSREQLLNHVWGTNVYVEDRTVDVHIRRLRKALEPGGHDRMVQTVRGTGYRFSTRF

>d1fsea\_ a.4.6.2 (A:) Germination protein GerE {Bacillus subtilis}

SKPLLTKREREVFELLVQDKTTKEIASELFISEKTVRNHISNAMQKLGVKGRSQAVVELLRMGELEL

>d1a04a1 a.4.6.2 (A:150-216) Nitrate/nitrite response regulator (NarL) {Escherichia coli}

ERDVNQLTPRERDILKLIAQGLPNKMIARRLDITESTVKVHVKHMLKKMKLKSRVEAAVWVHQERIF

>d1fc3a\_ a.4.6.3 (A:) SpoOA {Bacillus stearothermophilus}

NKPKNLDASITSIIHEIGVPAHIKGYLYLREAIAMVYHDIELLGSITKVLYPDIAKKYNTTASRVERAIRHAIEVAWSRGNLESISSLFGYTVSVSKAKPTNSEFIAMVADKLRLEHKA

>d1fox\_\_ a.4.7.1 (-) Ribosomal protein L11, C-terminal domain {Bacillus stearothermophilus}

MTFITKTPPAAVLLKKAAGIESGSGEPNRNKVATIKRDKVREIAELKMPDLNAASIEAAMRMIEGTARSMGIVVED

>d1qa6a\_ a.4.7.1 (A:) Ribosomal protein L11, C-terminal domain {Bacillus stearothermophilus}

KTPPAAVLLKKAAGIESGSGEPNRNKVATIKRDKVREIAELKMPDLNAASIEAAMRMIEGTARSMGI

>d1mmsa1 a.4.7.1 (A:71-140) Ribosomal protein L11, C-terminal domain {Thermotoga maritima}

KTPPASFLLKKAAGIEKGSSEPKRKIVGKVTRKQIEEIAKTKMPDLNANSLEAAMKIIEGTAKSMGIEVV

>d1fjgr\_ a.4.8.1 (R:) Ribosomal protein S18 {Thermus thermophilus}

PSRKAKVKATLGEFDLRDYRNVEVLKRFLSETGKILPRRRTGLSGKEQRILAKTIKRARILGLLPFTEKLVRK

>d1g1xc\_ a.4.8.1 (C:) Ribosomal protein S18 {Thermus thermophilus}

DLRDYRNVEVLKRFLSETGKILPRRRTGLSGKEQRILAKTIKRARILGLLPFT

>d1i94r\_ a.4.8.1 (R:) Ribosomal protein S18 {Thermus thermophilus}

KPKKEAQRRPSRKAKVKATLGEFDLRDYRNVEVLKRFLSETGKILPRRRTGLSGKEQRILAKTIKRARILGLLPFTEKLVRK

>d1e3ha1 a.4.9.1 (A:263-345) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 {Streptomyces antibioticus}

YQDDVLEALSAAVRPELSAALTIAGKQDREAELDRVKALAAEKLLPEFEGREKEISAAYRALTKSLVRERVIAEKKRIDGRGV

>d1k6ya1 a.4.10.1 (A:1-46) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 1}

FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLK

>d1wjba\_ a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 1}

FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLKGEAMHGQVD

>d1e0ea\_ a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 2}

FLEKIEPAQEEHEKYHSNVKELSHKFGIPNLVARQIVNSCAQCQQK

>d1ef4a\_ a.4.11.1 (A:) RNA polymerase subunit RPB10 {Archaeon Methanobacterium thermoautotrophicum}

MIPVRCLSCGKPVSAYFNEYQRRVADGEDPKDVLDDLGLKRYCCRRMLISHVETW

>d1i50j\_ a.4.11.1 (J:) RNA polymerase subunit RPB10 {Baker's yeast (Saccharomyces cerevisiae)}

MIVPVRCFSCGKVVGDKWESYLNLLQEDELDEGTALSRLGLKRYCCRRMILTHVDLIEKFLRYNP

>d1cuk\_1 a.5.1.1 (156-203) DNA helicase RuvA subunit, C-terminal domain {Escherichia coli}

TDDAEQEAVARLVALGYKPQEASRMVSKIARPDASSETLIREALRAAL

>d1bvsa1 a.5.1.1 (A:148-203) DNA helicase RuvA subunit, C-terminal domain {Mycobacterium leprae}

NAVRGSVVEALVGLGFAAKQAEEATDQVLDGELGKDGAVATSSALRAALSLLGKTR

>d1f4ia\_ a.5.2.1 (A:) C-terminal UBA domain of the hhr23a DNA repair protein {Human (Homo sapiens)}

QEKEAIERLKALGFEESLVIQAYFACEKNENLAANFLLSQNFDDE

>d1efub3 a.5.2.2 (B:1-54) Elongation factor Ts (EF-Ts), N-terminal domain {Escherichia coli}

AEITASLVKELRERTGAGMMDCKKALTEANGDIELAIENMRKSGAIKAAKKAGN

>d1aipc1 a.5.2.2 (C:2-53) Elongation factor Ts (EF-Ts), N-terminal domain {Thermus thermophilus}

SQMELIKKLREATGAGMMDVKRALEDAGWDEEKAVQLLRERGAMKAAKKADR

>d1go5a\_ a.5.2.3 (A:) FG-binding, C-terminal domain of TAP {Human (Homo sapiens)}

PAPTPSSSPVPTLSPEQQEMLQAFSTQSGMNLEWSQKCLQDNNWDYTRSAQAFTHLKAKGEIPEVAFMK

>d1aua\_1 a.5.3.1 (4-96) N-terminal domain of phosphatidylinositol transfer protein sec14p {Baker's yeast (Saccharomyces cerevisiae)}

QQEKEFLESYPQNCPPDALPGTPGNLDSAQEKALAELRKLLEDAGFIERLDDSTLLRFLRARKFDVQLAKEMFENCEKWRKDYGTDTILQDFH

>d1enwa\_ a.5.4.1 (A:) Elongation factor TFIIS domain 2 {Baker's yeast (Saccharomyces cerevisiae)}

GSHMPRNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESEHPPQSILHTAKAIESEMNKVNNCDTNEAAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP

>d1fjgm\_ a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}

ARIAGVEIPRNKRVDVALTYIYGIGKARAKEALEKTGINPATRVKDLTEAEVVRLREYVENTWKLEGELRAEVAANIKRLMDIGCYRGLRHRRGLPVRGQRTRTNARTRKGPRKTVAGKKKAPRK

>d1i94m\_ a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}

ARIAGVEIPRNKRVDVALTYIYGIGKARAKEALEKTGINPATRVKDLTEAEVVRLREYVENTWKLEGELRAEVAANIKRLMDIGCYRGLRHRR

>d1eija\_ a.5.6.1 (A:) Hypothetical protein MTH1615 {Archaeon Methanobacterium thermoautotrophicum}

MRQQLEMQKKQIMMQILTPEARSRLANLRLTRPDFVEQIELQLIQLAQMGRVRSKITDEQLKELLKRVAGKK

>d1jjcb1 a.6.1.1 (B:1-38,B:152-190) Domains B1 and B5 of PheRS-beta, PheT {Thermus thermophilus (Thermus aquaticus)}

MRVPFSWLKAYVPELESPEVLEERLAGLGFETDRIERVXEEVVLDLEVTPNRPDALGLLGLARDLHALGYALVEPEAA

>d1jjcb2 a.6.1.1 (B:400-474) Domains B1 and B5 of PheRS-beta, PheT {Thermus thermophilus (Thermus aquaticus)}

PPEAIPFRPEYANRLLGTSYPEAEQIAILKRLGCRVEGEGPTYRVTPPSHRLDLRLEEDLVEEVARIQGYETIPL

>d1d4ua1 a.6.1.2 (A:37-111) DNA repair factor XPA DNA- and RPA-binding domain, C-terminal subdomain {Human (Homo sapiens)}

DKHKLITKTEAKQEYLLKDCDLEKREPPLKFIVKKNPHHSQWGDMKLYLKLQIVKRSLEVWGSQEALEEAKEVRQ

>d1exja1 a.6.1.3 (A:3-120) Transcription activator BmrR {Bacillus subtilis}

ESYYSIGEVSKLANVSIKALRYYDKIDLFKPAYVDPDTSYRYYTDSQLIHLDLIKSLKYIGTPLEEMKKAQDLEMEELFAFYTEQERQIREKLDFLSALEQTISLVKKRMKRQMEYPA

>d1jbga\_ a.6.1.3 (A:) Multidrug transporter activator MtaN {Bacillus subtilis}

KYQVKQVAEISGVSIRTLHHYDNIELLNPSALTDAGYRLYSDADLERLQQILFFKEIGFRLDEIKEMLDHPNFDRKAALQSQKEILMKKKQRMDEMIQTIDRTLLS

>d2spca\_ a.7.1.1 (A:) Spectrin {Fruit fly (Drosophila sp.)}

QNLDLQLYMRDCELAESWMSAREAFLNADDDANAGGNVEALIKKHEDFDKAINGHEQKIAALQTVADQLIAQNHYASNLVDEKRKQVLERWRHLKEGLIEKRSRLGD

>d1aj3\_\_ a.7.1.1 (-) Spectrin {Chicken (Gallus gallus)}

HQFFRDMDDEESWIKEKKLLVSSEDYGRDLTGVQNLRKKHKRLEAELAAHEPAIQGVLDTGKKLSDDNTIGKEEIQQRLAQFVDHWKELKQLAAARGQ

>d1cuna1 a.7.1.1 (A:7-115) Spectrin {Chicken (Gallus gallus)}

MVHQFFRDMDDEESWIKEKKLLVSSEDYGRDLTGVQNLRKKHKRLEAELAAHEPAIQSVLDTGKKLSDDNTIGKEEIQQRLAQFVDHWKELKQLAAARGQRLEESLEYQ

>d1cuna2 a.7.1.1 (A:116-219) Spectrin {Chicken (Gallus gallus)}

QFVANVEEEEAWINEKMTLVASEDYGDTLAAIQGLLKKHEAFETDFTVHKDRVNDVCANGEDLIKKNNHHVENITAKMKGLKGKVSDLEKAAAQRKAKLDENSA

>d1hcia1 a.7.1.1 (A:272-396) alpha-actinin {Human (Homo sapiens)}

SSAVNQENERLMEEYERLASELLEWIRRTIPWLENRTPEKTMQAMQKKLEDFRDYRRKHKPPKVQEKCQLEINFNTLQTKLRISNRPAFMPSEGKMVSDIAGAWQRLEQAEKGYEEWLLNEIRRL

>d1hcia4 a.7.1.1 (A:633-746) alpha-actinin {Human (Homo sapiens)}

HANERLRRQFAAQANAIGPWIQNKMEEIARSSIQITGALEDQMNQLKQYEHNIINYKNNIDKLEGDHQLIQEALVFDNKHTNYTMEHIRVGWELLLTTIARTINEVETQILTRD

>d1quua1 a.7.1.1 (A:1-124) alpha-actinin {Human (Homo sapiens)}

GSSNEIRRLERLEHLAEKFRQKASTHETWAYGKEQILLQKDYESASLTEVRALLRKHEAFESDLAAHQDRVEQIAAIAQELNELDYHDAVNVNDRCQKICDQWDRLGTLTQKRREALERMEKLL

>d1quua2 a.7.1.1 (A:125-248) alpha-actinin {Human (Homo sapiens)}

ETIDQLHLEFAKRAAPFNNWMEGAMEDLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSIMAIQNEVEKVIQSYNIRISSSNPYSTVTMDELRTKWDKVKQLVPIRDQSLQEELARQHAN

>d1e2aa\_ a.7.2.1 (A:) Enzyme IIa from lactose specific PTS, IIa-lac {Lactococcus lactis}

MNREEMTLLGFEIVAYAGDARSKLLEALKAAENGDFAKADSLVVEAGSCIAEAHSSQTGMLAREASGEELPYSVTMMHGQDHLMTTILLKDVIHHLIELYKR

>d1chua1 a.7.3.1 (A:423-533) L-aspartate oxidase {Escherichia coli}

DESRVENPDERVVIQHNWHELRLFMWDYVGIVRTTKRLERALRRITMLQQEIDEYYAHFRVSNNLLELRNLVQVAELIVRCAMMRKESRGLHFTLDYPELLTHSGPSILSP

>d1fuma1 a.7.3.1 (A:443-575) Fumarate reductase flavoprotein subunit {Escherichia coli}

DGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKLAELQERFKRVRITDTSSVFNTDLLYTIELGHGLNVAECMAHSAMARKESRGAHQRLDEGCTERDDVNFLKHTLAFRDADGTTRLEYSDVKITTLPP

>d1qlaa1 a.7.3.1 (A:458-655) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}

KGTEDVFKIKNRMKDVMDDNVGIFRDGPHLEKSVKELEELYKKSKNVGIKNKRLHANPELEEAYRVPMMLKVALCVAKGALDRTESRGAHNREDYPKRDDINWLNRTLASWPNPEQTLPTLEYEALDVNEMEIAPRYRGYGAKGNYIENPLSVKRQEEIDKIQSELEAAGKDRHAIQEALMPYELPAKYKARNERLGD

>d1jnra1 a.7.3.1 (A:503-643) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

TADDVNPEYILPWQGLVRLQKIMDEYAAGIATIYKTNEKMLQRALELLAFLKEDLEKLAARDLHELMRAWELVHRVWTAEAHVRHMLFRKETRWPGYYYRTDYPELNDEEWKCFVCSKYDAEKDEWTFEKVPYVQVIEWSF

>d1fewa\_ a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}

SLSSEALMRRAVSLVTDSTSTFLSQTTYALIEAITEYTKAVYTLTSLYRQYTSLLGKMNSEEEDEVWQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEMAAEAAYQTGADQASITARNHIQLVKLQVEEVHQLSRKAETKLAEAQIEELKQKTQEEGEERAESEQEAYLRED

>d1g73a\_ a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}

AVPIAQKSEPHSLSSEALMRRAVSLVTDSTSTDLSQTTYALIEAITEYTKAVYTLTSLYRQYTSLLGKMNSEEEDEVWQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEMAAEAAYQTGADQASITARNHIQLVKLQVEEVHQLSRKAETKLAEAQ

>d1hx1b\_ a.7.7.1 (B:) BAG-family molecular chaperon regulator-1, BAG1 {Human (Homo sapiens)}

GNSPQEEVELKKLKHLEKSVEKIADQLEELNKELTGIQQGFLPKDLQAEALCKLDRRVKATIEQFMKILEEIDTLILPENFKDSRLKRKGLVKKVQAFLAECDTVEQNICQE

>d1i6za\_ a.7.7.1 (A:) BAG-family molecular chaperon regulator-1, BAG1 {Mouse (Mus musculus)}

GSPEFMLIGEKSNPEEEVELKKLKDLEVSAEKIANHLQELNKELSGIQQGFLAKELQAEALCKLDRKVKATIEQFMKILEEIDTMVLPEQFKDSRLKRKNLVKKVQVFLAECDTVEQYICQETERLQSTNLALAE

>d1qsda\_ a.7.5.1 (A:) beta-Tubulin binding post-chaperonin cofactor Rbl2p {Baker's yeast (Saccharomyces cerevisiae)}

TQLDIKVKALKRLTKEEGYYQQELKDQEAHVAKLKEDKSVDPYDLKKQEEVLDDTKRLLPTLYEKIREFKEDLEQFLKTYQGTEDVSDARSAITSAQELLDS

>d1fjgt\_ a.7.6.1 (T:) Ribosomal protein S20 {Thermus thermophilus}

RNLSALKRHRQSLKRRLRNKAKKSAIKTLSKKAVQLAQEGKAEEALKIMRKAESLIDKAAKGSTLHKNAAARRKSRLMRKVRQLLEAAGAPLIGGGLSA

>d1bdc\_\_ a.8.1.1 (-) Immunoglobulin-binding protein A modules {Staphylococcus aureus}

TADNKFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSQSANLLAEAKKLNDAQAPKA

>d1deeg\_ a.8.1.1 (G:) Immunoglobulin-binding protein A modules {Staphylococcus aureus}

DQQSAFYEILNMPNLNEAQRNGFIQSLKDDPSQSTNVLGEAKKLNESQAPK

>d1edj\_\_ a.8.1.1 (-) Immunoglobulin-binding protein A modules {Staphylococcus aureus}

AQHDEAQQNAFYQVLNMPNLNADQRNGFIQSLKDDPSQSANVLGEAQKLNDSQAPK

>d1fc2c\_ a.8.1.1 (C:) Immunoglobulin-binding protein A modules {Staphylococcus aureus}

FNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSQSANLLAEA

>d2spza\_ a.8.1.1 (A:) Immunoglobulin-binding protein A modules {Staphylococcus aureus}

VDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKLNDAQAPK

>d1gab\_\_ a.8.1.2 (-) PAB {Peptostreptococcus magnus}

TIDQWLLKNAKEDAIAELKKAGITSDFYFNAINKAKTVEEVNALKNEILKAHA

>d1gjta\_ a.8.1.2 (A:) IgG binding protein G {Streptococcus sp., group G}

MKAIFVLNAQHDEAVDANSLAEAKVLANRELDKYGVSDYYKNLINNAKTVEGVKALIDEILAALP

>d1ebdc\_ a.9.1.1 (C:) E3-binding domain of dihydrolipoamide acetyltransferase {Bacillus stearothermophilus}

IAMPSVRKYAREKGVDIRLVQGTGKNGRVLKEDIDAFLAGG

>d1bal\_\_ a.9.1.1 (-) E3-binding domain of dihydrolipoamide succinyltransferase {Escherichia coli}

YASLEEQNNDALSPAIRRLLAEHNLDASAIKGTGVGGRLTREDVEKHLAKA

>d1bbl\_\_ a.9.1.1 (-) E3-binding domain of dihydrolipoamide succinyltransferase {Escherichia coli}

LSPAIRRLLAEHNLDASAIKGTGVGGRLTREDVEKHL

>d2erl\_\_ a.10.1.1 (-) ER-1 {Euplotes raikovi}

DACEQAAIQCVESACESLCTEGEDRTGCYMYIYSNCPPYV

>d1erd\_\_ a.10.1.1 (-) ER-2 {Euplotes raikovi}

DPMTCEQAMASCEHTMCGYCQGPLYMTCIGITTDPECGLP

>d1erp\_\_ a.10.1.1 (-) ER-10 {Euplotes raikovi}

DLCEQSALQCNEQGCHNFCSPEDKPGCLGMVWNPELCP

>d1ery\_\_ a.10.1.1 (-) ER-11 {Euplotes raikovi}

DECANAAAQCSITLCNLYCGPLIEICELTVMQNCEPPFS

>d1hd6a\_ a.10.1.1 (A:) ER-22 {Euplotes raikovi}

DICDIAIAQCSLTLCQDCENTPICELAVKGSCPPPWS

>d1aca\_\_ a.11.1.1 (-) Acyl-CoA binding protein {Cow (Bos taurus)}

SQAEFDKAAEEVKHLKTKPADEEMLFIYSHYKQATVGDINTERPGMLDFKGKAKWDAWNELKGTSKEDAMKAYIDKVEELKKKYGI

>d1hbka\_ a.11.1.1 (A:) Acyl-CoA binding protein {Plasmodium falciparum}

HMAQQVFEEECVSFINGLPRTINNLPNELKLDLYKYYKQSTIGNCNIKEPSAHKYIDRKKYEEAWKSVENLNREDAQKKRYVDIVSEIFPYWQD

>d1ef1a1 a.11.2.1 (A:88-198) Moesin {Human (Homo sapiens)}

DVSEELIQDITQRLFFLQVKEGILNDDIYCPPETAVLLASYAVQSKYGDFNKEVHKSGYLAGDKLLPQRVLEQHKLNKDQWEERIQVWHEEHRGMLREDAVLEYLKIAQDL

>d1gc7a1 a.11.2.1 (A:88-198) Radixin {Mouse (Mus musculus)}

DVSEELIQEITQRLFFLQVKEAILNDEIYCPPETAVLLASYAVQAKYGDYNKEIHKPGYLANDRLLPQRVLEQHKLTKEQWEERIQNWHEEHRGMLREDSMMEYLKIAQDL

>d1gg3a1 a.11.2.1 (A:82-187) Erythroid membrane protein 4.1R {Human (Homo sapiens)}

PDPAQLTEDITRYYLCLQLRQDIVAGRLPCSFATLALLGSYTIQSELGDYDPELHGVDYVSDFKLAPNQTKELEEKVMELHKSYRSMTPAQADLEFLENAKKLSMY

>d1h4ra1 a.11.2.1 (A:104-214) Merlin {Human (Homo sapiens)}

NAEEELVQEITQHLFFLQVKKQILDEKIYCPPEASVLLASYAVQAKYGDYDPSVHKRGFLAQEELLPKRVINLYQMTPEMWEERITAWYAEHRGRARDEAEMEYLKIAQDL

>d1kdxa\_ a.12.1.1 (A:) Kix domain of CBP (creb binding protein) {Mouse (Mus musculus)}

GVRKGWHEHVTQDLRSHLVHKLVQAIFPTPDPAALKDRRMENLVAYAKKVEGDMYESANSRDEYYHLLAEKIYKIQKELEE

>d1lre\_\_ a.13.1.1 (-) alpha-2-Macroglobulin receptor associated protein (RAP) domain 1 {Human (Homo sapiens)}

GEEFRMEKLNQLWEKAQRLHLPPVRLAELHADLKIQERDELAWKKLKLDGLDEDGEKEARLIRNLNVILAKYGLDGKKDAR

>d1qqva\_ a.14.1.1 (A:) Thermostable subdomain from chicken villin headpiece {Chicken (Gallus gallus)}

PTKLETFPLDVLVNTAAEDLPRGVDPSRKENHLSDEDFKAVFGMTRSAFANLPLWKQQNLKKEKGLF

>d1vii\_\_ a.14.1.1 (-) Thermostable subdomain from chicken villin headpiece {Chicken (Gallus gallus)}

MLSDEDFKAVFGMTRSAFANLPLWKQQNLKKEKGLF

>d1tbaa\_ a.15.1.1 (A:) TAF(II)230 TBP-binding fragment {Fruit fly (Drosophila melanogaster)}

EGSIGNGLDLTGILFGNIDSEGRLLQDDDGEGRGGTGFDAELRENIGSLSKLGLDSMLLEVIDLKEA

>d1ail\_\_ a.16.1.1 (-) N-terminal, RNA-binding domain of nonstructural protein NS1 {Influenza A virus}

MDSNTVSSFQVDCFLWHVRKQVVDQELGDAPFLDRLRRDQKSLRGRGSTLGLNIEAATHVGKQIVEKILK

>d1a32\_\_ a.16.1.2 (-) Ribosomal protein S15 {Bacillus stearothermophilus}

LTQERKREIIEQFKVHENDTGSPEVQIAILTEQINNLNEHLRVHKKDHHSRRGLLKMVGKRRRLLAYLRNKDVARYREIVEKLGL

>d1dk1a\_ a.16.1.2 (A:) Ribosomal protein S15 {Thermus thermophilus}

PITKEEKQKVMQEFARFPGDTGSTEVQVALLTLRINRLSEHLKVHKKDHHSHRGLLMMVGQRRRLLRYLQREDPERYRMLIEKLGI

>d1g1xb\_ a.16.1.2 (B:) Ribosomal protein S15 {Thermus thermophilus}

PITKEEKQKVIQEFARFPGDTGSTEVQVALLTLRINRLSEHLKVHKKDHHSHRGLLMMVGQRRRLLRYLQREDPERYREIVEKLGLRG

>d1d2da\_ a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS) second repeated element {Chinese hamster (Cricetulus griseus)}

MVYDKIAAQGEVVRKLKAEKAPKAKVTEAVECLLSLKAEYKEKTGKEYVPGLEHHH

>d1fyja\_ a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS) second repeated element {Human (Homo sapiens)}

DSLVLYNRVAVQGDVVRELKAKKAPKEDVDAAVKQLLSLKAEYKEKTGQEYKPGNPP

>d2hp8\_\_ a.17.1.1 (-) p8-MTCP1 {Human (Homo sapiens)}

MPQKDPCQKQACEIQKCLQANSYMESKCQAVIQELRKCCAQYPKGRSVVCSGFEKEEEENLTRKSASK

>d1ijxa\_ a.141.1.1 (A:) Secreted Frizzled-related protein 3 (SFRP-3;fzb) {Mouse (Mus musculus)}

AACEPVRIPLCKSLPWEMTKMPNHLHHSTQANAILAMEQFEGLLGTHCSPDLLFFLCAMYAPICTIDFQHEPIKPCKSVCERARQGCEPILIKYRHSWPESLACDELPVYDRGVCISPEAIVTAD

>d1ijya\_ a.141.1.1 (A:) Frizzled 8 (FZ8) {Mouse (Mus musculus)}

ELACQEITVPLCKGIGYEYTYMPNQFNHDTQDEAGLEVHQFWPLVEIQCSPDLKFFLCSMYTPICLEDYKKPLPPCRSVCERAKAGCAPLMRQYGFAWPDRMRCDRLPEQGNPDTLCMDYER

>d2end\_\_ a.18.1.1 (-) T4 endonuclease V {Bacteriophage T4 (Escherichia coli)}

TRINLTLVSELADQHLMAEYRELPRVFGAVRKHVANGKRVRDFKISPTFILGAGHVTFFYDKLEFLRKRQIELIAECLKRGFNIKDTTVQDISDIPQEFRGDYIPHEASIAISQARLDEKIAQRPTWYKYYGKAIYA

>d2lisa\_ a.19.1.1 (A:) Lysin {Red abalone (Haliotis rufescens)}

HYVEPKFLNKAFEVALKVQIIAGFDRGLVKWLRVHGRTLSTVQKKALYFVNRRYMQTHWANYMLWINKKIDALGRTPVVGDYTRLGAEIGRRIDMAYFYDFLKDKNMIPKYLPYMEEINRMRPADVPVKYM

>d3lyna\_ a.19.1.1 (A:) Lysin {Green abalone (Haliotis fulgens)}

INKAYEVTMKIQIISGFDRQLTAWLRVHGRRLTNNQKKTLFFVNRRYMQTHWQNYMLWVKRKIKALGRPAAVGDYTRLGAEIGRRVDMVFFYNFLSGRKMIPPYSAYMAKLNALRPADVPVK

>d1gaka\_ a.19.1.1 (A:) SP18 {Abalone (Haliotis fulgens)}

FDDVVVSRQEQSYVQRGMVNFLDEEMHKLVKRFRDMRWNLGPGFVFLLKKVNRERMMRYCMDYARYSKKILQLKHLPVNKKTLTKMGRFVGYRNYGVIRELYADVFRDVQGFRGPKMTAAMRKYSSKDPGTFPCKNE

>d1lbu\_1 a.20.1.1 (1-83) Zn2+ DD-carboxypeptidase, N-terminal domain {Streptomyces albus G}

DGCYTWSGTLSEGSSGEAVRQLQIRVAGYPGTGAQLAIDGQFGPATKAAVQRFQSAYGLAADGIAGPATFNKIYQLQDDDCTP

>d1ck7a6 a.20.1.2 (A:31-107) Gelatinase A {Human (Homo sapiens)}

PSPIIKFPGDVAPKTDKELAVQYLNTFYGCPKESCNLFVLKDTLKKMQKFFGLPQTGDLDQNTIETMRKPRCGNPDV

>d1slm\_1 a.20.1.2 (16-80) Stromelysin-1 (MMP-3) {Human (Homo sapiens), fibroblast}

LVQKYLENYYDLKKDVKQFVRRKDSGPVVKKIREMQKFLGLEVTGKLDSDTLEVMRKPRCGVPDV

>d1aab\_\_ a.21.1.1 (-) HMG1, domains A and B {Rat (Rattus norvegicus)}

GKGDPKKPRGKMSSYAFFVQTSREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGE

>d1ckta\_ a.21.1.1 (A:) HMG1, domains A and B {Rat (Rattus norvegicus)}

KPRGKMSSYAFFVQTCREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTY

>d1hme\_\_ a.21.1.1 (-) HMG1, domains A and B {Rat (Rattus norvegicus)}

FKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAK

>d1hsm\_\_ a.21.1.1 (-) HMG1, domains A and B {Hamster (Cricetulus griseus)}

NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAAKLKEKYEKDIAAYRAKGKPDAA

>d1qrva\_ a.21.1.1 (A:) HMG-D {Drosophila melanogaster}

SDKPKRPLSAYMLWLNSARESIKRENPGIKVTEVAKRGGELWRAMKDKSEWEAKAAKAKDDYDRAVKEFEANG

>d1cg7a\_ a.21.1.1 (A:) NHP6a {Baker's yeast (Saccharomyces cerevisiae)}

MVTPREPKKRTTRKKKDPNAPKRALSAYMFFANENRDIVRSENPDITFGQVGKKLGEKWKALTPEEKQPYEAKAQADKKRYESEKELYNATLA

>d1hrza\_ a.21.1.1 (A:) SRY {Human (Homo sapiens)}

DRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQAMHREKYPNYKYR

>d1j46a\_ a.21.1.1 (A:) SRY {Human (Homo sapiens)}

MQDRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQAMHREKYPNYKYRPRRKAKMLPK

>d1i11a\_ a.21.1.1 (A:) Sox-5 {Mouse (Mus musculus)}

PHIKRPMNAFMVWAKDERRKILQAFPDMHNSNISKILGSRWKAMTNLEKQPYYEEQARLSKQHLEKYPDY

>d2lefa\_ a.21.1.1 (A:) Lymphoid enhancer-binding factor, LEF1 {Mouse (Mus musculus)}

MHIKKPLNAFMLYMKEMRANVVAESTLKESAAINQILGRRWHALSREEQAKYYELARKERQLHMQLYPGWSARDNYGKKKKRKREK

>d1k99a\_ a.21.1.1 (A:) Upstream binding factor, the first HMG box {Human (Homo sapiens)}

MKKLKKHPDFPKKPLTPYFRFFMEKRAKYAKLHPEMSNLDLTKILSKKYKELPEKKKMKYIQDFQREKQEFERNLARFREDHPDLIQNAKK

>d1eqza\_ a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus), erythrocytes}

SGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTDSHKA

>d1hioa\_ a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus), erythrocytes}

KSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLP

>d1hq3a\_ a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus), erythrocytes}

KAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPK

>d1aoic\_ a.22.1.1 (C:) Histone H2A {African clawed frog (Xenopus laevis)}

GKQGGKTRAKAKTRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAVRNDEELNKLLGRVTIAQGGVLPNIQSVLLPK

>d1f66c\_ a.22.1.1 (C:) Histone H2A {Human (Homo sapiens), variant H2A.Z}

AVSRSQRAGLQFPVGRIHRHLKSRTTSHGRVGATAAVYSAAILEYLTAEVLELAGNASKDLKVKRITPRHLQLAIRGDEELDSLIKATIAGGGVIPHIHKSLI

>d1id3c\_ a.22.1.1 (C:) Histone H2A {Baker's yeast (Saccharomyces cerevisiae), H2A.1}

QSRSAKAGLTFPVGRVHRLLRRGNYAQRIGSGAPVYLTAVLEYLAAEILELAGNAARDNKKTRIIPRHLQLAIRNDDELNKLLGNVTIAQGGVLPNIHQNLLPKKSAKAT

>d1eqzb\_ a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus), erythrocytes}

VTKTQKKGDKKRKKSRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSK

>d1hiob\_ a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus), erythrocytes}

SYSIYVYKVLKQVHPDTGISSKAMGSMNSFVNDIFERIAGLASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKHTSSK

>d1hq3b\_ a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus), erythrocytes}

RKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSS

>d1aoid\_ a.22.1.1 (D:) Histone H2B {African clawed frog (Xenopus laevis)}

KKRRKTRKESYAIYVYKVLKQVHPDTGISSKAMSIMNSFVNDVFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSAK

>d1id3d\_ a.22.1.1 (D:) Histone H2B {Baker's yeast (Saccharomyces cerevisiae), H2B.2}

RKETYSSYIYKVLKQTHPDTGISQKSMSILNSFVNDIFERIATEASKLAAYNKKSTISAREIQTAVRLILPGELAKHAVSEGTRAVTKYSSST

>d1eqzc\_ a.22.1.1 (C:) Histone H3 {Chicken (Gallus gallus), erythrocytes}

APATGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

>d1eqzg\_ a.22.1.1 (G:) Histone H3 {Chicken (Gallus gallus), erythrocytes}

PRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

>d1hq3c\_ a.22.1.1 (C:) Histone H3 {Chicken (Gallus gallus), erythrocytes}

YRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

>d1id3a\_ a.22.1.1 (A:) Histone H3 {Baker's yeast (Saccharomyces cerevisiae)}

PHRYKPGTVALREIRRFQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAIGALQESVEAYLVSLFEDTNLAAIHAKRVTIQKKEIKLARRLRGER

>d1eqzh\_ a.22.1.1 (H:) Histone H4 {Chicken (Gallus gallus), erythrocytes}

KGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVTYTEHAKRKTVTAMDVVYALKRQGRTLYGFGG

>d1hq3d\_ a.22.1.1 (D:) Histone H4 {Chicken (Gallus gallus), erythrocytes}

KVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVTYTEHAKRKTVTAMDVVYALKRQGRTLYGFGG

>d1id3b\_ a.22.1.1 (B:) Histone H4 {Baker's yeast (Saccharomyces cerevisiae)}

DNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSFLESVIRDSVTYTEHAKRKTVTSLDVVYALKRQGRTLYGFGG

>d1b67a\_ a.22.1.2 (A:) Archaeal histone {Archaeon Methanothermus fervidus, histone A}

GELPIAPIGRIIKNAGAERVSDDARIALAKVLEEMGEEIASEAVKLAKHAGRKTIKAEDIELARKMFK

>d1a7w\_\_ a.22.1.2 (-) Archaeal histone {Archaeon Methanothermus fervidus, histone B}

MELPIAPIGRIIKDAGAERVSDDARITLAKILEEMGRDIASEAIKLARHAGRKTIKAEDIELAVRRFK

>d1f1ea\_ a.22.1.2 (A:) Archaeal histone {Archaeon Methanopyrus kandleri}

ELPKAAIERIFRQGIGERRLSQDAKDTIYDFVPTMAEYVANAAKSVLDASGKKTLMEEHLKALADVLMVEGVEDYDGELFGRATVRRILKRAGIERASSDAVDLYNKLICRATEELGEKAAEYADEDGRKTVQGEDVEKAITYSMPKGGEL

>d1tafa\_ a.22.1.3 (A:) TAF(II)42 {Fruit fly (Drosophila melanogaster)}

PKDAQVIMSILKELNVQEYEPRVVNQLLEFTFRYVTSILDDAKVYANHARKKTIDLDDVRLATEVTLD

>d1tafb\_ a.22.1.3 (B:) TAF(II)62 {Fruit fly (Drosophila melanogaster)}

MLYGSSISAESMKVIAESIGVGSLSDDAAKELAEDVSIKLKRIVQDAAKFMNHAKRQKLSVRDIDMSLKV

>d1bh9a\_ a.22.1.3 (A:) TAF(II)18 {Human (Homo sapiens)}

LFSKELRCMMYGFGDDQNPYTESVDILEDLVIEFITEMTHKAMSI

>d1bh9b\_ a.22.1.3 (B:) TAF(II)28 {Human (Homo sapiens)}

FSEEQLNRYEMYRRSAFPKAAIKRLIQSITGTSVSQNVVIAMSGISKVFVGEVVEEALDVCEKWGEMPPLQPKHMREAVRRLKSKGQIP

>d1jfia\_ a.22.1.3 (A:) Negative cofactor 2, NC2, alpha chain {Human (Homo sapiens)}

ARFPPARIKKIMQTDEEIGKVAAAVPVIISRALELFLESLLKKACQVTQSRNAKTMTTSHLKQCIE

>d1jfib\_ a.22.1.3 (B:) Negative cofactor 2, NC2, beta chain {Human (Homo sapiens)}

DDLTIPRAAINKMIKETLPNVRVANDARELVVNCCTEFIHLISSEANEICNKSEKKTISPEHVIQALESLGFGSYISEVKEVLQECKTVALKRRKASSRLENLGIPEEELLRQQQELFAKARQQQAELAQQEWLQ

>d1fpoa2 a.23.1.1 (A:77-171) HSC20 (HSCB), C-terminal oligomerisation domain {Escherichia coli}

FDLASEQHTVRDTAFLMEQLELREELDEIEQAKDEARLESFIKRVKKMFDTRHQLMVEQLDNETWDAAADTCRKLRFLDKLRSSAEQLEEKLLDF

>d1eexg\_ a.23.2.1 (G:) Diol dehydratase, gamma subunit {Klebsiella oxytoca}

SARVSDYPLANKHPEWVKTATNKTLDDFTLENVLSNKVTAQDMRITPETLRLQASIAKDAGRDRLAMNFERAAELTAVPDDRILEIYNALRPYRSTKEELLAIADDLESRYQAKICAAFVREAATLYVERKKLKGDD

>d1mtyg\_ a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit {Methylococcus capsulatus}

LGIHSNDTRDAWVNKIAHVNTLEKAAEMLKQFRMDHTTPFRNSYELDNDYLWIEAKLEEKVAVLKARAFNEVDFRHKTAFGEDAKSVLDGTVAKMNAAKDKWEAEKIHIGFRQAYKPPIMPVNYFLDGERQLGTRLMELRNLNYYDTPLEELRKQRGVRVVH

>d1mhyg\_ a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit {Methylosinus trichosporium}

AKREPIHDNSIRTEWEAKIAKLTSVDQATKFIQDFRLAYTSPFRKSYDIDVDYQYIERKIEEKLSVLKTEKLPVADLITKATTGEDAAAVEATWIAKIKAAKSKYEAEAIHIEFRQLYKPPVLPVNVFLRTDAALGTVLMEIRNTDYYGTPLEGLRKERGVKVLHLQ

>d1om2a\_ a.23.4.1 (A:) Mitochondrial import receptor subunit Tom20 {Rat (Rattus norvegicus)}

RAGLSKLPDLKDAEAVQKFFLEEIQLGEELLAQGDYEKGVDHLTNAIAVCGQPQQLLQVLQQTLPPPVFQMLLTKLPTISQRIVSAQSLGEDDVE

>d1jw2a\_ a.23.5.1 (A:) Hemolysin expression modulating protein HHA {Escherichia coli}

MSEKPLTKTDYLMRLRRCQTIDTLERVIEKNKYELSDNELAVFYSAADHRLAELTMNKLYDKIPSSVWKFIR

>d1nfn\_\_ a.24.1.1 (-) Apolipoprotein E3 {Human (Homo sapiens)}

GQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELRALMDETMKELKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGRLVQYRGEVQAMLGQSTEELRVRLASHLRKLRKRLLRDADDLQKRLAVYQA

>d2asr\_\_ a.24.2.1 (-) Aspartate receptor, ligand-binding domain {Escherichia coli}

KSFVVSNQLREQQGELTSTWDLMLQTRINLSRSAVRMMMDSSNQQSNAKVELLDSARKTLAQAATHYKKFKSMAPLPEMVATSRNIDEKYKNYYTALTELIDYLDYGNTGAYFAQPTQGMQNAMGERFAQYALSSEKLYRDI

>d1vlta\_ a.24.2.1 (A:) Aspartate receptor, ligand-binding domain {Salmonella typhimurium}

GFVISNELRQQQSELTSTWDLMLQTRINLSRSAARMMMDASNQQSSAKTDLLQNAKTTLAQAAAHYANFKNMTPLPAMAEASANVDEKYQRYQAALAELIQFLDNGNMDAYFAQPTQGMQNALGEALGNYARVSENLYRQTF

>d2liga\_ a.24.2.1 (A:) Aspartate receptor, ligand-binding domain {Salmonella typhimurium}

MGGLLFSSLQHCQQGFVISNELRQQQSELTSTWDLMLQTRINLSRSAARMMMDASNQQSSAKTDLLQNAKTTLAQAAAHYANFKNMTPLPAMAEASANVDEKYQRYQAALAELIQFLDNGNMDAYFAQPTQGMQNALGEALGNYARVSENLYRQTFD

>d256ba\_ a.24.3.1 (A:) Cytochrome b562 {Escherichia coli}

ADLEDNMETLNDNLKVIEKADNAAQVKDALTKMRAAALDAQKATPPKLEDKSPDSPEMKDFRHGFDILVGQIDDALKLANEGKVKEAQAAAEQLKTTRNAYHQKYR

>d2ccya\_ a.24.3.2 (A:) Cytochrome c' {Rhodospirillum molischianum}

QSKPEDLLKLRQGLMQTLKSQWVPIAGFAAGKADLPADAAQRAENMAMVAKLAPIGWAKGTEALPNGETKPEAFGSKSAEFLEGWKALATESTKLAAAAKAGPDALKAQAAATGKVCKACHEEFKQD

>d1bbha\_ a.24.3.2 (A:) Cytochrome c' {Chromatium vinosum}

AGLSPEEQIETRQAGYEFMGWNMGKIKANLEGEYNAAQVEAAANVIAAIANSGMGALYGPGTDKNVGDVKTRVKPEFFQNMEDVGKIAREFVGAANTLAEVAATGEAEAVKTAFGDVGAACKSCHEKYRAK

>d1e85a\_ a.24.3.2 (A:) Cytochrome c' {Alcaligenes sp.}

EFAKPEDAVKYRQSALTLMASHFGRMTPVVKGQAPYDAAQIKANVEVLKTLSALPWAAFGPGTEGGDARPEIWSDAASFKQKQQAFQDNIVKLSAAADAGDLDKLRAAFGDVGASCKACHDAYRK

>d1jafa\_ a.24.3.2 (A:) Cytochrome c' {Rhodocyclus gelatinosus}

QFQKPGDAIEYRQSAFTLIANHFGRVAAMAQGKAPFDAKVAAENIALVSTLSKLPLTAFGPGTDKGHGTEAKPAVWSDAAGFKAAADKFAAAVDKLDAAGKTGDFAQIKAAVGETGGACKGCHDKFKE

>d1cpq\_\_ a.24.3.2 (-) Cytochrome c' {Rhodobacter capsulatus}

ADTKEVLEAREAYFKSLGGSMKAMTGVAKAFDAEAAKVEAAKLEKILATDVAPLFPAGTSSTDLPGQTEAKAAIWANMDDFGAKGKAMHEAGGAVIAAANAGDGAAFGAALQKLGGTCKACHDDYREED

>d1a7va\_ a.24.3.2 (A:) Cytochrome c' {Rhodopseudomonas palustris}

QTDVIAQRKAILKQMGEATKPIAAMLKGEAKFDQAVVQKSLAAIADDSKKLPALFPADSKTGGDTAALPKIWEDKAKFDDLFAKLAAAATAAQGTIKDEASLKANIGGVLGNCKSCHDDFRAKKS

>d2hmza\_ a.24.4.1 (A:) Hemerythrin {Sipunculid worm (Themiste dyscrita)}

GFPIPDPYCWDISFRTFYTIVDDEHKTLFNGILLLSQADNADHLNELRRCTGKHFLNEQQLMQASQYAGYAEHKKAHDDFIHKLDTWDGDVTYAKNWLVNHIKTIDFKYRGKI

>d1hrb\_\_ a.24.4.1 (-) Hemerythrin {Phascolopsis gouldii}

GFPIPDPYVWDPSFRTFYSIIDDEHKTLFNGIFHLAIDDNADNLGELRRCTGKHFLNQEVLMEASQYQFYDEHKKEHDGFINALDNWKGDVKWAKAWLVNHIKTIDFKYKGKI

>d1i4ya\_ a.24.4.1 (A:) Hemerythrin {Phascolopsis gouldii}

GFPIPDPYVWDPSFRTFYSIIDDEHKTLFNGIFHLAIDDNADNLGELRRCTGKHFLNEQVLMQASQYQFYDEHKKEHETFIHALDNWKGDVKWAKSWLVNHIKTIDFKYKGKI

>d2mhr\_\_ a.24.4.1 (-) Myohemerythin {Sipunculan worm (Themiste zostericola)}

GWEIPEPYVWDESFRVFYEQLDEEHKKIFKGIFDCIRDNSAPNLATLVKVTTNHFTHEEAMMDAAKYSEVVPHKKMHKDFLEKIGGLSAPVDAKNVDYCKEWLVNHIKGTDFKYKGKL

>d1ei7a\_ a.24.5.1 (A:) Tobacco mosaic virus coat protein {Tobacco mosaic virus, vulgare strain}

SYSITTPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSEVWKPSPQVTVRFPDSDFKVYRYNAVLDPLVTALLGAFDTRNRIIEVENQANPTTAETLDATRRVDDATVAIRSAINNLIVELIRGTGSYNRSSFESSSGLVWTSGPAT

>d1vtmp\_ a.24.5.1 (P:) Tobacco mosaic virus coat protein {Tobacco mosaic virus, vulgare strain}

PYTINSPSQFVYLSSAYADPVELINLCTNALGNQFQTQQARTTVQQQFADAWKPSPVMTVRFPASDFYVYRYNSTLDPLITALLNSFDTRNRIIEVNNQPAPNTTEIVNATQRVDDATVAIRASINNLANELVRGTGMFNQAGFETASGLVWTTTPAT

>d1cgme\_ a.24.5.1 (E:) Cucumber green mottle mosaic virus {Cucumber green mottle mosaic virus, strain watermelon}

AYNPITPSKLIAFSASYVPVRTLLNFLVASQGTAFQTQAGRDSFRESLSALPSSVVDINSRFPDAGFYAFLNGPVLRPIFVSLLSSTDTRNRVIEVVDPSNPTTAESLNAVKRTDDASTAARAEIDNLIESISKGFDVYDRASFEAAFSVVWSEATTSKA

>d1rmva\_ a.24.5.1 (A:) Ribgrass mosaic virus {Ribgrass mosaic virus}

SYNITNSNQYQYFAAVWAEPTPMLNQCVSALSQSYQTQAGRDTVRQQFANLLSTIVAPNQRFPDTGFRVYVNSAVIKPLYEALMKSFDTRNRIIETEEESRPSASEVANATQRVDDATVAIRSQIQLLLNELSNGHGYMNRAEFEAILPWTTAPAT

>d3fapb\_ a.24.7.1 (B:) FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) {Human (Homo sapiens)}

VAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQTLKETSFNQAYGRDLMEAQEWCRKYMKSGNVKDLTQAWDLYYHVFRRIS

>g1avo.1 a.24.8.1 (A:,B:) Proteasome activator reg(alpha) {Human (Homo sapiens)}

LRVQPEAQAKVDVFREDLCTKTENLLGSYFPKKISELDAFLKEPALNEANLSNLKAPLDIXAVNCNEKIVVLLQRLKPEIKDVIEQLNLVTTWLQLQIPRIEDGNNFGVAVQEKVFELMTSLHTKLEGFHTQISKYFSERGDAVTKAAKQPHVGDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKNFEKLKKPRG

>d1dova\_ a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}

ESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCSSVKRGNMVRAARALLSAVTRLLILADMADVYKLLVQLKVVEDGILKLRNAGNEQDLGIQYKALKPEVDKLNIMAAKRQQELKDVGNRDQMAAARGILQKNVPILYTASQACLQHPDVAAYKANRDLIYKQLQQAVTGISNAAQAT

>d1dowa\_ a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}

KAHVLAASVEQATENFLEKGDKIAKESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCSSVKRGNMVRAARALLSAVTRLLILADMADVYKLLVQLKVVEDGILKLRNAGNEQDLGIQYKALKPEVDKLNIMAAKRQQELKDVGNRDQMAAARGILQKNVPILYTASQACLQHPDVAAYKANRDLIYKQLQQAVTGISNAAQA

>d1h6ga1 a.24.9.1 (A:377-507) alpha-catenin {Human (Homo sapiens)}

DLRRQLRKAVMDHVSDSFLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACSISNNEEGVKLVRMSASQLEALCPQVINAALALAAKPQSKLAQENMDLFKEQWEKQVRVLTDAVDDITS

>d1h6ga2 a.24.9.1 (A:508-631) alpha-catenin {Human (Homo sapiens)}

IDDFLAVSENHILEDVNKCVIALQEKDVDGLDRTAGAIRGRAARVIHVVTSEMDNYEPGVYTEKVLEATKLLSNTVMPRFTEQVEAAVEALSSDPAQPMDENEFIDASRLVYDGIRDIRKAVLM

>d1h6gb1 a.24.9.1 (B:392-507) alpha-catenin {Human (Homo sapiens)}

DSFLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACSISNNEEGVKLVRMSASQLEALCPQVINAALALAAKPQSKLAQENMDLFKEQWEKQVRVLTDAVDDITS

>d1qkra\_ a.24.9.1 (A:) Vinculin {Chicken (Gallus gallus)}

KDEEFPEQKAGEAINQPMMMAARQLHDEARKWSSKGNDIIAAAKRMALLMAEMSRLVRGGSGNKRALIQCAKDIAKASDEVTRLAKEVAKQCTDKRIRTNLLQVCERIPTISTQLKILSTVKATMLGRTNISDEESEQATEMLVHNAQNLMQSVKETVREAEAASIKIRTDAGFTLRWVRK

>d1k04a\_ a.24.14.1 (A:) FAT domain of focal adhesion kinase {Human (Homo sapiens)}

EISPPPTANLDRSNDKVYENVTGLVKAVIEMSSKIQPAPPEEYVPMVKEVGLALRTLLATVDETIPLLPASTHREIEMAQKLLNSDLGELINKMKLAQQYVMTSLQQEYKKQMLTAAHALAVDAKNLLDVIDQARLKMLGQT

>d1k40a\_ a.24.14.1 (A:) FAT domain of focal adhesion kinase {Mouse (Mus musculus)}

NDKVYENVTGLVKAVIEMSSKIQPAPPEEYVPMVKEVGLALRTLLATVDETIPALPASTHREIEMAQKLLNSDLGELISKMKLAQQYVMTSLQQEYKKQMLTAAHALAVDAKNLLDVIDQARLKML

>d2a0b\_\_ a.24.10.1 (-) Aerobic respiration control sensor protein, ArcB {Escherichia coli}

SKSEALLDIPMLEQYLELVGPKLITDGLAVFEKMMPGYVSVLESNLTAQDKKGIVEEGHKIKGAAGSVGLRHLQQLGQQIQSPDLPAWEDNVGEWIEEMKEEWRHDVEVLKAWVAKAT

>d1c02a\_ a.24.10.2 (A:) Phosphorelay protein ypd1 {Baker's yeast (Saccharomyces cerevisiae)}

STIPSEIINWTILNEIISMDDDDSDFSKGLIIQFIDQAQTTFAQMQRQLDGEKNLTELDNLGHFLKGSSAALGLQRIAWVCERIQNLGRKMQHFFPNKTELVNTLSDKSIINGINIDEDDEEIKIQVDDKDENSIYLILIAKALNQSRLEFKLARIELSKYYNTNL

>d1i5na\_ a.24.10.3 (A:) Chemotaxis protein CheA P1 domain {Salmonella typhimurium}

DISDFYQTFFDEADELLADMEQHLLDLVPESPDAEQLNAIFRAAHSIKGGAGTFGFTILQETTHLMENLLDEARRGEMQLNTDIINLFLETKDIMQEQLDAYKNSEEPDAASFEYICNALRQLALEAK

>d1he1a\_ a.24.11.1 (A:) ExoS toxin {Pseudomonas aeruginosa}

ASSAVVFKQMVLQQALPMTLKGLDKASELATLTPEGLAREHSRLASGDGALRSLSTALAGIRAGSQVEESRIQAGRLLERSIGGIALQQWGTTGGAASQLVLDASPELRREITDQLHQVMSEVALLRQAVESEVS

>d1g4us1 a.24.11.1 (S:167-296) SptP tyrosine phosphatase {Salmonella typhimurium}

SKQPLLDIALKGLKRTLPQLEQMDGNSLRENFQEMASGNGPLRSLMTNLQNLNKIPEAKQLNDYVTTLTNIQVGVARFSQWGTCGGEVERWVDKASTHELTQAVKKIHVIAKELKNVTAELEKIEAGAPM

>d1hy5a\_ a.24.11.1 (A:) YopE {Yersinia pestis}

TSFSDSIKQLAAETLPKYMQQLNSLDAEMLQKNHDQFATGSGPLRGSITQCQGLMQFCGGELQAEASAILNTPVCGIPFSQWGTIGGAASAYVASGVDLTQAANEIKGLAQQMQKLLSLM

>d1f1ma\_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}

PNLTEISKKITESNAVVLAVKEVETLLTSIDELAKAIGKKIKSDVSLDNEADHNGSLMSGAYLISTLITKKISAIKDSGELKAEIEKAKKCSEEFTAKLKGEHTDLGKEGVTDDNAKKAILKTNNDKTKGADELEKLFESVKNLSKAAKEMLTNSVKELTSP

>d1g5za\_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}

PNLTEISKKITESNAVVLAVKEVETLLASIDELATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEELKEKIDTAKQCSTEFTNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNAVKELTSPIVA

>d1ggqa\_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}

GPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLDTENNHNGSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAAKKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKTNGTKTKGAEELGKLFESVEVLSKAAKEMLANSVKELTS

>d1jpna1 a.24.13.1 (A:1-88) Signal sequence recognition protein Ffh {Thermus aquaticus}

MFQQLSARLQEAIGRLRGRGRITEEDLKATLREIRRALMDADVNLEVARDFVERVREEALGKQVLESLTPAEVILATVYEALKEALGG

>d1j8mf1 a.24.13.1 (F:3-86) Signal sequence recognition protein Ffh {Archaeon Acidianus ambivalens}

LLDNLRDTVRKFLTGSSSYDKAVEDFIKELQKSLISADVNVKLVFSLTNKIKERLKNEKPPTYIERREWFIKIVYDELSNLFGG

>d1fts\_1 a.24.13.1 (201-284) Signal recognition particle receptor, FtsY {Escherichia coli}

RSLLKTKENLGSGFISLFRGKKIDDDLFEELEEQLLIADVGVETTRKIITNLTEGASRKQLRDAEALYGLLKEEMGEILAKVDE

>d1jr8a\_ a.24.15.1 (A:) Thiol oxidase Erv2p {Baker's yeast (Saccharomyces cerevisiae)}

DDKVKKEVGRASWKYFHTLLARFPDEPTPEEREKLHTFIGLYAELYPCGECSYHFVKLIEKYPVQTSSRTAAAMWGCHIHNKVNEYLKKDIYDCATILEDYDCGC

>d1h99a1 a.142.1.1 (A:54-168) Transcriptional antiterminator LicT {Bacillus subtilis}

GAMEKFKTLLYDIPIECMEVSEEIISYAKLQLGKKLNDSIYVSLTDHINFAIQRNQKGLDIKNALLWETKRLYKDEFAIGKEALVMVKNKTGVSLPEDEAGFIALHIVNAELNEE

>d1h99a2 a.142.1.1 (A:169-275) Transcriptional antiterminator LicT {Bacillus subtilis}

MPNIINITKVMEEILSIVKYHFKIEFNEESLHYYRFVTDLKFFAQRLFNGTHMESEDDFLLDTVKEKYHRAYECTKKIQTYIEREYEHKLTSDELLYLTIDIERVVK

>d1dvba1 a.25.1.1 (A:1-147) Rubrerythrin, N-terminal domain {Desulfovibrio vulgaris}

MKSLKGSRTEKNILTAFAGESQARNRYNYFGGQAKKDGFVQISDIFAETADQEREHAKRLFKFLEGGDLEIVAAFPAGIIADTHANLIASAAGEHHEYTEMYPSFARIAREEGYEEIARVFASIAVAEEFHEKRFLDFARNIKEGRV

>d1bcfa\_ a.25.1.1 (A:) Bacterioferritin (cytochrome b1) {Escherichia coli}

MKGDTKVINYLNKLLGNELVAINQYFLHARMFKNWGLKRLNDVEYHESIDEMKHADRYIERILFLEGLPNLQDLGKLNIGEDVEEMLRSDLALELDGAKNLREAIGYADSVHDYVSRDMMIEILRDEEGHIDWLETELDLIQKMGLQNYLQAQIREEG

>d1jgca\_ a.25.1.1 (A:) Bacterioferritin (cytochrome b1) {Rhodobacter capsulatus}

MKGDAKVIEFLNAALRSELTAISQYWVHFRLQEDWGLAKMAKKSREESIEEMGHADKIIARILFLEGHPNLQKLDPLRIGEGPRETLECDLAGEHDALKLYREARDYCAEVGDIVSKNIFESLITDEEGHVDFLETQISLYDRLGPQGFALLNAAPMDAA

>d1euma\_ a.25.1.1 (A:) Non-hem ferritin {Escherichia coli, ecFtnA}

LKPEMIEKLNEQMNLELYSSLLYQQMSAWCSYHTFEGAAAFLRRHAQEEMTHMQRLFDYLTDTGNLPRINTVESPFAEYSSLDELFQETYKHEQLITQKINELAHAAMTNQDYPTFNFLQWYVSEQHEEEKLFKSIIDKLSLAGKSGEGLYFIDKELSTLD

>d1krqa\_ a.25.1.1 (A:) Non-hem ferritin {Campylobacter jejuni}

MLSKEVVKLLNEQINKEMYAANLYLSMSSWCYENSLDGAGAFLFAHASEESDHAKKLITYLNETDSHVELQEVKQPEQNFKSLLDVFEKTYEHEQFITKSINTLVEHMLTHKDYSTFNFLQWYVSEQHEEEALFRGIVDKIKLIGEHGNGLYLADQYIKNIALSR

>d1dpsa\_ a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Escherichia coli}

SKATNLLYTRNDVSDSEKKATVELLNRQVIQFIDLSLITKQAHWNMRGANFIAVHEMLDGFRTALIDHLDTMAERAVQLGGVALGTTQVINSKTPLKSYPLDIHNVQDHLKELADRYAIVANDVRKAIGEAKDDDTADILTAASRDLDKFLWFIECNIE

>d1qgha\_ a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Listeria innocua}

VDTKEFLNHQVANLNVFTVKIHQIHWYMRGHNFFTLHEKMDDLYSEFGEQMDEVAERLLAIGGSPFSTLKEFLENASVEEAPYTKPKTMDQLMEDLVGTLELLRDEYKQGIELTDKEGDDVTNDMLIAFKASIDKHIWMFKAFLGKAPLE

>d2fha\_\_ a.25.1.1 (-) (Apo)ferritin {Human (Homo sapiens), H chain}

TSQVRQNYHQDSEAAINRQINLELYASYVYLSMSYYFDRDDVALKNFAKYFLHQSHEEREHAEKLMKLQNQRGGRIFLQDIQKPDCDDWESGLNAMECALHLEKNVNQSLLELHKLATDKNDPHLCDFIETHYLNEQVKAIKELGDHVTNLRKMGAPESGLAEYLFDKHTLG

>d1aew\_\_ a.25.1.1 (-) (Apo)ferritin {Horse (Equus caballus), L chain}

SQIRQNYSTEVEAAVNRLVNLYLRASYTYLSLGFYFDRDDVALEGVCHFFRELAEEKREGAERLLKMQNQRGGRALFQDLQKPSQDEWGTTPDAMKAAIVLEKSLNQALLDLHALGSAQADPHLCDFLESHFLDEEVKLIKKMGDHLTNIQRLVGSQAGLGEYLFERLTL

>d1h96a\_ a.25.1.1 (A:) (Apo)ferritin {Mouse (Mus musculus)}

TSQIRQNYSTEVEAAVNRLVNLHLRASYTYLSLGFFFDRDDVALEGVGHFFRELAEEKREGAERLLEFQNDRGGRALFQDVQKPSQDEWGKTQEAMEAALAMEKNLNQALLDLHALGSARADPHLCDFLESHYLDKEVKLIKKMGNHLTNLRRVAGPQPAQTGAPQGSLGEYLFERLTLK

>d1bg7\_\_ a.25.1.1 (-) (Apo)ferritin {Bullfrog (Rana catesbeiana)}

DSQVRQNFHRDCEAAINRMVNMELYASYTYLSMAFYFDRDDIALHNVAKFFKEQSHEEREHAEKLMKDQNKRGGRIVLQDVQKPERDEWGNTLEAMQAALQLEKTVNQALLDLHKVGSDKVDPHLCDFLETEYPEEQVKSIKQLGDYITNLKRLGLPQNGMGEYLFDKHTMGE

>d1mfra\_ a.25.1.1 (A:) (Apo)ferritin {Bullfrog (Rana catesbeiana)}

VSQVRQNYHSDCEAAVNRMLNLELYASYTYSSMYAFFDRDDVALHNVAEFFKEHSHEEREHAEKFMKYQNKRGGRVVLQDIKKPERDEWGNTLEAMQAALQLEKTVNQALLDLHKLATDKVDPHLCDFLESEYLEEQVKDIKRIGDFITNLKRLGLPENGMGEYLFDKHSV

>d1rcd\_\_ a.25.1.1 (-) (Apo)ferritin {Bullfrog (Rana catesbeiana)}

SQVRQNFHQDCEAGLNRTVNLKFHSSYVYLSMASYFNRDDVALSNFAKFFRERSEEEKEHAEKLIEYQNQRGGRVFLQSVEKPERDDWANGLEALQTALKLQKSVNQALLDLHAVAADKSDPHMTDFLESPYLSESVETIKKLGDHITSLKKLWSSHPGMAEYLFNKHTLG

>d1mtyb\_ a.25.1.2 (B:) Methane monooxygenase hydrolase, beta and alpha subunits {Methylococcus capsulatus}

ERRRGLTDPEMAAVILKALPEAPLDGNNKMGYFVTPRWKRLTEYEALTVYAQPNADWIAGGLDWGDWTQKFHGGRPSWGNETTELRTVDWFKHRDPLRRWHAPYVKDKAEEWRYTDRFLQGYSADGQIRAMNPTWRDEFINRYWGAFLFNEYGLFNAHSQGAREALSDVTRVSLAFWGFDKIDIAQMIQLERGFLAKIVPGFDESTAVPKAEWTNGEVYKSARLAVEGLWQEVFDWNESAFSVHAVYDALFGQFVRREFFQRLAPRFGDNLTPFFINQAQTYFQIAKQGVQDLYYNCLGDDPEFSDYNRTVMRNWTGKWLEPTIAALRDFMGLFAKLPAGTTDKEEITASLYRVVDDWIEDYASRIDFKADRDQIVKAVLAGLK

>d1mtyd\_ a.25.1.2 (D:) Methane monooxygenase hydrolase, beta and alpha subunits {Methylococcus capsulatus}

AANRAPTSVNAQEVHRWLQSFNWDFKNNRTKYATKYKMANETKEQFKLIAKEYARMEAVKDERQFGSLQVALTRLNAGVRVHPKWNETMKVVSNFLEVGEYNAIAATGMLWDSAQAAEQKNGYLAQVLDEIRHTHQCAYVNYYFAKNGQDPAGHNDARRTRTIGPLWKGMKRVFSDGFISGDAVECSLNLQLVGEACFTNPLIVAVTEWAAANGDEITPTVFLSIETDELRHMANGYQTVVSIANDPASAKYLNTDLNNAFWTQQKYFTPVLGMLFEYGSKFKVEPWVKTWDRWVYEDWGGIWIGRLGKYGVESPRSLKDAKQDAYWAHHDLYLLAYALWPTGFFRLALPDQEEMEWFEANYPGWYDHYGKIYEEWRARGCEDPSSGFIPLMWFIENNHPIYIDRVSQVPFCPSLAKGASTLRVHEYNGEMHTFSDQWGERMWLAEPERYECQNIFEQYEGRELSEVIAELHGLRSDGKTLIAQPHVRGDKLWTLDDIKRLNCVFKNPVKAF

>d1mhyb\_ a.25.1.2 (B:) Methane monooxygenase hydrolase, beta and alpha subunits {Methylosinus trichosporium}

KRGLTDPERAAIIAAAVPDHALDTQRKYHYFIQPRWKPLSEYEQLSCYAQPNPDWIAGGLDWGDWTQKFHGGRPSWGNESTELRTTDWYRHRDPARRWHHPYVKDKSEEARYTQRFLAAYSSEGSIRTIDPYWRDEILNKYFGALLYSEYGLFNAHSSVGRDCLSDTIRQTAVFAALDKVDNAQMIQMERLFIAKLVPGFDASTDVPKKIWTTDPIYSGARATVQEIWQGVQDWNEILWAGHAVYDATFGQFARREFFQRLATVYGDTLTPFFTAQSQTYFQTTRGAIDDLFVYCLANDSEFGAHNRTFLNAWTEHYLASSVAALKDFVGLYAKVEKVAGATDSAGVSEALQRVFGDWKIDYADKIGFRVDVDQKVDAVLAGY

>d1mhyd\_ a.25.1.2 (D:) Methane monooxygenase hydrolase, beta and alpha subunits {Methylosinus trichosporium}

NRAPVGVEPQEVHKWLQSFNWDFKENRTKYPTKYHMANETKEQFKVIAKEYARMEAAKDERQFGTLLDGLTRLGAGNKVHPRWGETMKVISNFLEVGEYNAIAASAMLWDSATAAEQKNGYLAQVLDEIRHTHQCAFINHYYSKHYHDPAGHNDARRTRAIGPLWKGMKRVFADGFISGDAVECSVNLQLVGEACFTNPLIVAVTEWASANGDEITPTVFLSVETDELRHMANGYQTVVSIANDPASAKFLNTDLNNAFWTQQKYFTPVLGYLFEYGSKFKVEPWVKTWNRWVSEDWGGIWIGRLGKYGVESPRSLRDAKRDAYWAHHDLALAAYAMWPLGFARLALPDEEDQAWFEANYPGWADHYGKIFNEWKKLGYEDPKSGFIPYQWLLANGHDVYIDRVSQVPFIPSLAKGTGSLRVHEFNGKKHSLTDDWGERQWLIEPERYECHNVFEQYEGRELSEVIAEGHGVRSDGKTLIAQPHTRGDNLWTLEDIKRAGCVFPDPLAKF

>d1jqca\_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Escherichia coli}

AYTTFSQTKNDQLKEPMFFGQPVNVARYDQQKYDIFEKLIEKQLSFFWRPEEVDVSRDRIDYQALPEHEKHIFISNLKYQTLLDSIQGRSPNVALLPLISIPELETWVETWAFSETIHSRSYTHIIRNIVNDPSVVFDDIVTNEQIQKRAEGISSYYDELIEMTSYWHLLGEGTHTVNGKTVTVSLRELKKKLYLCLMSVNALEAIRFYVSFACSFAFAERELMEGNAKIIRLIARDEALHLTGTQHMLNLLRSGADDPEMAEIAEECKQECYDLFVQAAQQEKDWADYLFRDGSMIGLNKDILCQYVEYITNIRMQAVGLDLPFQTRSNPIPWINTWLV

>d1r2fa\_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Salmonella typhimurium}

ISAINWNKIQDDKDLEVWNRLTSNFWLPEKVPLSNDIPAWQTLSAAEQQLTIRVFTGLTLLDTIQNIAGAPSLMADAITPHEEAVLSNISFMEAVHARSYSSIFSTLCQTKEVDAAYAWSEENPPLQRKAQIILAHYVSDEPLKKKIASVFLESFLFYSGFWLPMYFSSRGKLTNTADLIRLIIRDEAVHGYYIGYKYQIALQKLSAIEREELKLFALDLLMELYDNEIRYTEALYAETGWVNDVKAFLCYNANKALMNLGYEALFPPEMADVNPAILAALSP

>d1kgna\_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Corynebacterium ammoniagenes}

SNEYDEYIANHTDPVKAINWNVIPDEKDLEVWDRLTGNFWLPEKIPVSNDIQSWNKMTPQEQLATMRVFTGLTLLDTIQGTVGAISLLPDAETMHEEAVYTNIAFMESVHAKSYSNIFMTLASTPQINEAFRWSEENENLQRKAKIIMSYYNGDDPLKKKVASTLLESFLFYSGFYLPMYLSSRAKLTNTADIIRLIIRDESVHGYYIGYKYQQGVKKLSEAEQEEYKAYTFDLMYDLYENEIEYTEDIYDDLGWTEDVKRFLRYNANKALNNLGYEGLFPTDETKVSPAILSSLS

>d1xsm\_\_ a.25.1.2 (-) Ribonucleotide reductase R2 {Mouse (Mus musculus)}

NPSVEDEPLLRENPRRFVVFPIEYHDIWQMYKKAEASFWTAEEVDLSKDIQHWEALKPDERHFISHVLAFFAASDGIVNENLVERFSQEVQVTEARCFYGFQIAMENIHSEMYSLLIDTYIKDPKEREYLFNAIETMPCVKKKADWALRWIGDKEATYGERVVAFAAVEGIFFSGSFASIFWLKKRGLMPGLTFSNELISRDEGLHCDFACLMFKHLVHKPAEQRVREIITNAVRIEQEFLTEALPVKLIGMNCTLMKQYIEFVADRLMLELGFNKIFRVENPFDFME

>d1jk0a\_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Baker's yeast (Saccharomyces cerevisiae)}

LNKELETLREENRVKSDMLKEKLSKDAENHKAYLKSHQVHRHKLKEMEKEEPLLNEDKERTVLFPIKYHEIWQAYKRAEASFWTAEEIDLSKDIHDWNNRMNENERFFISRVLAFFAASDGIVNENLVENFSTEVQIPEAKSFYGFQIMIENIHSETYSLLIDTYIKDPKESEFLFNAIHTIPEIGEKAEWALRWIQDADALFGERLVAFASIEGVFFSGSFASIFWLKKRGMMPGLTFSNELICRDEGLHTDFACLLFAHLKNKPDPAIVEKIVTEAVEIEQRYFLDALPVALLGMNADLMNQYVEFVADRLLVAFGNKKYYKVENPFDFMEN

>d1jk0b\_ a.25.1.2 (B:) Ribonucleotide reductase R2 {Baker's yeast (Saccharomyces cerevisiae)}

FQKERHDMKEAEKDEILLMENSRRFVMFPIKYHEIWAAYKKVEASFWTAEEIELAKDTEDFQKLTDDQKTYIGNLLALSISSDNLVNKYLIENFSAQLQNPEGKSFYGFQIMMENIYSEVYSMMVDAFFKDPKNIPLFKEIANLPEVKHKAAFIERWISNDDSLYAERLVAFAAKEGIFQAGNYASMFWLTDKKIMPGLAMANRNICRDRGAYTDFSCLLFAHLRTKPNPKIIEKIITEAVEIEKEYYSNSLPVEKFGMDLKSIHTYIEFVADGLLQGFGNEKYY

>d1afra\_ a.25.1.2 (A:) delta 9-stearoyl-acyl carrier protein desaturase {Castor bean (Ricinus communis)}

MPPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKCWQPQDFLPDPASDGFDEQVRELRERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDHFSAVAQRLGVYTAKDYADILEFLVGRWKVDKLTGLSAEGQKAQDYVCRLPPRIRRLEERAQGRAKEAPTMPFSWIFDRQVKL

>d1rhga\_ a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF) {Human (Homo sapiens)}

LPQSFLLKCLEQVRKIQGDGAALQEKLCATYKLCHPEELVLLGHSLGIPWAPLSSCPSQALQLAGCLSQLHSGLFLYQGLLQALEGISPELGPTLDTLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLRHLA

>d1bgc\_\_ a.26.1.1 (-) Granulocyte-colony stimulating factor (G-CSF) {Cow (Bos taurus)}

SLPQSFLLKCLEQVRKIQADGAELQERLCAAHKLCHPEELMLLRHSLGIPQAPLSSCSSQSLQLRGCLNQLHGGLFLYQGLLQALAGISPELAPTLDTLQLDVTDFATNIWLQMEDLGAAPAVQPTQGAMPTFTSAFQRRAGGVLVASQLHRFLELAYRGLRYLA

>d1bgea\_ a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF) {Dog (Canis familiaris)}

PLPQSFLLKCLEQMRKVQADGTALQETLCATHQLCHPEELVLLGHALGIPQPPLSSCSSQALQLMGCLRQLHSGLFLYQGLLQALAGISPELAPTLDTLQLDTTDFAINIWQQMEDLGMAPAVPPTQGTMPAFTSAFQRRAGGVLVASNLQSFLELAYRALRHFAK

>d1alu\_\_ a.26.1.1 (-) Interleukin-6 {Human (Homo sapiens)}

LTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRALRQM

>d1i1rb\_ a.26.1.1 (B:) Interleukin-6 {Human herpesvirus 8, Kaposi's sarcoma herpes-virus}

EFEKDLLIQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNETSCLKKLADGFFEFEVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVLDSIP

>d1a7m\_\_ a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (Mus musculus)}

SPLPITPVNATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEPFPNNLDKLCGPNVTDFPPFHANGTEKAKLVELYRMVAYLSASLTNITRDQKVLNPSAVSLHSKLNATIDVMRGLLSNVLCRLCNKYRVGHVDVPPVPDHSDKEVFQKKKLGCQLLGTYKQVISVVVQAF

>d1lki\_\_ a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (Mus musculus)}

NATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEPFPNNVEKLCAPNMTDFPSFHGNGTEKTKLVELYRMVAYLSASLTNITRDQKVLNPTAVSLQVKLNATIDVMRGLLSNVLCRLCNKYRVGHVDVPPVPDHSDKEAFQRKKLGCQLLGTYKQVISVVVQAF

>d1emra\_ a.26.1.1 (A:) Leukemia inhibitory factor (LIF) {Human (Homo sapiens)}

LMNQIRSQLAQLNGSANALFILYYTAQGEPFPNNLEKLCGPNVTDFPPFHANGTEKAKLVELYRIVVYLGTSLGNITRDQKILNPSALSLHSKLNATADILRGLLSNVLCRLCSKYHVGHVDVTYGPDTSGKDVFQKKKLGCQLLGKYKQVISVLAQAF

>d1a22a\_ a.26.1.1 (A:) Growth hormone, somatotropin {Human (Homo sapiens)}

FPTIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEERIQTLMGRLEGQIFKQTYSKFDTDALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF

>d1axia\_ a.26.1.1 (A:) Growth hormone, somatotropin {Human (Homo sapiens)}

TIPLSRLFDNAMLRAHRLHQLAFDTYQEFEEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEERIQTLMGRLTDGSPRTGQIFKQTYSKFDTNSHNDDALLKNYGLLYCFRRDMTYVATYLRIVQCRSVEGSCGF

>d1hgu\_\_ a.26.1.1 (-) Growth hormone, somatotropin {Human (Homo sapiens)}

PTIPLSRLFQNAMLRAHRLHQLAFDTYEEFEEAYIPKEQKYSFLQAPQASLCFSESIPTPSNREQAQQKSNLQLLRISLLLIQSWLEPVGFLRSVFANSLVYGASDSDVYDLLKDLEEGIQTLMGRLEDGSPRTGQAFKQTYAKFDANSHNDDALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCG

>d1huw\_\_ a.26.1.1 (-) Growth hormone, somatotropin {Human (Homo sapiens)}

FPTIPLSRLADNAWLRADRLNQLAFDTYQEFEEAYIPKEQIHSFWWNPQTSLCPSESIPTPSNKEETQQKSNLELLRISLLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEALLKNYGLLYCFNKDMSKVSTYLRTVQCRSVEGSCGF

>d1f6fa\_ a.26.1.1 (A:) Placental lactogen {Sheep (Ovis aries)}

AQHPPYCRNQPGKCQIPLQSLFDRATTVANYNSKLAGEMVNRFDEQYGQGINSESKVINCHTSSITTPNSKAEAINTEDKILFKLVISLLHSWDEPLHHAVTELANSKGTSPALLTKAQEIKEKAKVLVDGVEVIQKRIHPGEKNEPYPVWSEQSSLTSQDENVRRVAFYRLFHCLHRDSSKIYTYLRILKCRLTSC

>d1cnt1\_ a.26.1.1 (1:) Ciliary neurotrophic factor (CNTF) {Human (Homo sapiens)}

PHRRDLCSRSIWLARKIRSDLTALTESYVKHQGLNKNINLDSADGMPVASTDQWSELTEAERLQENLQAYRTFHVLLARLLEDQQVHFTPTEGDFHQAIHTLLLQVAAFAYQIEELMILLEYKIPRNEADGMPINVGDGGLFEKKLWGLKVLQELSQWTVRSIHDLRFISSHQTGIP

>d1ax8\_\_ a.26.1.1 (-) Leptin (obesity protein) {Human (Homo sapiens)}

IQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPEASGLETLDSLGGVLEASGYSTEVVALSRLQGSLQDMLWQLDLSPGC

>d1evsa\_ a.26.1.1 (A:) Oncostatin M {Human (Homo sapiens)}

GSCSKEYRVLLGQLQKQTDLMQDTSRLLDPYIRIQGLDVPKLREHCRERPGAFPSEETLRGLGRRGFLQTLNATLGCVLHRLADLEQRLPKAQDLERSGLNIEDLEKLQMARPNILGLRNNIYCMAQLLDNSDTAEPTKAGRGASQPPTPTPASDAFQRKLEGCRFLHGYHRFMHSVGRVFSKW

>d1f45b\_ a.26.1.1 (B:) Heterodimeric interleukin-12 alpha chain {Human (Homo sapiens)}

QNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS

>d1eera\_ a.26.1.2 (A:) Erythropoietin {Human (Homo sapiens)}

APPRLICDSRVLERYLLEAKEAEKITTGCAEHCSLNEKITVPDTKVNFYAWKRMEVGQQAVEVWQGLALLSEAVLRGQALLVKSSQPWEPLQLHVDKAVSGLRSLTTLLRALGAQKEAISNSDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR

>d2gmfa\_ a.26.1.2 (A:) Granulocyte-macrophage colony-stimulating factor (GM-CSF) {Human (Homo sapiens)}

RSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFDCWEP

>d1hzia\_ a.26.1.2 (A:) Interleukin-4 (IL-4) {Human (Homo sapiens)}

HKCDITLQAIIKTLNSLTEQKTLCTELTVTDIFAASKNTTEKETFCRAATVLRQFYSHHEKDTRCLGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTIMREKYSKCSS

>d1hula\_ a.26.1.2 (A:) Interleukin-5 {Human (Homo sapiens)}

IPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEWI

>d1hmca\_ a.26.1.2 (A:) Macrophage colony-stimulating factor (M-CSF) {Human (Homo sapiens)}

SEYCSHMIGSGHLQSLQRLIDSQMETSCQITFEFVDQEQLKDPVCYLKKAFLLVQDIMEDTMRFRDNTPNAIAIVQLQELSLRLKSCFTKDYEEHDKACVRTFYETPLQLLEKVKNVFNETKNLLDKDWNIFSKNCNNSFAECSSQGH

>d1etea\_ a.26.1.2 (A:) Flt3 ligand {Human (Homo sapiens)}

TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDDELCGGLWRLVLAQRWMERLKTVAGSKMQGLLERVNTEIHFVTKCAFQPPPSCLRFVQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP

>d1scfa\_ a.26.1.2 (A:) Stem cell factor, SCF {Human (Homo sapiens)}

NVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVS

>d1scfc\_ a.26.1.2 (C:) Stem cell factor, SCF {Human (Homo sapiens)}

NVKDVTKLVANLPKDYMITLKYVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFNRSIDAF

>d3inkc\_ a.26.1.2 (C:) Interleukin-2 (IL-2) {Human (Homo sapiens)}

STKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

>d1jli\_\_ a.26.1.2 (-) Interleukin-3 (IL-3) {Human (Homo sapiens)}

ANCSIMIDEIIHHLKRPPNPLLDPNNLNSEDMDILMERNLRTPNLLAFVRAVKHLENASAIESILKNLLPCLPLATAAPTRHPIHIKDGDWNEFRRKLTFYLKTLENAQAQQ

>d1ga3a\_ a.26.1.2 (A:) Interleukin-13 (IL-13) {Human (Homo sapiens)}

GGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEKTQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKKLFREGRFN

>d2ilk\_\_ a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory factor, CSIF) {Human (Homo sapiens)}

TQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQLDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAENQDPDIKAHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQVKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRN

>d1vlk\_\_ a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory factor, CSIF) {Epstein-Barr virus}

CDNFPQMLRDLRDAFSRVKTFFQTKDEVDNLLLKESLLEDFKGYLGCQALSEMIQFYLEEVMPQAENQDPEAKDHVNSLGENLKTLRLRLRRCHRFLPCENKSKAVEQIKNAFNKLQEKGIYKAMSEFDIFINYIEAYMTIK

>d1au1a\_ a.26.1.3 (A:) Interferon-beta {Human (Homo sapiens)}

MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN

>d1rmi\_\_ a.26.1.3 (-) Interferon-beta {Mouse (Mus musculus)}

INYKQLQLQERTNIRKCQELLEQLNGKINLTYRADFKIPMEMTEKMQKSYTAFAIQEMLQNVFLVFRNNFSSTGWNETIVVRLLDELHQQTVFLKTVLEEKQEERLTWEMSSTALHLKSYYWRVQRYLKLMKYNSYAWMVVRAEIFRNFLIIRRLTRNFQ

>d1rh2a\_ a.26.1.3 (A:) Interferon-alpha 2b {Human (Homo sapiens)}

THSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDETLLDKFYTELYQQLNDLEACVIQGVGVTETPLMNEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQE

>d1b5l\_\_ a.26.1.3 (-) Interferon-tau {Sheep (Ovis aries)}

CYLSRKLMLDARENLKLLDRMNRLSPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLYEMLQQSFNLFYTEHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMGEEDSELGNMDPIVTVKKYFQGIYDYLQEKGYSDCAWEIVRVEMMRALTVSTTLQKRLTK

>d1d9ca\_ a.26.1.3 (A:) Interferon-gamma {Cow (Bos taurus)}

QGQFFREIENLKEYFNASSPDVAKGGPLFSEILKNWKDESDKKIIQSQIVSFYFKLFENLKDNQVIQRSMDIIKQDMFQKFLNGSSEKLEDFKKLIQIPVDDLQIQRKAINELIKVMNDLS

>d1fyha1 a.26.1.3 (A:0-124) Interferon-gamma {Human (Homo sapiens)}

MQDPYVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIDELIQVMAELGANV

>d1fyha2 a.26.1.3 (A:201-324) Interferon-gamma {Human (Homo sapiens)}

SGEFVKEAENLKKYFNAGHSDVADNGTLFLGILKNWKEESDRKIMQSQIVSFYFKLFKNFKDDQSIQKSVETIKEDMNVKFFNSNKKKRDDFEKLTNYSVTDLNVQRKAIHELIQVMAELSPAA

>d2rig\_\_ a.26.1.3 (-) Interferon-gamma {Rabbit (Oryctolagus cuniculus)}

QDTLTRETEHLKAYLKANTSDVANGGPLFLNILRNWKEESDNKIIQSQIVSFYFKLFDNLKDHEVIKKSMESIKEDIFVKFFNSNLTKMDDFQNLTRISVDDRLVQRKAVSELSNVLNF

>d1a8h\_1 a.27.1.1 (349-500) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}

LADDLGNLVQRTRAMLFRFAEGRIPEPVAGEELAEGTGLAGRLRPLVRELKFHVALEEAMAYVKALNRYINEKKPWELFKKEPEEARAVLYRVVEGLRIASILLTPAMPDKMAELRRALGLKEEVRLEEAERWGLAEPRPIPEEAPVLFPKK

>d1f4la1 a.27.1.1 (A:389-548) Methionyl-tRNA synthetase (MetRS) {Escherichia coli}

VVNLASRNAGFINKRFDGVLASELADPQLYKTFTDAAEVIGEAWESREFGKAVREIMALADLANRYVDEQAPWVVAKQEGRDADLQAICSMGINLFRVLMTYLKPVLPKLTERAEAFLNTELTWDGIQQPLLGHKVNPFKALYNRIDMRQVEALVEASKE

>d1ile\_1 a.27.1.1 (642-821) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}

YFLTLWNVYSFFVTYANLDRPDLKNPPPPEKRPEMDRWLLARMQDLIQRVTEALEAYDPTTSARALRDFVVEDLSQWYVRRNRRRFWKNEDALDREAAYATLYEALVLVATLAAPFTPFLAEVLWQNLVRSVRLEAKESVHLADWPEADPALADEALVAQMRAVLKVVDLARAARAKSGV

>d1ffya1 a.27.1.1 (A:645-917) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

YRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNIYQEVQNFINVELSNFYLDYGKDILYIEQRDSHIRRSMQTVLYQILVDMTKLLAPILVHTAEEVWSHTPHVKEESVHLADMPKVVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNASEFLTSFDALHQLFIVSQVKVVDKLDDQATAYEHGDIVIEHADGEKCERCWNYSEDLGAVDELTHLCPRCQQVVKSLV

>d1qu3a1 a.27.1.1 (A:645-881) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

YRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNIYQEVQNFINVELSNFYLDYGKDILYIEQRDSHIRRSMQTVLYQILVDMTKLLAPILVHTAEEVWSHTPHVKEESVHLADMPKVVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNASEFLTSFDALHQLFIVSQVKVVDKLDDQATAYEHGDIVIEHA

>d1gaxa1 a.27.1.1 (A:579-862) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}

ANKLYNAARFVLLSREGFQAKEDTPTLADRFMRSRLSRGVEEITALYEALDLAQAAREVYELVWSEFCDWYLEAAKPALKAGNAHTLRTLEEVLAVLLKLLHPMMPFLTSELYQALTGKEELALEAWPEPGGRDEEAERAFEALKQAVTAVRALKAEAGLPPAQEVRVYLEGETAPVEENLEVFRFLSRADLLPERPAKALVKAMPRVTARMPLEGLLDVEEWRRRQEKRLKELLALAERSQRKLASPGFREKAPKEVVEAEEARLKENLEQAERIREALSQIG

>d1f7ua1 a.27.1.1 (A:484-607) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast (Saccharomyces cerevisiae)}

DTGPYLQYAHSRLRSVERNASGITQEKWINADFSLLKEPAAKLLIRLLGQYPDVLRNAIKTHEPTTVVTYLFKLTHQVSSCYDVLWVAGQTEELATARLALYGAARQVLYNGMRLLGLTPVERM

>d1iq0a1 a.27.1.1 (A:467-592) Arginyl-tRNA synthetase (ArgRS) {Thermus thermophilus}

GDTGPYVQYAHARAHSILRKAGEWGAPDLSQATPYERALALDLLDFEEAVLEAAEERTPHVLAQYLLDLAASWNAYYNARENGQPATPVLTAPEGLRELRLSLVQSLQRTLATGLDLLGIPAPEVM

>d1acp\_\_ a.28.1.1 (-) Acyl carrier protein {Escherichia coli}

STIEERVKKIIGEQLGVKQEEVTNNASFVEDLGADSLDTVELVMALEEEFDTEIPDEEAEKITTVQAAIDYINGHQA

>d1f80d\_ a.28.1.1 (D:) Acyl carrier protein {Bacillis subtilis}

SADTLERVTKIIVDRLGVDEADVKLEASFKEDLGADXLDVVELVMELEDEFDMEISDEDAEKIATVGDAVNYIQ

>d1af8\_\_ a.28.1.1 (-) Actinorhodin polyketide synthase acyl carrier protein, ACT ACP {Streptomyces coelicolor, A3(2)}

MATLLTTDDLRRALVECAGETDGTDLSGDFLDLRFEDIGYDSLALMETAARLESRYGVSIPDDVAGRVDTPRELLDLINGALAEAA

>d1dnya\_ a.28.1.2 (A:) Peptidyl carrier protein (PCP), thioester domain {Bacillus brevis}

YVAPTNAVESKLAEIWERVLGVSGIGILDNFFQIGGHSLKAMAVAAQVHREYQVELPLKVLFAQPTIKALAQYVAT

>d1dv5a\_ a.28.1.3 (A:) apo-D-alanyl carrier protein {Lactobacillus casei}

ADEAIKNGVLDILADLTGSDDVKKNLDLNLFETGLLDSMGTVQLLLELQSQFGVDAPVSEFDRKEWDTPNKIIAKVEQAQ

>d1unka\_ a.28.2.1 (A:) ImmE7 protein (Im7) {Escherichia coli}

MELKNSISDYTEAEFVQLLKEIEKENVAATDDVLDVLLEHFVKITEHPDGTDLIYYPSDNRDDSPEGIVKEIKEWRAANGKPGFKQG

>d1imy\_\_ a.28.2.1 (-) ImmE8 (Im8) {Escherichia coli}

MELKNSISDYTETEFKKIIEDIINCEGDEKKQDDNLEHFISVTEHPSGSDLIYYPEGNNDGSPEAVIKEIKEWRAANGKSGFKQG

>d1emva\_ a.28.2.1 (A:) ImmE9 protein (Im9) {Escherichia coli}

LKHSISDYTEAEFLQLVTTICNADTSSEEELVKLVTHFEEMTEHPSGSDLIYYPKEGDDDSPSGIVNTVKQWRAANGKSGFKQ

>d2eiaa1 a.28.3.1 (A:148-222) EIAV capsid protein p26 {Equine infectious anemia virus}

PKAQNIRQGAKEPYPEFVDRLLSQIKSEGHPQEISKFLTDTLTIQNANEECRNAMRHLRPEDTLEEKMYACRDIG

>d1qrjb1 a.28.3.1 (B:131-214) HTLV-I capsid protein {Human T-cell leukemia virus type 1}

PSWASILQGLEEPYHAFVERLNIALDNGLPEGTPKDPILRSLAYSNANKECQKLLQARGHTNSPLGDMLRACQTWTPKDKTKVL

>d1a8o\_\_ a.28.3.1 (-) HIV capsid protein, dimerisation domain {Human immunodeficiency virus type 1}

MDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQNANPDCKTILKALGPGATLEEMMTACQG

>d1d1da1 a.28.3.1 (A:151-230) RSV capsid protein {Rous sarcoma virus}

GPWADITQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRAAPSTLTTPGEIIKYVLDRQKIAP

>d1eoqa\_ a.28.3.1 (A:) RSV capsid protein {Rous sarcoma virus}

MDIMQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRTAPSTLTTPGEIIKYVLDRQKTAP

>d1e6ia\_ a.29.2.1 (A:) GCN5 {Baker's yeast (Saccharomyces cerevisiae)}

RGPHDAAIQNILTELQNHAAAWPFLQPVNKEEVPDYYDFIKEPMDLSTMEIKLESNKYQKMEDFIYDARLVFNNCRMYNGENTSYYKYANRLEKFFNNKVKEIPEYSHLID

>d1f68a\_ a.29.2.1 (A:) GCN5 {Human (Homo sapiens)}

GDQLYTTLKNLLAQIKSHPSAWPFMEPVKKSEAPDYYEVIRFPIDLKTMTERLRSRYYVTRKLFVADLQRVIANCREYNPPDSEYCRCASALEKFFYFKLKEG

>d1b91a\_ a.29.2.1 (A:) P300/CAF histone acetyltransferase bromodomain {Human (Homo sapiens)}

GSHMSKEPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYYEVIRSPMDLKTMSERLKNRYYVSKKLFMADLQRVFTNCKEYNAPESEYYKCANILEKFFFSKIKEAGLIDK

>d1eqfa1 a.29.2.1 (A:1359-1497) TAFII250 double bromodomain module {Human (Homo sapiens)}

GTTVHCDYLNRPHKSIHRRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVVKDYYKIITRPMDLQTLRENVRKRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINP

>d1eqfa2 a.29.2.1 (A:1498-1625) TAFII250 double bromodomain module {Human (Homo sapiens)}

LLDDDDQVAFSFILDNIVTQKMMAVPDSWPFHHPVNKKFVPDYYKVIVNPMDLETIRKNISKHKYQSRESFLDDVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAKEAA

>d1gm5a1 a.29.4.1 (A:7-105) RecG, N-terminal domain {Thermotoga maritima}

FTSSLFLWGEALPTLLEEFLNEVEKMLKNQVNTRRIHQLLKELDDPLLENKDLEEKLQAFLDYVKEIPNLPEARKRYRIQKSLEMIEKLRSWFLIDYLE

>d1gkza1 a.29.5.1 (A:38-185) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK) {Rat (Rattus norvegicus)}

VRLTPTMMLYSGRSQDGSHLLKSGRYLQQELPVRIAHRIKGFRSLPFIIGCNPTILHVHELYIRAFQKLTDFPPIKDQADEAQYCQLVRQLLDDHKDVVTLLAEGLRESRKHIEDEKLVRYFLDKTLTSRLGIRMLATHHLALHEDKP

>d1jm6a1 a.29.5.1 (A:1003-1169) Pyruvate dehydrogenase kinase {Rat (Rattus norvegicus), isozyme 2}

ASLAGAPKYIEHFSKFSPSPLSMKQFLDFGSSNACEKTSFTFLRQELPVRLANIMKEINLLPDRVLSTPSVQLVQSWYVQSLLDIMEFLDKDPEDHRTLSQFTDALVTIRNRHNDVVPTMAQGVLEYKDTYGDDPVSNQNIQYFLDRFYLSRISIRMLINQHTLIFD

>d1buca1 a.29.3.1 (A:233-383) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}

GKGFKIAMMTLDGGRIGVAAQALGIAEAALADAVEYSKQRVQFGKPLCKFQSISFKLADMKMQIEAARNLVYKAACKKQEGKPFTVDAAIAKRVASDVAMRVTTEAVQIFGGYGYSEEYPVARHMRDAKITQIYEGTNEVQLMVTGGALLR

>d1jqia1 a.29.3.1 (A:235-387) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus)}

MGFKIAMQTLDMGRIGIASQALGIAQASLDCAVKYAENRHAFGAPLTKLQNIQFKLADMALALESARLLTWRAAMLKDNKKPFTKESAMAKLAASEAATAISHQAIQILGGMGYVTEMPAERYYRDARITEIYEGTSEIQRLVIAGHLLRSYR

>d3mdda1 a.29.3.1 (A:242-395) Medium chain acyl-CoA dehydrogenase {Pig (Sus scrofa)}

GAGFKIAMGTFDKTRPPVAAGAVGLAQRALDEATKYALERKTFGKLLAEHQGISFLLADMAMKVELARLSYQRAAWEIDSGRRNTYYASIAKAYAADIANQLATDAVQVFGGNGFNTEYPVEKLMRDAKIYQIYEGTAQIQRIIIAREHIGRYK

>d1egda1 a.29.3.1 (A:242-396) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens)}

GAGFKVAMGAFDKERPVVAAGAVGLAQRALDEATKYALERKTFGKLLVEHQAISFMLAEMAMKVELARMSYQRAAWEVDSGRRNTYYASIAKAFAGDIANQLATDAVQILGGNGFNTEYPVEKLMRDAKIYQIYGGTSQIQRLIVAREHIDKYKN

>d1ivha1 a.29.3.1 (A:242-392) Isovaleryl-CoA dehydrogenase {Human (Homo sapiens)}

KGVYVLMSGLDLERLVLAGGPLGLMQAVLDHTIPYLHVREAFGQKIGHFQLMQGKMADMYTRLMACRQYVYNVAKACDEGHCTAKDCAGVILYSAECATQVALDGIQCFGGNGYINDFPMGRFLRDAKLYEIGAGTSEVRRLVIGRAFNAD

>d1b6q\_\_ a.30.1.1 (-) ROP protein {Escherichia coli}

MTKQEKTALNMARFIRSQTLTLLEKLNELDPDEQADICESLHDHADELYRSCLARF

>d1f4na\_ a.30.1.1 (A:) ROP protein {Escherichia coli}

GTKQEKTILNMARFIRSQALTILEKANELDADEIADIAESIHDHADEIYRSALARFGDDG

>d1f4nb\_ a.30.1.1 (B:) ROP protein {Escherichia coli}

EKTILNMARFIRSQALTILEKANELDADEIADIAESIHDHADEIYRSALAR

>d1gtoa\_ a.30.1.1 (A:) ROP protein {Escherichia coli}

GTKQEKTALNMARFIRSQTLTLLEKLNELGADEQADICESLHDHADELYRSCLARFGDDGEN

>d1nkd\_\_ a.30.1.1 (-) ROP protein {Escherichia coli}

MTKQEKTALNMARFIRSQTLTLLEKLNELADAADEQADICESLHDHADELYRSCLARFG

>d1joya\_ a.30.2.1 (A:) EnvZ histidine kinase {Escherichia coli}

MAAGVKQLADDRTLLMAGVSHDLRTPLTRIRLATEMMSEQDGYLAESINKDIEECNAIIEQFIDYLR

>d1b3qa1 a.30.2.1 (A:293-354) Histidine kinase CheA {Thermotoga maritima}

SQTVRVDIEKLDNLMDLMGELVIARSRILETLKKYNIKELDESLSHLSRITLDLQNVVMKIR

>d1r2aa\_ a.31.1.1 (A:) Dimerization-anchoring domain of cAMP-dependent type II PK regulatory subunit {Mouse (Mus musculus)}

HMGHIQIPPGLTELLQGYTVEVLRQQPPDLVDFAVEYFTRLREARR

>d1ytfb1 a.32.1.1 (B:) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

SNAEASRVYEIIVESVVNEVREDFENAGIDEQTLQDLKNIWQKKLT

>d1ytfd1 a.32.1.1 (D:5-54) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

GYYELYRRSTIGNSLVDALDTLISDGRIEASLAMRVLETFDKVVAETLKD

>d1ecia\_ a.33.1.1 (A:) Ectatomin, A & B chains {Ant (Ectatomma tuberculatum), venom}

GVIPKKIWETVCPTVEPWAKKCSGDIATYIKRECGKL

>d1ecib\_ a.33.1.1 (B:) Ectatomin, A & B chains {Ant (Ectatomma tuberculatum), venom}

WSTIVKLTICPTLKSMAKKCEGSIATMIKKKCDK

>d1b0na1 a.34.1.1 (A:74-108) SinR repressor (dimerisation domain)-SinI anti-repressor complex {Bacillus subtilis}

LDSEWEKLVRDAMTSGVSKKQFREFLDYQKWRKSQ

>d1b0nb1 a.34.1.1 (B:) SinR repressor (dimerisation domain)-SinI anti-repressor complex {Bacillus subtilis}

FELDQEWVELMVEAKEANISPEEIRKYLLLN

>d1f93f\_ a.34.1.1 (F:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}

LSQLQTELLAALLESGLSKEALIQALG

>d1g2ya\_ a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}

MVSKLSQLQTEMLAALLESGLSKEALIQALG

>d1g2za\_ a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}

MVSKLSQLQTELMAALLESGLSKEALIQALGE

>d1g39a\_ a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}

MVSKLSQLQTELLAALLESGLSKEALIQ

>d1jb6b\_ a.34.1.1 (B:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}

SKLSQLQTELMAALLESGLSKEALIQAL

>d1e3oc2 a.35.1.1 (C:1-75) Oct-1 {Human (Homo sapiens)}

EEPSDLEELEQFAKTFKQRRIKLGFTQGDVGLAMGKLYGNDFSQTTISRFEALNLSFKNMSKLKPLLEKWLNDAE

>d1au7a2 a.35.1.1 (A:5-76) Pit-1 {Rat (Rattus norvegicus)}

GMRALEQFANEFKVRRIKLGYTQTNVGEALAAVHGSEFSQTTICRFENLQLSFKNACKLKAILSKWLEEAEQ

>d1llib\_ a.35.1.2 (B:) lambda C1 repressor, DNA-binding domain {Bacteriophage lambda (Escherichia coli)}

STKKKPLTQEQLEDARRLKAIYEKKKNELGLSQESLADKLGMGQSGIGALFNGINALNAYNAALLAKILKVSVEEFSPSIAREIYEMYEAVS

>d1lmb3\_ a.35.1.2 (3:) lambda C1 repressor, DNA-binding domain {Bacteriophage lambda (Escherichia coli)}

PLTQEQLEDARRLKAIYEKKKNELGLSQESVADKMGMGQSGVGALFNGINALNAYNAALLAKILKVSVEEFSPSIAREIYEMYEAVS

>d1r69\_\_ a.35.1.2 (-) 434 C1 repressor, DNA-binding domain {Bacteriophage 434 (Escherichia coli)}

SISSRVKSKRIQLGLNQAELAQKVGTTQQSIEQLENGKTKRPRFLPELASALGVSVDWLLNGT

>d2cro\_\_ a.35.1.2 (-) cro 434 {Bacteriophage 434}

MQTLSERLKKRRIALKMTQTELATKAGVKQQSIQLIEAGVTKRPRFLFEIAMALNCDPVWLQYGT

>d1adr\_\_ a.35.1.2 (-) P22 C2 repressor, DNA-binding domain {Salmonella bacteriophage P22}

MNTQLMGERIRARRKKLKIRQAALGKMVGVSNVAISQWERSETEPNGENLLALSKALQCSPDYLLKGDLSQTNVAY

>d1copd\_ a.35.1.2 (D:) cro lambda repressor {Bacteriophage lambda (Escherichia coli)}

MEQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEEVKPFPSNKKTTA

>d1d1la\_ a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda (Escherichia coli)}

MEQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEEVKPWPSN

>d3orca\_ a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda (Escherichia coli)}

EQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEEVKDGEVKPFPSN

>d1ner\_\_ a.35.1.2 (-) Ner {Bacteriophage mu}

CSNEKARDWHRADVIAGLKKRKLSLSALSRQFGYAPTTLANALERHWPKGEQIIANALETKPEVIWPSRYQAGE

>d1b0na2 a.35.1.3 (A:1-68) SinR repressor, DNA-binding domain {Bacillus subtilis}

MIGQRIKQYRKEKGYSLSELAEKAGVAKSYLSSIERNLQTNPSIQFLEKVSAVLDVSVHTLLDEKHET

>d1dw9a1 a.35.1.4 (A:1-86) Cyanase N-terminal domain {Escherichia coli}

MIQSQINRNIRLDLADAILLSKAKKDLSFAEIADGTGLAEAFVTAALLGQQALPADAARLVGAKLDLDEDSILLLQMIPLRGCIDD

>d1pru\_\_ a.35.1.5 (-) Purine repressor (PurR), N-terminal domain {Escherichia coli}

MATIKDVAKRANVSTTTVSHVINKTRFVAEETRNAVWAAIKELHYSPSAVARSLKV

>d1vpwa1 a.35.1.5 (A:3-58) Purine repressor (PurR), N-terminal domain {Escherichia coli}

TIKDVAKRANVSTTTVSHVINKTRFVAEETRNAVWAAIKELHYSPSAVARSMKVNH

>d1efaa1 a.35.1.5 (A:2-60) Lac repressor (LacR), N-terminal domain {Escherichia coli}

KPVTLYDVAEYAGVSYQTVSRVVNQASHVSAKTREKVEAAMAELNYIPNRVAQQLAGKQ

>d1lcca\_ a.35.1.5 (A:) Lac repressor (LacR), N-terminal domain {Escherichia coli}

MKPVTLYDVAEYAGVSYQTVSRVVNQASHVSAKTREKVEAAMAELNYIPNR

>d1uxc\_\_ a.35.1.5 (-) Fructose repressor (FruR), N-terminal domain {Escherichia coli}

MKLDEIARLAGVSRTTASYVINGKAKQYRVSDKTVEKVMAVVREHNYHPN

>d1uxd\_\_ a.35.1.5 (-) Fructose repressor (FruR), N-terminal domain {Escherichia coli}

MKLDEIARLAGVSRTTASYVINGKAKQYRVSDKTVEKVMAVVREHNYHPNAVAAGLRLQ

>d1dula\_ a.36.1.1 (A:) Signal sequence binding protein Ffh {Escherichia coli}

FDLNDFLEQKVLVRMEAIINSMTMKERAKPEIIKGSRKRRIAAGSGMQVQDVNRLLKQFDDMQRMMKKM

>d1hq1a\_ a.36.1.1 (A:) Signal sequence binding protein Ffh {Escherichia coli}

GFDLNDFLEQLRQMKNMGGMASLMGKLPGMGQIPDNVKSQMDDKVLVRMEAIINSMTMKERAKPEIIKGSRKRRIAAGSGMQVQDVNRLLKQFDDMQRMMKKMK

>d2ffha2 a.36.1.1 (A:319-418) Signal sequence binding protein Ffh {Thermus aquaticus}

ELSLEDFLKQMQNLKRLGPFSEILGLLPGVPQGLKVDEKAIKRLEAIVLSMTPEERKDPRILNGSRRKRIAKGSGTSVQEVNRFIKAFEEMKALMKSLEK

>d1qb2a\_ a.36.1.1 (A:) SRP54M {Human (Homo sapiens)}

QFTLRDMYEQFQNIMKMGPFSQILGMIPGFGTDFMSKGNEQESMARLKKLMTIMDSMNDQELDSTDGAKVFSKQPGRIQRVARGSGVSTRDVQELLTQYTKFAQMVK

>d1sknp\_ a.37.1.1 (P:) Binding domain of Skn-1 {Caenorhabditis elegans}

GRQSKDEQLASDNELPVSAFQISEMSLSELQQVLKNESLSEYQRQLIRKIRRRGKNKVAARTCRQRRTDRHDKM

>d1hloa\_ a.38.1.1 (A:) Max protein {Human (Homo sapiens)}

NDDIEVESDADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRRKNHTHQQDIDDLKRQN

>d1an2a\_ a.38.1.1 (A:) Max protein {Mouse (Mus musculus)}

ADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRRKNHTHQQDIDDLKRQNALLEQQVRALEKARS

>d1mdya\_ a.38.1.1 (A:) Myod B/HLH domain {Mouse (Mus musculus)}

MELKRKTTNADRRKAATMRERRRLSKVNEAFETLKRSTSSNPNQRLPKVEILRNAIRYIEGLQALLRD

>d1an4a\_ a.38.1.1 (A:) Usf B/HLH domain {Human (Homo sapiens)}

MDEKRRAQHNEVERRRRDKINNWIVQLSKIIPDSSMESTKSGQSKGGILSKASDYIQELRQSNHR

>d1a0aa\_ a.38.1.1 (A:) Pho4 B/HLH domain {Baker's yeast (Saccharomyces cerevisiae)}

MKRESHKHAEQARRNRLAVALHELASLIPAEWKQQNVSAAPSKATTVEAACRYIRHLQQNGST

>d1am9a\_ a.38.1.1 (A:) SREBP-1a {Human (Homo sapiens)}

QSRGEKRTAHNAIEKRYRSSINDKIIELKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKLKQENLSLRTAVHKSKSLK

>d1bod\_\_ a.39.1.1 (-) Calbindin D9K {Cow (Bos taurus)}

MKSPEELKGIFEKYDKEGDGQLSKEELKLLLQTEFPSLLKGMSTLDELFEELDKNGDGEVSFEEFQVLVKKISQ

>d1ig5a\_ a.39.1.1 (A:) Calbindin D9K {Cow (Bos taurus)}

KSPEELKGIFEKYAAKEGDPNQLSKEELKLLLQTEFPSLLKGPSTLDELFEELDKNGDGEVSFEEFQVLVKKISQ

>d1cb1\_\_ a.39.1.1 (-) Calbindin D9K {Pig (Sus scrofa)}

SAQKSPAELKSIFEKYAAKEGDPNQLSKEELKQLIQAEFPSLLKGPRTLDDLFQELDKNGDGEVSFEEFQVLVKKISQ

>d1a03a\_ a.39.1.2 (A:) Calcyclin (S100) {Rabbit (Oryctolagus cuniculus)}

MASPLDQAIGLLIGIFHKYSGKEGDKHTLSKKELKELIQKELTIGSKLQDAEIVKLMDDLDRNKDQEVNFQEYITFLGALAMIYNEALKG

>d1k2ha\_ a.39.1.2 (A:) Calcyclin (S100) {Rat (Rattus norvegicus), s100a1}

GSELETAMETLINVFHAHSGKEGDKYKLSKKELKDLLQTELSSFLDVQKDADAVDKIMKELDENGDGEVDFQEFVVLVAALTVACNNFFWENS

>d1qlka\_ a.39.1.2 (A:) Calcyclin (S100) {Rat (Rattus norvegicus), s100b}

MSELEKAMVALIDVFHQYSGREGDKHKLKKSELKELINNELSHFLEEIKEQEVVDKVMETLDEDGDGECDFQEFMAFVSMVTTACHEFFEHE

>d1mho\_\_ a.39.1.2 (-) Calcyclin (S100) {Cow (Bos taurus), s100b}

SELEKAVVALIDVFHQYSGREGDKHKLKKSELKELINNELSHFLEEIKEQEVVDKVMETLDSDGDGECDFQEFMAFVAMITTACHEFF

>d1a4pa\_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), P11 s100a10, calpactin}

PSQMEHAMETMMFTFHKFAGDKGYLTKEDLRVLMEKEFPGFLENQKDPLAVDKIMKDLDQCRDGKVGFQSFFSLIAGLTIACNDYFVVHMKQ

>d1psra\_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), psoriasin s100a7}

SNTQAERSIIGMIDMFHKYTRRDDKIDKPSLLTMMKENFPNFLSACDKKGTNYLADVFEKKDKNEDKKIDFSEFLSLLGDIATDYHKQSHGAAPCSGGSQ

>d1qlsa\_ a.39.1.2 (A:) Calcyclin (S100) {Pig (Sus scrofa), calgizzarin s100c (s100a11)}

PTETERCIESLIAIFQKHAGRDGNNTKISKTEFLIFMNTELAAFTQNQKDPGVLDRMMKKLDLDSDGQLDFQEFLNLIGGLAIACHDSFIKSTQK

>d1mr8a\_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), calgranulin s100a8, MRP8}

MLTELEKALNSIIDVYHKYSLIKGNFHAVYRDDLKKLLETECPQYIRKKGADVWFKELDINTDGAVNFQEFLILVIKMGVAAHKKSHEES

>d1e8aa\_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), calgranulin C, s100a12}

TKLEEHLEGIVNIFHQYSVRKGHFDTLSKGELKQLLTKELANTIKNIKDKAVIDEIFQGLDANQDEQVDFQEFISLVAIALKAAHYH

>d1irja\_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), s100a9 (mrp14)}

TCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKNEKVIEHIMEDLDTNADKQLSFEEFIMLMARL

>d1sra\_\_ a.39.1.3 (-) C-terminal (EC) domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}

PPCLDSELTEFPLRMRDWLKNVLVTLYERDEDNNLLTEKQKLRVKKIHENEKRLEAGDHPVELLARDFEKNYNMYIFPVHWQFGQLDQHPIDGYLSHTELAPLRAPLIPMEHCTTRFFETCDLDNDKYIALDEWAGCFGIKQKDIDKDLVI

>d1rro\_\_ a.39.1.4 (-) Oncomodulin {Rat (Rattus norvegicus)}

SITDILSAEDIAAALQECQDPDTFEPQKFFQTSGLSKMSASQVKDIFRFIDNDQSGYLDGDELKYFLQKFQSDARELTESETKSLMDAADNDGDGKIGADEFQEMVHS

>d1cdp\_\_ a.39.1.4 (-) Parvalbumin {Carp (Cyprinus carpio)}

AFAGVLNDADIAAALEACKAADSFNHKAFFAKVGLTSKSADDVKKAFAIIDQDKSGFIEEDELKLFLQNFKADARALTDGETKTFLKAGDSDGDGKIGVDEFTALVKA

>d1pvaa\_ a.39.1.4 (A:) Parvalbumin {Pike (Esox lucius)}

AAKDLLKADDIKKALDAVKAEGSFNHKKFFALVGLKAMSANDVKKVFKAIDADASGFIEEEELKFVLKSFAADGRDLTDAETKAFLKAADKDGDGKIGIDEFETLVHEA

>d2pvba\_ a.39.1.4 (A:) Parvalbumin {Pike (Esox lucius)}

SFAGLKDADVAAALAACSAADSFKHKEFFAKVGLASKSLDDVKKAFYVIDQDKSGFIEEDELKLFLQNFSPSARALTDAETKAFLADGDKDGDGMIGVDEFAAMIKA

>d5pal\_\_ a.39.1.4 (-) Parvalbumin {Leopard shark (Triakis semifasciata)}

PMTKVLKADDINKAISAFKDPGTFDYKRFFHLVGLKGKTDAQVKEVFEILDKDQSGFIEEEELKGVLKGFSAHGRDLNDTETKALLAAGDSDHDGKIGADEFAKMVAQA

>d1a75a\_ a.39.1.4 (A:) Parvalbumin {Whiting (Merlangius merlangus)}

AGILADADCAAAVKACEAADSFSYKAFFAKCGLSGKSADDIKKAFVFIDQDKSGFIEEDELKLFLQVFKAGARALTDAETKAFLKAGDSDGDGAIGVEEWVALVKA

>d1bu3\_\_ a.39.1.4 (-) Parvalbumin {Silver hake (Merluccius bilinearis)}

AFSGILADADVAAALKACEAADSFNYKAFFAKVGLTAKSADDIKKAFFVIDQDKSGFIEEDELKLFLQVFSAGARALTDAETKAFLKAGDSDGDGAIGVDEWAALVKA

>d1g33a\_ a.39.1.4 (A:) Parvalbumin {Rat (Rattus rattus)}

MKSADDVKKVFHILDKDKSGFIEEDELGSILKGFSSDARDLSAKETKTLMAAGDKDGDGKIGVEEFSTLVAES

>d1rtp1\_ a.39.1.4 (1:) Parvalbumin {Rat (Rattus rattus)}

SMTDLLSAEDIKKAIGAFTAADSFDHKKFFQMVGLKKKSADDVKKVFHILDKDKSGFIEEDELGSILKGFSSDARDLSAKETKTLMAAGDKDGDGKIGVEEFSTLVAES

>d1avsa\_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}

QAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEELDAIIEEVDEDGSGTIDFEEFLVMMVRQMK

>d1ctda\_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}

KSEEELANAFRIFDKNADGYIDIEELGEILRATG

>d1dtla\_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}

YKAAVEQLTEEQKNEFKAAFDIFVLGAEDGSISTKELGKVMRMLGQNPTPEELQEMIDEVDEDGSGTVDFDEFLVMMVRSMKDDSKGKSEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNNDGRIDYDEFLEFMKGV

>d1jc2a\_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}

EDAKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVIEEDIEDLMKDSDKNNDGRIDFDEFLKMMEGVQ

>d1ncx\_\_ a.39.1.5 (-) Troponin C {Chicken (Gallus gallus)}

ASMTDQQAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEELDAIIEEVDEDGSGTIDFEEFLVMMVRQMKEDAKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVTEEDIEDLMKDSDKNNDGRIDFDEFLKMMEGVQ

>d1smg\_\_ a.39.1.5 (-) Troponin C {Chicken (Gallus gallus)}

ASMTDQQAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKALGTVMRMLGQNPTKEELDAIIEEVDEDGSGTIDFEEFLVMMVRQMKEDA

>g1pon.1 a.39.1.5 (A:,B:) Troponin C {Chicken (Gallus gallus)}

KSEEELANAFRIFDKNADGYIDIEELGEILRATGXVTEEDIEDLMKDSDKNNDGRIDFDEFLKMMEGVQ

>d1tn4\_\_ a.39.1.5 (-) Troponin C {Rabbit (Oryctolagus cuniculus)}

TDQQAEARSYLSEEMIAEFKAAFDMFDADGGGDISVKELGTVMRMLGQTPTKEELDAIIEEVDEDGSGTIDFEEFLVMMVRQMKEDAKGKSEEELAELFRIFDRNADGYIDAEELAEIFRASGEHVTDEEIESLMKDGDKNNDGRIDFDEFLKMMEG

>d1fi5a\_ a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus), cardiac isoform}

MVRCMKDDSKGKTEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNNDGRIDYDEFLEFMKGVE

>d1ap4\_\_ a.39.1.5 (-) Troponin C {Human (Homo sapiens), cardiac isoform}

MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEMIDEVDEDGSGTVDFDEFLVMMVRCMKDDS

>d1ih0a\_ a.39.1.5 (A:) Troponin C {Human (Homo sapiens), cardiac isoform}

GKSEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNNDGRIDYDEFLEFMKGVE

>d2scpa\_ a.39.1.5 (A:) Sarcoplasmic calcium-binding protein {Sandworm (Nereis diversicolor)}

SDLWVQKMKTYFNRIDFDKDGAITRMDFESMAERFAKESEMKAEHAKVLMDSLTGVWDNFLTAVAGGKGIDETTFINSMKEMVKNPEAKSVVEGPLPLFFRAVDTNEDNNISRDEYGIFFGMLGLDKTMAPASFDAIDTNNDGLLSLEEFVIAGSDFFMNDGDSTNKVFWGPLV

>d2sas\_\_ a.39.1.5 (-) Sarcoplasmic calcium-binding protein {Amphioxus (Branchiostoma lanceolatum)}

GLNDFQKQKIKFTFDFFLDMNHDGSIQDNDFEDMMTRYKEVNKGSLSDADYKSMQASLEDEWRDLKGRADINKDDVVSWEEYLAMWEKTIATCKSVADLPAWCQNRIPFLFKGMDVSGDGIVDLEEFQNYCKNFQLQCADVPAVYNVITDGGKVTFDLNRYKELYYRLLTSPAADAGNTLMGQKP

>d1c7va\_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma lanceolatum)}

EEEILRAFKVFDANGDGVIDFDEFKFIMQKVGEEPLTDAEVEEAMKEADEDGNGVIDIPEFMDLIKKS

>d1j7qa\_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma lanceolatum)}

AAPKARALGPEEKDECMKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEARGPKGDKKNIGPEEWLTLCSKWVRQDD

>d1j7ra\_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma lanceolatum)}

LGPEEKDECMKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEARGPKGDKKNIGPEEWLTLCSKWVRQ

>d1ej3a\_ a.39.1.5 (A:) Calcium-regulated photoprotein {Jellyfish (Aequorea aequorea), aequorin}

LTSDFDNPRWIGRHKHMFNFLDVNHNGKISLDEMVYKASDIVINNLGATPEQAKRHKDAVEAFFGGAGMKYGVETDWPAYIEGWKKLATDELEKYAKNEPTLIRIWGDALFDIVDKDQNGAITLDEWKAYTKAAGIIQSSEDCEETFRVCDIDESGQLDVDEMTRQHLGFWYTMDPACEKLYGGAVP

>d1el4a\_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa (Obelia longissima), obelin}

SSKYAVKLKTDFDNPRWIKRHKHMFDFLDINGNGKITLDEIVSKASDDICAKLEATPEQTKRHQVCVEAFFRGCGMEYGKEIAFPQFLDGWKQLATSELKKWARNEPTLIREWGDAVFDIFDKDGSGTITLDEWKAYGKISGISPSQEDCEATFRHCDLDNSGDLDVDEMTRQHLGFWYTLDPEADGLYGNGVP

>d1jf0a\_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa (Obelia geniculata), obelin}

KYAVKLQTDFDNPKWIKRHKFMFDYLDINGNGQITLDEIVSKASDDICKNLGATPAQTQRHQDCVEAFFRGCGLEYGKETKFPEFLEGWKNLANADLAKWARNEPTLIREWGDAVFDIFDKDGSGTITLDEWKAYGRISGISPSEEDCEKTFQHCDLDNSGELDVDEMTRQHLGFWYTLDPEADGLYGNGVP

>d1jfja\_ a.39.1.5 (A:) EHCABP {Entamoeba (Entamoeba histolytica)}

MAEALFKEIDVNGDGAVSYEEVKAFVSKKRAIKNEQLLQLIFKSIDADGNGEIDQNEFAKFYGSIQGQDLSDDKIGLKVLYKLMDVDGDGKLTKEEVTSFFKKHGIEKVAEQVMKADANGDGYITLEEFLEFSL

>d1cmg\_\_ a.39.1.5 (-) Calmodulin {Cow (Bos taurus)}

MKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMMTAK

>d1fw4a\_ a.39.1.5 (A:) Calmodulin {Cow (Bos taurus)}

SEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMM

>d1g4yr\_ a.39.1.5 (R:) Calmodulin {Rat (Rattus rattus)}

ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDKDGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQMMTA

>d1f70a\_ a.39.1.5 (A:) Calmodulin {African frog (Xenopus laevis)}

ADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLTMMARKM

>d1exra\_ a.39.1.5 (A:) Calmodulin {Ciliate (Paramecium tetraurelia)}

EQLTEEQIAEFKEAFALFDKDGDGTITTKELGTVMRSLGQNPTEAELQDMINEVDADGNGTIDFPEFLSLMARKMKEQDSEEELIEAFKVFDRDGNGLISAAELRHVMTNLGEKLTDDEVDEMIREADIDGDGHINYEEFVRMMVS

>d1ggwa\_ a.39.1.5 (A:) Cdc4p {Fission yeast (Schizosaccharomyces pombe)}

STDDSPYKQAFSLFDRHGTGRIPKTSIGDLLRACGQNPTLAEITEIESTLPAEVDMEQFLQVLNRPNGFDMPGDPEEFVKGFQVFDKDATGMIGVGELRYVLTSLGEKLSNEEMDELLKGVPVKDGMVNYHDFVQMILAN

>d1wdcb\_ a.39.1.5 (B:) Myosin Essential Chain {Bay scallop (Aequipecten irradians)}

LPQKQIQEMKEAFSMIDVDRDGFVSKEDIKAISEQLGRAPDDKELTAMLKEAPGPLNFTMFLSIFSDKLSGTDSEETIRNAFAMFDEQETKKLNIEYIKDLLENMGDNFNKDEMRMTFKEAPVEGGKFDYVKFTAMIKGSGE

>d1br1b\_ a.39.1.5 (B:) Myosin Essential Chain {Chicken (Gallus gallus)}

FSEEQTAEFKEAFQLFDRTGDGKILYSQCGDVMRALGQNPTNAEVMKVLGNPKSDEMNLKTLKFEQFLPMMQTIAKNKDQGCFEDYVEGLRVFDKEGNGTVMGAEIRHVLVTLGEKMTEEEVEQLVAGHEDSNGCINYEELVRMVLSG

>d2mysb\_ a.39.1.5 (B:) Myosin Essential Chain {Chicken (Gallus gallus)}

FDETEIEDFKEAFTVIDQNADGIIDKDDLRETFAAMGRLNVKNEELDAMIKEASGPINFTVFLTMFGEKLKGADPEDVIMGAFKVLDPDGKGSIKKSFLEELLTTGGGRFTPEEIKNMWAAFPPDVAGNVDYKNICYVITHGEDA

>d1wdcc\_ a.39.1.5 (C:) Myosin Regulatory Chain {Bay scallop (Aequipecten irradians)}

LSQDEIDDLKDVFELFDFWDGRDGAVDAFKLGDVCRCLGINPRNEDVFAVGGTHKMGEKSLPFEEFLPAYEGLMDCEQGTFADYMEAFKTFDREGQGFISGAELRHVLTALGERLSDEDVDEIIKLTDLQEDLEGNVKYEDFVKKVMAGPYP

>d2mysc\_ a.39.1.5 (C:) Myosin Regulatory Chain {Chicken (Gallus gallus)}

AAADDFKEAFLLFDRTGDAKITASQVGDIARALGQNPTNAEINKILGNPSKEEMNAAAITFEEFLPMLQAAANNKDQGTFEDFVEGLRVFDKEGNGTVMGAELRHVLATLGEKMTEEEVEELMKGQEDSNGCINYEAFVKHIMSV

>d1auib\_ a.39.1.5 (B:) Calcineurin regulatory subunit (B-chain) {Human (Homo sapiens)}

SYPLEMCSHFDADEIKRLGKRFKKLDLDNSGSLSVEEFMSLPELQQNPLVQRVIDIFDTDGNGEVDFKEFIEGVSQFSVKGDKEQKLRFAFRIYDMDKDGYISNGELFQVLKMMVGNNLKDTQLQQIVDKTIINADKDGDGRISFEEFCAVVGGLDIHKKMVVDV

>d1rec\_\_ a.39.1.5 (-) Recoverin {Cow (Bos taurus)}

LSKEILEELQLNTKFTEEELSSWYQSFLKECPSGRITRQEFQTIYSKFFPEADPKAYAQHVFRSFDANSDGTLDFKEYVIALHMTSAGKTNQKLEWAFSLYDVDGNGTISKNEVLEIVTAIFKMISPEDTKHLPEDENTPEKRAEKIWGFFGKKDDDKLTEKEFIEGTLANKEILRLIQFEPQKVKEKLK

>d1g8ia\_ a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Human (Homo sapiens)}

SNSKLKPEVVEELTRKTYFTEKEVQQWYKGFIKDCPSGQLDAAGFQKIYKQFFPFGDPTKFATFVFNVFDENKDGRIEFSEFIQALSVTSRGTLDEKLRWAFKLYDLDNDGYITRNEMLDIVDAIYQMVGNTVELPEEENTPEKRVDRIFAMMDKNADGKLTLQEFQEGSKADPSIVQALSLYDGLV

>d1fpwa\_ a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Baker's yeast (Saccharomyces cerevisiae)}

MGAKTSKLSKDDLTCLKQSTYFDRREIQQWHKGFLRDCPSGQLAREDFVKIYKQFFPFGSPEDFANHLFTVFDKDNNGFIHFEEFITVLSTTSRGTLEEKLSWAFELYDLNHDGYITFDEMLTIVASVYKMMGSMVTLNEDEATPEMRVKKIFKLMDKNEDGYITLDEFREGSKVDPSIIGALNLYDGLI

>d1jbaa\_ a.39.1.5 (A:) Guanylate cyclase activating protein 2, GCAP-2 {Cow (Bos taurus)}

GQQFSWEEAEENGAVGAADAAQLQEWYKKFLEECPSGTLFMHEFKRFFKVPDNEEATQYVEAMFRAFDTNGDNTIDFLEYVAALNLVLRGTLEHKLKWTFKIYDKDRNGCIDRQELLDIVESIYKLKKACSVEVEAEQQGKLLTPEEVVDRIFLLVDENGDGQLSLNEFVEGARRDKWVMKMLQMDLNP

>d1bjfa\_ a.39.1.5 (A:) Neurocalcin {Cow (Bos taurus)}

NSKLRPEVMQDLLESTDFTEHEIQEWYKGFLRDCPSGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGDGTIDFREFIIALSVTSRGKLEQKLKWAFSMYDLDGNGYISKAEMLEIVQAIYKMVSSVMKMPEDESTPEKRTEKIFRQMDTNRDGKLSLEEFIRGAKSDPSIVRLLQC

>d1dgua\_ a.39.1.5 (A:) Calcium- and integrin-binding protein, CIB {Human (Homo sapiens)}

SKELLAEYQDLTFLTKQEILLAHRRFCELLPQEQRSVESSLRAQVPFEQILSLPELKANPFKERICRVFSTSPAKDSLSFEDFLDLLSVFSDTATPDIKSHYAFRIFDFDDDGTLNREDLSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFASSFKIVL

>d1qjta\_ a.39.1.6 (A:) Eps15 {Mouse (Mus musculus)}

LSLTQLSSGNPVYEKYYRQVEAGNTGRVLALDAAAFLKKSGLPDLILGKIWDLADTDGKGVLSKQEFFVALRLVACAQNGLEVSLSSLSLAVPPPRFHD

>d1c07a\_ a.39.1.6 (A:) Eps15 {Human (Homo sapiens)}

TWVVSPAEKAKYDEIFLKTDKDMDGFVSGLEVREIFLKTGLPSTLLAHIWSLCDTKDCGKLSKDQFALAFHLISQKLIKGIDPPHVLTPEMIPPS

>d1f8ha\_ a.39.1.6 (A:) Eps15 {Human (Homo sapiens)}

PWAVKPEDKAKYDAIFDSLSPVNGFLSGDKVKPVLLNSKLPVDILGRVWELSDIDHDGMLDRDEFAVAMFLVYCALEKEPVPMSLPPALVPPSKR

>d1iq3a\_ a.39.1.6 (A:) Pob1 {Human (Homo sapiens)}

GSLQDNSSYPDEPWRITEEQREYYVNQFRSLQPDPSSFISGSVAKNFFTKSKLSIPELSYIWELSDADCDGALTLPEFCAAFHLIVARKNGYPLPEGLPPTLQPEFIVTD

>d1fi6a\_ a.39.1.6 (A:) Reps1 {Mouse (Mus musculus)}

WKITDEQRQYYVNQFKTIQPDLNGFIPGSAAKEFFTKSKLPILELSHIWELSDFDKDGALTLDEFCAAFHLVVARKNGYDLPEKLPESLMPK

>d1hqva\_ a.39.1.8 (A:) Apoptosis-linked protein alg-2 {Mouse (Mus musculus)}

PGPGGGPGPAAGAALPDQSFLWNVFQRVDKDRSGVISDNELQQALSNGTWTPFNPVTVRSIISMFDRENKAGVNFSEFTGVWKYITDWQNVFRTYDRDNSGMIDKNELKQALSGFGYRLSDQFHDILIRKFDRQGRGQIAFDDFIQGCIVLQRLTDIFRRYDTDQDGWIQVSYEQYLSMVF

>d1juoa\_ a.39.1.8 (A:) Sorcin {Human (Homo sapiens)}

FPGQTQDPLYGYFAAVAGQDGQIDADELQRCLTQSGIAGGYKPFNLETCRLMVSMLDRDMSGTMGFNEFKELWAVLNGWRQHFISFDTDRSGTVDPQELQKALTTMGFRLSPQAVNSIAKRYSTNGKITFDDYIACCVKLRALTDSFRRRDTAQQGVVNFPYDDFIQCVMSV

>d1djxb1 a.39.1.7 (B:158-298) Phosphoinositide-specific phospholipase C, isozyme D1 (PLC-D!) {Rat (Rattus norvegicus)}

NKMNFKELKDFLKELNIQVDDGYARKIFRECDHSQTDSLEDEEIETFYKMLTQRAEIDRAFEEAAGSAETLSVERLVTFLQHQQREEEAGPALALSLIERYEPSETAKAQRQMTKDGFLMYLLSADGNAFSLAHRRVYQDM

>d1qasa1 a.39.1.7 (A:205-298) Phosphoinositide-specific phospholipase C, isozyme D1 (PLC-D!) {Rat (Rattus norvegicus)}

YKMLTQRAEIDRAFEEAAGSAETLSVERLVTFLQHQQREEEAGPALALSLIERYEPSETAKAQRQMTKDGFLMYLLSADGNAFSLAHRRVYQDM

>d1k94a\_ a.39.1.7 (A:) Grancalcin {Human (Homo sapiens)}

SVYTYFSAVAGQDGEVDAEELQRCLTQSGINGTYSPFSLETCRIMIAMLDRDHTGKMGFNAFKELWAALNAWKENFMTVDQDGSGTVEHHELRQAIGLMGYRLSPQTLTTIVKRYSKNGRIFFDDYVACCVKLRALTDFFRKRDHLQQGSANFIYDDFLQGTMAI

>d1kfus\_ a.39.1.7 (S:) Calpain small (regulatory) subunit (domain VI) {Human (Homo sapiens)}

THYSNIEANESEEVRQFRRLFAQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTCRSMVAVMDSDTTGKLGFEEFKYLWNNIKRWQAIYKQFDTDRSGTICSSELPGAFEAAGFHLNEHLYNMIIRRYSDESGNMDFDNFISCLVRLDAMFRAFKSLDKDGTGQIQVNIQEWLQLTMYS

>d1dvia\_ a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI) {Rat (Rattus norvegicus)}

EEERQFRKLFVQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTSRSMVAVMDSDTTGKLGFEEFKYLWNNIKKWQGIYKRFDTDRSGTIGSNELPGAFEAAGFHLNQHIYSMIIRRYSDETGNMDFDNFISCLVRLDAMFRAFRSLDKNGTGQIQVNIQEWLQLTMYS

>d1alva\_ a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI) {Pig (Sus scrofa)}

EEVRQFRRLFAQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTCRSMVAVMDSDTTGKLGFEEFKYLWNNIKKWQAIYKQFDVDRSGTIGSSELPGAFEAAGFHLNEHLYSMIIRRYSDEGGNMDFDNFISCLVRLDAMFRAFKSLDKDGTGQIQVNIQEWLQLTMYS

>d1kful1 a.39.1.7 (L:515-700) Calpain large subunit, C-terminal domain (domain IV) {Human (Homo sapiens)}

EIEANLEEFDISEDDIDDGVRRLFAQLAGEDAEISAFELQTILRRVLAKRQDIKSDGFSIETCKIMVDMLDSDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETLFKIFKQLDPENTGTIELDLISWLCFSVL

>d1df0a1 a.39.1.7 (A:515-700) Calpain large subunit, C-terminal domain (domain IV) {Rat (Rattus norvegicus)}

EIEANIEEIEANEEDIGDGFRRLFAQLAGEDAEISAFELQTILRRVLAKREDIKSDGFSIETCKIMVDMLDEDGSGKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKLPCQLHQVIVARFADDELIIDFDNFVRCLVRLEILFKIFKQLDPENTGTIQLDLISWLSFSVL

>d1eg3a1 a.39.1.7 (A:85-209) Dystrophin {Human (Homo sapiens)}

HPKMTELYQSLADLNNVRFSAYRTAMKLRRLQKALCLDLLSLSAACDALDQHNLKQNDQPMDILQIINCLTTIYDRLEQEHNNLVNVPLCVDMCLNWLLNVYDTGRTGRIRVLSFKTGIISLCKA

>d1eg3a2 a.39.1.7 (A:210-306) Dystrophin {Human (Homo sapiens)}

HLEDKYRYLFKQVASSTGFCDQRRLGLLLHDSIQIPRQLGEVASFGGSNIEPSVRSCFQFANNKPEIEAALFLDWMRLEPQSMVWLPVLHRVAAAET

>d2cbla1 a.39.1.7 (A:178-263) Cbl {Human (Homo sapiens)}

TFRITKADAAEFWRKAFGEKTIVPWKSFRQALHEVHPISSGLEAMALKSTIDLTCNDYISVFEFDIFTRLFQPWSSLLRNWNSLAV

>d1h8ba\_ a.39.1.7 (A:) alpha-Actinin {Human (Homo sapiens)}

MADTDTAEQVIASFRILASDKPYILAEELRRELPPDQAQYCIKRMPAYSGPGSVPGALDYAAFSSALYGESDL

>d1c3za\_ a.39.2.1 (A:) Thp12-carrier protein {Yellow mealworm (Tenebrio molitor)}

ETPREKLKQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAFCILKRAGFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPQHSSADFFKCVHDNRS

>d1dqea\_ a.39.2.1 (A:) Pheromone binding protein {Silkworm (Bombyx mori)}

SQEVMKNLSLNFGKALDECKKEMTLTDAINEDFYNFWKEGYEIKNRETGCAIMCLSTKLNMLDPEGNLHHGNAMEFAKKHGADETMAQQLIDIVHGCEKSTPANDDKCIWTLGVATCFKAEIHKLNWAPSMDVAVGE

>d1iioa\_ a.39.4.1 (A:) Hypothetical protein MTH865 {Archaeon Methanobacterium thermoautotrophicum}

GSHMKMGVKEDIRGQIIGALAGADFPINSPEELMAALPNGPDTTCKSGDVELKASDAGQVLTADDFPFKSAEEVADTIVNKAGL

>d1cpo\_1 a.39.3.1 (0-119) Cloroperoxidase {Fungus (Caldariomyces fumago)}

EEPGSGIGYPYDNNTLPYVAPGPTDSRAPCPALNALANHGYIPHDGRAISRETLQNAFLNHMGIANSVIELALTNAFVVCEYVTGSDCGDSLVNLTLLAEPHAFEHDHSFSRKDYKQGVA

>d1cpo\_2 a.39.3.1 (120-298) Cloroperoxidase {Fungus (Caldariomyces fumago)}

NSNDFIDNRNFDAETFQTSLDVVAGKTHFDYADMNEIRLQRESLSNELDFPGWFTESKPIQNVESGFIFALVSDFNLPDNDENPLVRIDWWKYWFTNESFPYHLGWHPPSPAREIEFVTSASSAVLAASVTSTPSSLPSGAIGPGAEAVPLSFASTMTPFLLATNAPYYAQDPTLGPND

>d1h67a\_ a.40.1.1 (A:) Calponin {Chicken (Gallus gallus)}

MPQTERQLRVWIEGATGRRIGDNFMDGLKDGVILCELINKLQPGSVQKVNDPVQNWHKLENIGNFLRAIKHYGVKPHDIFEANDLFENTNHTQVQSTLIALASQAKTK

>d1bkra\_ a.40.1.1 (A:) beta-spectrin {Human (Homo sapiens)}

KSAKDALLLWCQMKTAGYPNVNIHNFTTSWRDGMAFNALIHKHRPDLIDFDKLKKSNAHYNLQNAFNLAEQHLGLTKLLDPEDISVDHPDEKSIITYVVTYYHYFSKM

>d1aoa\_1 a.40.1.1 (121-251) N-terminal actin-crosslinking domain from fimbrin {Human (Homo sapiens)}

YSEEEKYAFVNWINKALENDPDCRHVIPMNPNTDDLFKAVGDGIVLCKMINLSVPDTIDERAINKKKLTPFIIQENLNLALNSASAIGCHVVNIGAEDLRAGKPHLVLGLLWQIIKIGLFADIELSRNEAL

>d1aoa\_2 a.40.1.1 (260-375) N-terminal actin-crosslinking domain from fimbrin {Human (Homo sapiens)}

TLEELMKLSPEELLLRWANFHLENSGWQKINNFSADIKDSKAYFHLLNQIAPKGQKEGEPRIDINMSGFNETDDLKRAESMLQQADKLGCRQFVTPADVVSGNPKLNLAFVANLFN

>d1bhda\_ a.40.1.1 (A:) Utrophin {Human (Homo sapiens)}

LQQTNSEKILLSWVRQTTRPYSQVNVLNFTTSWTDGLAFNAVLHRHKPDLFSWDKVVKMSPIERLEHAFSKAQTYLGIEKLLDPEDVAVRLPDKKSIIMYLTSLFEVL

>d1qaga1 a.40.1.1 (A:31-151) Utrophin {Human (Homo sapiens)}

DVQKKTFTKWINARFSKSGKPPINDMFTDLKDGRKLLDLLEGLTGTSLPKERGSTRVHALNNVNRVLQVLHQNNVELVNIGGTDIVDGNHKLTLGLLWSIILHWQVKDVMKDVMSDLQQTN

>d1dxxa1 a.40.1.1 (A:9-119) Dystrophin {Human (Homo sapiens)}

DSYEREDVQKKTFTKWVNAQFSKFGKQHIENLFSDLQDGRRLLDLLEGLTGQKLPKEKGSTRVHALNNVNKALRVLQNNNVDLVNIGSTDIVDGNHKLTLGLIWNIILHWQ

>d1dxxa2 a.40.1.1 (A:120-246) Dystrophin {Human (Homo sapiens)}

VKNVMKNIMAGLQQTNSEKILLSWVRQSTRNYPQVNVINFTTSWSDGLALNALIHSHRPDLFDWNSVVSQQSATQRLEHAFNIARYQLGIEKLLDPEDVDTTYPDKKSILMYITSLFQVLPQQVSIE

>d1a26\_1 a.41.1.1 (662-796) Domain of poly(ADP-ribose) polymerase {Chicken (Gallus gallus)}

KSKLAKPIQDLIKMIFDVESMKKAMVEFEIDLQKMPLGKLSKRQIQSAYSILNEVQQAVSDGGSESQILDLSNRFYTLIPHDFGMKKPPLLSNLEYIQAKVQMLDNLLDIEVAYSLLRGGNEDGDKDPIDINYEK

>d1ycqa\_ a.42.1.1 (A:) MDM2 {African clawed frog (Xenopus laevis)}

EKLVQPTPLLLSLLKSAGAQKETFTMKEVIYHLGQYIMAKQLYDEKQQHIVHCSNDPLGELFGVQEFSVKEPRRLYAMISRNLVSANV

>d1ycra\_ a.42.1.1 (A:) MDM2 {Human (Homo sapiens)}

ETLVRPKPLLLKLLKSVGAQKDTYTMKEVLFYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIYRNLVV

>d1b28a\_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}

MKGMSKMPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFKKEGRIGA

>d1baza\_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}

SKMPQVNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIGA

>d1bazb\_ a.43.1.1 (B:) Arc repressor {Salmonella bacteriophage P22}

KMPQVNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFK

>d1bdta\_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}

MKGMSKMPQFNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIG

>d1myka\_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}

KMLQFNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIG

>d1myla\_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}

KMPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFKKEGR

>d1mylb\_ a.43.1.1 (B:) Arc repressor {Salmonella bacteriophage P22}

MPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFK

>d1mnta\_ a.43.1.1 (A:) Mnt repressor {Salmonella bacteriophage P22}

ARDDPHFNFRMPMEVREKLKFRAEANGRSMNSELLQIVQDALSKPSPVTGYRNDAERLADEQSELV

>d2cpga\_ a.43.1.2 (A:) Transcriptional repressor CopG {Streptococcus agalactiae}

MKKRLTITLSESVLENLEKMAREMGLSKSAMISVALENYKKGQ

>d1irqa\_ a.43.1.2 (A:) Omega transcriptional repressor {Streptococcus pyogenes}

IMGDKTVRVRADLHHIIKIETAKNGGNVKEVMDQALEEYIRKYLPDKL

>d1cmba\_ a.43.1.2 (A:) Met repressor, MetR {Escherichia coli}

AEWSGEYISPYAEHGKKSEQVKKITVSIPLKVLKILTDERTRRQVNNLRHATNSELLCEAFLHAFTGQPLPDDADLRKERSDEIPEAAKEIMREMGINPETWEY

>d1fvka1 a.44.1.1 (A:65-128) Disulphide-bond formation facilitator (DSBA), insertion domain {Escherichia coli}

GGDLGKDLTQAWAVAMALGVEDKVTVPLFEGVQKTQTIRSASDIRDVFINAGIKGEEYDAAWNS

>d1bed\_1 a.44.1.1 (63-126) Disulphide-bond formation facilitator (DSBA), insertion domain {Vibrio cholerae}

GNMGQAMSKAYATMIALEVEDKMVPVMFNRIHTLRKPPKDEQELRQIFLDEGIDAAKFDAAYNG

>d1aqwa1 a.45.1.1 (A:77-209) Glutathione S-transferase {Human (Homo sapiens), class pi}

GLYGKDQQEAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDYVKALPGQLKPFETLLSQNQGGKTFIVGDQISFADYNLLDLLLIHEVLAPGCLDAFPLLSAYVGRLSARPKLKAFLASPEYVNLPINGNGKQ

>d2gsra1 a.45.1.1 (A:77-207) Glutathione S-transferase {Pig (Sus scrofa), class pi}

YGKDQKEAALVDMVNDGVEDLRCKYATLIYTNYEAGKEKYVKELPEHLKPFETLLSQNQGGQAFVVGSQISFADYNLLDLLRIHQVLNPSCLDAFPLLSAYVARLSARPKIKAFLASPEHVNRPINGNGKQ

>d1glqa1 a.45.1.1 (A:79-209) Glutathione S-transferase {Mouse (Mus musculus), class pi}

YGKNQREAAQMDMVNDGVEDLRGKYVTLIYTNYENGKNDYVKALPGHLKPFETLLSQNQGGKAFIVGDQISFADYNLLDLLLIHQVLAPGCLDNFPLLSAYVARLSARPKIKAFLSSPEHVNRPINGNGKQ

>d1gtua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Human (Homo sapiens), class mu}

LCGETEEEKIRVDILENQTMDNHMQLGMICYNPEFEKLKPKYLEELPEKLKLYSEFLGKRPWFAGNKITFVDFLVYDVLDLHRIFEPKCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPRPVFSKMAVWGNK

>d1hna\_1 a.45.1.1 (85-217) Glutathione S-transferase {Human (Homo sapiens), class mu}

LCGESEKEQIREDILENQFMDSRMQLAKLCYDPDFEKLKPEYLQALPEMLKLYSQFLGKQPWFLGDKITFVDFIAYDVLERNQVFEPSCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPRPVFTKMAVFGNK

>d3gtub1 a.45.1.1 (B:85-224) Glutathione S-transferase {Human (Homo sapiens), class mu}

RKHNMCGETEEEKIRVDIIENQVMDFRTQLIRLCYSSDHEKLKPQYLEELPGQLKQFSMFLGKFSWFAGEKLTFVDFLTYDILDQNRIFDPKCLDEFPNLKAFMCRFEALEKIAAYLQSDQFCKMPINNKMAQWGNKPVC

>d4gtua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Human (Homo sapiens), class mu}

LCGETEEEKIRVDILENQAMDVSNQLARVCYSPDFEKLKPEYLEELPTMMQHFSQFLGKRPWFVGDKITFVDFLAYDVLDLHRIFEPNCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPKPLYTRVAVWGNK

>d2gsta1 a.45.1.1 (A:85-217) Glutathione S-transferase {Rat (Rattus norvegicus), class mu}

LCGETEEERIRADIVENQVMDNRMQLIMLCYNPDFEKQKPEFLKTIPEKMKLYSEFLGKRPWFAGDKVTYVDFLAYDILDQYHIFEPKCLDAFPNLKDFLARFEGLKKISAYMKSSRYLSTPIFSKLAQWSNK

>d1gsua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Chicken (Gallus gallus), class mu}

MCGETEVEKQRVDVLENHLMDLRMAFARLCYSPDFEKLKPAYLEQLPGKLRQLSRFLGSRSWFVGDKLTFVDFLAYDVLDQQRMFVPDCPELQGNLSQFLQRFEALEKISAYMRSGRFMKAPIFWYTALWNNK

>d1gsea1 a.45.1.1 (A:81-222) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}

LYGKDIKERALIDMYIEGIADLGEMILLLPVCPPEEKDAKLALIKEKIKNRYFPAFEKVLKSHGQDYLVGNKLSRADIHLVELLYYVEELDSSLISSFPLLKALKTRISNLPTVKKFLQPGSPRKPPMDEKSLEEARKIFRF

>d1gula1 a.45.1.1 (A:81-220) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}

LFGKNLKERTLIDMYVEGTLDLLELLIMHPFLKPDDQQKEVVNMAQKAIIRYFPVFEKILRGHGQSFLVGNQLSLADVILLQTILALEEKIPNILSAFPFLQEYTVKLSNIPTIKRFLEPGSKKKPPPDEIYVRTVYNIF

>d1ev4a1 a.45.1.1 (A:80-222) Glutathione S-transferase {Rat (Rattus norvegicus), class alpha (a1-1)}

DLYGKDMKERALIDMYSEGILDLTEMIMQLVICPPDQKEAKTALAKDRTKNRYLPAFEKVLKSHGQDYLVGNKLTRVDIHLLELLLYVEEFDASLLTSFPLLKAFKSRISSLPNVKKFLQPGSQRKLPMDAKQIEEARKIYKF

>d1ev4c1 a.45.1.1 (C:80-208) Glutathione S-transferase {Rat (Rattus norvegicus), class alpha (a1-1)}

DLYGKDMKERALIDMYSEGILDLTEMIMQLVICPPDQKEAKTALAKDRTKNRYLPAFEKVLKSHGQDYLVGNKLTRVDIHLLELLLYVEEFDASLLTSFPLLKAFKSRISSLPNVKKFLQPGSQRKLPM

>d1f3aa1 a.45.1.1 (A:80-221) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-1)}

LYGKDMKERALIDMYSEGILDLTEMIGQLVLCPPDQREAKTALAKDRTKNRYLPAFEKVLKSHGQDYLVGNRLTRVDIHLLEVLLYVEEFDASLLTPFPLLKAFKSRISSLPNVKKFLQPGSQRKPPMDAKQIQEARKAFKI

>d1b48a1 a.45.1.1 (A:80-222) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-4)}

NLYGKDLKERVRIDMYADGTQDLMMMIAVAPFKTPKEKEESYDLILSRAKTRYFPVFEKILKDHGEAFLVGNQLSWADIQLLEAILMVEELSAPVLSDFPLLQAFKTRISNIPTIKKFLQPGSQRKPPPDGPYVEVVRIVLKF

>d1ljra1 a.45.1.1 (A:80-244) Glutathione S-transferase {Human (Homo sapiens), class theta}

TPDHWYPSDLQARARVHEYLGWHADCIRGTFGIPLWVQVLGPLIGVQVPEEKVERNRTAMDQALQWLEDKFLGDRPFLAGQQVTLADLMALEELMQPVALGYELFEGRPRLAAWRGRVEAFLGAELCQEAHSIILSILEQAAKKTLPTPSPEAYQAMLLRIARIP

>d1pd211 a.45.1.1 (1:76-199) Glutathione S-transferase {Rat (Rattus norvegicus), class sigma}

DLAGKTELEQCQVDAVVDTLDDFMSLFPWAEENQDLKERTFNDLLTRQAPHLLKDLDTYLGDKEWFIGNYVTWADFYWDICSTTLLVLKPDLLGIYPRLVSLRNKVQAIPAISAWILKRPQTKL

>d2gsq\_1 a.45.1.1 (76-202) Glutathione S-transferase {Squid (Ommastrephes sloani pacificus), class sigma}

LDGKTSLEKYRVDEITETLQDIFNDVVKIKFAPEAAKEAVQQNYEKSCKRLAPFLEGLLVSNGGGDGFFVGNSMTLADLHCYVALEVPLKHTPELLKDCPKIVALRKRVAECPKIAAYLKKRPVRDF

>d1eema1 a.45.1.1 (A:103-241) Glutathione S-transferase {Human (Homo sapiens), class omega}

LPDDPYEKACQKMILELFSKVPSLVGSFIRSQNKEDYAGLKEEFRKEFTKLEEVLTNKKTTFFGGNSISMIDYLIWPWFERLEAMKLNECVDHTPKLKLWMAAMKEDPTVSALLTSEKDWQGFLELYLQNSPEACDYGL

>d1fw1a1 a.45.1.1 (A:88-212) Glutathione S-transferase {Human (Homo sapiens), class zeta}

LLPQDPKKRASVRMISDLIAGGIQPLQNLSVLKQVGEEMQLTWAQNAITCGFNALEQILQSTAGIYCVGDEVTMADLCLVPQVANAERFKVDLTPYPTISSINKRLLVLEAFQVSHPCRQPDTPT

>d1bg5\_1 a.45.1.1 (81-254) Glutathione S-transferase {Schistosoma japonicum}

MLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLVPRGSSYYQEAKSSKIMESFKNMVPQQALVNSS

>d1duga1 a.45.1.1 (A:81-220) Glutathione S-transferase {Schistosoma japonicum}

LGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDP

>d1gne\_1 a.45.1.1 (80-232) Glutathione S-transferase {Schistosoma japonicum}

MLGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLVPRGSMELDKWA

>d1fhe\_1 a.45.1.1 (81-214) Glutathione S-transferase {Fasciola hepatica}

LGTTPEERARISMIEGAAMDLRIGFGRVCYNPKFEEVKEEYVKELPKTLKMWSDFLGDRHYLTGSSVSHVDFMLYETLDSIRYLAPHCLDEFPKLKEFKSRIEALPKIKAYMESKRFIKWPLNGWAASFGAGDA

>d2fhea1 a.45.1.1 (A:81-216) Glutathione S-transferase {Fasciola hepatica}

IGTTSEERARVSMIEGAAVDLRQGISRISYQPKFEQLKEGYLKDLPTTMKMWSDFLGKNPYLRGTSVSHVDFMVYEALDAIRYLEPHCLDHFPNLQQFMSRIEALPSIKAYMESNRFIKWPLNGWHAQFGGGDAPP

>d1gnwa1 a.45.1.1 (A:86-211) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}

LQTDSKNISQYAIMAIGMQVEDHQFDPVASKLAFEQIFKSIYGLTTDEAVVAEEEAKLAKVLDVYEARLKEFKYLAGETFTLTDLHHIPAIQYLLGTPTKKLFTERPRVNEWVAEITKRPASEKVQ

>d1axda1 a.45.1.1 (A:81-210) Glutathione S-transferase {Maize (Zea mays), type I}

ELLREGNLEEAAMVDVWIEVEANQYTAALNPILFQVLISPMLGGTTDQKVVDENLEKLKKVLEVYEARLTKCKYLAGDFLSLADLNHVSVTLCLFATPYASVLDAYPHVKAWWSGLMERPSVQKVAALM

>d1aw9\_1 a.45.1.1 (83-217) Glutathione S-transferase {Maize (Zea mays), type III}

GTDLLPATASAAKLEVWLEVESHHFYPNASPLVFQLLVRPLLGGAPDAAVVDKHAEQLAKVLDVYEAHLARNKYLAGDEFTLADANHASYLLYLSKTPKAGLVAARPHVKAWWEAIVARPAFQKTVAAIPLPPPP

>d1e6ba1 a.45.1.1 (A:88-220) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana), class zeta}

PLLPRDLHKRAVNYQAMSIVLSGIQPHQNLAVIRYIEEKINVEEKTAWVNNAITKGFTALEKLLVNCAGKHATGDEIYLADLFLAPQIHGAINRFQINMEPYPTLAKCYESYNELPAFQNALPEKQPDAPSST

>d1a0fa1 a.45.1.1 (A:81-201) Glutathione S-transferase {Escherichia coli}

QLLAPVNSISRYKTIEWLNYIATELHKGFTPLFRPDTPEEYKPTVRAQLEKKLQYVNEALKDEHWICGQRFTIADAYLFTVLRWAYAVKLNLEGLEHIAAFMQRMAERPEVQDALSAEGLK

>d1b8xa1 a.45.1.1 (A:81-260) Glutathione S-transferase {Escherichia coli}

LGGCPKERAEISMLEGAVLDIRYGVSRIAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLYDALDVVLYMDPMCLDAFPKLVCFKKRIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLVPRGSRRASVGSRMHYPGAFTYSPTPVTSGIGIGMSAMGS

>d1pmt\_1 a.45.1.1 (81-201) Glutathione S-transferase {Proteus mirabilis}

NLIAPPKALERYHQIEWLNFLASEVHKGYSPLFSSDTPESYLPVVKNKLKSKFVYINDVLSKQKCVCGDHFTVADAYLFTLSQWAPHVALDLTDLSHLQDYLARIAQRPNVHSALVTEGLI

>d1f2ea1 a.45.1.1 (A:81-201) Glutathione S-transferase {Sphingomonas paucimobilis}

GLAPAEGSLDRYRLLSRLSFLGSEFHKAFVPLFAPATSDEAKAAAAESVKNHLAALDKELAGRDHYAGNAFSVADIYLYVMLGWPAYVGIDMAAYPALGAYAGKIAQRPAVGAALKAEGLA

>d1g7oa1 a.45.1.1 (A:76-215) Glutaredoxin 2 {Escherichia coli}

PLLTGKRSPAIEEWLRKVNGYANKLLLPRFAKSAFDEFSTPAARKYFVDKKEASAGNFADLLAHSDGLIKNISDDLRALDKLIVKPNAVNGELSEDDIQLFPLLRNLTLVAGINWPSRVADYRDNMAKQTQINLLSSMAI

>d1k0da1 a.45.1.1 (A:201-351) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}

LWSDDLADQSQINAWLFFQTSGHAPMIGQALHFRYFHSQKIASAVERYTDEVRRVYGVVEMALAERREALVMELDTENAAAYSAGTTPMSQSRFFDYPVWLVGDKLTIADLAFVPWNNVVDRIGINIKIEFPEVYKWTKHMMRRPAVIKAL

>d1k0ma1 a.45.1.1 (A:92-240) Chloride intracellular channel 1 (clic1) {Human (Homo sapiens)}

RYPKLAALNPESNTAGLDIFAKFSAYIKNSNPALNDNLEKGLLKALKVLDNYLTSPLPEGVDETSAEDEGVSQRKFLDGNELTLADCNLLPKLHIVQVVCKKYRGFTIPEAFRGVHRYLSNAYAREEFASTCPDDEEIELAYEQVAKAL

>d1bmta1 a.46.1.1 (A:651-740) Methionine synthase domain {Escherichia coli}

QAEWRSWEVNKRLEYSLVKGITEFIEQDTEEARQQATRPIEVIEGPLMDGMNVVGDLFGEGKMFLPQVVKSARVMKQAVAYLEPFIEASK

>d2tpt\_1 a.46.2.1 (1-70) Thymidine phosphorylase {Escherichia coli}

LFLAQEIIRKKRDGHALSDEEIRFFINGIRDNTISEGQIAALAMTIFFHDMTMPERVSLTMAMRDSGTVL

>d1brwa1 a.46.2.1 (A:1-70) Pyrimidine nucleoside phosphorylase {Bacillus stearothermophilus}

MRMVDLIAKKRDGKALTKEEIEWIVRGYTNGDIPDYQMSALAMAIYFRGMTEEETAALTMAMVQSGEMLD

>d1bf5a1 a.47.1.1 (A:136-316) STAT-1, coiled coil domain {Human (Homo sapiens)}

LDKQKELDSKVRNVKDKVMCIEHEIKSLEDLQDEYDFKCKTLQNREHLLLKKMYLMLDNKRKEVVHKIIELLNVTELTQNALINDELVEWKRRQQSACIGGPPNACLDQLQNWFTIVAESLQQVRQQLKKLEELEQKYTYEHDPITKNKQVLWDRTFSLFQQLIQSS

>d1bg1a1 a.47.1.1 (A:136-321) STAT3b {Mouse (Mus musculus)}

VVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIVSELAGLLSAMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAF

>d1dn1b\_ a.47.2.1 (B:) Syntaxin 1A N-terminal domain {Rat (Rattus norvegicus)}

DRFMDEFFEQVEEIRGFIDKIAENVEEVKRKHSAILASPNPDEKTKEELEELMSDIKKTANKVRSKLKSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKFVEVMSEYNATQSDYRERCKGRIQRQLEITGRTTTSEELEDMLESGNPAIFASGIIMDSSISKQALSEIETRHSEIIKLENSIRELHDMFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAV

>d1ez3a\_ a.47.2.1 (A:) Syntaxin 1A N-terminal domain {Rat (Rattus norvegicus)}

RDRFMDEFFEQVEEIRGFIDKIAENVEEVKRKHSAILASPNPDEKTKEELEELMSDIKKTANKVRSKLKSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKFVEVMSEYNATQSDYRERCKGRI

>d1fioa\_ a.47.2.1 (A:) Sso1 {Baker's yeast (Saccharomyces cerevisiae)}

MHDFVGFMNKISQINRDLDKYDHTINQVDSLHKRLLTEVNEEQASHLRHSLDNFVAQATDLQFKLKNEIKSAQRDGIHDTNKQAQAENSRQRFLKLIQDYRIVDSNYKEENKEQAKRQYMIIQPEATEDEVEAAISDVGGQQIFSQALLNANRRGEAKTALAEVQARHQELLKLEKSMAELTQLFNDMEELVIEQQ

>d1hs7a\_ a.47.2.1 (A:) Vam3p N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

TNQKTKELSNLIETFAEQSRVLEKECTKIGSKRDSKELRYKIETELIPNCTSVRDKIESNILIHQNGKLSADFKNLKTKYQSLQQSYNQRKSLFPLK

>d2cbla2 a.48.1.1 (A:47-177) N-terminal domain of cbl (N-cbl) {Human (Homo sapiens)}

PPGTVDKKMVEKCWKLMDKVVRLCQNPKLALKNSPPYILDLLPDTYQHLRTILSRYEGKMETLGENEYFRVFMENLMKKTKQTISLFKEGKERMYEENSQPRRNLTKLSLIFSHMLAELKGIFPSGLFQGD

>d1de4c1 a.48.2.1 (C:609-756) Transferrin receptor ectodomain, C-terminal domain {Human (Homo sapiens)}

LDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFGNAEKTDRFVMKKLNDRVMRVEYHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQNNGAFNETLFRNQLALATWTIQGAANALSGDVWDI

>d1eo0a\_ a.48.3.1 (A:) Transcription elongation factor TFIIS N-domain {Baker's yeast (Saccharomyces cerevisiae)}

MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDKEFVPTEKLLRETKVGVEVNKFKKSTNVEISKLVKKMISSWKDAIN

>d1f6va\_ a.49.1.1 (A:) C-terminal domain of B transposition protein {Bacteriophage mu}

GSRIAKRTAINKTKKADVKAIADAWQINGEKELELLQQIAQKPGALRILNHSLRLAAMTAHGKGERVNEDYLRQAFRELDLDVDISTLLRN

>d1i6ve\_ a.143.1.1 (E:) RNA polymerase omega subunit {Thermus aquaticus}

MAEPGIDKLFGMVDSKYRLTVVVAKRAQQLLRHRFKNTVLEPEERPKMRTLEGLYDDPNAVTWAMKELLTGRLFFGENLVPEDRLQKEMERLYPTEEE

>d1cfaa\_ a.50.1.1 (A:) C5a anaphylotoxin {Human (Homo sapiens)}

MLQKKIEEIAAKYKHSVVKKCCYDGASVNNDETCEQRAARISLGPRCIKAFTECCVVASQLRANISHKDMC

>d1c5a\_\_ a.50.1.1 (-) C5a anaphylotoxin {Pig (Sus scrofa domestica)}

MLQKKIEEEAAKYKYAMLKKCCYDGAYRNDDETCEERAARIKIGPKCVKAFKDCCYIANQVRAEQS

>d0c3a\_\_ a.50.1.1 (-) C3a anaphylotoxin {Human (Homo sapiens)}

SVQLTEKRMNKVGKYPKELRKCCEDGMRQNPMRFSCQRRTRFISLGEACKKVFLDCCNYITELRRQHARASHLGLAR

>d1ocrh\_ a.51.1.1 (H:) Cytochrome c oxidase subunit h {Cow (Bos taurus)}

KIKNYQTAPFDSRFPNQNQTRNCWQNYLDFHRCEKAMTAKGGDVSVCEWYRRVYKSLCPISWVSTWDDRRAEGTFPGKI

>d1hyp\_\_ a.52.1.1 (-) Soybean hydrophobic protein {Soybean (Glycine max)}

PSCPDLSICLNILGGSLGTVDDCCALIGGLGDIEAIVCLCIQLRALGILNLNRNLQLILNSCGRSYPSNATCPRT

>d1bwoa\_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Wheat (Triticum aestivum), L. seeds}

IDCGHVDSLVRPCLSYVQGGPGPSGQCCDGVKNLHNQARSQSDRQSACNCLKGIARGIHNLNEDNARSIPPKCGVNLPYTISLNIDCSRV

>d1be2\_\_ a.52.1.1 (-) Plant non-specific lipid-transfer protein (ns-LTP) {Barley (Hordeum vulgare)}

LNCGQVDSKMKPCLTYVQGGPGPSGECCNGVRDLHNQAQSSGDRQTVCNCLKGIARGIHNLNLNNAASIPSKCNVNVPYTISPDIDCSRIY

>d1fk5a\_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Maize (Zea mays)}

AISCGQVASAIAPCISYARGQGSGPSAGCCSGVRSLNNAARTTADRRAACNCLKNAAAGVSGLNAGNAASIPSKCGVSIPYTISTSTDCSRVN

>d1rzl\_\_ a.52.1.1 (-) Plant non-specific lipid-transfer protein (ns-LTP) {Rice (Oryza sativa)}

ITCGQVNSAVGPCLTYARGGAGPSAACCSGVRSLKAAASTTADRRTACNCLKNAARGIKGLNAGNAASIPSKCGVSVPYTISASIDCSRVS

>d1hssa\_ a.52.1.2 (A:) 0.19 alpha-amylase inhibitor {Wheat (Triticum aestivum)}

MCYPGQAFQVPALPACRPLLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSMLDSMYKEHGAQEGQAGTGAFPRCRREVVKLTAASITAVCRLPIVVDASGDGAYVCKDVAAYPDA

>d1tmqb\_ a.52.1.2 (B:) Trypsin/alpha-amylase inhibitor RBI {Ragi (Elucine coracana gaertneri), seeds}

SVGTSCIPGMAIPHNPLDSCRWYVSTRTCGVGPRLATQEMKARCCRQLEAIPAYCRCEAVRILMDGVVTSSGQHEGRLLQDLPGCPRQVQRAFAPKLVTEVECNLATIHGGPFCLSL

>d1bea\_\_ a.52.1.2 (-) Hageman factor/amylase inhibitor {Maize (Zea mays)}

SCVPGWAIPHNPLPSCRWYVTSRTCGIGPRLPWPELKRRCCRELADIPAYCRCTALSILMDGAIPPGPDAQLEGRLEDLPGCPREVQRGFAATLVTEAECNLATISGVAECPWILG

>g1pnb.1 a.52.1.3 (A:,B:) Napin BNIb {Rape (Brassica napus)}

QPQKCQREFQQEQHLRACQQWIRQQLAGSPFXQSGPQQGPWLREQCCNELYQEDQVCVCPTLKQAAKSVRVQGQHGPFQSTRIYQIAKNLPNVCNMKQIGTCPFIAI

>d1a1ua\_ a.53.1.1 (A:) p53 tetramerization domain {Human (Homo sapiens)}

EYFTLQIRGRERFEKIREYNEALELKDAQ

>d1aie\_\_ a.53.1.1 (-) p53 tetramerization domain {Human (Homo sapiens)}

EYFTLQIRGRERFEMFRELNEALELKDAQAG

>d1hs5a\_ a.53.1.1 (A:) p53 tetramerization domain {Human (Homo sapiens)}

DGEYFTLQIRGRERFEQFRERNEALELKDAQAGK

>d1saia\_ a.53.1.1 (A:) p53 tetramerization domain {Human (Homo sapiens)}

KKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG

>d1k1fa\_ a.147.1.1 (A:) Bcr-Abl oncoprotein oligomerization domain {Human (Homo sapiens)}

MVDPVGFAEAWKAQFPDSEPPRMELRSVGDIEQELERAKASIRRLEQEVNQERFRMIYLQTLLAKEK

>d1adt\_1 a.54.1.1 (176-265) Domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}

PIVSAWEKGMEAARALMDKYHVDNDLKANFKLLPDQVEALAAVCKTWLNEEHRGLQLTFTSNKTFVTMMGRFLQAYLQSFAEVTYKHHEP

>d1ihfa\_ a.55.1.1 (A:) Integration host factor (IHF) {Escherichia coli}

ALTKAEMSEYLFDKLGLSKRDAKELVELFFEEIRRALENGEQVKLSGFGNFDLRDKNQRPGRNPKTGEDIPITARRVVTFRPGQKLKSRVENASPK

>d1ihfb\_ a.55.1.1 (B:) Integration host factor (IHF) {Escherichia coli}

MTKSELIERLATQQSHIPAKTVEDAVKEMLEHMASTLAQGERIEIRGFGSFSLHYRAPRTGRNPKTGDKVELEGKYVPHFKPGKELRDRANIYG

>d1hns\_\_ a.55.1.1 (-) DNA-binding domain of H1 protein, (H-NS) {Escherichia coli}

AQRPAKYSYVDENGETKTWTGQGRTPAVIKKAMDEQGKSLDDFLIKQ

>d1huua\_ a.55.1.1 (A:) HU protein {Bacillus stearothermophilus}

MNKTELINAVAETSGLSKKDATKAVDAVFDSITEALRKGDKVQLIGFGNFEVRERAARKGRNPQTGEEMEIPASKVPAFKPGKALKDAVK

>d1b8za\_ a.55.1.1 (A:) HU protein {Thermotoga maritima}

MNKKELIDRVAKKAGAKKKDVKLILDTILETITEALAKGEKVQIVGFGSFEVRKAAARKGVNPQTRKPITIPERKVPKFKPGKALKEKVK

>d1exea\_ a.55.1.1 (A:) Transcription factor 1, TF1 {Bacteriophage SPO1 (Bacillus subtilis)}

MNKTELIKAIAQDTGLTQVSVSKMLASFEKIITETVAKGDKVQLTGFLNIKPVARQARKGFNPQTQEALEIAPSVGVSVKPGESLKKAAEGLKYEDFAK

>d1dp3a\_ a.55.1.2 (A:) DNA-binding domain (fragment?) of the TraM protein {Escherichia coli}

AKVQAYVSDEIVYKINKIVERRRAEGAKSTDVSFSSISTMLLELGLRVYEAQMER

>d1hlra1 a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2 {Desulfovibrio gigas}

QPENLHPLQKAWVLHGGAQCGFCSPGFIVSAKGLLDTNADPSREDVRDWFQKHRNACRCTGYKPLVDAVMDAAAVINGKKPETDLEFKMPADGRIWGSKYPRPTAVAKVTGTL

>d1dgja1 a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2 {Desulfovibrio desulfuricans}

APDCLHPLQHAWIQHGAAQCGFCTPGFIVSAKALLDENVAPSREDVRDWFQKHHNICRCTGYKPLVDAVMDAAAILRGEKTVEEISFKMPADGRIWGSSIPRPSAVAKVTGLA

>d1fo4a1 a.56.1.1 (A:93-165) Xanthine oxidase, domain 2 {Cow (Bos taurus)}

STKTRLHPVQERIAKSHGSQCGFCTPGIVMSMYTLLRNQPEPTVEEIEDAFQGNLCRCTGYRPILQGFRTFAK

>d1jroa1 a.56.1.1 (A:85-166) Xanthine dehydrogenase chain A, domain 2 {Rhodobacter capsulatus}

DGRLHPVQQAMIDHHGSQCGFCTPGFIVSMAAAHDRDRKDYDDLLAGNLCRCTGYAPILRAAEAAAGEPPADWLQADAAFTL

>d1qj2a1 a.56.1.1 (A:82-161) Carbon monoxide (CO) dehydrogenase iron-sulfur protein, C-domain {Pseudomonas carboxydovorans}

APDGTLSALQEGFRMMHGLQCGYCTPGMIMRSHRLLQENPSPTEAEIRFGIGGNLCRCTGYQNIVKAIQYAAAKINGVPF

>d1ffva1 a.56.1.1 (A:82-157) Carbon monoxide (CO) dehydrogenase iron-sulfur protein, C-domain {Hydrogenophaga pseudoflava}

NKGVLHAVQEGFYKEHGLQCGFCTPGMLMRAYRFLQENPNPTEAEIRMGMTGNLCRCTGYQNIVKAVQYAARKLQE

>d1dj8a\_ a.57.1.1 (A:) Protein HNS-dependent expression A; HdeA {Escherichia coli}

NKKPVNSWTCEDFLAVDESFQPTAVGFAEALNNKDKPEDAVLDVQGIATVTPAIVQACTQDKQANFKDKVKGEWDKIKK

>d1g9la\_ a.144.1.1 (A:) poly(A) binding protein {Human (Homo sapiens)}

GPLGSAAAATPAVRTVPQYKYAAGVRNPQQHLNAQPQVTMQQPAVHVQGQEPLTASMLASAPPQEQKQMLGERLFPLIQAMHPTLAGKITGMLLEIDNSELLHMLESPESLRSKVDEAVAVLQAHQAKEAAQKAVNSATGVPTV

>d1i2ta\_ a.144.1.1 (A:) hyperplastic discs protein {Human (Homo sapiens)}

HRQALGERLYPRVQAMQPAFASKITGMLLELSPAQLLLLLASEDSLRARVDEAMELIIAHG

>d1af7\_1 a.58.1.1 (11-91) Chemotaxis receptor methyltransferase CheR, N-terminal domain {Salmonella typhimurium}

SVLLQMTQRLALSDAHFRRICQLIYQRAGIVLADHKRDMVYNRLVRRLRALGLDDFGRYLSMLEANQNSAEWQAFINALTT

>d1e91a\_ a.59.1.1 (A:) Sin3B {Mouse (Mus musculus)}

ESDSVEFNNAISYVNKIKTRFLDHPEIYRSFLEILHTYQKEQLHTKGRPFRGMSEEEVFTEVANLFRGQEDLLSEFGQFLPEAKR

>d1g1eb\_ a.59.1.1 (B:) Sin3A {Mouse (Mus musculus)}

SLQNNQPVEFNHAINYVNKIKNRFQGQPDIYKAFLEILHTYQKEQRNAKEAGGNYTPALTEQEVYAQVARLFKNQEDLLSEFGQFLPDA

>d1bqv\_\_ a.60.1.1 (-) Ets-1 transcription factor pointed domain {Mouse (Mus musculus)}

MECADVPLLTPSSKEMMSQALKATFSGFTKEQQRLGIPKDPRQWTETHVRDWVMWAVNEFSLKGVDFQKFCMSGAALCALGKECFLELAPDFVGDILWEHLEILQKEDVK

>d1b0xa\_ a.60.1.2 (A:) EphA4 receptor tyrosine kinases {Mouse (Mus musculus)}

FSAVVSVGDWLQAIKMDRYKDNFTAAGYTTLEAVVHMSQDDLARIGITAITHQNKILSSVQAMRTQMQQMHG

>d1b4fa\_ a.60.1.2 (A:) EphB2 receptor {Human (Homo sapiens)}

PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMMEDILRVGVTLAGHQKKILNSIQVMRAQMNQIQS

>d1sgg\_\_ a.60.1.2 (-) EphB2 receptor {Chicken (Gallus gallus)}

YTSFNTVDEWLDAIKMSQYKESFASAGFTTFDIVSQMTVEDILRVGVTLAGHQKKILNSIQVMRAQM

>d1coka\_ a.60.1.2 (A:) C-terminal domain of p73 {Human (Homo sapiens)}

YHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDLKQGHDY

>d1dxsa\_ a.60.1.2 (A:) C-terminal domain of p73 {Human (Homo sapiens)}

SLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGLQDL

>d1cuk\_2 a.60.2.1 (65-142) DNA helicase RuvA subunit, middle domain {Escherichia coli}

NKQERTLFKELIKTNGVGPKLALAILSGMSAQQFVNAVEREEVGALVKLPGIGKKTAERLIVEMKDRFKGLHGDLFTP

>d1bvsa2 a.60.2.1 (A:64-134) DNA helicase RuvA subunit, middle domain {Mycobacterium leprae}

DAENRDLFLALLSVSGVGPRLAMATLAVHDAAALRQALADSDVASLTRVPGIGRRGAERIVLELADKVGPV

>d1dgsa1 a.60.2.2 (A:401-581) NAD+-dependent DNA ligase, domain 3 {Thermus filiformis}

RWPEACPECGHRLVKEGKVHRCPNPLCPAKRFEAIRHYASRKAMDIEGLGEKLIERLLEKGLVRDVADLYHLRKEDLLGLERMGEKSAQNLLRQIEESKHRGLERLLYALGLPGVGEVLARNLARRFGTMDRLLEASLEELIEVEEVGELTARAILETLKDPAFRDLVRRLKEAGVSMESK

>d1coo\_\_ a.60.3.1 (-) C-terminal domain of RNA polymerase alpha subunit {Escherichia coli}

FDPILLRPVDDLELTVRSANCLKAEAIHYIGDLVQRTEVELLKTPNLGKKSLTEIKDVLASRGLSLGMRLENWPPASIADE

>d1doqa\_ a.60.3.1 (A:) C-terminal domain of RNA polymerase alpha subunit {Thermus thermophilus}

EQEEELDLPLEELGLSTRVLHSLKEEGIESVRALLALNLKDLKNIPGIGERSLEEIKEALEKKGFTLKE

>d1b22a\_ a.60.4.1 (A:) DNA repair protein Rad51, N-terminal domain {Human (Homo sapiens)}

EEESFGPQPISRLEQCGINANDVKKLEEAGFHTVEAVAYAPKKELINIKGISEAKADKILAEAAKLVPMG

>d1ci4a\_ a.60.5.1 (A:) Barrier-to-autointegration factor, BAF {Human (Homo sapiens)}

MTTSQKHRDFVAEPMGEKPVGSLAGIGEVLGKKLEERGFDKAYVVLGQFLVLKKDEDLFREWLKDTCGANAKQSRDCFGCLREWCDAFL

>d1bpya1 a.60.6.1 (A:10-91) DNA polymerase beta, N-terminal (8 kD)-domain {Human (Homo sapiens)}

TLNGGITDMLTELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKKLPGVGTKIAEKIDEFLATGKLRKLEKIRQD

>d1dk2a\_ a.60.6.1 (A:) DNA polymerase beta, N-terminal (8 kD)-domain {Rat (Rattus norvegicus)}

SKRKAPQETLNGGITDMLVELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKKLPGVGTKIAEKIDEFLATGKLRKLEK

>d1jmsa1 a.60.6.1 (A:148-242) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}

KKISQYACQRRTTLNNYNQLFTDALDILAENDELRENEGSCLAFMRASSVLKSLPFPITSMKDTEGIPCLGDKVKSIIEGIIEDGESSEAKAVLN

>d1tfr\_1 a.60.7.1 (183-305) T4 RNase H {Bacteriophage T4}

GSAEIDCMTKILKGDKKDNVASVKVRSDFWFTRVEGERTPSMKTSIVEAIANDREQAKVLLTESEYNRYKENLVLIDFDYIPDNIASNIVNYYNSYKLPPRGKIYSYFVKAGLSKLTNSINEF

>d1bgxt1 a.60.7.1 (T:174-289) 5' to 3' exonuclease domain of DNA polymerase Taq {Thermus aquaticus}

LRPDQWADYRALTGDESDNLPGVKGIGEKTARKLLEEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREPDRERLRAFLERLEFGSLLHEFGLLE

>d1xo1a1 a.60.7.1 (A:186-290) T5 5'-exonuclease {Bacteriophage T5}

VDDVEQFISLKAIMGDLGDNIRGVEGIGAKRGYNIIREFGNVLDIIDQLPLPGKQKYIQNLNASEELLFRNLILVDLPTYCVDAIAAVGQDVLDKFTKDILEIAE

>d1a77\_1 a.60.7.1 (209-316) Flap endonuclease-1 {Archaeon Methanococcus jannaschii}

ISLDDLIDIAIFMGTDYNPGGVKGIGFKRAYELVRSGVAKDVLKKEVEYYDEIKRIFKEPKVTDNYSLSLKLPDKEGIIKFLVDENDFNYDRVKKHVDKLYNLIANKT

>d1b43a1 a.60.7.1 (A:220-339) Fen-1 nuclease {Archaeon Pyrococcus furiosus}

LTREKLIELAILVGTDYNPGGIKGIGLKKALEIVRHSKDPLAKFQKQSDVDLYAIKEFFLNPPVTDNYNLVWRDPDEEGILKFLCDEHDFSEERVKNGLERLKKAIKSGKQSTLESWFKR

>d1d8ba\_ a.60.8.1 (A:) HRDC domain from RecQ helicase {Baker's yeast (Saccharomyces cerevisiae)}

ELNNLRMTYERLRELSLNLGNRMVPPVGNFMPDSILKKMAAILPMNDSAFATLGTVEDKYRRRFKYFKATIADLSKKRSSE

>d1go3f\_ a.60.8.2 (F:) RNA polymerase II subunit RBP7 (RpoF) {Archaeon Methanococcus jannaschii}

MIGKKILGERYVTVSEAAEIMYNRAQIGELSYEQGCALDYLQKFAKLDKEEAKKLVEELISLGIDEKTAVKIADILPEDLDDLRAIYYKRELPENAEEILEIVRKYI

>d1f44a1 a.60.9.1 (A:20-129) Cre recombinase {Bacteriophage P1}

SDEVRKNLMDMFRDRQAFSEHTWKMLLSVCRSWAAWCKLNNRKWFPAEPEDVRDYLLYLQARGLAVKTIQQHLGQLNMLHRRSGLPRPSDSNAVSLVMRRIRKENVDAGE

>d1a0p\_1 a.60.9.1 (3-100) Recombinase XerD {Escherichia coli}

QDLARIEQFLDALWLEKNLAENTLNAYRRDLSMMVEWLHHRGLTLATAQSDDLQALLAERLEGGYKATSSARLLSAVRRLFQYLYREKFREDDPSAHL

>d1floa1 a.60.9.1 (A:2-129) Flp recombinase {Baker's yeast (Saccharomyces cerevisiae)}

PQFDILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWMITHNGTAIKRATFMSYNTIISNSLSFDIVNKSLQFKYKTQKATILEASLKKLIPAWEFTIIPYYGQKHQSDITDIVSSLQLQFES

>d1zyma1 a.60.10.1 (A:22-144) Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain {Escherichia coli}

DEIVIDRKKISADQVDQEVERFLSGRAKASAQLETIKTKAGETFGEEKEAIFEGHIMLLEDEELEQEIIALIKDKHMTADAAAHEVIEGQASALEELDDEYLKERAADVRDIGKRLLRNILGL

>d1jyga\_ a.60.11.1 (A:) Hypothetical protein YjbJ {Escherichia coli}

MNKDEAGGNWKQFKGKVKEQWGKLTDDDMTIIEGKRDQLVGKIQERYGYQKDQAEKEVVDWETRNEYRW

>d1hiwa\_ a.61.1.1 (A:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}

VLSGGELDKWEKIRLRPGGKKQYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSEELRSLYNTIAVLYCVHQRIDVKDTKEALDKIEEEQNKSKKKAQQAAAD

>d1hiws\_ a.61.1.1 (S:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}

VLSGGELDKWEKIRLRPGGKKQYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSEELRSLYNTIAVLYCVHQRIDVKDTKEALDKIEEEQN

>d1tam\_\_ a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}

MGARASVLSGGELDRWEKIRLRPGGKKKYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSEELRSLYNTVATLYCVHQRIEIKDTKEALDKIEEEQNKSKKKAQQAAA

>d2hmx\_\_ a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}

HMGARASVLSGGELDKWEKIRLRPGGKKQYKLKHIVWASRELERFAVNPGLLETSEGCRQILGQLQPSLQTGSEELRSLYNTIAVLYCVHQRIDVKDTKEALDKIEEEQNKSKKKAQQAAADTGNNSQVSQNY

>d1ed1a\_ a.61.1.1 (A:) SIV matrix antigen {Simian immunodeficiency virus}

SVLSGKKADELEKIRLRPGGKKKYMLKHVVWAANELDRFGLAESLLENKEGCQKILSVLAPLVPTGSENLKSLYNTVCVIWCIHAEEKVKHTEEAKQIVQRHLVVETGTAETMP

>d1jvr\_\_ a.61.1.2 (-) HTLV-II matrix protein {Human T-cell leukemia virus type 2}

HMGQIHGLSPTPIPKAPRGLSTHHWLNFLQAAYRLQPGPSDFDFQQLRRFLKLALKTPIWLNPIDYSLLASLIPKGYPGRVVEIINILVKNQVSPSAPAAPVPTPICPTTTPPPPPPPSPEAHVPPPYVEPTTTQCF

>d1bax\_\_ a.61.1.3 (-) Mason-pfizer monkey virus matrix protein {Simian mason-pfizer virus}

MGQELSQHERYVEQLKQALKTRGVKVKYADLLKFFDFVKDTCPWFPQEGTIDIKRWRRVGDCFQDYYNTFGPEKVPVTAFSYWNLIKELIDKKE

>d1a6s\_\_ a.61.1.4 (-) GAG polyprotein M-domain {Rous sarcoma virus}

GEAVIKVISSACKTYCGKTSPSKKEIGAMLSLLQKEGLLMSPSDLYSPGSWDPITAALSQRAMILGKSGELKTWGLVLGALKAAREE

>d1heka\_ a.61.1.5 (A:) EIAV matrix antigen {Equine infectious anemia virus, EIAV}

AMADIGSMGDPLTWSKALKKLEKVTVQGSQKLTTGNCNWALSLVDLFHDTNFVKEKDWQLRDVIPLLEDVTQTLSGQEREAFERTWWAISAVKMGLQINNVVDGKASFQLLRAKYE

>d1qgta\_ a.62.1.1 (A:) Hepatitis B viral capsid (hbcag) {Hepatitis B virus}

MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHTALRQAILCWGELMTLATWVGNNLEDPASRDLVVNYVNTNMGLKIRQLLWFHISCLTFGRETVLEYLVSFGVWIRTPPAYRPPNAPILST

>d1aep\_\_ a.63.1.1 (-) Apolipophorin-III {African locust (Locusta migratoria)}

NIAEAVQQLNHTIVNAAHELHETLGLPTPDEALNLLTEQANAFKTKIAEVTTSLKQEAEKHQGSVAEQLNAFARNLNNSIHDAATSLNLQDQLNSLQSALTNVGHQWQDIATKTQASAQEAWAPVQSALQEAAEKTKEAAANLQNSIQSAVQK

>d1eq1a\_ a.63.1.1 (A:) Apolipophorin-III {Manduca sexta}

DAPAGGNAFEEMEKHAKEFQKTFSEQFNSLVNSKNTQDFNKALKDGSDSVLQQLSAFSSSLQGAISDANGKAKEALEQARQNVEKTAEELRKAHPDVEKEANAFKDKLQAAVQTTVQESQKLAKEVASNMEETNKKLAPKIKQAYDDFVKHAEEVQKKLHEAATKQ

>d1nkl\_\_ a.64.1.1 (-) NK-lysin {Pig (Sus scrofa)}

GYFCESCRKIIQKLEDMVGPQPNEDTVTQAASQVCDKLKILRGLCKKIMRSFLRRISWDILTGKKPQAICVDIKICKE

>d1qdma1 a.64.1.2 (A:1S-104S) (Pro)phytepsin {Barley (Hordeum vulgare)}

VVSQECKTIVSQYGQQILDLLLAETQPKKICSQVGLCTFDGTRGVSAGIRSVVDDEPVKSNGLRADPMCSACEMAVVWMQNQLAQNKTQDLILDYVNQLCNRLP

>d1e68a\_ a.64.2.1 (A:) Bacteriocin AS-48 {Enterococcus faecalis}

MAKEFGIPAAVAGTVLNVVEAGGWVTTIVSILTAVGSGGLSLLAAAGRESIKAYLKKEIKKKGKRAVIAW

>d1ain\_\_ a.65.1.1 (-) Annexin I {Human (Homo sapiens)}

GSAVSPYPTFNPSSDVAALHKAIMVKGVDEATIIDILTKRNNAQRQQIKAAYLQETGKPLDETLKKALTGHLEEVVLALLKTPAQFDADELRAAMKGLGTDEDTLIEILASRTNKEIRDINRVYREELKRDLAKDITSDTSGDFRNALLSLAKGDRSEDFGVNEDLADSDARALYEAGERRKGTDVNVFNTILTTRSYPQLRRVFQKYTKYSKHDMNKVLDLELKGDIEKCLTAIVKCATSKPAFFAEKLHQAMKGVGTRHKALIRIMVSRSEIDMNDIKAFYQKMYGISLCQAILDETKGDYEKILVALCGGN

>d1bo9a\_ a.65.1.1 (A:) Annexin I {Human (Homo sapiens)}

TFNPSSDVAALHKAIMVKGVDEATIIDILTKRNNAQRQQIKAAYLQETGKPLDETLKKALTGHLEEVVLALLK

>d1hm6a\_ a.65.1.1 (A:) Annexin I {Pig (Sus scrofa)}

AMVSEFLKQAWFIDNEEQEYIKTVKGSKGGPGSAVSPYPTFNPSSDVEALHKAITVKGVDEATIIEILTKRTNAQRQQIKAAYLQEKGKPLDEALKKALTGHLEEVALALLKTPAQFDADELRAAMKGLGTDEDTLNEILASRTNREIREINRVYKEELKRDLAKDITSDTSGDYQKALLSLAKGDRSEDLAINDDLADTDARALYEAGERRKGTDLNVFITILTTRSYPHLRRVFQKYSKYSKHDMNKVLDLELKGDIENCLTVVVKCATSKPMFFAEKLHQAMKGIGTRHKTLIRIMVSRSEIDMNDIKACYQKLYGISLCQAILDETKGDYEKILVALCG

>d1axn\_\_ a.65.1.1 (-) Annexin III {Human (Homo sapiens)}

SASIWVGHRGTVRDYPDFSPSVDAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEYQAAYGKELKDDLKGDLSGHFEHLMVALVTPPAVFDAKQLKKSMKGAGTNEDALIEILTTRTSRQMKDISQAYYTVYKKSLGDDISSETSGDFRKALLTLADGRRDESLKVDEHLAKQDAQILYKAGENRWGTDEDKFTEILCLRSFPQLKLTFDEYRNISQKDIVDSIKGELSGHFEDLLLAIVNCVRNTPAFLAERLHRALKGIGTDEFTLNRIMVSRSEIDLLDIRTEFKKHYGYSLYSAIKSDTSGDYEITLLKICGGDD

>d1i4aa\_ a.65.1.1 (A:) Annexin IV {Cow (Bos taurus)}

ASGFNAAEDAQTLRKAMKGLGTDEDAIINVLAYRSTAQRQEIRTAYKTTIGRDLMDDLKSELSGNFEQVILGMMTPTVLYDVQELRKAMKGAGTDEGCLIEILASRTPEEIRRINQTYQLQYGRSLEDDIRSDTSFMFQRVLVSLSAGGRDESNYLDDALMRQDAQDLYEAGEKKWGTDEVKFLTVLCSRNRNHLLHVFDEYKRIAQKDIEQSIKSETSGSFEDALLAIVKCMRNKSAYFAERLYKSMKGLGTDDDTLIRVMVSRAEIDMLDIRANFKRLYGKSLYSFIKGDTSGDYRKVLLILCGGDD

>d1ala\_\_ a.65.1.1 (-) Annexin V {Chicken (Gallus gallus)}

KYTRGTVTAFSPFDARADAEALRKAMKGMGTDEETILKILTSRNNAQRQEIASAFKTLFGRDLVDDLKSELTGKFETLMVSLMRPARIFDAHALKHAIKGAGTNEKVLTEILASRTPAEVQNIKQVYMQEYEANLEDKITGETSGHFQRLLVVLLQANRDPDGRVEEALVEKDAQVLFRAGELKWGTDEETFITILGTRSVSHLRRVFDKYMTISGFQIEETIDRETSGDLEKLLLAVVKCIRSVPAYFAETLYYSMKGAGTDDDTLIRVMVSRSEIDLLDIRHEFRKNFAKSLYQMIQKDTSGDYRKALLLLCGG

>d1hvd\_\_ a.65.1.1 (-) Annexin V {Human (Homo sapiens)}

VLRGTVTDFPGFDGRADAETLRKAMKGLGTDEESILTLLTSRSNAQRQEISAAFKTLFGRDLLDDLKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEEYGSSLEDDVVGDTSGYYQRMLVVLLQANRDPDAGIDEAQVEQDAQALFQAGELKWGTDEEKFITIFGTRSVSHLRKVFDKYMTISGFQIEETIDRETSGNLEQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLC

>d1g5na\_ a.65.1.1 (A:) Annexin V {Rat (Rattus norvegicus)}

ALRGTVTDFSGFDGRADAEVLRKAMKGLGTDEDSILNLLTARSNAQRQQIAEEFKTLFGRDLVNDMKSELTGKFEKLIVALMKPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPEELRAIKQAYEEEYGSNLEDDVVGDTSGYYQRMLVVLLQANRDPDTAIDDAQVELDAQALFQAGELKWGTDEEKFITILGTRSVSHLRRVFDKYMTISGFQIEETIDRETSGNLENLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMIKGDTSGDYKKALLLLCGGEDD

>d1avc\_1 a.65.1.1 (10-350) Annexin VI {Cow (Bos taurus)}

YRGSIRDFPDFNPSQDAETLYNAMKGFGSDKEAIINLITSRSNKQRQEICQNYKSLYGKDLIADLKYELTGKFERLIVGLMRPPAYADAKEIKDAISGIGTDEKCLIEILASRTNEQIHQLVAAYKDAYERDLEADITGDTSGHFRKMLVVLLQGTREEDDVVSEDLVQQDVQDLYEAGELKWGTDEAQFIYILGNRSKQHLRLVFDEYLKTTGKPIEASIRGELSGDFEKLMLAVVKCIRSTAEYFAERLFKAMKGLGTRDNTLIRIMVSRSELDMLDIREIFRTKYEKSLYSMIKNDTSGEYKKTLLKLCGGDDDAAGQFFPEAAQVAYQMWELSAVAR

>d1avc\_2 a.65.1.1 (351-671) Annexin VI {Cow (Bos taurus)}

VELKGTVRPAGDFNPDADAKALRKAMKGLGTDEDTIIDIITHRSNAQRQQIRQTFKSHFGRDLMADLKSELSGDLARLILGLMMPPAHYDAKQLKKAMEGAGTDEKALIEILATRTNAEIQAINKAYKEDYHKTLEDALSSDTSGHFKRILISLATGNREEGGEDRERAREDAQVAAEILEIADTTSGDKSSLETRFMMILCTRSYPDLRRVFQEFVKMTNYDVEHTIKKEMSGDVRDVFVAIVQSVKNKPLFFADKLYKSMKGAGTEEKTLTRIMVSRSEIDLLNIRREFIEKYDKSLHQAIEGDTSGHFLKALLAICGG

>d1dm5a\_ a.65.1.1 (A:) Annexin XII {Hydra vulgaris}

VVQGTVKPHASFNSREDAETLRKAMKGIGTDEKSITHILATRSNAQRQQIKTDYTTLFGKHLEDELKSELSGNYEAAALALLRKPDEFLAEQLHAAMKGLGTDKNALIDILCTQSNAQIHAIKAAFKLLYKEDLEKEIISETSGNFQRLLVSMLQGGRKEDEPVNAAHAAEDAAAIYQAGEGQIGTDESRFNAVLATRSYPQLHQIFHEYSKISNKTILQAIENEFSGDIKNGLLAIVKSVENRFAYFAERLHHAMKGLGTSDKTLIRILVSRSEIDLANIKETFQAMYGKSLYEFIADDCSGDYKDLLLQITGH

>d1dk5a\_ a.65.1.1 (A:) Annexin 24(ca32) {Bell pepper (Capsicum annuum)}

HHHHMASLTVPAHVPSAAEDCEQLRSAFKGWGTNEKLIISILAHRTAAQRKLIRQTYAETFGEDLLKELDRELTHDFEKLVLVWTLDPSERDAHLAKEATKRWTKSNFVLVELACTRSPKELVLAREAYHARYKKSLEEDVAYHTTGDHRKLLVPLVSSYRYGGEEVDLRLAKAESKILHEKISDKAYSDDEVIRILATRSKAQLNATLNHYKDEHGEDILKQLEDGDEFVALLRATIKGLVYPEHYFVEVLRDAINRRGTEEDHLTRVIATRAEVDLKIIADEYQKRDSIPLGRAIAKDTRGDYESMLLALLGQE

>d1azsc1 a.66.1.1 (C:86-201) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}

GEKATKVQDIKNNLKEAIETIVAAMSNLVPPVELANPENQFRVDYILSVMNVPDFDFPPEFYEHAKALWEDEGVRACYERSNEYQLIDCAQYFLDKIDVIKQDDYVPSDQDLLRCR

>d1tada1 a.66.1.1 (A:57-177) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}

YSLEECLEFIAIIYGNTLQSILAIVRAMTTLNIQYGDSARQDDARKLMHMADTIEEGTMPKEMSDIIQRLWKDSGIQACFDRASEYQLNDSAGYYLSDLERLVTPGYVPTEQDVLRSRVKT

>d1cipa1 a.66.1.1 (A:61-181) Transducin (alpha subunit), insertion domain {Rat (Rattus norvegicus)}

YSEEECKQYKAVVYSNTIQSIIAIIRAMGRLKIDFGDAARADDARQLFVLAGAAEEGFMTAELAGVIKRLWKDSGVQACFNRSREYQLNDSAAYYLNDLDRIAQPNYIPTQQDVLRTRVKT

>d1ej5a\_ a.68.1.1 (A:) Wiscott-Aldrich syndrome protein, WASP, C-terminal domain {Human (Homo sapiens)}

SGFKHVSHVGWDPQNGFDVNNLDPDLRSLFSRAGISEAQLTDAETSKLIYDFIEDQGGLEAVRQEMRRQGGSGGSQSSEGLVGALMHVMQKRSRAIHSSDEGEDQAG

>d1e79a1 a.69.1.1 (A:380-510) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

TRAMKQVAGTMKLELAQYREVAAFAQFGSDLDAATQQLLSRGVRLTELLKQGQYSPMAIEEQVAVIYAGVRGYLDKLEPSKITKFENAFLSHVISQHQALLGKIRTDGKISEESDAKLKEIVTNFLAGFEA

>d1e79d1 a.69.1.1 (D:358-475) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

MDPNIVGSEHYDVARGVQKILQDYKSLQDIIAILGMDELSEEDKLTVSRARKIQRFLSQPFQVAEVFTGHLGKLVPLKETIKGFQQILAGEYDHLPEQAFYMVGPIEEAVAKADKLAE

>d1skyb1 a.69.1.1 (B:372-502) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

IKAMKKVAGTLRLDLAAYRELEAFAQFGSDLDKATQANVARGARTVEVLKQDLHQPIPVEKQVLIIYALTRGFLDDIPVEDVRRFEKEFYLWLDQNGQHLLEHIRTTKDLPNEDDLNQAIEAFKKTFVVSQ

>d1skye1 a.69.1.1 (E:357-470) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

EIVGEEHYQVARKVQQTLERYKELQDIIAILGMDELSDEDKLVVHRARRIQFFLSQNFHVAEQFTGQPGSYVPVKETVRGFKEILEGKYDHLPEDRFRLVGRIEEVVEKAKAMG

>d1fx0a1 a.69.1.1 (A:373-501) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

IKAMKKVAGKLKLELAQFAELEAFAQFASDLDKATQNQLARGQRLRELLKQPQSAPLTVEEQVMTIYTGTNGYLDSLELDQVRKYLVELRTYVKTNKPEFQEIISSTKTFTEEAEALLKEAIQEQMERF

>d1fx0b1 a.69.1.1 (B:378-485) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

RIVGEEHYEIAQRVKETLQRYKELQDIIAILGLDELSEEDRLTVARARKIERFLSQPFFVAEVFTGSPGKYVGLAETIRGFQLILSGELDSLPEQAFYLVGNIDEATA

>d1fkma1 a.69.2.1 (A:249-442) Ypt/Rab-GAP domain of gyp1p {Baker's yeast (Saccharomyces cerevisiae)}

NSIIQRISKFDNILKDKTIINQQDLRQISWNGIPKIHRPVVWKLLIGYLPVNTKRQEGFLQRKRKEYRDSLKHTFSDQHSRDIPTWHQIEIDIPRTNPHIPLYQFKSVQNSLQRILYLWAIRHPASGYVQGINDLVTPFFETFLTEYLPPSQIDDVEIKDPSTYMVDEQITDLEADTFWCLTKLLEQITDNYIH

>d1fkma2 a.69.2.1 (A:443-630) Ypt/Rab-GAP domain of gyp1p {Baker's yeast (Saccharomyces cerevisiae)}

GQPGILRQVKNLSQLVKRIDADLYNHFQNEHVEFIQFAFRWMNCLLMREFQMGTVIRMWDTYLSETSQEVTSSYSMSSNDIKPPVTPTEPRVASFVTPTKDFQSPTTALSNMTPNNAVEDSGKMRQSSLNEFHVFVCAAFLIKWSDQLMEMDFQETITFLQNPPTKDWTETDIEMLLSEAFIWQSLYK

>d1k5ha1 a.69.3.1 (A:301-398) 1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain {Escherichia coli}

KLSALTFAAPDYDRYPCLKLAMEAFEQGQAATTALNAANEITVAAFLAQQIRFTDIAALNLSVLEKMDMREPQCVDDVLSVDANAREVARKEVMRLAS

>d1abv\_\_ a.70.1.1 (-) N-terminal domain of the delta subunit of the F1F0-ATP synthase {Escherichia coli}

SEFITVARPYAKAAFDFAVEHQSVERWQDMLAFAAEVTKNEQMAELLSGALAPETLAESFIAVCGEQLDENGQNLIRVMAENGRLNALPDVLEQFIHLRAVSEAT

>d1g7da\_ a.71.1.1 (A:) Endoplasmic reticulum protein ERP29, C-domain {Rat (Rattus norvegicus)}

PGCLPAYDALAGQFIEASSREARQAILKQGQDGLSGVKETDKKWASQYLKIMGKILDQGEDFPASELARISKLIENKMSEGKKEELQRSLNILTAFRKKGAEKEEL

>d1dvka\_ a.72.1.1 (A:) Functional domain of the splicing factor Prp18 {Baker's yeast (Saccharomyces cerevisiae)}

MRIQEAIAQDKTISVIIDPSQIGSTEGKPLLSMKCNLYIHEILSRWKASLEAYHPELFLDTKKALFPLLLQLRRNQLAPDLLISLATVLYHLQQPKEINLAVQSYMKLSIGNVAWPIGVTSVGIHARSAHSKIQGGRNAANIMIDERTRLWITSIKRLITFEEWYTSNH

>d1ak4c\_ a.73.1.1 (C:) HIV-1 capsid protein {Human immunodeficiency virus type 1}

PIVQNLQGQMVHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRLHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTHNPPIPVGEIYKRWIILGLNKIVRMY

>d1e6jp2 a.73.1.1 (P:11-147) HIV-1 capsid protein {Human immunodeficiency virus type 1}

VHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDRVHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMTNNPPIPVGEIYKRWIILGLNKIVRMYSP

>d2eiaa2 a.73.1.1 (A:17-147) EIAV capsid protein p26 {Equine infectious anemia virus}

PRGYTTWVNTIQTNGLLNEASQNLFGILSVDCTSEEMNAFLDVVPGQAGQKQILLDAIDKIADDWDNRHPLPNAPLVAPPQGPIPMTARFIRGLGVPRERQMEPAFDQFRQTYRQWIIEAMSEGIKVMIGK

>d1g03a\_ a.73.1.1 (A:) HTLV-I capsid protein {Human T-cell leukemia virus type 1}

PVMHPHGAPPNHRPWQMKDLQAIKQEVSQAAPGSPQFMQTIRLAVQQFDPTAKDLQDLLQYLCSSLVASLHHQQLDSLISEAETRGITSYNPLAGPLRVQANNPQQQGLRREYQQLWLAAFAALPGSAKDPSWA

>g1qrj.1 a.73.1.1 (A:,B:16-130) HTLV-I capsid protein {Human T-cell leukemia virus type 1}

HHHHHSSGHIEGRHMXQMKDLQAIKQEVSQAAPGSPQFMQTIRLAVQQFDPTAKDLQDLLQYLCSSLVASLHHQQLDSLISEAETRGITGYNPLAGPLRVQANNPQQQGLRREYQQLWLAAFAALPGSAKD

>d1d1da2 a.73.1.1 (A:11-150) RSV capsid protein {Rous sarcoma virus}

WTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVILGPAPYALWMDAWGVQLQTVIAAATRDPRHPANGQGRGERTNLDRLKGLADGMVGNPQGQAALLRPGELVAITASALQAFREVARLAEPA

>d1em9a\_ a.73.1.1 (A:) RSV capsid protein {Rous sarcoma virus}

PVVIKTEGPAWTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVILGPAPYALWMDAWGVQLQTVIAAATRDPRHPANGQGRGERTNLNRLKGLADGMVGNPQGQAALLRPGELVAITASALQAFREVARLA

>d1jsub2 a.74.1.1 (B:310-432) Cyclin A {Human (Homo sapiens)}

TVNQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSVIAGAAFHLALYTVTGQSWPESLIRKTGYTLESLKPCLMDLHQTYLKAPQHAQQSIREKYKNSKYHGVSLLNPPETLNL

>d1vin\_1 a.74.1.1 (181-308) Cyclin A {Cow (Bos taurus)}

DIHTYLREMEVKCKPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYIDRFLSSMSVLRGKLQLVGTAAMLLASKFEEIYPPEVAEFVYITDDTYTKKQVLRMEHLVLKVLAFDLAA

>d1vin\_2 a.74.1.1 (309-432) Cyclin A {Cow (Bos taurus)}

PTINQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSVIAAAAFHLALYTVTGQSWPESLVQKTGYTLETLKPCLLDLHQTYLRAPQHAQQSIREKYKNSKYHGVSLLNPPETLNL

>d1jkw\_1 a.74.1.1 (11-161) Cyclin H (mcs2) {Human (Homo sapiens)}

WTFSSEEQLARLRADANRKFRCKAVANGKVLPNDPVFLEPHEEMTLCKYYEKRLLEFCSVFKPAMPRSVVGTACMYFKRFYLNNSVMEYHPRIIMLTCAFLACKVDEFNVSSPQFVGNLRESPLGQEKALEQILEYELLLIQQLNFHLIVH

>d1jkw\_2 a.74.1.1 (162-287) Cyclin H (mcs2) {Human (Homo sapiens)}

NPYRPFEGFLIDLKTRYPILENPEILRKTADDFLNRIALTDAYLLYTPSQIALTAILSSASRAGITMESYLSESLMLKENRTCLSQLLDIMKSMRNLVKKYEPPRSEEVAVLKQKLDRCHSAELAL

>d1bu2a1 a.74.1.1 (A:22-148) Viral cyclin {Herpes virus saimiri}

RVLNNLKLRELLLPKFTSLWEIQTEVTVDNRTILLTWMHLLCESFELDKSVFPLSVSILDRYLCKKQGTKKTLQKIGAACVLIGSKIRTVKPMTVSKLTYLSCDCFTNLELINQEKDILEALKWDTE

>d1bu2a2 a.74.1.1 (A:149-250) Viral cyclin {Herpes virus saimiri}

AVLATDFLIPLCNALKIPEDLWPQLYEAASTTICKALIQPNIALLSPGLICAGGLLTTIETDNTNCRPWTCYLEDLSSILNFSTNTVRTVKDQVSEAFSLYD

>d1f5qb1 a.74.1.1 (B:6-146) Viral cyclin {Murine herpes virus gamma 68}

FQGFLDSSLLNEEDCRQMIYRSEREHDARMVGVNVDQHFTSQYRKVLTTWMFCVCKDLRQDNNVFPLAVALLDELFLSTRIDRENYQSTAAVALHIAGKVRAYMPIKATQLAYLCGGATTADKLLTLEVKSLDTLSWVADR

>d1f5qb2 a.74.1.1 (B:147-252) Viral cyclin {Murine herpes virus gamma 68}

CLSTDLICYILHIMHAPREDYLNIYNLCRPKIFCALCDGRSAMKRPVLITLACMHLTMNQKYDYYENRIDGVCKSLYITKEELHQCCDLVDIAIVSFDENYFKINA

>d1g3nc1 a.74.1.1 (C:16-147) Viral cyclin {Kaposi sarcoma-associated virus}

LCEDRIFYNILEIEPRFLTSDSVFGTFQQSLTSHMRKLLGTWMFSVCQEYNLEPNVVALALNLLDRLLLIKQVSKEHFQKTGSACLLVASKLRSLTPISTSSLCYAAADSFSRQELIDQEKELLEKLAWRTE

>d1g3nc2 a.74.1.1 (C:148-253) Viral cyclin {Kaposi sarcoma-associated virus}

AVLATDVTSFLLLKLVGGSQHLDFWHHEVNTLITKALVDPLTGSLPASIISAAGCALLVPANVIPQDTHSGGVVPQLASILGCDVSVLQAAVEQILTSVSDFDLRI

>d1vola1 a.74.1.2 (A:113-207) Transcription factor IIB (TFIIB), core domain {Human (Homo sapiens)}

AMMNAFKEITTMADRINLPRNKVDRTNNLFRQAYEQKSLKGRANDAIASACLYIACRQEGVPRTFKEICAVSRISKKEIGRCFKLILKALETSVD

>d1vola2 a.74.1.2 (A:208-316) Transcription factor IIB (TFIIB), core domain {Human (Homo sapiens)}

LITTGDFMSRFCSNLCLPKQVQMAATHIARKAVELDLVPGRSPISVAAAAIYMASQASAEKRTQKEIGDIAGVADVTIRQSYRLIYPRAPDLFPTDFKFDTPVDKLPQL

>d1aisb1 a.74.1.2 (B:1108-1205) Transcription factor IIB (TFIIB), core domain {Archaeon Pyrococcus woesei}

NLAFALSELDRITAQLKLPRHVEEEAARLYREAVRKGLIRGRSIESVMAACVYAACRLLKVPRTLDEIADIARVDKKEIGRSYRFIARNLNLTPKKLF

>d1aisb2 a.74.1.2 (B:1206-1300) Transcription factor IIB (TFIIB), core domain {Archaeon Pyrococcus woesei}

VKPTDYVNKFADELGLSEKVRRRAIEILDEAYKRGLTSGKSPAGLVAAALYIASLLEGEKRTQREVAEVARVTEVTVRNRYKELVEKLKIKVPIA

>d1guxa\_ a.74.1.3 (A:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}

NTIQQLMMILNSASDQPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGVRLYYRVMESMLKSEEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSGTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLAWLSDSPLFDLIKQSK

>d1guxb\_ a.74.1.3 (B:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}

TSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEEYDSIIVFYNSVFMQRLKTNILQYASTRPPTLSPIPHI

>d1k8ke\_ a.148.1.1 (E:) Arp2/3 complex 21 kDa subunit ARPC3 {Cow (Bos taurus)}

PAYHSSLMDPDTKLIGNMALLPIRSQFKGPAPRETKDTDIVDEAIYYFKANVFFKNYEIKNEADRTLIYITLYISECLKKLQKCNSKSQGEKEMYTLGITNFPIPGEPGFPLNAIYAKPANKQEDEVMRAYLQQLRQETGLRLCEKVFDPQNDKPSKWWTCFVKRQFMNKSLSG

>d1jfza\_ a.149.1.1 (A:) RNase III endonuclease domain {Aquifex aeolicus}

GMKMLEQLEKKLGYTFKDKSLLEKALTHVSYSKKEHYETLEFLGDALVNFFIVDLLVQYSPNKREGFLSPLKAYLISEEFFNLLAQKLELHKFIRIKRGKINETIIGDVFEALWAAVYIDSGRDANFTRELFYKLFKEDILSAIKEGR

>d1hus\_\_ a.75.1.1 (-) Ribosomal protein S7 {Bacillus stearothermophilus}

RDVLPDPIYNSKLVTRLINKIMIDGKKSKAQKILYTAFDIIRERTGKDPMEVFEQALKNVMPVLEVRARRVGGANYQVPVEVRPDRRVSLGLRWLVQYARLRNEKTMEERLANEIMDAANNTGAAVKKREDTHKMAEAN

>d1rss\_\_ a.75.1.1 (-) Ribosomal protein S7 {Thermus thermophilus}

LQPDLVYGDVLVTAFINKIMRDGKKNLAARIFYDACKIIQEKTGQEPLKVFKQAVENVKPRMEVRSRRVGGANYQVPMEVSPRRQQSLALRWLVQAANQRPERRAAVRIAHELMDAAEGKGGAVKKKEDVERMAEANRAYAHYRW

>d1iqva\_ a.75.1.1 (A:) Ribosomal protein S7 {Archaeon Pyrococcus horikoshii}

IKVMGRWSTEDVEVKDPSLKPYINLEPRLLPHTHGRHAKKHFGKANVHIVERLINKVMRSGGSHYKVAGHFMRREHRSLNSKKVRAYEVVKEAFKIIEKRTGKNPIQVLVWAIENAAPREDTTSVMFGGIRYHVAVDISPLRRLDVALRNIALGASAKCYRTKMSFAEALAEEIILAANKDPKSYAYSKKLEIERIAESSR

>d1jr3a1 a.80.1.1 (A:243-368) gamma subunit {Escherichia coli}

TLDDDQALSLVEAMVEANGERVMALINEAAARGIEWEALLVEMLGLLHRIAMVQLSPAALGNDMAAIELRMRELARTIPPTDIQLYYQTLLIGRKELPYAPDRRMGVEMTLLRALAFHPRMPLPEP

>d1a5t\_1 a.80.1.1 (208-330) delta prime subunit {Escherichia coli}

DNWQARETLCQALAYSVPSGDWYSLLAALNHEQAPARLHWLATLLMDALKRHHGAAQVTNVDVPGLVAELANHLSPSRLQAILGDVCHIREQLMSVTGINRELLITDLLLRIEHYLQPGVVLP

>d1jr3d1 a.80.1.1 (D:212-338) delta subunit {Escherichia coli}

FTPFHWVDALLMGKSKRALHILQQLRLEGSEPVILLRTLQRELLLLVNLKRQSAHTPLRALFDKHRVWQNRRGMMGEALNRLSQTQLRQAVQLLTRTELTLKQDYGQSVWAELEGLSLLLCHKPLAD

>d1iqpa1 a.80.1.1 (A:233-327) Replication factor C {Archaeon Pyrococcus furiosus}

RARPEDIREMMLLALKGNFLKAREKLREILLKQGLSGEDVLVQMHKEVFNLPIEEPKKVLLADKIGEYNFRLVEGANEIIQLEALLAQFTLIGKK

>d1jr5a\_ a.150.1.1 (A:) Anti-sigma factor Asia {Bacteriophage T4}

MNKNIDTVREIITVASILIKFSREDIVENRANFIAFLNEIGVTHEGRKLNQNSFRKIVSELTQEDKKTLIDEFNEGFEGVYRYLEMYTNK

>d1f5ta2 a.76.1.1 (A:1065-1121) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}

TPTGRTLATAVMRKHRLAERLLTDIIGLDINKVHDEADRWEHVMSDEVERRLVKVLK

>d1g3sa2 a.76.1.1 (A:65-140) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}

TPTGRTLATAVMRKHRLAERLLTDIIGLDINKVHDEASRWEHVMSDEVERRLVKVLKDVSRSPFGNPIPGLDELGV

>d1fx7a2 a.76.1.1 (A:65-144) Iron-dependent regulator {Mycobacterium tuberculosis}

TEKGRALAIAVMRKHRLAERLLVDVIGLPWEEVHAEACRWEHVMSEDVERRLVKVLNNPTTSPFGNPIPGLDELGVGPEP

>d1gpja1 a.151.1.1 (A:303-404) Glutamyl tRNA-reductase dimerization domain {Archaeon Methanopyrus kandleri}

EIPKVEKLIEEELSTVEEELEKLKERRLVADVAKSLHEIKDRELERALRRLKTGDPENVLQDFAEAYTKRLINVLTSAIMELPDEYRRAASRALRRASELNG

>d1ngr\_\_ a.77.1.1 (-) p75 low affinity neurotrophin receptor {Rat (Rattus norvegicus)}

GNLYSSLPLTKREEVEKLLNGDTWRHLAGELGYQPEHIDSFTHEACPVRALLASWGAQDSATLDALLAALRRIQRADIVESLCSE

>d1ddf\_\_ a.77.1.1 (-) Fas {Human (Homo sapiens)}

METVAINLSDVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLVLEHHHHHH

>d1a1w\_\_ a.77.1.1 (-) FADD (Mort1) {Human (Homo sapiens)}

MDPFLVLLHSVSSSLSSSELTELKYLCLGRVGKRKLERVQSGLDLFSMLLEQNDLEPGHTELLRELLASLRRHDLLRRVDDFE

>d1e41a\_ a.77.1.1 (A:) FADD (Mort1) {Human (Homo sapiens)}

GSHMGEEDLCAAFNVICDNVGKDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTEKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGA

>d1fada\_ a.77.1.1 (A:) FADD (Mort1) {Mouse (Mus musculus)}

AAPPGEAYLQVAFDIVCDNVGRDWKRLARELKVSEAKMDGIEEKYPRSLSERVRESLKVWKNAEKKNASVAGLVKALRTCRLNLVADLVEEAQES

>d3crd\_\_ a.77.1.1 (-) Raidd CARD domain {Human (Homo sapiens)}

MEARDKQVLRSLRLELGAEVLVEGLVLQYLYQEGILTENHIQEINAQTTGLRKTMLLLDILPSRGPKAFDTFLDSLQEFPWVREKLKKAREEAMTDLPAG

>d1cy5a\_ a.77.1.1 (A:) Apoptotic protease activating factor 1, APAF-1 {Human (Homo sapiens)}

MDAKARNCLLQHREALEKDIKTSYIMDHMISDGFLTISEEEKVRNEPTQQQRAAMLIKMILKKDNDSYVSFYNALLHEGYKDLAALLHDGIPV

>d3ygsp\_ a.77.1.1 (P:) Procaspase 9 prodomain {Human (Homo sapiens)}

SMDEADRRLLRRCRLRLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRRDQARQLIIDLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAG

>d1dgna\_ a.77.1.1 (A:) Iceberg {Human (Homo sapiens)}

ADQLLRKKRRIFIHSVGAGTINALLDCLLEDEVISQEDMNKVRDENDTVMDKARVLIDLVTGKGPKSCCKFIKHLCEEDPQLASKMGLH

>d1d2za\_ a.77.1.1 (A:) Pelle death domain {Drosophila melanogaster}

LDNTMAIRLLPLPVRAQLCAHLDALDVWQQLATAVKLYPDQVEQISSQKQRGRSASNEFLNIWGGQYNHTVQTLFALFKKLKLHNAMRLIKDYVSEDLHKYI

>d1d2zb\_ a.77.1.1 (B:) Tube death domain {Drosophila melanogaster}

LSSKYSRNTELRRVEDNDIYRLAKILDENSCWRKLMSIIPKGMDVQACSGAGCLNFPAEIKKGFKYTAQDVFQIDEAANRLPPDQSKSQMMIDEWKTSGKLNERPTVGVLLQLLVQAELFSAADFVALDFLNESTPARPVDGPGALISLE

>d1hw1a2 a.78.1.1 (A:79-230) Fatty acid responsive transcription factor FadR, C-terminal domain {Escherichia coli}

GLNILETLARLDHESVPQLIDNLLSVRTNISTIFIRTAFRQHPDKAQEVLATANEVADHADAFAELDYNIFRGLAFASGNPIYGLILNGMKGLYTRIGRHYFANPEARSLALGFYHKLSALCSEGAHDQVYETVRRYGHESGEIWHRMQKNL

>d1eyva\_ a.79.1.1 (A:) Antitermination factor NusB {Mycobacterium tuberculosis}

GRHQARKRAVALLFEAEVRGISAAEVVDTRAALAEAKPDIARLHPYTAAVARGVSEHAAHIDDLITAHLRGWTLDRLPAVDRAILRVSVWELLHAADVPEPVVVDEAVQLAKELSTDDSPGFVNGVLGQVM

>d1ey1a\_ a.79.1.1 (A:) Antitermination factor NusB {Escherichia coli}

MKPAARRRARECAVQALYSWQLSQNDIADVEYQFLAEQDVKDVDVLYFRELLAGVATNTAYLDGLMKPYLSRLLEELGQVEKAVLRIALYELSKRSDVPYKVAINEAIELAKSFGAEDSHKFVNGVLDKAAPVIRPNKK

>d1b79a\_ a.81.1.1 (A:) N-terminal domain of DnaB helicase {Escherichia coli}

PPHSIEAEQSVLGGLMLDNERWDDVAERVVADDFYTRPHRHIFTEMARLQESGSPIDLITLAESLERQGQLDSVGGFAYLAELSKNTPSAANISAYADIVRE

>d1jwea\_ a.81.1.1 (A:) N-terminal domain of DnaB helicase {Escherichia coli}

MKVPPHSIEAEQSVLGGLMLDNERWDDVAERVVADDFYTRPHRHIFTEMARLQESGSPIDLITLAESLERQGQLDSVGGFAYLAELSKNTPSAANISAYADIVRERAVVREMIS

>d1qc7a\_ a.82.1.1 (A:) FliG C-terminal domain {Thermotoga maritima}

MFVFEDILKLDDRSIQLVLREVDTRDLALALKGASDELKEKIFKNMSKRAAALLKDELEYMGPVRLKDVEEAQQKIINIIRRLEEAGEIVIARGGGEELIM

>d1qc7b\_ a.82.1.1 (B:) FliG C-terminal domain {Thermotoga maritima}

MFVFEDILKLDDRSIQLVLREVDTRDLALALKGASDELKEKIFKNMSKRAAALLKDELEYMGPVRLKDVEEAQQKIINIIRRLEEAGEIV

>d1crka1 a.83.1.1 (A:1-98) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), mitochondria}

TVHEKRKLFPPSADYPDLRKHNNCMAECLTPAIYAKLRDKLTPNGYSLDQCIQTGVDNPGHPFIKTVGMVAGDEESYEVFAEIFDPVIKARHNGYDPR

>d1qh4a1 a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), brain-type}

PFSNSHNLLKMKYSVDDEYPDLSVHNNHMAKVLTLDLYKKLRDRQTSSGFTLDDVIQTGVDNPGHPFIMTVGCVAGDEESYEVFKELFDPVIEDRHGGYKP

>d1qk1a1 a.83.1.1 (A:1-102) Creatine kinase, N-terminal domain {Human (Homo sapiens), mitochondria}

AASERRRLYPPSAEYPDLRKHNNCMASHLTPAVYARLCDKTTPTGWTLDQCIQTGVDNPGHPFIKTVGMVAGDEETYEVFADLFDPVIQERHNGYDPRTMKH

>d2crka1 a.83.1.1 (A:8-102) Creatine kinase, N-terminal domain {Rabbit (Oryctolagus cuniculus)}

NKYKLNYKSEEEYPDLSKHNNHMAKVLTPDLYKKLRDKETPSGFTLDDVIQTGVDNPGHPFIMTVGCVAGDEESYTVFKDLFDPIIQDRHGGFKP

>d1g0wa1 a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Cow (Bos taurus), retinal isoform}

PFSNSHNTLKLRFPAEDEFPDLSGHNNHMAKVLTPELYAELRAKSTPSGFTVDDVIQTGVDNPGHPYIMTVGCVAGDEESYDVFKELFDPIIEDRHGGYKP

>d1bg0\_1 a.83.1.1 (2-95) Arginine kinase {Horseshoe crab (Limulus polyphemus)}

VDQATLDKLEAGFKKLQEASDCKSLLKKHLTKDVFDSIKNKKTGMGATLLDVIQSGVENLDSGVGIYAPDAESYRTFGPLFDPIIDDYHGGFKL

>d1al01\_ a.84.1.1 (1:) Scaffolding protein gpD of bacteriophage procapsid {Bacteriophage phi-X174}

EQSVRFQTALASIKLIQASAVLDLTEDDFDFLTSNKVWIATDRSRARRCVEACVYGTLDFVGYPRFPAPVEFIAAVIAYYVHPVNIQTACLIMEGAEFTENIINGVERPVKAAELFAFTLRVRAGNTDVLTDAEENVRQKLRA

>d1ll1\_1 a.85.1.1 (1-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus polyphemus)}

TLHDKQIRVCHLFEQLSSATVIRLKNVGKLQPGAIFSCFHPDHLEEARHLYEVFWEAGDFNDFIEIAKEARTFVNEGLFAFAAEVAVLHRDDCKGLYVP

>d1lla\_1 a.85.1.1 (2-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus polyphemus)}

LHDKQIRICHLFEQLSSATVIGDGDKHKHSDRLKNVGKLQPGAIFSCFHPDHLEEARHLYEVFWEAGDFNDFIEIAKEARTFVNEGLFAFAAEVAVLHRDDCKGLYVP

>d1hc2\_1 a.85.1.1 (5-135) Hemocyanin, N-terminal domain {Spiny lobster (Panulirus interruptus)}

TGNAQKQQDINHLLDKIYEPTKYPDLKDIAENFNPLGDTSIYNDHGAAVETLMKELNDHRLLEQRHWYSLFNTRQRKEALMLFAVLNQCKEWYCFRSNAAYFRERMNEGEFVYALYVSVIHSKLGDGIVLP

>d1lla\_2 a.86.1.1 (110-379) Hemocyanin {Horseshoe crab (Limulus polyphemus)}

PVQEIFPDKFIPSAAINEAFKKAHVRPEFDESPILVDVQDTGNILDPEYRLAYYREDVGINAHHWHWHLVYPSTWNPKYFGKKKDRKGELFYYMHQQMCARYDCERLSNGMHRMLPFNNFDEPLAGYAPHLTHVASGKYYSPRPDGLKLRDLGDIEISEMVRMRERILDSIHLGYVISEDGSHKTLDELHGTDILGALVESSYESVNHEYYGNLHNWGHVTMARIHDPDGRFHEEPGVMSDTSTSLRDPIFYNWHRFIDNIFHEYKNTLK

>d1hc2\_2 a.86.1.1 (136-398) Hemocyanin {Spiny lobster (Panulirus interruptus)}

PLYQITPHMFTNSEVIDKAYSAKMTQKPGTFNVSFTGTKKNREQRVAYFGEDIGMNIHHVTWHMDFPFWWEDSYGYHLDRKGELFFWVHHQLTARFDFERLSNWLDPVDELHWDRIIREGFAPLTSYKYGGEFPVRPDNIHFEDVDGVAHVHDLEITESRIHEAIDHGYITDSDGHTIDIRQPKGIELLGDIIESSKYSSNVQYYGSLHNTAHVMLGRQGDPHGKFNLPPGVMEHFETATRDPSFFRLHKYMDNIFKKHTDSF

>d1js8a1 a.86.1.1 (A:2503-2791) Functional unit from octopus hemocyanin {Giant octopus (Octopus dofleini)}

AIIRKNVNSLTPSDIKELRDAMAKVQADTSDNGYQKIASYHGIPLSCHYENGTAYACCQHGMVTFPNWHRLLTKQMEDALVAKGSHVGIPYWDWTTTFANLPVLVTEEKDNSFHHAHIDVANTDTTRSPRAQLFDDPDKGDKSFFYRQIALALEQTDFCDFEIQFEIGHNAIHSWVGGSSPYGMSTLHYTSYDPLFYLHHSNTDRIWSVWQALQKYRGLPYNTANCEINKLVKPLKPFNLDTNPNAVTKAHSTGATSFDYHKLGYDYDNLNFHGMTIPELEEHLKEIQH

>d1bt3a\_ a.86.1.2 (A:) Catechol oxidase {Sweet potato (Ipomoea batatas)}

APIQAPEISKCVVPPADLPPGAVVDNCCPPVASNIVDYKLPAVTTMKVRPAAHTMDKDAIAKFAKAVELMKALPADDPRNFYQQALVHCAYCNGGYDQVNFPDQEIQVHNSWLFFPFHRWYLYFYERILGKLIGDPSFGLPFWNWDNPGGMVLPDFLNDSTSSLYDSNRNQSHLPPVVVDLGYNGADTDVTDQQRITDNLALMYKQMVTNAGTAELFLGKAYRAGDAPSPGAGSIETSPHIPIHRWVGDPRNTNNEDMGNFYSAGRDIAFYCHHSNVDRMWTIWQQLAGKPRKRDYTDSDWLNATFLFYDENGQAVKVRIGDSLDNQKMGYKYAKTPLPWL

>d1dbha1 a.87.1.1 (A:198-404) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}

EQTYYDLVKAFMAEIRQYIRELNLIIKVFREPFVSNSKLFSANDVENIFSRIVDIHELSVKLLGHIEDTVEMTDEGSPHPLVGSCFEDLAEELAFDPYESYARDILRPGFHDRFLSQLSKPGAALYLQSIGEGFKEAVQYVLPRLLLAPVYHCLHYFELLKQLEEKSEDQEDKECLKQAITALLNVQSGMEKICSKSLAKRRLSESA

>d1by1a\_ a.87.1.1 (A:) beta-pix {Human (Homo sapiens)}

MKGFDTTAINKSYYNVVLQNILETENEYSKELQTVLSTYLRPLQTSEKLSSANISYLMGNLEEICSFQQMLVQSLEECTKLPEAQQRVGGCFLNLMPQMKTLYLTYCANHPSAVNVLTEHSEELGEFMETKGASSPGILVLTTGLSKPFMRLDKYPTLLKELERHMEDYHTDRQDIQKSMAAFKNLSAQCQEVRKRKELELQILTEAIR

>d1f5xa\_ a.87.1.1 (A:) RhoGEF Vav {Mouse (Mus musculus)}

MKGDEIYEDLMRLESVPTPPKMTEYDKRCCCLREIQQTEEKYTDTLGSIQQHFMKPLQRFLKPQDMETIFVNIEELFSVHTHFLKELKDALAGPGATTLYQVFIKYKERFLVYGRYCSQVESASKHLDQVATAREDVQMKLEECSQRANNGRFTLRDLLMVPMQRVLKYHLLLQELVKHTQDATEKENLRLALDAMRDLAQCVNEVKR

>d1foea1 a.87.1.1 (A:1034-1239) GEF of TIAM1 (T-Lymphoma invasion and metastasis indusing protein 1) {Mouse (Mus musculus)}

QLSDADKLRKVICELLETERTYVKDLNCLMERYLKPLQKETFLTQDELDVLFGNLTEMVEFQVEFLKTLEDGVRLVPDLEKLEKVDQFKKVLFSLGGSFLYYADRFKLYSAFCASHTKVPKVLVKAKTDTAFKAFLDAQNPRQQHSSTLESYLIKPIQRVLKYPLLLRELFALTDAESEEHYHLDVAIKTMNKVASHINEMQKIHE

>d1boua\_ a.88.1.1 (A:) LigA subunit of an aromatic-ring-opening dioxygenase LigAB {Sphingomonas paucimobilis, formerly Pseudomonas paucimobilis}

IDVHAYLAEFDDIPGTRVFTAQRARKGYNLNQFAMSLMKAENRERFKADESAYLDEWNLTPAAKAAVLARDYNAMIDEGGNVYFLSKLFSTDGKSFQFAAGSMTGMTQEEYAQMMIDGGRSPAGVRSIKGGY

>d1hbna1 a.89.1.1 (A:270-549) Alpha chain {Archaeon Methanobacterium thermoautotrophicum}

RRARGENEPGGVPFGYLADICQSSRVNYEDPVRVSLDVVATGAMLYDQIWLGSYMSGGVGFTQYATAAYTDNILDDFTYFGKEYVEDKYGLCEAPNNMDTVLDVATEVTFYGLEQYEEYPALLEDQFGGSQRAAVVAAAAGCSTAFATGNAQTGLSGWYLSMYLHKEQHSRLGFYGYDLQDQCGASNVFSIRGDEGLPLELRGPNYPNYAMNVGHQGEYAGISQAPHAARGDAFVFNPLVKIAFADDNLVFDFTNVRGEFAKGALREFEPAGERALITPA

>d1e6va1 a.89.1.1 (A:273-552) Alpha chain {Archaeon Methanopyrus kandleri}

RRARGENEPGGVPFGVLADCVQTMRKYPDDPAKVALEVIAAGAMLYDQIWLGSYMSGGVGFTQYATAVYPDNILDDYVYYGLEYVEDKYGIAEAEPSMDVVKDVATEVTLYGLEQYERYPAAMETHFGGSQRAAVCAAAAGCSTAFATGHAQAGLNGWYLSQILHKEGQGRLGFYGYALQDQCGAANSLSVRSDEGLPLELRGPNYPNYAMNVGHLGEYAGIVQAAHAARGDAFCVHPVIKVAFADENLVFDFTEPRKEFAKGALREFEPAGERDLIVPA

>d1e6ya1 a.89.1.1 (A:1284-1569) Alpha chain {Archaeon Methanosarcina barkeri}

RRARGPNEPGGLSFGHLSDIVQTSRVSEDPAKIALEVVGAGCMLYDQIWLGSYMSGGVGFTQYATAAYTDDILDNNTYYDVDYINDKYNGAATVGKDNKVKASLEVVKDIATESTLYGIETYEKFPTALEDHFGGSQRATVLAAAAGVACSLATGNANAGLSGWYLSMYLHKEAWGRLGFFGFDLQDQCGATNVLSYQGDEGLPDELRGPNYPNYAMNVGHQGGYAGIAQAAHSGRGDAFTVNPLLKVCFADDLLPFNFAEPRREFGRGAIREFVPAGERSLVIPA

>d1hbnb1 a.89.1.1 (B:189-443) Beta chain {Archaeon Methanobacterium thermoautotrophicum}

GYALRNIMVNHVVAATLKNTLQAAALSTILEQTAMFEMGDAVGAFERMHLLGLAYQGMNADNLVFDLVKANGKEGTVGSVIADLVERALEDGVIKVEKELTDYKVYGTDDLAMWNAYAAAGLMAATMVNQGAARAAQGVSSTLLYYNDLIEFETGLPSVDFGKVEGTAVGFSFFSHSIYGGGGPGIFNGNHIVTRHSKGFAIPCVAAAMALDAGTQMFSPEATSGLIKEVFSQVDEFREPLKYVVEAAAEIKNEI

>d1e6vb1 a.89.1.1 (B:190-442) Beta chain {Archaeon Methanopyrus kandleri}

GYALRNIMVNHIVAATRKNTMQAVCLAATLQQTAMFEMGDALGPFERLHLLGYAYQGLNADNMVYDIVKKHGKEGTVGTVVREVVERALEDGVIEVKEELPSFKVYKANDMDLWNAYAAAGLVAAVMVNQGAARAAQGVSATILYYNDLLEYETGLPGVDFGRAEGTAVGFSFFSHSIYGGGGPGIFHGNHIVTRHSKGFAIPPVAAAMALDAGTQMFSPEVTSKLIGDVFGEIDEFREPMKYITEAAAEEAK

>d1e6yb1 a.89.1.1 (B:2186-2433) Beta chain {Archaeon Methanosarcina barkeri}

GFSLRNIMANHVAAISNRNAMNASALSSIYEQSGIFEMGGAVGMFERHQLLGLAYQGLNANNLLYDIVKENGKDGTIGTVIESVVRRAIEAGIISVDKTAPSGYNFYKANDVPKWNACAAVGTLAATLVNCGAGRAAQNVSSTLLYFNDILEKETGLPGCDYGKVEGTAVGFSFFSHSIYGGGGPGVFNGNHVVTRHSRGFAIPCVCAAVALDAGTQMFSIESTSGLIGDVFGAIPEFREPIKAVAGV

>d1bgf\_\_ a.90.1.1 (-) Transcription factor STAT-4 N-domain {Mouse (Mus musculus)}

GGSQWNQVQQLEIKFLEQVDQFYDDNFPMEIRHLLAQWIETQDWEVASNNETMATILLQNLLIQLDEQLGRVSKEKNLLLIHNLKRIRKVLQGKFHGNPMHVAVVISNCLREERRILAAANMPI

>d1agre\_ a.91.1.1 (E:) Regulator of G-protein signalling 4, RGS4 {Rat (Rattus norvegicus)}

VSQEEVKKWAESLENLINHECGLAAFKAFLKSEYSEENIDFWISCEEYKKIKSPSKLSPKAKKIYNEFISVQATKEVNLDSCTREETSRNMLEPTITCFDEAQKKIFNLMEKDSYRRFLKSRFYLDLT

>d1fqia\_ a.91.1.1 (A:) RGS9, RGS domain {Cow (Bos taurus)}

KLVDIPTKMRVERWAFNFSELIRDPKGRQSFQHFLRKEFSGENLGFWEACEDLKYGDQSKVKEKAEEIYKLFLAPGARRWINIDGKTMDITVKGLKHPHRYVLDAAQTHIYMLMKKDSYARYLKSPIYKEMLAKAIEP

>d1cmza\_ a.91.1.1 (A:) Galpha interacting protein, GaIP {Human (Homo sapiens)}

PSPEEVQSWAQSFDKLMHSPAGRSVFRAFLRTEYSEENMLFWLACEELKAEANQHVVDEKARLIYEDYVSILSPKEVSLDSRVREGINKKMQEPSAHTFDDAQLQIYTLMHRDSYPRFLSSPTYRALL

>d1dk8a\_ a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}

GSASPTPPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAIYRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLEYTRTGSESPKV

>d1emua\_ a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}

PPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAIYRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLEYT

>d1iapa\_ a.91.1.1 (A:) p115RhoGEF {Human (Homo sapiens)}

SQFQSLEQVKRRPAHLMALLQHVALQFEPGPLLCCLHADMLGSLGPKEAKKAFLDFYHSFLEKTAVLRVPVPPNVAFELDRTRADLISEDVQRRFVQEVVQSQQVAVGRQLEDFRSKRLMGMTPWEQELAQLEAWVGRDRASYEARERHVAERLLMHLEEMQHTISTDEEKSAAVVNAIGLYMRHLGVRT

>d1htjf\_ a.91.1.1 (F:) Pdz-RhoGEF RGS-like domain {Human (Homo sapiens)}

ESDIIFQDLEKLKSRPAHLGVFLRYIFSQADPSPLLFYLCAEVYQQASPKDSRSLGKDIWNIFLEKNAPLRVKIPEMLQAEIDSRLRNSEDARGVLCEAQEAAMPEIQEQIHDYRTKRTLGLGSLYGENDLLDLDGDPLRERQVAEKQLAALGDILSAYAADRSAPMDFALNTYMSHAGIRL

>d1a9xa1 a.92.1.1 (A:403-555) Carbamoyl phosphate synthetase, large subunit connection domain {Escherichia coli}

EVGATGFDPKVSLDDPEALTKIRRELKDAGADRIWYIADAFRAGLSVDGVFNLTNIDRWFLVQIEELVRLEEKVAEVGITGLNADFLRQLKRKGFADARLAKLAGVREAEIRKLRDQYDLHPVYKRVDTCAAEFATDTAYMYSTYEEECEANP

>d1b80a\_ a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete (Phanerochaete chrysosporium)}

VIEKRATCSNGKTVGDASCCAWFDVLDDIQQNLFHGGQCGAEAHESIRLVFHDSIAISPAMEAQGKFGGGGADGSIMIFDDIETAFHPNIGLDEIVKLQKPFVQKHGVTPGDFIAFAGAVALSNCPGAPQMNFFTGRAPATQPAPDGLVPEPFHTVDQIINRVNDAGEFDELELVWMLSAHSVAAVNDVDPTVQGLPFDSTPGIFDSQFFVETQLRGTAFPGSGGNQGEVESPLPGEIRIQSDHTIARDSRTACEWQSFVNNQSKLVDDFQFIFLALTQLGQDPNAMTDCSDVIPQSKPIPGNLPFSFFPAGKTIKDVEQACAETPFPTLTTLPGPETSVQRIPPPPGA

>d1llp\_\_ a.93.1.1 (-) Lignin peroxidase {White rot basidiomycete (Phanerochaete chrysosporium)}

ATCANGKTVGDASCCAWFDVLDDIQANMFHGGQCGAEAHESIRLVFHDSIAISPAMEAKGKFGGGGADGSIMIFDTIETAFHPNIGLDEVVAMQKPFVQKHGVTPGDFIAFAGAVALSNCPGAPQMNFFTGRKPATQPAPDGLVPEPFHTVDQIIARVNDAGEFDELELVWMLSAHSVAAVNDVDPTVQGLPFDSTPGIFDSQFFVETQFRGTLFPGSGGNQGEVESGMAGEIRIQTDHTLARDSRTACEWQSFVGNQSKLVDDFQFIFLALTQLGQDPNAMTDCSDVIPLSKPIPGNGPFSFFPPGKSHSDIEQACAETPFPSLVTLPGPATSVARIPPHKA

>d1qpaa\_ a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete (Phanerochaete chrysosporium)}

VACPDGVHTASNAACCAWFPVLDDIQQNLFHGGQCGAEAHEALRMVFHDSIAISPKLQSQGKFGGGGADGSIITFSSIETTYHPNIGLDEVVAIQKPFIAKHGVTPGDFIAFAGAVGVSNCPGAPQMQFFLGRPEATQAAPDGLVPEPFHTIDQVLARMLDAGGFDEIETVWLLSAHSIAAANDVDPTISGLPFDSTPGQFDSQFFVETQLRGTAFPGKTGIQGTVMSPLKGEMRLQTDHLFARDSRTACEWQSFVNNQTKLQEDFQFIFTALSTLGHDMNAMIDCSEVIPAPKPVNFGPSFFPAGKTHADIEQACASTPFPTLITAPGPSASVARIPPPPSPN

>d1aru\_\_ a.93.1.1 (-) Peroxidase {Arthromyces ramosus}

SVTCPGGQSTSNSQCCVWFDVLDDLQTNFYQGSKCESPVRKILRIVFHDAIGFSPALTAAGQFGGGGADGSIIAHSNIELAFPANGGLTDTIEALRAVGINHGVSFGDLIQFATAVGMSNCPGSPRLEFLTGRSNSSQPSPPSLIPGPGNTVTAILDRMGDAGFSPDEVVDLLAAHSLASQEGLNSAIFRSPLDSTPQVFDTQFYIETLLKGTTQPGPSLGFAEELSPFPGEFRMRSDALLARDSRTACRWQSMTSSNEVMGQRYRAAMAKMSVLGFDRNALTDCSDVIPSAVSNNAAPVIPGGLTVDDIEVSCPSEPFPEIATASGPLPSLAPAP

>d1jdra\_ a.93.1.1 (A:) Cytochrome c peroxidase, CCP {Baker's yeast (Saccharomyces cerevisiae)}

TTPLVHVASVEKGRSYEDFQKVYNAIALKLREDDEYDNYIGYGPVLVRLAWHTSGTWDKHDNTGGSYGGTYRFKKEFNDPSNAGLQNGFKFLEPIHKEFPWISSGDLFSLGGVTAVQEMQGPKIPWRCGRVDTPEDTTPDNGRLPDADKDADYVRTFFQRLNMNDREVVALMGAHTLGKTHLKNSGYEGPWTANNNVFDNSFYLNLLNEDWKLEKNDANNEQWDSKSGYMMLPTDYSLIQDPKYLSIVKEYANDQDKFFKDFSKAFEKLLENGITFPKDAPSPFIFKTLEEQGL

>d1mn2\_\_ a.93.1.1 (-) Manganese peroxidase {Basidomycetos fungus (Phanerochaete chrysosporium)}

AVCPDGTRVSHAACCAFIPLAQDLQETIFQNECGQDAHEVIRLTFHDAIAISRSQGPKAGGGADGSMLLFPTVEPNFSANNGIDDSVNNLIPFMQKHNTISAADLVQFAGAVALSNCPGAPRLEFLAGRPNKTIAAVDGLIPEPQDSVTKILQRFEDAGGFTPFEVVSLLASHSVARANKVDQTIDAAPFDSTPFTFDTQVFLEVLLKGVGFPGSANNTGEVASPLPLGSGSDTGEMRLQSDFALAHDPRTACIWQGFVNEQAFMAASFRAAMSKLAVLGHNRNSLIDCSDVVPVPKPATGQPAMFPASTGPQDLELSCPSERFPTLTTQPGASQSLIAHCPDGSMSCPGVQFNGPA

>d1apxa\_ a.93.1.1 (A:) Ascorbate peroxidase {Pea (Pisum sativum)}

GKSYPTVSPDYQKAIEKAKRKLRGFIAEKKCAPLILRLAWHSAGTFDSKTKTGGPFGTIKHQAELAHGANNGLDIAVRLLEPIKEQFPIVSYADFYQLAGVVAVEITGGPEVPFHPGREDKPEPPPEGRLPDATKGSDHLRDVFGKAMGLSDQDIVALSGGHTIGAAHKERSGFEGPWTSNPLIFDNSYFTELLTGEKDGLLQLPSDKALLTDSVFRPLVEKYAADEDVFFADYAEAHLKLSELGFAEA

>d7atja\_ a.93.1.1 (A:) Plant peroxidase {Horseradish (Armoracia rusticana)}

QLTPTFYDNSCPNVSNIVRDTIVNELRSDPRIAASILRLHFHDCFVNGCDASILLDNTTSFRTEKDAFGNANSARGFPVIDRMKAAVESACPRTVSCADLLTIAAQQSVTLAGGPSWRVPLGRRDSLQAFLDLANANLPAPFFTLPQLKDSFRNVGLNRSSDLVALSGGHTFGKNQCRFIMDRLYNFSNTGLPDPTLNTTYLQTLRGLCPLNGNLSALVDFDLRTPTIFDNKYYVNLEEQKGLIQSDQELFSSPNATDTIPLVRSFANSTQTFFNAFVEAMDRMGNITPLTGTQGQIRLNCRVVN

>d1scha\_ a.93.1.1 (A:) Plant peroxidase {Peanut (Arachis hypogaea)}

ELSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFVQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCPGVVSCADILAVAARDSVVALGGASWNVLLGRRDSTTASLSSANSDLPAPFFNLSGLISAFSNKGFTTKELVTLSGAHTIGQAQCTAFRTRIYNESNIDPTYAKSLQANCPSVGGDTNLSPFDVTTPNKFDNAYYINLRNKKGLLHSDQQLFNGVSTDSQVTAYSNNAATFNTDFGNAMIKMGNLSPLTGTSGQIRTNCRKTN

>d1fhfa\_ a.93.1.1 (A:) Plant peroxidase {Soybean (Glycine max)}

QLTPTFYRETCPNLFPIVFGVIFDASFTDPRIGASLMRLHFHDCFVQGCDGSVLLNNTDTIESEQDALPNINSIRGLDVVNDIKTAVENSCPDTVSCADILAIAAEIASVLGGGPGWPVPLGRRDSLTANRTLANQNLPAPFFNLTQLKASFAVQGLNTLDLVTLSGGHTFGRARCSTFINRLYNFSNTGNPDPTLNTTYLEVLRARCPQNATGDNLTNLDLSTPDQFDNRYYSNLLQLNGLLQSDQELFSTPGADTIPIVNSFSSNQNTFFSNFRVSMIKMGNIGVLTGDEGEIRLQCNFVNG

>d1bgp\_\_ a.93.1.1 (-) Plant peroxidase {Barley (Hordeum vulgare), peroxidase 1}

AEPPVAPGLSFDFYWQTCPRAESIVREFVQEAVRKDIGLAAGLLRLHFHDCFVQGCDASVLLDGSATGPGEQQAPPNLTLRPSAFKAVNDIRDRLERECRGAVVSCSDILALAARDSVVVSGGPDYRVPLGRRDSRSFASTQDVLSDLPGPSSNVQSLLALLGRLGLDATDLVTISGGHTIGLAHCSSFEDRLFPRPDPTISPTFLSRLKRTCPAKGTDRRTVLDVRTPNVFDNKYYIDLVNREGLFVSDQDLFTNAITRPIVERFAQSQQDFFEQFGVSIGKMGQMRVRTSDQGEVRRNCSVRNPGPG

>d1qgja\_ a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (Arabidopsis thaliana), peroxidase N}

QLSPDIYAKSCPNLVQIVRKQVAIALKAEIRMAASLIRLHFHDCFVNGCDASLLLDGADSEKLAIPNINSARGFEVIDTIKAAVENACPGVVSCADILTLAARDSVVLSGGPGWRVALGRKDGLVANQNSANNLPSPFEPLDAIIAKFVAVNLNITDVVALSGAHTFGQAKCAVFSNRLFNFTGAGNPDATLETSLLSNLQTVCPLGGNSNITAPLDRSTTDTFDNNYFKNLLEGKGLLSSDQILFSSDLAVNTTKKLVEAYSRSQSLFFRDFTCAMIRMGNISNGASGEVRTNCRVINN

>d1pa2a\_ a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (Arabidopsis thaliana), peroxidase A2}

MQLNATFYSGTCPNASAIVRSTIQQALQSDTRIGASLIRLHFHDCFVNGCDASILLDDTGSIQSEKNAGPNVNSARGFNVVDNIKTALENACPGVVSCSDVLALASEASVSLAGGPSWTVLLGRRDSLTANLAGANSSIPSPIESLSNITFKFSAVGLNTNDLVALSGAHTFGRARCGVFNNRLFNFSGTGNPDPTLNSTLLSTLQQLCPQNGSASTITNLDLSTPDAFDNNYFANLQSNDGLLQSDQELFSTTGSSTIAIVTSFASNQTLFFQAFAQSMINMGNISPLTGSNGEIRLDCKKVNGS

>g1cxp.1 a.93.1.2 (A:,C:) Myeloperoxidase {Human (Homo sapiens)}

CPEQDKYRTITGMCNNRRSPTLGASNRAFVRWLPAEYEDGFSLPYGWTPGVKRNGFPVALARAVSNEIVRFPTDQLTPDQERSLMFMQWGQLLDHDLDFTPEPAXVNCETSCVQQPPCFPLKIPPNDPRIKNQADCIPFFRSCPACPGSNITIRNQINALTSFVDASMVYGSEEPLARNLRNMSNQLGLLAVNQRFQDNGRALLPFDNLHDDPCLLTNRSARIPCFLAGDTRSSEMPELTSMHTLLLREHNRLATELKSLNPRWDGERLYQEARKIVGAMVQIITYRDYLPLVLGPTAMRKYLPTYRSYNDSVDPRIANVFTNAFRYGHTLIQPFMFRLDNRYQPMEPNPRVPLSRVFFASWRVVLEGGIDPILRGLMATPAKLNRQNQIAVDEIRERLFEQVMRIGLDLPALNMQRSRDHGLPGYNAWRRFCGLPQPETVGQLGTVLRNLKLARKLMEQYGTPNNIDIWMGGVSEPLKRKGRVGPLLACIIGTQFRKLRDGDRFWWENEGVFSMQQRQALAQISLPRIICDNTGITTVSKNNIFMSNSYPRDFVNCSTLPALNLASWREA

>d1eqga1 a.93.1.2 (A:74-583) Prostaglandin H2 synthase {Sheep (Ovis aries)}

IWTWLRTTLRPSPSFIHFLLTHGRWLWDFVNATFIRDTLMRLVLTVRSNLIPSPPTYNIAHDYISWESFSNVSYYTRILPSVPRDCPTPMGTKGKKQLPDAEFLSRRFLLRRKFIPDPQGTNLMFAFFAQHFTHQFFKTSGKMGPGFTKALGHGVDLGHIYGDNLERQYQLRLFKDGKLKYQMLNGEVYPPSVEEAPVLMHYPRGIPPQSQMAVGQEVFGLLPGLMLYATIWLREHNRVCDLLKAEHPTWGDEQLFQTARLILIGETIKIVIEEYVQQLSGYFLQLKFDPELLFGAQFQYRNRIAMEFNQLYHWHPLMPDSFRVGPQDYSYEQFLFNTSMLVDYGVEALVDAFSRQPAGRIGGGRNIDHHILHVAVDVIKESRVLRLQPFNEYRKRFGMKPYTSFQELTGEKEMAAELEELYGDIDALEFYPGLLLEKCHPNSIFGESMIEMGAPFSLKGLLGNPICSPEYWKASTFGGEVGFNLVKTATLKKLVCLNTKTCPYVSFHVP

>d1cvua1 a.93.1.2 (A:74-583) Prostaglandin H2 synthase {Mouse (Mus musculus)}

FLTRIKLLLKPTPNTVHYILTHFKGVWNIVNNIPFLRSLIMKYVLTSRSYLIDSPPTYNVHYGYKSWEAFSNLSYYTRALPPVADDCPTPMGVKGNKELPDSKEVLEKVLLRREFIPDPQGSNMMFAFFAQHFTAQFFKTDHKRGPGFTRGLGHGVDLNHIYGETLDRQHKLRLFKDGKLKYQVIGGEVYPPTVKDTQVEMIYPPHIPENLQFAVGQEVFGLVPGLMMYATIWLREHQRVCDILKQEHPEWGDEQLFQTSKLILIGETIKIVIEDYVQHLSGYHFKLKFDPELLFNQQFQYQNRIASEFNTLYHWHPLLPDTFNIEDQEYSFKQFLYNNSILLEHGLTQFVESFTRQIAGRVAGGRNVPIAVQAVAKASIDQSREMKYQSLNEYRKRFSLKPYTSFEELTGEKEMAAELKALYSDIDVMELYPALLVEKPRPDAIFGETMVELGAPFSLKGLMGNPICSPQYWKPSTFGGEVGFKIINTASIQSLICNNVKGCPFTSFNVQ

>d1jj2o\_ a.94.1.1 (O:) Ribosomal protein L19 (L19e) {Archaeon Haloarcula marismortui}

TDLSAQKRLAADVLDVGKNRVWFNPERQGDIADAITREDVRELVDEGAIQAKDKKGNSRGRARERQKKRAKGHQKGAGSRKGKAGARQNSKEDWESRIRAQRTKLRELRDEGTLSSSQYRDLYDKAGGGEFDSVADLERYIDA

>d1aa7a\_ a.95.1.1 (A:) Influenza virus matrix protein M1 {Influenza virus}

MSLLTEVETYVLSIIPSGPLKAEIAQRLEDVFAGKNTDLEVLMEWLKTRPILSPLTKGILGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDKAVKLYRKLKREITFHGAKEISLSYSAGALASCMGLIYNRMGAVTTEVAFGLVCATCEQIADSQ

>d2abk\_\_ a.96.1.1 (-) Endonuclease III {Escherichia coli}

MNKAKRLEILTRLRENNPHPTTELNFSSPFELLIAVLLSAQATDVSVNKATAKLYPVANTPAAMLELGVEGVKTYIKTIGLYNSKAENIIKTCRILLEQHNGEVPEDRAALEALPGVGRKTANVVLNTAFGWPTIAVDTHIFRVCNRTQFAPGKNVEQVEEKLLKVVPAEFKVDCHHWLILHGRYTCIARKPRCGSCIIEDLCEYKEKVDI

>d1mun\_\_ a.96.1.2 (-) Catalytic domain of MutY {Escherichia coli}

MQASQFSAQVLDWYDKYGRKTLPWQIDKTPYKVWLSEVMLQQTQVATVIPYFERFMARFPTVTDLANAPLDEVLHLWTGLGYYARARNLHKAAQQVATLHGGKFPETFEEVAALPGVGRSTAGAILSLSLGKHFPILNGNVKRVLARCYAVSGWPGKKEVENKLWSLSEQVTPAVGVERFNQAMMDLGAMICTRSKPKCSLCPLQNGCIAAANNSWALYPGKKPK

>d1keaa\_ a.96.1.2 (A:) Thymine-DNA glycosylase {Archaeon Methanobacterium thermoformicicum}

DATNKKRKVFVSTILTFWNTDRRDFPWRHTRDPYVILITEILLRRTTAGHVKKIYDKFFVKYKCFEDILKTPKSEIAKDIKEIGLSNQRAEQLKELARVVINDYGGRVPRNRKAILDLPGVGKYTCAAVMCLAFGKKAAMVDANFVRVINRYFGGSYENLNYNHKALWELAETLVPGGKCRDFNLGLMDFSAIICAPRKPKCEKCGMSKLCSYYEKC

>d1mpga1 a.96.1.3 (A:100-282) 3-Methyladenine DNA glycosylase II (gene alkA or aidA) {Escherichia coli}

AARPGLRLPGCVDAFEQGVRAILGQLVSVAMAAKLTARVAQLYGERLDDFPEYICFPTPQRLAAADPQALKALGMPLKRAEALIHLANAALEGTLPMTIPGDVEQAMKTLQTFPGIGRWTANYFALRGWQAKDVFLPDDYLIKQRFPGMTPAQIRRYAERWKPWRSYALLHIWYTEGWQPDEA

>d1ko9a1 a.96.1.3 (A:136-323) 8-oxoguanine glycosylase {Human (Homo sapiens)}

DPIECLFSFICSSNNNIARITGMVERLCQAFGPRLIQLDDVTYHGFPSLQALAGPEVEAHLRKLGLGYRARYVSASARAILEEQGGLAWLQQLRESSYEEAHKALCILPGVGTKVADCICLMALDKPQAVPVDVHMWHIAQRDYSWHPTTSQAKGPSPQTNKELGNFFRSLWGPYAGWAQAVLFSADL

>d1gln\_1 a.97.1.1 (306-468) Anticodon-binding (C-terminal) domain of glutamyl-tRNA synthetase (GluRS) {Thermus thermophilus}

DLEKLRWMNGKYIREVLSLEEVAERVKPFLREAGLSWESEAYLRRAVELMRPRFDTLKEFPEKARYLFTEDYPVSEKAQRKLEEGLPLLKELYPRLRAQEEWTEAALEALLRGFAAEKGVKLGQVAQPLRAALTGSLETPGLFEILALLGKERALRRLERALA

>d1rlr\_1 a.98.1.1 (10-221) R1 subunit of ribonucleotide reductase, N-terminal domain {Escherichia coli}

RDGSTERINLDKIHRVLDWAAEGLHNVSISQVELRSHIQFYDGIKTSDIHETIIKAAADLISRDAPDYQYLAARLAIFHLRKKAYGQFEPPALYDHVVKMVEMGKYDNHLLEDYTEEEFKQMDTFIDHDRDMTFSYAAVKQLEGKYLVQNRVTGEIYESAQFLYILVAACLFSNYPRETRLQYVKRFYDAVSTFKISLPTPIMSGVRTPTRQ

>d1dnpa1 a.99.1.1 (A:201-469) FAD-binding (C-terminal) domain of DNA photolyase {Escherichia coli}

PVEEKAAIAQLRQFCQNGAGEYEQQRDFPAVEGTSRLSASLATGGLSPRQCLHRLLAEQPQALDGGAGSVWLNELIWREFYRHLITYHPSLCKHRPFIAWTDRVQWQSNPAHLQAWQEGKTGYPIVDAAMRQLNSTGWMHNRLRMITASFLVKDLLIDWREGERYFMSQLIDGDLAANNGGWQWAASTGTDAAPYFRIFNPTTQGEKFDHEGEFIRQWLPELRDVPGKVVHEPWKWAQKAGVTLDYPQPIVEHKEARVQTLAAYEAARK

>d1iqra1 a.99.1.1 (A:172-416) FAD-binding (C-terminal) domain of DNA photolyase {Thermus thermophilus}

LPLPEPGEEAALAGLRAFLEAKLPRYAEERDRLDGEGGSRLSPYFALGVLSPRLAAWEAERRGGEGARKWVAELLWRDFSYHLLYHFPWMAERPLDPRFQAFPWQEDEALFQAWYEGKTGVPLVDAAMRELHATGFLSNRARMNAAQFAVKHLLLPWKRCEEAFRHLLLDGDRAVNLQGWQWAGGLGVDAAPYFRVFNPVLQGERHDPEGRWLKRWAPEYPSYAPKDPVVDLEEARRRYLRLARD

>d1qnf\_1 a.99.1.1 (205-475) FAD-binding (C-terminal) domain of DNA photolyase {Anacystis nidulans}

PVEPGETAAIARLQEFCDRAIADYDPQRNFPAEAGTSGLSPALKFGAIGIRQAWQAASAAHALSRSDEARNSIRVWQQELAWREFYQHALYHFPSLADGPYRSLWQQFPWENREALFTAWTQAQTGYPIVDAAMRQLTETGWMHNRCRMIVASFLTKDLIIDWRRGEQFFMQHLVDGDLAANNGGWQWSASSGMDPKPLRIFNPASQAKKFDATATYIKRWLPELRHVHPKDLISGEITPIERRGYPAPIVNHNLRQKQFKALYNQLKAAI

>d2pgd\_1 a.100.1.1 (177-473) 6-phosphogluconate dehydrogenase (6PGD) {Sheep (Ovis orientalis aries)}

GAGHFVKMVHNGIEYGDMQLICEAYHLMKDVLGLGHKEMAKAFEEWNKTELDSFLIEITASILKFQDADGKHLLPKIRDSAGQKGTGKWTAISALEYGVPVTLIGEAVFARCLSSLKDERIQASKKLKGPQNIPFEGDKKSFLEDIRKALYASKIISYAQGFMLLRQAATEFGWTLNYGGIALMWRGGCIIRSVFLGKIKDAFDRNPGLQNLLLDDFFKSAVENCQDSWRRAISTGVQAGIPMPCFTTALSFYDGYRHAMLPANLIQAQRDYFGAHTYELLAKPGQFIHTNWTGHGG

>d1pgja1 a.100.1.1 (A:179-478) 6-phosphogluconate dehydrogenase (6PGD) {Trypanosoma brucei}

GAGSCVKMYHNSGEYAILQIWGEVFDILRAMGLNNDEVAAVLEDWKSKNFLKSYMLDISIAAARAKDKDGSYLTEHVMDRIGSKGTGLWSAQEALEIGVPAPSLNMAVVSRQFTMYKTERQANASNAPGITQSPGYTLKNKSPSGPEIKQLYDSVCIAIISCYAQMFQCLREMDKVHNFGLNLPATIATFRAGCILQGYLLKPMTEAFEKNPNISNLMCAFQTEIRAGLQNYRDMVALITSKLEVSIPVLSASLNYVTAMFTPTLKYGQLVSLQRDVFGRHGYERVDKDGRESFQWPELQ

>d1qmga1 a.100.1.2 (A:308-595) Acetohydroxy acid isomeroreductase, ketoacid reductoisomerase (KARI) {Spinach (Spinacia oleracea)}

LEQEYKSDIFGERGILLGAVHGIVECLFRRYTESGMSEDLAYKNTVECITGVISKTISTKGMLALYNSLSEEGKKDFQAAYSASYYPSMDILYECYEDVASGSEIRSVVLAGRRFYEKEGLPAFPMGKIDQTRMWKVGEKVRSVRPAGDLGPLYPFTAGVYVALMMAQIEILRKKGHSYSEIINESVIEAVDSLNPFMHARGVSFMVDNCSTTARLGSRKWAPRFDYILSQQALVAVDNGAPINQDLISNFLSDPVHEAIGVCAQLRPSVDISVTADADFVRPELRQA

>d1f0ya1 a.100.1.3 (A:204-302) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (Homo sapiens)}

GFIVNRLLVPYLMEAIRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIVDGWHEMDAENPLHQPSPSLNKLVAENKFGKKTGEGFYKYK

>d3hdha1 a.100.1.3 (A:204-302) Short chain L-3-hydroxyacyl CoA dehydrogenase {Pig (Sus scrofa)}

GFIVNRLLVPYLIEAVRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIIDGWHEMDSQNPLFQPSPAMNKLVAENKFGKKTGEGFYKYK

>d1dlja1 a.100.1.4 (A:197-294) UDP-glucose dehydrogenase (UDPGDH), middle domain {Streptococcus pyogenes}

ASEAEAVKLFANTYLALRVAYFNELDTYAESRKLNSHMIIQGISYDDRIGMHYNNPSFGYGGYSLPKDTKQLLANYNNIPQTLIEAIVSSNNVRKSYI

>d1bg6\_1 a.100.1.5 (188-359) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}

NVLHTSLTNVNAVMHPLPTLLNAARCESGTPFQYYLEGITPSVGSLAEKVDAERIAIAKAFDLNVPSVCEWYKESYGQSPATIYEAVQGNPAYRGIAGPINLNTRYFFEDVSTGLVPLSELGRAVNVPTPLIDAVLDLISSLIDTDFRKEGRTLEKLGLSGLTAAGIRSAVE

>d1evya1 a.100.1.6 (A:189-357) Glycerol-3-phosphate dehydrogenase {Trypanosome (Leishmania mexicana)}

DRSFVCWATTDTVGCEVASAVKNVLAIGSGVANGLGMGLNARAALIMRGLLEIRDLTAALGGDGSAVFGLAGLGDLQLTCSSELSRNFTVGKKLGKGLPIEEIQRTSKAVAEGVATADPLMRLAKQLKVKMPLCHQIYEIVYKKKNPRDALADLLSCGLQDEGLPPLFK

>d1ks9a1 a.100.1.7 (A:168-291) Ketopantoate reductase PanE {Escherichia coli}

NIRAELWRKLAVNCVINPLTAIWNCPNGELRHHPQEIMQICEEVAAVIEREGHHTSAEDLRDYVMQVIDATAENISSMLQDIRALRHTEIDYINGFLLRRARAHGIAVPENTRLFEMVKRKESE

>d1utg\_\_ a.101.1.1 (-) Uteroglobin {Rabbit (Oryctolagus cuniculus)}

GICPRFAHVIENLLLGTPSSYETSLKEFEPDDTMKDAGMQMKKVLDSLPQTTRENIMKLTEKIVKSPLCM

>d1ccd\_\_ a.101.1.1 (-) Clara cell 17kDa protein {Rat (Rattus norvegicus)}

SSDICPGFLQVLEALLLGSESNYEAALKPFNPASDLQNAGTQLKRLVDTLPQETRINIVKLTEKILTSPLCEQDLRV

>d1utra\_ a.101.1.1 (A:) Clara cell 17kDa protein {Rat (Rattus norvegicus)}

ICPGFLQVLEALLLGSESNYEAALKPFNPASDLQNAGTQLKRLVDTLPQETRINIVKLTEKILTSPLC

>d1gai\_\_ a.102.1.1 (-) Glucoamylase {Aspergillus awamori, variant x100}

ATLDSWLSNEATVARTAILNNIGADGAWVSGADSGIVVASPSTDNPDYFYTWTRDSGLVIKTLVDLFRNGDTDLLSTIEHYISSQAIIQGVSNPSGDLSSGGLGEPKFNVDETAYTGSWGRPQRDGPALRATAMIGFGQWLLDNGYTSAATEIVWPLVRNDLSYVAQYWNQTGYDLWEEVNGSSFFTIAVQHRALVEGSAFATAVGSSCSWCDSQAPQILCYLQSFWTGSYILANFDSSRSGKDTNTLLGSIHTFDPEAGCDDSTFQPCSPRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGRYPEDSYYNGNPWFLCTLAAAEQLYDALYQWDKQGSLEITDVSLDFFKALYSGAATGTYSSSSSTYSSIVSAVKTFADGFVSIVETHAASNGSLSEQFDKSDGDELSARDLTWSYAALLTANNRRNSVVPPSWGETSASSVPGTCAATSASGTYSSVTVTSWPSIVATG

>d1ayx\_\_ a.102.1.1 (-) Glucoamylase {Baker's yeast (Saccharomycopsis fibuligera)}

AYPSFEAYSNYKVDRTDLETFLDKQKEVSLYYLLQNIAYPEGQFNNGVPGTVIASPSTSNPDYYYQWTRDSAITFLTVLSELEDNNFNTTLAKAVEYYINTSYNLQRTSNPSGSFDDENHKGLGEPKFNTDGSAYTGAWGRPQNDGPALRAYAISRYLNDVNSLNEGKLVLTDSGDINFSSTEDIYKNIIKPDLEYVIGYWDSTGFDLWEENQGRHFFTSLVQQKALAYAVDIAKSFDDGDFANTLSSTASTLESYLSGSDGGFVNTDVNHIVENPDLLQQNSRQGLDSATYIGPLLTHDIGESSSTPFDVDNEYVLQSYYLLLEDNKDRYSVNSAYSAGAAIGRYPEDVYNGDGSSEGNPWFLATAYAAQVPYKLAYDAKSASNDITINKINYDFFNKYIVDLSTINSAYQSSDSVTIKSGSDEFNTVADNLVTFGDSFLQVILDHINDDGSLNEQLNRYTGYSTGAYSLTWSSGALLEAIRLRNKVKALA

>d1cem\_\_ a.102.1.2 (-) CelA cellulase {Clostridium thermocellum}

AGVPFNTKYPYGPTSIADNQSEVTAMLKAEWEDWKSKRITSNGAGGYKRVQRDASTNYDTVSEGMGYGLLLAVCFNEQALFDDLYRYVKSHFNGNGLMHWHIDANNNVTSHDGGDGAATDADEDIALALIFADKQWGSSGAINYGQEARTLINNLYNHCVEHGSYVLKPGDRWGGSSVTNPSYFAPAWYKVYAQYTGDTRWNQVADKCYQIVEEVKKYNNGTGLVPDWCTASGTPASGQSYDYKYDATRYGWRTAVDYSWFGDQRAKANCDMLTKFFARDGAKGIVDGYTIQGSKISNNHNASFIGPVAAASMTGYDLNFAKELYRETVAVKDSEYYGYYGNSLRLLTLLYITGNFPNPLSDL

>d1tf4a1 a.102.1.2 (A:1-460) Endo/exocellulase:cellobiose E-4, N-terminal domain {Thermomonospora fusca}

EPAFNYAEALQKSMFFYEAQRSGKLPENNRVSWRGDSGLNDGADVGLDLTGGWYDAGDHVKFGFPMAFTATMLAWGAIESPEGYIRSGQMPYLKDNLRWVNDYFIKAHPSPNVLYVQVGDGDADHKWWGPAEVMPMERPSFKVDPSCPGSDVAAETAAAMAASSIVFADDDPAYAATLVQHAKQLYTFADTYRGVYSDCVPAGAFYNSWSGYQDELVWGAYWLYKATGDDSYLAKAEYEYDFLSTEQQTDLRSYRWTIAWDDKSYGTYVLLAKETGKQKYIDDANRWLDYWTVGVNGQRVPYSPGGMAVLDTWGALRYAANTAFVALVYAKVIDDPVRKQRYHDFAVRQINYALGDNPRNSSYVVGFGNNPPRNPHHRTAHGSWTDSIASPAENRHVLYGALVGGPGSPNDAYTDDRQDYVANEVATDYNAGFSSALAMLVEEYGGTPLADFPPTEEPDG

>d1clc\_1 a.102.1.2 (135-575) CelD cellulase {Clostridium thermocellum}

AMNVYEDAFKTAMLGMYLLRCGTSVSATYNGIHYSHGPCHTNDAYLDYINGQHTKKDSTKGWHDAGDYNKYVVNAGITVGSMFLAWEHFKDQLEPVALEIPEKNNSIPDFLDELKYEIDWILTMQYPDGSGRVAHKVSTRNFGGFIMPENEHDERFFVPWSSAATADFVAMTAMAARIFRPYDPQYAEKCINAAKVSYEFLKNNPANVFANQSGFSTGEYATVSDADDRLWAAAEMWETLGDEEYLRDFENRAAQFSKKIEADFDWDNVANLGMFTYLLSERPGKNPALVQSIKDSLLSTADSIVRTSQNHGYGRTLGTTYYWGCNGTVVRQTMILQVANKISPNNDYVNAALDAISHVFGRNYYNRSYVTGLGINPPMNPHDRRSGADGIWEPWPGYLVGGGWPGPKDWVDIQDSYQTNEIAINWNAALIYALAGFVNYN

>d1faea\_ a.102.1.2 (A:) Processive endocellulase CelF (Cel48F) {Clostridium cellulolyticum}

ASSPANKVYQDRFESMYSKIKDPANGYFSEQGIPYHSIETLMVEAPDYGHVTTSEAMSYYMWLEAMHGRFSGDFTGFDKSWSVTEQYLIPTEKDQPNTSMSRYDANKPATYAPEFQDPSKYPSPLDTSQPVGRDPINSQLTSAYGTSMLYGMHWILDVDNWYGFGARADGTSKPSYINTFQRGEQESTWETIPQPCWDEHKFGGQYGFLDLFTKDTGTPAKQFKYTNAPDADARAVQATYWADQWAKEQGKSVSTSVGKATKMGDYLRYSFFDKYFRKIGQPSQAGTGYDAAHYLLSWYYAWGGGIDSTWSWIIGSSHNHFGYQNPFAAWVLSTDANFKPKSSNGASDWAKSLDRQLEFYQWLQSAEGAIAGGATNSWNGRYEAVPSGTSTFYGMGYVENPVYADPGSNTWFGMQVWSMQRVAELYYKTGDARAKKLLDKWAKWINGEIKFNADGTFQIPSTIDWEGQPDTWNPTQGYTGNANLHVKVVNYGTDLGCASSLANTLTYYAAKSGDETSRQNAQKLLDAMWNNYSDSKGISTVEQRGDYHRFLDQEVFVPAGWTGKMPNGDVIKSGVKFIDIRSKYKQDPEWQTMVAALQAGQVPTQRLHRFWAQSEFAVANGVYAILFPD

>d1fp3a\_ a.102.1.3 (A:) N-acyl-D-glucosamine 2-epimerase {Pig (Sus scrofa)}

MEKERETLQAWKERVGQELDRVMAFWLEHSHDREHGGFFTCLGRDGRVYDDLKYVWLQGRQVWMYCRLYRKLERFHRPELLDAAKAGGEFLLRHARVAPPEKKCAFVLTRDGRPVKVQRSIFSECFYTMAMNELWRVTAEARYQSEAVDMMDQIVHWVREDPSGLGRPQLPGAVASESMAVPMMLLCLVEQLGEEDEELAGRYAQLGHWCARRILQHVQRDGQAVLENVSEDGEELSGCLGRHQNPGHALEAGWFLLRHSSRSGDAKLRAHVIDTFLLLPFRSGWDADHGGLFYFQDADGLCPTQLEWAMKLWWPHSEAMIAFLMGYSESGDPALLRLFYQVAEYTFRQFRDPEYGEWFGYLNREGKVALTIKGGPFKGCFHVPRCLAMCEEMLSALLSRLA

>d1h54a1 a.102.1.4 (A:269-753) Lactobacillus maltose phosphorylase, central domain {Lactobacillus brevis}

DTQESLTAAMHQLSDKVAQSSYEDLLNAHTAIWAQRWEKSDVVIKGDDESQQGIRFNLFQLFSTYYGEDARLNIGPKGFTGEKYGGATYWDTEAFAFPVYLGITDPKVTRNLLMYRYKQLDGAYINAQEQGLKGALFPMVTFDGIECHNEWEITFEEIHRNGDIAFAIYNYTRYTGDDSYVLHEGAKVLTEISRFWADRVHFSKRNNQYMIHGVTGADEYENNVDNNWDTNMLAQWTLKYTLEILGKVDQDTAKQLDVSDEEKTKWQDIVDRMYLPYDKDLNIFVQHDGFLDKDIEPVSSIPADQRPINQNWSWDKILRSPYIKQGDVLQGIWDFIDDYTPEQKKANFDFYEPLTVHESSLSPAIHSVLAADLHYEDKAVELYSRTARLDLDNYNNDTTDGLHITSMTGAWIAVVQGFAGMRVRDGQLHYAPFLPKTWTSYTFRQVFRDRLIEVSVHADGPHFKLLSGEPLTIDVAGAAAAAAAA

>d1dl2a\_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

GAGEMRDRIESMFLESWRDYSKHGWGYDVYGPIEHTSHNMPRGNQPLGWIIVDSVDTLMLMYNSSTLYKSEFEAEIQRSEHWINDVLDFDIDAEVNVFETTIRMLGGLLSAYHLSDVLEVGNKTVYLNKAIDLGDRLALAFLSTQTGIPYSSINLHSGQAVKNHADGGASSTAEFTTLQMEFKYLAYLTGNRTYWELVERVYEPLYKNNDLLNTYDGLVPIYTFPDTGKFGASTIRFGSRGDSFYEYLLKQYLLTHETLYYDLYRKSMEGMKKHLLAQSKPSSLWYIGEREQGLHGQLSPKMDHLVCFMGGLLASGSTEGLSIHEARRRPFFSKSDWDLAKGITDTCYQMYKQSSSGLAPEIVVFNDGNIKQDGWWRSSVGDFFVKPLDRHNLQRPETVESIMFMYHLSHDHKYREWGAEIATSFFENTCVDCNDPKLRRFTSLSDCITLPTKKSNNMESFWLAETLKYLYILFLDEFDLTKVVFNTEAHPFPVLDEEILKSQSLTTGWSL

>d1hcua\_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Trichoderma reesei}

KRGSPNPTRAAAVKAAFQTSWNAYHHFAFPHDDLHPVSNSFDDERNGWGSSAIDGLDTAILMGDADIVNTILQYVPQINFTTTAVANQGSSVFETNIRYLGGLLSAYDLLRGPFSSLATNQTLVNSLLRQAQTLANGLKVAFTTPSGVPDPTVFFNPTVRRSGASSNNVAEIGSLVLEWTRLSDLTGNPQYAQLAQKGESYLLNPKGSPEAWPGLIGTFVSTSNGTFQDSSGSWSGLMDSFYEYLIKMYLYDPVAFAHYKDRWVLGADSTIGHLGSHPSTRKDLTFLSSYNGQSTSPNSGHLASFGGGNFILGGILLNEQKYIDFGIKLASSYFGTYTQTASGIGPEGFAWVDSVTGAGGSPPSSQSGFYSSAGFWVTAPYYILRPETLESLYYAYRVTGDSKWQDLAWEALSAIEDACRAGSAYSSINDVTQANGGGASDDMESFWFAEALKYAYLIFAEESDVQVQATGGNKFVFNTEAHPFSIRS

>d1krea\_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Fungus (Penicillium citrinum)}

SNQAKADAVKEAFQHAWNGYMKYAFPHDELTPVSNGHADSRNGWGASAVDALSTAVIMGKADVVNAILEHVADIDFSKTSDTVSLFETTIRYLAGMLSGYDLLQGPAKNLVDNQDLIDGLLDQSRNLADVLKFAFDTPSGVPYNNINITSHGNDGATTNGLAVTGTLVLEWTRLSDLTGDEEYAKLSQKAESYLLKPQPSSSEPFPGLVGSSININDGQFADSRVSWNGGDDSFYEYLIKMYVYDPKRFETYKDRWVLAAESTIKHLKSHPKSRPDLTFLSSYSNRNYDLSSQHLTCFDGGSFLLGGTVLDRQDFIDFGLELVDGCEATYNSTLTKIGPDSWGWDPKKVPSDQKEFYEKAGFYISSGSYVLRPEVIESFYYAHRVTGKEIYRDWVWNAFVAINSTCRTDSGFAAVSDVNKANGGSKYDNQESFLFAEVMKYSYLAHSEDAAWQVQKGGKNTFVYNTEAHPISVAR

>d1fo3a\_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Human (Homo sapiens)}

QGPVHLNYRQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEARKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKIPYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELSRLTGDKKFQEAVEKVTQHIHGLSGKKDGLVPMFINTHSGLFTHLGVFTLGARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRTHLLRHSEPSKLTFVGELAHGRFSAKMDHLVCFLPGTLALGVYHGLPASHMELAQELMETCYQMNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLLRPETVESLFYLYRVTGDRKYQDWGWEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLDAYVFNTEAHPLPIWT

>d1qaza\_ a.102.3.1 (A:) Alginate lyase A1-III {Sphingomonas sp., A1}

GSHPFDQAVVKDPTASYVDVKARRTFLQSGQLDDRLKAALPKEYDCTTEATPNPQQGEMVIPRRYLSGNHGPVNPDYEPVVTLYRDFEKISATLGNLYVATGKPVYATCLLNMLDKWAKADALLNYDPKSQSWYQVEWSAATAAFALSTMMAEPNVDTAQRERVVKWLNRVARHQTSFPGGDTSCCNNHSYWRGQEATIIGVISKDDELFRWGLGRYVQAMGLINEDGSFVHEMTRHEQSLHYQNYAMLPLTMIAETASRQGIDLYAYKENGRDIHSARKFVFAAVKNPDLIKKYASEPQDTRAFKPGRGDLNWIEYQRARFGFADELGFMTVPIFDPRTGGSATLLAYKP

>d1cb8a1 a.102.3.2 (A:26-335) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

GTAELIMKRVMLDLKKPLRNMDKVAEKNLNTLQPDGSWKDVPYKDDAMTNWLPNNHLLQLETIIQAYIEKDSHYYGDDKVFDQISKAFKYWYDSDPKSRNWWHNEIATPQALGEMLILMRYGKKPLDEALVHKLTERMKRGEPEKKTGANKTDIALHYFYRALLTSDEALLSFAVKELFYPVQFVHYEEGLQYDYSYLQHGPQLQISSYGAVFITGVLKLANYVRDTPYALSTEKLAIFSKYYRDSYLKAIRGSYMDFNVEGRGVSRPDILNKKAEKKRLLVAKMIDLKHTEEWADAIARTDSTVAAGYK

>d1egua1 a.102.3.2 (A:171-540) Hyaluronate lyase {Streptococcus pneumoniae}

KDTYTDRLDDWNGIIAGNQYYDSKNDQMAKLNQELEGKVADSLSSISSQADRIYLWEKFSNYKTSANLTATYRKLEEMAKQVTNPSSRYYQDETVVRTVRDSMEWMHKHVYNSEKSIVGNWWDYEIGTPRAINNTLSLMKEYFSDEEIKKYTDVIEKFVPDPEHFRKTTDNPFKALGGNLVDMGRVKVIAGLLRKDDQEISSTIRSIEQVFKLVDQGEGFYQDGSYIDHTNVAYTGAYGNVLIDGLSQLLPVIQKTKNPIDKDKMQTMYHWIDKSFAPLLVNGELMDMSRGRSISRANSEGHVAAVEVLRGIHRIADMSEGETKQRLQSLVKTIVQSDSYYDVFKNLKTYKDISLMQSLLSDAGVASVPR

>d1f1sa1 a.102.3.2 (A:249-619) Hyaluronate lyase {Streptococcus agalactiae}

EDNFTKLLDKWNDVTIGNYVYDTNDSNMQKLNQKLDETNAKNIEAIKLDSNRTFLWKDLDNLNNSAQLTATYRRLEDLAKQITNPHSTIYKNEKAIRTVKESLAWLHQNFYNVNKDIEGSANWWDFEIGVPRSITGTLSLMNNYFTDAEIKTYTDPIEHFVPDAEYFRKTLVNPFKALGGNLVDMGRVKIIEGLLRKDNTIIEKTSHSLKNLFTTATKAEGFYADGSYIDHTNVAYTGAYGNVLIDGLTQLLPIIQETDYKISNQELDMVYKWINQSFLPLIVKGELMDMSRGRSISREAASSHAAAVEVLRGFLRLANMSNEERNLDLKSTIKTIITSNKFYNVFNNLKSYSDIANMNKLLNDSTVATKP

>d5eau\_1 a.102.4.1 (21-220) 5-Epi-aristolochene synthase, N-terminal domain {Tobacco (Nicotiana tabacum)}

SPSLWGDQFLSFSIDNQVAEKYAKEIEALKEQTRNMLLATGMKLADTLNLIDTIERLGISYHFEKEIDDILDQIYNQNSNCNDLCTSALQFRLLRQHGFNISPEIFSKFQDENGKFKESLASDVLGLLNLYEASHVRTHADDILEDALAFSTIHLESAAPHLKSPLREQVTHALEQCLHKGVPRVETRFFISSIYDKEQS

>d2sqca1 a.102.4.2 (A:8-36,A:308-630) Squalene-hopene cyclase {Alicyclobacillus acidocaldarius}

APAYARTLDRAVEYLLSCQKDEGYWWGPLXISPVWDTGLAVLALRAAGLPADHDRLVKAGEWLLDRQITVPGDWAVKRPNLKPGGFAFQFDNVYYPDVCDTAVVVWALNTLRLPDERRRRDAMTKGFRWIVGMQSSNGGWGAYDVDNTSDLPNHIPFSDFGEVTDPPSEDVTAHVLECFGSFGYDDAWKVIRRAVEYLKREQKPDGSWFGRWGVNYLYGTGAVVSALKAVGIDTREPYIQKALDWVEQHQNPDGGWGEDCRSYEDPAYAGKGASTPSQTAWALMALIAGGRAESEAARRGVQYLVETQRPDGGWDEPYYTGTGFPGDFYLGYTMYRHVFPTLALGRYKQAIER

>d2sqca2 a.102.4.2 (A:37-307) Squalene-hopene cyclase {Alicyclobacillus acidocaldarius}

LSNVTMEAEYVLLCHILDRVDRDRMEKIRRYLLHEQREDGTWALYPGGPPDLDTTIEAYVALKYIGMSRDEEPMQKALRFIQSQGGIESSRVFTRMWLALVGEYPWEKVPMVPPEIMFLGKRMPLNIYEFGSWARATVVALSIVMSRQPVFPLPERARVPELYETDVPPRRRGAKGGGGWIFDALDRALHGYQKLSVHPFRRAAEIRALDWLLERQAGDGSWGGIQPPWFYALIALKILDMTQHPAFIKGWEGLELYGVELDYGGWMFQAS

>d1d8db\_ a.102.4.3 (B:) Protein farnesyltransferase, beta-subunit {Rat (Rattus norvegicus)}

PVWSEPLYSLRPEHARERLQDDSVETVTSIEQAKVEEKIQEVFSSYKFNHLVPRLVLQREKHFHYLKRGLRQLTDAYECLDASRPWLCYWILHSLELLDEPIPQIVATDVCQFLELCQSPDGGFGGGPGQYPHLAPTYAAVNALCIIGTEEAYNVINREKLLQYLYSLKQPDGSFLMHVGGEVDVRSAYCAASVASLTNIITPDLFEGTAEWIARCQNWEGGIGGVPGMEAHGGYTFCGLAALVILKKERSLNLKSLLQWVTSRQMRFEGGFQGRCNKLVDGCYSFWQAGLLPLLHRALHAQGDPALSMSHWMFHQQALQEYILMCCQCPAGGLLDKPGKSRDFYHTCYCLSGLSIAQHFGSGAMLHDVVMGVPENVLQPTHPVYNIGPDKVIQATTHFLQKPVPGF

>d1dceb\_ a.102.4.3 (B:) Rab geranylgeranyltransferase, beta subunit {Rat (Rattus norvegicus)}

TQQKDVTIKSDAPDTLLLEKHADYIASYGSKKDDYEYCMSEYLRMSGVYWGLTVMDLMGQLHRMNKEEILVFIKSCQHECGGVSASIGHDPHLLYTLSAVQILTLYDSIHVINVDKVVAYVQSLQKEDGSFAGDIWGEIDTRFSFCAVATLALLGKLDAINVEKAIEFVLSCMNFDGGFGCRPGSESHAGQIYCCTGFLAITSQLHQVNSDLLGWWLCERQLPSGGLNGRPEKLPDVCYSWWVLASLKIIGRLHWIDREKLRSFILACQDEETGGFADRPGDMVDPFHTLFGIAGLSLLGEEQIKPVSPVFCMPEEVLQRVNVQPELVS

>d1c3d\_\_ a.102.4.4 (-) C3D, a C3 fragment and ligand for complement receptor 2 {Human (Homo sapiens)}

MLDAERLKHLIVTPSGAGEQNMIGMTPTVIAVHYLDETEQWEKFGLEKRQGALELIKKGYTQQLAFRQPSSAFAAFVKRAPSTWLTAYVVKVFSLAVNLIAIDSQVLCGAVKWLILEKQKPDGVFQEDAPVIHQEMIGGLRNNNEKDMALTAFVLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRSYTVAIAGYALAQMGRLKGPLLNKFLTTAKDKNRWEDPGKQLYNVEATSYALLALLQLKDFDFVPPVVRWLNEQRYYGGGYGSTQATFMVFQALAQYQKDAP

>d1qqfa\_ a.102.4.4 (A:) C3D, a C3 fragment and ligand for complement receptor 2 {Rat (Rattus norvegicus)}

CGEQNMIGMTPTVIAVHYLDQTEQWEKFGLEKRQEALELIKKGYTQQLAFKQPISAYAAFNNRPPSTWLTAYVSRVFSLAANLIAIDSQVLCGAVKWLILEKQKPDGVFQEDGPVIHQEMIGGFRNTKEADVSLTAFVLIALQEARDICEGQVNSLPGSINKAGEYLEASYLNLQRPYTVAIAGYALALMNKLEEPYLTKFLNTAKDRNRWEEPGQQLYNVEATSYALLALLLLKDFDSVPPVVRWLNDERYYGGGYGSTQATFMVFQALAQYRADV

>d1csc\_\_ a.103.1.1 (-) Citrate synthase {Chicken (Gallus gallus)}

ASSTNLKDVLAALIPKEQARIKTFRQQHGGTALGQITVDMSYGGMRGMKGLVYETSVLDPDEGIRFRGFSIPECQKLLPKGGXGGEPLPEGLFWLLVTGQIPTGAQVSWLSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGILRTKYWEMVYESAMDLIAKLPCVAAKIYRNLYRAGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLGWLAQLQKAXXXAGADASLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPGDPMFKLVAQLYKIVPNVLLEQGAAANPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTDGLIAL

>d1csh\_\_ a.103.1.1 (-) Citrate synthase {Chicken (Gallus gallus)}

STNLKDVLASLIPKEQARIKTFRQQHGNTAVGQITVDMSYGGMRGMKGLIYETSVLDPDEGIRFRGFSIPECQKLLPKAGGGEEPLPEGLFWLLVTGQIPTPEQVSWVSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGINRTKYWEFVYEDAMDLIAKLPCVAAKIYRNLYRAGSSIGAIDSKLDWSHNFTNMLGYTDPQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLLWLSQLQKDLGADASDEKLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPSDPMFKLVAQLYKIVPNVLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTAGLEKLSAGG

>d2cts\_\_ a.103.1.1 (-) Citrate synthase {Pig (Sus scrofa)}

ASSTNLKDILADLIPKEQARIKTFRQQHGNTAVGQITVDMMYGGMRGMKGLVYETSVLDPDEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEGIHRTKYWELIYEDCMDLIAKLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSDEKLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKHLPHDPMFKLVAQLYKIVPNVLLEQGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTDGLIKLVDSK

>d1aj8a\_ a.103.1.1 (A:) Citrate synthase {Archaeon Pyrococcus furiosus}

LAKGLEDVYIDQTNICYIDGKEGKLYYRGYSVEELAELSTFEEVVYLLWWGKLPSLSELENFKKELAKSRGLPKEVIEIMEALPKNTHPMGALRTIISYLGNIDDSGDIPVTPEEVYRIGISVTAKIPTIVANWYRIKNGLEYVPPKEKLSHAANFLYMLHGEEPPKEWEKAMDVALILYAEHEINASTLAVMTVGSTLSDYYSAILAGIGALKGPIHGGAVEEAIKQFMEIGSPEKVEEWFFKALQQKRKIMGAGHRVYKTYDPRARIFKKYASKLGDKKLFEIAERLERLVEEYLSKKGISINVDYWSGLVFYGMKIPIELYTTIFAMGRIAGWTAHLAEYVSHNRIIRPRLQYVGEIGKKYLPIELRR

>d1a59\_\_ a.103.1.1 (-) Citrate synthase {Antarctic bacterium DS2-3R}

EPTIHKGLAGVTADVTAISKVNSDTNSLLYRGYPVQELAAKCSFEQVAYLLWNSELPNDSELKAFVNFERSHRKLDENVKGAIDLLSTACHPMDVARTAVSVLGANHARAQDSSPEANLEKAMSLLATFPSVVAYDQRRRRGEELIEPREDLDYSANFLWMTFGEEAAPEVVEAFNVSMILYAEHSFNASTFTARVITSTLADLHSAVTGAIGALKGPLHGGANEAVMHTFEEIGIRKDESLDEAATRSKAWMVDALAQKKKVMGFGHRVYKNGDSRVPTMKSALDAMIKHYDRPEMLGLYNGLEAAMEEAKQIKPNLDYPAGPTYNLMGFDTEMFTPLFIAARITGWTAHIMEQVADNALIRPLSEYNGPEQRQVP

>d1dz4a\_ a.104.1.1 (A:) Cytochrome P450-CAM {Pseudomonas putida}

LAPLPPHVPEHLVFDFDMYNPSNLSAGVQEAWAVLQESNVPDLVWTRCNGGHWIATRGQLIREAYEDYRHFSSECPFIPREAGEAYDFIPTSMDPPEQRQFRALANQVVGMPVVDKLENRIQELACSLIESLRPQGQCNFTEDYAEPFPIRIFMLLAGLPEEDIPHLKYLTDQMTRPDGSMTFAEAKEALYDYLIPIIEQRRQKPGTDAISIVANGQVNGRPITSDEAKRMCGLLLVGGLDTVVNFLSFSMEFLAKSPEHRQELIQRPERIPAACEELLRRFSLVADGRILTSDYEFHGVQLKKGDQILLPQMLSGLDERENACPMHVDFSRQKVSHTTFGHGSHLCLGQHLARREIIVTLKEWLTRIPDFSIAPGAQIQHKSGIVSGVQALPLVWDPATTKAV

>d1jpza\_ a.104.1.1 (A:) Cytochrome P450 bm-3 {Bacillus megaterium}

TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMVDIAVQLVQKWERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSMVRALDEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLLTHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWGDDVEEFRPERFENPSAIPQHAFKPFGNGQRACIGQQFALHEATLVLGMMLKHFDFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGI

>d1jfba\_ a.104.1.1 (A:) Cytochrome P450-NOR, nitric reductase {Fungus (Fusarium oxysporum)}

APSFPFSRASGPEPPAEFAKLRATNPVSQVKLFDGSLAWLVTKHKDVCFVATSEKLSKVRTRQGFPELSASGKQAAKAKPTFVDMDPPEHMHQRSMVEPTFTPEAVKNLQPYIQRTVDDLLEQMKQKGCANGPVDLVKEFALPVPSYIIYTLLGVPFNDLEYLTQQNAIRTNGSSTAREASAANQELLDYLAILVEQRLVEPKDDIISKLCTEQVKPGNIDKSDAVQIAFLLLVAGNATMVNMIALGVATLAQHPDQLAQLKANPSLAPQFVEELCRYHTASALAIKRTAKEDVMIGDKLVRANEGIIASNQSANRDEEVFENPDEFNMNRKWPPQDPLGFGFGDHRCIAEHLAKAELTTVFSTLYQKFPDLKVAVPLGKINYTPLNRDVGIVDLPVIF

>d1jipa\_ a.104.1.1 (A:) Cytochrome P450-ERYF {Saccaropolyspora erythraea}

TTVPDLESDSFHVDWYRTYAELRETAPVTPVRFLGQDAWLVTGYDEAKAALSDLRLSSDPKKKYPGVEVEFPAYLGFPEDVRNYFATNMGTSDPPTHTRLRKLVSQEFTVRRVEAMRPRVEQITAELLDEVGDSGVVDIVDRFAHPLPIKVICELLGVDEKYRGEFGRWSSEILVMDPERAEQRGQAAREVVNFILDLVERRRTEPGDDLLSALIRVQDDDDGRLSADELTSIALVLLLAGFESSVSLIGIGTYLLLTHPDQLALVRRDPSALPNAVEEILRYIAPPETTTRFAAEEVEIGGVAIPQYSTVLVANGAANRDPKQFPDPHRFDVTRDTRGHLSFGQGIHFCMGRPLAKLEGEVALRALFGRFPALSLGIDADDVVWRRSLLLRGIDHLPVRLDG

>d1cpt\_\_ a.104.1.1 (-) Cytochrome P450-TERP {Pseudomonas sp.}

MDARATIPEHIARTVILPQGYADDEVIYPAFKWLRDEQPLAMAHIEGYDPMWIATKHADVMQIGKQPGLFSNAEGSEILYDQNNEAFMRSISGGCPHVIDSLTSMDPPTHTAYRGLTLNWFQPASIRKLEENIRRIAQASVQRLLDFDGECDFMTDCALYYPLHVVMTALGVPEDDEPLMLKLTQDFFGVEAARRFHETIATFYDYFNGFTVDRRSCPKDDVMSLLANSKLDGNYIDDKYINAYYVAIATAGHDTTSSSSGGAIIGLSRNPEQLALAKSDPALIPRLVDEAVRWTAPVKSFMRTALADTEVRGQNIKRGDRIMLSYPSANRDEEVFSNPDEFDITRFPNRHLGFGWGAHMCLGQHLAKLEMKIFFEELLPKLKSVELSGPPRLVATNFVGGPKNVPIRFTKA

>d1e9xa\_ a.104.1.1 (A:) Cytochrome p450 14 alpha-sterol demethylase (cyp51) {Mycobacterium tuberculosis}

MSAVALPRVSGGHDEHGHLEEFRTDPIGLMQRVRDECGDVGTFQLAGKQVVLLSGSHANEFFFRAGDDDLDQAKAYPFMTPIFGEGVVFDASPERRKEMLHNAALRGEQMKGHAATIEDQVRRMIADWGEAGEIDLLDFFAELTIYTSSACLIGKKFRDQLDGRFAKLYHELERGTDPLAYVDPYLPIESFRRRDEARNGLVALVADIMNGRIANPPTDKSDRDMLDVLIAVKAETGTPRFSADEITGMFISMMFAGHHTSSGTASWTLIELMRHRDAYAAVIDELDELYGDGRSVSFHALRQIPQLENVLKETLRLHPPLIILMRVAKGEFEVQGHRIHEGDLVAASPAISNRIPEDFPDPHDFVPARYEQPRQEDLLNRWTWIPFGAGRHRCVGAAFAIMQIKAIFSVLLREYEFEMAQPPESYRNDHSKMVVQLAQPACVRYRRRT

>d1io7a\_ a.104.1.1 (A:) CYP119 {Archaeon Sulfolobus solfataricus}

MYDWFSEMRKKDPVYYDGNIWQVFSYRYTKEVLNNFSKFSSDLTGYHERLEDLRNGKIRFDIPTRYTMLTSDPPLHDELRSMSADIFSPQKLQTLETFIRETTRSLLDSIDPREDDIVKKLAVPLPIIVISKILGLPIEDKEKFKEWSDLVAFRLGKPGEIFELGKKYLELIGYVKDHLNSGTEVVSRVVNSNLSDIEKLGYIILLLIAGNETTTNLISNSVIDFTRFNLWQRIREENLYLKAIEEALRYSPPVMRTVRKTKERVKLGDQTIEEGEYVRVWIASANRDEEVFHDGEKFIPDRNPNPHLSFGSGIHLCLGAPLARLEARIAIEEFSKRFRHIEILDTEKVPNEVLNGYKRLVVRLKS

>d1dt6a\_ a.104.1.1 (A:) Mammalian cytochrome p450 2c5 {Rabbit (Oryctolagus cuniculus)}

PPGPTPFPIIGNILQIDAKDISKSLTKFSECYGPVFTVYLGMKPTVVLHGYEAVKEALVDLGEEFAGRGSVPILEKVSKGLGIAFSNAKTWKEMRRFSLMTLRNFGMGKRSIEDRIQEEARCLVEELRKTNASPCDPTFILGCAPCNVICSVIFHNRFDYKDEEFLKLMESLHENVELLGTPWLQVYNNFPALLDYFPGIHKTLLKNADYIKNFIMEKVKEHQKLLDVNNPRDFIDCFLIKMEQENNLEFTLESLVIAVSDLFGAGTETTSTTLRYSLLLLLKHPEVAARVQEEIERVIGRHRSPCMQDRSRMPYTDAVIHEIQRFIDLLPTNLPHAVTRDVRFRNYFIPKGTDIITSLTSVLHDEKAFPNPKVFDPGHFLDESGNFKKSDYFMPFSAGKRMCVGEGLARMELFLFLTSILQNFKLQSLVEPKDLDITAVVNGFVSVPPSYQLCFIPIHH

>d1etob\_ a.105.1.1 (B:) FIS protein {Escherichia coli}

MFEQRVNSDVLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVEQPLLDMVMQYTLGNQTRAALMMGINRGTLRKKLKKYGMN

>d1etxa\_ a.105.1.1 (A:) FIS protein {Escherichia coli}

VLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVEQPLLDMVMQYTRGNATRAALMMGINRGTLRKKLKKYGMN

>d1fipa\_ a.105.1.1 (A:) FIS protein {Escherichia coli}

PLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVEQALLDMVMQYTRGNQTRAALMMGINRGTLRKKLKKYGMN

>d1ntca\_ a.105.1.1 (A:) DNA-binding domain of NTRC {Salmonella typhimurium}

MDLPGELFEASTPDSPSHLPPDSWATLLAQWADRALRSGHQNLLSEAQPELERTLLTTALRHTQGHKQEAARLLGWGAATLTAKLKELGME

>d1g8ea\_ a.145.1.1 (A:) Flagellar transcriptional activator FlhD {Escherichia coli}

MHTSELLKHIYDINLSYLLLAQRLIVQDKASAMFRLGINEEMATTLAALTLPQMVKLAETNQLVCHFRFDSHQTITQLTQDSRVDDLQQIHTGIMLST

>d1g8eb\_ a.145.1.1 (B:) Flagellar transcriptional activator FlhD {Escherichia coli}

TSELLKHIYDINLSYLLLAQRLIVQDKASAMFRLGINEEMATTLAALTLPQMVKLAETNQLVCHFRFDSHQTITQLTQDS

>d1jhga\_ a.107.1.1 (A:) Trp repressor {Escherichia coli}

SAAMAEQRHQEWLRFVDLLKNAYQNDLHLPLLNLMLTPDEREALGTRVRIIEELLRGEMSQRELKNELGAGIATITRGSNSLKAAPVELRQWLEEVLLKSD

>d1trra\_ a.107.1.1 (A:) Trp repressor {Escherichia coli}

AQQSPYSAAMAEQRHEEWLRFVDLLKNAYQNDLHLPLLNLMLTPDEREALGTRVRIVEELLRGEMSQRELKNELGAGIATITRGSNSLKAAPVELRQWLEEVLLK

>d1dd3a1 a.108.1.1 (A:1-57) Ribosomal protein L7/12, oligomerisation (N-terminal) domain {Thermotoga maritima}

MTIDEIIEAIEKLTVSELAELVKKLEDKFGVTAAAPVAVAAAPVAGAAAGAAQEEKT

>d1dd3c1 a.108.1.1 (C:) Ribosomal protein L7/12, oligomerisation (N-terminal) domain {Thermotoga maritima}

MTIDEIIEAIEKLTVSELAELVKKLEDKFGVT

>d1dd4d1 a.108.1.1 (D:) Ribosomal protein L7/12, oligomerisation (N-terminal) domain {Thermotoga maritima}

MTIDEIIEAIEKLTVSELAELVKKLEDKFGVTAAAPVAVA

>d1iiea\_ a.109.1.1 (A:) MHC class II-associated invariant chain ectoplasmic trimerization domain {Human (Homo sapiens)}

YGNMTEDHVMHLLQNADPLKVYPPLKGSFPENLRHLKNTMETIDWKVFESWMHHWLLFEMSRHSLEQKPTDAPPK

>d1aora1 a.110.1.1 (A:211-605) Aldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

IADKQKFMLVVREKVNKLRNDPVAGGGLPKYGTAVLVNIINENGLYPVKNFQTGVYPYAYEQSGEAMAAKYLVRNKPCYACPIGCGRVNRLPTVGETEGPEYESVWALGANLGINDLASIIEANHMCDELGLDTISTGGTLATAMELYEKGHIKDEELGDAPPFRWGNTEVLHYYIEKIAKREGFGDKLAEGSYRLAESYGHPELSMTVKKLELPAYDPRGAEGHGLGYATNNRGGCHIKNYMISPEILGYPYKMDPHDVSDDKIKMLILFQDLTALIDSAGLCLFTTFGLGADDYRDLLNAALGWDFTTEDYLKIGERIWNAERLFNLKAGLDPARDDTLPKRFLEEPMPEGPNKGHTVRLKEMLPRYYKLRGWTEDGKIPKEKLEELGIAEFY

>d1b25a1 a.110.1.1 (A:211-619) Formaldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

DKEELKKLSQEAYNEILNSPGYPFWKRQGTMAAVEWCNTNYALPTRNFSDGYFEFARSIDGYTMEGMKVQQRGCPYCNMPCGNVVLDAEGQESELDYENVALLGSNLGIGKLNEVSVLNRIADEMGMDTISLGVSIAHVMEAVERGILKEGPTFGDFKGAKQLALDIAYRKGELGNLAAEGVKAMAEKLGTHDFAMHVKGLEVSGYNCYIYPAMALAYGTSAIGAHHKEAWVIAWEIGTAPIEGEKAEKVEYKISYDPIKAQKVVELQRLRGGLFEMLTACRLPWVEVGLSLDYYPKLLKAITGVTYTWDDLYKAADRVYSLIRAYWVREFNGKWDRKMDYPPKRWFTEGLKSGPHKGEHLDEKKYDELLSEYYRIRGWDERGIPKKETLKELDLDFVIPELEKVTNLE

>d1d2ta\_ a.111.1.1 (A:) Acid phosphatase {Escherichia blattae}

GNDTTTKPDLYYLKNSEAINSLALLPPPPAVGSIAFLNDQAMYEQGRLLRNTERGKLAAEDANLSSGGVANAFSGAFGSPITEKDAPALHKLLTNMIEDAGDLATRSAKDHYMRIRPFAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLAEINPQRQNEILKRGYELGQSRVICGYHWQSDVDAARVVGSAVVATLHTNPAFQQQLQKAKAEFAQHQK

>d1qi9a\_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Ascophyllum nodosum}

TCSTSDDADDPTPPNERDDEAFASRVAAAKRELEGTGTVCQINNGETDLAAKFHKSLPHDDLGQVDADAFAALEDCILNGDLSICEDVPVGNSEGDPVGRLVNPTAAFAIDISGPAFSATTIPPVPTLPSPELAAQLAEVYWMALARDVPFMQYGTDDITVTAAANLAGMEGFPNLDAVSIGSDGTVDPLSQLFRATFVGVETGPFISQLLVNSFTIDSITVEPKQETFAPDVNYMVDFDEWLNIQNGGPPAGPELLDDELRFVRNARDLARVTFTDNINTEAYRGALILLGLDAFNRAGVNGPFIDIDRQAGFVNFGISHYFRLIGAAELAQRSSWYQKWQVHRFARPEALGGTLHLTIKGELNADFDLSLLENAELLKRVAAINAAQNPNNEVTYLLPQAIQEGSPTHPSYPSGHATQNGAFATVLKALIGLDRGGDCYPDPVYPDDDGLKLIDFRGSCLTFEGEINKLAVNVAFGRQMLGIHYRFDGIQGLLLGETITVRTLHQELMTFAEESTFEFRLFTGEVIKLFQDGTFTIDGFKCPGLVYTGVENCV

>d1qhba\_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Red algae (Corallina officinalis)}

GIPADNLQSRAKASFDTRVAAAELALARGAVPSFANGEELLYRNSETGDPSFIGSFTKGLPHDDNGAIIDPDDFLAFVRAINSGDEKEIAALTLGPARDPETGLPIWRSDLANSLDLEVRGWENSSAGLTFDLEGPDAQSVAMPPAPVLTSPELIAEMAELYLMALGRDIEFSEFDSPKNAAFIRSAIERLNGLEWFNTPAKLGDPPAEIRRRRGEVTVGNLFRGILPGSEVGPYLSQFIIVGSKQIGSATVGNKTLVSPNAADEFDGEIAYGSITISQRVRIATPGRDFMTDLKVFLDVQDAADFRGFESYEPGARLIRTIRDLATWVHFDSLYEAYLNACLILLANGVPFDPNLPFQQEDKLDNQDVFVNFGSAHVLSLVTEVATRALKAVRYQKFNIHRRLRPEATGGLISVNKNAFLKSESVFPEVDVLVEELSSILDDSASSNEKQNIADGDVSPGKSFLLPMAFAEGSPFHPSYGSGHAVVAGACVTILKAFFDANFQIDQVFEVDTDEDKLVKSSFPGPLTVAGELNKLADNVAIGRNMAGVHYFSDQFESLLLGEQIAIGILEEQSLTYGENFFFNLPKFDGTTIQI

>d1vns\_\_ a.111.1.3 (-) Chloroperoxidase {Curvularia inaequalis}

VTPIPLPKIDEPEEYNTNYILFWNHVGLELNRVTHTVGGPLTGPPLSARALGMLHLAIHDAYFSICPPTDFTTFLSPDTENAAYRLPSPNGANDARQAVAGAALKMLSSLYMKPVEQPNPNPGANISDNAYAQLGLVLDRSVLEAPGGVDRESASFMFGEDVADVFFALLNDPRGASQEGYHPTPGRYKFDDEPTHPVVLIPVDPNNPNGPKMPFRQYHAPFYGKTTKRFATQSEHFLADPPGLRSNADETAEYDDAVRVAIAMGGAQALNSTKRSPWQTAQGLYWAYDGSNLIGTPPRFYNQIVRRIAVTYKKEEDLANSEVNNADFARLFALVDVACTDAGIFSWKEKWEFEFWRPLSGVRDDGRPDHGDPFWLTLGAPATNTNDIPFKPPFPAYPSGHATFGGAVFQMVRRYYNGRVGTWKDDEPDNIAIDMMISEELNGVNRDLRQPYDPTAPIEDQPGIVRTRIVRHFDSAWELMFENAISRIFLGVHWRFDAAAARDILIPTTTKDVYAVDNNGATVFQNVEDIRYTTRGTREDEEGLFPIGGVPLGIEIADEIFNNGLKPTPPEIQP

>d1sig\_\_ a.112.1.1 (-) sigma70 subunit fragment from RNA polymerase {Escherichia coli}

MEGEIDIAKRIEDGINQVQCSVAEYPEAITYLLEQYNRVEAEEARLSDLITGFVDPNAEEDLAPTATHVGSELSQEDLDDDEDEDEEDGDDDSADDDNSIDPELAREKFAELRAQYVVTRDTIKAKGRSHATAQEEILKLSEVFKQFRLVPKQFDYLVNSMRVMMDRVRTQERLIMKLCVEQCKMPKKNFITLFTGNETSDTWFNAAIAMNKPWSEKLHDVSEEVHRALQKLQQIEEETGLTIEQVKDINRRMSIGEAKARRAKKEMVEANLRLVISIAKKYTNRGLQFLDLIQEGNIGLMKAVDKFEYRRGYKFSTYATWWIRQAITRSIADQ

>d1ewqa1 a.113.1.1 (A:267-541) DNA repair protein MutS, domain III {Thermus aquaticus}

RGQDTLFSVLDETRTAPGRRLLQSWLRHPLLDRGPLEARLDRVEGFVREGALREGVRRLLYRLADLERLATRLELGRASPKDLGALRRSLQILPELRALLGEEVGLPDLSPLKEELEAALVEDPPLKVSEGGLIREGYDPDLDALRAAHREGVAYFLELEERERERTGIPTLKVGYNAVFGYYLEVTRPYYERVPKEYRPVQTLKDRQRYTLPEMKEKEREVYRLEALIRRREEEVFLEVRERAKRQAEALREAARILAELDVYAALAEVAVRYG

>d1e3ma1 a.113.1.1 (A:270-566) DNA repair protein MutS, domain III {Escherichia coli}

DAATRRNLEITQNLAGGAENTLASVLDCTVTPMGSRMLKRWLHMPVRDTRVLLERQQTIGALQDFTAGLQPVLRQVGDLERILARLALRTARPRDLARMRHAFQQLPELRAQLETVDSAPVQALREKMGEFAELRDLLERAIIDTPPVLVRDGGVIASGYNEELDEWRALADGATDYLERLEVRERERTGLDTLKVGFNAVHGYYIQISRGQSHLAPINYMRRQTLKNAERYIIPELKEYEDKVLTSKGKALALEKQLYEELFDLLLPHLEALQQSASALAELDVLVNLAERAYTLN

>d1f5na1 a.114.1.1 (A:284-583) Interferon-induced guanylate-binding protein 1 (GBP1), C-terminal domain {Human (Homo sapiens)}

GGIQVNGPRLESLVLTYVNAISSGDLPCMENAVLALAQIENSAAVQKAIAHYEQQMGQKVQLPTESLQELLDLHRDSEREAIEVFIRSSFKDVDHLFQKELAAQLEKKRDDFCKQNQEASSDRCSGLLQVIFSPLEEEVKAGIYSKPGGYRLFVQKLQDLKKKYYEEPRKGIQAEEILQTYLKSKESMTDAILQTDQTLTEKEKEIEVERVKAESAQASAKMLHEMQRKNEQMMEQKERSYQEHLKQLTEKMENDRVQLLKEQERTLALKLQEQEQLLKEGFQKESRIMKNEIQDLQTKM

>d1bvp11 a.115.1.1 (1:1-120,1:255-349) Bluetongue virus capsid protein vp7 (BTV-10 vp7) {Bluetongue virus}

MDTIAARALTVMRACATLQEARIVLEANVMEILGIAINRYNGLTLRGVTMRPTSLAQRNEMFFMCLDMMLSAAGINVGPISPDYTQHMATIGVLATPEIPFTTEAANEIARVTGETSTWGXKTLNQYPALTAEIFNVYSFRDHTWHGLRTAILNRTTLPNMLPPIFPPNDRDSILTLLLLSTLADVYTVLRPEFAIHGVNPMPGPLTRAIARAAYV

>d1qhda1 a.115.1.2 (A:1-148,A:333-397) vp6, the major capsid protein of group A rotavirus {Bovine rotavirus}

MDVLYSLSKTLKDARDKIVEGTLYSNVSDLIQQFNQMIITMNGNEFQTGGIGNLPIRNWNFDFGLLGTTLLNLDANYVETARNTIDYFVDFVDNVCMDEMVRESQRNGIAPQSDSLIKLSGIKFKRINFDNSSEYIENWNLQNRRQRTXSVLADASETMLANVTSVRQEYAIPVGPVFPPGMNWTDLITNYSPSREDNLQRVFTVASIRSMLVK

>d1tx4a\_ a.116.1.1 (A:) p50 RhoGAP domain {Human (Homo sapiens)}

PLPNQQFGVSLQHLQEKNPEQEPIPIVLRETVAYLQAHALTTEGIFRRSANTQVVREVQQKYNMGLPVDFDQYNALHLPAVILKTFLRELPEPLLTFDLYPHVVGFLNIDESQRVPATLQVLQTLPEENYQVLRFLTAFLVQISAHSDQNKMTNTNLAVVFGPNLLWAKDAAITLKAINPINTFTKFLLDHQGELF

>d1pbwa\_ a.116.1.1 (A:) p85 alpha subunit RhoGAP domain {Human (Homo sapiens)}

LPDLAEQFAPPDIAPPLLIKLVEAIEKKGLECSTLYRTQSSSNLAELRQLLDCDTPSVDLEMIDVHVLADAFKRYLLDLPNPVIPAAVYSEMISLAPEVQSSEEYIQLLKKLIRSPSIPHQYWLTLQYLLKHFFKLSQTSSKNLLNARVLSEIFSPMLFRFSAASSDNTENLIKVIEILISTEW

>d1f7ca\_ a.116.1.1 (A:) Graf {Chicken (Gallus gallus)}

AQLDSIGFSIIKKCIHAVETRGINEQGLYRIVGVNSRVQKLLSILMDPKTATETETEICAEWEIKTITSALKTYLRMLPGPLMMYQFQRSFIKAAKLENQESRVSEIHSLVHRLPEKNRQMLHLLMNHLAKVADNHKQNLMTVANLGVVFGPTLLRPQEETVAAIMDIKFQNIVIEILIENHEKIFNTVPE

>d1wer\_\_ a.116.1.2 (-) p120GAP domain {Human (Homo sapiens)}

MPEEEYSEFKELILQKELHVVYALSHVCGQDRTLLASILLRIFLHEKLESLLLCTLNDREISMEDEATTLFRATTLASTLMEQYMKATATQFVHHALKDSILKIMESKQSCELSPSKLEKNEDVNTNLTHLLNILSELVEKIFMASEILPPTLRYIYGCLQKSVQHKWPTNTTMRTRVVSGFVFLRLICPAILNPRMFNIISDSPSPIAARTLILVAKSVQNLANLVEFGAKEPYMEGVNPFIKSNKHRMIMFLDELGNVPELPDTTEHSRTDLSRDLAALHEICVAHSDELRTLSNERGAQQHVLKKLLAITELLQQKQNQYT

>d1nf1a\_ a.116.1.2 (A:) GAP related domain of neurofibromin {Human (Homo sapiens)}

ERLVELVTMMGDQGELPIAMALANVVPCSQWDELARVLVTLFDSRHLLYQLLWNMFSKEVELADSMQTLFRGNSLASKIMTFCFKVYGATYLQKLLDPLLRIVITSSDWQHVSFEVDPTRLEPSESLEENQRNLLQMTEKFFHAIISSSSEFPPQLRSVCHCLYQVVSQRFPQNSIGAVGSAMFLRFINPAIVSPYEAGILDKKPPPIIERGLKLMSKILQSIANHVLFTKEEHMRPFNDFVKSNFDAARRFFLDIASDCPTSDAVNHSLSFISDGNVLALHRLLWNNQEKIGQYLSSNRDHKAVGRRPFDKMATLLAYLGPPE

>d1bkds\_ a.117.1.1 (S:) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}

RLPSADVYRFAEPDSEENIIFEEGIPIIKAGTVIKLIERLTYHMYADPNFVRTFLTTYRSFCKPQELLSLIIERFEIPEPRFRKEYIQPVQLRVLNVCRHWVEHHFYDFERDAYLLQRMEEFIGTVRGKAMKKWVESITKIIQRKKITFQSSPPTVEWHISRPGHIETFDLLTLHPIEIARQLTLLESDLYRAVQPSELVGSVWTKEDKEINSPNLLKMIRHTTNLTLWFEKCIVETENLEERVAVVSRIIEILQVFQELNNFNGVLEVVSAMNSSPVYRLDHTFEQIPSRQKKILEEAHELSEDHYKKYLAKLRSINPPCVPFFGIYLTNILKTEEGNPEVLKRHGKELINFSKRRKVAEITGEIQQYQNQPYCLRVESDIKRFFENLNPMGNSMEKEFTDYLFNKSLEIEPRNPKPLPRFPKKYSYPLKSPGVRPSN

>d1h6oa\_ a.146.1.1 (A:) TRF1 {Human (Homo sapiens)}

EDAGLVAEAEAVAAGWMLDFLCLSLCRAFRDGRSEDFRRTRNSAEAIIHGLSSLTACQLRTIYICQFLTRIAAGKTLDAQFENDERITPLESALMIWGSIEKEHDKLHEEIQNLIKIQAIAVCMENGNFKEAEEVFERIFGDPNSHMPFKSKLLMIISQKDTFHSFFQHFSYNHMMEKIKSYVNYVLSEKSSTFLMKAAAKVVE

>d1h6pa\_ a.146.1.1 (A:) TRF2 {Human (Homo sapiens)}

AGEARLEEAVNRWVLKFYFHEALRAFRGSRYGDFRQIRDIMQALLVRPLGKEHTVSRLLRVMQCLSRIEEGENLDCSFDMEAELTPLESAINVLEMIKTEFTLTEAVVESSRKLVKEAAVIICIKNKEFEKASKILKKHMSKDPTTQKLRNDLLNIIREKNLAHPVIQNFSYETFQQKMLRFLESHLDDAEPYLLTMAKKALK

>d1g3jc\_ a.118.1.1 (C:) beta-Catenin {Human (Homo sapiens)}

HHREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLLHQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSVCSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSDAATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTSRHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRIVIRGLNTIPLFVQLLYSPIENIQRVAAGVLCELAQDKEAAEAIEAEGATAPLTELLHSRNEGVATYAAAVLFRMSE

>d1jdha\_ a.118.1.1 (A:) beta-Catenin {Human (Homo sapiens)}

AVVNLINYQDDAELATRAIPELTKLLNDEDQVVVNKAAVMVHQLSKKEASRHAIMRSPQMVSAIVRTMQNTNDVETARCTAGTLHNLSHHREGLLAIFKSGGIPALVKMLGSPVDSVLFYAITTLHNLLLHQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLIILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSVCSSNKPAIVEAGGMQALGLHLTDPSQRLVQNCLWTLRNLSDAATKQEGMEGLLGTLVQLLGSDDINVVTCAAGILSNLTCNNYKNKMMVCQVGGIEALVRTVLRAGDREDITEPAICALRHLTSRHQEAEMAQNAVRLHYGLPVVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRIVIRGLNTIPLFVQLLYSPIENIQRVAAGVLCELAQDKEAAEAIEAEGATAPLTELLHSRNEGVATYAAAVLFRMS

>d1iala\_ a.118.1.1 (A:) Importin alpha {Mouse (Mus musculus)}

DEQMLKRRNVSSFPDDATSPLQENRNNQGTVNWSVEDIVKGINSNNLESQLQATQAARKLLSREKQPPIDNIIRAGLIPKFVSFLGKTDCSPIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHAHISEQAVWALGNIAGDGSAFRDLVIKHGAIDPLLALLAVPDLSTLACGYLRNLTWTLSNLCRNKNPAPPLDAVEQILPTLVRLLHHNDPEVLADSCWAISYLTDGPNERIEMVVKKGVVPQLVKLLGATELPIVTPALRAIGNIVTGTDEQTQKVIDAGALAVFPSLLTNPKTNIQKEATWTMSNITAGRQDQIQQVVNHGLVPFLVGVLSKADFKTQKEAAWAITNYTSGGTVEQIVYLVHCGIIEPLMNLLSAKDTKIIQVILDAISNIFQAAEKLGETEKLSIMIEECGGLDKIEALQRHENESVYKASLNLIEKYF

>d1ibrb\_ a.118.1.1 (B:) Importin beta {Human (Homo sapiens)}

ELITILEKTVSPDRLELEAAQKFLERAAVENLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLTSKDPDIKAQYQQRWLAIDANARREVKNYVLQTLGTETYRPSSASQCVAGIACAEIPVNQWPELIPQLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAIIQGMRKEEPSNNVKLAATNALLNSLEFTKANFDKESERHFIMQVVCEATQCPDTRVRVAALQNLVKIMSLYYQYMETYMGPALFAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEASEAAEQGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDDDDDWNPCKAAGVCLMLLATCCEDDIVPHVLPFIKEHIKNPDWRYRDAAVMAFGCILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTVGRICELLPEAAINDVYLAPLLQCLIEG

>d1qgra\_ a.118.1.1 (A:) Importin beta {Human (Homo sapiens)}

MELITILEKTVSPDRLELEAAQKFLERAAVENLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLTSKDPDIKAQYQQRWLAIDANARREVKNYVLHTLGTETYRPSSASQCVAGIACAEIPVNQWPELIPQLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAIIQGMRKEEPSNNVKLAATNALLNSLEFTKANFDKESERHFIMQVVCEATQCPDTRVRVAALQNLVKIMSLYYQYMETYMGPALFAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEASEAAEQGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDDDDDWNPCKAAGVCLMLLATCCEDDIVPHVLPFIKEHIKNPDWRYRDAAVMAFGCILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTVGRICELLPEAAINDVYLAPLLQCLIEGLSAEPRVASNVCWAFSSLAEAAYEAADVADDQEEPATYCLSSSFELIVQKLLETTDRPDGHQNNLRSSAYESLMEIVKNSAKDCYPAVQKTTLVIMERLQQVLQMESHIQSTSDRIQFNDLQSLLCATLQNVLRKVQHQDALQISDVVMASLLRMFQSTAGSGGVQEDALMAVSTLVEVLGGEFLKYMEAFKPFLGIGLKNYAEYQVCLAAVGLVGDLCRALQSNIIPFCDEVMQLLLENLGNENVHRSVKPQILSVFGDIALAIGGEFKKYLEVVLNTLQQASQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDQENVHPDVMLVQPRVEFILSFIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLKLVEARPMIHELLTEGRRSKTNKAKTLARWATKELRKLKNQA

>d1qbkb\_ a.118.1.1 (B:) Karyopherin beta2 {Human (Homo sapiens)}

YEWKPDEQGLQQILQLLKESQSPDTTIQRTVQQKLEQLNQYPDFNNYLIFVLTKLKSEDEPTRSLSGLILKNNVKAHFQNFPNGVTDFIKSECLNNIGDSSPLIRATVGILITTIASKGELQNWPDLLPKLCSLLDSEDYNTCEGAFGALQKICEDSAEILDSDVLDRPLNIMIPKFLQFFKHSSPKIRSHAVACVNQFIISRTQALMLHIDSFTENLFALAGDEEPEVRKNVCRALVMLLEVRMDRLLPHMHNIVEYMLQRTQDQDENVALEACEFWLTLAEQPICKDVLVRHLPKLIPVLVNGMKYSDIDIILLKGDVEEDETIPDSEQDIRPRFHRSRTVAQQHDEDGIEEEDDDDDEIDDDDTISDWNLRKCSAAALDVLANVYRDELLPHILPLLKELLFHHEWVVKESGILVLGAIAEGCMQGMIPYLPELIPHLIQCLSDKKALVRSITCWTLSRYAHWVVSQPPDTYLKPLMTELLKRILDSNKRVQEAACSAFATLEEEACTELVPYLAYILDTLVFAFSKYQHKNLLILYDAIGTLADSVGHHLNKPEYIQMLMPPLIQKWNMLKDEDKDLFPLLECLSSVATALQSGFLPYCEPVYQRCVNLVQKTLAQAMLNNAQPDQYEAPDKDFMIVALDLLSGLAEGLGGNIEQLVARSNILTLMYQCMQDKMPEVRQSSFALLGDLTKACFQHVKPCIADFMPILGTNLNPEFISVCNNATWAIGEISIQMGIEMQPYIPMVLHQLVEIINRPNTPKTLLENTAITIGRLGYVCPQEVAPMLQQFIRPWCTSLRNIRDNEEKDSAFRGICTMISVNPSGVIQDFIFFCDAVASWINPKDDLRDMFCKILHGFKNQVGDENWRRFSDQFPLPLKERLAAFYGV

>d1ee4a\_ a.118.1.1 (A:) Karyopherin alpha {Baker's yeast (Saccharomyces cerevisiae)}

QELPQMTQQLNSDDMQEQLSATVKFRQILSREHRPPIDVVIQAGVVPRLVEFMRENQPEMLQLEAAWALTNIASGTSAQTKVVVDADAVPLFIQLLYTGSVEVKEQAIWALGNVAGDSTDYRDYVLQCNAMEPILGLFNSNKPSLIRTATWTLSNLCRGKKPQPDWSVVSQALPTLAKLIYSMDTETLVDACWAISYLSDGPQEAIQAVIDVRIPKRLVELLSHESTLVQTPALRAVGNIVTGNDLQTQVVINAGVLPALRLLLSSPKENIKKEACWTISNITAGNTEQIQAVIDANLIPPLVKLLEVAEDKTKKEACWAISNASSGGLQRPDIIRYLVSQGCIKPLCDLLEIADNRIIEVTLDALENILKMGEADKEARGLNINENADFIEKAGGMEKIFNCQQNENDKIYEKAYKIIETYF

>d1b3ua\_ a.118.1.2 (A:) Constant regulatory domain of protein phosphatase 2a, pr65alpha {Human (Homo sapiens)}

AAADGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSTIALALGVERTRSELLPFLTDTIYDEDEVLLALAEQLGTFTTLVGGPEYVHCLLPPLESLATVEETVVRDKAVESLRAISHEHSPSDLEAHFVPLVKRLAGGDWFTSRTSACGLFSVCYPRVSSAVKAELRQYFRNLCSDDTPMVRRAAASKLGEFAKVLELDNVKSEIIPMFSNLASDEQDSVRLLAVEACVNIAQLLPQEDLEALVMPTLRQAAEDKSWRVRYMVADKFTELQKAVGPEITKTDLVPAFQNLMKDCEAEVRAAASHKVKEFCENLSADCRENVIMSQILPCIKELVSDANQHVKSALASVIMGLSPILGKDNTIEHLLPLFLAQLKDECPEVRLNIISNLDCVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIIEYMPLLAGQLGVEFFDEKLNSLCMAWLVDHVYAIREAATSNLKKLVEKFGKEWAHATIIPKVLAMSGDPNYLHRMTTLFCINVLSEVCGQDITTKHMLPTVLRMAGDPVANVRFNVAKSLQKIGPILDNSTLQSEVKPILEKLTQDQDVDVKYFAQEALTVLSLA

>d1hu3a\_ a.118.1.2 (A:) Eukaryotic initiation factor eIF4G {Human (Homo sapiens)}

SDPENIKTQELFRKVRSILNKLTPQMFNQLMKQVSGLTVDTEERLKGVIDLVFEKAIDEPSFSVAYANMCRCLVTLKVPMADKPGNTVNFRKLLLNRCQKEFEKDKADDDVFEKKQKELEAASAPEERTRLHDELEEAKDKARRRSIGNIKFIGELFKLKMLTEAIMHDCVVKLLKNHDEESLECLCRLLTTIGKDLDFEKAKPRMDQYFNQMEKIVKERKTSSRIRFMLQDVIDLRLCNWVS

>d1h6ka1 a.118.1.2 (A:27-290) CBP80, 80KDa nuclear cap-binding protein {Human (Homo sapiens)}

TEDHLESLICKVGEKSACSLESNLEGLAGVLEADLPNYKSKILRLLCTVARLLPEKLTIYTTLVGLLNARNYNFGGEFVEAMIRQLKESLKANNYNEAVYLVRFLSDLVNCHVIAAPSMVAMFENFVSVTQEEDVPQVRRDWYVYAFLSSLPWVGKELYEKKDAEMDRIFANTESYLKRRQKTHVPMLQVWTADKPHPQEEYLDCLWAQIQKLKKDRWQERHILRPYLAFDSILCEALQHNLPPFTPPPHTEDSVYPMPRVIFR

>d1h6ka2 a.118.1.2 (A:291-480) CBP80, 80KDa nuclear cap-binding protein {Human (Homo sapiens)}

MFDYTDDPEGPVMPGSHSVERFVIEENLHCIIKSHWKERKTCAAQLVSYPGKNKIPLNYHIVEVIFAELFQLPAPPHIDVMYTTLLIELCKLQPGSLPQVLAQATEMLYMRLDTMNTTCVDRFINWFSHHLSNFQFRWSWEDWSDCLSQDPESPKPKFVREVLEKCMRLSYHQRILDIVPPTFSALCPSN

>d1h6ka3 a.118.1.2 (A:481-790) CBP80, 80KDa nuclear cap-binding protein {Human (Homo sapiens)}

PTCIYKYGDESSNSLPGHSVALCLAVAFKSKATNDEIFSILKDVPNPNQDDDDDEGFSFNPLKIEVFVQTLLHLAAKSFSHSFSALAKFHEVFKTLAESDEGKLHVLRVMFEVWRNHPQMIAVLVDKMIRTQIVDCAAVANWIFSSELSRDFTRLFVWEILHSTIRKMNKHVLKIQKELEEAKEKLARQHDGVLEEQIERLQEKVESAQSEQKNLFLVIFQRFIMILTEHLVRCETDGTSVLTPWYKNCIERLQQIFLQHHQIIQQYMVTLENLLFTAELDPHILAVFQQFCALQA

>d1hs6a1 a.118.1.7 (A:461-610) Leukotriene A4 hydrolase C-terminal domain {Human (Homo sapiens)}

DMTLTNACIALSQRWITAKEDDLNSFNATDLKDLSSHQLNEFLAQTLQRAPLPLGHIKRMQEVYNFNAINNSEIRFRWLRLCIQSKWEDAIPLALKMATEQGRMKFTRPLFKDLAAFDKSHDQAVRTYQEHKASMHPVTAMLVGKDLKVD

>d1b89a\_ a.118.1.3 (A:) Clathrin heavy chain proximal leg segment {Cow (Bos taurus)}

RLAELEEFINGPNNAHIQQVGDRCYDEKMYDAAKLLYNNVSNFGRLASTLVHLGEYQAAVDGARKANSTRTWKEVCFACVDGKEFRLAQMCGLHIVVHADELEELINYYQDRGYFEELITMLEAALGLERAHMGMFTELAILYSKFKPQKMREHLELFWSRVNIPKVLRAAEQAHLWAELVFLYDKYEEYDNAIITMMNHPTDAWKEGQFKDIITKVANVELYYRAIQFYLEFKPLLLNDLLMVLSPRLDHTRAVNYFSKVKQLPLVKPYLRSVQNHNNKSVNESLNNLFITEEDYQALRTSIDAYDNFDNISLAQRLEKHELIEFRRIAAYLFKG

>d1bpoa1 a.118.1.4 (A:331-487) Clathrin heavy-chain linker domain {Rat (Rattus norvegicus)}

EENIIPYITNVLQNPDLALRMAVRNNLAGAEELFARKFNALFAQGNYSEAAKVAANAPKGILRTPDTIRRFQSVPAQPGQTSPLLQYFGILLDQGQLNKYESLELCRPVLQQGRKQLLEKWLKEDKLECSEELGDLVKSVDPTLALSVYLRANVPNK

>d1c9la1 a.118.1.4 (A:331-359) Clathrin heavy-chain linker domain {Rat (Rattus norvegicus)}

EENIIPYITNVLQNPDLALRMAVRNNLAG

>d1lrv\_\_ a.118.1.5 (-) Leucine-rich repeat variant {Azotobacter vinelandii}

TPIGDCRVCSFRMSLLLTGRCTPGDACVAVESGRQIDRFFRNNPHLAVQYLADPFWERRAIAVRYSPVEALTPLIRDSDEVVRRAVAYRLPREQLSALMFDEDREVRITVADRLPLEQLEQMAADRDYLVRAYVVQRIPPGRLFRFMRDEDRQVRKLVAKRLPEESLGLMTQDPEPEVRRIVASRLRGDDLLELLHDPDWTVRLAAVEHASLEALRELDEPDPEVRLAIAGRL

>d1e8xa1 a.118.1.6 (A:525-725) Phoshoinositide 3-kinase (PI3K) helical domain {Pig (Sus scrofa)}

HPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWGQQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLHYLLQLVQAVKFEPYHDSALARFLLKRGLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCG

>d1ib2a\_ a.118.1.8 (A:) Pumilio 1 {Human (Homo sapiens)}

GRSRLLEDFRNNRYPNLQLREIAGHIMEFSQDQHGSRFIQLKLERATPAERQLVFNEILQAAYQLMVDVFGNYVIQKFFEFGSLEQKLALAERIRGHVLSLALQMYGCRVIQKALEFIPSDQQNEMVRELDGHVLKCVKDQNGNHVVQKCIECVQPQSLQFIIDAFKGQVFALSTHPYGCRVIQRILEHCLPDQTLPILEELHQHTEQLVQDQYGNYVIQHVLEHGRPEDKSKIVAEIRGNVLVLSQHKFASNVVEKCVTHASRTERAVLIDEVCTMNDGPHSALYTMMKDQYANYVVQKMIDVAEPGQRKIVMHKIRPHIA

>d1ho8a\_ a.118.1.9 (A:) Regulatory subunit H of the V-type ATPase {Baker's yeast (Saccharomyces cerevisiae)}

GATKILMDSTHFNEIRSIIRSRSVAWDALARSEELSEIDASTAKALESILVKKNIGDGLSSSNNAHSGFKVNGKTLIPLIHLLSTSDNEDCKKSVQNLIAELLSSDKYGDDTVKFFQEDPKQLEQLFDVSLKGDFQTVLISGFNVVSLLVQNGLHNVKLVEKLLKNNNLINILQNIEQMDTCYVCIRLLQELAVIPEYRDVIWLHEKKFMPTLFKILQRATDSQLATRIVATNSNHLGIQLQYHSLLLIWLLTFNPVFANELVQKYLSDFLDLLKLVKITIKEKVSRLCISIILQCCSTRVKQHKKVIKQLLLLGNALPTVQSLSERKYSDEELRQDISNLKEILENEYQELTSFDEYVAELDSKLLCWSPPHVDNGFWSDNIDEFKKDNYKIFRQLIELLQAKVRNGDVNAKQEKIIIQVALNDITHVVELLPESIDVLDKTGGKADIMELLNHSDSRVKYEALKATQAIIGYTFK

>d1ycsb1 a.118.2.1 (B:327-456) 53BP2 {Human (Homo sapiens)}

PLALLLDSSLEGEFDLVQRIIYEVDDPSLPNDEGITALHNAVCAGHTEIVKFLVQFGVNVNAADSDGWTPLHCAASCNNVQVCKFLVESGAAVFAMTYSDMQTAADKCEEMEEGYTQCSQFLYGVQEKMG

>d1awcb\_ a.118.2.1 (B:) GA bindinig protein (GABP) beta 1 {Mouse (Mus musculus)}

DLGKKLLEAARAGQDDEVRILMANGAPFTTDWLGTSPLHLAAQYGHFSTTEVLLRAGVSRDARTKVDRTPLHMAASEGHANIVEVLLKHGADVNAKDMLKMTALHWATEHNHQEVVELLIKYGADVHTQSKFCKTAFDISIDNGNEDLAEILQ

>d1bd8\_\_ a.118.2.1 (-) Cell cycle inhibitor p19ink4D {Human (Homo sapiens)}

RAGDRLSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSTAIALELLKQGASPNVQDTSGTSPVHDAARTGFLDTLKVLVEHGADVNVPDGTGALPIHLAVQEGHTAVVSFLAAESDLHRRDARGLTPLELALQRGAQDLVDILQGHM

>d1blxb\_ a.118.2.1 (B:) Cell cycle inhibitor p19ink4D {Mouse (Mus musculus)}

VCVGDRLSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALELLKQGASPNVQDASGTSPVHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFLAPESDLHHRDASGLTPLELARQRGAQNLMDILQGHMMIP

>d1ihba\_ a.118.2.1 (A:) p18ink4C(ink6) {Human (Homo sapiens)}

WGNELASAAARGDLEQLTSLLQNNVNVNAQNGFGRTALQVMKLGNPEIARRLLLRGANPDLKDRTGFAVIHDAARAGFLDTLQTLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFLVKHTASNVGHRNHKGDTACDLARLYGRNEVVSLMQANG

>d1a5e\_\_ a.118.2.1 (-) Cell cycle inhibitor p16ink4A {Human (Homo sapiens)}

MEPAAGSSMEPSADWLATAAARGRVEEVRALLEAGALPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAAGGTRGSNHARIDAAEGPSDIPD

>d1bi7b\_ a.118.2.1 (B:) Cell cycle inhibitor p16ink4A {Human (Homo sapiens)}

EPSADWLATAAARGRVEEVRALLEAGANPNAPNSYGRRPIQVMMMGSARVAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDLAEELGHRDVARYLRAAA

>d1iknd\_ a.118.2.1 (D:) I-kappa-B-alpha {Human (Homo sapiens)}

DGDSFLHLAIIHEEKALTMEVIRQVKGDLAFLNFQNNLQQTPLHLAVITNQPEIAEALLGAGCDPELRDFRGNTPLHLACEQGCLASVGVLTQSCTTPHLHSILKATNYNGHTCLHLASIHGYLGIVELLVSLGADVNAQEPCNGRTALHLAVDLQNPDLVSLLLKCGADVNRVTYQGYSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTES

>d1k1aa\_ a.118.2.1 (A:) bcl-3 {Human (Homo sapiens)}

EDGDTPLHIAVVQGNLPAVHRLVNLFQQGGRELDIYNNLRQTPLHLAVITTLPSVVRLLVTAGASPMALDRHGQTAAHLACEHRSPTCLRALLDSAAPGTLDLEARNYDGLTALHVAVNTECQETVQLLLERGADIDAVDIKSGRSPLIHAVENNSLSMVQLLLQHGANVNAQMYSGSSALHSASGRGLLPLVRTLVRSGADSSLKNCHNDTPLMVARSRRVIDILRG

>d1myo\_\_ a.118.2.1 (-) Myotrophin {Rat (Rattus norvegicus)}

MCDKEFMWALKNGDLDEVKDYVAKGEDVNRTLEGGRKPLHYAADCGQLEILEFLLLKGADINAPDKHHITPLLSAVYEGHVSCVKLLLSKGADKTVKGPDGLTALEATDNQAIKALLQ

>d1sw6a\_ a.118.2.1 (A:) Swi6 ankyrin-repeat fragment {Baker's yeast (Saccharomyces cerevisiae)}

GPIITFTHDLTSDFLSSPLKIMKALPSPVVNDNEQKMKLEAFLQRLLFPEIQEMPTSLNNDSSNRNSEGGSSNQQQQHVSFDSLLQEVNDAFPNTQLNLNIPVDEHGNTPLHWLTSIANLELVKHLVKHGSNRLYGDNMGESCLVKAVKSVNNYDSGTFEALLDYLYPCLILEDSMNRTILHHIIITSGMTGCSAAAKYYLDILMGWIVKKQNRPIQSGTNEKESKPNDKNGERKDSILENLDLKWIIANMLNAQDSNGDTCLNIAARLGNISIVDALLDYGADPFIANKSGLRPVDFGAG

>d1dcqa1 a.118.2.1 (A:369-522) Pyk2-associated protein beta {Mouse (Mus musculus)}

ADTAAKLHSLCEAVKTRDIFGLLQAYADGVDLTEKIPLANGHEPDETALHLAVRSVDRTSLHIVDFLVQNSGNLDKQTGKGSTALHYCCLTDNAECLKLLLRGKASIEIANESGETPLDIAKRLKHEHCEELLTQALSGRFNSHVHVEYEWRLL

>d1pbv\_\_ a.118.3.1 (-) Exchange factor ARNO {Human (Homo sapiens)}

ANEGSKTLQRNRKMAMGRKKFNMDPKKGIQFLVENELLQNTPEEIARFLYKGEGLNKTAIGDYLGEREELNLAVLHAFVDLHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFAQRYCLCNPGVFQSTDTCYVLSFAVIMLNTSLHNPNVRDKPGLERFVAMNRGINEGGDLPEELLRNLYDSIRNEPFKIP

>d1bc9\_\_ a.118.3.1 (-) Cytohesin-1/b2-1 {Human (Homo sapiens)}

MKNMQRNKQVAMGRKKFNMDPKKGIQFLIENDLLKNTCEDIAQFLYKGEGLNKTAIGDYLGERDEFNIQVLHAFVELHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFAQRYCQCNNGVFQSTDTCYVLSFAIIMLNTSLHNPNVKDKPTVERFIAMNRGINDGGDLPEELLRNLYESIKNEPFKIPELEHHHHHH

>d1qsaa1 a.118.5.1 (A:1-450) 70 KDa soluble lytic transglycosylase (SLT70), superhelical domain {Escherichia coli}

DSLDEQRSRYAQIKQAWDNRQMDVVEQMMPGLKDYPLYPYLEYRQITDDLMNQPAVTVTNFVRANPTLPPARTLQSRFVNELARREDWRGLLAFSPEKPGTTEAQCNYYYAKWNTGQSEEAWQGAKELWLTGKSQPNACDKLFSVWRASGKQDPLAYLERIRLAMKAGNTGLVTVLAGQMPADYQTIASAIISLANNPNTVLTFARTTGATDFTRQMAAVAFASVARQDAENARLMIPSLAQAQQLNEDQIQELRDIVAWRLMGNDVTDEQAKWRDDAIMRSQSTSLIERRVRMALGTGDRRGLNTWLARLPMEAKEKDEWRYWQADLLLERGREAEAKEILHQLMQQRGFYPMVAAQRIGEEYELKIDKAPQNVDSALTQGPEMARVRELMYWNLDNTARSEWANLVKSKSKTEQAQLARYAFNNQWWDLSVQATIAGKLWDHLEERFP

>d1d8da\_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Rat (Rattus norvegicus)}

FLSLDSPTYVLYRDRAEWADIDPVPQNDGPSPVVQIIYSEKFRDVYDYFRAVLQRDERSERAFKLTRDAIELNAANYTVWHFRRVLLRSLQKDLQEEMNYIIAIIEEQPKNYQVWHHRRVLVEWLKDPSQELEFIADILNQDAKNYHAWQHRQWVIQEFRLWDNELQYVDQLLKEDVRNNSVWNQRHFVISNTTGYSDRAVLEREVQYTLEMIKLVPHNESAWNYLKGILQDRGLSRYPNLLNQLLDLQPSHSSPYLIAFLVDIYEDMLENQCDNKEDILNKALELCEILAKEKDTIRKEYWRYIGRSLQSKHSRESDIPASV

>d1jcqa\_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Human (Homo sapiens)}

FVSLDSPSYVLYRDRAEWADIDPVPQNDGPNPVVQIIYSDKFRDVYDYFRAVLQRDERSERAFKLTRDAIELNAANYTVWHFRRVLLKSLQKDLHEEMNYITAIIEEQPKNYQVWHHRRVLVEWLRDPSQELEFIADILNQDAKNYHAWQHRQWVIQEFKLWDNELQYVDQLLKEDVRNNSVWNQRYFVISNTTGYNDRAVLEREVQYTLEMIKLVPHNESAWNYLKGILQDRGLSKYPNLLNQLLDLQPSHSSPYLIAFLVDIYEDMLENQCDNKEDILNKALELCEILAKEKDTIRKEYWRYIGRSLQSKH

>d1dcea1 a.118.6.1 (A:1-240,A:351-443) Rab geranylgeranyltransferase alpha-subunit, N-terminal domain {Rat (Rattus norvegicus)}

MHGRLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQAGELDESVLELTSQILGANPDFATLWNCRREVLQHLETEKSPEESAALVKAELGFLESCLRVNPKSYGTWHHRCWLLSRLPEPNWARELELCARFLEADERNFHCWDYRRFVAAQAAVAPAEELAFTDSLITRNFSNYSSWHYRSCLLPQLHPQPDSGPQGRLPENVLLKELELVQNAFFTDPNDQSAWFYHRWLLGRAEXLFRCELSVEKSTVLQSELESCKELQELEPENKWCLLTIILLMRALDPLLYEKETLQYFSTLKAVDPMRAAYLDDLRSKFLLENSVLKMEYADV

>d1qjba\_ a.118.7.1 (A:) zeta isoform {Human (Homo sapiens)}

MDKNELVQKAKLAEQAERYDDMAACMKSVTEQGAELSNEERNLLSVAYKNVVGARRSSWRVVSSIEQKTEGAEKKQQMAREYREKIETELRDICNDVLSLLEKFLIPNASQAESKVFYLKMKGDYYRYLAEVAAGDDKKGIVDQSQQAYQEAFEISKKEMQPTHPIRLGLALNFSVFYYEILNSPEKACSLAKTAFDEAIAELDTLSEESYKDSTLIMQLLRDNLTLWTSDT

>d1a17\_\_ a.118.8.1 (-) Protein phosphatase 5 {Human (Homo sapiens)}

PPADGALKRAEELKTQANDYFKAKDYENAIKFYSQAIELNPSNAIYYGNRSLAYLRTECYGYALGDATRAIELDKKYIKGYYRRAASNMALGKFRAALRDYETVVKVKPHDKDAKMKYQECNKIVKQKAFERAIAGDEHKRSVVDSLDIESMTIEDEYS

>d1elra\_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}

GKQALKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMTYITNQAAVYFEKGDYNKCRELCEKAIEVGRENREDYRQIAKAYARIGNSYFKEEKYKDAIHFYNKSLAEHRTPDVLKKCQQAEKILKEQ

>d1elwa\_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}

EQVNELKEKGNKALSVGNIDDALQCYSEAIKLDPHNHVLYSNRSAAYAKKGDYQKAYEDGCKTVDLKPDWGKGYSRKAAALEFLNRFEEAKRTYEEGLKHEANNPQLKEGLQNMEAR

>d1qqea\_ a.118.8.1 (A:) Vesicular transport protein sec17 {Baker's yeast (Saccharomyces cerevisiae)}

ISDPVELLKRAEKKGVPSSGFMKLFSGSDSYKFEEAADLCVQAATIYRLRKELNLAGDSFLKAADYQKKAGNEDEAGNTYVEAYKCFKSGGNSVNAVDSLENAIQIFTHRGQFRRGANFKFELGEILENDLHDYAKAIDCYELAGEWYAQDQSVALSNKCFIKCADLKALDGQYIEASDIYSKLIKSSMGNRLSQWSLKDYFLKKGLCQLAATDAVAAARTLQEGQSEDPNFADSRESNFLKSLIDAVNEGDSEQLSEHCKEFDNFMRLDKWKITILNKIKESIQQQEDD

>d1hh8a\_ a.118.8.1 (A:) Neutrophil cytosolic factor 2 (NCF-2, p67-phox) {Human (Homo sapiens)}

SLVEAISLWNEGVLAADKKDWKGALDAFSAVQDPHSRICFNIGCMYTILKNMTEAEKAFTRSINRDKHLAVAYFQRGMLYYQTEKYDLAIKDLKEALIQLRGNQLIDYKILGLQFKLFACEVLYNIAFMYAKKEEWKKAEEQLALATSMKSEPRHSKIDKAMECVWKQKLYEPVVIPVGRLFRPNERQVAQL

>d1fcha\_ a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Human (Homo sapiens)}

SATYDKGYQFEEENPLRDHPQPFEEGLRRLQEGDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLELKPDNQTALMALAVSFTNESLQRQACEILRDWLRYTPAYAHLVTPAEEGAGGAGLGPSKRILGSLLSDSLFLEVKELFLAAVRLDPTSIDPDVQCGLGVLFNLSGEYDKAVDCFTAALSVRPNDYLLWNKLGATLANGNQSEEAVAAYRRALELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGAMSENIWSTLRLALSMLGQSDAYGAADARDLSTLLTMFGLPQ

>d1hxia\_ a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Trypanosoma brucei}

NNTDYPFEANNPYMYHENPMEEGLSMLKLANLAEAALAFEAVCQKEPEREEAWRSLGLTQAENEKDGLAIIALNHARMLDPKDIAVHAALAVSHTNEHNANAALASLRAWLL

>d1ihga1 a.118.8.1 (A:197-365) Cyclophilin 40 {Cow (Bos taurus)}

GSGDSHPDFPEDADVDLKDVDKILLISEDLKNIGNTFFKSQNWEMAIKKYTKVLRYVEGSRAAAEDADGAKLQPVALSCVLNIGACKLKMSDWQGAVDSCLEALEIDPSNTKALYRRAQGWQGLKEYDQALADLKKAQEIAPEDKAIQAELLKVKQKIKAQKDKEKAAY

>d1iipa1 a.118.8.1 (A:197-298) Cyclophilin 40 {Cow (Bos taurus)}

GSGDSHPDFPEDADVDLKDVDKILLISEDLKNIGNTFFKSQNWEMAIKKYTKVLRYVEGSRAAAEDADGAKLQPVALSCVLNIGACKLKMSDWQGAVDSCLE

>d1hz4a\_ a.118.8.2 (A:) Transcription factor MalT domain III {Escherichia coli}

EIKDIREDTMHAEFNALRAQVAINDGNPDEAERLAKLALEELPPGWFYSRIVATSVLGEVLHCKGELTRSLALMQQTEQMARQHDVWHYALWSLIQQSEILFAQGFLQTAWETQEKAFQLINEQHLEQLPMHEFLVRIRAQLLWAWARLDEAEASARSGIEVLSSYQPQQQLQCLAMLIQCSLARGDLDNARSQLNRLENLLGNGKYHSDWISNANKVRVIYWQMTGDKAAAANWLRHTAKPEFANNHFLQGQWRNIARAQILLGEFEPAEIVLEELNENARSLRLMSDLNRNLLLLNQLYWQAGRKSDAQRVLLDALKLANRTGFISHFVIEGEAMAQQLRQLIQLNTLPELEQHRAQRILREIN

>d1eyha\_ a.118.9.1 (A:) Epsin 1 {Rat (Rattus norvegicus)}

HNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVAFSEIMSMIWKRLNDHGKNWRHVYKAMTLMEYLIKTGSERVSQQCKENMYAVQTLKDFQYVDRDGKDQGVNVREKAKQLVALLRDEDRLREERAHALKTKEKLAQTA

>d1inza\_ a.118.9.1 (A:) Epsin 1 {Human (Homo sapiens)}

GSSRMSTSSLRRQMKNIVHNYSEAEIKVREATSNDPWGPSSSLMSEIADLTYNVVAFSEIMSMIWKRLNDHGKNWRHVYKAMTLMEYLIKTGSERVSQQCKENMYAVQTLKDFQYVDRDGKDQGVNVREKAKQLVALLRDEDRLREER

>d1dvpa1 a.118.9.2 (A:1-145) Hrs {Fruit fly (Drosophila melanogaster)}

MFRSSFCKNLENATSHLRLEPDWPSILLICDEINQKDVTPKNAFAAIKKKMNSPNPHSSCYSLLVLESIVKNCGAPVHEEVFTKENCEMFSSFLESTPHENVRQKMLELVQTWAYAFRSSDKYQAIKDTMTILKAKGHTFPELRE

>d1elka\_ a.118.9.2 (A:) Tom1 protein {Human (Homo sapiens)}

SDFLLGNPFSSPVGQRIEKATDGSLQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVLETCVKNCGHRFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVLNLIQSWADAFRSSPDLTGVVTIYEDLRRKGLEFPM

>d1juqa\_ a.118.9.2 (A:) Gga3 {Human (Homo sapiens)}

ESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEGPQIAVRLLAHKIQSPQEWEALQALTVLEACMKNCGRRFHNEVGKFRFLNELIKVVSPKYLGDRVSEKVKTKVIELLYSWTMALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLI

>d1hf8a\_ a.118.10.1 (A:) Clathrin assembly lymphoid myeloid leukaemia protein, Calm {Rat (Rattus norvegicus)}

GSAVSKTVCKATTHEIMGPKKKHLDYLIQCTNEMNVNIPQLADSLFERTTNSSWVVVFKSLITTHHLMVYGNERFIQYLASRNTLFNLSNFLDKSGLQGYDMSTFIRRYSRYLNEKAVSYRQVAFDFTKVKRGADGVMRTMNTEKLLKTVPIIQNQMDALLDFNVNSNELTNGVINAAFMLLFKDAIRLFAAYNEGIINLLEKYFDMKKNQCKEGLDIYKKFLTRMTRISEFLKVAEQVGIDRGDIPDLSQAPSSLLDALEQH

>d1hx8a\_ a.118.10.1 (A:) AP180 (Lap) {Fruit fly (Drosophila melanogaster)}

QGLAKSVCKATTEECIGPKKKHLDYLVHCANEPNVSIPHLANLLIERSQNANWVVVYKSLITTHHLMAYGNERFMQYLASSNSTFNLSSFLDKGTVQDGGMGVPGGRMGYDMSPFIRRYAKYLNEKSLSYRAMAFDFCKVKRGKEEGSLRSMNAEKLLKTLPVLQAQLDALLEFDCQSNDLSNGVINMSFMLLFRDLIRLFACYNDGIINLLEKYFDMNKKHARDALDLYKKFLVRMDRVGEFLKVAENVGIDKGDIPDLTKAPSSLLDALEQHLATL

>d1kpsb\_ a.118.12.1 (B:) Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain {Mouse (Mus musculus)}

TDLSTFLSFPSPEKLLRLGPKVSVLIVQQTDTSDPEKVVSAFLKVASVFRDDASVKTAVLDAIDALMKKAFSCSSFNSNTFLTRLLIHMGLLKSEDKIKAIPSLHGPLMVLNHVVRQDYFPKALAPLLLAFVTKPNGALETCSFARHNLLQTLYNI

>d1k8kg\_ a.118.13.1 (G:) Arp2/3 complex 16 kDa subunit ARPC5 {Cow (Bos taurus)}

ARFRKVDVDEYDENKFVDEDDGGDGQAGPDEGEVDSCLRQGNMTAALQAALKNPPINTKSQAVKDRAGSIVLKVLISFKANDIEKAVQSLDKNGVDLLMKYIYKGFESPSDNSSAVLLQWHEKALAAGGVGSIVRVLTARKTV

>d1ocre\_ a.118.11.1 (E:) Cytochrome c oxidase subunit E {Cow (Bos taurus)}

SHGSHETDEEFDARWVTYFNKPDIDAWELRKGMNTLVGYDLVPEPKIIDAALRACRRLNDFASAVRILEVVKDKAGPHKEIYPYVIQELRPTLNELGISTPEELGLDKV

>d1f8na1 a.119.1.1 (A:150-839) Lipoxigenase, C-terminal domain {Soybean (Glycine max), isozyme L1}

VPSETPAPLVSYREEELKSLRGNGTGERKEYDRIYDYDVYNDLGNPDKSEKLARPVLGGSSTFPYPRRGRTGRGPTVTDPNTEKQGEVFYVPRDENLGHLKSKDALEIGTKSLSQIVQPAFESAFDLKSTPIEFHSFQDVHDLYEGGIKLPRDVISTIIPLPVIKELYRTDGQHILKFPQPHVVQVSQSAWMTDEEFAREMIAGVNPCVIRGLEEFPPKSNLDPAIYGDQSSKITADSLDLDGYTMDEALGSRRLFMLDYHDIFMPYVRQINQLNSAKTYATRTILFLREDGTLKPVAIELSLPHSAGDLSAAVSQVVLPAKEGVESTIWLLAKAYVIVNDSCYHQLMSHWLNTHAAMEPFVIATHRHLSVLHPIYKLLTPHYRNNMNINALARQSLINANGIIETTFLPSKYSVEMSSAVYKNWVFTDQALPADLIKRGVAIKDPSTPHGVRLLIEDYPYAADGLEIWAAIKTWVQEYVPLYYARDDDVKNDSELQHWWKEAVEKGHGDLKDKPWWPKLQTLEDLVEVCLIIIWIASALHAAVNFGQYPYGGLIMNRPTASRRLLPEKGTPEYEEMINNHEKAYLRTITSKLPTLISLSVIEILSTHASDEVYLGQRDNPHWTSDSKALQAFQKFGNKLKEIEEKLVRRNNDPSLQGNRLGPVQLPYTLLYPSSEEGLTFRGIPNSISI

>d1ik3a1 a.119.1.1 (A:168-857) Lipoxigenase, C-terminal domain {Soybean (Glycine max), isozyme L3}

LPSETPAPLVKYREEELHNLRGDGTGERKEWERIYDYDVYNDLGDPDKGENHARPVLGGNDTFPYPRRGRTGRKPTRKDPNSESRSNDVYLPRDEAFGHLKSSDFLTYGLKSVSQNVLPLLQSAFDLNFTPREFDSFDEVHGLYSGGIKLPTDIISKISPLPVLKEIFRTDGEQALKFPPPKVIQVSKSAWMTDEEFAREMLAGVNPNLIRCLKDFPPRSKLDSQVYGDHTSQITKEHLEPNLEGLTVDEAIQNKRLFLLDHHDPIMPYLRRINATSTKAYATRTILFLKNDGTLRPLAIELSLPHPQGDQSGAFSQVFLPADEGVESSIWLLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFIIATNRHLSVVHPIYKLLHPHYRDTMNINGLARLSLVNDGGVIEQTFLWGRYSVEMSAVVYKDWVFTDQALPADLIKRGMAIEDPSCPHGIRLVIEDYPYTVDGLEIWDAIKTWVHEYVFLYYKSDDTLREDPELQACWKELVEVGHGDKKNEPWWPKMQTREELVEACAIIIWTASALHAAVNFGQYPYGGLILNRPTLSRRFMPEKGSAEYEELRKNPQKAYLKTITPKFQTLIDLSVIEILSRHASDEVYLGERDNPNWTSDTRALEAFKRFGNKLAQIENKLSERNNDEKLRNRCGPVQMPYTLLLPSSKEGLTFRGIPNSISI

>d1lox\_1 a.119.1.2 (113-663) 15-Lipoxygenase {Rabbit (Oryctolagus cuniculus)}

TGCTTVGDPQGLFQKHREQELEERRKLYQWGSWKEGLILNVAGSKLTDLPVDERFLEDKKIDFEASLAWGLAELALKNSLNILAPWKTLDDFNRIFWCGRSKLARRVRDSWQEDSLFGYQFLNGANPMLLRRSVQLPARLVFPPGMEELQAQLEKELKAGTLFEADFALLDNIKANVILYCQQYLAAPLVMLKLQPDGKLMPMVIQLHLPKIGSSPPPLFLPTDPPMVWLLAKCWVRSSDFQVHELNSHLLRGHLMAEVFTVATMRCLPSIHPVFKLIVPHLRYTLEINVRARNGLVSDFGIFDQIMSTGGGGHVQLLQQAGAFLTYRSFCPPDDLADRGLLGVESSFYAQDALRLWEIISRYVQGIMGLYYKTDEAVRDDLELQSWCREITEIGLQGAQKQGFPTSLQSVAQACHFVTMCIFTCTGQHSSIHLGQLDWFTWVPNAPCTMRLPPPTTKDATLETVMATLPNLKQSSLQMSIVWQLGRDQPIMVPLGQHQEEYFSGPEPRAVLEKFREELAIMDKEIEVRNEKLDIPYEYLRPSIVENSVAI

>d1c1ka\_ a.120.1.1 (A:) gene 59 helicase assembly protein {Bacteriophage T4}

MIKLRMPAGGERYIDGKSVYKLYLMIKQHMNGKYDVIKYNWCMRVSDAAYQKRRDKYFFQKLSEKYKLKELALIFISNLVANQDAWIGDISDADALVFYREYIGRLKQIKFKFEEDIRNIYYFSKKVEVSAFKEIFEYNPKVQSSYIFKLLQSNIISFETFILLDSFLNIIDKHDEQTDNLVWNNYSIKLKAYRKILNIDSQKAKNVFIETVKSCKY

>d2tct\_2 a.121.1.1 (68-208) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}

LPAAGESWQSFLRNNAMSFRRALLRYRDGAKVHLGTRPDEKQYDTVETQLRFMTENGFSLRDGLYAISAVSHFTLGAVLEQQEHTAALTDRPAAPDENLPPLLREALQIMDSDDGEQAFLHGLESLIRGFEVQLTALLQIV

>d1jt6a2 a.121.1.1 (A:73-187) Multidrug binding protein QacR {Staphylococcus aureus}

KTNREKFYLYNELSLTTEYYYPLQNAIIEFYTEYYKTNSINEKMNKLENKYIDAYHVIFKEGNLNGEWSINDVNAVSKIAANAVNGIVTFTHEQNINERIKLMNKFSQIFLNGLS

>d1fqva1 a.122.1.1 (A:107-145) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}

VSWDSLPDELLLGIFSCLCLPELLKVSGVCKRWYRLASD

>d1fqvb1 a.122.1.1 (B:85-160) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}

IPVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPEEIRKTFNIKNDFTEEEEAQVRKENQWC

>d1fs1a1 a.122.1.1 (A:109-149) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}

WDSLPDELLLGIFSCLCLPELLKVSGVCKRWYRLASDESLW

>d1fs1b1 a.122.1.1 (B:86-140) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}

PVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPEEIRKTFN

>d1fs2b1 a.122.1.1 (B:80-146) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}

KRTDDIPVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPEEIRKTFNIKNDFT

>d1g5ya\_ a.123.1.1 (A:) Retinoid-X receptor (RXR-alpha) {Human (Homo sapiens)}

PVERILEAELAVEPKTETYVEANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHFSELPLDDQVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSAGVGAIFDRVLTELVSKMRDMQMDKTELGCLRAIVLFNPDSKGLSNPAEVEALREKVYASLEAYCKHKYPEQPGRFAKLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEAP

>d1dkfb\_ a.123.1.1 (B:) Retinoic acid receptor alpha (RAR-alpha) {Human (Homo sapiens)}

PEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLEN

>d1fcya\_ a.123.1.1 (A:) Retinoic acid receptor gamma (RAR-gamma) {Human (Homo sapiens)}

ASPQLEELITKVSKAHQETFPSLCQLGKYTTNSSADHRVQLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLSIADQITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQMHNAGFGPLTDLVFAFAGQLLPLEMDDTETGLLSAICLICGDRMDLEEPEKVDKLQEPLLEALRLYARRRRPSQPYMFPRMLMKITDLRGISTKGAERAITLKMEIPGPMPPLIREMLE

>d1a28a\_ a.123.1.1 (A:) Progesterone receptor {Human (Homo sapiens)}

QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFGLGWRSYKHVSGQMLYFAPDLILNEQRMKESSFYSLCLTMWQIPQEFVKLQVSQEEFLCMKVLLLLNTIPLEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVEFPEMMSEVIAAQLPKILAGMVKPLLFHK

>d3erda\_ a.123.1.1 (A:) Estrogen receptor alpha {Human (Homo sapiens)}

SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPGKLLFAPNLLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLLEMLDAHRLH

>d1qkma\_ a.123.1.1 (A:) Estrogen receptor beta {Human (Homo sapiens)}

LDALSPEQLVLTLLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLLESCWMEVLMMGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLVTATQDADSSRKLAHLLNAVTDALVWVIAKSGISSQQQSMRLANLLMLLSHVRHASNKGMEHLLNMKCKNVVPVYDLLLEMLNAHVL

>d1qkna\_ a.123.1.1 (A:) Estrogen receptor beta {Rat (Rattus norvegicus)}

TLSPEQLVLTLLEAEPPNVLVSRPSMPFTEASMMMSLTKLADKELVHMIGWAKKIPGFVELSLLDQVRLLESCWMEVLMVGLMWRSIDHPGKLIFAPDLVLDRDEGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLNSSMYPLASANQEAESSRKLTHLLNAVTDALVWVIAKSGISSQQQSVRLANLLMLLSHVRHISNKGMEHLLSMKCKNVVPVYDLLLEMLNA

>d1i37a\_ a.123.1.1 (A:) Androgen receptor {Rat (Rattus norvegicus)}

IFLNVLEAIEPGVVCAGHDNNQPDSFAALLSSLNELGERQLVHVVKWAKALPGFRNLHVDDQMAVIQYSWMGLMVFAMGWRSFTNVNSRMLYFAPDLVFNEYRMHKSRMYSQCVRMRHLSQEFGWLQITPQEFLCMKALLLFSIIPVDGLKNQKFFDELRMNYIKELDRIIACKRKNPTSCSRRFYQLTKLLDSVQPIARELHQFTFDLLIKSHMVSVDFPEMMAEIISVQVPKILSGKVKPIYFH

>d1k7la\_ a.123.1.1 (A:) Peroxisome proliferator activated receptor alpha, PPAR-alpha {Human (Homo sapiens)}

DLKSLAKRIYEAYLKNFNMNKVKARVILSGKASNNPPFVIHDMETLCMAEKTLVAKLVANGIQNKEAEVRIFHCCQCTSVETVTELTEFAKAIPGFANLDLNDQVTLLKYGVYEAIFAMLSSVMNKDGMLVAYGNGFITREFLKSLRKPFCDIMEPKFDFAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGHIEKMQEGIVHVLRLHLQSNHPDDIFLFPKLLQKMADLRQLVTEHAQLVQIIKKTESDAALHPLLQEIYRDMY

>d2prga\_ a.123.1.1 (A:) Peroxisome proliferator activated receptor gamma, PPAR-gamma {Human (Homo sapiens)}

ESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESSQLFAKLLQKMTDLRQIVTEHVQLLQVIKKTETDMSLHPLLQEIYKDLY

>d2gwxa\_ a.123.1.1 (A:) Peroxisome proliferator-activated receptor delta, PPAR-DELTA {Human (Homo sapiens)}

LKAFSKHIYNAYLKNFNMTKKKARSILTGKASHTAPFVIHDIETLWQAEKGLVWKQLVNGLPPYKEISVHVFYRCQCTTVETVRELTEFAKSIPSFSSLFLNDQVTLLKYGVHEAIFAMLASIVNKDGLLVANGSGFVTREFLRSLRKPFSDIIEPKFEFAVKFNALELDDSDLALFIAAIILCGDRPGLMNVPRVEAIQDTILRALEFHLQANHPDAQQLFPKLLQKMADLRQLVTEHAQMMQRIKKTETETSLHPLLQEIYKDM

>d1ilga\_ a.123.1.1 (A:) Pregnane x receptor, PXR {Human (Homo sapiens)}

GLTEEQRMMIRELMDAQMKTFDTTFSHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQVRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAGGFQQLLLEPMLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSYIECNRPQPAHRFLFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLMQELFGI

>d1ie9a\_ a.123.1.1 (A:) Vitamin D nuclear receptor {Human (Homo sapiens)}

DSLRPKLSEEQQRIIAILLDAHHKTYDPTYSDFCQFRPPVRVNDGGGSVTLELSQLSMLPHLADLVSYSIQKVIGFAKMIPGFRDLTSEDQIVLLKSSAIEVIMLRSNESFTMDDMSWTCGNQDYKYRVSDVTKAGHSLELIEPLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAALIEAIQDRLSNTLQTYIRCRHPPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSMKLTPLVLEVFG

>d1bsxa\_ a.123.1.1 (A:) Thyroid hormone receptor beta (TR-beta) {Human (Homo sapiens)}

KPEPTDEEWELIKTVTEAHVATNAQGSHWKQKRKFLPEDIGQAPIVNAPEGGKVDLEAFSHFTKIITPAITRVVDFAKKLPMFCELPCEDQIILLKGCCMEIMSLRAAVRYDPESETLTLNGEMAVTRGQLKNGGLGVVSDAIFDLGMSLSSFNLDDTEVALLQAVLLMSSDRPGLACVERIEKYQDSFLLAFEHYINYRKHHVTHFWPKLLMKVTDLRMIGACHASRFLHMKVECPTELFPPLFLEVFED

>d1hg4a\_ a.123.1.1 (A:) Ultraspiracle protein, usp {Drosophila melanogaster}

FSIERIIEAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVSALCQVVNKQLFQMVEYARMMPHFAQVPLDDQVILLKAAWIELLIANVAWCSIVSLDDGGAGGGGGGLGHDGSFERRSPGLQPQQLFLNQSFSYHRNSAIKAGVSAIFDRILSELSVKMKRLNLDRRELSCLKAIILYNPDIRGIKSRAEIEMCREKVYACLDEHCRLEHPGDDGRFAQLLLRLPALRSISLKCQDHLFLFRITSDRPLEELFLEQLEAPPPPG

>d1g2na\_ a.123.1.1 (A:) Ultraspiracle protein, usp {Heliothis virescens}

AAVQELSIERLLEMESLVADPSEEFQFLRVGPDSNVPPKFRAPVSSLCQIGNKQIAALVVWARDIPHFSQLEMEDQILLIKGSWNELLLFAIAWRSMEFLTEERDGVDGTGNRTTSPPQLMCLMPGMTLHRNSALQAGVGQIFDRVLSELSLKMRTLRVDQAEYVALKAIILLNPDVKGLKNRQEVEVLREKMFLCLDEYCRRSRSSEEGRFAALLLRLPALRSISLKSFEHLFFFHLVADTSIAGYIRDALRNHA

>d1ah7\_\_ a.124.1.1 (-) Bacterial phosholipase C {Bacillus cereus}

WSAEDKHKEGVNSHLWIVNRAIDIMSRNTTLVKQDRVAQLNEWRTELENGIYAADYENPYYDNSTFASHFYDPDNGKTYIPFAKQAKETGAKYFKLAGESYKNKDMKQAFFYLGLSLHYLGDVNQPMHAANFTNLSYPQGFHSKYENFVDTIKDNYKVTDGNGYWNWKGTNPEEWIHGAAVVAKQDYSGIVNDNTKDWFVKAAVSQEYADKWRAEVTPMTGKRLMDAQRVTAGYIQLWFDTYGDR

>d1ca1\_1 a.124.1.1 (1-249) Alpha-toxin, N-terminal domain {Clostridium perfringens}

WDGKIDGTGTHAMIVTQGVSILENDLSKNEPESVRKNLEILKENMHELQLGSTYPDYDKNAYDLYQDHFWDPDTDNNFSKDNSWYLAYSIPDTGESQIRKFSALARYEWQRGNYKQATFYLGEAMHYFGDIDTPYHPANVTAVDSAGHVKFETFAEERKEQYKINTVGCKTNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSHSWDDWDYAAKVTLANSQKGTAGYIYRFLHDVSEGNDP

>d1ak0\_\_ a.124.1.2 (-) P1 nuclease {Penicillium citrinum}

WGALGHATVAYVAQHYVSPEAASWAQGILGSSSSSYLASIASWADEYRLTSAGKWSASLHFIDAEDNPPTNCNVDYERDCGSSGCSISAIANYTQRVSDSSLSSENHAEALRFLVHFIGDMTQPLHDEAYAVGGNKINVTFDGYHDNLHSDWDTYMPQKLIGGHALSDAESWAKTLVQNIESGNYTAQAIGWIKGDNISEPITTATRWASDANALVCTVVMPHGAAALQTGDLYPTYYDSVIDTIELQIAKGGYRLANWINEIH

>d1f0ja\_ a.125.1.1 (A:) Catalytic domain of cyclic nucleotide phosphodiesterase 4b2b {Human (Homo sapiens)}

SISRFGVNTENEDHLAKELEDLNKWGLNIFNVAGYSHNRPLTCIMYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPALDAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLLQEEHCDIFMNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLDNYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWADLVQPDAQDILDTLEDNRNWYQSMIPQAPAPPLDEQNRDCQGLMEKFQF

>d1gnia1 a.126.1.1 (A:3-196) Serum albumin {Human (Homo sapiens)}

HKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPKLDELRDEGKASSAKQ

>d1gnia2 a.126.1.1 (A:197-388) Serum albumin {Human (Homo sapiens)}

RLKCASLQKFGERAFKAWAVARLSQRFPKAEFAEVSKLVTDLTKVHTECCHGDLLECADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLLLRLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNLI

>d1gnia3 a.126.1.1 (A:389-584) Serum albumin {Human (Homo sapiens)}

KQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCCKHPEAKRMPCAEDYLSVVLNQLCVLHEKTPVSDRVTKCCTESLVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCCKADDKETCFAEEGKKLVAASQAALG

>d1j78a1 a.126.1.1 (A:13-198) Vitamin D binding protein {Human (Homo sapiens)}

CKEFSHLGKEDFTSLSLVLYSRKFPSGTFEQVSQLVKEVVSLTEACCAEGADPDCYDTRTSALSAKSCESNSPFPVHPGTAECCTKEGLERKLCMAALKHQPQEFPTYVEPTNDEICEAFRKDPKEYANQFMWEYSTNYGQAPLSLLVSYTKSYLSMVGSCCTSASPTVCFLKERLQLKHLSLLTT

>d1j78a2 a.126.1.1 (A:199-386) Vitamin D binding protein {Human (Homo sapiens)}

LSNRVCSQYAAYGEKKSRLSNLIKLAQKVPTADLEDVLPLAEDITNILSKCCESASEDCMAKELPEHTVKLCDNLSTKNSKFEDCCQEKTAMDVFVCTYFMPAAQLPELPDVELPTNKDVCDPGNTKVMDKYTFELSRRTHLPEVFLSKVLEPTLKSLGECCDVEDSTTCFNAKGPLLKKELSSFIDK

>d1j78a3 a.126.1.1 (A:387-457) Vitamin D binding protein {Human (Homo sapiens)}

GQELCADYSENTFTEYKKKLAERLKAKLPDATPTELAKLVNKRSDFASNCCSINSPPLYCDSEIDAELKNI

>d1jswa\_ a.127.1.1 (A:) L-aspartate ammonia lyase {Escherichia coli}

MSNNIRIEEDLLGTREVPADAYYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKKAAAMANKELQTIPKSVANAIIAACDEVLNNGKCMDQFPVDVYQGGAGTSVNMNTNEVLANIGLELMGHQKGEYQYLNPNDHVNKCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAVEFQDILKMGRTQLQDAVPMTLGQEFRAFSILLKEEVKNIQRTAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPAEDLIEATSDCGAYVMVHGALKRLAVKMSKICNDLRLLSSGPRAGLNEINLPELQAGSSIMPAKVNPVVPEVVNQVCFKVIGNDTTVTMAAEAGQLQLNVMEPVIGQAMFESVHILTNACYNLLEKCINGITANKEVCEGYVYNSIGIVTYLNPFIGHHNGDIVGKICAETGKSVREVVLERGLLTEAELDDIFSV

>d1jswc\_ a.127.1.1 (C:) L-aspartate ammonia lyase {Escherichia coli}

IRIEEDLLGTREVPADAYYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKKAAAMANKELQTIPKSVANAIIAACDEVLNNGKCMDQFPVDVYQGGAGTSVNMNTNEVLANIGLELMGHQKGEYQYLNPNDHVNKCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAVEFQDILKMGRTQLQDAVPMTLGQEFRAFSILLKEEVKNIQRTAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPAEDLIEATSDCGAYVMVHGALKRLAVKMSKICNDLRLLSSGPRAGLNEINLPELQAGSSIMPAKVNPVVPEVVNQVCFKVIGNDTTVTMAAEAGQLQLNVMEPVIGQAMFESVHILTNACYNLLEKCINGITANKEVCEGYVYNSIGIVTYLNP

>d1fura\_ a.127.1.1 (A:) Fumarase {Escherichia coli}

VRSEKDSMGAIDVPADKLWGAQTQRSLEHFRISTEKMPTSLIHALALTKRAAAKVNEDLGLLSEEKASAIRQAADEVLAGQHDDEFPLAIWQTGSGTQSNMNMNEVLANRASELLGGVRGMERKVHPNDDVNKSQSSNDVFPTAMHVAALLALRKQLIPQLKTLTQTLNEKSRAFADIVKIGRTNLQDATPLTLGQEISGWVAMLEHNLKHIEYSLPHVAELALGGTAVGTGLNTHPEYARRVADELAVITCAPFVTAPNKFEALATCDALVQAHGALKGLAASLMKIANDVRWLASGPRCGIGEISIPENEPGSSIMPGKVNPTQCEALTMLCCQVMGNDVAINMGGASGNFELNVFRPMVIHNFLQSVRLLADGMESFNKHCAVGIEPNRERINQLLNESLMLVTALNTHIGYDKAAEIAKKAHKEGLTLKAAALALGYLSEAEFDSWVRPEQM

>d1yfm\_\_ a.127.1.1 (-) Fumarase {Baker's yeast (Saccharomyces cerevisiae)}

SFRTETDAFGEIHVPADKYWGAQTQRSFQNFKIGGARERMPLPLVHAFGVLKKSAAIVNESLGGLDPKISKAIQQAADEVASGKLDDHFPLVVFQTGSGTQSNMNANEVISNRAIEILGGKIGSKQVHPNNHCNQSQSSNDTFPTVMHIAASLQIQNELIPELTNLKNALEAKSKEFDHIVKIGRTHLQDATPLTLGQEFSGYVQQVENGIQRVAHSLKTLSFLAQGGTAVGTGLNTKPGFDVKIAEQISKETGLKFQTAPNRFEALAAHDAIVECSGALNTLACSLFKIAQDIRYLGSGPRCGYHELMLPENEPGSSIMPGKVNPTQNEALTQVCVQVMGNNAAITFAGSQGQFELNVFKPVMIANLLNSIRLITDAAYSFRVHCVEGIKANEPRIHELLTKSLMLVTALNPKIGYDAASKVAKNAHKKGITLKESALELGVLTEKEFDEWVVPEHML

>d1k62a\_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Human (Homo sapiens)}

GAVDPIMEKFNASIAYDRHLWEVDVQGSKAYSRGLEKAGLLTKAEMDQILHGLDKVAEEWAQGTFKLNSNDEDIHTANERRLKELIGATAGKLHTGRSRNDQVVTDLRLWMRQTCSTLSGLLWELIRTMVDRAEAERDVLFPGYTHLQRAQPIRWSHWILSHAVALTRDSERLLEVRKRINVLPLGSGAIAGNPLGVDRELLRAELNFGAITLNSMDATSERDFVAEFLFWRSLCMTHLSRMAEDLILYCTKEFSFVQLSDAYSTGSSLMPRKKNPDSLELIRSKAGRVFGRCAGLLMTLKGLPSTYNKDLQEDKEAVFEVSDTMSAVLQVATGVISTLQIHQENMGQALSPDMLATDLAYYLVRKGMPFRQAHEASGKAVFMAETKGVALNQLSLQELQTISPLFSGDVICVWDYRHSVEQYGALGGTARSSVDWQIRQVRALLQAQQA

>d1auwa\_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas platyrhynchos), delta-crystallin}

TDPIMEKLNSSIAYDQRLSEVDIQGSMAYAKALEKAGILTKTELEKILSGLEKISEEWSKGVFVVKQSDEDINTANERRLKELIGDIAGKLHTGRSRNDQVVTDLKLFMKNSLSIISTHLLQLIKTLVERAAIEIDVILPGYTHLQKAQPIRWSQFLLSHAVALTRDSERLGEVKKRINVLPLGSGALAGNPLDIDREMLRSELEFASISLNSMDAISERDFVVEFLSFATLLMIHLSKMAEDLIIYSTSEFGFLTDSDAFSTGSSLMPQKKNPDSLELIRSKAGRVFGRLASILMVLKGLPSTYNKDLQEDKEAVFDVVDTLTAVLQVATGVISTLQISKENMEKALTPEMLATDLALYLVRKGVPFRQAHTASGKAVHLAETKGITINKLSLEDLKSISPQFSSDVSQVFNFVNSVEQYTALGGTAKSSVTTQIEQLRELMKKQK

>d1dcnb\_ a.127.1.1 (B:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas platyrhynchos), delta-crystallin}

DPIMAKLNSSIAYDQRLSEVDIQGSMAYAKALEKAGILTKTELAKILSGLEKISEEDIHTANERRLKELIGDIAGKLNTGRSRNDQVVTDLKLFMKNSLSIISTHLLQLIKTLVERAAIEIDVILPGYTNLQKAQPIRWSQFLLSHAVALTRDSERLGEVKKRINVLPLGSGALAGNPLDIDREMLRSELEFASISLNSMDAISERDFVVEFLSFATLLMIHLSKMAEDLIIYSTSEFGFLTLSPDSLELIRSKSGRVFGRLASILMVLKGLPSTYNKDLQEDKEAVFDVVDTLTAVLQVATGVISTLQISKENMEKALTPEMLATDLALYLVRKGVPFRQAHTASGKAVHLAETKGITINNLSLEDLKSISPQFSSDVSQVFNFVNSVEQYTALGGTAKSSVTTQIEQLRELMKKQK

>d1hy0a\_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas platyrhynchos), delta-crystallin}

DPIMQMLSTSISTEQRLSEVDIQASIAYAKALEKAGILTKTELEKILSGLEKISEELSKGVIVVTQSDEDIQTANERRLKELIGDIAGKLHTGRSRNEQVVTDLKLFMKNSLSIISTHLLQLIKTLVERAAIEIDVILPGYTHLQKAQPIRWSQFLLSHAVALTRDSERLGEVKKRINVLPLGSGALAGNPLDIDREMLRSELEFASISLNSMDAISERDFVVEFLSVATLLLIHLSKMAEDLIIYSTSEFGFLTLSDAFSTGSSLMPQKKNPDSLELIRSKSGRVFGRLASILMVLKGLPSTYNKDLQEDKEAVIDVVDTLTAVLQVATGVISTLQISKENMEKALTPEMLATDLALYLVRKGMPFRQAHTASGKAVHLAETKGIAINNLTLEDLKSISPLFSSDVSQVFNFVNSVEQYTALGGTAKSSVTTQIEQLRELMKKQKE

>d1i0aa\_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Turkey (Meleagris gallopavo), delta-crystallin}

GRFVGSVDPIMEILSSSISTEQRLTEVDIQASMAYAKALEKASILTKTELEKILSGLEKISEESSKGVLVMTQSDEDIQTAIERRLKELIGDIAGKLQTGRSRNEQVVTDLKLLLKSSISVISTHLLQLIKTLVERAAIEIDIIMPGYTHLQKALPIRWSQFLLSHAVALTRDSERLGEVKKRITVLPLGSGVLAGNPLEIDRELLRSELDMTSITLNSIDAISERDFVVELISVATLLMIHLSKLAEDLIIFSTTEFGFVTLSDAYSTGSSLLPQKKNPDSLELIRSKAGRVFGRLAAILMVLKGIPSTFSKDLQEDKEAVLDVVDTLTAVLQVATGVISTLQINKENMEKALTPELLSTDLALYLVRKGMPIRQAQTASGKAVHLAETKGITINNLTLEDLKSISPLFASDVSQVFSVVNSVEQYTAVGGTAKSSVTAQIEQLRELLKKQK

>d1c3ca\_ a.127.1.1 (A:) Adenylosuccinate lyase {Thermotoga maritima}

VERYSLSPMKDLWTEEAKYRRWLEVELAVTRAYEELGMIPKGVTERIRNNAKIDVELFKKIEEKTNHDVVAFVEGIGSMIGEDSRFFHYGLTSSDVLDTANSLALVEAGKILLESLKEFCDVLWEVANRYKHTPTIGRTHGVHAEPTSFGLKVLGWYSEMKRNVQRLERAIEEVSYGKISGAVGNYANVPPEVEEKALSYLGLKPEPVSTQVVPRDRHAFYLSTLAIVAAGIERIAVEIRHLQRTEVLEVEEPFRKGQRGSSAMPHKKNPITCERLTGLSRMMRAYVDPSLENIALWHERDISHSSVERYVFPDATQTLYYMIVTATNVVRNMKVNEERMKKNIDLTKGLVFSQRVLLKLIEKGLTRKEAYDIVQRNALKTWNSEKHFLEYLLEDEEVKKLVTKEELEELFDISYYLKHVDHIFERFEK

>d1dofa\_ a.127.1.1 (A:) Adenylosuccinate lyase {Archaeon Pyrobaculum aerophilum}

HVSPFDWRYGSEEIRRLFTNEAIINAYLEVERALVCALEELGVAERGCCEKVNKASVSADEVYRLERETGHDILSLVLLLEQKSGCRYVHYGATSNDIIDTAWALLIRRALAAVKEKARAVGDQLASMARKYKTLEMVGRTHGQWAEPITLGFKFANYYYELYIACRQLALAEEFIRAKIGGAVGTMASWGELGLEVRRRVAERLGLPHHVITTQVAPRESFAVLASALALMAAVFERLAVEIRELSRPEIGEVVEGGGGSSAMPHKANPTASERIVSLARYVRALTHVAFENVALWHERDLTNSANERVWIPEALLALDEILTSALRVLKNVYIDEERITENLQKALPYILTEFHMNRMIKEGASRAEAYKKAKEVKALTFEYQKWPVERLIEDALSLKLC

>d1f1oa\_ a.127.1.1 (A:) Adenylosuccinate lyase {Bacillus subtilis}

EMSAIWTDENRFQAWLEVEILACEAWAELGVIPKEDVKVMRENASFDINRILEIEKDTRHDVVAFTRAVSESLGEERKWVHYGLTSTDVVDTALSYLLKQANDILLKDLERFVDIIKEKAKEHKYTVMMGRTHGVHAEPTTFGLKLALWHEEMKRNLERFKQAKAGIEVGKISGAVGTYANIDPFVEQYVCEKLGLKAAPISTQTLQRDRHADYMATLALIATSIEKFAVEIRGLQKSETREVEEFFAKGQKGSSAMPHKRNPIGSENMTGMARVIRGYMMTAYENVPLWHERDISHSSAERIILPDATIALNYMLNRFSNIVKNLTVFPENMKRNMDRTLGLIYSQRVLLALIDTGLTREEAYDTVQPKAMEAWEKQVPFRELVEAEEKITSRLSPEKIADCFDYNY

>d1gk2a\_ a.127.1.2 (A:) Histidine ammonia-lyase (HAL) {Pseudomonas putida}

TELTLKPGTLTLAQLRAIHAAPVRLQLDASAAPAIDASVACVEQIIAEDRTAYGINTGFGLLASTRIASHDLENLQRSLVLSHAAGIGAPLDDDLVRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGASGDLAPLAHMSLVLLGEGKARYKGQWLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSVEAVLGSRSPFDARIHEARGQRGQIDTAACFRDLLGDSSEVSLSHKNADKVQDPYSLRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVISGGNGHAEPVAMAADNLALAIAEIGSLSERRISLMMDKHMSQLPPFLVENGGVNSGFMIAQVTAAALASENKALSHPHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVLAIEWLGACQGLDLRKGLKTSAKLEKARQALRSEVAHYDRDRFFAPDIEKAVELLAKGSLTGLLPAGVLPSL

>d1uby\_\_ a.128.1.1 (-) Farnesyl diphosphate synthase {Chicken (Gallus gallus)}

SPVVVEREREEFVGFFPQIVRDLTEDGIGHPEVGDAVARLKEVLQYNAPGGKCNRGLTVVAAYRELSGPGQKDAESLRCALAVGWCIELFQAASLVADDIMDQSLTRRGQLCWYKKEGVGLDAINDSFLLESSVYRVLKKYCRQRPYYVHLLELFLQTAYQTELGQMLDLITAPVSKVDLSHFSEERYKAIVKYKTAFYSFYLPVAAAMYMVGIDSKEEHENAKAILLEMGEYFQIQDDYLDCFGDPALTGAVGTDIQDNKCSWLVVQCLQRVTPEQRQLLEDNYGRKEPEKVAKVKELYEAVGMRAAFQQYEESSYRRLQELIEKHSNRLPKEIFLGLAQKIYKRQK

>d1ezfa\_ a.128.1.2 (A:) Squalene synthase {Human (Homo sapiens)}

NSLKTCYKYLNQTSRSFAAVIQALDGEMRNAVCIFYLVLRALDTLEDDMTISVEKKVPLLHNFHSFLYQPDWRFMESKEKDRQVLEDFPTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVGIGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIRDYLEDQQGGREFWPQEVWSRYVKKLGDFAKPENIDLAVQCLNELITNALHHIPDVITYLSRLRNQSVFNFCAIPQVMAIATLAACYNNQQVFKGAVKIRKGQAVTLMMDATNMPAVKAIIYQYMEEIYHRIPDSDPSSSKTRQIISTIRTQN

>d5eau\_2 a.128.1.3 (221-548) 5-Epi-aristolochene synthase, C-terminal domain {Tobacco (Nicotiana tabacum)}

KNNVLLRFAKLDFNLLQMLHKQELAQVSRWWKDLDFVTTLPYARDRVVECYFWALGVYFEPQYSQARVMLVKTISMISIVDDTFDAYGTVKELEAYTDAIQRWDINEIDRLPDYMKISYKAILDLYKDYEKELSSAGRSHIVCHAIERMKEVVRNYNVESTWFIEGYTPPVSEYLSNALATTTYYYLATTSYLGMKSATEQDFEWLSKNPKILEASVIICRVIDDTATYEVEKSRGQIATGIECCMRDYGISTKEAMAKFQNMAETAWKDINEGLLRPTPVSTEFLTPILNLARIVEVTYIHNLDGYTHPEKVLKPHIINLLVDSIKI

>d1di1a\_ a.128.1.4 (A:) Aristolochene synthase {Fungus (Penicillium roqueforti)}

TPPPTQWSYLCHPRVKEVQDEVDGYFLENWKFPSFKAVRTFLDAKFSEVTCLYFPLALDDRIHFACRLLTVLFLIDDVLEHMSFADGEAYNNRLIPISRGDVLPDRTKPEEFILYDLWESMRAHDAELANEVLEPTFVFMRAQTDRARLSIHELGHYLEYREKDVGKALLSALMRFSMGLRLSADELQDMKALEANCAKQLSVVNDIYSYDKEEEASRTGHKEGAFLCSAVKVLAEESKLGIPATKRVLWSMTREWETVHDEIVAEKIASPDGCSEAAKAYMKGLEYQMSGNEQWSKTTR

>d1ps1a\_ a.128.1.4 (A:) Pentalenene synthase {Streptomyces sp., UC5319}

QDVDFHIPLPGRQSPDHARAEAEQLAWPRSLGLIRSDAAAERHLRGGYADLASRFYPHATGADLDLGVDLMSWFFLFDDLFDGPRGENPEDTKQLTDQVAAALDGPLPDTAPPIAHGFADIWRRTCEGMTPAWCARSARHWRNYFDGYVDEAESRFWNAPCDSAAQYLAMRRHTIGVQPTVDLAERAGRFEVPHRVFDSAVMSAMLQIAVDVNLLLNDIASLEKEEARGEQNNMVMILRREHGWSKSRSVSHMQNEVRARLEQYLLLESCLPKVGEIYQLDTAEREALERYRTDAVRTVIRGSYDWHRSSG

>d1jfaa\_ a.128.1.5 (A:) Trichodiene synthase {Fusarium sporotrichioides}

MENFPTEYFLNTTVRLLEYIRYRDSNYTREERIENLHYAYNKAAHHFAQPRQQQLLKVDPKRLQASLQTIVGMVVYSWAKVSKECMADLSIHYTYTLVLDDSKDDPYPTMVNYFDDLQAGREQAHPWWALVNEHFPNVLRHFGPFCSLNLIRSTLDFFEGCWIEQYNFGGFPGSHDYPQFLRRMNGLGHCVGASLWPKEQFNERSLFLEITSAIAQMENWMVWVNDLMSFYKEFDDERDQISLVKNYVVSDEISLHEALEKLTQDTLHSSKQMVAVFSDKDPQVMDTIECFMHGYVTWHLCDRRYRLSEIYEKVKEEKTEDAQKFCKFYEQAANVGAVSPSEWAYPPVAQLANV

>d1oela1 a.129.1.1 (A:2-136,A:410-525) GroEL {Escherichia coli}

AAKDVKFGNDAGVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGAPTITKDGVSVAREIELEDKFENMGAQMVKEVASKANDAAGDGTTTATVLAQAIITEGLKAVAAGMNPMDLKRGIDKAVTVAVEELKALSVXGVVAGGGVALIRVASKLADLRGQNEDQNVGIKVALRAMEAPLRQIVLNCGEEPSVVANTVKGGDGNYGYNAATEEYGNMIDMGILDPTKVTRSALQYAASVAGLMITTECMVTDLP

>d1ioka1 a.129.1.1 (A:2-136,A:410-526) GroEL {Paracoccus denitrificans}

AAKEVKFNSDARDRMLKGVNILADAVKVTLGPKGRNVVIDKSFGAPRITKDGVSVAKEIELSDKFENMGAQMVREVASRTNDEAGDGTTTATVLAQAIVREGLKAVAAGMNPMDLKRGIDVATAKVVEAIKSAARXGIVVGGGVALVQGAKVLEGLSGANSDQDAGIAIIRRALEAPMRQIAENAGVDGAVVAGKVRESSDKAFGFNAQTEEYGDMFKFGVIDPAKVVRTALEDAASVAGLLITTEAMIAEKP

>d1a6da1 a.129.1.2 (A:17-145,A:404-519) Thermosome {Archaeon Thermoplasma acidophilum}

REQGKNAQRNNIEAAKAIADAVRTTLGPKGMDKMLVDSIGDIIISNDGATILKEMDVEHPTAKMIVEVSKAQDTAVGDGTTTAVVLSGELLKQAETLLDQGVHPTVISNGYRLAVNEARKIIDEIAEKSXFLWGGGAVEAELAMRLAKYANSVGGREQLAIEAFAKALEIIPRTLAENAGIDPINTLIKLKADDEKGRISVGVDLDNNGVGDMKAKGVVDPLRVKTHALESAVEVATMILRIDDVI

>d1a6db1 a.129.1.2 (B:20-144,B:404-521) Thermosome {Archaeon Thermoplasma acidophilum}

KDAMKENIEAAIAISNSVRSSLGPRGMDKMLVDSLGDIVITNDGVTILKEMDVEHPAAKMMVEVSKTQDSFVGDGTTTAVIIAGGLLQQAQGLINQNVHPTVISEGYRMASEEAKRVIDEISTKIXAYAAGGGATAAEIAFRLRSYAQKIGGRQQLAIEKFADAIEEIPRALAENAGLDPIDILLKLRAEHAKGNKTYGINVFTGEIEDMVKNGVIEPIRVGKQAIESATEAAIMILRIDDVIA

>d1ecma\_ a.130.1.1 (A:) Chorismate mutase domain of P-protein {Escherichia coli}

NPLLALREKISALDEKLLALLAERRELAVEVGKAKLLSHRPVRDIDRERDLLERLITLGKAHHLDAHYITRLFQLIIEDSVLTQQALLQQH

>d5csma\_ a.130.1.2 (A:) Allosteric chorismate mutase {Baker's yeast (Saccharomyces cerevisiae)}

MDFTKPETVLNLQNIRDELVRMEDSIIFKFIERSHFATCPSVYEANHPGLEIPNFKGSFLDWALSNLEIAHSRIRRFESPDETPFFPDKIQKSFLPSINYPQILAPYAPEVNYNDKIKKVYIEKIIPLISKRDGDDKNNFGSVATRDIECLQSLSRRIHFGKFVAEAKFQSDIPLYTKLIKSKDVEGIMKNITNSAVEEKILERLTKKAEVYGVDPTERRIERRISPEYLVKIYKEIVIPITKEVEVEYLLRRLEE

>d1pprm1 a.131.1.1 (M:1-156) Peridinin-chlorophyll protein {Dinoflagellate (Amphidinium carterae)}

DEIGDAAKKLGDASYAFAKEVDWNNGIFLQAPGKLQPLEALKAIDKMIVMGAAADPKLLKAAAEAHHKAIGSISGPNGVTSRADWDNVNAALGRVIASVPENMVMDVYDSVSKITDPKVPAYMKSLVNGADAEKAYEGFLAFKDVVKKSQVTSAAG

>d1pprm2 a.131.1.1 (M:157-312) Peridinin-chlorophyll protein {Dinoflagellate (Amphidinium carterae)}

PATVPSGDKIGVAAQQLSEASYPFLKEIDWLSDVYMKPLPGVSAQQSLKAIDKMIVMGAQADGNALKAAAEAHHKAIGSIDATGVTSAADYAAVNAALGRVIASVPKSTVMDVYNAMAGVTDTSIPLNMFSKVNPLDANAAAKAFYTFKDVVQAAQ

>d1qq8a\_ a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Human (Homo sapiens)}

PQDLSEALKEATKEVHTQAENAEFMRNFQKGQVTRDGFKLVMASLYHIYVALEEEIERNKESPVFAPVYFPEELHRKAALEQDLAFWYGPRWQEVIPYTPAMQRYVKRLHEVGRTEPELLVAHAYTRYLGDLSGGQVLKKIAQKALDLPSSGEGLAFFTFPNIASATKFKQLYRSRMNSLEMTPAVRQRVIEEAKTAFLLNIQLFEELQELLTH

>d1dvga\_ a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Rat (Rattus norvegicus)}

SQDLSEALKEATKEVHIRAENSEFMRNFQKGQVSREGFKLVTASLYHIYTALEEEIERNKQNPVYAPLYFPEELHRRAALEQDLAFWYGPHWQEAIPYTPATQHYVKRLHEVGGTHPELLVAHAYTRYLGDLSGGQVLKKIAQKALALPSSGEGLASFTFPSIDNPTKFKQLYRARMNTLELTPEVKHRVTEEAKTAFLLNIELFEELQALLTE

>d1j77a\_ a.132.1.2 (A:) Gram-negative bacterial heme oxygenase {Neisseria meningitidis}

ALTFAKRLKADTTAVHDSVDNLVMSVQPFVSKENYIKFLKLQSVFHKAVDHIYKDAELNKAIPELEYMARYDAVTQDLKDLGEEPYKFDKELPYEAGNKAIGWLYCAEGSNLGAAFLFKHAQKLDYNGEHGARHLAPHPDGRGKHWRAFVEHLNALNLTPEAEAEAIQGAREAFAFYKVVLRETFGLAADAEAPEGMMPH

>d1knca\_ a.152.1.1 (A:) Antioxidant defence protein AhpD {Mycobacterium tuberculosis}

SIEKLKAALPEYAKDIKLNLSSITRSSVLDQEQLWGTLLASAAATRNPQVLADIGAEATDHLSAAARHAALGAAAIMGMNNVFYRGRGFLEGRYDDLRPGLRMNIIANPGIPKANFELWSFAVSAINGCSHCLVAHEHTLRTVGVDREAIFEALKAAAIVSGVAQALATIEALS

>d1poa\_\_ a.133.1.2 (-) Snake phospholipase A2 {Taiwan cobra (Naja naja atra)}

NLYQFKNMIQCTVPSRSWWDFADYGCYCGRGGSGTPVDDLDRCCQVHDNCYNEAEKISGCWPYFKTYSYECSQGTLTCKGGNNACAAAVCDCDRLAAICFAGAPYNDNDYNINLKARC

>d1pp2l\_ a.133.1.2 (L:) Snake phospholipase A2 {Western diamondback rattlesnake (Crotalus atrox)}

SLVQFETLIMKIAGRSGLLWYSAYGCYCGWGGHGLPQDATDRCCFVHDCCYGKATDCNPKTVSYTYSEENGEIICGGDDPCGTQICECDKAAAICFRDNIPSYDNKYWLFPPKDCREEPEPC

>d1bjja\_ a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}

NLLQFNKMIKEETGKNAIPFYAFYGCYCGWGGQGKPKDGTDRCCFVHDCCYGRLVNCNTKSDIYSYSLKEGYITCGKGTNCEEQICECDRVAAECFRRNLDTYNNGYMFYRDSKCTETSEEC

>d1jiaa\_ a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}

HLLQFRKMIKKMTGKEPVVSYAFYGCYCGSGGRGKPKDATDRCCFVHDCCYEKVTGCDPKWDDYTYSWKNGTIVCGGDDPCKKEVCECDKAAAICFRDNLKTYKKRYMAYPDILCSSKSEKC

>d1psj\_\_ a.133.1.2 (-) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}

SLIQFETLIMKVAKKSGMFWYSNYGCYCGWGGQGRPQDATDRCCFVHDCCYGKVTGCDPKMDVYSFSEENGDIVCGGDDPCKKEICECDRAAAICFRDNLTLYNDKKYWAFGAKNCPQEESEPC

>d1ppa\_\_ a.133.1.2 (-) Snake phospholipase A2 {Eastern cottonmouth snake (Agkistridon piscivorus)}

SVLELGKMILQETGKNAITSYGSYGCNCGWGHRGQPKDATDRCCFVHKCCYKKLTDCNHKTDRYSYSWKNKAIICEEKNPCLKEMCECDKAVAICLRENLDTYNKKYKAYFKLKCKKPDTC

>d1vapa\_ a.133.1.2 (A:) Snake phospholipase A2 {Eastern cottonmouth snake (Agkistridon piscivorus)}

NLFQFEKLIKKMTGKSGMLWYSAYGCYCGWGGQGRPKDATDRCCFVHDCCYGKVTGCNPKMDIYTYSVDNGNIVCGGTNPCKKQICECDRAAAICFRDNLKTYDSKTYWKYPKKNCKEESEPC

>d1ijla\_ a.133.1.2 (A:) Snake phospholipase A2 {Viper (Deinagkistrodon acutus)}

SLIQFETLIMKVVKKSGMFWYSAYGCYCGWGGHGRPQDATDRCCFVHDCCYGKVTGCDPKMDSYTYSEENGDIVCGGDDPCKREICECDRVAADCFRDNLDTYNSDTYWRYPRQDCEESPEPC

>d1fe7a\_ a.133.1.2 (A:) Snake phospholipase A2 {Snake (Daboia russelli pulchella)}

SLLEFGKMILEETGKLAIPSYSSYGCYCGWGGKGTPKDATDRCCFVHDCCYGNLPDCNPKSDRYKYKRVNGAIVCEKGTSCENRICECDKAAAICFRQNLNTYSKKYMLYPDFLCKGELKC

>d1ae7\_\_ a.133.1.2 (-) Snake phospholipase A2 {Mainland tiger snake (Notechis scutatus scutatus), notexin}

NLVQFSYLIQCANHGKRPTWHYMDYGCYCGAGGSGTPVDELDRCCKIHDDCYDEAGKKGCFPKMSAYDYYCGENGPYCRNIKKKCLRFVCDCDVEAAFCFAKAPYNNANWNIDTKKRCQ

>d2nota\_ a.133.1.2 (A:) Snake phospholipase A2 {Mainland tiger snake (Notechis scutatus scutatus), notechis II-5}

NLVQFSYLIQCANHGRRPTRHYMDYGCYCGWGGSGTPVDELDRCCKIHDDCYSDAEKKGCSPKMSAYDYYCGENGPYCRNIKKKCLRFVCDCDVEAAFCFAKAPYNNANWNIDTKKRCQ

>d1qlla\_ a.133.1.2 (A:) Snake phospholipase A2 {Bothrops pirajai, Piratoxin-II (PRTX-II)}

SLFELGKMILQETGKNPAKSYGAYGCNCGVLGRGKPKDATDRCCYVHKCCYKKLTGCNPKKDRYSYSWKDKTIVCGENNPCLKELCECDKAVAICLRENLGTYNKKYRYHLKPFCKKADKC

>d1vip\_\_ a.133.1.2 (-) Snake phospholipase A2 {Russell's viper (Vipera russelli)}

NLFQFAEMIVKMTGKNPLSSYSDYGCYCGWGGKGKPQDATDRCCFVHDCCYEKVKSCKPKLSLYSYSFQNGGIVCGDNHSCKRAVCECDRVAATCFRDNLNTYDKKYHNYPPSQCTGTEQC

>d1jlta\_ a.133.1.2 (A:) Snake phospholipase A2 {Sand viper (Vipera ammodytes meridionalis), vipoxin}

NLFQFGDMILQKTGKEAVHSYAIYGCYCGWGGQARAQDATDRCCFAQDCCYGRVNDCNPKTATYTYSFENGDIVCGDNDLCLRAVCECDRAAAICLGENVNTYDKNYEYYSISHCTEESEQC

>d1jltb\_ a.133.1.2 (B:) Snake phospholipase A2 {Sand viper (Vipera ammodytes meridionalis), vipoxin}

NLFQFAKMINGKLGAFSVWNYISYGCYCGWGGQGTPKDATDRCCFVHDCCYGRVRGCNPKLAIYSYSFKKGNIVCGKNNGCLRDICECDRVAANCFHQNKNTYNKNYKFLSSSRCRQTSEQC

>d1dpya\_ a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (Bungarus caeruleus), different isoforms}

NLIQFKNMIQCAGTRIWTAYVAYGCYCGKGGSGTPVDELDRCCYTHDHCYNEAEKIPGCNPNIKTYSYTCTQPNLTCTDSADTCAQFLCECDRTAAICFASAPYNSNNIMLSSSTSCQ

>d1fe5a\_ a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (Bungarus caeruleus), different isoforms}

NLIQFKNMIQCAGTRPWTAYVNYGCYCGKGGSGTPVDELDRCCYTHDNCYNEAEKIPGCNPNIKTYSYTCTEPNLTCTDTADTCARFLCNCDRTAAICFASAPYNSNNVMISSSTNCQ

>d1kvoa\_ a.133.1.2 (A:) Phospholipase A2 {Human (Homo sapiens), synovial fluid}

NLVNFHRMIKLTTGKEAALSYGFYGCHCGVGGRGSPKDATDRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGSTPRC

>d1g4ia\_ a.133.1.2 (A:) Phospholipase A2 {Cow (Bos taurus), pancreas}

ALWQFNGMIKCKIPSSEPLLDFNNYGCYCGLGGSGTPVDDLDRCCQTHDNCYKQAKKLDSCKVLVDNPYTNNYSYSCSNNEITCSSENNACEAFICNCDRNAAICFSKVPYNKEHKNLDKKNC

>d1hn4a\_ a.133.1.2 (A:) Phospholipase A2 {Pig (Sus scrofa), pancreas}

GISSRALWQFRSMIKCAIPGSHPLMDFNNYGCYCGLGGSGTPVDELDRCCETHDNCYRDAKNLDSCKFLVDNPYTESYSYSCSNTEITCNSKNNACEAFICNCDRNAAICFSKAPYNKEHKNLDTKKYC

>d5p2pa\_ a.133.1.2 (A:) Phospholipase A2 {Pig (Sus scrofa), pancreas}

ALFQFRSMIKCAIPGSHPLMDFNNYGCYCGWGGSGTPVDELDRCCETHDNCYRDAKNLSGCYPYTESYSYSCSNTEITCNSKNNACEAFICNCDRNAAICFSKAPYNKEHKNLDTKKYC

>d1buna\_ a.133.1.2 (A:) beta2-bungarotoxin, phospholipase A2 chain {Many-banded krait (Bungarus multicinctus), elapid}

NLINFMEMIRYTIPCEKTWGEYADYGCYCGAGGSGRPIDALDRCCYVHDNCYGDAEKKHKCNPKTQSYSYKLTKRTIICYGAAGTCARIVCDCDRTAALCFGNSEYIEGHKNIDTARFCQ

>d1goda\_ a.133.1.2 (A:) Myotoxin II {Bothrops godmani}

SMYQLWKMILQETGKNAVPSYGLYGCNCGVGSRGKPKDATDRCCFVHKCCYKKLTDCSPKTDSYSYSWKDKTIVCGDNNPCLQEMCECDKAVAICLRENLDTYNKNYKIYPKPLCKKADAC

>d1gmza\_ a.133.1.2 (A:) Myotoxin II {Snake (Bothrops pirajai), piratoxin III}

DLWQFGKMILKETGKLPFPYYVTYGCYCGVGGRGGPKDATDRCCFVHDCCYGKLTSCKPKTDRYSYSRKDGTIVCGENDPCRKEICECDKAAAVCFRENLDTYNKKYMSYLKSLCKKXADDC

>d1poc\_\_ a.133.1.1 (-) Phospholipase A2 {European honeybee (Apis mellifera)}

IIYPGTLWCGHGNKSSGPNELGRFKHTDACCRTHDMCPDVMSAGESKHGLTNTASHTRLSCDCDDKFYDCLKNSADTISSYFVGKMYFNLIDTKCYKLEHPVTGCGERTEGRCLHYTVDKSKPKVYQWFDLRKY

>d1faza\_ a.133.1.3 (A:) Prokaryotic phospholipase A2 {Streptomyces violaceoruber}

APADKPQVLASFTQTSASSQNAWLAANRNQSAWAAYEFDWSTDLCTQAPDNPFGFPFNTACARHDFGYRNYKAAGSFDANKSRIDSAFYEDMKRVCTGYTGEKNTACNSTAWTYYQAVKIFG

>d1bxm\_\_ a.134.1.1 (-) beta-cryptogein {Phytophthora cryptogea}

RGTCTATQQTAAYHTLVSILSDASFNQCSTDSGYSMLTAKALPTTAQYKLMCASTACNTMIKKIVTLNPPNCDLTVPTSGLVLNVYSYANGFSNKCSSL

>d1g8qa\_ a.135.1.1 (A:) CD81 extracellular domain {Human (Homo sapiens)}

FVNKDQIAKDVKQFYDQALQQAVVDDDANNAKAVVKTFHETLDCCGSSTLTALTTSVLKNNLCPSGSNIISNLFKEDCHQKIDDLFSGKH

>d1dvoa\_ a.136.1.1 (A:) Repressor of bacterial conjugation FinO {Escherichia coli}

PPKWKVKKQKLAEKAAREAELTAKKAQARQALSIYLNLPTLDEAVNTLKPWWPGLFDGDTPRLLACGIRDVLLEDVAQRNIPLSHKKLRRAMKAITRSESYLCAMKAGACRYDTEGYVTEHISQEEEVYAAERLDKIRRQNRIKAELQAVLD

>d1jjsa\_ a.153.1.1 (A:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}

ALQDLLRTLKSPSSPQQQQQVLNILKSNPQLMAAFIKQRTAKYVAN

>d1kbhb\_ a.153.1.1 (B:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}

PNRSISPSALQDLLRTLKSPSSPQQQQQVLNILKSNPQLMAAFIKQRTAKYVANQPGMQ

>d1kbha\_ a.153.1.1 (A:) Nuclear receptor coactivator ACTR {Human (Homo sapiens)}

EGQSDERALLDQLHTLLSNTDATGLEEIDRALGIPELVNQGQALEPK

>d1ffky\_ a.137.1.1 (Y:) Ribosomal protein L39e {Archaeon Haloarcula marismortui}

GKKSKATKKRKAKLDNQNSRVPAYVMLKTDREVQRNHKRRHWRRNDTDE

>d1jj21\_ a.137.1.1 (1:) Ribosomal protein L39e {Archaeon Haloarcula marismortui}

GKKSKATKKRLAKLDNQNSRVPAWVMLKTDEVQRNHKRRHWRRNDTDE

>d1g72b\_ a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylophilus methylotrophus, w3a1}

YDGQNCKEPGNCWENKPGYPEKIAGSKYDPKHDPVELNKQEESIKAMDARNAKRIAN

>d4aahb\_ a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylophilus methylotrophus, w3a1}

YDGQNCKEPGNCWENKPGYPEKIAGSKYDPKHDPVELNKQEESIKAMDARNAKRIANAKSSGNFVFDVK

>d1h4ib\_ a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylobacterium extorquens}

YDGTKCKAAGNCWEPKPGFPEKIAGSKYDPKHDPKELNKQADSIKQMEERNKKRVENFKKTGKFEYDVAKISA

>d1gg2g\_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

SIAQARKLVEQLKMEANIDRIKVSKAAADLMAYCEAHAKEDPLLTPVPASENPF

>d1gotg\_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

LTEKDKLKMEVDQLKKEVTLERMLVSKCCEEFRDYVEERSGEDPLVKGIPEDKNPFKE

>d1tbge\_ a.137.3.1 (E:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

APVINIEDLTEKDKLKMEVDQLKKEVTLERMLVSKCCEEFRDYVEERSGEDPLVKGIPEDKNPFKELK

>d1hfes\_ a.137.4.1 (S:) Fe-only hydrogenase smaller subunit {Desulfovibrio desulfuricans}

VKQIKDYMLDRINGVYGADAKFPVRASQDNTQVKALYKSYLEKPLGHKSHDLLHTHWFDKSKGVKELTTAGKLPNPRASEFEGPYPYE

>d1ef1c\_ a.137.5.1 (C:) Moesin tail domain {Human (Homo sapiens)}

AEASADLRADAMAKDRSEEERTTEAEKNERVQKHLKALTSELANARDESKKTANDMIHAENMRLGRDKYKTLRQIRQGNTKQRIDEFESM

>d2prgc\_ a.137.6.1 (C:) Nuclear receptor coactivator Src-1 {Human (Homo sapiens)}

QTSHKLVQLLTTTAEQQLRHADIDTSCKDVLSCTGTSNSASANSSGGSCPSSHSSLTERHKILHRLLQEGSPSDIT

>d1dp5b\_ a.137.7.1 (B:) Proteinase A inhibitor IA3 {Baker's yeast (Saccharomyces cerevisiae)}

NTDQQKVSEIFQSSKEKLQGDAKVVSDAFMM

>d1dpjb\_ a.137.7.1 (B:) Proteinase A inhibitor IA3 {Baker's yeast (Saccharomyces cerevisiae)}

TDQQKVSEIFQSSKEKLQGDAKVVSDAFK

>d1e79i\_ a.137.8.1 (I:) Epsilon subunit of mitochondrial F1F0-ATP synthase {Cow (Bos taurus)}

VAYWRQAGLSYIRYSQICAKAVRDALKTEFKANAMKTSGSTIKIVKV

>d1jjuc\_ a.137.9.1 (C:) Quinohemoprotein amine dehydrogenase C chain {Paracoccus denitrificans}

MNALVGCTTSFDPGWEVDAFGAVSNLCQPMEADLYGCADPCWXPAQVADTLNTYPNWSAGADDVMQDWRKLQSVFPETK

>d1jmxg\_ a.137.9.1 (G:) Quinohemoprotein amine dehydrogenase C chain {Pseudomonas putida}

AVAGCTATTDPGWEVDAFGGVSSLCQPMEADLYGCSDPCWXPAQVPDMMSTYQDWNAQASNSAEDWRNLGTVFPKDK

>d1aqe\_\_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

TFEIPESVTMSPKQFEGYTPKKGDVTFNHASHMDIACQQCHHTVPDTYTIESCMTEGCHDNIKERTEISSVERTFHTTKDSEKSCVGCHRELKRQGPSDAPLACNSCHVQ

>d1i77a\_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

APAAPDKPLEFKGSQKTVMFPHAVHAKVECVTCHHQVDGKESFAKCGSSGCHDDLAGKQGEKSLYYVVHTKKELKHTNCIGCHSKVVEGKPELKKDLTACAKSKCHP

>d2cy3\_\_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

ADAPGDDYVISAPEGMKAKPKGDKPGALQKTVPFPHTKHATVECVQCHHTLEADGGAVKKCTTSGCHDSLEFRDKANAKDIKLVENAFHTQCIDCHKALKKDKKPTGPTACGKCHTTN

>d3cyr\_\_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

APAVPNKPVEVKGSQKTVMFPHAPHEKVECVTCHHLVDGKESYAKCGSSGCHDDLTAKKGEKSLYYVVHAKGELKHTSCLACHSKVVAEKPELKKDLTGCAKSKCHP

>d2cdv\_\_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio vulgaris}

APKAPADGLKMDKTKQPVVFNHSTHKAVKCGDCHHPVNGKENYQKCATAGCHDNMDKKDKSAKGYYHAMHDKGTKFKSCVGCHLETAGADAAKKKELTGCKGSKCHS

>d2ctha\_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio vulgaris}

APKAPADGLKMEATKQPVVFNHSTHKSVKCGDCHHPVNGKEDYRKCGTAGCHDSMDKKDKSAKGYYHVMHDKNTKFKSCVGCHVEVAGADAAKKKDLTGCKKSKCHE

>d1wad\_\_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio gigas}

VDVPADGAKIDFIAGGEKNLTVVFNHSTHKDVKCDDCHHDPGDKQYAGCTTDGCHNILDKADKSVNSWYKVVHDAKGGAKPTCISCHKDKAGDDKELKKKLTGCKGSACHP

>d3caoa\_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio africanus}

EDMTHVPTDAFGKLERPAAVFNHDEHNEKAGIESCNACHHVWVNGVLAEDEDSVGTPCSDCHALEQDGDTPGLQDAYHQQCWGCHEKQAKGPVMCGECHVKN

>d1hh5a\_ a.138.1.1 (A:) Cytochrome c7 (cytochrome c551.5) {Desulfuromonas acetoxidans}

ADVVTYENKKGNVTFDHKAHAEKLGCDACHEGTPAKIAIDKKSAHKDACKTCHKSNNGPTKCGGCHIK

>d19hca\_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

AALEPTDSGAPSAIVMFPVGEKPNPKGAAMKPVVFNHLIHEKKIADCETCHHTGDPVSCSTCHTVEGKAEGDYITLDRAMHATDIAARAKGNTPTSCVSCHQSETKERRECAGCHAITTPKDDEAWCATCHDITPSMTPSEMQKGIAGTLLPGDNEALAAETVLAEATVAPVSPMLAPYKVVIDALADKYEPSDFTHRRHLTSLMESIKDDKLAQAFHDKPEILCATCHHRSPLSLTPPKCGSCHTKEIDAADPGRPNLMAAYHLECMGCHKGMAVARPRDTDCTTCHKAAA

>d1duwa\_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 29577}

EPTDSGAPSAIVMFPVSAKPNPKGAAMKPAVFNHLAHEKKIANCETCHHTGDPVACSTCHTTEGKAEGNFVTLDRAMHATNIAKRAKGNTPVSCVSCHEQQTKERRECAGCHAIVTPKRDQAWCATCHNVTSSMTPEQMQQGIKGKLPPDQNEALAAETVLNHKPVQPLTAMQGPYKVSIDALADKYEPSNFTHRRHMASLMERIKGDKLAEAFHNKPETLCATCHHRSPLSATPPKCGSCHTKEIDPANPNRPNLKAAYHLQCMGCHQGMNVGRPKNTDCTTCHKARP

>d1dxrc\_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit) {Rhodopseudomonas viridis}

CFEPPPATTTQTGFRGLSMGEVLHPATVKAKKERDAQYPPALAAVKAEGPPVSQVYKNVKVLGNLTEAEFLRTMTAITEWVSPQEGCTYCHDENNLASEAKYPYVVARRMLEMTRAINTNWTQHVAQTGVTCYTCHRGTPLPPYVRYLEPTLPLNNRETPTHVERVETRSGYVVRLAKYTAYSALNYDPFTMFLANDKRQVRVVPQTALPLVGVSRGKERRPLSDAYATFALMMSISDSLGTNCTFCHNAQTFESWGKKSTPQRAIAWWGIRMVRDLNMNYLAPLNASLPASRLGRQGEAPQADCRTCHQGVTKPLFGASRLKDYPELGPIK

>d1eysc\_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit) {Thermochromatium tepidum}

CEGPPPGTEQIGYRGVGMENYYVKRQRALSIQANQPVESLPAADSTGPKASEVYQSVQVLKDLSVGEFTRTMVAVTTWVSPKEGCNYCHVPGNWASDDIYTKVVSRRMFELVRAANSDWKAHVAETGVTCYTCHRGNPVPKYAWVTDPGPKYPSGLKPTGQNYGSKTVAYASLPFDPLTPFLDQANEIRITGNAALAGSNPASLKQAEWTFGLMMNISDSLGVGCTSCHNTRAFNDWTQSTPKRTTAWYAIRHVRDINQNYIWPLNDVLPASRKGPYGDPLRVSCMTCHQAVNKPLYGAQMAKDYPGLYK

>d1fgja\_ a.138.1.3 (A:) Hydroxylamine oxidoreductase, HAO {Nitrosomonas europaea}

DISTVPDETYDALKLDRGKATPKETYEALVKRYKDPAHGAGKGTMGDYWEPIAISIYMDPNTFYKPPVSPKEVAERKDCVECHSDETPVWVRAWKRSTHANLDKIRNLKSDDPLYYKKGKLEEVENNLRSMGKLGEKETLKEVGCIDCHVDVNKKDKADHTKDIRMPTADTCGTCHLREFAERESERDTMVWPNGQWPAGRPSHALDYTANIETTVWATMPQREVAEGCTMCHTNQNKCDNCHTRHEFSAAESRKPEACATCHSGVDHNNWEAYTMSKHGKLAEMNRDKWNWEVRLKDAFSKGGQNAPTCAACHMEYEGEYTHNITRKTRWANYPFVPGIAENITSDWSEARLDSWVLTCTQCHSERFARSYLDLMDKGTLEGLAKYQEANAIVHKMYEDGTLTGQKTNRPNPPEPEKPGFGIFTQLFWSKGNNPASLELKVLEMGENNLAKMHVGLAHVNPGGWTYTEGWGPMNRAYVEIQDEYTKMQELSALQARVN

>d1ft5a\_ a.138.1.3 (A:) Cytochrome c554 {Nitrosomonas europaea}

ADAPFEGRKKCSSCHKAQAQSWKDTAHAKAMESLKPNVKKEAKQKAKLDPAKDYTQDKDCVGCHVDGFGQKGGYTIESPKPMLTGVGCESCHGPGRNFRGDHRKSGQAFEKSGKKTPRKDLAKKGQDFHFEERCSACHLNYEGSPWKGAKAPYTPFTPEVDAKYTFKFDEMVKEVKAMHEHYKLEGVFEGEPKFKFHDEFQASAKPAKKGK

>d1ddca\_ a.138.1.3 (A:) Dimeric di-heme split-soret cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

RFDQVGGAFGWKPHKLDPKECAQVAYDGYWYKGFGCGFGAFYSIVGLMGEKYGAPYNQFPFAMLEANKGGISDWGTIYGALYGAAATFSLFWGRKEVHPMVNELFRWYEVTKLPIFNPGDAAQGVKGDLPMSASDSVLCHISVSKWCYENKIEATSKQRSERAGRLTADAAFKAAEIINTKIDQGKDFKSTFPMQASVSSCGECHMTKGNDANWAKGIMDCTPCHSGTAATQNKFVNH

>d1qdba\_ a.138.1.3 (A:) Cytochrome c nitrite reductase {Sulfurospirillum deleyianum}

GIAGKEKSEEWAKYYPRQFDSWKKTKEYDSFTDMLAKDPALVIAWSGYAFSKDYNSPRGHYYALQDNVNSLRTGAPVDAKTGPLPTACWTCKSPDVPRLIEEDGELEYFTGKWAKYGSQIVNVIGCANCHDDKTAELKVRVPHLNRGLQAAGLKTFEESTHQDKRTLVCAQCHVEYYFKKTEWKDAKGADKTAMVVTLPWANGVGKDGNAGVEGMIKYYDEINFSDWTHNISKTPMLKAQHPGFEFWKSGIHGQKGVSCADCHMPYTQEGSVKYSDHQVKENPLDSMDQSCMNCHRESESKLRGIVHQKYERKEFLNKVAFDNIGKAHLETGKAIEAGASDEELKEVRKLIRHGQFKADMAIAAHGNYFHAPEETLRLLAAGSDDAQKARLLLVKILAKHGVMDYIAPDFDTKDKAQKLAKVDIAALAAEKMKFKQTLEQEWKKEAKAKGRANPELYKDVDTINDGKSSWNKK

>d1fs7a\_ a.138.1.3 (A:) Cytochrome c nitrite reductase {Wolinella succinogenes}

KTAHSQGIEGKAMSEEWARYYPRQFDSWKKTKESDNITDMLKEKPALVVAWAGYPFSKDYNAPRGHYYALQDNINTLRTGAPVDGKTGPLPSACWTCKSPDVPRIIEQDGELEYFTGKWAKYGDEIVNTIGCYNCHDDKSAELKSKVPYLDRGLSAAGFKTFAESTHQEKRSLVCAQCHVEYYFKKTEWKDDKGVDKTAMVVTLPWSKGISTEQMEAYYDEINFADWTHGISKTPMLKAQHPDWELYKTGIHGQKGVSCADCHMPYTQEGAVKYSDHKVGNPLDNMDKSCMNCHRESEQKLKDIVKQKFERKEFLQDIAFDNIGKAHLETGKAMELGATDAELKEIRTHIRHAQWRADMAIAGHGSFFHAPEEVLRLLASGNEEAQKARIKLVKVLAKYGAIDYVAPDFETKEKAQKLAKVDMEAFIAEKLKFKQTLEQEWKKQAIAKGRLNPESLKGVDEKSSYYDKTKK

>d1e39a1 a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella frigidimarina}

ADNLAEFHVQNQECDSCHTPDGELSNDSLTYENTQCVSCHGTLAEVAETTKHEHYNAHASHFPGEVACTSCHSAHEKSMVYCDSCHSFDFNMPYAKKWLRDE

>d1qo8a1 a.138.1.3 (A:2-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella frigidimarina}

TPDMGSFHADMGSCQSCHAKPIKVTDSETHENAQCKSCHGEYAELANDKLQFDPHNSHLGDINCTSCHKGHEEPKFYCNECHSFDIKPMPFSDAKKKKSWD

>d1d4ca1 a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella putrefaciens}

APEVLADFHGEMGGCDSCHVSDKGGVTNDNLTHENGQCVSCHGDLKELAAAAPKDKVSPHKSHLIGEIACTSCHKGHEKSVAYCDACHSFGFDMPFGGKWER

>d1neu\_\_ b.1.1.1 (-) Myelin membrane adhesion molecule P0 {Rat (Rattus norvegicus)}

IVVYTDREVYGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAKGQPYIDEVGTFKERIQWVGDPSWKDGSIVIHNLDYSDNGTFTCDVKNPPDIVGKTSQVTLYVFE

>d1eaja\_ b.1.1.1 (A:) Coxsackie virus and adenovirus receptor (Car), domain 1 {Human (Homo sapiens)}

FARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVDQVIILYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKKAPGVANKKIHLVVLV

>d1qfoa\_ b.1.1.1 (A:) N-terminal domain of sialoadhesin {Mouse (Mus musculus)}

TWGVSSPKNVQGLSGSCLLIPCIFSYPADVPVSNGITAIWYYDYSGKRQVVIHSGDPKLVDKRFRGRAELMGNMDHKVCNLLLKDLKPEDSGTYNFRFEISDSNRWLDVKGTTVTVTT

>d1akjd\_ b.1.1.1 (D:) CD8 {Human (Homo sapiens)}

SQFRVSPLDRTWNLGETVELKCQVLLSNPTSGCSWLFQPRGAAASPTFLLYLSQNKPKAAEGLDTQRFSGKRLGDTFVLTLSDFRRENEGYYFCSALSNSIMYFSHFVPVFLPA

>d1bqhg\_ b.1.1.1 (G:) CD8 {Mouse (Mus musculus)}

KPQAPELRIFPKKMDAELGQKVDLVCEVLGSVSQGCSWLFQNSSSKLPQPTFVVYMASSHNKITWDEKLNSSKLFSAMRDTNNKYVLTLNKFSKENEGYYFCSVISNSVMYFSSVVPVLQKV

>d1cdy\_1 b.1.1.1 (1-97) N-terminal domain of CD4 {Human (Homo sapiens)}

KKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKSPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLV

>d1wioa2 b.1.1.1 (A:179-291) N-terminal domain of CD4 {Human (Homo sapiens)}

FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSVKRVTQDPKLQMGKKLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVV

>d1cid\_1 b.1.1.1 (1-105) N-terminal domain of CD4 {Rat (Rattus rattus)}

TSITAYKSEGESAEFSFPLNLGEESLQGELRWKAEKAPSSQSWITFSLKNQKVSVQKSTSNPKFQLSETLPLTLQIPQVSLQFAGSGNLTLTLDRGILYQEVNLV

>d1hnf\_1 b.1.1.1 (4-104) CD2, first domain {Human (Homo sapiens)}

TNALETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDKKKIAQFRKEKETFKEKDTYKLFKNGTLKIKHLKTDDQDIYKVSIYDTKGKNVLEKIFDLKIQE

>d1hnga1 b.1.1.1 (A:2-99) CD2, first domain {Rat (Rattus norvegicus)}

DSGTVWGALGHGINLNIPNFQMTDDIDEVRWERGSTLVAEFKRKMKPFLKSGAFEILANGDLKIKNLTRDDSGTYNVTVYSTNGTRILNKALDLRILE

>d1ccza1 b.1.1.1 (A:1-93) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}

FSQQIYGVVYGNVTFHVPSNVPLKEVLWKKQKDKVAELENSEFRAFSSFKNRVYLDTVSGSLTIYNLTSSDEDEYEMESPNITDTMKFFLYVL

>d1qa9b\_ b.1.1.1 (B:) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}

SSQQIYGVKYGNVTFHVPSNQPLKEVLWKKQKDKVAELENSEFRAFSSFKNRVYLDTKSGSLTIYNLTSSDEDEYEMESPNITDSMKFFLYVGES

>d1dr9a1 b.1.1.1 (A:1-105) CD80, N-terminal domain {Human (Homo sapiens)}

VIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLTMMSGDMNIWPEYKNRTIFDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLSVK

>d1i85a\_ b.1.1.1 (A:) CD86 (b7-2), N-terminal domain {Human (Homo sapiens)}

MLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQENLVLNEVYLGKEKFDSVHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLA

>d1f97a1 b.1.1.1 (A:27-128) Junction adhesion molecule, JAM, N-terminal domain {Mouse (Mus musculus)}

KGSVYTAQSDVQVPENESIKLTCTYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSSGITFSSVTRKDNGEYTCMVSEEGGQNYGEVSIHLTVL

>d1jmaa\_ b.1.1.1 (A:) HSV glycoprotein D {Herpes simplex virus type 1}

KYALADASLKMADPNRFRGKDLPVLDQLTDPPGVRRVYHIQAGLPDPFQPPSLPITVYYAVLERACRSVLLNAPSEAPQIVRGASEDVRKQPYNLTIAWFRMGGNCAIPITVMEYTECSYNKSLGACPIRTQPRWNYYDSFSAVSEDNLGFLMHAPAFETAGTYLRLVKINDWTEITQFILEHRAKGSCKYALPLRIPPSACLSPQAYQQGVTVDSIGMLPRFIPENQRTVAVYSLKIAGWHGPKAPYTSTLLPPELSE

>d1igta1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}

DIVLTQSPSSLSASLGDTITITCHASQNINVWLSWYQQKPGNIPKLLIYKASNLHTGVPSRFSGSGSGTGFTLTISSLQPEDIATYYCQQGQSYPLTFGGGTKLEIKR

>d1igtb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}

EVKLQESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQTPEKRLEWVAYISNGGGSTYYPDTVKGRFTISRDNAKNTLYLQMSRLKSEDTAMYYCARHGGYYAMDYWGQGTTVTVSSA

>d1igya1 b.1.1.1 (A:2-107) Immunoglobulin (variable domains of L and H chains) {Intact IgG1 antibody Mab61.1.3 (mouse), kappa L chain}

KCAHTVSKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGYSYPYTFGGGTKLEIK

>d1igyb1 b.1.1.1 (B:2-113) Immunoglobulin (variable domains of L and H chains) {Intact IgG1 antibody Mab61.1.3 (mouse), kappa L chain}

VKLQESGAELARPGASVKMSCKASGYTFTTYTIHWIKQRPGQGLEWIGYINPSSVYTNYNQRFKDKATLTRDRSSNTANIHLSSLTSDDSAVYYCVREGEVPYWGQGTTVTVSS

>d1hzhh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}

QVQLVQSGAEVKKPGASVKVSCQASGYRFSNFVIHWVRQAPGQRFEWMGWINPYNGNKEFSAKFQDRVTFTADTSANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYYMDVWGKGTTVIVSS

>d1hzhl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}

EIVLTQSPGTLSLSPGERATFSCRSSHSIRSRRVAWYQHKPGQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTITRVEPEDFALYYCQVYGASSYTFGQGTKLERK

>d8faba1 b.1.1.1 (A:3-105) Immunoglobulin (variable domains of L and H chains) {Fab HIL (human), lambda L chain}

ELTQPPSVSVSPGQTARITCSANALPNQYAYWYQQKPGRAPVMVIYKDTQRPSGIPQRFSSSTSGTTVTLTISGVQAEDEADYYCQAWDNSASIFGGGTKLTV

>d8fabb1 b.1.1.1 (B:1-121) Immunoglobulin (variable domains of L and H chains) {Fab HIL (human), lambda L chain}

AVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYYGDSVKGRFTISRDNSKRTLYMQMNSLRTEDTAVYYCARDPDILTAFSFDYWGQGVLVTVSS

>d7fabh1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and H chains) {Fab NEW (human), lambda L chain}

AVQLEQSGPGLVRPSQTLSLTCTVSGTSFDDYYWTWVRQPPGRGLEWIGYVFYTGTTLLDPSLRGRVTMLVNTSKNQFSLRLSSVTAADTAVYYCARNLIAGGIDVWGQGSLVTVS

>d7fabl1 b.1.1.1 (L:1-103) Immunoglobulin (variable domains of L and H chains) {Fab NEW (human), lambda L chain}

ASVLTQPPSVSGAPGQRVTISCTGSSSNIGAGHNVKWYQQLPGTAPKLLIFHNNARFSVSKSGTSATLAITGLQAEDEADYYCQSYDRSLRVFGGGTKLTVLR

>d1bafh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab ANO2 (mouse), kappa L chain}

DVQLQESGPGLVKPSQSQSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYMSYSGSTRYNPSLRSRISITRDTSKNQFFLQLKSVTTEDTATYFCARGWPLAYWGQGTQVSVSE

>d1bafl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab ANO2 (mouse), kappa L chain}

QIVLTQSPAIMSASPGEKVTMTCSASSSVYYMYWYQQKPGSSPRLLIYDTSNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSSYPPITFGVGTKLELKR

>d1a3rh1 b.1.1.1 (H:2-119) Immunoglobulin (variable domains of L and H chains) {Fab 8F5 (mouse), kappa L chain}

VQLQQSGAELVRPGASVKLSCTTSGFNIKDIYIHWVKQRPEQGLEWIGRLDPANGYTKYDPKFQGKATITVDTSSNTAYLHLSSLTSEDTAVYYCDGYYSYYDMDYWGPGTSVTVSSAKTTAP

>d1a3rl1 b.1.1.1 (L:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 8F5 (mouse), kappa L chain}

DIVMTQSPSSLTVTTGEKVTMTCKSSQSLLNSRTQKNYLTWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLSISGVQAEDLAVYYCQNNYNYPLTFGAGTKLELKRADAAPT

>d1bbjh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab B72.3 (mouse/human chimera), kappa L chain}

EVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWAKQKPEQGLEWIGYISPGNDDIKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVYFCKRSYYGHWGQGTTLTVSSA

>d1bbjl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab B72.3 (mouse/human chimera), kappa L chain}

DIQMTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKQGKSPQLLVYAATNLADGVPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWGTPYTFGGGTRLEIKRA

>d1hila1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 17/9 (mouse), kappa L chain}

DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSNPLTFGGGTKLELKR

>d1hilb1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 17/9 (mouse), kappa L chain}

EVQLVESGGDLVKPGGSLKLSCAASGFSFSSYGMSWVRQTPDKRLEWVATISNGGGYTYYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDSAMYYCARRERYDENGFAYWGQGTLVTVS

>d1dbbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab DB3 (mouse), kappa L chain}

QIQLVQSGPELKKPGETVKISCKASGYAFTNYGVNWVKEAPGKELKWMGWINIYTGEPTYVDDFKGRFAFSLETSASTAYLEINNLKNEDTATYFCTRGDYVNWYFDVWGAGTTVTVS

>d1dbbl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab DB3 (mouse), kappa L chain}

DVVMTQIPLSLPVNLGDQASISCRSSQSLIHSNGNTYLHWYLQKPGQSPKLLMYKVSNRFYGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQSSHVPPTFGGGTKLEIK

>d1dfbh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and H chains) {Fab 3D6 (human), kappa L chain}

EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDMALYYCVKGRDYYDSGGYFTVAFDIWGQGTMVTVSS

>d1dfbl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab 3D6 (human), kappa L chain}

DIQMTQSPSTLSASVGDRVTITCRASQSISRWLAWYQQKPGKVPKLLIYKASSLESGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCQQYNSYSFGPGTKVDIKR

>d1igfh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab B13I2 (mouse), kappa L chain}

EVQLVESGGDLVKPGGSLKLSCAASGFTFSRCAMSWVRQTPEKRLEWVAGISSGGSYTFYPDTVKGRFIISRNNARNTLSLQMSSLRSEDTAIYYCTRYSSDPFYFDYWGQGTTLTVSS

>d1igfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab B13I2 (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASISCRSNQTILLSDGDTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGGTKLEIK

>d1igja1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 26-10 (mouse), kappa L chain}

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLNWYLQKAGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGIYFCSQTTHVPPTFGGGTKLEIK

>d1igjb1 b.1.1.1 (B:2-114) Immunoglobulin (variable domains of L and H chains) {Fab 26-10 (mouse), kappa L chain}

VQLQQSGPELVKPGASVRMSCKSSGYIFTDFYMNWVRQSHGKSLDYIGYISPYSGVTGYNQKFKGKATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSGNKWAMDYWGHGASVTVSSA

>d1igmh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv POT (human) IgM, kappa L chain}

EVHLLESGGNLVQPGGSLRLSCAASGFTFNIFVMSWVRQAPGKGLEWVSGVFGSGGNTDYADAVKGRFTITRDNSKNTLYLQMNSLRAEDTAIYYCAKHRVSYVLTGFDSWGQGTLVTVSSGSASAPTL

>d1igml\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv POT (human) IgM, kappa L chain}

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLAWYQQKPGKAPELRIYDASNLETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYQNLPLTFGPGTKVDIKRTVAAPSV

>d1dqlh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv MEZ (human) IgM, kappa L chain}

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISSDGGNKYYTDSVKGRFTISRNDSKNTLYLQMNSLRTEDTAVFYCARGNPPYSSGWGGGDYWGQGTMVTVSS

>d1dqll\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv MEZ (human) IgM, kappa L chain}

DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPGKAPKKLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCLQQNSNWTFGQGTKVDIK

>d1dn0a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab Kau cold agglutinin (human) IgM, kappa L chain}

EIVLTQSPATLSLSPGERATLSCGASQSVSSNYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQQYGSSPLTFGGGTKVEI

>d1dn0b1 b.1.1.1 (B:1-120) Immunoglobulin (variable domains of L and H chains) {Fab Kau cold agglutinin (human) IgM, kappa L chain}

EVQLQQWGAGLLKPSETLSLTCAVYGGSFSDYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCARPPHDTSGHYWNYWGQGTLVTVSS

>d1indh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab Cha255 (mouse), lambda L chain}

EVTLVESGGDSVKPGGSLKLSCAASGFTLSGETMSWVRQTPEKRLEWVATTLSGGGFTFYSASVKGRFTISRDNAQNNLYLQLNSLRSEDTALYFCASHRFVHWGHGTLVTVSA

>d1faih1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Fab R19.9 (mouse), kappa L chain}

QVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGVNWVKQRPGQGLEWIGYINPGKGYLSYNEKFKGKTTLTVDRSSSTAYMQLRSLTSEDAAVYFCARSFYGGSDLAVYYFDSWGQGTTLTVS

>d1fail1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab R19.9 (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEHEDIATYFCQQGSTLPRTFGGGTKLEIKR

>d2fb4h1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab KOL (human), lambda L chain}

EVQLVQSGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHYADSVKGRFTISRNDSKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSSASCFGPDYWGQGTPVTVSSA

>d2fb4l1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab KOL (human), lambda L chain}

QSVLTQPPSASGTPGQRVTISCSGTSSNIGSSTVNWYQQLPGMAPKLLIYRDAMRPSGVPDRFSGSKSGASASLAIGGLQSEDETDYYCAAWDVSLNAYVFGTGTKVTVLG

>d2fbjh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and H chains) {Fab J539 (mouse), kappa L chain}

EVKLLESGGGLVQPGGSLKLSCAASGFDFSKYWMSWVRQAPGKGLEWIGEIHPDSGTINYTPSLKDKFIISRDNAKNSLYLQMSKVRSEDTALYYCARLHYYGYNAYWGQGTLVTVSA

>d2fbjl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab J539 (mouse), kappa L chain}

EIVLTQSPAITAASLGQKVTITCSASSSVSSLHWYQQKSGTSPKPWIYEISKLASGVPARFSGSGSGTSYSLTINTMEAEDAAIYYCQQWTYPLITFGAGTKLELKRAD

>d1fgvh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab H52 (synthetic, humanised version), kappa L chain}

EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSYADSVKGRFTISVDKSKNTLYLQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLVTVSS

>d1fgvl\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab H52 (synthetic, humanised version), kappa L chain}

DIQMTQSPSSLSASVGDRVTITCRASQDINNYLNWYQQKPGKAPKLLIYYTSTLESGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCQQGNTLPPTFGAGTKVEIK

>d2fgwh1 b.1.1.1 (H:1-124) Immunoglobulin (variable domains of L and H chains) {Fab H52 (synthetic, humanised version), kappa L chain}

EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSHNQRFMDRFTISVDKSTSTAYMQMNSLRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLVTVSS

>d1mcph1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab MCPC603 (human), kappa L chain}

EVKLVESGGGLVQPGGSLRLSCATSGFTFSDFYMEWVRQPPGKRLEWIAASRNKGNKYTTEYSASVKGRFIVSRDTSQSILYLQMNALRAEDTAIYYCARNYYGSTWYFDVWGAGTTVTVS

>d2imn\_\_ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Fab MCPC603 (human), kappa L chain}

DIVMTQSPSSLSVSAGERVTMSCKSSQSLLYKDGKNFLAWYQQKPGQPPKLLIYGASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLTFGAGTKLELKR

>d1fvca\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Fab 4D5 (synthetic, humanised version), kappa L chain}

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRT

>d1fvcb\_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Fab 4D5 (synthetic, humanised version), kappa L chain}

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDYWGQGTLVTVSS

>d1ggbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 50.1 (mouse), kappa L chain}

QVQLQESGPGILQPSQTLSLTCSFSGFSLSTYGMGVSWIRQPSGKGLEWLAHIFWDGDKRYNPSLKSRLKISKDTSNNQVFLKITSVDTADTATYYCVQEGYIYWGQGTSVTVS

>d1ggbl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 50.1 (mouse), kappa L chain}

DIVLTQSPGSLAVSLGQRATISCRASESVDDDGNSFLHWYQQKPGQPPKLLIYRSSNLISGIPDRFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGAGTKLEIK

>d1ai1h1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 59.1 (mouse), kappa L chain}

QVKLQESGPAVIKPSQSLSLTCIVSGFSITRTNYCWHWIRQAPGKGLEWMGRICYEGSIYYSPSIKSRSTISRDTSLNKFFIQLISVTNEDTAMYYCSRENHMYETYFDVWGQGTTVTVS

>d1ai1l1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 59.1 (mouse), kappa L chain}

DIVMTQSPASLVVSLGQRATISCRASESVDSYGKSFMHWYQQKPGQPPKVLIYIASNLESGVPARFSGSGSRTDFTLTIDPVEADDAATYYCQQNNEDPPTFGAGTKLEMRR

>d1mamh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab Yst9.1 (mouse), kappa L chain}

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMSWVRQPPGKALEWLGFIRNKADGYTTEYSASVKGRFTISRDNSQSILYLQMNTLRAEDSATYYCTRDPYGPAAYWGQGTLVTVSA

>d1maml1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab Yst9.1 (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTISCRASQDIYNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLNQEDMATYICQQGNTLPFTFGSGTKLEIKR

>d1mfa\_1 b.1.1.1 (1L-111L) Immunoglobulin (variable domains of L and H chains) {Fab SE155-4 (mouse), lambda L chain}

QIVVTQESALTTSPGETVTLTCRSSTGTVTSGNHANWVQEKPDHLFTGLIGDTNNRAPGVPARFSGSLIGDKAALTITGAQPEDEAIYFCALWSNNHWIFGGGTKLTVLGQ

>d1mfa\_2 b.1.1.1 (251H-367H) Immunoglobulin (variable domains of L and H chains) {Fab SE155-4 (mouse), lambda L chain}

EVQVQQSGTVVARPGASVKMSCKASGYTFTNYWMHWIKQRPGQGLEWIGAIYPGNSATFYNHKFRAKTKLTAVTSTTTAYMELSSLTSEDSAVYYCTRGGHGYYGDYWGQGASLTVS

>d1nbvh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab BV04-01 (mouse), kappa L chain}

EVQPVETGGGLVQPKGSLKLSCAASGFSFNTNAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSVKDRFTISRDDSQNMLYLQMNNLKTEDTAMYYCVRDQTGTAWFAYWGQGTLVTVSAA

>d1teth1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab TE33 (mouse), kappa L chain}

QIQLVQSGPELKTPGETVRISCKASGYTFTTYGMSWVKQTPGKGFKWMGWINTYSGVPTYADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARRSWYFDVWGTGTTVTVS

>d1tetl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TE33 (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASISCKSSQSIVHSSGNTYFEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHIPFTFGSGTKLEIK

>d1flrh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and H chains) {Fab 4-4-20 (mouse), kappa L chain}

EVKLDETGGGLVQPGRPMKLSCVASGFTFSDYWMNWVRQSPEKGLEWVAQIRNKPYNYETYYSDSVKGRFTISRDDSKSSVYLQMNNLRVEDMGIYYCTGSYYGMDYWGQGTSVTVSS

>d4fabl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 4-4-20 (mouse), kappa L chain}

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSQGNTYLRWYLQKPGQSPKVLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPWTFGGGTKLEIK

>d1jfqh1 b.1.1.1 (H:302-421) Immunoglobulin (variable domains of L and H chains) {Fab 36-71 (mouse), kappa L chain}

VQLQQSGVELVRAGSSVKMSCKASGYTFTSNGINWVKQRPGQGLEWIGYNNPGNGYITYNEKFKGKTTLTVDKSSNTAYMQLRSLTSEDSAVYFCARSEYYGGSYKFDYWGQGTTLTVSS

>d1jfql1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 36-71 (mouse), kappa L chain}

DIQMTQIPSSLSASLGDRVSISCRASQDINNFLNWYQQKPDGTIKLLIYFTSRSQSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNALPRTFGGGTKLEIKR

>d1gigh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab HC19 (mouse), lambda L chain}

QVQLKESGPGLVAPSQSLSITCTVSGFLLISNGVHWVRQPPGKGLEWLGVIWAGGNTNYNSALMSRVSISKDNSKSQVFLKMKSLQTDDTAMYYCARDFYDYDVFYYAMDYWGQGTSVTV

>d2cgrh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Fab, anti-sweetener (mouse), kappa L chain}

RVQLLESGAELMKPGASVQISCKATGYTFSEYWIEWVKERPGHGLEWIGEILPGSGRTNYREKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCTRGYSSMDYWGQGTSVTVSAA

>d2cgrl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab, anti-sweetener (mouse), kappa L chain}

ELVMTQSPLSLPVSLGDQASISCRPSQSLVHSNGNTYLHWYLQKPGQSPKLLIYRVSNRFSGVPDRFSGSGSGTAFTLKISRVEAEDLGVYFCSQGTHVPYTFGGGTKLELK

>d1figh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 1F7 (mouse), kappa L chain}

DVQLQQSGPELEKPGASVKISCKASGFSLPGHNINWIVQRNGKSLEWIGNIDPYYGGTNFNPKFKGKATLTVDKSSSTLYMHLTSLQSEDSAVYYCARRRDGNYGFTYWGQGTLVTVSA

>d1figl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 1F7 (mouse), kappa L chain}

ENVLTQSPAIMSASPGEKVTMACRASSSVSSTYLHWYQQKSGASPKLLIYSTSNLASGVPARFSGSGSGTSYSLTISSVEAEDAATYYCQQYSGYPLTFGAGTKLELKR

>d1frgh1 b.1.1.1 (H:218-336) Immunoglobulin (variable domains of L and H chains) {Fab 26/9 (mouse), kappa L chain}

EVLLVESGGDLVKPGGFLKLSCAASGFTFSSFGMSWVRHTPDKRLEWVATISNGGGYTYYQDSVKGRFTISRDNAKNTLFLEMTSLKSEDAGLYYCARRERYDEKGFAYWGRGTLVTVS

>d1frgl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 26/9 (mouse), kappa L chain}

DIVMTQSPSSLTVTAGEKVTMSCKSSQSLFNSGKRKNFLTWYHQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTITSVQAEDLAIYYCQNDYSHPLTFGAGTKLELK

>d1a2ya\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3 (mouse), kappa L chain}

DIVLTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYYTTTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPRTFGGGTKLEIK

>d1a2yb\_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3 (mouse), kappa L chain}

QVQLQESGPGLVAPSQSLSITCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWGDGNTDYNSALKSRLSISKDNSKSQVFLKMNSLHTDDTARYYCARERDYRLDYWGQGTTLTVSS

>d1a7ql\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3 (mouse), kappa L chain}

DIVLTQSPASLSASVGETVTITCRAGGNTHNYLAWYQQKQGKSPQLLVYYTTTLAAGVPSRFSGSGSGTQYSLKINSLQPDDFGSYYCQHFWSTPRSFGGGTKLEI

>d1cica1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-idiotope (D1.3) Fab E225, (mouse), kappa L chain}

DIVMTQSHKFMSTSVGDRVSITCKASQDVRIAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCQHCGSYPFTFGSGTKLEIK

>d1cicb1 b.1.1.1 (B:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-idiotope (D1.3) Fab E225, (mouse), kappa L chain}

QVQLQQPGSELVRPGASVKLSCKASGYTFTNYWMHWVKQRPGQGLEWIGNIYPGSGDSNYDEKFKSKATLTVDTSSSTAYMQLSGLTSEDSAVYYCARGLAFYFDHWGQGTTLTVSS

>d1jhlh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv D11.15 (mouse), kappa L chain}

QVQLQQSGAELVRPGASVKLSCKASGYTFISYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQKFKDKATLTVDKSSSTAYMQLSSPTSEDSAVYYCTRDDNYGAMDYWGQGTTVTV

>d1jhll\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv D11.15 (mouse), kappa L chain}

DIELTQSPSYLVASPGETITINCRASKSISKSLAWYQEKPGKTNNLLIYSGSTLQSGIPSRFSGSGSGTDFTLTISSLEPEDFAMYICQQHNEYPWTFGGGTKLEIKR

>d1bqlh1 b.1.1.1 (H:2-116) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-5 (mouse), kappa L chain}

VQLQQSGAELMKPGASVKISCKASGYTFSDYWIEWVKQRPGHGLEWIGEILPGSGSTNYHERFKGKATFTADTSSSTAYMQLNSLTSEDSGVYYCLHGNYDFDGWGQGTTLTVSS

>d1bqll1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-5 (mouse), kappa L chain}

DIVLTQSPAIMSASPGEKVTMTCSASSSVNYMYWYQQKSGTSPKRWIYDTSKLASGVPVRFSGSGSGTSYSLTISSMETEDAATYYCQQWGRNPTFGGGTKLEIKR

>d1ic7h\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-10 (mouse), kappa L chain}

DVQLQESGPSLVKPSQTLSLTCSVTGDSITSAYWSWIRKFPGNRLEYMGYVSYSGSTYYNPSLKSRISITRDTSKNQYYLDLNSVTTEDTATYYCANWAGDYWGQGTLVTVSAA

>d2jelh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab JE142 (mouse), kappa L chain}

QVQLAQSGPELVRPGVSVKISCKGSGYTFTTYAMHWVKQSHAKSLEWIGLISTYSGYTNYNQKFKGKATMTVDKSSSTAYMELARLTSEDSAIYYCARVMGEQYFDVWGAGTTVIVSS

>d1ncbh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab NC41 (mouse), kappa L chain}

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLEWMGWINTNTGEPTYGEEFKGRFAFSLETSASTANLQINNLKNEDKATFFCARGEDNFGSLSDYWGQGTTLTVSS

>d1ncbl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab NC41 (mouse), kappa L chain}

DIVMTQSPKFMSTSVGDRVTITCKASQDVSTAVVWYQQKPGQSPKLLIYWASTRHIGVPDRFAGSGSGTDYTLTISSVQAEDLALYYCQQHYSPPWTFGGGTKLEIKR

>d1forh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 17-Ia (mouse), kappa L chain}

QGQLQQSGAELVRPGSSVKISCKASGYAFSSFWVNWVKQRPGQGLEWIGQIYPGDGDNKYNGKFKGKATLTADKSSTTAYMQLYSLTSEDSAVYFCARSGNYPYAMDYWGQGTSVTVSSA

>d1forl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 17-Ia (mouse), kappa L chain}

QIVLTQSPAIMSAFPGEKVTITCSATSSVNYMHWFQQKPGTSPKLWIYSSSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPITFGSGTKLEIKR

>d1knoa1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Fab CNJ206 (mouse), kappa L chain}

QIQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYAASTLDSGVPKRFSGSRSGSDYSLTISSLESEDFADYYCLQYASSPYTFGGGTKLEILR

>d1knob1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Fab CNJ206 (mouse), kappa L chain}

DVKLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTIYYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAMYYCARGDYYGSRGAYWGQGTLVTVSA

>d1eapb1 b.1.1.1 (B:1-124) Immunoglobulin (variable domains of L and H chains) {Fab 17E8 (mouse), kappa L chain}

EVQLQESGTELVKPGASVKISCKASGYISTDHAIHWVKQRPEQGLEWIGYISPGNGDIKYNEKFKVKATLTADQSSSTAYMQLNSLTSEDSAVYFCKRSYYGSSYVDYWGQGTTLTVSS

>d1mrdh1 b.1.1.1 (H:2-115) Immunoglobulin (variable domains of L and H chains) {Fab Jel 103 (mouse), kappa L chain}

VQLQQSGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGEIDPSDSYTNYNQKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYYCANLRGYFDYWGQGTTLTVSSAK

>d1fbih1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab F9.13.7 (mouse), kappa L chain}

QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQGPGQGLEWIGEIDPSDSYPNYNEKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCASLYYYGTSYGVLDYWGQGTSVTVS

>d1fbil1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab F9.13.7 (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQKKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTIRNLEQEDIATYFCQQGYTLPYTFGGGTKLEIK

>d1rmfh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab R6.5 (mouse), kappa L chain}

QVQLQQSGPELVRPGVSVKISCKGSGYTFIDYAIHWVKESHAKSLEWIGVISAYSGDTNYNQKFKGKATMTVDKSSNTAYLELARLTSEDSAIYYCARGGWLLLSFDYWGQGTTLTVSS

>d1rmfl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab R6.5 (mouse), kappa L chain}

DVVMTQSPLSLPVSLGDQASISCRSSQSLVHSNGNNYLHWYLQKSGQAPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPLTFGGGTKLEIK

>d1fpth1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab C3, neutralizing type 1 poliovirus, (mouse), kappa L chain}

QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIQWIKQRPGQGLEWIGVINPGSGGTDYNANFKGKATLTADKSSSIVYMQLSSLTSDDSAVYFCARDFYDYDVGFDYWGQGTTLTVSS

>d1fptl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab C3, neutralizing type 1 poliovirus, (mouse), kappa L chain}

DVVMTQTPLSLPVSLGDQASISCSSSQSLVHSNGKTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTYFTLKISRVEAEDLGVYFCSQSTHVPYTFGGGTKLEIKR

>d1ikfh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and H chains) {Fab, anti-cyclosporin A, (mouse), kappa L chain}

EVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQNSEKRLEWVAFISNGGGSAFYADIVKGRFTISRDNAKNTLYLQMSRLKSEDTAMYYCTRHTLYDTLYGNYPVWFADWGQGTLVTVSA

>d1ikfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab, anti-cyclosporin A, (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTISCRASQDISTYLNWYQQKPDGTVKLLIFYTSRLRSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGSRIPPTFGGGTKLEIL

>d1lmka1 b.1.1.1 (A:2-127) Immunoglobulin (variable domains of L and H chains) {scFv dimer (L5MK16 diabody), based on: (mouse), kappa L chain}

VQLQQSGTELMKPGRSLKISCKTTGYIFSNYWIEWVKQRPGHGLEWIGKILPGGGSNTYNDKFKGKATFTADTSSNIAYMQLSSLTSEDSAVYYCARGEDYYAYWYVLDYWGQGTTVTVSSGGGGS

>d1lmka2 b.1.1.1 (A:201-312) Immunoglobulin (variable domains of L and H chains) {scFv dimer (L5MK16 diabody), based on: (mouse), kappa L chain}

DIELTQSPLSLPVSLGDQASISCRSSQSLVHSNGNTSLHWYLKKPGQSPKLLIYKVSTRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPFTFGSGTKLELK

>d1nqba2 b.1.1.1 (A:121-233) Immunoglobulin (variable domains of L and H chains) {scFv trivalent antibody, based on: (mouse), kappa L chain}

DIELTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLEIKR

>d1igch1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab MoPC21 (mouse), kappa L chain}

DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTGMYYCARWGNYPYYAMDYWGQGTSVTVS

>d1igcl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab MoPC21 (mouse), kappa L chain}

NIVMTQSPKSMSMSVGERVTLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQGNSYPYTFGGGTKLEIKR

>d1ibgh1 b.1.1.1 (H:2-113) Immunoglobulin (variable domains of L and H chains) {Fab 40-50 (mouse), kappa L chain}

VHLVQSGPGLVAPSQSLSITCTVSGFSLTTYGVHWFRQPPGKGLEWLGLIWAGGNTDYNSALMSRLSINKDNSKSQVFLKMNSLQADDTAMYYCARFRFASYYDYAVDYWGQGTSVTVSS

>d1ibgl1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and H chains) {Fab 40-50 (mouse), kappa L chain}

IVLTQSPASLAVSLGQRATISCRASKSVSTSGYSHIHWYQQKPGQPPKLLIYLASILESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSREYPLTFGAGTELELK

>d1mlbb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and H chains) {Fab D44.1 (mouse), kappa L chain}

QVQLQESGAEVMKPGASVKISCKATGYTFSTYWIEWVKQRPGHGLEWIGEILPGSGSTYYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARGDGNYGYWGQGTTLTVSSAS

>d1a14h\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab NC10 (mouse), kappa L chain}

QVQLQQSGAELVKPGASVRMSCKASGYTFTNYNMYWVKQSPGQGLEWIGIFYPGNGDTSYNQKFKDKATLTADKSSNTAYMQLSSLTSEDSAVYYCARSGGSYRYDGGFDYWGQGTTVTV

>d1a14l\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab NC10 (mouse), kappa L chain}

DIELTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTAA

>d1nmbl\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab NC10 (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTKLEIRRA

>d1bm3h1 b.1.1.1 (H:1-125) Immunoglobulin (variable domains of L and H chains) {Anti-integrin Fab OPG2 (mouse), kappa L chain}

EVQLVQSGGGLVNPGRSLKLSCAASGFTFSSYGMSWVRQTPEKRLEWVAAISGGGTYIHYPDSVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCTRHPFYRYDGGNYYAMDHWGQGTSVTVSA

>d1nsnh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab N10 (mouse), kappa L chain}

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYITYSGTTSYNPSLKSRISISRDTSKNQFFMQLNSVTTEDTGTFYCTRGNGDWGQGTTLTVSSA

>d1nsnl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab N10 (mouse), kappa L chain}

DIVLTQSPSSLAVSLGQRATISCRASQSVSTSSFRYMHWYQQKPGQPPRLLIKYASNLESGVPARFSGSGSGTDFTLNIHPVEEEDTATYYCQHSWEIPYTFGGGTKLEIK

>d1iaih1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab 730.1.4 (mouse), kappa L chain}

QIQLVQSGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMAWINTYTGEPTYADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARDGYYENYYAMDYWGQGTSVTVSS

>d1iail1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 730.1.4 (mouse), kappa L chain}

DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYQYTGVPDRFTGSGSRTDFTFTINSVQAEDLAVYYCHQHYSTPFTFGSGTKLEIKR

>d1iaii1 b.1.1.1 (I:1-121) Immunoglobulin (variable domains of L and H chains) {Fab 409.5.3 (mouse), kappa L chain}

EVKLQESGGGLVQPGGSMKLSCVASGFTFNNYWMSWVRQSPEKGLEWVAEIRLNSDNFATHYAESVKGKFIISRDDSKSRLYLQMNSLRAEDTGIYYCVLRPLFYYAVDYWGQGTSVTVSS

>d1iaim1 b.1.1.1 (M:1-109) Immunoglobulin (variable domains of L and H chains) {Fab 409.5.3 (mouse), kappa L chain}

DIQLTQSPAFMAASPGEKVTITCSVSSSISSSNLHWYQQKSETSPKPWIYGTSNLASGVPVRFSGSGSGTSYSLTISSMEAEDAATYYCQQWNSYPYTFGGGTKLEIKR

>d1plgh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Polysialic acid-binding Fab (mouse), kappa L chain}

QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKYNEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYWGQGTSVTVSS

>d1plgl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Polysialic acid-binding Fab (mouse), kappa L chain}

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLYWYLQKPGQSPKPLIYRVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCFQGTHVPYTFGGGTRLEIK

>d1aj7h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 48G7 (mouse/human), kappa L chain}

QVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCASYYGIYWGQGTTLTVSSA

>d1gafh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 48G7 (mouse/human), kappa L chain}

QVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANVDTKYDPKFQDKATITADTSSKTTYLQLSSLTSEDTAVYYCASYYGIYWGQGTTLTVSS

>d1gafl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab 48G7 (mouse/human), kappa L chain}

DIQMTQSPSSLSASLGERVSLTCRASQEINGYLGWLQQKPDGTIKRLIYAASTLHSGVPKRFSGSRSGSDYSLTISSLESEDFADYYCLQYASYPRTFGGGTKVEIKRT

>d1vgeh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab TR1.9 (mouse/human), kappa L chain}

QVKLLEQSGAEVKKPGASVKVSCKASGYSFTSYGLHWVRQAPGQRLEWMGWISAGTGNTKYSQKFRGRVTFTRDTSATTAYMGLSSLRPEDTAVYYCARDPYGGGKSEFDYWGQGTLVTVSS

>d1vgel1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TR1.9 (mouse/human), kappa L chain}

ELVMTQSPSSLSASVGDRVNIACRASQGISSALAWYQQKPGKAPRLLIYDASNLESGVPSRFSGSGSGTDFTLTISSLQPEDFAIYYCQQFNSYPLTFGGGTKVEIK

>d1yuhb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and H chains) {Fab anti-nitrophenol (mouse), lambda L chain}

QVQFQQSGAELVKPGASVKLSCKASGYTFTSYLMHWIKQRPGRGLEWIGRIDPNNVVTKFNEKFKSKATLTVDKPSSTAYMELSSLTSEDSAVYYCARYAYCRPMDYWGQGTTVTVSS

>d1ucbh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab CBR96 (mouse/human), kappa L chain}

EVNLVESGGGLVQPGGSLKVSCVTSGFTFSDYYMYWVRQTPEKRLEWVAYISQGGDITDYPDTVKGRFTISRDNAKNSLYLQMSRLKSEDTAMYYCARGLDDGAWFAYWGQGTLVTVSV

>d1ucbl1 b.1.1.1 (L:4-108) Immunoglobulin (variable domains of L and H chains) {Fab CBR96 (mouse/human), kappa L chain}

MTQIPVSLPVSLGDQASISCRSSQIIVHNNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFTFGSGTKLEIKR

>d1dvfc\_ b.1.1.1 (C:) Immunoglobulin (variable domains of L and H chains) {Fv E5.2 (mouse), kappa L chain}

DIQLTQSPSSLSASLGDRVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGGGTKLEIK

>d1dvfd\_ b.1.1.1 (D:) Immunoglobulin (variable domains of L and H chains) {Fv E5.2 (mouse), kappa L chain}

QVQLQQSGTELVKSGASVKLSCTASGFNIKDTHMNWVKQRPEQGLEWIGRIDPANGNIQYDPKFRGKATITADTSSNTAYLQLSLTSEDTAVYYCATKVIYYQGRGAMDYWGQGTTLTVS

>d1ghfh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab GH1002 (mouse), kappa L chain}

VQLQQSGPELKKPGETVKISCKLWYTFTDYGMNWVKQAPGKGLKWMGWIQTNTEEPTYGAEFKGRFAFSLETSAFTAYKQINNLKNEDMATYFCARVEAGFDYWAQGTTLTVSS

>d1ghfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab GH1002 (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTISCRESQDISNSLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGTGTDYSLTISNLEQEDFATYFCQQGNTLPYTFGGGTKLEIK

>d1nldh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 1583, against an epitope of gp41 of HIV-1, (mouse), kappa L chain}

QVKLQQSGPGLVQPSQSLSITCTVSGFSLTCYGVHWVRQSPGKGLEWLGVIWSGGDTDYNAAFISRLSITKDNSKSQVFFKMNSLQPNDRAIYYCARRGGDFWGQGTTVTVS

>d1nldl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 1583, against an epitope of gp41 of HIV-1, (mouse), kappa L chain}

DVVMTQTPLTLSVTIGQPASISCKSSQSLLDSDGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHFPRTFGGGTKLEIK

>d1kelh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab 28B4 (mouse), kappa L chain}

EVKLVESGGGLGQPGGSLRLSCATSGFTFTDYYFNWARQPPGKALEWLGFIRNKAKGYTTEYSASVKGRFTISRDNSQGILYLQMNTLRAEDSATYYCARWGSYAMDYWGQGTSV

>d1kell1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 28B4 (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASISCRFSQSIVHSNGNTYLEWYLQKSGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPRTFGGGTKLEIK

>d1osph1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}

EVQLQESGPSLVKPSQTLSLTCSVTGEPITSGFWDWIRKFPGNKLEFMGYIRYGGGTYYNPSLKSPISITRDTSKNHYYLQLNSVVTEDTATYYCARSRDYYGSSGFAFWGEGTLVTVSA

>d1ospl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}

DIQMSQSSSSFSVSLGDRVTITCKASEDIYSRLAWYQQKPGNAPRLLISGATSLETWVPSRFSGSDSGKDYTLSITSLQTEDVATYFCQQYWSPPPTFGGGTKLEIK

>d1fj1a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab LA-2 (mouse), kappa L chain}

DIQMTQSPSSLSATLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGNPSRFSGSGSGRDYSFSISNLEAEDIAIYYCLQYDNLQRTFGGGTKVEIK

>d1fj1b1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Fab LA-2 (mouse), kappa L chain}

QIQLVQSGPELKKPGETVKISCKASGYTFTDYSMYWVKQAPGKGLKRMGWINTETGEPTYADDFKGRFALSLDTSASTAYLHISNLKNEDTATYFCARGLDSWGQGTSVTVSSA

>d1cloh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (mouse), kappa L chain}

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKSQSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLTVSS

>d1clol1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (mouse), kappa L chain}

QTVLSQSPAILSASPGEKVTMTCRASSSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQHWSSKPPTFGGGTKLEIK

>d1ad0a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (engineered human construct), kappa L chain}

QTVLTQSPSSLSVSVGDRVTITCRASSSVTYIHWYQQKPGLAPKSLIYATSNLASGVPSRFSGSGSGTDYTFTISSLQPEDIATYYCQHWSSKPPTFGQGTKVEVKR

>d1ad0b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (engineered human construct), kappa L chain}

EVQLLESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKGLEWLGFIGNKANGYTTEYSASVKGRFTISRDKSKSTLYLQMNTLQAEDSAIYYCTRDRGLRFYFDYWGQGTLVTVSS

>d1mimh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab CHI621 (mouse), kappa L chain}

QLQQSGTVLARPGASVKMSCKASGYSFTRYWMHWIKQRPGQGLEWIGAIYPGNSDTSYNQKFEGKAKLTAVTSASTAYMELSSLTHEDSAVYYCSRDYGYYFDFWGQGTTLTVSS

>d1miml1 b.1.1.1 (L:1-105) Immunoglobulin (variable domains of L and H chains) {Fab CHI621 (mouse), kappa L chain}

QIVSTQSPAIMSASPGEKVTMTCSASSSRSYMQWYQQKPGTSPKRWIYDTSKLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQRSSYTFGGGTKLEIKR

>d1afvh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 25.3 (mouse), kappa L chain}

QVQLQQPGSVLVRPGASVKLSCKASGYTFTSSWIHWAKQRPGQGLEWIGEIHPNSGNTNYNEKFKGKATLTVDTSSSTAYVDLSSLTSEDSAVYYCARWRYGSPYYFDYWGQGTTLTVSS

>d1afvl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 25.3 (mouse), kappa L chain}

DIVLTQSPASLAVSLGQRATISCRASESVDNYGISFMNWFQQKPGQPPKLLIYAASNLGSGVPARFSGSGSGTDFSLNIHPMEEEDTAMYFCQQSKEVPLTFGAGTKVELKR

>d2mpah1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Bactericidal Fab MN12H2, (mouse), kappa L chain}

EVNLQQSGTVLARPGASVRMSCKASGYSFTSYWLHWIKQRPGQGLEWIGGIYPGNRDTRYTQRFKDKAKLTAVTSANTAYMELSSLTNEDSAVYYCSIIYFDYADFIMDYWGQGTTVTVSS

>d2mpal1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Bactericidal Fab MN12H2, (mouse), kappa L chain}

DIVMTQTPLSLPVSLGDKASISCRSSQALVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVFFCSQSTHVPRTFGGGTKLEIK

>d1qkzh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab MN14C11.6 (mouse), kappa L chain}

DVKLVESGGGLVKPGRSLKLSCAASGFTFSDYYMFWVRQTPEQRLEWVATISDGGAYTYYPDSVKGRFTISRDNAKNNLYLQMNSLKSEDTGMYYCARDPLEYYGMDYWGQGTSVAVSS

>d1qkzl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab MN14C11.6 (mouse), kappa L chain}

NIVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYTVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHFPTFGGGTKLEIK

>d1pskh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab against a ganglioside (mouse), kappa L chain}

EVQLQQSGPELVKPGASVKISCKTSGYTFTKYTMHWVKQSHGKSLEWIGDINPNNGGTNYNQKFKGTATLTVHKSSTTAYMELRSLTSEDSAVYYCTSKSFDYWGQGTTLTVSS

>d1pskl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab against a ganglioside (mouse), kappa L chain}

QIVLTQSPAIMSASPGEKVTITCSASSSVSNIHWFQQKPGTFPKLWIYSTSTLASGVPGRFSGSGSGTSYSLTISRMGAEDAATYYCQQRSGYPFTFGSGTKLEIK

>d1yejh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.3 (mouse), kappa L chain}

EMQLQQSGAELLRPGTSVKLSCKTSGYIFTSYWIHWVKQRSGQGLEWIARIYPGTGSTYYNEKFKGKATLTADKSSSTAYMQLSTLKSEDSAVYFCTRWGFIPVREDYVMDYWGQGTLVTVSS

>d1yejl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab D2.3 (mouse), kappa L chain}

DIVMTQSPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLLQRPGQSPKRLIHLVSKLDSGVPDRITGSGSGTDFTLKISRVEAADLGVYYCVQGTHFPYTFGGGTKLEIL

>d1yedb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.4 (mouse), kappa L chain}

AVKLQQSGPELVRPGTSVKLSCKTSGYIFTSYWIHWLKQSSGQGLEWIARIYPGTGGTYYNEKFKGKATLTADKSSSTAYMQLSSLKSEDSAVYFCTRWGFTTVRENYYAMDYWGQGTLVTVSS

>d1yeeh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.5 (mouse), kappa L chain}

EVKLQESGAELVRPGASVKLSCKTSGYIFTSYWIHWVKQRAAAGLEWIARIYPGTGSSYYNVKFKGKATLTADKSSSTAYMQLSSLKSDDSAVYFCVRWGFIPVREDYVLDYWGQGTLVTVSS

>d1cfvh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv 4155 (mouse), kappa L chain}

QVQLQESGGGLVNLGGSMTLSCVASGFTFNTYYMSWVRQTPEKTLELVAAINSDGEPIYYPDTLKGRVTISRDNAKKTLYLQMSSLNFEDTALYYCARLNYAVYGMDYWGQGTTVTVSS

>d1cfvl\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv 4155 (mouse), kappa L chain}

DIELTQSPPSLPVSLGDQVSISCRSSQSLVSNNRRNYLHWYLQKPGQSPKLVIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVAAEDLGLYFCSQSSHVPLTFGSGTKLEIKR

>d1hyxh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 6D9 (mouse), kappa L chain}

EVKLLESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVRQTPEKRLEWVVSISSGGSIYYLDSVKGRFTVSRDNARNILYLQMTSLRSEDTAMYFCARVSHYDGSRDWYFDVWGAGTSVTVSS

>d1hyxl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 6D9 (mouse), kappa L chain}

ELVMTQTPLSLPVSLGDQASISCRSSQTIVHSNGDTYLDWFLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPPTFGGGTKLEIK

>d2hrph1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab F11.2.32 (mouse), kappa L chain}

DVQLVESGGGLVQPGGSRKLSCAASGFTFMRFGMHWVRQAPEKGLEWVAYISSGSSTIYYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTALYYCARSGGIERYDGTYYVMDYWGQGTSVTVSS

>d2hrpl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab F11.2.32 (mouse), kappa L chain}

DTVLTQSPASLAVSLGQRATISCRASESVDYYGKSFMNWFQQKPGQPPKLLIYAASNQGSGVPARFSGSGSGTDFSLHIHPMEEDDSAMYFCQQSKEVPWTFGGGTKLEIK

>d2ap2a\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {scFv C219, (mouse sequence-based), kappa L chain}

FVRDIVMTQSPSSLTVTAGEKVTMSCKSSQSLLNSGNQKNYLTWYQQKPGQPPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEP

>d2ap2b\_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {scFv C219, (mouse sequence-based), kappa L chain}

EVQLQQSGAELVRPGASVKLSCTASGFNIKDDFMHWVKQRPEQGLEWIGRIDPANDNTKYAPKFQDKATIIADTSSNTAYLQLSSLTSEDTAVYYCARREVYSYYSPLDVWGAGTTVTVPSG

>d1nfde1 b.1.1.1 (E:2-107) Immunoglobulin (variable domains of L and H chains) {Fab H57 (hamster), lambda L chain}

YELIQPSSASVTVGETVKITCSGDQLPKNFAYWFQQKSDKNILLLIYMDNKRPSGIPERFSGSTSGTTATLTISGAQPEDEAAYYCLSSYGDNNDLVFGSGTQLTVLR

>d1nfdf1 b.1.1.1 (F:1-114) Immunoglobulin (variable domains of L and H chains) {Fab H57 (hamster), lambda L chain}

EVYLVESGGDLVQPGSSLKVSCAASGFTFSDFWMYWVRQAPGKGLEWVGRIKNIPNNYATEYADSVRGRFTISRDDSRNSIYLQMNRLRVDDTAIYYCTRAGRFDHFDYWGQGTMVTVSSA

>d2h1ph1 b.1.1.1 (H:301-420) Immunoglobulin (variable domains of L and H chains) {Fab 2H1 (mouse), kappa L chain}

DVKLVESGGGLVKLGGSLKLSCAASGFTFSSYFLSWVRQTPEKRLELVATINSNGDKTYHPDTMKGRFTISRDNAKNTLYLQMSSLKSEDTALYYCARRDSSASLYFDYWGQGTTLTVSS

>d2h1pl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 2H1 (mouse), kappa L chain}

DVVMTQTPLSLPVSLGDPASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDKFSGSGSGTDFTLKISRVEAEDQGVYFCSQSTHVPWTFGGGTKLEIKR

>d1aqkh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}

EVQLVESGGGVVQPGRSLRLSCAASGFTFNNYAIHWVRQAPGKGLEWVAFISYDGSKNYYADSVKGRFTISRDNSKNTLFLQMNSLRPEDTAIYYCARVLFQQLVLYAPFDIWGQGTMVTVSS

>d1aqkl1 b.1.1.1 (L:1-111) Immunoglobulin (variable domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}

ENVLTQPPSVSGAPGQRVTISCTGSNSNIGAGFTVHWYQHLPGTAPKLLIFANTNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDSSLSARFGGGTRLTVLG

>d1axsa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Oxy-cope catalytic Fab az-28, chimeric (mouse V domains/human C1 domains)}

ELVLTQSPSSMYASLGERVTITCKASQDINSYLNWFQQKPGKSPKTLIYRTNRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGSGTKLEIK

>d1d5ih1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Oxy-cope catalytic Fab az-28, chimeric (mouse V domains/human C1 domains)}

QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIEWVKQRPGHGLEWIGEILPGSGSTNYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCARGHSYYFYDGDYWGQGTSVTVSS

>d1d5il1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Oxy-cope catalytic Fab az-28, chimeric (mouse V domains/human C1 domains)}

DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSLEYEDMGIYYCLQYDEFPYTFGSGTKLEIK

>d1ar1c\_ b.1.1.1 (C:) Immunoglobulin (variable domains of L and H chains) {Fv against Paracoccus denitrificans cytochrome c oxidase (mouse), kappa L chain}

EVKLQESGGDLVQPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVASINNGGGRTYYPDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYYCVRHEYYYAMDYWGQGTTVTVSS

>d1ar1d\_ b.1.1.1 (D:) Immunoglobulin (variable domains of L and H chains) {Fv against Paracoccus denitrificans cytochrome c oxidase (mouse), kappa L chain}

DIELTQTPVSLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQFLVYNAKTLGEGVPSRFSGSGSGTQFSLKINSLLPEDFGSYYCQHHYGTPPLTFGGGTKLEIK

>d1ae6h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab CTM01 (mouse), kappa L chain}

QIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWMKQKPGQGLEWIGWIDPGSGNTKYNEKFKGKATLTVDTSSSTAYMQLSSLTSEDTAVYFCAREKTTYYYAMDYWGQGTSVTVSAA

>d1ae6l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and H chains) {Fab CTM01 (mouse), kappa L chain}

DIVMTQAAPSVPVTPGESLSISCRSSKSLLHSNGDTFLYWFLQRPGQSPQLLIYRMSNLASGVPDRFSGSGSGTAFTLRVSRVEAEDVGVYYCMQHLEYPFTFGAGTKLELK

>d1ad9a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab CTM01 (human construct), kappa L chain}

DIQMTQSPSTLSASVGDRVTITCRSSKSLLHSNGDTFLYWFQQKPGKAPKLLMYRMSNLASGVPSRFSGSGSGTEFTLTISSLQPDDFATYYCMQHLEYPFTFGQGTKVEVKR

>d1ad9b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab CTM01 (human construct), kappa L chain}

EIQLVQSGAEVKKPGSSVKVSCKASGYTFTDYYINWMRQAPGQGLEWIGWIDPGSGNTKYNEKFKGRATLTVDTSTNTAYMELSSLRSEDTAFYFCAREKTTYYYAMDYWGQGTLVTVSS

>d1fgnh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-human tissue factor Fab 5G9 (mouse), kappa L chain}

EIQLQQSGAELVRPGALVKLSCKASGFNIKDYYMHWVKQRPEQGLEWIGLIDPENGNTIYDPKFQGKASITADTSSNTAYLQLSSLTSEDTAVYYCARDNSYYFDYWGQGTTLTVSS

>d1fgnl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Anti-human tissue factor Fab 5G9 (mouse), kappa L chain}

DIKMTQSPSSMYASLGERVTITCKASQDIRKYLNWYQQKPWKSPKTLIYYATSLADGVPSRFSGSGSGQDYSLTISSLESDDTATYYCLQHGESPYTFGGGTKLEINR

>d1jpth1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-human tissue humanised factor Fab D3H44}

EVQLVESGGGLVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGNTIYDPKFQDRATISADNSKNTAYLQMNSLRAEDTAVYYCARDTAAYFDYWGQGTLVTVSS

>d1jptl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-human tissue humanised factor Fab D3H44}

DIQMTQSPSSLSASVGDRVTITCRASRDIKSYLNWYQQKPGKAPKVLIYYATSLAEGVPSRFSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPWTFGQGTKVEIK

>d1jrhh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A6 (mouse), kappa L chain}

AVKLQESGPGILKPSQTLSLTCSFSGFSLTTYGMGVGWIRQSSGKGLEWLAHIWWDDDKYYNPSLKSRLTISKDTSRNQVFLKITSVATADTATYYCARRAPFYGNHAMDYWGQGTTVTVSS

>d1jrhl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A6 (mouse), kappa L chain}

SVEMTQSPSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPRLLISGATSLETEVPSRFSGSGSGKDYTLSITSLQTEDVATYYCQQYWSTWTFGGGTKLEIK

>d1gpoh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab M41 (artificial design)}

EVKLQESGPSLVKPSQTLSLTCSVTGDSITSDFWSWIRQFPGNRLEYMGFVQYSGETAYNPSLKSRISITRDTSKNQYYLDLNSVTTEDTAVYYCANWHGDYWGQGTTVTVSS

>d1gpol1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab M41 (artificial design)}

DIELTQSPATLSVTPGNSVSISCRASQSLVNEDGNTYLFWYQQKSHESPRLLIKYASQSISGIPSRFSGSGSGTDFTLSINSVETEDLAVYFCQQITDWPFTFGGGTKLEIK

>d1kb5h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab Desire-1 (mouse), kappa L chain}

EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSNGKSLEWIGNIDPYYGGISYNQKFKGRATLTVDKSSSTAYMQLKSLTSEDSAVYYCARSRTDLYYFDYWGQGTTLTVSS

>d1kb5l1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab Desire-1 (mouse), kappa L chain}

DIQMTQSPASLSASVGETVTITCRASKNIYSYLAWYQQKQGKSPQLLVYNAKTLGEGVPSRFSGSGSGTQFSLKINSLQPEDFGSYYCQHHYGTPYTFGGGTKLEIKR

>d1a4jb1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Diels alder catalytic Fab (mouse), kappa L chain}

QVQLLESGPELKKPGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTYADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCVQAERLRRTFDYWGAGTTVTVSS

>d1a4ka1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and H chains) {Diels alder catalytic Fab (mouse), kappa L chain}

ELVMTQTPLSLPVSLGDQASISCRSSQSLLHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQVTHVPPTFGGGTKLEIKRTVAA

>d1c1eh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Diels alder catalytic Fab 1E9 (mouse), kappa L chain}

QIQLVQSGPELKKPGETVKISCKASGYMFTNYGMNWVKQAPGKALKLMGWINPYTGESTFADDFKGRFAFFLETSATTAYLQINNLKNEDMATYFCARGTTIVRAMDYWGQGTSLTVSSAKTTPP

>d1c1el1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Diels alder catalytic Fab 1E9 (mouse), kappa L chain}

ELVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKFLIYKVSNRFSGVPDRFGGSGSGTDFILKISRVEAEDLGVYFCFQSTHFFPTFGGGTKLEIKSADAA

>d1a3lh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Diels alder catalytic Fab 13G5 (mouse), kappa L chain}

EVQLEESGPELVRPGTSVKISCKASGYTFTNYWLGWVKQRPGHGFEWIGDIYPGGVYTTNNEKFRGKAILTADTSSSTAYMQLSSLTSEDSAVYFCARAGGYYTGGDYWGQGTSVTVSS

>d1a3ll1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Diels alder catalytic Fab 13G5 (mouse), kappa L chain}

DIVLTQAAFSNPVTLGASASISCRSSKSLLNSNGIIHMYWYLQKPGQSPQLLIYQMSKLASGAPDRFSGSGSGTDFTLRISRVEAEDVGVYYCAQNLELPYTFGGGTKLEIK

>d1ay1h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab TP7 (mouse), kappa L chain}

EVQLQESGPGLVKPYQSLSLSCTVTGYSITSDYAWNWIRQFPGNKLEWMGYITYSGTTDYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCARYYYGYWYFDVWGQGTTLTVSS

>d1ay1l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TP7 (mouse), kappa L chain}

DIQMTQSPAIMSASPGEKVTMTCSASSSVSYMYWYQQKPGSSPRLLIYDSTNLASGVPVRFSGSGSGTSYSLTISRMEAEDAATYYCQQWSTYPLTFGAGTKLELK

>d1dsfh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anticancer Fv B1 (mouse)}

QLVESGGGLVKPGGSLKLSCAASGFIFSDNYMYWVRQTPEKCLEWVATISDGGTYIDYSDSVKGRFTISRDNAKNNLYLQMSSLRSEDTGMYYCGRSPIYYDYAPFTYWGQGTLVTVSA

>d1dsfl\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anticancer Fv B1 (mouse)}

DVVMTQTPLSLPVSLGDQASISCRSSQNLVHSDGKTYLHWFLQKPGQSPTLLIYKVSNRFSGVPDRFSGSGSGTDFILKISRVEAEDLGVYFCSQSTHVPLTFGCGTKLELK

>d1a6ta1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab Mab1-IA (mouse), kappa L chain}

QSVLSQSPAILSASPGEKVIMTCSPSSSVSYMQWYQQKPGSSPKPWIYSTSNLASGVPGRFSGGGSGTSFSLTISGVEAEDAATYYCQQYSSHPLTFGGGTKLELK

>d1a6tb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab Mab1-IA (mouse), kappa L chain}

EVQLQQSGPDLVKPGASVKISCKASGYSFSTYYMHWVKQSHGKSLEWIGRVDPDNGGTSFNQKFKGKAILTVDKSSSTAYMELGSLTSEDSAVYYCARRDDYYFDFWGQGTSLTVSS

>d1a6wh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv B1-8 (mouse), lambda L chain}

QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGRIDPNSGGTKYNEKFKSKATLTVDKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWGQGTTVTVSS

>d1a6wl\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv B1-8 (mouse), lambda L chain}

AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTNNRAPGVPARFSGSLIGNKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLE

>d1g9mh1 b.1.1.1 (H:1-129) Immunoglobulin (variable domains of L and H chains) {HIV-1 neutralizing Fab 17B (human), kappa L chain}

QVQLLESGAEVKKPGSSVKVSCKASGDTFIRYSFTWVRQAPGQGLEWMGRIITILDVAHYAPHLQGRVTITADKSTSTVYLELRNLRSDDTAVYFCAGVYEGEADEGEYRNNGFLKHWGQGTLVTVTSA

>d1g9ml1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {HIV-1 neutralizing Fab 17B (human), kappa L chain}

ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPARFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWPPRYTFGQGTRLEIK

>d12e8h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 2E8 (mouse), kappa L chain}

EVQLQQSGAEVVRSGASVKLSCTASGFNIKDYYIHWVKQRPEKGLEWIGWIDPEIGDTEYVPKFQGKATMTADTSSNTAYLQLSSLTSEDTAVYYCNAGHDYDRGRFPYWGQGTLVTVSAA

>d12e8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 2E8 (mouse), kappa L chain}

DIVMTQSQKFMSTSVGDRVSITCKASQNVGTAVAWYQQKPGQSPKLMIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQSEDLADYFCQQYSSYPLTFGAGTKLELK

>d1adqh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {IgM rheumatoid factor Fab (human), lambda L chain}

EVQLVESGGGLVQPGRSLRLSCVTSGFTFDDYAMHWVRQSPGKGLEWVSGISWNTGTIIYADSVKGRFIISRDNAKNSLYLQMNSLRVEDTALYYCAKTRSYVVAAEYYFHYWGQGILVTVSS

>d1adql1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and H chains) {IgM rheumatoid factor Fab (human), lambda L chain}

YVLTQPPSVSVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVVYDDSDRPPGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDSSSDHAVFGGGTKLTVLG

>d2hmic1 b.1.1.1 (C:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 28 against HIV-1 RT (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTISCSASQDISSYLNWYQQKPEGTVKLLIYYTSSLHSGVPSAFSGSGSGTDYSLTISNLEPEDFATYYCQQYSKFPWTFGGGTKLEIK

>d2hmid1 b.1.1.1 (D:1-123) Immunoglobulin (variable domains of L and H chains) {Fab 28 against HIV-1 RT (mouse), kappa L chain}

QITLKESGPGIVQPSQPFRLTCTFSGFSLSTSGIGVTWIRQPSGKGLEWLATIWWDDDNRYNPSLKSRLTVSKDTSNNQAFLNMMTVETADTAIYYCAQSAITSVTDSAMDHWGQGTSVTVSS

>d1bvka\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Humanized anti-lysozyme Fv HuLys11 (mouse), kappa L chain}

DIQMTQSPSSLSASVGDRVTITCRASGNIHNYLAWYQQKPGKAPKLLIYYTTTLADGVPSRFSGSGSGTDYTFTISSLQPEDIATYYCQHFWSTPRTFGQGTKVEIKR

>d1bvkb\_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Humanized anti-lysozyme Fv HuLys11 (mouse), kappa L chain}

QVQLQESGPGLVRPSQTLSLTCTVSGFSLTGYGVNWVRQPPGRGLEWIGMIWGDGNTDYNSALKSRVTMLKDTSKNQFSLRLSSVTAADTAVYYCARERDYRLDYWGQGSLVTVSS

>d1a0qh1 b.1.1.1 (H:2-114) Immunoglobulin (variable domains of L and H chains) {Fab 29G11 (mouse), kappa L chain}

VQLQESDAELVKPGASVKISCKASGYTFTDHVIHWVKQKPEQGLEWIGYISPGNGDIKYNEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVYLCKRGYYGRSNVDYWGQGTTLTVSSA

>d1a0ql1 b.1.1.1 (L:2-108) Immunoglobulin (variable domains of L and H chains) {Fab 29G11 (mouse), kappa L chain}

IELTQSPSSLSASLGGKVTITCKASQDIKKYIGWYQHKPGKQPRLLIHYTSTLLPGIPSRFRGSGSGRDYSFSISNLEPEDIATYYCLQYYNLRTFGGGTKLEIKR

>d1fnsh1 b.1.1.1 (H:215-336) Immunoglobulin (variable domains of L and H chains) {Fab NMC-4 (mouse), kappa L chain}

QVQLKESGPGLVAPSQSLSITCTVSGFSLTDYGVDWVRQPPGKGLEWLGMIWGDGSTDYNSALKSRLSITKDNSKSQVFLKMNSLQTDDTARYYCVRDPADYGNYDYALDYWGQGTSVTVSS

>d1fnsl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab NMC-4 (mouse), kappa L chain}

DIQMTQSPSSLSASLGDRVTISCSASQDINKYLNWYQQKPDGAVKLLIFYTSSLHSGVPSRFSGSGSGTDYSLTISNLEPEDIATYYCQQYEKLPWTFGGGTKLEVK

>d1qfuh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Influenza virus hemagglutinin-neutralizing Fab (mouse), kappa L chain}

QVQLQQPGAELVRPGASVKLSCKASGYTLTTYWMNWFKQRPDQGLEWIGRIDPYDSETHYNQKFKDKAILTVDRSSSTAYMQLSSLTSEDSAVYYCTRFLQITTIIYGMDYWGQGTSVTVSS

>d1eo8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Influenza virus hemagglutinin-neutralizing Fab BH151 (mouse), kappa L chain}

QVQLQQSGAELMKPGPSVKISCKATGYSFSTYFIEWIRQRPGHGLEWIGEILPGSDNTNFNEKFKDRATFTADTPSNTAYMQLSSLTSEDSAVYYCARPTGRLWFSYWGQGTLVTVSA

>d1eo8l1 b.1.1.1 (L:1-106B) Immunoglobulin (variable domains of L and H chains) {Influenza virus hemagglutinin-neutralizing Fab BH151 (mouse), kappa L chain}

QIILTQSPAIMSASPGEKVTMTCSASSDISYMHWYQQKSDTSPKIWIYDTSKLASGVPARFSGSGSGTSYSLTISTMEAEDAATYYCHQRSSYPTFGGGTKLEIK

>d35c8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 5C8 (mouse), kappa L chain}

EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQKPEQGLEWIAQIDPANGNTKYDPKFQGKATITADTSSNTAYLHLSSLTSEDSAVYYCAADPPYYGHGDYWGQGTTLTVSS

>d35c8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 5C8 (mouse), kappa L chain}

DIVLTQSPAIMSASLGERVTMTCTASSSVSSSNLHWYQQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAATYYCHQYHRSPYTFGGGTKLEIK

>d1a5fh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Anti-E-selectin Fab (mouse), kappa L chain}

EVALQQSGAELVKPGASVKLSCAASGFTIKDAYMHWVKQKPEQGLEWIGRIDSGSSNTNYDPTFKGKATITADDSSNTAYLQMSSLTSEDTAVYYCARVGLSYWYAMDYWGQGTSVTVSS

>d1axth1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 33F12 (mouse), kappa L chain}

EVKLEESGGGLVQPGGSMKLSCVVSGLTFSRFWMSWVRQSPEKGLEWVAEIRLKSDNYATHYAESVKGKFTISRDDSKSRLYLQMNSLRTEDTGIYYCKIYFYSFSYWGQGTLVTVSA

>d1axtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 33F12 (mouse), kappa L chain}

ELVMTQTPLSLPVSLGDQASISCRSSQSLVHSYGNTFLNWYLQKSGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQGTHVPYTFGGGTKLEIK

>d1b2wh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Humanized and chimeric anti-gamma-interferon Fab}

EVQLVQSGGGVVQPGRSLKLSCLASGYIFTSSWINWVKQRPGRGLEWIGRIDPSDGEVHYNQDFKDRFTISRDKSKNTLYLQMNSLRPEDTAVYYCARGFLPWFADWGQGTLVTVSS

>d1b2wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Humanized and chimeric anti-gamma-interferon Fab}

DIQMTQSPSTLSASVGDRVTITCKASENVDTYVSWYQQKPGKAPKLLIYGASNRYTGVPSRFSGSGSGTDFTLTISSLQPDDFATYYCGQSYNYPFTFGQGTKVEVK

>d1b4jh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Humanized and chimeric anti-gamma-interferon Fab}

EVQLQQPGADLVMPGAPVKLSCLASGYIFTSSWINWVKQRPGRGLEWIGRIDPSDGEVHYNQDFKDKATLTVDKSSSTAYIQLNSLTSEDSAVYYCARGFLPWFADWGQGTLVTVSA

>d1b4jl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Humanized and chimeric anti-gamma-interferon Fab}

NIVMTQSPKSMYVSIGERVTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISSVQAEDLADYHCGQSYNYPFTFGSGTKLEIK

>d1bfoa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {CAMPATH-1G igg2b monoclonal fab (rat), kappa L chain}

DIKMTQSPSFLSASVGDRVTLNCKASQNIDKYLNWYQQKLGESPKLLIYNTNNLQTGIPSRFSGSGSGTDFTLTISSLQPEDVATYFCLQHISRPRTFGTGTKLELK

>d1bfob1 b.1.1.1 (B:1-121) Immunoglobulin (variable domains of L and H chains) {CAMPATH-1G igg2b monoclonal fab (rat), kappa L chain}

EVKLLESGGGLVQPGGSMRLSCAGSGFTFTDFYMNWIRQPAGKAPEWLGFIRDKAKGYTTEYNPSVKGRFTISRDNTQNMLYLQMNTLRAEDTATYYCAREGHTAAPFDYWGQGVMVTVSS

>d1ce1h1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Therapeutic CAMPATH-1H humanized fab (rat), kappa L chain}

QVQLQESGPGLVRPSQTLSLTCTVSGFTFTDFYMNWVRQPPGRGLEWIGFIRDKAKGYTTEYNPSVKGRVTMLVDTSKNQFSLRLSSVTAADTAVYYCAREGHTAAPFDYWGQGSLVTVSS

>d1ce1l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Therapeutic CAMPATH-1H humanized fab (rat), kappa L chain}

DIQMTQSPSSLSASVGDRVTITCKASQNIDKYLNWYQQKPGKAPKLLIYNTNNLQTGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCLQHISRPRTFGQGTKVEIK

>d1bj1h1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {VEGF neutralizing Fab-12 (mouse), kappa L chain}

EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVRQAPGKGLEWVGWINTYTGEPTYAADFKRRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAKYPHYYGSSHWYFDVWGQGTLVTVSS

>d1bj1j1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and H chains) {VEGF neutralizing Fab-12 (mouse), kappa L chain}

DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIYFTSSLHSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQYSTVPWTFGQGTKVEIK

>d1blna1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-p-glycoprotein Fab MRK-16 (mouse), kappa L chain}

DVLMTQTPVSLSVSLGDQASISCRSSQSIVHSTGNTYLEWYLQKPGQSPKLLIYKISNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQASHAPRTFGGGTKLEIK

>d1blnb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-p-glycoprotein Fab MRK-16 (mouse), kappa L chain}

EVILVESGGGLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGGNTYYPDSVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARYYRYEAWFASWGQGTLVTVSA

>d1boga1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-p24 (HIV-1) Fab CB 4-1 (mouse), kappa L chain}

DIKMTQSPSSMYTSLGERVTITCKASQDINSFLTWFLQKPGKSPKTLIYRANRLMIGVPSRFSGSGSGQTYSLTISSLEYEDMGIYYCLQYDDFPLTFGAGTKLDLK

>d1bogb1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and H chains) {Anti-p24 (HIV-1) Fab CB 4-1 (mouse), kappa L chain}

QDQLQQSGAELVRPGASVKLSCKALGYIFTDYEIHWVKQTPVHGLEWIGGIHPGSSGTAYNQKFKGKATLTADKSSTTAFMELSSLTSEDSAVYYCTRKDYWGQGTLVTVSA

>d1f58h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-gp120 (HIV-1) Fab 58.2, (mouse), kappa L chain}

DVQLQQSGPDLVKPSQSLSLTCTVTGYSITSGYSWHWIRQFPGNKLEWMGYIHYSAGTNYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCAREEAMPYGNQAYYYAMDCWGQGTTVTVSS

>d1f58l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-gp120 (HIV-1) Fab 58.2, (mouse), kappa L chain}

DIVLTQSPASLAVSLGQRATISCKASQGVDFDGASFMNWYQQKPGQPPKLLIFAASTLESGIPARFSGRGSGTDFTLNIHPVEEEDAATYYCQQSHEDPLTFGAGTKLELK

>d1wejh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Anti-cytochrome c Fab E8, (mouse), kappa L chain}

EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIDPASGNTKYDPKFQDKATITADTSSNTAYLQLSSLTSEDTAVYYCAGYDYGNFDYWGQGTT

>d1wejl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-cytochrome c Fab E8, (mouse), kappa L chain}

DIQMTQSPASLSASVGETVTITCRASGNIHNYLAWYQQKQGKSPQLLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFWSTPWTFGGGTKLEIK

>d1sbsh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Anti-HCG Fab 3A2, (mouse), kappa L chain}

EVNLEESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVADIRLKSNNYATLYAESVKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTRGAYYRYDYAMDYWGQGTSVTVSS

>d1sbsl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-HCG Fab 3A2, (mouse), kappa L chain}

DIVMSQSPSSLAVSVGEKVTMTCKSSQSLLYSSNQMNYLAWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVEAEDLAVYYCQQYHSYPFTFGSGTKLEIK

>d1sm3h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Tumor-specific Fab SM3, (mouse), lambda L chain}

QVQLQESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSNNYATHYAESVKGRFTISRDDSKSSVYLQMNNLRAEDTGIYYCTGVGQFAYWGQGTTVTVSS

>d2pcpa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 6B5, (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASISCRSSQTIVHSNGNTYLEWYLQKPGQSPKLLIYKVTNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGTHAPYTFGGGTKLEIK

>d2pcpb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 6B5, (mouse), kappa L chain}

EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYIHWNKQSHGKSLEWIGYIYPNNGGNGYNHKFKGKATLTVDKSSSTAYMDVRTLTSEDSAVYYCGRSTWDDFDYWGQGTTLTVSS

>d3fcta1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Mature metal chelatase catalytic Fab, (human), kappa L chain}

ELVMTQTPKFMSTTVGDRVSITCKASQNVGTPVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQSEDLADYFCQQYSSYPLTFGGGTKVEIK

>d3fctb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Mature metal chelatase catalytic Fab, (human), kappa L chain}

QVQLLESGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGMIDPNSGGTKYNEKFKSKATLTVDKPSNTAYMQLSSLTSEDSAVYYCTRRDMDYWGAGTTVTVSS

>d1cf8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 19A4 (mouse), kappa L chain}

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSGYAWNWIRQFPGNKLEWMGYIRYSGDTRYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCAIGYGNSDYWGQGTLVTVSA

>d1cf8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 19A4 (mouse), kappa L chain}

DIVLTQSPTIMSVSPGEKVTLTCSASSSVSSNYVYWYQQKPGSSPKVWIYSTSNLASGVPARFSGSGSGTSYSLTISSMEAEDAASYFCLQWSSFPYTFGGGTKLELK

>d1c12a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab directed agains the musk odorant traseolide, (mouse), kappa L chain}

DIELTQSPSSMSVSLGDTVSITCHASQGISSNIGWLQQKPGKSFKGLIYHGTNLEDGVPSRFSGSGSGADYSLTISSLESEDFADYYCVQYVQFPFTFGSGTKLEIK

>d1c12b1 b.1.1.1 (B:301-413) Immunoglobulin (variable domains of L and H chains) {Fab directed agains the musk odorant traseolide, (mouse), kappa L chain}

QVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSYSPSLKSRISLTRDTSKNQFFLQLNSVTTEDTATYYCVTSLTWLLRRKRSYWGQGTTVTVSS

>d1dlfh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv, (mouse), kappa L chain}

EVKLEESGGGLVQPGGSMKLSCATSGFTFSDAWMDWVRQSPEKGLEWVAEIRNKANNHATYYAESVKGRFTISRDDSKRRVYLQMNTLRAEDTGIYYCTGIYYHYPWFAYWGQGTLVTVS

>d1dlfl\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv, (mouse), kappa L chain}

DVVMTQTPLSLPVSLGNQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPFTFGSGTKLEIKR

>d43c9a\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and amidolytic Fv 43c9, (mouse), kappa L chain}

DVVMTQTPSSLAMSVGQKVTMSCKSSQSLLNISNQKNYLAWYQQKPGQSPKLLVYFASTRESGVPDRFIGSGSGTDFTLTISSVQAEDQADYFCQQHYRAPRTFGGGTKLEIK

>d43c9b\_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and amidolytic Fv 43c9, (mouse), kappa L chain}

GQVQLVESGPGLVAPSQSLSITCTVSGISLSRYNVHWVRQSPGKGLEWLGMIWGGGSIEYNPALKSRLSISKDNSKSQIFLKMNSLQTDDSAMYYCVSYGYGGDRFSYWGQGTLVTVS

>d1bz7a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab R24, (mouse), kappa L chain}

DIQMTQITSSLSVSLGDRVIISCRASQDIGNFLNWYQQKPDGSLKLLIYYTSRLQSGVPSRFSGWGSGTDYSLTISNLEEEDIATFFCQQGKTLPYTFGGGTKLEIK

>d1bz7b1 b.1.1.1 (B:1-122) Immunoglobulin (variable domains of L and H chains) {Fab R24, (mouse), kappa L chain}

DVQLVESGGGLVQPGGSRKLSCAASGFTFSNFGMHWVRQAPEKGLEWVAYISSGGSSINYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTAIYYCTRGGTGTRSLYYFDYWGQGATLIVSS

>d1ct8a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 7C8, (mouse), kappa L chain}

ELVMTQTPATLSVTPGDSVSLSCRASQSVSNKLHWYQQKSHESPRLLIKFASQSIPGIPSRFSGSGSGSDFTLSINSVETEDFGIYFCHQTHGRPLTFGAGTKLELK

>d1ct8b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 7C8, (mouse), kappa L chain}

QVKLLESGAVLVKPGASVKLSCKTSGFTFSSSYINWLKQKPGQSLEWIAWIYAGSGGTVYNQHFTDKARLTVDTSSSTAYMQFSSLTTEDSAIYYCARYRYDEGFAYWGQGTLVTVSA

>d1c5da1 b.1.1.1 (A:1-106) Immunoglobulin (variable domains of L and H chains) {Fab against the main immunogenic region of the human muscle acetylcholine receptor, (rat), kappa L chain}

DIQMTQSPPSLSASLGDKVTITCQASQDINKYIAWYQQKPGKAPRQLIRYTSILVLGTPSRFSGSGSGRDFSFSISNVASEDIASYYCLQYGNLYTFGAGTKLEIK

>d1c5db1 b.1.1.1 (B:1-117) Immunoglobulin (variable domains of L and H chains) {Fab against the main immunogenic region of the human muscle acetylcholine receptor, (rat), kappa L chain}

EVKLLESGPGLVQPSQTLSLTCTVSGFPLTTNGVSWVRQPPGKGLEWIAAISSGGSPYYNSALKSRLSINRDTSKSQVFLKMNSLQTEDTAIYFCTREDGWNYFDYWGPGTMVTVSS

>d1f3rb2 b.1.1.1 (B:139-257) Immunoglobulin (variable domains of L and H chains) {scFv MAB198, (rat), kappa L chain}

DIKLTQSPSLLSASVGDRVTLSCKGSQNINNYLAWYQQKLGEAPKLLIYNTNSLQTGIPSRFSGSGSGTDYTLTISSLQPEDVATYFCYQYNNGYTFGAGTKLELKAAEQKLISEEDLN

>d1dqqa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme Fab HYHEL-63, (mouse), kappa L chain}

DIVLTQSPATLSVTPGDSVSLSCRASQSISNNLHWYQQKSHESPRLLIKYASQSISGIPSRFSGSGSGTDFTLSINSVETEDFGMYFCQQSNSWPYTFGGGTKLEIK

>d1dqqb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme Fab HYHEL-63, (mouse), kappa L chain}

EVQLQESGPSLVKPSQTLSLTCSVTGDSVTSDYWSWIRKFPGNKLEYMGYISYSGSTYYHPSLKSRISITRDTSKNQYYLQLNSVTTEDTATYYCASWGGDVWGAGTTVTVSS

>d1ejoh1 b.1.1.1 (H:2501-2619) Immunoglobulin (variable domains of L and H chains) {Anti-FMDV Fab 4C4, (mouse), kappa L chain}

QMLVESGGDLVKPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVATISSGGAYTYYPDSVKGRFTISDDNAESTLYLQMSSLRSEDTAMYYCVRRAFDSDVGFASWGHRTLVTVSA

>d1ejol1 b.1.1.1 (L:2001-2111) Immunoglobulin (variable domains of L and H chains) {Anti-FMDV Fab 4C4, (mouse), kappa L chain}

DIVLTQSPASLAVSLGQRATISCRASESVDSYGNSFMHWYQQKPGQPPKLLIYRASNLESGIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEDPLTFGAGTKLELK

>d1cr9h1 b.1.1.1 (H:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-prion Fab 3F4, (mouse), kappa L chain}

KVKLQQSGAELVRSGASVKLSCTASGFNIKDYYIQWVKQRPEQGLEWIGWIDPENGNSEYAPRFQGKATMTADTLSNTAYLQLSSLTSEDTAVYYCNADLHDYWGQGTTLTVSS

>d1cr9l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and H chains) {Anti-prion Fab 3F4, (mouse), kappa L chain}

DVVMTQTPLSLSVTIGQPASISCKSSQSLLDSDGKTYLIWVFQRPGQSPKRLIFLVSKRDSGVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPHTVGGGTKLEIA

>d1qfwh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin alpha subunit] Fv, kappa L chain}

QLQQSGAELVKPGASVKLSCKASDYTFTSYWMHWVKQRPGQGLEWIGEINPTNGRTYYNEKFKSKATLTVAASASTAAMQASSLTSEDSAVYYCARRYGNSFDYWGQGTTVTVSS

>d1qfwl\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin alpha subunit] Fv, kappa L chain}

DIELTQSPDSLAVSLGQRATISCRASESVDSYGNSFMQWYQQKPGQPPKLLIYRASNLESGIPARFSGTGSRTDFTLTINPVEADDVATYYCQQSDEYPYMYTFGGGTKLEIKR

>d1qfwi\_ b.1.1.1 (I:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin beta subunit] Fv, kappa L chain}

QVQLQESGGHLVKPGGSLKLSCAASGFAFSSFDMSWIRQTPEKRLEWVASITNVGTYTYYPGSVKGRFSISRDNARNTLNLQMSSLRSEDTALYFCARQGTAAQPYWYFDVWGAGTTVTVS

>d1qfwm\_ b.1.1.1 (M:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin beta subunit] Fv, kappa L chain}

DIELTQSPKSMSMSVGERVTLSCKASETVDSFVSWYQQKPEQSPKLLIFGASNRFSGVPDRFTGSGSATDFTLTISSVQAEDFADYHCGQTYNHPYTFGGGTKLEIKR

>d32c2a1 b.1.1.1 (A:1-110) Immunoglobulin (variable domains of L and H chains) {Fab 32C2 against P450-arom, (mouse), kappa L chain}

DIVLTQSPASLAVSLGQRATISCRASKSVSTSGYGYMHWNQQKPGQPPRLLIYLVSNLESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHIREPLTFGGGTKLEIK

>d32c2b1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Fab 32C2 against P450-arom, (mouse), kappa L chain}

DVQLQESGPGLVKPSQSLSLTCTVTGYSISSDYAWNWIRQFPGNKLEWMGYISYSGSTSYNPSLKSRISITRDTSKNQFFLQLSSVTTEDTATYYCARGYYGSSHSPVWGAGTTVTVSS

>d1dqdh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab HGR-2 F6, (mouse), kappa L chain}

EVQLQESGPSLVKPSQTLSLTCSVTGDSITSGYWNWIRKFPGNKLEYMGYISYSGSTYYNPSLKSRLSITRDTSRNQYYLQLKSVTPEDTATYYCASPPGYYGSGPYAMDYWGQGTSVTVSS

>d1dqdl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab HGR-2 F6, (mouse), kappa L chain}

DIVLSQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLCIYTTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSTYPPTFGSGTKLEIK

>d1deea1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}

DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSAPRTFGQGTKVEIK

>d1deeb1 b.1.1.1 (B:501-621) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}

QVQLVESGGGVVQPGKSLRLSCAASGFTFSGYGMHWVRQAPGKGLEWVALISYDESNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKVKFYDPTAPNDYWGQGTLVTVSS

>d1qnzh\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fv 0.5B, (mouse), kappa L chain}

QVQLQQSGAELVKPGASVKMSCKASGYTFTTYPIEWMKQNHGKSLEWIGNFHPYSDDTNYNEKFKGKAKLTVEKSSSTVYLEFSRLTSDDSAVYYCAIHYGSAYAMDYWGQGTSVTVSS

>d1f4xh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-carbohydrate Fab S-20-4 (mouse), lambda L chain}

EVQLEESGGGLVTPGGSLRLSCAASGYVFSTYDMSWVRQTPEKRLEWVAFISSGGGRTSYPDTVKGRFTISRDDAKNTLYLQMSSLQSEDTAMYYCTRHFYAVLDYWGRGTTLTVSS

>d1f4xl1 b.1.1.1 (L:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-carbohydrate Fab S-20-4 (mouse), lambda L chain}

QAVVTQESALTTSPGETVTLTCRSSTGTVTTSNYANWVQEKPDHLFTGLIGATNNRAAGVPVRFSGSLIGGKAALTITGAQTEDEAIYFCALWYSGHWVFGGGTKLTVLG

>d1f11b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-Pres2 Fab F124, (mouse), kappa L chain}

EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTGYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCANDYGSTYGFAYWGQGTLVTVSA

>d1f3dh1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}

EIQLQQSGPELVKPGASVKVSCKASGYSFIDYNIHWVKQSHGKSLEWIGYIVPYSGGTTFNQKFKGKATLTVDKSSSTAFMHLNSLTFEDSAVYYCANDYDGVYWGQGTTLTVSS

>d1f3dj1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQVSISCRSSQSIFHSDGKTYLEWHLQKPGQSPKLLIYKVSKRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPYTFGGGTKLEIK

>d1fh5h1 b.1.1.1 (H:4-120) Immunoglobulin (variable domains of L and H chains) {Fab MAK33, (human), kappa L chain}

SGGGLVKPAGSLKLSCAASGFTFSSYYMYWVRQTPDKRLEWVATISDGGSYTYYPDSVKGRFTISRDNAKNNLYLQMSSLKSEDTAMYYCARDAMDYWGQGTLVTVSA

>d1fskb1 b.1.1.1 (B:1-107) Immunoglobulin (variable domains of L and H chains) {Anti bet v1 Fab BV16, (mouse), kappa L chain}

NIVLTQSPKSMSVSVGERVTLSCKASENVDTYVFWFQQKPDQSPKLLLYGPSNRYTGVPDRFTGSGSTTDFTLTISSVQAEDLADYHCGQSYSYPYTFGGGTKLEIK

>d1fskc1 b.1.1.1 (C:1-118) Immunoglobulin (variable domains of L and H chains) {Anti bet v1 Fab BV16, (mouse), kappa L chain}

QVQLQQPGTELVRPGASVILSCKASGYTFTSYWINWVKQRPGQGLEWVGNIFPSDSYTNYNQKFKDKATLTVDKSSSTAYMQVNSPTSEDSAVYYCTRGARDTWFAYWGQGTLVTVSV

>d1c5ch1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Decarboxylase catalytic Fab 21D8, chimeric (mouse V domains/human C1 domains)}

QVQLLEPGTELVKPGASVKLSCRASGYSFTSYWMHWVKQRPGQGLEWIGLIDPSNGRTNFNDKFKSRATLTVDTSSSTAYMQLSSLTSEDSAVYYCVRIAYWGQGTLVTVSS

>d1c5cl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Decarboxylase catalytic Fab 21D8, chimeric (mouse V domains/human C1 domains)}

EIQLTQSPSSLSASLGERVSLTCRTSQEISGYLSWLQQKPDGTIKRLIYDATKLDSGAPKRFSGSRSGSDYSLTISSLESEDFADYYCLQYASFPRTFGGGTKLEIK

>d1etza1 b.1.1.1 (A:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-sweetener Fab NC10.14, (mouse), lamba L chain}

FAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYAIWVQEKPDHLFSGLIGGTNNRVPGVPARFSGSLIGDKAALTVTGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLG

>d1etzb1 b.1.1.1 (B:1-126) Immunoglobulin (variable domains of L and H chains) {Anti-sweetener Fab NC10.14, (mouse), lamba L chain}

QVTLKESGPGILQPSQTLSLTCSFSGFSLSTSGMGVGWIRQPSGEGLEWLADIWWNDKKYYNPSLKSRLTVSKDTSSNQVFLKITSVDTSDTATYHCARRTFSYYYGSSFYYFDNWGQGTTLTVSS

>d1emth1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}

QVHLQESGPELVRPGASVKISCKTSGYVFSSSWMNWVKQRPGQGLKWIGRIYPGNGNTNYNEKFKGKATLTADKSSNTAYMQLSSLTSVDSAVYFCATSSAYWGQGTLLTVSA

>d1emtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVTFSCSASQDISNYLNWYQQKPDGTIKLLIYYTSSLRSGVPSRFSGSGSGTDYSLTINNLEPEDIATYFCQQYSRLPFTFGSGTKLEIK

>d1fl3a1 b.1.1.1 (A:2-116) Immunoglobulin (variable domains of L and H chains) {Blue fluorescent Fab 19G2, (mouse), kappa L chain}

AALLESGGGLVKPGGSLKLSCTASGITFSRYIMSWVRQIPEKRLEWVASISSGGITYYPDSVAGRFTISRDNVRNILYLQMSSLRSEDTALYYCARGQGRPYWGQGTSVTVSA

>d1fl3b1 b.1.1.1 (B:2-113) Immunoglobulin (variable domains of L and H chains) {Blue fluorescent Fab 19G2, (mouse), kappa L chain}

AALTQSPVSNPVTLGTSASISCRSTKSLLHSNGITYLYWYLQKPGQSPQLLIYQMSNLASGVPNRFSSSGSGTDFTLRINTVEAEDVGVYYCAQNLELPPTFGAGTKLELKR

>d1dzba1 b.1.1.1 (A:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}

QVKLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSSLTSEDTAVYYCARWDWYFDVWGQGTTVTVSSG

>d1dzba2 b.1.1.1 (A:201-307) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}

DIELTQSPSSMYTSLGERVTITCKASQDINSYLRWFQQKPGKSPKTLIYYATSLADGVPSRFSGSGSGQDYSLTISSLESDDTTTYYCLQHGESPYTFGGGTKLEIK

>d1qoka1 b.1.1.1 (A:27-147) Immunoglobulin (variable domains of L and H chains) {Anti-carcinoembryonic scFv MFE-23, (mouse), kappa L chain}

QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQGKATFTTDTSSNTAYLQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSSG

>d1qoka2 b.1.1.1 (A:162-267) Immunoglobulin (variable domains of L and H chains) {Anti-carcinoembryonic scFv MFE-23, (mouse), kappa L chain}

ENVLTQSPAIMSASPGEKVTITCSASSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPLTFGAGTKLELK

>d1e6oh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 13B5 against HIV-1 capsid protein p24, (mouse), kappa L chain}

EVQLQQSGAELARPGASVKMSCKASGYTFTSYTMHWVKQRPGQGLEWIGYINPSSGYSNYNQKFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYCSRPVVRLGYNFDYWGQGSTLTVSS

>d1e6ol1 b.1.1.1 (L:1-105) Immunoglobulin (variable domains of L and H chains) {Fab 13B5 against HIV-1 capsid protein p24, (mouse), kappa L chain}

EIVLTQSPAITAASLGQKVTITCSASSSVSYMHWYQQKSGTSPKPWIYEISKLASGVPARFSGSGSGTSYSLTISSMEAEDAAIYYCQQWNYPFTFGSGTKLEIK

>d1dl7h\_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv M3C65, (human), lambda L chain}

QVQLKESGPGLVAPSQSLSITCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWGDGSTDYNSALKSRLNISKDKSKSQVFLRMYSLQTDDTARYYCARDYGPYWGQGTLVTVS

>d1dl7l\_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv M3C65, (human), lambda L chain}

QAVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDHLFTGLIGGTKHRTPGAPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVL

>d1egjh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab against cytokyne receptor common beta chain domain 4, (mouse), kappa L chain}

EVQLQQSGPELVKPGTSVKMSCKASGYTFTDYYMKWVKHSHGKSLEWIGDINPSNGGTLYNQKFKGKATLTVDKSSSTASMQLSRLTSEDSAVYYCSRGDGIHGGFAYWGQGTTVTVSS

>d1egjl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab against cytokyne receptor common beta chain domain 4, (mouse), kappa L chain}

NIVLTQSPASLAVSLGQRATISCRANESVYSYGDSFMHWYQQKPGQPPKLLIYLASNLASGVPARFSGSGSRTDFTLTIDPVETDDAATYYCQQNNEDPWTFGGGTKLEIK

>d1ehlh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-photoproduct Fab 64M-2, (mouse), kappa L chain}

EVQLQQSGTVLARPGASVKMSCKASGYSFTSFWMHWVKQRPGQGLEWIGTIYPGNSDTSYNQKFKGKAKLTAVTSASTAYMEVSSLTNEDSAVYYCTRRSGYKYYALDYWGQGTSVTVSS

>d1fe8h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

DVKLVQSGPGLVAPSQSLSITCTVSGFSLTTYGVSWVRQPPGKGLEWLGVIWGDGNTTYHSALISRLSISKDNSRSQVFLKLNSLHTDDTATYYCAGNYYGMDYWGQGTSVTVSS

>d1fe8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

DIAMTQTTSSLSASLGQKVTISCRASQDIGNYLNWYQQKPDGTVRLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISNLESEDIATYFCQNGGTNPWTFGGGTKLEVK

>d1ezvx\_ b.1.1.1 (X:) Immunoglobulin (variable domains of L and H chains) {Fv against Rieske protein from the yeast cytochrome bc1 complex, (mouse), kappa L chain}

EVKLQESGAGLVQPSQSLSLTCSVTGYSITSGYYWNWIRLFPGNKLEWVGYISNVGDNNYNPSLKDRLSITRDTSKNQFFLKLNSVTTEDTATYYCARSEYYSVTGYAMDYWGQGTTVTVSSAWRHP

>d1ezvy\_ b.1.1.1 (Y:) Immunoglobulin (variable domains of L and H chains) {Fv against Rieske protein from the yeast cytochrome bc1 complex, (mouse), kappa L chain}

DIELTQTPVSLAASLGDRVTISCRASQDINNFLNWYQQKPDGTIKLLIYYTSRLHAGVPSRFSGSGSGTDYSLTISNLEPEDIATYFCQHHIKFPWTFGAGTKLEIK

>d1il1a1 b.1.1.1 (A:3-121) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fab G3-519, (mouse), kappa L chain}

QLQQSGAELVRSGASVKLSCATSDFNIKDYYIHWVRQRPEQGLEWIGWLDPENGDTESAPKFQGKATMTADTSSNTAYLQLSSLTSEASAVYYCNAISTTRDYYALDYWGQGTSVTVSS

>d1il1b1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fab G3-519, (mouse), kappa L chain}

DIVMSQSPSSLAVSVGEKVTMSCKSSQSLLYSRNQMNYLSWYQQKPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISSVKAEDLAVYYCQQYYHYRTFGGGTRLEIR

>d1f8th1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-IL2 Fab LNKB-2, (mouse), kappa L chain}

GVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWIRQFPGNKLEWMGYITYSGSTGYNPSLKSRISITRDTSKNQFFLQLNSVTTEDTATYYCASYDDYTWFTYWGQGTLVTVSA

>d1f8tl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-IL2 Fab LNKB-2, (mouse), kappa L chain}

DVQMTQTPLTLSVTIGQPASISCESSQSLLYSNGKTYLNWLLQRPGQSPKRLIYLVSKLDSGVPDRFTGSGSGTDFTLRISRVEAEDLGVYYCVQGTHFPRTFGGGTKLEIK

>d1e4wh1 b.1.1.1 (H:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-TGFalpha Fab TAB2, (mouse), kappa L chain}

QVQLQQPGAELVKPGASVKLSCKASGFTFTNYWMHWVKQRPGQGLEWIGEILPSNGRTNYNEKFKTKATLTVDKSSNTAYMQLSSLTSEDSAVYYCARSPSDYWGQGTTLTVSS

>d1e4wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-TGFalpha Fab TAB2, (mouse), kappa L chain}

DIQMTQTPSSLSASLGDRVTISCRASQDISHYLNWFQQKPDGTVKLLIYYTSTLHSGVPSRFSGSGSGTDYSLTISNLEEEDIAFYFCQQGGALPFTFGSGTKLAIK

>d1h8na1 b.1.1.1 (A:3-109) Immunoglobulin (variable domains of L and H chains) {Anti-ampicillin scFv, (mouse), kappa L chain}

KDIVLTQSHKFMSTSVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGTDFTLTISNVQSEDLADYFCQQYSSYPLTFGAGTKLEL

>d1h8na2 b.1.1.1 (A:132-243) Immunoglobulin (variable domains of L and H chains) {Anti-ampicillin scFv, (mouse), kappa L chain}

QVQLQESGGELVRPGASVKLSCKASGYTFTSYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQKFKDKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARWGYWGQGTLVTVSA

>d1i7za1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab GNC92H2, (mouse/human chimera), kappa L chain}

DLVLTQSPASLAVSLGQRATISCRASKSVSTSGYNYMHWYQQKPGQPPKLLIYLASNLASGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCLYSREFPPWTFGGGTKLEIK

>d1i7zb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab GNC92H2, (mouse/human chimera), kappa L chain}

QVQLQQSGPELKKPGETVKISCKTSGYSFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTYADDFRGRFAFSLATSASTAYLQIINLKNEDTATYFCETYDSPLGDYWGQGTTVTVSS

>d1iqda1 b.1.1.1 (A:2-108) Immunoglobulin (variable domains of L and H chains) {Fab BO2C11 against the C2 domain of factor VIII, (human), kappa L chain}

IALTQSPGTLSLSPGERATLSCRASQSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFGQGTRLEIK

>d1iqdb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Fab BO2C11 against the C2 domain of factor VIII, (human), kappa L chain}

QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVRQAPGKGLEWVGSFDPESGESIYAREFQGSVTMTADTSTNIAYMELSSLRSDDTAVYYCAVPDPDAFDIWGQGTMVTVSS

>d1fn4a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 198 against actylcholine receptor, (rat)}

DIKLTQSPSLLSASVGDRVTLSCKGSQNINNYLAWYQQKLGEAPKLLIYNTNSLQTGIPSRFSGSGSGTDYTLTISSLQPEDVATYFCYQYNNGYTFGAGTKLELKR

>d1fn4b1 b.1.1.1 (B:1-106) Immunoglobulin (variable domains of L and H chains) {Fab 198 against actylcholine receptor, (rat)}

QVQLLESGPGLVRPSETLSLTCTVSGFSLTSFSVSWVRHPSGKGPEWMGRMWYDGYTAYNSALKSRLSISRDTSKNQVFLKMNSLQTDDTGTYYCTRDLYGGYPLGFWYFDFWGPG

>d1jglh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 57-2, (mouse), kappa L chain}

QIQLVQSGPELKKPGETVRISCKASDYSFMTSGMQWVQQMPGKGLKWIGWLNTQSGVPEYAEDFKGRFAFSLETSATTAYLQINNLKNEDTATYFCATWGGNSAYWGQGTTLTVSS

>d1jp5a1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and H chains) {scFv 1695, (mouse), kappa L chain}

DILMTQTPLYLPVSLGDQASISCRSSQTIVHNNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGIYYCFQGSHFPPTFGGGTKLEIK

>d1jp5a2 b.1.1.1 (A:128-247) Immunoglobulin (variable domains of L and H chains) {scFv 1695, (mouse), kappa L chain}

EVQLQQSGPELKKPGETVKISCKATNYAFTDYSMHWVKQAPGGDLKYVGWINTETDEPTFADDFKGRFAFSLDTSTSTAFLQINNLKNEDTATYFCVRDRHDYGEIFTYWGQGTTVTVSS

>d1fl5b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Sulfide oxidase catalytic Fab 28b4 germline precursor, (mouse/human?), kappa L chain}

QVQLVESGGGLVQPGGSLRLSCATSGFTFTDYYMSWVRQPPGKALEWLGFIRNKANGYTTEYSASVKGRFTISRDNSQSILYLQMNTLRAEDSATYYCARDGSYAMDYWGQGTSVTVSS

>d1k4ca1 b.1.1.1 (A:1-118) Immunoglobulin (variable domains of L and H chains) {Fab against potassium channel KcsA, (mouse), kappa L chain}

QVQLQQPGAELVKPGASVKLSCKASGYTFTSDWIHWVKQRPGHGLEWIGEIIPSYGRANYNEKIQKKATLTADKSSSTAFMQLSSLTSEDSAVYYCARERGDGYFAVWGAGTTVTVSS

>d1k4cb1 b.1.1.1 (B:1-107) Immunoglobulin (variable domains of L and H chains) {Fab against potassium channel KcsA, (mouse), kappa L chain}

DILLTQSPAILSVSPGERVSFSCRASQSIGTDIHWYQQRTNGSPRLLIKYASESISGIPSRFSGSGSGTDFTLSINSVESEDIANYYCQQSNRWPFTFGSGTKLEIK

>d1jguh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

EVKLVESRGGLVKPGGSLQLSCAASGFTFSGYAMSWFRLTPEKRLEWVASIYNGFRIHYLDSVKGRFTISSDYARNILYLQMSTLRSEDTAMYYCSRGDAYSRYFDVWGAGTTVTVSA

>d1jgul1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

EVVMTQSPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK

>d1i8ma1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Anti ssDNA Fab, (mouse), kappa L chain}

ELQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQLLVYNAKTLAEGVPSRFSGSGSGTQFSLKINSLQPEDFGSYYCQHHYGTPLTFGAGTKLELK

>d1i8mb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Anti ssDNA Fab, (mouse), kappa L chain}

QVKLLESGPELVKPGASVKMSCKASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTKYNEKFKGKATLTSDKSSSTAYMELSSLTSEDSAVYYCVRGGYRPYYAMDYWGQGTSVTVSS

>d1jv5b\_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Anti-blood group A Fv, (human), kappa L chain}

QVQLQQPGAELVKPGTSVKLSCKASGYNFTSYWINWVKLRPGQGLEWIGDIYPGSGITNYNEKFKSKATLTVDTSSSTAYMQLSSLASEDSALYYCAGQYGNLWFAYWGQGTLVTVS

>d1iqwh1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Anti-human Fas Fab hfe7a, (mouse), kappa L chain}

QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGEIDPSDSYTNYNQKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYYCARNRDYSNNWYFDVWGTGTTVTVSS

>d1iqwl1 b.1.1.1 (L:1-111) Immunoglobulin (variable domains of L and H chains) {Anti-human Fas Fab hfe7a, (mouse), kappa L chain}

DIVLTQSPASLAVSLGQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDFTLNIHPVEEEDAATYYCQQSNEDPRTFGGGTKLEIK

>d1jnha1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 10G6D6, (mouse), lambda L chain}

QAVVTQESALTTSPGETVTLTCRSSSGAITTSHYANWIQEKPDHLFTGLISGTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYICALWFSNQFIFGSGTKVTV

>d1jnhb1 b.1.1.1 (B:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 10G6D6, (mouse), lambda L chain}

EVQLQQSGAELARPGASVKLSCRTSGYSFTTYWMQWVRQRPGQGLEWIAAIYPGDDDARYTQKFKGKATLTADRSSSIVYLQLNSLTSEDSAVYSCSRGRSLYYTMDYWGQGTSVTV

>d1jnlh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}

EVQLQQSGAELVKPGASVRLSCSASGFNIKDTYMFWVKQRPEQGLDWIGRINPANGISKYDPRFQGKATLTADTSSNTAYLQLDNLTSEDTAVYYCAIEKDLPWGQGTLVTVSV

>d1jnll1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}

QIVMTQTPASLSASVGETVTITCRASGNIYNYLAWYQQKQGKSPQLLVYNAKTLVDGVPLRFSGSGSGTQYSLKINSLQPEDFGNYYCHHFWNTPYTFGGGTKLEIK

>d1vhp\_\_ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {VH-P8 domain (human), camelized monomer}

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKEREIVSAVSGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARLKKYAFDYWGQGTLVTVSS

>d1jtpa\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-lysozyme antibody}

DVQLQASGGGSVQAGGSLRLSCAASGYTIGPYCMGWFRQAPGKEREGVAAINMGGGITYYADSVKGRFTISQDNAKNTVYLLMNSLEPEDTAIYYCAADSTIYASYYECGHGLSTGGYGYDSWGQGTQVTVSSRR

>d1bzqk\_ b.1.1.1 (K:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-RNase A antibody}

QVQLVESGGGLVQAGGSLRLSCAASGYAYTYIYMGWFRQAPGKEREGVAAMDSGGGGTLYADSVKGRFTISRDKGKNTVYLQMDSLKPEDTATYYCAAGGYELRDRTYGQWGQGTQVTVSSRGR

>d1f2xk\_ b.1.1.1 (K:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), antibody cab-ca05}

QVQLVESGGGSVQAGGSLRLSCAASGYTVSTYCMGWFRQAPGKEREGVATILGGSTYYGDSVKGRFTISQDNAKNTVYLQMNSLKPEDTAIYYCAGSTVASTGWCSRLRPYDYHYRGQGTQVTVSS

>d1hcv\_\_ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), anti-gonadotropin alpha subunit VH domain}

VQLQESGGGLVQAGGSLRLSCAASGRTGSTYDMGWFRQAPGKERESVAAINWDSARTYYASSVRGRFTISRDNAKKTVYLQMNSLKPEDTAVYTCGAGEGGTWDSWGQGTQVTVSS

>d1qd0a\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), anti-RR6 VH domain}

QVQLQESGGGLVQAGGSLRLSCAASGRAASGHGHYGMGWFRQVPGKEREFVAAIRWSGKETWYKDSVKGRFTISRDNAKTTVYLQMNSLKGEDTAVYYCAARPVRVADISLPVGFDYWGQGTQVTVSS

>d1i3ua\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), the dye RR1-binding VHh domain}

VQLQESGGGLVQAGDSLKLSCEASGDSIGTYVIGWFRQAPGKERIYLATIGRNLVGPSDFYTRYADSVKGRFAVSRDNAKNTVNLQMNSLKPEDTAVYYCAAKTTTWGGNDPNNWNYWGQGTQVTV

>d1ivla\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {VL domain (kappa) of antibody M29B, dimer synthetic}

DIELTQSPATLSVTPGNSVSISCRASQSIGNRLFWYQQKSHESPRLLIKYASQSISGIPSRFSGSGSGTDFTLSINSVETEDLAVYFCQQVSEWPFTFGGGTKLEIK

>d1bwwa\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) dimer REI (human)}

TPDIQMTQSPSSLSASVGDRVTITCQASQDIIKYLNWYQQKPGKAPKLLIYEASNLQAGVPSRFSGSGSGTDYTFTISSLQPEDIATYYCQQYQSLPYTFGQGTKLQIT

>d2rhe\_\_ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda) dimer RHE (human)}

ESVLTQPPSASGTPGQRVTISCTGSATDIGSNSVIWYQQVPGKAPKLLIYYNDLLPSGVSDRFSASKSGTSASLAISGLESEDEADYYCAAWNDSLDEPGFGGGTKLTVLGQPK

>d1bjma1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and H chains) {Bence-Jones lambda L chain dimer LOC (human)}

ESVLTQPPSASGTPGQRVTISCSGSSSNIGENSVTWYQHLSGTAPKLLIYEDNSRASGVSDRFSASKSGTSASLAISGLQPEDETDYYCAAWDDSLDVAVFGTGTKVTVLG

>d1wtla\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) dimer WAT (human)}

DIQMTQSPSSLSASVGDRVTITCRASQDITNYVNWFQQRPGQAPKVLIYGASILETGVPSRFSGSGSGTDFTFTISSLQPEDIATYYCQQYDTLPLTFGGGTKVDIKR

>d1b0wa\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) dimer BRE (human)}

DIQMTQSPSSLSASVGDRVTITCQASQDISDYLIWYQQKLGKAPNLLIYDASTLETGVPSRFSGSGSGTEYTFTISSLQPEDIATYYCQQYDDLPYTFGQGTKVEIKR

>d1eeqa\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) domain LEN (human)}

DIVLTQSPDSLAVSLGERATINCKSSQSVLDSSNSKNYLAWYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSHPYSFGQGTKLEIK

>d1lila1 b.1.1.1 (A:2-107) Immunoglobulin (variable domains of L and H chains) {Bence-Jones lambda L chain dimer CLE (human)}

YEVTQPPSLSVSPGQTARITCSGEKLGDAYVCWYQQRPGQSPVVVIYQDNRRPSGIPERFSGSSSGNTATLTISGTQTLDEADYYCQVWDSNASVVFGGGTKLTVLG

>d1cd0a\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda) dimer JTO (human)}

NFMLNQPHSVSESPGKTVTISCTRSSGNIDSNYVQWYQQRPGSAPITVIYEDNQRPSGVPDRFAGSIDRSSNSASLTISGLKTEDEADYYCQSYDARNVVFGGGTRLTVLG

>d2cd0a\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda) dimer WIL (human)}

NFLLTQPHSVSESPGKTVTISCTRSSGSIANNYVHWYQQRPGSSPTTVIFEDDHRPSGVPDRFSGSVDTSSNSASLTISGLKTEDEADYYCQSYDHNNQVFGGGTKLTVLG

>d1b6da1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Bence-Jones kappa L chain DEL (human)}

DIQMTQSPSSLSASVGDRVTITCQASQDISSYLNWYQQKPGKAPKLLIHAASSLETGVPSRFSGSGSGTDFSFTISSLQPEDLATYYCQQYDSLPLTFGGGTKVEIK

>d1ek3a\_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Kappa-4 VL REC (human)}

DIVMTQSPDSLAVSPGERATINCKSSQNLLDSSFDTNTLAWYQQKPGQPPKLLIYWASSRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSTPPTFGGGTKVEIKR

>d1mcoh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Intact antibody (lambda) MCG (human)}

PLVLQESGPGLVKPSEALSLTCTVSGDSINTILYYWSWIRQPPGKGLEWIGYIYYSGSTYGNPSLKSRVTISVNTSKNQFYSKLSSVTAADTAVYYCARVPLVVNPWGQGTLVTVSS

>d1dcla1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and H chains) {Lambda L chain dimer MCG (human)}

PSALTQPPSASGSLGQSVTISCTGTSSNVGGYNYVSWYQQHAGKAPKVIIYEVNKRPSGVPDRFSGSKSGNTASLTVSGLQAEDEADYYCSSYEGSDNFVFGTGTKVTVLG

>d1mcww1 b.1.1.1 (W:1-111) Immunoglobulin (variable domains of L and H chains) {Heterologous L chain dimer MCG-WEIR hybrid (human)}

ESALTQPASVSGSPGQSITVSCAGHTSDVADSNSISWFQQHPDKAPKLLIYAVTFRPSGIPLRFSGSKSGNTASLTISGLLPDDEADYFCMSYLSDASFVFGSGTKVTVLR

>d1ac6a\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

DSVTQTEGQVALSEEDFLTIHCNYSASGYPALFWYVQYPGEGPQFLFRASRDKEKGSSRGFEATYNKEATSFHLQKASVQESDSAVYYCALSGGNNKLTFGAGTKLTIKP

>d1b88a\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

MQQVRQSPQSLTVWEGETAILNCSYENSAFDYFPWYQQFPGEGPALLISILSVSNKKEDGRFTIFFNKREKKLSLHIADSQPGDSATYFCAASASFGDNSKLIWGLGTSLVVNP

>d1d9ka\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

QVRQSPQSLTVWEGETTILNCSYEDSTFDYFPWYRQFPGKSPALLIAISLVSNKKEDGRFTIFFNKREKKLSLHITDSQPGDSATYFCAATGSFNKLTFGAGTRLAVSPY

>d1fo0a\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

KVTQTQTSISVMEKTTVTMDCVYETQDSSYFLFWYKQTASGEIVFLIRQDSYKKENATVGHYSLNFQKPKSSIGLIITATQIEDSAVYFCAMRGDYGGSGNKLIFGTGTLLSVKP

>d1h5ba\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

GDQVEQSPSALSLHEGTDSALRCNFTTTMRSVQWFRQNSRGSLISLFYLASGTKENGRLKSAFDSERARYSTLHIRDAQLEDSGTYFCAAEASSGSWQLIFGSGTQLTVMPVT

>d1i9ea\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

QSVTQPDARVTVSEGASLQLRCKYSYSATPYLFWYVQYPRQGLQLLLKYYSGDPVVQGVNGFEAEFSKSNSSFHLRKASVHWSDSAVYFCAVSGFASALTFGSGTKVIVLPYIQN

>d1kb5a\_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

QQVRQSPQSLTVWEGETAILNCSYEDSTFNYFPWYQQFPGEGPALLISIRSVSDKKEDGRFTIFFNKREKKLSLHITDSQPGDSATYFCAARYQGGRALIFGTGTTVSVSPGSAD

>d1nfda1 b.1.1.1 (A:1-117) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

DSVTQTEGLVTVTEGLPVKLNCTYQTTYLTIAFFWYVQYLNEAPQVLLKSSTDNKRTEHQGFHATLHKSSSSFHLQKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKVIAH

>d1bd2d1 b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}

QQVKQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISISSIKDKNADGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAAMEGAQKLVFGQGTRLTINPN

>d1fytd1 b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}

QSVTQLGSHVSVSEGALVLLRCNYSSSVPPYLFWYVQYPNQGLQLLLKYTSAATLVKGINGFEAEFKKSETSFHLTKPSAHMSDAAEYFCAVSESPFGNEKLTFGTGTRLTIIPN

>d1qrnd1 b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}

KEVEQNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGKSPELIMSIYSNGDKEDGRFTAQLNKASQYVSLLIRDSQPSDSATYLCAVTTDSWGKLQFGAGTQVVVTPD

>d1bec\_1 b.1.1.1 (3-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

AVTQSPRNKVAVTGGKVTLSCQQTNNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDIPDGYKASRPSQEQFSLILELATPSQTSVYFCASGGGRGSYAEQFFGPGTRLTVLE

>d1fo0b\_ b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

VTLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANMSQGRTLYCTCSADRVGNTLYFGEGSRLIV

>d1kb5b\_ b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

VTLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEVKSLPGADYLATRVTDTELRLQVANMSQGRTLYCTCSAAPDWGASAETLYFGSGTRLTVL

>d1nfdb1 b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

DSGVVQSPRHIIKEKGGRSVLTCIPISGHSNVVWYQQTLGKELKFLIQHYEKVERDKGFLPSRFSVQQFDDYHSEMNMSALELEDSAMYFCASSLRWGDEQYFGPGTRLTVLE

>d1tcrb1 b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

EAAVTQSPRNKVAVTGGKVTLSCNQTNNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDIPDGYKASRPSQENFSLILELATPSQTSVYFCASGGGGTLYFGAGTRLSVLE

>d1bd2e1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}

GVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVSRSTTEDFPLRLLSAAPSQTSVYFCASSYPGGGFYEQYFGPGTRLTVTE

>d1fyte1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}

KVTQSSRYLVKRTGEKVFLECVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKEKGDIPEGYSVSREKKERFSLILESASTNQTSMYLCASSSTGLPYGYTFGSGTRLTVVE

>d1hxma1 b.1.1.1 (A:1-120) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}

AIELVPEHQTVPVSIGVPATLRCSMKGEAIGNYYINWYRKTQGNTMTFIYREKDIYGPGFKDNFQGDIDIAKNLAVLKILAPSERDEGSYYCACDTLGMGGEYTDKLIFGKGTRVTVEPR

>d1hxmb1 b.1.1.1 (B:1-123) T-cell antigen receptor {Human (Homo sapiens), delta-chain}

AGHLEQPQISSTKTLSKTARLECVVSGITISATSVYWYRERPGEVIQFLVSISYDGTVRKESGIPSGKFEVDRIPETSTSTLTIHNVEKQDIATYYCALWEAQQELGKKIKVFGPGTKLIITD

>d1tvda\_ b.1.1.1 (A:) T-cell antigen receptor {Human (Homo sapiens), delta-chain}

DKVTQSSPDQTVASGSEVVLLCTYDTVYSNPDLFWYRIRPDYSFQFVFYGDDSRSEGADFTQGRFSVKHILTQKAFHLVISPVRTEDSATYYCAFTLPPPTDKLIFGKGTRVTVEP

>d1ah1\_\_ b.1.1.1 (-) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}

AMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYYLGIGNGTQIYVIDPEPCPDSDQEPK

>d1i8lc\_ b.1.1.1 (C:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}

MHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYYLGIGNGAQIYVIDPE

>d1dqta\_ b.1.1.1 (A:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Mouse (Mus musculus)}

IQVTQPSVVLASSHGVASFPCEYSPSHNTDEVRVTVLRQTNDQMTEVCATTFTEKNTVGFLDYPFCSGTFNESRVNLTIQGLRAVDTGLYLCKVELMYPPPYFVGMGNGTQIYVIDP

>d3frua1 b.1.1.2 (A:179-269) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}

KEPPSMRLKARPGNSGSSVLTCAAFSFYPPELKFRFLRNGLASGSGNCSTGPNGDGSFHAWSLLEVKRGDEHHYQCQVEHEGLAQPLTVDL

>d3frub1 b.1.1.2 (B:) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}

IQKTPQIQVYSRHPPENGKPNFLNCYVSQFHPPQIEIELLKNGKKIPNIEMSDLSFSKDWSFYILAHTEFTPTETDVYACRVKHVTLKEPKTVTWDRDM

>d1bmg\_\_ b.1.1.2 (-) Class I MHC, beta2-microglobulin and alpha-3 domain {Cow (Bos taurus)}

IQRPPKIQVYSRHPPEDGKPNYLNCYVYGFHPPQIEIDLLKNGEKIKSEQSDLSFSKDWSFYLLSHAEFTPNSKDQYSCRVKHVTLEQPRIVKWDRDL

>d1i4fa1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-A2.1}

TDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGQEQRYTCHVQHEGLPKPLTLRWE

>d1i4fb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-A2.1}

MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVKWDRDM

>d1agda1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-B0801}

ADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFQKWAAVVVPSGEEQRYTCHVQHEGLPKPLTLRWEP

>d1qqda1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-CW4}

AEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPLTLRW

>d1mhea1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-E}

LEPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQQDGEGHTQDTELVETRPAGDGTFQKWAAVVVPSGEEQRYTCHVQHEGLPEPVTLRW

>d1de4a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), hemochromatosis protein Hfe}

QQVPPLVKVTHHVTSSVTTLRCRALNYYPQNITMKWLKDKQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTCQVEHPGLDQPLIVIW

>d1fzka1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2KB}

TDSPKAHVTHHSRPEDKVTLRCWALGFYPADITLTWQLNGEELIQDMELVETRPAGDGTFQKWASVVVPLGKEQYYTCHVYHQGLPEPLTLRW

>d1fzkb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2KB}

IQKTPQIQVYSRHPPENGKPNILNCYVTQFHPPHIEIQMLKNGKKIPKVEMSDMSFSKDWSFYILAHTEFTPTETDTYACRVKHDSMAEPKTVYWDRDM

>d1jpfa1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2DB}

TDSPKAHVTHHPRSKGEVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFQKWASVVVPLGKEQNYTCRVYHEGLPEPLTLRWEP

>d1mhca1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2M3}

ADPPKAHVAHHPRPKGDVTLRCWALGFYPADITLTWQKDEEDLTQDMELVETRPSGDGTFQKWAAVVVPSGEEQRYTCYVHHEGLTEPLALKWRS

>d1qo3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2DD}

TDPPKAHVTHHRRPEGDVTLRCWALGFYPADITLTWQLNGEELTQEMELVETRPAGDGTFQKWASVVVPLGKEQKYTCHVEHEGLPEPLTLRWG

>d1k8da1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), IB QA-2}

TDPPKAHVTHHPRSYGAVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFQKWASVVVPLGKEQNYTCHVNHEGLPEPLTLRW

>d1ed3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Rat (Rattus norvegicus), RT1-AA}

SDPPEAHVTLHPRPEGDVTLRCWALGFYPADITLTWQLNGEDLTQDMELVETRPAGDGTFQKWASVVVPLGKEQNYTCRVEHEGLPKPLSQRWE

>d1zaga1 b.1.1.2 (A:184-277) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}

QDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGDVLHNGNGTYQSWVVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEA

>d1hyrc1 b.1.1.2 (C:181-274) MHC I homolog {Human (Homo sapiens), Mic-a}

TVPPMVNVTRSEASEGNITVTCRASGFYPWNITLSWRQDGVSLSHDTQQWGDVLPDGNGTYQTWVATRICQGEEQRFTCYMEHSGNHSTHPVPS

>d1c16a1 b.1.1.2 (A:181-276) MHC I homolog {Mouse (Mus musculus), t22}

RSDPPKAHVTRHPRPEGDVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFQKWAAVVVPLGKEQSYTCHVYHEGLPEPLILRWGG

>d1exua1 b.1.1.2 (A:177-267) MHC-related Fc receptor {Human (Homo sapiens)}

KEPPSMRLKARPSSPGFSVLTCSAFSFYPPELQLRFLRNGLAAGTGQGDFGPNSDGSFHASSSLTVKSGDEHHYCCIVQHAGLAQPLRVEL

>d1igtb3 b.1.1.2 (B:236-361) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}

PCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKG

>d1igtb4 b.1.1.2 (B:363-474) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}

SVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSR

>d1igyb3 b.1.1.2 (B:236-361) Immunoglobulin (constant domains of L and H chains) {Intact IgG1 antibody Mab61.1.3 (mouse), kappa L chain}

GCKPCICTVPEVSSVFIFPPKPKDTLLITVTPKVTCVVVDISKDDPEVQFSWFVDNVEVHTAQTQPREEQFNSTFRVVSALPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKG

>d1igyb4 b.1.1.2 (B:363-474) Immunoglobulin (constant domains of L and H chains) {Intact IgG1 antibody Mab61.1.3 (mouse), kappa L chain}

KPRAPQVYTIPPPKEQMAKDKVSLTCMITDFFPEDITVEWQSDGQAPENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSH

>d1hzhh3 b.1.1.2 (H:236-359) Immunoglobulin (constant domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}

THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA

>d8faba2 b.1.1.2 (A:106-208) Immunoglobulin (constant domains of L and H chains) {Fab HIL (human), lambda L chain}

LGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPIKAGVETTTPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAP

>d1dn0b2 b.1.1.2 (B:121-225) Immunoglobulin (constant domains of L and H chains) {Fab Kau cold agglutinin (human) IgM, kappa L chain}

GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVMAGTDEHVVCKVQHPNGNKEKNVPLPV

>d2fb4l2 b.1.1.2 (L:110-214) Immunoglobulin (constant domains of L and H chains) {Fab KOL (human), lambda L chain}

QPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKTVAPTECS

>d2ig2h2 b.1.1.2 (H:120-231) Immunoglobulin (constant domains of L and H chains) {Fab KOL (human), lambda L chain}

STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP

>d2fbjh2 b.1.1.2 (H:119-220) Immunoglobulin (constant domains of L and H chains) {Fab J539 (mouse), kappa L chain}

ESARNPTIYPLTLPPALSSDPVIIGCLIHDYFPSGTMNVTWGKSGKDITTVNFPPALASGGRYTMSNQLTLPAVECPEGESVKCSVQHDSNPVQELDVNCSG

>d1mfbl2 b.1.1.2 (L:112-212) Immunoglobulin (constant domains of L and H chains) {Fab SE155-4 (mouse), lambda L chain}

PKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTVDWKVDGTPVTQGMETTQPSKQSNNKYMASSYLTLTARAWERHSSYSCQVTHEGHTVEKSLSRA

>d1teth2 b.1.1.2 (H:113-213) Immunoglobulin (constant domains of L and H chains) {Fab TE33 (mouse), kappa L chain}

SAKTTPPSVYPLAPGSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPR

>d2jelh2 b.1.1.2 (H:114-226) Immunoglobulin (constant domains of L and H chains) {Fab JE142 (mouse), kappa L chain}

AATTPPSVYPLAPGSGGQGNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLAADLYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIAPG

>d2jell2 b.1.1.2 (L:109-212) Immunoglobulin (constant domains of L and H chains) {Fab JE142 (mouse), kappa L chain}

ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIGDGARQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSDSPIVKSFNRN

>d1eapb2 b.1.1.2 (B:125-221) Immunoglobulin (constant domains of L and H chains) {Fab 17E8 (mouse), kappa L chain}

AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGGLSSSVHTFPALLQSGLYTMSSSVTVPGGGWPSATVTCSVAHPASSTTVDKKL

>d1yuhb2 b.1.1.2 (B:119-218) Immunoglobulin (constant domains of L and H chains) {Fab anti-nitrophenol (mouse/human), lambda L chain}

AATTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQSDLYTLSSSVTVPASTWPSGTVTCNVAHPASSTAVDKKIVPR

>d1clzh2 b.1.1.2 (H:115-231) Immunoglobulin (constant domains of L and H chains) {Fab MBR96 (mouse), kappa L chain}

TTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQSGFYSLSSLVTVPSSTWPSQTVICNVAHPASKTELIKRIEPR

>d1nldh2 b.1.1.2 (H:113-215) Immunoglobulin (constant domains of L and H chains) {Fab 1583, against an epitope of gp41 of HIV-1, (mouse), kappa L chain}

SASTTAPSVYPLAPVSGDQTNSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSPWPSETITCNVAHPASSTKVDKKIEPRGC

>d1kelh2 b.1.1.2 (H:116-218) Immunoglobulin (constant domains of L and H chains) {Fab 28B4 (mouse), kappa L chain}

TVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVP

>d1osph2 b.1.1.2 (H:121-218) Immunoglobulin (constant domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}

AKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPESVTVTWNSGSLSSSVHTFPALLQSGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDKKLE

>d1nfde2 b.1.1.2 (E:108-215) Immunoglobulin (constant domains of L and H chains) {Fab H57 (hamster), lambda L chain}

GPKSSPKVTVFPPSPEELRTNKATLVCLVNDFYPGSATVTWKANGATINDGVKTTKPSKQGQNYMTSSYLSLTADQWKSHNRVSCQVTHEGETVEKSLSPAECL

>d1nfdf2 b.1.1.2 (F:115-228) Immunoglobulin (constant domains of L and H chains) {Fab H57 (hamster), lambda L chain}

TTTAPSVYPLAPACDSTTSTTDTVTLGCLVKGYFPEPVTVSWNSGALTSGVHTFPSVLHSGLYSLSSSVTVPSSTWPKQPITCNVAHPASSTKVDKKIEPR

>d1aqkl2 b.1.1.2 (L:112-216) Immunoglobulin (constant domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}

QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVNAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPAECS

>d1a4kh2 b.1.1.2 (H:120-211) Immunoglobulin (constant domains of L and H chains) {Diels alder catalytic Fab (mouse), kappa L chain}

SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV

>d1c1eh2 b.1.1.2 (H:120-228) Immunoglobulin (constant domains of L and H chains) {Diels alder catalytic Fab 1E9 (mouse), kappa L chain}

SVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPR

>d2hmic2 b.1.1.2 (C:108-214) Immunoglobulin (constant domains of L and H chains) {Fab 28 against HIV-1 RT (mouse), kappa L chain}

RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVAWAIDGSAAANGVLNSWTDQDSKDSTYSMSSTLTLTADEYEAANSYTCAATHKTSTSPIVKSFNANEC

>d1a5fh2 b.1.1.2 (H:121-217) Immunoglobulin (constant domains of L and H chains) {Anti-E-selectin Fab (mouse), kappa L chain}

AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVSVPTSTETVTCNVAHAPSSTKVDKKIVPR

>d1bfoa2 b.1.1.2 (A:108-214) Immunoglobulin (constant domains of L and H chains) {CAMPATH-1G igg2b monoclonal fab (rat), kappa L chain}

RANAAPTVSIFPPSTEQLATGGASVVCLMNKFYPRDISVKWKIDGTERNGVLNSVTDQDSADSTYSMSSTLSLTKADYQSHNLYTCQVVHKTSSSPVVAKNFNRNEC

>d1bogb2 b.1.1.2 (B:113-213) Immunoglobulin (constant domains of L and H chains) {Anti-p24 (HIV-1) Fab CB 4-1 (mouse), kappa L chain}

AKTTAPSVYPLVPVCGGTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPALLQSGLYTLSSSVTVTSNTWPSQTITCNVAHPASSTKVDKKIEPRV

>d1wejh2 b.1.1.2 (H:113-223) Immunoglobulin (constant domains of L and H chains) {Anti-cytochrome c Fab E8, (mouse), kappa L chain}

LTVSSAETTPPSVYPLAPGTAALKSSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLTSSVTVPSSTWPSQTVTCNVAHPASSTKVDKKIVPRNCGGDC

>d1sm3h2 b.1.1.2 (H:114-213) Immunoglobulin (constant domains of L and H chains) {Tumor-specific Fab SM3, (mouse), lambda L chain}

AKTTPPTVYPLAPGSNAASQSMVTLGCLVKGYFPEPVTVTWNSGSLASGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDAKIVPR

>d1c12b2 b.1.1.2 (B:414-513) Immunoglobulin (constant domains of L and H chains) {Fab directed agains the musk odorant traseolide, (mouse), kappa L chain}

ASTKGPSVYPLAPGSKAAASMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSPRPSETVTCNVAHPASSTKVDKKIVPE

>d1r24b2 b.1.1.2 (B:123-217) Immunoglobulin (constant domains of L and H chains) {Fab R24, (mouse), kappa L chain}

ATTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPGPVTVKWNYGALSSGVRTVSSVLQSGFYSLSSLVTVPSSTWPSQTVICNVAHPASKTDLIK

>d1c5da2 b.1.1.2 (A:107-213) Immunoglobulin (constant domains of L and H chains) {Fab against the main immunogenic region of the human muscle acetylcholine receptor, (rat), kappa L chain}

RADAAPTVSIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSVTDQDSKDSTYSMSSTLSLTKADYESHNLYTCEVVHKTSSSPVVKSFNRNEC

>d1c5db2 b.1.1.2 (B:118-215) Immunoglobulin (constant domains of L and H chains) {Fab against the main immunogenic region of the human muscle acetylcholine receptor, (rat), kappa L chain}

AQTTAPSVYPLAPGCGDTTSSTVTLGCLVKGYFPEPVTVTWNSGALSSDVHTFPAVLQSGLYTLTSSVTSSTWPSQTVTCNVAHPASSTKVDKKLERR

>d32c2b2 b.1.1.2 (B:120-218) Immunoglobulin (constant domains of L and H chains) {Fab 32C2 against P450-arom, (mouse), kappa L chain}

AKTTPPPVYPLVPGSLAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIEP

>d1deeb2 b.1.1.2 (B:622-723) Immunoglobulin (constant domains of L and H chains) {Fab of human IgM RF 2A2}

GSASAPTLFPLVSCENSNPSSTVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVAQGTNEHVVCKVQHPNGNKEKDVPL

>d1f3dh2 b.1.1.2 (H:122-223) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}

AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDC

>d1fh5h2 b.1.1.2 (H:121-215) Immunoglobulin (constant domains of L and H chains) {Fab MAK33, (human), kappa L chain}

AKTTPPSVYPLAVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSETVTCNVAHPASSTKVDKKIVPR

>d1c5ch2 b.1.1.2 (H:114-230) Immunoglobulin (constant domains of L and H chains) {Decarboxylase catalytic Fab 21D8, chimeric (mouse V domains/human C1 domains)}

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSC

>d1c5cl2 b.1.1.2 (L:108-214) Immunoglobulin (constant domains of L and H chains) {Decarboxylase catalytic Fab 21D8, chimeric (mouse V domains/human C1 domains)}

RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

>d1fe8h2 b.1.1.2 (H:116-216) Immunoglobulin (constant domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

AETTAPSVYKLEPVSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEPRG

>d1iqdb2 b.1.1.2 (B:115-212) Immunoglobulin (constant domains of L and H chains) {Fab BO2C11 against the C2 domain of factor VIII, (human), kappa L chain}

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTATYTCNVDHKPSNTKVDKRV

>d1fn4b2 b.1.1.2 (B:107-208) Immunoglobulin (constant domains of L and H chains) {Fab 198 against actylcholine receptor, (rat)}

TMVTVSSVFPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGALSSGVHTFPAVLQSGLYTLTSSVTVPSSTWSSQAVTCNVAHPASSTKVDKKIVPRDC

>d1jguh2 b.1.1.2 (H:114-212) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

AKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEPVTLTWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIEP

>d1jgul2 b.1.1.2 (L:108-214) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

>d1mcoh2 b.1.1.2 (H:118-219) Immunoglobulin (constant domains of L and H chains) {Intact antibody (lambda) MCG (human)}

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVAPEL

>d1adqa1 b.1.1.2 (A:238-341) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgG1 class}

PSVFLFPPKPKDTLMISRTPEVTCVVVDVSQEDPQVQFNWYVDGVQVHNAKTKPREQQFNSTYRVVSVLTVLHQNWLDGKEYKCKVSNKGLPSSIEKTISKAKG

>d1dn2a1 b.1.1.2 (A:237-341) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgG1 class}

GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHENPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG

>d1dn2a2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgG1 class}

QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL

>d1fc2d1 b.1.1.2 (D:238-341) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgG1 class}

PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPQVKFNWYVDGVQVHNAKTKPREQQYNSTYRVVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTISKAKG

>d1fp5a1 b.1.1.2 (A:336-438) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgE}

VSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSG

>d1fp5a2 b.1.1.2 (A:439-543) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgE}

PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSV

>d1i1ca1 b.1.1.2 (A:239-341) Immunoglobulin (constant domains of L and H chains) {Fc (rat) IgG}

SVFIFPPKTKDVLGGGLTPKVTCVVVDISQNDPEVRFSWFIDDVEVHTAQTHAPEKQSNSTLRSVSELPIVERDWLNGKTFKCKVNSGAFPAPIEKSISKPEG

>d1i1ca2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L and H chains) {Fc (rat) IgG}

TPRGPQVYTMAPPKEEMTQSQVSITCMVKGFYPPDIYTEWKMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKKETWQQGNTFTCSVLHEGLENEHTEKSLSH

>d1pfc\_\_ b.1.1.2 (-) Immunoglobulin (constant domains of L and H chains) {Fc (guinea pig)}

RTISKAKGPPRIPEVYLLPPPRNELSKKKVSLTCMITGFYPADINVEWDSSEPSDYKNTPPVFDTDGSFFLYSRLKVDTDAWNNGESFTCSVMHEALPNHVIQKSISRSPG

>d1cqka\_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {Fc MAK33 (mouse)}

PAAPQVYTIPPPLEQMAKDLVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNVQKSNWEAGNTFTCSVLHEGLHNHHTEKSLSH

>d1g84a\_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {C epsilon2 domain from IgE (human)}

SRDFTPPTVKILQSSSDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKSA

>d1tcra2 b.1.1.2 (A:118-213) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

IQNPEPAVYALKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDATVLDMKAMDSKSNGAIAWSNQTSFTCQDIFKETNATYPSSDVPC

>d1bd2d2 b.1.1.2 (D:118-203) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}

IQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNVSQSKDSDVYITDKTVLDMRSMDFKSNSAVAWSNKSDFACANAFNNSIIPEDTF

>d1bec\_2 b.1.1.2 (118-246) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

DLRQVTPPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVQFHGLSEEDKWPEGSPKPVTQNISAEAWGRAD

>d1bd2e2 b.1.1.2 (E:119-247) T-cell antigen receptor {Human (Homo sapiens), beta-chain}

DLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVSTDPQPLKEQPALNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTQIVSAEAWGRAD

>d1hxma2 b.1.1.2 (A:121-206) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}

SQPHTKPSVFVMKNGTNVACLVKEFYPKDIRINLVSSKKITEFDPAIVISPSGKYNAVKLGKYEDSNSVTCSVQHDNKTVHSTDFE

>d1hxmb2 b.1.1.2 (B:124-230) T-cell antigen receptor {Human (Homo sapiens), delta-chain}

KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLLEKFFPDVIKIHWEEKKSNTILGSQEGNTMKTNDTYMKFSWLTVPEKSLDKEHRCIVRHENNKNGVDQEIIFPPI

>d1cd1a1 b.1.1.2 (A:186-279) CD1, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus)}

QEKPVAWLSSVPSSAHGHRQLVCHVSGFYPKPVWVMWMRGDQEQQGTHRGDFLPNADETWYLQATLDVEAGEEAGLACRVKHSSLGGQDIILYW

>d1hdma1 b.1.1.2 (A:94-196) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}

SRGFPIAEVFTLKPLEFGKPNTLVCFVSNLFPPMLTVNWHDHSVPVEGFGPTFVSAVDGLSFQAFSYLNFTPEPSDIFSCIVTHEPDRYTAIAYWVPRNALPS

>d1hdmb1 b.1.1.2 (B:88-185) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}

TRPPSVQVAKTTPFNTREPVMLACYVWGFYPAEVTITWRKNGKLVMHSSAHKTAQPNGDWTYQTLSHLALTPSYGDTYTCVVEHIGAPEPILRDWTPG

>d1aqdb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR1}

RRVEPKVTVYPSKTQPLQHHNLLVCSVSGFYPGSIEVRWFRNGQEEKAGVVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSVTSPLTVEWRA

>d1fv1a1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

ITNVPPEVTVLTNSPVELREPNVLICFIDKFTPPVVNVTWLRNGKPVTTGVSETVFLPREDHLFRKFHYLPFLPSTEDVYDCRVEHWGLDEPLLKHWEFD

>d1fv1b1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

RRVEPKVTVYPARTQTLQHHNLLVCSVNGFYPGSIEVRWFRNSQEEKAGVVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSVTSPLTVEWRA

>d1d5zb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR4}

RRVYPEVTVYPAKTQPLQHHNLLVCSVNGFYPGSIEVRWFRNGQEEKTGVVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSLTSPLTVEWRA

>d1jk8a1 b.1.1.2 (A:85-181) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}

EVPEVTVFSKSPVTLGQPNTLICLVDNIFPPVVNITWLSNGHSVTEGVSETSFLSKSDHSFFKISYLTFLPSDDEIYDCKVEHWGLDEPLLKHWEPE

>d1jk8b1 b.1.1.2 (B:95-192) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}

VEPTVTISPSRTEALNHHNLLVCSVTDFYPAQIKVRWFRNDQEETTGVVSTPLIRNGDWTFQILVMLEMTPQRGDVYTCHVEHPSLQNPIIVEWRAQS

>d1iaka1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}

ATNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFFVNRDYSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPE

>d1iakb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}

RLEQPSVVISLSRTEALNHHNTLVCSVTDFYPAKIKVRWFRNGQEETVGVSSTQLIRNGDWTFQVLVMLEMTPRRGEVYTCHVEHPSLTSPITVEWRA

>d1fnga1 b.1.1.2 (A:82-182) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

DANVAPEVTVLSRSPVNLGEPNILICFIDKFSPPVVNVTWLRNGRPVTEGVSETVFLPRDDHLFRKFHYLTFLPSTDDFYDCEVDHWGLEEPLRKHWEFEE

>d1fngb1 b.1.1.2 (B:93-188) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

RRVEPTVTVYPTKTQPLEHHNLLVCSVSDFYPGNIEVRWFRNGKEEKTGIVSTGLVRNGDWTFQTLVMLETVPQSGEVYTCQVEHPSLTDPVTVEW

>d2iada1 b.1.1.2 (A:83-186) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AD}

TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEISSADLVPR

>d1es0a1 b.1.1.2 (A:83-180) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-A(G7)}

TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHSFHKLSYLTFIPSDDDIYDCKVEHWGLEEPVLKHWSS

>d1es0b1 b.1.1.2 (B:94-189) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-A(G7)}

RLEQPNVAISLSRTEALNHHNTLVCSVTDFYPAKIKVRWFRNGQEETVGVSSTQLIRNGDWTFQVLVMLEMTPHQGEVYTCHVEHPSLKSPITVEWS

>d1k8ia1 b.1.1.2 (A:93-191) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

VSRGLPVAEVFTLKPLEFGKPNTLVCFISNLFPPTLTVNWQLHSAPVEGASPTSISAVDGLTFQAFSYLNFTPEPFDLYSCTVTHEIDRYTAIAYWVPQ

>d1k8ib1 b.1.1.2 (B:95-190) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

APSVRVAQTTPFNTREPVMLACYVWGFYPADVTITWMKNGQLVPSHSNKEKTAQPNGDWTYQTVSYLALTPSYGDVYTCVVQHSGTSEPIRGDWTP

>d1vcaa1 b.1.1.3 (A:91-199) Second domain of vascular cell adhesion molecule-1 (VCAM-1) {Human (Homo sapiens)}

FPKDPEIHLSGPLEAGKPITVKCSVADVYPFDRLEIDLLKGDHLMKSQEFLEDADRKSLETKSLEVTFTPVIEDIGKVLVCRAKLHIDEMDSVPTVRQAVKELQVYISP

>d1iam\_1 b.1.1.3 (83-185) Second domain of intercellular cell adhesion molecule-1 (ICAM-1) {Human (Homo sapiens)}

YWTPERVELAPLPSWQPVGKQLTLRCQVEGGAPRAQLTVVLLRGEKELKREPAVGEPAEVTTTVLVRRDHHGAQFSCRTELDLRPQGLELFENTSAPYQLQTF

>d1ic1a1 b.1.1.3 (A:83-190) Second domain of intercellular cell adhesion molecule-1 (ICAM-1) {Human (Homo sapiens)}

YWTPERVELAPLPSWQPVGKNLTLRCQVEGGAPRANLTVVLLRGEKELKREPAVGEPAEVTTTVLVRRDHHGANFSCRTELDLRPQGLELFENTSAPYQLQTFVLPAT

>d1zxq\_1 b.1.1.3 (87-192) Second domain of intercellular cell adhesion molecule-2 (ICAM-2) {Human (Homo sapiens)}

PPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGHRNFSCLAVLDLMSRGGNIFHKHSAPKMLEIY

>d1cdy\_2 b.1.1.3 (98-178) CD4 {Human (Homo sapiens)}

FGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLA

>d1wioa4 b.1.1.3 (A:292-363) CD4 {Human (Homo sapiens)}

MRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWVLNPEAGMWQCLLSDSGQVLLESNIKVLP

>d1cid\_2 b.1.1.3 (106-177) CD4 {Rat (Rattus rattus)}

VMKVTQPDSNTLTCEVMGPTSPKMRLILKQENQEARVSRQEKVIQVQAPEAGVWQCLLSEGEEVKMDSKIQV

>d1hnf\_2 b.1.1.3 (105-182) CD2, second domain {Human (Homo sapiens)}

RVSKPKISWTCINTTLTCEVMNGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVSKESSVEPVSCPEK

>d1ccza2 b.1.1.3 (A:94-171) CD2-binding domain of CD58, second domain {Human (Homo sapiens)}

EMVSKPMIYWECSNATLTCEVLEGTDVELKLYQGKEHLRSLRQKTMSYQWTNLRAPFKCKAVNRVSQESEMEVVNCPE

>d1dr9a2 b.1.1.3 (A:106-200) CD80, second domain {Human (Homo sapiens)}

ADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTA

>d1vcaa2 b.1.1.4 (A:1-90) N-terminal domain of vascular cell adhesion molecule-1 (VCAM-1) {Human (Homo sapiens)}

FKIETTPESRYLAQIGDSVSLTCSTTGCESPFFSWRTQIDSPLNGKVTNEGTTSTLTMNPVSFGNEHSYLCTATCESRKLEKGIQVEIYS

>d1iam\_2 b.1.1.4 (1-82) N-terminal domain of intracellular adhesion molecule-1, ICAM-1 {Human (Homo sapiens)}

QTSVSPSKVILPRGGSVLVTCSTSCDQPKLLGIETPLPKKELLLPGNNRKVYELSNVQEDSQPMCYSNCPDGQSTAKTFLTV

>d1zxq\_2 b.1.1.4 (1-86) N-terminal domain of intracellular adhesion molecule-2, ICAM-2 {Human (Homo sapiens)}

KVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVGGLETSLNKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESMNSNVSVYQ

>d1epfa1 b.1.1.4 (A:1-97) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}

LQVDIVPSQGEISVGESKFFLCQVAGDAKDKDISWFSPNGEKLSPNQQRISVVWNDDDSSTLTIYNANIDDAGIYKCVVTAEDGTQSEATVNVKIFQ

>d1epfa2 b.1.1.4 (A:98-189) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}

KLMFKNAPTPQEFKEGEDAVIVCDVVSSLPPTIIWKHKGRDVILKKDVRFIVLSNNYLQIRGIKKTDEGTYRCEGRILARGEINFKDIQVIV

>d1ie5a\_ b.1.1.4 (A:) Neural cell adhesion molecule (NCAM) {Chicken (Gallus gallus)}

GKDIQVIVNVPPSVRARQSTMNATANLSQSVTLACDADGFPEPTMTWTKDGEPIEQEDNEEKYSFNYDGSELIIKKVDKSDEAEYICIAENKAGEQDATIHLKVFAK

>d1gsma1 b.1.1.4 (A:1-90) Mucosal addressin cell adhesion molecule-1 (MADCAM-1) {Human (Homo sapiens)}

VKPLQVEPPEPVVAVALGASRQLTCRLACADRGASVQWRGLDTSLGAVQSDTGRSVLTVRNASLSAAGTRVCVGSCGGRTFQHTVQLLVY

>d1gsma2 b.1.1.4 (A:91-206) Mucosal addressin cell adhesion molecule-1 (MADCAM-1) {Human (Homo sapiens)}

AFPNQLTVSPAALVPGDPEVACTAHKVTPVDPNALSFSLLVGGQELEGAQALGPEVQEEEEEPQGDEDVLFRVTERWRLPPLGTPVPPALYCQATMRLPGLELSHRQAIPVLIEGR

>d1fhga\_ b.1.1.4 (A:) Telokin {Turkey (Meleagris gallopavo)}

AEEKPHVKPYFTKTILDMEVVEGSAARFDCKVEGYPDPEVMWFKDDNPVKESRHFQIDYDEEGNCSLTISEVCGDDDAKYTCKAVNSLGEATCTAELLVETM

>d1g1ca\_ b.1.1.4 (A:) Titin {Human (Homo sapiens), different modules}

SMEAPKIFERIQSQTVGQGSDAHFRVRVVGKPDPECEWYKNGVKIERSDRIYWYWPEDNVCELVIRDVTGEDSASIMVKAINIAGETSSHAFLLVQAK

>d1nct\_\_ b.1.1.4 (-) Titin {Human (Homo sapiens), different modules}

SKTTLAARILTKPRSMTVYEGESARFSCDTDGEPVPTVTWLRKGQVLSTSARHQVTTTKYKSTFEISSVQASDEGNYSVVVENSEGKQEAEFTLTIQK

>d1koa\_1 b.1.1.4 (6265-6361) Twitchin {Nematode (Caenorhabditis elegans)}

QPRFIVKPYGTEVGEGQSANFYCRVIASSPPVVTWHKDDRELKQSVKYMKRYNGNDYGLTINRVKGDDKGEYTVRAKNSYGTKEEIVFLNVTRHSEP

>d1wiu\_\_ b.1.1.4 (-) Twitchin {Nematode (Caenorhabditis elegans)}

LKPKILTASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGDSGAALAPELLVDAKSSTTSIFFPSAKRADSGNYKLKVKNELGEDEAIFEVIVQ

>d1tiu\_\_ b.1.1.4 (-) Twitchin {Human (Homo sapiens), Ig repeat 27}

LIEVEKPLYGVEVFVGETAHFEIELSEPDVHGQWKLKGQPLTASPDCEIIEDGKKHILILHNCQLGMTGEVSFQAANAKSAANLKVKEL

>d1iray1 b.1.1.4 (Y:1-101) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

DKCKEREEKIILVSSANEIDVRPCPLNPNEHKGTITWYKDDSKTPVSTEQASRIHQHKEKLWFVPAKVEDSGHYYCVVRNSSYCLRIKISAKFVENEPNLC

>d1iray2 b.1.1.4 (Y:102-204) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

YNAQAIFKQKLPVAGDGGLVCPYMEFFKNENNELPKLQWYKDCKPLLLDNIHFSGVKDRLIVMNVAEKHRGNYTCHASYTYLGKQYPITRVIEFITLEENKPT

>d1iray3 b.1.1.4 (Y:205-311) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

RPVIVSPANETMEVDLGSQIQLICNVTGQLSDIAYWKWNGSVIDEDDPVLGEDYYSVENPANKRRSTLITVLNISEIESRFYKHPFTCFAKNTHGIDAAYIQLIYPV

>d1cvsc1 b.1.1.4 (C:149-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}

MPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPQPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVVPSDKGNYTCIVENEYGSINHTYQLDVVER

>d1cvsc2 b.1.1.4 (C:251-359) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}

SPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILKTAGVNTTDKEMEVLHLRNVSFEDAGEYTCLAGNSIGLSHHSAWLTVL

>d1ev2e1 b.1.1.4 (E:150-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR2}

NKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPTMRWLKNGKEFKQEHRIGGYKVRNQHWSLIMESVVPSDKGNYTCVVENEYGSINHTYHLDVVE

>d1ev2e2 b.1.1.4 (E:251-360) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR2}

RSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDGLPYLKVLKAAGVNTTDKEIEVLYIRNVTFEDAGEYTCLAGNSIGISFHSAWLTVL

>d1biha1 b.1.1.4 (A:5-98) Hemolin {Moth (Hyalophora cecropia)}

KYPVLKDQPAEVLFRENNPTVLECIIEGNDQGVKYSWKKDGKSYNWQEHNAALRKDEGSLVFLRPQASDEGHYQCFAETPAGVASSRVISFRKT

>d1biha2 b.1.1.4 (A:99-209) Hemolin {Moth (Hyalophora cecropia)}

YLIASPAKTHEKTPIEGRPFQLDCVLPNAYPKPLITWKKRLSGADPNADVTDFDRRITAGPDGNLYFTIVTKEDVSDIYKYVCTAKNAAVDEEVVLVEYEIKGVTKDNSGY

>d1biha3 b.1.1.4 (A:210-306) Hemolin {Moth (Hyalophora cecropia)}

KGEPVPQYVSKDMMAKAGDVTMIYCMYGSNPMGYPNYFKNGKDVNGNPEDRITRHNRTSGKRLLFKTTLPEDEGVYTCEVDNGVGKPQKHSLKLTVV

>d1biha4 b.1.1.4 (A:307-395) Hemolin {Moth (Hyalophora cecropia)}

SAPKYEQKPEKVIVVKQGQDVTIPCKVTGLPAPNVVWSHNAKPLSGGRATVTDSGLVIKGVKNGDKGYYGCRATNEHGDKYFETLVQVN

>d1cs6a1 b.1.1.4 (A:7-103) Axonin-1 {Ckicken (Gallus gallus)}

RSYGPVFEEQPAHTLFPEGSAEEKVTLTCRARANPPATYRWKMNGTELKMGPDSRYRLVAGDLVISNPVKAKDAGSYQCVATNARGTVVSREASLRF

>d1cs6a2 b.1.1.4 (A:104-208) Axonin-1 {Ckicken (Gallus gallus)}

GFLQEFSAEERDPVKITEGWGVMFTCSPPPHYPALSYRWLLNEFPNFIPADGRRFVSQTTGNLYIAKTEASDLGNYSCFATSHIDFITKSVFSKFSQLSLAAEDA

>d1cs6a3 b.1.1.4 (A:209-299) Axonin-1 {Ckicken (Gallus gallus)}

RQYAPSIKAKFPADTYALTGQMVTLECFAFGNPVPQIKWRKLDGSQTSKWLSSEPLLHIQNVDFEDEGTYECEAENIKGRDTYQGRIIIHA

>d1cs6a4 b.1.1.4 (A:300-388) Axonin-1 {Ckicken (Gallus gallus)}

QPDWLDVITDTEADIGSDLRWSCVASGKPRPAVRWLRDGQPLASQNRIEVSGGELRFSKLVLEDSGMYQCVAENKHGTVYASAELTVQA

>d1gl4b\_ b.1.1.4 (B:) Perlecan Ig3 domain {Mouse (Mus musculus)}

PIMVTVEEQRSQSVRPGADVTFICTAKSKSPAYTLVWTRLHNGKLPSRAMDFNGILTIRNVQPSDAGTYVCTGSNMFAMDQGTATLHVQ

>d1f97a2 b.1.1.4 (A:129-238) Junction adhesion molecule, JAM, C-terminal domain {Mouse (Mus musculus)}

VPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPSEYSWFKDGISMLTADAKKTRAFMNSSFTIDPKSGDLIFDPVTAFDSGEYYCQAQNGYGTAMRSEAAHMDAVELNVGG

>d1fltx\_ b.1.1.4 (X:) Second domain of the Flt-1 receptor {Human (Homo sapiens)}

GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATVNGHLYKTNYLTHRQT

>d1he7a\_ b.1.1.4 (A:) NGF binding domain of trkA receptor {Human (Homo sapiens)}

SHMPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLRLNQPTHVNNGNYTLLAANPFGQASASIMAAFMDNPFEFNPE

>d1wwwx\_ b.1.1.4 (X:) NGF binding domain of trkA receptor {Human (Homo sapiens)}

VSFPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLRLNQPTHVNNGNYTLLAANPFGQASASIMAAFMDNP

>d1wwbx\_ b.1.1.4 (X:) Ligand binding domain of trkB receptor {Human (Homo sapiens)}

VHFAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFYNGAILNESKYICTKIHVTNHTEYHGCLQLDNPTHMNNGDYTLIAKNEYGKDEKQISAHFMGWPGID

>d1wwca\_ b.1.1.4 (A:) NT3 binding domain of trkC receptor {Human (Homo sapiens)}

TVYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGNYTLIAKNPLGTANQTINGHFLKEPFPVDE

>d1fcga1 b.1.1.4 (A:4-88) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIa}

APPKAVLKLEPPWINVLQEDSVTLTCQGARSPESDSIQWFHNGNLIPTHTQPSYRFKANNNDSGEYTCQTGQTSLSDPVHLTVLF

>d1fcga2 b.1.1.4 (A:89-174) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIa}

EWLVLQTPHLEFQEGETIMLRCHSWKDKPLVKVTFFQNGKSQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITVQV

>d2fcba1 b.1.1.4 (A:6-90) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIb}

APPKAVLKLEPQWINVLQEDSVTLTCRGTHSPESDSIQWFHNGNLIPTHTQPSYRFKANNNDSGEYTCQTGQTSLSDPVHLTVLS

>d2fcba2 b.1.1.4 (A:91-178) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIb}

EWLVLQTPHLEFQEGETIVLRCHSWKDKPLVKVTFFQNGKSKKFSRSDPNFSIPQANHSHSGDYHCTGNIGYTLYSSKPVTITVQAPA

>d1fnla1 b.1.1.4 (A:3-86) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), III}

EDLPKAVVFLEPQWYSVLEKDSVTLKCQGAYSPEDNSTQWFHNESLISSQASSYFIDAATVNDSGEYRCQTNLSTLSDPVQLEV

>d1fnla2 b.1.1.4 (A:87-175) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), III}

HIGWLLLQAPRWVFKEEDPIHLRCHSWKNTALHKVTYLQNGKDRKYFHHNSDFHIPKATLKDSGSYFCRGLVGSKNVSSETVNITITQA

>d1f2qa1 b.1.1.4 (A:4-85) IgE high affinity receptor alpha subunit {Human (Homo sapiens)}

KPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFS

>d1f2qa2 b.1.1.4 (A:86-174) IgE high affinity receptor alpha subunit {Human (Homo sapiens)}

DWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPR

>d1efxd1 b.1.1.4 (D:4-103) Killer cell inhibitory receptor {Human (Homo sapiens), kir2dl3}

VHRKPSLLAHPGRLVKSEETVILQCWSDVRFEHFLLHREGKFKDTLHLIGEHHDGVSKANFSIGPMMQDLAGTYRCYGSVTHSPYQLSAPSDPLDIVITG

>d1efxd2 b.1.1.4 (D:104-200) Killer cell inhibitory receptor {Human (Homo sapiens), kir2dl3}

LYEKPSLSAQPGPTVLAGESVTLSCSSRSSYDMYHLSREGEAHECRFSAGPKVNGTFQADFPLGPATHGGTYRCFGSFRDSPYEWSNSSDPLLVSVI

>d1nkr\_1 b.1.1.4 (6-101) Killer cell inhibitory receptor {Human (Homo sapiens), p58-cl42 kir}

RKPSLLAHPGPLVKSEETVILQCWSDVMFEHFLLHREGMFNDTLRLIGEHHDGVSKANFSISRMTQDLAGTYRCYGSVTHSPYQVSAPSDPLDIVI

>d1nkr\_2 b.1.1.4 (102-200) Killer cell inhibitory receptor {Human (Homo sapiens), p58-cl42 kir}

IGLYEKPSLSAQPGPTVLAGENVTLSCSSRSSYDMYHLSREGEAHERRLPAGPKVNGTFQADFPLGPATHGGTYRCFGSFHDSPYEWSKSSDPLLVSVT

>d1g0xa1 b.1.1.4 (A:2-97) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}

HLPKPTLWAEPGSVITQGSPVTLRCQGGQETQEYRLYREKKTAPWITRIPQELVKKGQFPIPSITWEHAGRYRCYYGSDTAGRSESSDPLELVVTG

>d1g0xa2 b.1.1.4 (A:98-198) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}

AYIKPTLSAQPSPVVNSGGNVTLQCDSQVAFDGFILCKEGEDEHPQCLNSQPHARGSSRAIFSVGPVSPSRRWWYRCYAYDSNSPYEWSLPSDLLELLVLG

>d1f42a1 b.1.1.4 (A:1-87) The p40 domain of interleukin-12 (IL-12 beta chain), N-teminal domain {Human (Homo sapiens)}

IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKED

>d1jbja1 b.1.1.4 (A:101-186) CD3 gamma chain ectodomain fragment {Mouse (Mus musculus)}

KKDGSQTNKAKNLVQVDGSRGDGSVLLTCGLTDKTIKWLKDGSIISPLNATKNTWNLGNNAKDPRGTYQCQGAKETSNPLQVYYRM

>d1jbja2 b.1.1.4 (A:1-100) CD3 epsilon chain ectodomain fragment {Mouse (Mus musculus)}

DDAENIEYKVSISGTSVELTCPLDSDENLKWEKNGQELPQKHDKHLVLQDFSEVEDSGYYVCYTPASNKNTYLYLKARVGSADDAKKDAAKKDDAKKDDA

>d1k3ia1 b.1.1.5 (A:538-639) Galactose oxidase, C-terminal domain {Fungi (Fusarium spp)}

GNLATRPKITRTSTQSVKVGGRITISTDSSISKASLIRYGTATHTVNTDQRRIPLTLTNNGGNSYSFQVPSDSGVALPGYWMLFVMNSAGVPSVASTIRVTQ

>d1qba\_1 b.1.1.5 (781-885) Bacterial chitobiase, c-terminal domain {Serratia marcescens}

GETHFVDTQALEKDWLRFANILGQRELAKLDKGGVAYRLPVPGARVAGGKLEANIALPGLGIEYSTDGGKQWQRYDAKAKPAVSGEVQVRSVSPDGKRYSRAEKV

>d1svb\_1 b.1.1.5 (303-395) Envelope glycoprotein, domain III (C-terminal) {Tick-borne encephalitis virus}

TYTMCDKTKFTWKRAPTDSGHDTVVMEVTFSGTKPCRIPVRAVAHGSPDVNVAMLITPNPTIENNGGGFIEMQLPPGDNIIYVGELSHQWFQK

>d1cgt\_1 b.1.1.5 (495-579) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans, different strains}

ETTPTIGHVGPVMGKPGNVVTIDGRGFGSTKGTVYFGTTAVTGAAITSWEDTQIKVTIPSVAAGNYAVKVAASGVNSNAYNNFTI

>d1kcla1 b.1.1.5 (A:496-581) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans, different strains}

TATPTIGHVGPMMAKPGVTITIDGRGFGSSKGTVYFGTTAVSGADITSWEDTQIKVKIPAVAGGNYNIKVANAAGTASNVYDNFEV

>d1cyg\_1 b.1.1.5 (492-574) Cyclodextrin glycosyltransferase, domain E {Bacillus stearothermophilus}

ESTPIIGHVGPMMGQVGHQVTIDGEGFGTNTGTVKFGTTAANVVSWSNNQIVVAVPNVSPGKYNITVQSSSGQTSAAYDNFEV

>d1qhoa1 b.1.1.5 (A:496-576) Cyclodextrin glycosyltransferase, domain E {Bacillus stearothermophilus, maltogenic alpha-amylase}

ASAPQIGSVAPNMGIPGNVVTIDGKGFGTTQGTVTFGGVTATVKSWTSNRIEVYVPNMAAGLTDVKVTAGGVSSNLYSYNI

>d1pama1 b.1.1.5 (A:497-582) Cyclodextrin glycosyltransferase, domain E {Bacillus sp., strain 1011}

TTPIIGNVGPMMAKPGVTITIDGRGFGSGKGTVYFGTTAVTGADIVAWEDTQIQVKIPAVPGGIYDIRVANAAGAASNIYDNFEVL

>d1ciu\_1 b.1.1.5 (496-578) Cyclodextrin glycosyltransferase, domain E {Thermoanaerobacterium thermosulfurigenes, EM1}

SNSPLIGHVGPTMTKAGQTITIDGRGFGTTSGQVLFGSTAGTIVSWDDTEVKVKVPSVTPGKYNISLKTSSGATSNTYNNINI

>d1smaa1 b.1.1.5 (A:1-123) Maltogenic amylase, N-terminal domain {Thermus sp.}

MRKEAIHHRSTDNFAYAYDSETLHLRLQTKKNDVDHVELLFGDPYEWHDGAWQFQTMPMRKTGSDGLFDYWLAEVKPPYRRLRYGFVLRAGGEKLVYTEKGFYHEAPSDDTAYYFCFPFLHRV

>d1bvza1 b.1.1.5 (A:1-120) Maltogenic amylase, N-terminal domain {Thermoactinomyces vulgaris, TVAII}

MLLEAIFHEAKGSYAYPISETQLRVRLRAKKGDVVRCEVLYADRYASPEEELAHALAGKAGSDERFDYFEALLECSTKRVKYVFLLTGPQGEAVYFGETGFSAERSKAGVFQYAYIHRSE

>d1eh9a1 b.1.1.5 (A:1-90) Glycosyltrehalose trehalohydrolase, N-terminal domain {Archaeon Sulfolobus solfataricus, km1}

TFAYKIDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVLDDASEIPDPASRYQPEGVHGPSQIIQESKE

>d1bf2\_1 b.1.1.5 (1-162) Isoamylase, N-terminal domain {Pseudomonas amyloderamosa}

AINSMSLGASYDAQQANITFRVYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVWAVTVPVSSIKAAGITGAVYYGYRAWGPNWPYASNWGKGSQAGFVSDVDANGDRFNPNKLLLDPYAQEVSQDPLNPSNQNGNVFASGASYRTTDSGIYAPKGVVLV

>d1lla\_3 b.1.1.5 (380-628) Hemocyanin, C-terminal domain {Horseshoe crab (Limulus polyphemus)}

PYDHDVLNFPDIQVQDVTLHARVDNVVHTFMREQELELKHGINPGNARSIKARYYHLDHEPFSYAVNVQNNSASDKHATVRIFLAPKYDELGNEIKADELRRTAIELDKFKTDLHPGKNTVVRHSLDSSVTLSHQPTFEDLLHGVGLNEHKSEYCSCGWPSHLLVPKGNIKGMEYHLFVMLTDWDKDKVDGSESVACVDAVSYCGARDHKYPDKKPMGFPFDRPIHTEHISDFLTNNMFIKDIKIKFHE

>d1hc2\_3 b.1.1.5 (399-653) Hemocyanin, C-terminal domain {Spiny lobster (Panulirus interruptus)}

PPYTHDNLEFSGMVVNGVAIDGELITFFDEFQYSLINAVDSGENIEDVEINARVHRLNHNEFTYKITMSNNNDGERLATFRIFLCPIEDNNGITLTLDEARWFCIELDKFFQKVPSGPETIERSSKDSSVTVPDMPSFQSLKEQADNAVNGGHDLDLSAYERSCGIPDRMLLPKSKPEGMEFNLYVAVTDGDKDTEGHNGGHDYGGTHAQCGVHGEAYPDNRPLGYPLERRIPDERVIDGVSNIKHVVVKIVHHL

>d1js8a2 b.1.1.5 (A:2792-2892) C-terminal domain of octopus hemocyanin {Giant octopus (Octopus dofleini)}

EDRVFAGFLLRTIGQSADVNFDVCTKDGECTFGGTFCILGGEHEMFWAFDRLFKYDITTSLKHLRLDAHDDFDIKVTIKGIDGHVLSNKYLSPPTVFLAPA

>d1clc\_2 b.1.1.5 (35-134) CelD cellulase, N-terminal domain {Clostridium thermocellum}

IETKVSAAKITENYQFDSRIRLNSIGFIPNHSKKATIAANCSTFYVVKEDGTIVYTGTATSMFDNDTKETVYIADFSSVNEEGTYYLAVPGVGKSVNFKI

>d1f1sa2 b.1.1.5 (A:171-248) Hyaluronate lyase precatalytic domain {Streptococcus agalactiae}

SEHPQPVTTQIEKSVNTALNKNYVFNKADYQYTLTNPSLGKIVGGILYPNATGSTTVKISDKSGKIIKEVPLSVTAST

>d1edqa1 b.1.1.5 (A:24-132) Chitinase A, N-terminal domain {Serratia marcescens}

AAPGKPTIAWGNTKFAIVEVDQAATAYNNLVKVKNAADVSVSWNLWNGDTGTTAKVLLNGKEAWSGPSTGSSGTANFKVNKGGRYQMQVALCNADGCTASDATEIVVAD

>d1f13a1 b.1.1.5 (A:5-190) Transglutaminase N-terminal domain {Human (Homo sapiens)}

RTAFGGRRAVPPNNSNAAEDDLPTVELQGVVPRGVNLQEFLNVTSVHLFKERWDTNKVDHHTDKYENNKLIVRRGQSFYVQIDFSRPYDPRRDLFRVEYVIGRYPQENKGTYIPVPIVSELQSGKWGAKIVMREDRSVRLSIQSSPKCIVGKFRMYVAVWTPYGVLRTSRNPETDTYILFNPWCED

>d1g0da1 b.1.1.5 (A:6-140) Transglutaminase N-terminal domain {Red sea bream (Chrysophrys major)}

GLIVDVNGRSHENNLAHRTREIDRERLIVRRGQPFSITLQCSDSLPPKHHLELVLHLGKRDEVVIKVQKEHGARDKWWFNQQGAQDEILLTLHSPANAVIGHYRLAVLVMSPDGHIVERADKISFHMLFNPWCRD

>d1eut\_1 b.1.1.5 (403-505) Sialidase, "linker" domain {Micromonospora viridifaciens}

GICAPFTIPDVALEPGQQVTVPVAVTNQSGIAVPKPSLQLDASPDWQVQGSVEPLMPGRQAKGQVTITVPAGTTPGRYRVGATLRTSAGNASTTFTVTVGLLD

>d1ksr\_\_ b.1.1.5 (-) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}

ADPEKSYAEGPGLDGGECFQPSKFKIHAVDPDGVHRTDGGDGFVVTIEGPAPVDPVMVDNGDGTYDVEFEPKEAGDYVINLTLDGDNVNGFPKTVTVKPA

>d1qfha1 b.1.1.5 (A:646-749) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}

KPAPSAEHSYAEGEGLVKVFDNAPAEFTIFAVDTKGVARTDGGDPFEVAINGPDGLVVDAKVTDNNDGTYGVVYDAPVEGNYNVNVTLRGNPIKNMPIDVKCIE

>d1qfha2 b.1.1.5 (A:750-857) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}

GANGEDSSFGSFTFTVAAKNKKGEVKTYGGDKFEVSITGPAEEITLDAIDNQDGTYTAAYSLVGNGRFSTGVKLNGKHIEGSPFKQVLGNPGKKNPEVKSFTTTRTAN

>d1ds6b\_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}

GNYKPPPQKSLKELQEMDKDDESLIKYKKTLLGDGPVVTDPKAPNVVVTRLTLVCESAPGPITMDLTGDLEALKKETIVLKEGSEYRVKIHFKVNRDIVSGLKYVQHTYRTGVKVDKATFMVGSYGPRPEEYEFLTPVEEAPKGMLARGTYHNKSFFTDDDKQDHLSWEWNLSIKKEWG

>d1fsoa\_ b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}

MVPNVVVTGLTLVCSSAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRAGVAIDATDYMVGSYGPRAEEYEFLTPVEEAPKGMLARGSYSIKSRFTDDDKTDHLSWEWNFTIKKDWK

>d1hh4e\_ b.1.1.5 (E:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}

HSVNYKPPAQKSIQEIQELDKDDESLRKYKEALLGRVAVSADPNVPNVVVTGLTLVCSSAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMVGSYGPRAEEYEFLTPVEEAPKGMLARGSYSIKSRFTDDDKTDHLSWEWNLTIKKDW

>d1rhoa\_ b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}

VAVSADPNVPNVVVTGLTLVCSSAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIEHTYRKGVKIDKTDYMVGSYGPRAEEYEFLTPVEEAPKGMLARGSYSIKSRFTDDDKTDHLSWEWNLTIKKDWK

>d1ajw\_\_ b.1.1.5 (-) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}

AVSADPNVPNVVVTRLTLVCSTAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMVGSYGPRAEEYEFLTPMEEAPKGMLARGSYNIKSRFTDDDRTDHLSWEWNLTIKKEWKD

>d1doab\_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}

EPTAEQLAQIAAENEEDEHSVNYKPPAQKSIQEIQELDKDDESLRKYKEALLGRVAVSADPNVPNVVVTRLTLVCSTAPGPLELDLTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMVGSYGPRAEEYEFLTPMEEAPKGMLARGSYNIKSRFTDDDRTDHLSWEWNLTIKKEWKD

>d1ayra2 b.1.1.5 (A:183-368) Arrestin {Cow (Bos taurus), visual arrestin}

DMGPQPRAEASWQFFMSDKPLRLAVSLSKEIYYHGEPIPVTVAVTNSTEKTVKKIKVLVEQVTNVVLYSSDYYIKTVAAEEAQEKVPPNSSLTKTLTLVPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDKTVMGILVSYQIKVKLTVSGLLGELTSSEVATEVPFRLMHPQPEDPDTAKA

>d1cf1a1 b.1.1.5 (A:10-182) Arrestin {Cow (Bos taurus), visual arrestin}

HVIFKKISRDKSVTIYLGKRDYIDHVERVEPVDGVVLVDPELVKGKRVYVSLTCAFRYGQEDIDVMGLSFRRDLYFSQVQVFPPVGASGATTRLQESLIKKLGANTYPFLLTFPDYLPCSVMLQPAPQDVGKSCGVDFEIKAFATHSTDVEEDKIPKKSSVRLLIRKVQHAPR

>d1cf1a2 b.1.1.5 (A:183-393) Arrestin {Cow (Bos taurus), visual arrestin}

DMGPQPRAEASWQFFMSDKPLRLAVSLSKEIYYHGEPIPVTVAVTNSTEKTVKKIKVLVEQVTNVVLYSSDYYIKTVAAEEAQEKVPPNSSLTKTLTLVPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDKTVMGILVSYQIKVKLTVSGLLGELTSSEVATEVPFRLMHPQPEDPDTAKESFQDENFVFEEFARQNLKDAGEYKE

>d1g4ma1 b.1.1.5 (A:5-175) Arrestin {Cow (Bos taurus), beta-arrestin 1}

GTRVFKKASPNGKLTVYLGKRDFVDHIDLVEPVDGVVLVDPEYLKERRVYVTLTCAFRYGREDLDVLGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERLIKKLGEHAYPFTFEIPPNLPCSVTLQPGPEDTGKACGVDYEVKAFCAENLEEKIHKRNSVRLVIRKVQYAP

>d1g4ma2 b.1.1.5 (A:176-393) Arrestin {Cow (Bos taurus), beta-arrestin 1}

ERPGPQPTAETTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVKKIKISVRQYADICLFNTAQYKCPVAMEEADDTVAPSSTFCKVYTLTPFLANNREKRGLALDGKLKHEDTNLASSTLLREGANREILGIIVSYKVKVKLVVSRGGLLGDLASSDVAVELPFTLMHPKPKEEPPHREVPEHETPVDTNLIELDTNDDDIVFEDFAR

>d1a02n1 b.1.1.5 (N:577-678) Transcription factor NFATC, C-terminal domain {Human (Homo sapiens)}

LPMVERQDTDSCLVYGGQQMILTGQNFTSESKVVFTEKTTDGQQIWEMEATVDKDKSQPNMLFVEIPEYRNKHIRTPVKVNFYVINGKRKRSQPQHFTYHPV

>d1imhc1 b.1.1.5 (C:368-468) Transcription factor TONEBP, C-terminal domain {Human (Homo sapiens)}

VPEILKKSLHSCSVKGEEEVFLIGKNFLKGTKVIFQENVSDENSWKSEAEIDMELFHQNHLIVKVPPYHDQHITLPVSVGIYVVTNAGRSHDVQPFTYTPD

>d1bfs\_\_ b.1.1.5 (-) p50 subunit of NF-kappa B transcription factor, C-terminal domain {Mouse (Mus musculus)}

ASNLKIVRMDRTAGCVTGGEEIYLLCDKVQKDDIQIRFYEEEENGGVWEGFGDFSPTDVHRQFAIVFKTPKYKDVNITKPASVFVQLRRKSDLETSEPKPFLYYPE

>d1a3qa1 b.1.1.5 (A:227-327) p52 subunit of NF-kappa B (NFKB), C-terminal domain {Human (Homo sapiens)}

NLKISRMDKTAGSVRGGDEVYLLCDKVQKDDIEVRFYEDDENGWQAFGDFSPTDVHKQYAIVFRTPPYHKMKIERPVTVFLQLKRKRGGDVSDSKQFTYYP

>d1bfta\_ b.1.1.5 (A:) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Mouse (Mus musculus)}

TAELKICRVNRNSGSCLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTPPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPD

>d1ikna1 b.1.1.5 (A:192-303) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Mouse (Mus musculus)}

AELKICRVNRNSGSCLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTPPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPDTDDRHRIEEKRK

>d1nfia1 b.1.1.5 (A:190-314) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Human (Homo sapiens)}

NTAELKICRVNRNSGSCLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTPPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPDTDDRHRIEEKRKRTYETFKSIMK

>d1ahm\_\_ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides farinae), Der f 2}

DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFTLEALFDANQNTKTAKIEIKASLDGLEIDVPGIDTNACHFVKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKLIGDNGVLACAIATHGKIRD

>d1a9v\_\_ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides pteronyssinus), Der p 2}

SQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKIEIKASIDGLEVDVPGIDPNACHYMKCPLVKGQQYDIKYTWNVPKIAPKSENVVVTVKVMGDDGVLACAIATHAKIRD

>d1soxa1 b.1.1.5 (A:344-466) Sulfite oxidase, C-terminal domain {Chicken (Gallus gallus)}

ELPVQSAVTQPRPGAAVPPGELTVKGYAWSGGGREVVRVDVSLDGGRTWKVARLMGDKAPPGRAWAWALWELTVPVEAGTELEIVCKAVDSSYNVQPDSVAPIWNLRGVLSTAWHRVRVSVQD

>d1cvra1 b.1.1.5 (A:351-432) Gingipain R (RgpB), C-terminal domain {Porphyromonas gingivalis}

PTEMQVTAPANISASAQTFEVACDYNGAIATLSDDGDMVGTAIVKDGKAIIKLNESIADETNLTLTVVGYNKVTVIKDVKVE

>d1h6ta1 b.1.1.6 (A:241-321) Internalin B {Listeria monocytogenes}

ECLNKPINHQSNLVVPNTVKNTDGSLVTPEIISDDGDYEKPNVKWHLPEFTNEVSFIFYQPVTIGKAKARFHGRVTQPLKE

>d1h6ua1 b.1.1.6 (A:263-343) Internalin H {Listeria monocytogenes}

TITNQPVFYNNNLVVPNVVKGPSGAPIAPATISDNGTYASPNLTWNLTSFINNVSYTFNQSVTFKNTTVPFSGTVTQPLTE

>d1ehxa\_ b.1.1.6 (A:) Cellulosomal scaffoldin protein CipC, module x2.1 {Clostridium cellulolyticum}

MQDPTINPTSISAKAGSFADTKITLTPNGNTFNGISELQSSQYTKGTNEVTLLASYLNTLPENTTKTLTFDFGVGTKNPKLTITVLPKDIPGLE

>d1im3d\_ b.1.1.6 (D:) Cytomegalovirus protein US2 {Human cytomegalovirus}

PWFQIEDNRCYIDNGKLFARGSIVGNMSRFVFDPKADYGGVGENLYVHADDVEFVPGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPEL

>d1jjua3 b.1.1.6 (A:274-351) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}

AAPQVLAVAPARLKIGEETQLRVAGTGLGSDLTLPEGVAGSVESAGNGVTVLKLTATGTPGPVSLELGGQKVDLVAYD

>d1jjua4 b.1.1.6 (A:352-489) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}

RPDRISIVPDLTIARIGGNGGPIPKVPAQFEAMGWLNGPDGQPGTGDDIALGAFPASWATDNFDEEAEKMQDAKYAGSIDDTGLFTPAEAGPNPERPMQTNNAGNLKVIATVDAEGEPLSAEAHLYATVQRFVDAPIR

>d1jmxa3 b.1.1.6 (A:282-363) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Pseudomonas putida}

GKARLLAVQPAFIKAGGESEITLVGSGLAGKPDLGAGVEVTEVLEQTPTLVRLKARAAADAKPGQREVAVGTLKGVNLAVYD

>d1jmxa4 b.1.1.6 (A:364-494) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Pseudomonas putida}

KVEEVKVVPAFSIARIGENGASVPKVQGRFEAEAWGKDANGQPLRIGYLPASWKVEPFNERAVEDEDVKFAGKMQADGVFVPGGAGPNPERKMMTNNAGNLKVIATLADGGQTGEGHMIVTVQRWNNPPLP

>d2hft\_1 b.1.2.1 (1-106) Extracellular region of human tissue factor {Human (Homo sapiens)}

SGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLET

>d2hft\_2 b.1.2.1 (107-211) Extracellular region of human tissue factor {Human (Homo sapiens)}

NLGQPTIQSFEQVGTKVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSQEKGEFRSGKKTAKTNTNEFLIDVDKGENYCFSVQAVIPSRTVNRKSTDSPVECMG

>g1dan.1 b.1.2.1 (T:,U:91-106) Extracellular region of human tissue factor {Human (Homo sapiens)}

TVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAXEPLYENSPEFTPYLET

>d1a21a1 b.1.2.1 (A:4-106) Extracellular region of human tissue factor {Rabbit (Oryctolagus cuniculus)}

TGRAYNLTWKSTNFKTILEWEPKSIDHVYTVQISTRLENWKSKCFLTAETECDLTDEVVKDVGQTYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNL

>d1a21a2 b.1.2.1 (A:107-208) Extracellular region of human tissue factor {Rabbit (Oryctolagus cuniculus)}

GQPTIQSFEQVGTKLNVTVQDARTLVRRNGTFLSLRAVFGKDLNYTLYYWRASSTGKKTATTNTNEFLIDVDKGENYCFSVQAVIPSRKRKQRSPESLTECT

>d1fna\_\_ b.1.2.1 (-) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

RDLEVVAATPTSLLISWDAPAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPISINYRTEI

>d1fnf\_1 b.1.2.1 (1142-1235) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

PLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDDKESVPISDTIIPA

>d1fnf\_2 b.1.2.1 (1236-1326) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

VPPPTDLRFTNIGPDTMRVTWAPPPSIDLTNFLVRYSPVKNEEDVAELSISPSDNAVVLTNLLPGTEYVVSVSSVYEQHESTPLRGRQKTG

>d1fnf\_3 b.1.2.1 (1327-1415) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

LDSPTGIDFSDITANSFTVHWIAPRATITGYRIRHHPEHFSGRPREDRVPHSRNSITLTNLTPGTEYVVSIVALNGREESPLLIGQQST

>d1fnha1 b.1.2.1 (A:3-92) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

PAPTDLKFTQVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSSSVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLE

>d1fnha2 b.1.2.1 (A:93-182) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

NVSPPRRARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKPDVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTA

>d1fnha3 b.1.2.1 (A:183-271) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

IDAPSNLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRPRPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKT

>d1j8ka\_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

NIDRPKGLAFTDVDVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTAELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPA

>d2fnba\_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

MRGSEVPQLTDLSFVDITDSSIGLRWTPLNSSTIIGYRITVVAAGEGIPIFEDFVDSSVGYYTVTGLEPGIDYDISVITLINGGESAPTTLTQQT

>d2mfn\_1 b.1.2.1 (1-92) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}

GLDSPTGFDSSDITANSFTVHWVAPRAPITGYIIRHHAEHSVGRPRQDRVPPSRNSITLTNLNPGTEYVVSIIAVNGREESPPLIGQQATVS

>d2mfn\_2 b.1.2.1 (93-184) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}

DIPRDLEVIASTPTSLLISWEPPAVSVRYYRITYGETGGNSPVQEFTVPGSKSTATINNIKPGADYTITLYAVTGRGDSPASSKPVSINYKT

>d1qr4a1 b.1.2.1 (A:1-87) Tenascin {Chicken (Gallus gallus)}

DNPKDLEVSDPTETTLSLRWRRPVAKFDRYRLTYVSPSGKKNEMEIPVDSTSFILRGLDAGTEYTISLVAEKGRHKSKPTTIKGSTV

>d1qr4a2 b.1.2.1 (A:88-175) Tenascin {Chicken (Gallus gallus)}

VGSPKGISFSDITENSATVSWTPPRSRVDSYRVSYVPITGGTPNVVTVDGSKTRTKLVKLVPGVDYNVNIISVKGFEESEPISGILKT

>d1ten\_\_ b.1.2.1 (-) Tenascin {Human (Homo sapiens)}

RLDAPSQIEVKDVTDTTALITWFKPLAEIDGIELTYGIKDVPGDRTTIDLTEDENQYSIGNLKPDTEYEVSLISRRGDMSSNPAKETFTT

>d1cfb\_1 b.1.2.1 (610-709) Neuroglian, two amino proximal Fn3 repeats {Drosophila melanogaster}

IVQDVPNAPKLTGITCQADKAEIHWEQQGDNRSPILHYTIQFNTSFTPASWDAAYEKVPNTDSSFVVQMSPWANYTFRVIAFNKIGASPPSAHSDSCTTQ

>d1cfb\_2 b.1.2.1 (710-814) Neuroglian, two amino proximal Fn3 repeats {Drosophila melanogaster}

PDVPFKNPDNVVGQGTEPNNLVISWTPMPEIEHNAPNFHYYVSWKRDIPAAAWENNNIFDWRQNNIVIADQPTFVKYLIKVVAINDRGESNVAAEEVVGYSGEDR

>d1qg3a1 b.1.2.1 (A:1126-1217) Integin beta-4 subunit {Human (Homo sapiens)}

DLGAPQNPNAKAAGSRKIHFNWLPPSGKPMGYRVKYWIQGDSESEAHLLDSKVPSVELTNLYPYCDYEMKVCAYGAQGEGPYSSLVSCRTHQ

>d1qg3a2 b.1.2.1 (A:1218-1320) Integin beta-4 subunit {Human (Homo sapiens)}

EVPSEPGRLAFNVVSSTVTQLSWAEPAETNGEITAYEVCYGLVNDDNRPIGPMKKVLVDNPKNRMLLIENLRESQPYRYTVKARNGAGWGPEREAIINLATQP

>d1axib1 b.1.2.1 (B:32-130) Growth hormone receptor {Human (Homo sapiens)}

EPKFTKCRSPERETFSCHWTDEVHHGTKNEGPIQLFYTRRNTQEWTQEWKECPDYVSAGENSCYFNSSFTSIAIPYCIKLTSNGGTVDEKCFSVDEIVQ

>d1axib2 b.1.2.1 (B:131-236) Growth hormone receptor {Human (Homo sapiens)}

PDPPIALNWTLLNVSLTGIHADIQVRWEAPRNADIQKGWMVLEYELQYKEVNETKWKMMDPILTTSVPVYSLKVDKEYEVRVRSKQRNSGNYGEFSEVLYVTLPQM

>d1eerb1 b.1.2.1 (B:8-116) Erythropoietin (EPO) receptor {Human (Homo sapiens)}

DPKFESKAALLAARGPEELLCFTERLEDLVCFWEEAASAGVGPGQYSFSYQLEDEPWKLCRLHQAPTARGAVRFWCSLPTADTSSFVPLELRVTAASGAPRYHRVIHIN

>d1eerb2 b.1.2.1 (B:117-220) Erythropoietin (EPO) receptor {Human (Homo sapiens)}

EVVLLDAPVGLVARLADESGHVVLRWLPPPETPMTSHIRYEVDVSAGQGAGSVQRVEILEGRTECVLSNLRGRTRYTFAVRARMAEPSFGGFWSEWSEPVSLLT

>d1bp3b1 b.1.2.1 (B:202-300) Prolactin receptor {Human (Homo sapiens)}

LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYI

>d1bp3b2 b.1.2.1 (B:301-404) Prolactin receptor {Human (Homo sapiens)}

VQPDPPLELAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWEIHFAGQQTEFKILSLHPGQKYLVQVRCKPDHGYWSAWSPATFIQIPS

>d1f6fb1 b.1.2.1 (B:5-100) Prolactin receptor {Rat (Rattus norvegicus)}

GKPEIHKCRSPDKETFTCWWNPGTDGGLPTNYSLTYSKEGEKTTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYI

>d1f6fb2 b.1.2.1 (B:101-203) Prolactin receptor {Rat (Rattus norvegicus)}

VEPEPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIRLKPEEAEEWEIHFTGHQTQFKVFDLYPGQKYLVQTRCKPDHGYWSRWSQESSVEMP

>d1iarb1 b.1.2.1 (B:1-96) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}

FKVLQEPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPSEHV

>d1iarb2 b.1.2.1 (B:97-197) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}

KPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVNIWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQAYNTTWSEWSPSTKWH

>d1egja\_ b.1.2.1 (A:) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

IQMAPPSLNVTKDGDSYSLRWETMKMRYEHIDHTFEIQYRKDTATWKDSKTETLQNAHSMALPALEPSTRYWARVRVRTSRTGYNGIWSEWSEARSWDTES

>d1gh7a1 b.1.2.1 (A:1-103) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

EETIPLQTLRCYNDYTSHITCRWADTQDAQRLVNVTLIRRVNEDLLEPVSCDLSDDMPWSACPHPRCVPRRCVIPCQSFVVTDVDYFSFQPDRPLGTRLTVTL

>d1gh7a2 b.1.2.1 (A:104-217) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

TQHVQPPEPRDLQISTDQDHFLLTWSVALGSPQSHWLSPGDLEFEVVYKRLQDSWEDAAILLSNTSQATLGPEHLMPSSTYVARVRTRLAPGSRLSGRPSKWSPEVCWDSQPGD

>d1gh7a3 b.1.2.1 (A:218-316) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

EAQPQNLECFFDGAAVLSCSWEVRKEVASSVSFGLFYKPSPDAGSAVLLREEECSPVLREGLGSLHTRHHCQIPVPDPATHGQYIVSVQPRRAEKHIKS

>d1cd9b1 b.1.2.1 (B:1-107) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse (Mus musculus)}

AGYPPASPSNLSCLMHLTTNSLVCQWEPGPETHLPTSFILKSFRSRADCQYQGDTIPDCVAKKRQNNCSIPRKNLLLYQYMAIWVQAENMLGSSESPKLCLDPMDVV

>d1cd9b2 b.1.2.1 (B:108-213) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse (Mus musculus)}

KLEPPMLQALDIGPDVVSHQPGCLWLSWKPWKPSEYMEQECELRYQPQLKGANWTLVFHLPSSKDQFELCGLHQAPVYTLQMRCIRSSLPGFWSPWSPGLQLRPTM

>d1fyhb1 b.1.2.1 (B:12-109) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}

VPTPTNVTIESYNMNPIVYWEYQIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPSNSLWVRVKARVGQKESAYAKSEEFAVCRDGK

>d1fyhb2 b.1.2.1 (B:110-223) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}

IGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVYNVYVRMNGSEIQYKILTQKEDDCDEIQCQLAIPVSSLNSQYCVSAEGVLHVWGVTTEKSKEVCITIFN

>d1bqua1 b.1.2.1 (A:5-99) Cytokyne receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

GLPPEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVDYSTVYFVNIEVWVEAENALGKVTSDHINFDPV

>d1bqua2 b.1.2.1 (A:100-214) Cytokyne receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

YKVKPNPPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDTASTRSSFTVQDLKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRPSKEPSF

>d1i1ra1 b.1.2.1 (A:2-101) Cytokyne receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

LLDPCGYISPESPVVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIASLNIQLTCNILTFGQLEQNVYGITIISG

>d1j7vr1 b.1.2.1 (R:2-100) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}

GTELPSPPSVWFEAEFFHHILHWTPIPQQSESTCYEVALLRYGIESWNSISQCSQTLSYDLTAVTLDLYHSNGYRARVRAVDGSRHSQWTVTNTRFSVD

>d1j7vr2 b.1.2.1 (R:101-206) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}

EVTLTVGSVNLEIHNGFILGKIQLPRPKMAPAQDTYESIFSHFREYEIAIRKVPGQFTFTHKKVKHEQFSLLTSGEVGEFCVQVKPSVASRSNKGMWSKEECISLT

>d1bpv\_\_ b.1.2.1 (-) Type I titin module {Human (Homo sapiens)}

SPIDPPGKPVPLNITRHTVTLKWAKPEYTGGFKITSYIVEKRDLPNGRWLKANFSNILENEFTVSGLTEDAAYEFRVIAKNAAGAISPPSEPSDAITCRDDVEA

>d1f42a2 b.1.2.1 (A:88-211) The p40 domain of interleukin-12 (IL-12 beta chain), domains 2 and 3 {Human (Homo sapiens)}

GIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEYEYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDII

>d1f42a3 b.1.2.1 (A:212-306) The p40 domain of interleukin-12 (IL-12 beta chain), domains 2 and 3 {Human (Homo sapiens)}

KPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS

>d1b4ra\_ b.1.3.1 (A:) Polycystein-1, PKD-1 {Human (Homo sapiens)}

ATLVGPHGPLASGQLAAFHIAAPLPVTATRWDFGDGSAEVDAAGPAASHRYVLPGRYHVTAVLALGAGSALLGTDVQVEA

>d1jz8a1 b.1.4.1 (A:220-333) beta-Galactosidase, domains 2 and 4 {Escherichia coli}

TQISDFHVATRFNDDFSRAVLEAEVQMCGELRDYLRVTVSLWQGETQVASGTAPFGGEIIDERGGYADRVTLRLNVENPKLWSAEIPNLYRAVVELHTADGTLIEAEACDVGFR

>d1jz8a2 b.1.4.1 (A:626-730) beta-Galactosidase, domains 2 and 4 {Escherichia coli}

FFQFRLSGQTIEVTSEYLFRHSDNELLHWMVALDGKPLASGEVPLDVAPQGKQLIELPELPQPESAGQLWLTVRVVQPNATAWSEAGHISAWQQWRLAENLSVTL

>d1bhga1 b.1.4.1 (A:226-328) beta-Glucuronidase {Human (Homo sapiens)}

TYIDDITVTTSVEQDSGLVNYQISVKGSNLFKLEVRLLDAENKVVANGTGTQGQLKVPGVSLWWPYLMHERPAYLYSLEVQLTAQTSLGPVSDFYTLPVGIRT

>d1f13a2 b.1.5.1 (A:516-627) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}

SNVDMDFEVENAVLGKDFKLSITFRNNSHNRYTITAYLSANITFYTGVPKAEFKKETFDVTLEPLSFKKEAVLIQAGEYMGQLLEQASLHFFVTARINETRDVLAKQKSTVL

>d1f13a3 b.1.5.1 (A:628-728) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}

TIPEIIIKVRGTQVVGSDMTVTVEFTNPLKETLRNVWVHLDGPGVTRPMKKMFREIRPNSTVQWEEVCRPWVSGHRKLIASMSSDSLRHVYGELDVQIQRR

>d1g0da2 b.1.5.1 (A:472-583) Transglutaminase, two C-terminal domains {Red sea bream (Chrysophrys major)}

RLQLSIKHAQPVFGTDFDVIVEVKNEGGRDAHAQLTMLAMAVTYNSLRRGECQRKTISVTVPAHKAHKEVMRLHYDDYVRCVSEHHLIRVKALLDAPGENGPIMTVANIPLS

>d1g0da3 b.1.5.1 (A:584-684) Transglutaminase, two C-terminal domains {Red sea bream (Chrysophrys major)}

TPELLVQVPGKAVVWEPLTAYVSFTNPLPVPLKGGVFTLEGAGLLSATQIHVNGAVAPSGKVSVKLSFSPMRTGVRKLLVDFDSDRLKDVKGVTTVVVHKK

>d1ncia\_ b.1.6.1 (A:) N-cadherin (neural) {Mouse (Mus musculus)}

GSDWVIPPINLPENSRGPFPQELVRIRSGRDKNLSLRYSVTGPGADQPPTGIFIINPISGQLSVTKPLDRELIARFHLRAHAVDINGNQVENPIDIVINVID

>d1ncja2 b.1.6.1 (A:102-215) N-cadherin (neural) {Mouse (Mus musculus)}

NDNRPEFLHQVWNGSVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRIVSQAPSTPSPNMFTINNETGDIITVAAGLDREKVQQYTLIIQATDMEGNPTYGLSNTATAVITVTD

>d1edha1 b.1.6.1 (A:3-101) E-cadherin (epithelial) {Mouse (Mus musculus)}

VIPPISCPENEKGEFPKNLVQIKSNRDKETKVFYSITGQGADKPPVGVFIIERETGWLKVTQPLDREAIAKYILYSHAVSSNGEAVEDPMEIVITVTDQ

>d1edha2 b.1.6.1 (A:102-213) E-cadherin (epithelial) {Mouse (Mus musculus)}

NDNRPEFTQEVFEGSVAEGAVPGTSVMKVSATDADDDVNTYNAAIAYTIVSQDPELPHKNMFTVNRDTGVISVLTSGLDRESYPTYTLVVQAADLQGEGLSTTAKAVITVKD

>d2mcm\_\_ b.1.7.1 (-) Macromycin {Streptomyces macromomyceticus}

APGVTVTPATGLSNGQTVTVSATGLTPGTVYHVGQCAVVEPGVIGCDATTSTDVTADAAGKITAQLKVHSSFQAVVGADGTPWGTVNCKVVSCSAGLGSDSGEGAAQAITFA

>d1noa\_\_ b.1.7.1 (-) Neocarzinostatin {Streptomyces carzinostaticus}

AAPTATVTPSSGLSDGTVVKVAGAGLQAGTAYDVGQCAWVDTGVLACNPADFSSVTADANGSASTSLTVRRSFEGFLFDGTRWGTVDCTTAACQVGLSDAAGNGPEGVAISFN

>d1acx\_\_ b.1.7.1 (-) Actinoxanthin {Actinomyces globisporus, number 1131}

APAFSVSPASGASDGQSVSVSVAAAGETYYIAQCAPVGGQDACNPATATSFTTDASGAASFSFTVRKSYAGQTPSGTPVGSVDCATDACNLGAGNSGLNLGHVALTFG

>d1hzka\_ b.1.7.1 (A:) Antitumor antibiotic C-1027 apoprotein {Streptomyces globisporus}

APAFSVSPASGLSDGQSVSVSVSGAAAGETYYIAQCAPVGGQDACNPATATSFTTDASGAASFSFVVRKSYTGSTPEGTPVGSVDCATAACNLGAGNSGLDLGHVALTFG

>d1akp\_\_ b.1.7.1 (-) Kedarcidin (apo form) {Actimomycete, strain L585-6}

ASAAVSVSPATGLADGATVTVSASGFATSTSATALQCAILADGRGACNVAEFHDFSLSGGEGTTSVVVRRSFTGYVMPDGPEVGAVDCDTAPGGCEIVVGGNTGEYGNAAISFG

>d1cbja\_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Cow (Bos taurus)}

ATKAVCVLKGDGPVQGTIHFEAKGDTVVVTGSITGLTEGDHGFHVHQFGDNTQGCTSAGPHFNPLSKKHGGPKDEERHVGDLGNVTADKNGVAIVDIVDPLISLSGEYSIIGRTMVVHEKPDDLGRGGNEESTKTGNAGSRLACGVIGIAK

>d1azva\_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Human (Homo sapiens)}

ATKAVCVLKGDGPVQGIINFEQKESNGPVKVWGSIKRLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGVADVSIEDSVISLSGDHCIIGRTLVVHEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQ

>d1xsoa\_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {African clawed frog (Xenopus laevis)}

VKAVCVLAGSGDVKGVVHFEQQDEGAVSVEGKIEGLTDGLHGFHIHVFGDNTNGCMSAGSHFNPENKNHGAPGDTDRHVGDLGNVTAEGGVAQFKITDSLISLKGPNSIIGRTAVVHEKADDLGKGGNDESLKTGNAGGRLACGVIGYSP

>d1srda\_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Spinach (Spinacia oleracea)}

ATKKAVAVLKGTSNVEGVVTLTQEDDGPTTVNVRISGLAPGKHGFHLHEFGDTTNGCMSTGPHFNPDKKTHGAPEDEVRHAGDLGNIVANTDGVAEATIVDNQIPLTGPNSVVGRALVVHELEDDLGKGGHELSPTTGNAGGRLACGVVGLTPV

>d1jcv\_\_ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Baker's yeast (Saccharomyces cerevisiae)}

VQAVAVLKGDAGVSGVVKFEQASESEPTTVSYEIAGNSPNAERGFHIHEFGDATNGCVSAGPHFNPFKKTHGAPTDEVRHVGDMGNVKTDENGVAKGSFKDSLIKLIGPTSVVGRSVVIHAGQDDLGKGDTEESLKTGNAGPRPACGVIGLTN

>d1yaia\_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Photobacterium leiognathi}

QDLTVKMTDLQTGKPVGTIELSQNKYGVVFTPELADLTPGMHGFHIHQNGSCASSEKDGKVVLGGAAGGHYDPEHTNKHGFPWTDDNHKGDLPALFVSANGLATNPVLAPRLTLKELKGHAIMIHAGGDNHSDMPKALGGGGARVACGVIQ

>d1eso\_\_ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Escherichia coli}

ASEKVEMNLVTSQGVGQSIGSVTITETDKGLEFSPDLKALPPGEHGFHIHAKGSCQPATKDGKASAAESAGGHLDPQNTGKHEGPEGAGHLGDLPALVVNNDGKATDAVIAPRLKSLDEIKDKALMVHVGGDNMSDQPKPLGGGGERYACGVIK

>d1eqwa\_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Salmonella typhimurium}

NTLTVKMNDALSSGTGENIGEITVSETPYGLLFTPHLNGLTPGIHGFHVHTNPSCMPGMKDGKEVPALMAGGHLDPEKTGKHLGPYNDKGHLGDLPGLVVNADGTATYPLLAPRLKSLSELKGHSLMIHKGGDNYSDKPAPLGGGGARFACGVIE

>d2apsa\_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Actinobacillus pleuropneumoniae}

EKLVVQVQQLDPVKGNKDVGTVEITESAYGLVFTPHLHGLAQGLHGFHIHQNPSCEPKEKDGKLVAGLGAGGHWDPKETKQHGYPWSDNAHLGDLPALFVEHDGSATNPVLAPRLKKLDEVKGHSLMIHEGGDNHSDHPAPLGGGGPRMACGVIK

>d1ej8a\_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

SSAVAILETFQKYTIDQKKDTAVRGLARIVQVGENKTLFDITVNGVPEAGNYHASIHEKGDVSKGVESTGKVWHKFDEPIECFNESDLGKNLYSGKTFLSAPLPTWQLIGRSFVISKSLNHPENEPSSVKDYSFLGVIAR

>d1jk9b1 b.1.8.1 (B:74-245) Copper chaperone for superoxide dismutase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

GKPNSSAVAILETFQKYTIDQKKDTAVRGLARIVQVGENKTLFDITVNGVPEAGNYHASIHEKGDVSKGVESTGKVWHKFDEPIECFNESDLGKNLYSGKTFLSAPLPTWQLIGRSFVISKSLNHPENEPSSVKDYSFLGVIARSAGVWENNKQVCACTGKTVWEERKDALA

>d1do5a\_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase, C-terminal domain {Human (Homo sapiens)}

QNLGAAVAILGGPGTVQGVVRFLQLTPERCLIEGTIDGLEPGLHGLHVHQYGDLTNNCNSCGNHFNPDGASHGGPQDSDRHRGDLGNVRADADGRAIFRMEDEQLKVWDVIGRSLIIDEGEDDLGRGGHPLSKITGNSGERLACGIIARSAGLF

>d1d7ca\_ b.1.9.1 (A:) Cytochrome domain of cellobiose dehydrogenase {Fungus (Phanerochaete chrysosporium)}

ESASQFTDPTTGFQFTGITDPVHDVTYGFVFPPLATSGAQSTEFIGEVVAPIASKWIGIALGGAMNNDLLLVAWANGNQIVSSTRWATGYVQPTAYTGTATLTTLPETTINSTHWKWVFRCQGCTEWNNGGGIDVTSQGVLAWAFSNVAVDDPSDPQSTFSEHTDFGFFGIDYSTAHSANYQNYLNGDSG

>d1i8aa\_ b.1.9.2 (A:) Xylanase 10A {Thermotoga maritima}

MVATAKYGTPVIDGEIDEIWNTTEEIETKAVAMGSLDKNATAKVRVLWDENYLYVLAIVKDPVLNKDNSNPWEQDSVEIFIDENNHKTGYYEDDDAQFRVNYMNEQTFGTGGSPARFKTAVKLIEGGYIVEAAIKWKTIKPTPNTVIGFNIQVNDANEKGQRVGIISWSDPTNNSWRDPSKFGNLRLIK

>d1qtsa1 b.1.10.1 (A:692-824) Alpa-adaptin AP2, N-terminal subdomain {Mouse (Mus musculus)}

GSPGIRLGSSEDNFARFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFLNFTPTLICADDLQTNLNLQTKPVDPTVDGGAQVQQVVNIECISDFTEAPVLNIQFRYGGTFQNVSVKLPITLNK

>d1e42a1 b.1.10.1 (A:705-824) Beta2-adaptin AP2, N-terminal subdomain {Human (Homo sapiens)}

GGYVAPKAVWLPAVKAKGLEISGTFTHRQGHIYMEMNFTNKALQHMTDFAIQFNKNSFGVIPSTPLAIHTPLMPNQSIDVSLPLNTLGPVMKMEPLNNLQVAVKNNIDVFYFSCLIPLNV

>d1jv2a1 b.1.15.1 (A:439-598) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo sapiens)}

PVITVNAGLEVYPSILNQDNKTCSLPGTALKVSCFNVRFCLKADGKGVLPRKLNFQVELLLDKLKQKGAIRRALFLYSRSPSHSKNMTISRGGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAADTTGLQPILNQFTPANISRQAHILLDCGE

>d1jv2a2 b.1.15.1 (A:599-737) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo sapiens)}

DNVCKPKLEVSVDSDQKKIYIGDDNPLTLIVKAQNQGEGAYEAELIVSIPLQADFIGVVRNNEALARLSCAFKTENQTRQVVCDLGNPMKAGTQLLAGLRFSVHQQSEMDTSVKFDLQIQSSNLFDKVSPVVSHKVDLA

>d1jv2a3 b.1.15.1 (A:738-956) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo sapiens)}

VLAAVEIRGVSSPDHVFLPIPNWEHKENPETEEDVGPVVQHIYELRNNGPSSFSKAMLHLQWPYKYNNNTLLYILHYDIDGPMNCTSDMEINPLRIKISSLQTTEKNDTVAGQGERDHLITKRDLALSEGDIHTLGCGVAQCLKIVCQVGRLDRGKSAILYVKSLLWTETFMNKENQNHSYSLKSSASFNVIEFPYKNLPIEDITNSTLVTTNVTWGIQ

>d1jv2b1 b.1.15.1 (B:55-106,B:355-434) Hybrid domain of integrin beta {Human (Homo sapiens)}

EFPVSEARVLEDRPLSDKGSGDSSQVTQVSPQRIALRLRPDDSKNFSIQVRQXVELEVRDLPEELSLSFNATCLNNEVIPGLKSCMGLKIGDTVSFSIEAKVRGCPQEKEKSFTIKPVGFKDSLIVQVTFDCD

>d1qpxa1 b.1.11.1 (A:1-124) Pilus chaperone PapD, N-domain {Escherichia coli}

AVSLDRTRAVFDGSEKSMTLDISNDNKQLPYLAQAWIENENQEKIITGPVIATPPVQRLDPGAKSMVRLSTTPDISKLPQDRESLFYFNLREIPPRSEKANVVQIALCTKIKLFYRPAAIKTRP

>d1quna1 b.1.11.1 (A:1-121) Periplasmic chaperone FimC {Escherichia coli}

GVALGATRVIYPAGQKQVQLAVTNNDENSTYLIQSWVENADGVKDGRFIVTPPLFAMKGKKENTLRILDATNNQLPQDRESLFWMNVKAIPSMDKSKLTENTLQLAIISRIKLYYRPAKLA

>d1mspa\_ b.1.11.2 (A:) Major sperm protein, alpha isoform (recombinant), ph 4.6 {Pig roundworm (Ascaris suum)}

SVPPGDINTQPSQKIVFNAPYDDKHTYHIKITNAGGRRIGWAIKTTNMRRLSVDPPCGVLDPKEKVLMAVSCDTFNAATEDLNNDRITIEWTNTPDGAAKQFRREWFQGDGMVRRKNLPIEYNL

>d4kbpa1 b.1.12.1 (A:9-120) Purple acid phosphatase, N-terminal domain {Kidney bean (Phaseolus vulgaris)}

RDMPLDSDVFRVPPGYNAPQQVHITQGDLVGRAMIISWVTMDEPGSSAVRYWSEKNGRKRIAKGKMSTYRFFNYSSGFIHHTTIRKLKYNTKYYYEVGLRNTTRRFSFITPP

>d1dqia\_ b.1.13.1 (A:) Superoxide reductase (SOR) {Archaeon Pyrococcus furiosus}

MISETIRSGDWKGEKHVPVIEYEREGELVKVKVQVGKEIPHPNTTEHHIRYIELYFLPEGENFVYQVGRVEFTAHGESVNGPNTSDVYTEPIAYFVLKTKKKGKLYALSYCNIHGLWENEVTLE

>d1dfx\_1 b.1.13.1 (37-125) Desulfoferrodoxin C-terminal domain {Desulfovibrio desulfuricans}

VEGSTDGAMEKHVPVIEKVDGGYLIKVGSVPHPMEEKHWIEWIELLADGRSYTKFLKPGDAPEAFFAIDASKVTAREYCNLHGHWKAEN

>d1f00i1 b.1.14.1 (I:658-752) Intimin {Escherichia coli}

ASITEIKADKTTAVANGQDAITYTVKVMKGDKPVSNQEVTFTTTLGKLSNSTEKTDTNGYAKVTLTSTTPGKSLVSARVSDVAVDVKAPEVEFFT

>d1f00i2 b.1.14.1 (I:753-841) Intimin {Escherichia coli}

TLTIDDGNIEIVGTGVKGKLPTVWLQYGQVNLKASGGNGKYTWRSANPAIASVDASSGQVTLKEKGTTTISVISSDNQTATYTIATPNS

>d1cwva1 b.1.14.1 (A:503-596) Invasin {Yersinia pseudotuberculosis}

LTLTAAVIGDGAPANGKTAITVEFTVADFEGKPLAGQEVVITTNNGALPNKITEKTDANGVARIALTNTTDGVTVVTAEVEGQRQSVDTHFVKG

>d1cwva2 b.1.14.1 (A:597-692) Invasin {Yersinia pseudotuberculosis}

TIAADKSTLAAVPTSIIADGLMASTITLELKDTYGDPQAGANVAFDTTLGNMGVITDHNDGTYSAPLTSTTLGVATVTVKVDGAAFSVPSVTVNFT

>d1cwva3 b.1.14.1 (A:693-795) Invasin {Yersinia pseudotuberculosis}

ADPIPDAGRSSFTVSTPDILADGTMSSTLSFVPVDKNGHFISGMQGLSFTQNGVPVSISPITEQPDSYTATVVGNSVGDVTITPQVDTLILSTLQKKISLFPV

>d1cwva4 b.1.14.1 (A:796-886) Invasin {Yersinia pseudotuberculosis}

PTLTGILVNGQNFATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSSSFTPNVSVNDQGQVTITYQTYSEVAVTAKSKKFPSYSVSYRFYP

>d1f0la1 b.2.1.1 (A:381-535) Diphtheria toxin, C-terminal domain {Corynebacterium diphtheriae}

SPGHKTQPFLHDGYAVSWNTVEDSIIRTGFQGESGHDIKITAENTPLPIAGVLLPTIPGKLDVNKSKTHISVNGRKIRMRCRAIDGDVTFCRPKSPVYVGNGVHANLHVAFHRSSSEKIHSNEISSDSIGVLGYQKTVDHTKVNSKLSLFFEIKS

>d1exh\_\_ b.2.2.1 (-) Exo-1,4-beta-D-glycanase (cellulase, xylanase), cellulose-binding domain, CBD {Cellulomonas fimi}

ASSGPAGCQVLWGVNQWNTGFTANVTVKNTSSAPVDGWTLTFSFPSGQQVTQAWSSTVTQSGSAVTVRNAPWNGSIPAGGTAQFGFNGSHTGTNAAPTAFSLNGTPCTVG

>d1e5ba\_ b.2.2.1 (A:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas fimi}

TGCSVTATRAEEWSDGFNVTYSVSGSSAWTVNLALNGSQTIQASWNANVTGSGSTRTVTPNGSGNTFGVTVMKNGSSTTPAATCAGS

>d1hejc\_ b.2.2.1 (C:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas fimi}

TGSCSVSAVRGEEWADRFNVTYSVSGSSSWVVTLGLNGGQSVQSSWNAALTGSSGTVTARPNGSGNSFGVTFYKNGSSATPGATCATG

>d1nbca\_ b.2.2.2 (A:) Cellusomal scaffolding protein A, scafoldin {Clostridium thermocellum}

NLKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSKLTLRYYYTVDGQKDQTFWCDHAAIIGSNGSYNGITSNVKGTFVKMSSSTNNADTYLEISFTGGTLEPGAHVQIQGRFAKNDWSNYTQSNDYSFKSASQFVEWDQVTAYLNGVLVWGKEP

>d1g43a\_ b.2.2.2 (A:) Cellusomal scaffolding protein A, scafoldin {Clostridium cellulolyticum}

AGTGVVSVQFNNGSSPASSNSIYARFKVTNTSGSPINLADLKLRYYYTQDADKPLTFWCDHAGYMSGSNYIDATSKVTGSFKAVSPAVTNADHYLEVALNSDAGSLPAGGSIEIQTRFARNDWSNFDQSNDWSYTAAGSYMDWQKISAFVGGTLAYGSTP

>d1tf4a2 b.2.2.2 (A:461-605) Endo/exocellulase:cellobiose E-4, C-terminal domain {Thermomonospora fusca}

PEIFVEAQINTPGTTFTEIKAMIRNQSGWPARMLDKGTFRYWFTLDEGVDPADITVSSAYNQCATPEDVHHVSGDLYYVEIDCTGEKIFPGGQSEHRREVQFRIAGGPGWDPSNDWSFQGIGNELAPAPYIVLYDDGVPVWGTAP

>d1anu\_\_ b.2.2.2 (-) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

VVVEIGKVTGSVGTTVEIPVYFRGVPSKGIANCDFVFRYDPNVLEIIGIDPGDIIVDPNPTKSFDTAIYPDRKIIVFLFAEDSGTGAYAITKDGVFAKIRATVKSSAPGYITFDEVGGFADNDLVEQKVSFIDGGVNV

>d1aoha\_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

AVRIKVDTVNAKPGDTVRIPVRFSGIPSKGIANCDFVYSYDPNVLEIIEIEPGELIVDPNPTKSFDTAVYPDRKMIVFLFAEDSGTGAYAITEDGVFATIVAKVKSGAPNGLSVIKFVEVGGFANNDLVEQKTQFFDGGVNVG

>d1g1ka\_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

ASLKVTVGTANGKPGDTVTVPVTFADVAKMKNVGTCNFYLGYDASLLEVVSVDAGPIVKNAAVNFSSSASNGTISFLFLDNTITDELITADGVFANIKFKLKSVTAKTTTPVTFKDGGAFGDGTMSKIASVTKTNGSVTIDPG

>d1qba\_2 b.2.2.3 (28-200) Bacterial chitobiase, n-terminal domain {Serratia marcescens}

DQQLVDQLSQLKLNVKMLDNRAGENGVDCAALGADWASCNRVLFTLSNDGQAIDGKDWVIYFHSPRQTLRVDNDQFKIAHLTGDLYKLEPTAKFSGFPAGKAVEIPVVAEYWQLFRNDFLPRWYATSGDAKPKMLANTDTENLDQFVAPFTGDQWKRTKDDKNILMTPASRFV

>d1amx\_\_ b.2.3.1 (-) Collagen-binding domain of adhesin {Staphylococcus aureus}

TSSVFYYKTGDMLPEDTTHVRWFLNINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVTGTHSNYYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIPQGYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHN

>d1qunb1 b.2.3.2 (B:1-158) Mannose-specific adhesin FimH {Escherichia coli}

FACKTANGTAIPIGGGSANVYVNLAPVVNVGQNLVVDLSTQIFCHNDYPETITDYVTLQRGSAYGGVLSNFSGTVKYSGSSYPFPTTSETPRVVYNSRTDKPWPVALYLTPVSSAGGVAIKAGSLIAVLILRQTNNYNSDDFQFVWNIYANNDVVVPT

>d1qunb2 b.2.3.2 (B:159-279) Mannose-specific adhesin FimH {Escherichia coli}

GGCDVSARDVTVTLPDYPGSVPIPLTVYCAKSQNLGYYLSGTTADAGNSIFTNTASFSPAQGVGVQLTRNGTIIPANNTVSLGAVGTSAVSLGLTANYARTGGQVTAGNVQSIIGVTFVYQ

>d1pdkb\_ b.2.3.2 (B:) PapK pilus subunit {Escherichia coli}

LLDRPCHVSGDSLNKHVVFKTRASRDFWYPPGRSPTESFVIRLENCHATAVGKIVTLTFKGTEEAALPGHLKVTGVNAGRLGIALLDTDGSSLLKPGTSHNKGQGEKVTGNSLELPFGAYVVATPEALRTKSVVPGDYEATATFELTYR

>d1j8ra\_ b.2.3.3 (A:) PapG adhesin receptor-binding domain {Escherichia coli}

WNNIVFYSLGDVNSYQGGNVVITQRPQFITSWRPGIATVTWNQCNGPEFADGFWAYYREYIAWVVFPKKVMTQNGYPLFIEVHNKGSWSEENTGDNDSYFFLKGYKWDERAFDAGNLCQKPGEITRLTEKFDDIIFKVALPADLPLGDYSVKIPYTSGMQRHFASYLGARFKIPYNVAKTLPRENEMLFLFKNIGG

>d1edya\_ b.2.4.1 (A:) alpha-1-macroglobulin {Rat (Rattus norvegicus)}

EAPFTLKVNTLPLNFDKAEHHRKFQIHINVSYIGERPNSNMVIVDVKMVSGFIPVKPSVKKLQDQSNIQRTEVNTNHVLIYIEKLTNQTMGFSFAVEQDIPVKNLKPAPVKVYDYYETDEFAIEEYSAPFSSDS

>d1bv8a\_ b.2.4.1 (A:) alpha-2-macroglobulin {Human (Homo sapiens)}

EEFPFALGVQTLPQTCDEPKAHTSFQISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSNHVLIYLDKVSNQTLSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFAIAEYNAPCSKDLGNA

>d1ayoa\_ b.2.4.1 (A:) alpha-2-macroglobulin {Cow (Bos taurus)}

EFPFALEVQTLPQTCDGPKAHTSFQISLSVSYIGSRPASNMAIVDVKMVSGFIPLKPTVKMLERSNVSRTEVSNNHVLIYLDKVTNETLTLTFTVLQDIPVRDLKPAIVKVYDYYETDEFAVAEYSAPCS

>d1ycsa\_ b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Human (Homo sapiens)}

VPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRVRAMAIYKQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHSVVVPYEPPEVGSDCTTIHYNYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEE

>d1hu8a\_ b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Mouse (Mus musculus)}

TYQGNYGFHLGFLQSGTAKSVMCTYSPPLNKLFCQLAKTCPVQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRRCPHHERCSDGDGLAPPQHLIRVEGNLAPEYLEDRQTFRHSVVVPYEPPEAGSEYTTIHYKYMCNSSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEE

>d1a02n2 b.2.5.1 (N:399-576) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}

WPLSSQSGSYELRIEVQPKPHHRAHYETEGSRGAVKAPTGGHPVVQLHGYMENKPLGLQIFIGTADERILKPHAFYQVHRITGKTVTTTSYEKIVGNTKVLEIPLEPKNNMRATIDCAGILKLRNADIELRKGETDIGRKNTRVRLVFRVHIPESSGRIVSLQTASNPIECSQRSAHE

>d1a66a\_ b.2.5.1 (A:) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}

MKDWQLPSHSGPYELRIEVQPKSHHRARYETEGSRGAVKASAGGHPIVQLHGYLENEPLMLQLFIGTADDRLLRPHAFYQVHRITGKTVSTTSHEAILSNTKVLEIPLLPENSMRAVIDCAGILKLRNSDIELRKGETDIGRKNTRVRLVFRVHVPQPSGRTLSLQVASNPIECSQRS

>d1imhc2 b.2.5.1 (C:188-367) Transcription factor TONEBP, DNA-binding domain {Human (Homo sapiens)}

KKSPMLCGQYPVKSEGKELKIVVQPETQHRARYLTEGSRGSVKDRTQQGFPTVKLEGHNEPVVLQVFVGNDSGRVKPHGFYQACRVTGRNTTPCKEVDIEGTTVIEVGLDPSNNMTLAVDCVGILKLRNADVEARIGIAGSKKKSTRARLVFRVNIMRKDGSTLTLQTPSSPILCTQPAG

>d1nfka2 b.2.5.1 (A:39-250) p50 subunit of NF-kappa B (NFKB), N-terminal domain {Mouse (Mus musculus)}

GPYLQILEQPKQRGFRFRYVCEGPSHGGLPGASSEKNKKSYPQVKICNYVGPAKVIVQLVTNGKNIHLHAHSLVGKHCEDGVCTVTAGPKDMVVGFANLGILHVTKKKVFETLEARMTEACIRGYNPGLLVHSDLAYLQAEGGGDRQLTDREKEIIRQAAVQQTKEMDLSVVRLMFTAFLPDSTGSFTRRLEPVVSDAIYDSKAPNASNLKI

>d1a3qa2 b.2.5.1 (A:37-226) p52 subunit of NF-kappa B (NFKB), N-terminal domain {Human (Homo sapiens)}

GPYLVIVEQPKQRGFRFRYGCEGPSHGGLPGASSEKGRKTYPTVKICNYEGPAKIEVDLVTHSDPPRAHAHSLVGKQCSELGICAVSVGPKDMTAQFNNLGVLHVTKKNMMGTMIQKLQRQRLRSRPQGLTEAEQRELEQEAKELKKVMDLSIVRLRFSAFLRSLPLKPVISQPIHDSKSPGAS

>d1ikna2 b.2.5.1 (A:19-191) p65 subunit of NF-kappa B (NFKB), N-terminal domain {Mouse (Mus musculus)}

PYVEIIEQPKQRGMRFRYKCEGRSAGSIPGERSTDTTKTHPTIKINGYTGPGTVRISLVTKDPPHRPHPHELVGKDCRDGYYEADLCPDRSIHSFQNLGIQCVKKRDLEQAISQRIQTNNNPFHVPIEEQRGDYDLNAVRLCFQVTVRDPAGRPLLLTPVLSHPIFDNRAPNT

>d1nfia2 b.2.5.1 (A:20-189) p65 subunit of NF-kappa B (NFKB), N-terminal domain {Human (Homo sapiens)}

YVEIIEQPKQRGMRFRYKCEGRSAGSIPGERSTDTTKTHPTIKINGYTGPGTVRISLVTKDPPHRPHPHELVGKDCRDGFYEAELCPDRCIHSFQNLGIQCVKKRDLEQAISQRIQTNNNPFQVPIEEQRGDYDLNAVRLCFQVTVRDPSGRPLRLPPVLPHPIFDNRAP

>d1bvoa\_ b.2.5.1 (A:) Dorsal homologue Gambif1 {African malaria mosquito (Anopheles gambiae)}

PYVEITEQPHPKALRFRYECEGRSAGSIPGVNTTAEQKTFPSIQVHGYRGRAVVVVSCVTKEGPEHKPHPHNLVGKEGCKKGVCTVEINSTTMSYTFNNLGIQCVKKKDVEEALRLRQEIRVDPFRTGFGHAKEPGSIDLNAVRLCFQVFLEGQQRGRFTEPLTPVVSDIIYDKK

>d1xbra\_ b.2.5.1 (A:) T domain from Brachyury transcription factor {African clawed frog (Xenopus laevis)}

ELKVSLEERDLWTRFKELTNEMIVTKNGRRMFPVLKVSMSGLDPNAMYTVLLDFVAADNHRWKYVNGEWVPGGKPEPQAPSCVYIHPDSPNFGAHWMKDPVSFSKVKLTNKMNGGGQIMLNSLHKYEPRIHIVRVGGTQRMITSHSFPETQFIAVTAYQNEEITALKIKHNPFAKAFLDAKERN

>d1bf5a2 b.2.5.1 (A:317-568) STAT-1, DNA-binding domain {Human (Homo sapiens)}

FVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQELNYNLKVKVLFDKDVNERNTVKGFRKFNILGTHTKVMNMEESTNGSLAAEFRHLQLKEQKNAGTRTNEGPLIVTEELHSLSFETQLCQPGLVIDLETTSLPVVVISNVSQLPSGWASILWYNMLVAEPRNLSFFLTPPCARWAQLSEVLSWQFSSVTKRGLNVDQLNMLGEKLLGPNASPDGLIPWTRFCKENINDKNFPFWLWIESILELIKKH

>d1bg1a2 b.2.5.1 (A:322-575) STAT3b {Mouse (Mus musculus)}

VVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVLSWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYSGCQITWAKFCKENMAGKGFSFWVWLDNIIDLVKKY

>d1e50q\_ b.2.5.1 (Q:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}

LVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELRNATAAMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVD

>d1h9da\_ b.2.5.1 (A:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}

VLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGTLVTVMAGNDENYSAELRNATAAMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRR

>d1hcz\_1 b.2.6.1 (1-167,231-250) Cytochrome f, large domain {Turnip (Brassica rapa)}

YPIFAQQNYENPREATGRIVCANCHLASKPVDIEVPQAVLPDTVFEAVVKIPYDMQLKQVLANGKKGALNVGAVLILPEGFELAPPDRISPEMKEKIGNLSFQNYRPNKKNILVIGPVPGQKYSEITFPILAPDPATNKDVHFLKYPIYVGGNRGRGQIYPDGSKSNXPNVGGFGQGDAEIVLQDPLR

>d1e2wa1 b.2.6.1 (A:1-168,A:233-251) Cytochrome f, large domain {Chlamydomonas reinhardtii}

YPVFAQQNYANPREANGRIVCANCHLAQKAVEIEVPQAVLPDTVFEAVIELPYDKQVKQVLANGKKGDLNVGMVLILPEGFELAPPDRVPAEIKEKVGNLYYQPYSPEQKNILVVGPVPGKKYSEMVVPILSPDPAKNKNVSYLKYPIYFGGNRGRGQVYPDGKKSNFXNVGGFGQAETEIVLQNPAR

>d1ci3m1 b.2.6.1 (M:1-169,M:232-249) Cytochrome f, large domain {Phormidium laminosum}

YPFWAQQNYANPREATGRIVCANCHLAAKPAEIEVPQAVLPDSVFKAVVKIPYDHSVQQVQADGSKGPLNVGAVLMLPEGFTIAPEDRIPEEMKEEVGPSYLFQPYADDKQNIVLVGPLPGDEYEEIVFPVLSPNPATNKSVAFGKYSIHLGANRGRGQIYPTGEKSNNXNVGGFGQKDTEIVLQSPN

>d1i31a\_ b.2.7.1 (A:) Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor {Rat (Rattus norvegicus)}

IGWRREGIKYRRNELFLDVLESVNLLMSPQGQVLSAHVSGRVVMKSYLSGMPECKFGMNDKIVIEKQGKGTADETSKSGKQSIAIDDCTFHQCVRLSKFDSERSISFIPPDGEFELMRYRTTKDIILPFRVIPLVREVGRTKLEVKVVIKSNFKPSLLAQKIEVRIPTPLNTSGVQVICMKGKAKYKASENAIVWKIKRMAGMKESQISAEIELLPTNDKKKWARPPISMNFEVPFAPSGLKVRYLKVFEPKLNYSDHDVIKWVRYIGRSGIYETRC

>d1cgt\_2 b.3.1.1 (580-684) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}

LTGDQVTVRFVVNNASTTLGQNLYLTGNVAELGNWSTGSTAIGPAFNQVIHQYPTWYYDVSVPAGKQLEFKFFKKNGSTITWESGSNHTFTTPASGTATVTVNWQ

>d1kcla2 b.3.1.1 (A:582-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}

LSGDQVSVRFVVNNATTALGQNVYLTGSVSELGNWDPAKAIGPMYNQVVYQYPNWYYDVSVPAGKTIEFKFLKKQGSTVTWEGGSNHTFTAPSSGTATINVNWQP

>d1cyg\_2 b.3.1.1 (575-680) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus}

LTNDQVSVRFVVNNATTNLGQNIYIVGNVYELGNWDTSKAIGPMFNQVVYSYPTWYIDVSVPEGKTIEFKFIKKDSQGNVTWESGSNHVYTTPTNTTGKIIVDWQN

>d1qhoa2 b.3.1.1 (A:577-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus, maltogenic alpha-amylase}

LSGTQTSVVFTVKSAPPTNLGDKIYLTGNIPELGNWSTDTSGAVNNAQGPLLAPNYPDWFYVFSVPAGKTIQFKFFIKRADGTIQWENGSNHVATTPTGATGNITVTWQN

>d1pama2 b.3.1.1 (A:583-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus sp., strain 1011}

TGDQVTVRFVINNATTALGQNVFLTGNVSELGNWDPNNAIGPMYNQVVYQYPTWYYDVSVPAGQTIEFKFLKKQGSTVTWEGGANRTFTTPTSGTATVNVNWQP

>d1ciu\_2 b.3.1.1 (579-683) Cyclodextrin glycosyltransferase, C-terminal domain {Thermoanaerobacterium thermosulfurigenes, EM1}

LTGNQICVRFVVNNASTVYGENVYLTGNVAELGNWDTSKAIGPMFNQVVYQYPTWYYDVSVPAGTTIQFKFIKKNGNTITWEGGSNHTYTVPSSSTGTVIVNWQQ

>d1acz\_\_ b.3.1.1 (-) Glucoamilase, granular starch-binding domain {Aspergillus niger}

CTTPTAVAVTFDLTATTTYGENIYLVGSISQLGDWETSDGIALSADKYTSSDPLWYVTVTLPAGESFEYKFIRIESDDSVEWESDPNREYTVPQACGTSTATVTDTWR

>d1cqya\_ b.3.1.1 (A:) beta-amylase {Bacillus cereus}

TPVMQTIVVKNVPTTIGDTVYITGNRAELGSWDTKQYPIQLYYDSHSNDWRGNVVLPAERNIEFKAFIKSKDGTVKSWQTIQQSWNPVPLKTTSHTSSW

>d1h8la1 b.3.2.1 (A:305-383) Carboxypeptidase D, a regulatory domain {Crested duck (Lophonetta specularioides)}

GIWGFVLDATDGRGILNATISVADINHPVTTYKDGDYWRLLVQGTYKVTASARGYDPVTKTVEVDSKGGVQVNFTLSRT

>d1vcbc\_ b.3.3.1 (C:) VHL {Human (Homo sapiens)}

LRSVNSREPSQVIFCNRSPRVVLPVWLNFDGEPQPYPTLPPGTGRRIHSYRGHLWLFRDAGTHDGLLVNQTELFVPSLNVDGQPIFANITLPVYTLKERCLQVVRSLVKPENYRRLDIVRSLYEDLEDHPNVQKDLERLTQE

>d1f86a\_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (Homo sapiens)}

CPLMVKVLDAVRGSPAINVAVHVFRKAADDTWEPFASGKTSESGELHGLTTEEEFVEGIYKVEIDTKSYWKALGISPFHEHAEVVFTANDSGPRRYTIAALLSPYSYSTMAVVTN

>d1ttba\_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (Homo sapiens)}

GPTGTGESKCPLMVKVLDAVRGSPAINVAVHVFRKAADDTWEPFASGKTSESGELHGLTTEEEFVEGIYKVEIDTKSYWKALGISPFHEHAEVVFTANDSGPRRYTIATLLSPYSYSTTAVVTNPKE

>d1gkea\_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Rat (Rattus norvegicus)}

SKCPLMVKVLDAVRGSPAVDVAVKVFKKTADGSWEPFASGKTAESGELHGLTTDEKFTEGVYRVELDTKSYWKALGISPFHEYAEVVFTANDSGHRHYTIAALLSPYSYSTTAVVSNPQN

>d1tfpa\_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Chicken (Gallus gallus)}

CPLMVKVLDAVRGSPAANVAVKVFKKAADGTWQDFATGKTTEFGEIHELTTEEQFVEGVYRVEFDTSSYWKGLGLSPFHEYADVVFTANDSGHRHYTIAALLSPFSYSTTAVVS

>d1d2oa1 b.3.5.1 (A:535-624) B repeat unit of collagen binding surface protein (cna) {Staphylococcus aureus}

ETTSSIGEKVWDDKDNQDGKRPEKVSVNLLANGEKVKTLDVTSETNWKYEFKDLPKYDEGKKIEYTVTEDHVKDYTTDINGTTITNKYTP

>d1d2oa2 b.3.5.1 (A:625-721) B repeat unit of collagen binding surface protein (cna) {Staphylococcus aureus}

GETSATVTKNWDDNNNQDGKRPTEIKVELYQDGKATGKTAILNESNNWTHTWTGLDEKAKGQQVKYTVEELTKVKGYTTHVDNNDMGNLITTNKYTP

>d1dmha\_ b.3.6.1 (A:) Catechol 1,2-dioxygenase {Acinetobacter calcoaceticus}

VKIFNTQDVQDFLRVASGLEQEGGNPRVKQIIHRVLSDLYKAIEDLNITSDEYWAGVAYLNQLGANQEAGLLSPGLGFDHYLDMRMDAEDAALGIENATPRTIEGPLYVAGAPESVGYARMDDGSDPNGHTLILHGTIFDADGKPLPNAKVEIWHANTKGFYSHFDPTGEQQAFNMRRSIITDENGQYRVRTILPAGYGCPPEGPTQQLLNQLGRHGNRPAHIHYFVSADGHRKLTTQINVAGDPYTYDDFAYATREGLVVDAVEHTDPEAIKANDVEGPFAEMVFDLKLTRLVDGVDNQVVDRPRLAV

>d3pcca\_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Pseudomonas aeruginosa}

PIELLPETPSQTAGPYVHIGLALEAAGNPTRDQEIWNRLAKPDAPGEHILLLGQVYDGNGHLVRDSFLEVWQADANGEYQDAYNLENAFNSFGRTATTFDAGEWTLHTVKPGVVNNAAGVPMAPHINISLFARGINIHLHTRLYFDDEAQANAKCPVLNLIEQPQRRETLIAKRCEVDGKTAYRFDIRIQGEGETVFFDF

>d1eo9a\_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Acinetobacter calcoaceticus, adp1}

ELKETPSQTGGPYVHIGLLPKQANIEVFEHNLDNNLVQDNTQGQRIRLEGQVFDGLSLPLRDVLIEIWQADTNGVYPSQADTQGKQVDPNFLGWGRTGADFGTGFWSFNTIKPGAVPGRKGSTQAPHISLIIFARGINIGLHTRVYFDDEAEANAKDPVLNSIEWATRRQTLVAKREERDGEVVYRFDIRIQGENETVFFDI

>d3pccm\_ b.3.6.1 (M:) Protocatechuate-3,4-dioxygenase, beta chain {Pseudomonas aeruginosa}

PAQDNSRFVIRDRNWHPKALTPDYKTSIARSPRQALVSIPQSISETTGPNFSHLGFGAHDHDLLLNFNNGGLPIGERIIVAGRVVDQYGKPVPNTLVEMWQANAGGRYRHKNDRYLAPLDPNFGGVGRCLTDSDGYYSFRTIKPGPYPWRNGPNDWRPAHIHFGISGPSIATKLITQLYFEGDPLIPMCPIVKSIANPEAVQQLIAKLDMNNANPMDCLAYRFDIVLRGQRKTHFE

>d1eo9b\_ b.3.6.1 (B:) Protocatechuate-3,4-dioxygenase, beta chain {Acinetobacter calcoaceticus, adp1}

IIWGAYAQRNTEDHPPAYAPGYKTSVLRSPKNALISIAETLSEVTAPHFSADKFGPKDNDLILNYAKDGLPIGERVIVHGYVRDQFGRPVKNALVEVWQANASGRYRHPNDQYIGAMDPNFGGCGRMLTDDNGYYVFRTIKPGPYPWRNRINEWRPAHIHFSLIADGWAQRLISQFYFEGDTLIDSCPILKTIPSEQQRRALIALEDKSNFIEADSRCYRFDITLRGRRATYFENDLT

>d1c3ga1 b.4.1.1 (A:180-259) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}

ETVQVNLPVSLEDLFVGKKKSFKIGRKGPHGASEKTQIDIQLKPGWKAGTKITYKNQGDYNPQTGRRKTLQFVIQEKSHP

>d1c3ga2 b.4.1.1 (A:260-349) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}

NFKRDGDDLIYTLPLSFKESLLGFSKTIQTIDGRTLPLSRVQPVQPSQTSTYPGQGMPTPKNPSQRGNLIVKYKVDYPISLNDAQKRAID

>d1hd8a1 b.105.1.1 (A:263-356) Penicillin-binding protein 5, C-terminal domain {Escherichia coli}

FETVNPLKVGKEFASEPVWFGDSDRASLGVDKDVYLTIPRGRMKDLKASYVLNSSELHAPLQKNQVVGTINFQLDGKTIEQRPLVVLQEIPEGN

>d1hoe\_\_ b.5.1.1 (-) alpha-Amylase inhibitor tendamistat {Streptomyces tendae}

DTTVSEPAPSCVTLYQSWRYSQADNGCAETVTVKVVYEDDTEGLCYAVAPGQITTVGDGYIGSHGHARYLARCL

>d1aac\_\_ b.6.1.1 (-) Amicyanin {Paracoccus denitrificans}

DKATIPSESPFAAAEVADGAIVVDIAKMKYETPELHVKVGDTVTWINREAMPHNVHFVAGVLGEAALKGPMMKKEQAYSLTFTEAGTYDYHCTPHPFMRGKVVVE

>d1id2a\_ b.6.1.1 (A:) Amicyanin {Paracoccus versutus (Thiobacillus versutus)}

QDKITVTSEKPVAAADVPADAVVVGIEKMKYLTPEVTIKAGETVYWVNGEVMPHNVAFKKGIVGEDAFRGEMMTKDQAYAITFNEAGSYDYFCTPHPFMRGKVIVE

>d1plc\_\_ b.6.1.1 (-) Plastocyanin {Poplar (Populus nigra), variant italica}

IDVLLGADDGSLAFVPSEFSISPGEKIVFKNNAGFPHNIVFDEDSIPSGVDASKISMSEEDLLNAKGETFEVALSNKGEYSFYCSPHQGAGMVGKVTVN

>d9pcy\_\_ b.6.1.1 (-) Plastocyanin {French bean (Phaseolus vulgaris)}

LEVLLGSGDGSLVFVPSEFSVPSGEKIVFKNNAGFPHNVVFDEDEIPAGVDAVKISMPEEELLNAPGETYVVTLDTKGTYSFYCSPHQGAGMVGKVTVN

>d1pla\_\_ b.6.1.1 (-) Plastocyanin {Parsley (Petroselinum crispum)}

AEVKLGSDDGGLVFSPSSFTVAAGEKITFKNNAGFPHNIVFDEDEVPAGVNAEKISQPEYLNGAGETYEVTLTEKGTYKFYCEPHAGAGMKGEVTVN

>d1ag6\_\_ b.6.1.1 (-) Plastocyanin {Spinach (Spinacia oleracea)}

VEVLLGGDDGSLAFLPGDFSVASGEEIVFKNNAGFPHNVVFDEDEIPSGVDAAKISMSEEDLLNAPGETYKVTLTEKGTYKFYCSPHQGAGMVGKVTVN

>d1bypa\_ b.6.1.1 (A:) Plastocyanin {White campion (Silene pratensis)}

AEVLLGSSDGGLAFVPSDLSIASGEKITFKNNAGFPHNDLFDKKEVPAGVDVTKISMPEEDLLNAPGEEYSVTLTEKGTYKFYCAPHAGAGMVGKVTVN

>d1iuz\_\_ b.6.1.1 (-) Plastocyanin {Sea lettuce (Ulva pertusa)}

AQIVKLGGDDGSLAFVPSKISVAAGEAIEFVNNAGFPHNIVFDEDAVPAGVDADAISYDDYLNSKGETVVRKLSTPGVYGVYCEPHAGAGMKMTITVQ

>d2plt\_\_ b.6.1.1 (-) Plastocyanin {Green alga (Chlamydomonas reinhardtii)}

DATVKLGADSGALEFVPKTLTIKSGETVNFVNNAGFPHNIVFDEDAIPSGVNADAISRDDYLNAPGETYSVKLTAAGEYGYYCEPHQGAGMVGKIIVQ

>d7pcy\_\_ b.6.1.1 (-) Plastocyanin {Green alga (Enteromorpha prolifera)}

AAIVKLGGDDGSLAFVPNNITVGAGESIEFINNAGFPHNIVFDEDAVPAGVDADAISAEDYLNSKGQTVVRKLTTPGTYGVYCDPHSGAGMKMTITVQ

>d1kdj\_\_ b.6.1.1 (-) Plastocyanin {Fern (Adiantum capillus-veneris)}

AKVEVGDEVGNFKFYPDSITVSAGEAVEFTLVGETGHNIVFDIPAGAPGTVASELKAASMDENDLLSEDEPSFKAKVSTPGTYTFYCTPHKSANMKGTLTVK

>d1nin\_\_ b.6.1.1 (-) Plastocyanin {Anabaena variabilis}

ETYTVKLGSDKGLLVFEPAKLTIKPGDTVEFLNNKVPPHNVVFDAALNPAKSADLAKSLSHKQLLMSPGQSTSTTFPADAPAGEYTFYCEPHRGAGMVGKITVAG

>d1bawa\_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (Phormidium laminosum)}

ETFTVKMGADSGLLQFEPANVTVHPGDTVKWVNNKLPPHNILFDDKQVPGASKELADKLSHSQLMFSPGESYEITFSSDFPAGTYTYYCAPHRGAGMVGKITVEG

>d1pcs\_\_ b.6.1.1 (-) Plastocyanin {Cyanobacterium (Synechocystis sp.), pcc 6803}

ANATVKMGSDSGALVFEPSTVTIKAGEEVKWVNNKLSPHNIVFDADGVPADTAAKLSHKGLLFAAGESFTSTFTEPGTYTYYCEPHRGAGMVGKVVVE

>d1bxva\_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (Synechocystis sp.), pcc 7942}

QTVAIKMGADNGMLAFEPSTIEIQAGDTVQWVNNKLAPHNVVVEGQPELSHKDLAFSPGETFEATFSEPGTYTYYCEPHRGAGMVGKIVVQ

>d2b3ia\_ b.6.1.1 (A:) Plastocyanin {Photosynthetic prokaryote (Prochlorothrix hollandica)}

ASVQIKMGTDKYAPLYEPKALSISAGDTVEFVMNKVGPHNVIFDKVPAGESAPALSNTKLAIAPGSFYSVTLGTPGTYSFYCTPHRGAGMVGTITVE

>d1paz\_\_ b.6.1.1 (-) Pseudoazurin {Alcaligenes faecalis, strain s-6}

ENIEVHMLNKGAEGAMVFEPAYIKANPGDTVTFIPVDKGHNVESIKDMIPEGAEKFKSKINENYVLTVTQPGAYLVKCTPHYAMGMIALIAVGDSPANLDQIVSAKKPKIVQERLEKVIA

>d1pmy\_\_ b.6.1.1 (-) Pseudoazurin {Methylobacterium extorquens, strain am1}

DEVAVKMLNSGPGGMMVFDPALVRLKPGDSIKFLPTDKGHNVETIKGMAPDGADYVKTTVGQEAVVKFDKEGVYGFKCAPHYMMGMVALVVVGDKRDNLEAAKSVQHNKLTQKRLDPLFAQIQ

>d1bqk\_\_ b.6.1.1 (-) Pseudoazurin {Achromobacter cycloclastes}

ADFEVHMLNKGKDGAMVFEPASLKVAPGDTVTFIPTDKGHNVETIKGMIPDGAEAFKSKINENYKVTFTAPGVYGVKCTPHYGMGMVGVVQVGDAPANLEAVKGAKNPKKAQERLDAALAALGN

>d1adwa\_ b.6.1.1 (A:) Pseudoazurin {Thiosphaera pantotropha}

ATHEVHMLNKGESGAMVFEPAFVRAEPGDVINFVPTDKSHNVEAIKEILPEGVESFKSKINESYTLTVTEPGLYGVKCTPHFGMGMVGLVQVGDAPENLDAAKTAKMPKKARERMDAELAQVN

>d2cbp\_\_ b.6.1.1 (-) Plantacyanin {Cucumber (Cucumis sativus)}

AVYVVGGSGGWTFNTESWPKGKRFRAGDILLFNYNPSMHNVVVVNQGGFSTCNTPAGAKVYTSGRDQIKLPKGQSYFICNFPGHCQSGMKIAVNAL

>d1f56a\_ b.6.1.1 (A:) Plantacyanin {Spinach (Spinacia oleracea)}

AVYNIGWSFNVNGARGKSFRAGDVLVFKYIKGQHNVVAVNGRGYASCSAPRGARTYSSGQDRIKLTRGQNYFICSFPGHCGGGMKIAINAK

>d1azca\_ b.6.1.1 (A:) Azurin {Alcaligenes denitrificans}

AQCEATIESNDAMQYNLKEMVVDKSCKQFTVHLKHVGKMAKVAMGHNWVLTKEADKQGVATDGMNAGLAQDYVKAGDTRVIAHTKVIGGGESDSVTFDVSKLTPGEAYAYFCSFPGHWAMMKGTLKLSN

>d1dyza\_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015), different isoforms}

AQCEATVESNDAMQYNVKEIVVDKSCKQFTMHLKHVGKMAKVAMGHNLVLTKDADKQAVATDGMGAGLAQDYVKAGDTRVIAHTKVIGGGESDSVTFDVSKIAAGENYAYFCSFPGHWAMMKGTLKLGS

>d1rkra\_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015), different isoforms}

AECSVDIAGNDGMQFDKKEITVSKSCKQFTVNLKHPGKLAKNVMGHNWVLTKQADMQGAVNDGMAAGLDNNYVKKDDARVIAHTKVIGGGETDSVTFDVSKLAAGEDYAYFCSFPGHFALMKGVLKLVD

>d1cc3a\_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}

AECSVDIQGNDQMQFNTNAITVDKSCKQFTVNLSHPGNLPKNVMGHNWVLSTAADMQGVVTDGMASGLDKDYLKPDDSRVIAHTKLIGSGEKDSVTFDVSKLKEGEQYMFFCSELCGINHALMKGTLTLK

>d1jzga\_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}

AECSVDIQGNDQMQFNTNAITVDKSCKQFTVNLSHPGNLPKNVMGHNWVLSTAADMQGVVTDGMASGLDKDYLKPDDSRVIAHTKLIGSGEKDSVTFDVSKLKEGEQYMFFCTFPGHSALMKGTLTLK

>d1joi\_\_ b.6.1.1 (-) Azurin {Pseudomonas fluorescens}

AECKVTVDSTDQMSFNTKAIEIDKSCKTFTVELTHSGSLPKNVMGHNWVLSSAADMPGIASDGMAAGIDKNYLKEGDTRVIAHTKIIGAGEKDSVTFDVSKLAAGTDYAFFCSFPGHISMMKGTVTVK

>d1nwpa\_ b.6.1.1 (A:) Azurin {Pseudomonas putida}

AECKVTVDSTDQMSFNTKDIAIDKSCKTFTVELTHSGSLPKNVMGHNLVISKEADMQPIATDGLSAGIDKQYLKDGDARVIAHTKVIGAGEKDSVTFDVSKLAAGEKYGFFCSFPGHISMMKGTVTLK

>d1cuoa\_ b.6.1.1 (A:) Azurin {Methylomonas sp. j}

ASCETTVTSGDTMTYSTRSISVPASCAEFTVNFEHKGHMPKTGMGHNWVLAKSADVGDVAKEGAHAGADNNFVTPGDKRVIAFTPIIGGGEKTSVKFKVSALSKDEAYTYFCSYPGHFSMMRGTLKLEE

>d1qhqa\_ b.6.1.1 (A:) Auracyanin {Chloroflexus aurantiacus}

ANAPGGSNVVNETPAQTVEVRAAPDALAFAQTSLSLPANTVVRLDFVNQNNLGVQHNWVLVNGGDDVAAAVNTAAQNNADALFVPPPDTPNALAWTAMLNAGESGSVTFRTPAPGTYLYICTFPGHYLAGMKGTLTVTP

>d1e30a\_ b.6.1.1 (A:) Rusticyanin {Thiobacillus ferrooxidans}

LDTTWKEATLPQVKAMLEKDTGKVSGDTVTYSGKTVHVVAAAVLPGFPFPSFEVHDKKNPTLEIPAGATVDVTFINTNKGFGHSFDITKKGPPYAVMPVIDPIVAGTGFSPVPKDGKFGYTNFTWHPTAGTYYYVCQIPGHAATGQFGKIVVK

>d1jer\_\_ b.6.1.1 (-) Stellacyanin {Cucumber (Cucumis sativus)}

MQSTVHIVGDNTGWSVPSSPNFYSQWAAGKTFRVGDSLQFNFPANAHNVHEMETKQSFDACNFVNSDNDVERTSPVIERLDELGMHYFVCTVGTHCSNGQKLSINVVAAN

>d1ibya\_ b.6.1.4 (A:) Red copper protein nitrosocyanin {Nitrosomonas europaea}

EHNFNVVINAYDTTIPELNVEGVTVKNIRAFNVLNEPETLVVKKGDAVKVVVENKSPISEGFSIDAFGVQEVIKAGETKTISFTADKAGAFTIWCQLHPKNIHLPGTLNVVE

>d1qnia1 b.6.1.4 (A:451-581) Nitrous oxide reductase, C-terminal domain {Pseudomonas nautica}

KIYERNDPYFASCRAQAEKDGVTLESDNKVIRDGNKVRVYMTSVAPQYGMTDFKVKEGDEVTVYITNLDMVEDVTHGFCMVNHGVSMEISPQQTASVTFTAGKPGVYWYYCNWFCHALHMEMVGRMLVEAA

>d1fwxa1 b.6.1.4 (A:452-581) Nitrous oxide reductase, C-terminal domain {Paracoccus denitrificans}

SVWDRNDPMWAETRAQAEADGVDIDNWTEEVIRDGNKVRVYMSSVAPSFSIESFTVKEGDEVTVIVTNLDEIDDLTHGFTMGNYGVAMEIGPQMTSSVTFVAANPGVYWYYCQWFCHALHMEMRGRMLVEPK

>d1cyx\_\_ b.6.1.2 (-) Quinol oxidase (CyoA) {Escherichia coli}

KPITIEVVSMDWKWFFIYPEQGIATVNEIAFPANTPVYFKVTSNSVMHSFFIPRLGSQIYAMAGMQTRLHLIANEPGTYDGICAEICGPGHSGMKFKAIATPDRAAFDQWVAKAKQSPNTMSDMAAFEKLAAPSEYNQVEYFSNVKPDLFADVINKFM

>d1fftb1 b.6.1.2 (B:118-283) Quinol oxidase (CyoA) {Escherichia coli}

KPLAHDEKPITIEVVSMDWKWFFIYPEQGIATVNEIAFPANTPVYFKVTSNSVMNSFFIPRLGSQIYAMAGMQTRLHLIANEPGTYDGISASYSGPGFSGMKFKAIATPDRAAFDQWVAKAKQSPNTMSDMAAFEKLAAPSEYNQVEYFSNVKPDLFADVINKFMA

>d1ocrb1 b.6.1.2 (B:91-227) Cytochrome c oxidase {Cow (Bos taurus)}

NNPSLTVKTMGHQWYWSYEYTDYEDLSFDSYMIPTSELKPGELRLLEVDNRVVLPMEMTIRMLVSSEDVLHSWAVPSLGLKTDAIPGRLNQTTLMSSRPGLYYGQCSEICGSNHSFMPIVLELVPLKYFEKWSASML

>d1ar1b1 b.6.1.2 (B:108-252) Cytochrome c oxidase {Paracoccus denitrificans}

NDPDLVIKAIGHQWYWSYEYPNDGVAFDALMLEKEALADAGYSEDEYLLATDNPVVVPVGKKVLVQVTATDVIHAWTIPAFAVKQDAVPGRIAQLWFSVDQEGVYFGQCSELCGINHAYMPIVVKAVSQEKYEAWLAGAKEEFAA

>d2cuaa\_ b.6.1.2 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AGKLERVDPTTVRQEGPWADPAQAVVQTGPNQYTVYVLAFAFGYQPNPIEVPQGAEIVFKITSPDVIHGFHVEGTNINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE

>d2cuab\_ b.6.1.2 (B:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AYTLATHTAGVIPAGKLERVDPTTVRQEGPWADPAQAVVQTGPNQYTVYVLAFAFGYQPNPIEVPQGAEIVFKITSPDVIHGFHVEGTNINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE

>d1nif\_1 b.6.1.3 (8-166) Nitrite reductase, NIR {Achromobacter cycloclastes}

DISTLPRVKVDLVKPPFVHAHDQVAKTGPRVVEFTMTIEEKKLVIDREGTEIHAMTFNGSVPGPLMVVHENDYVELRLINPDTNTLLHNIDFHAATGALGGGALTQVNPGEETTLRFKATKPGVFVYHCAPEGMVPWHVTSGMNGAIMVLPRDGLKDEK

>d1nif\_2 b.6.1.3 (167-340) Nitrite reductase, NIR {Achromobacter cycloclastes}

GQPLTYDKIYYVGEQDFYVPKDEAGNYKKYETPGEAYEDAVKAMRTLTPTHIVFNGAVGALTGDHALTAAVGERVLVVHSQANRDTRPHLIGGHGDYVWATGKFRNPPDLDQETWLIPGGTAGAAFYTFRQPGVYAYVNHNLIEAFELGAAGHFKVTGEWNDDLMTSVVKPASM

>d1j9qa1 b.6.1.3 (A:4-166) Nitrite reductase, NIR {Alcaligenes faecalis, strain s-6}

ATAAEIAALPRQKVELVDPPFVHAHSQVAEGGPKVVEFTMVIEEKKIVIDDAGTEVHAMAFNGTVPGPLMVVHQDDYLELTLINPETNTLMHNINFHAATGALGGGGLTEINPGEKTILRFKATKPGVFVYHCAPPGMVPWHVVSGMNGAIMVLPREGLHDGK

>d1j9qa2 b.6.1.3 (A:167-339) Nitrite reductase, NIR {Alcaligenes faecalis, strain s-6}

GKALTYDKIYYVGEQDFYVPRDENGKYKKYEAPGDAYEDTVKVMRTLTPTHVVFNGAVGALTGDKAMTAAVGEKVLIVHSQANRDTRPHLIGGHGDYVWATGKFNTPPDVDQETWFIPGGAAGAAFYTFQQPGIYAYVNHNLIEAFELGAAAHFKVTGEWNDDLMTSVLAPSG

>d1gs7a1 b.6.1.3 (A:1-159) Nitrite reductase, NIR {Alcaligenes xylosoxidans}

QDADKLPHTKVTLVAPPQVHPHEQATKSGPKVVEFTMTIEEKKMVIDDKGTTLQAMTFNGSMPGPTLVVHEGDYVQLTLVNPATNAMPHNVDFHGATGALGGAKLTNVNPGEQATLRFKADRSGTFVYHCAPEGMVPWHVVSGMSGTLMVLPRDGLKDP

>d1gs7a2 b.6.1.3 (A:160-336) Nitrite reductase, NIR {Alcaligenes xylosoxidans}

QGKPLHYDRAYTIGEFDLYIPKGPDGKYKDYATLAESYGDTVQVMRTLTPSHIVFNGKVGALTGANALTAKVGETVLLIHSQANRDTRPHLIGGFGDWVWETGKFANPPQRDLETWFIRGGSAGAALYTFKQPGVYAYLNHNLIEAFELGAAGHIKVEGKWNDDLMKQIKAPAPIPR

>d1ndsa1 b.6.1.3 (A:11-166) Nitrite reductase, NIR {Alcaligenes xylosoxidans}

GLPRVAVDLVAPPLVHPHSQVAAGAPKVVQFRMSIEEKKMVADDDGTTAQAMTFNGSVPGPTLVVHEGDYIELTLVNPATNSMPHNVDFHAATGALGGAGLTQVVPGQEAVLRFKADRSGTFVYHCAPAGMVPWHVVSGMNGALMVLPRDGLRDAA

>d1ndsa2 b.6.1.3 (A:167-340) Nitrite reductase, NIR {Alcaligenes xylosoxidans}

GAALAYDRVYTIGESDLYVPKAADGNYSDYPALASAYADTVAVMRTLTPSHAVFNGAVGALTGANALTAAVGESVLIIHSQANRDSRPHLIGGHGDWVWTTGKFANPPQLNMETWFIPGGSAAAALYTFKQPGTYAYLSHNLIEAMELGAAAQASVEGQWDDDLMTSVAAPGPA

>d1kbva1 b.6.1.3 (A:13-163) Nitrite reductase, NIR {Neisseria gonorrhoeae, AniA}

ELPVIDAVTTHAPEVPPAIDRDYPAKVRVKMETVEKTMKMDDGVEYRYWTFDGDVPGRMIRVREGDTVEVEFSNNPSSTVPHNVDFHAATGQGGGAAATFTAPGRTSTFSFKALQPGLYIYHCAVAPVGMHIANGMYGLILVEPKEGLPKV

>d1kbva2 b.6.1.3 (A:164-314) Nitrite reductase, NIR {Neisseria gonorrhoeae, AniA}

DKEFYIVQGDFYTKGKKGAQGLQPFDMDKAVAEQPEYVVFNGHVGALTGDNALKAKAGETVRMYVGNGGPNLVSSFHVIGEIFDKVYVEGGKLINENVQSTIVPAGGSAIVEFKVDIPGNYTLVDHSIFRAFNKGALGQLKVEGAENPEIM

>d1kv7a1 b.6.1.3 (A:31-170) multi-copper oxidase CueO {Escherichia coli}

RPTLPIPDLLTTDARNRIQLTIGAGQSTFGGKTATTWGYNGNLLGPAVKLQRGKAVTVDIYNQLTEETTLHWHGLEVPGEVDGGPQGIIPPGGKRSVTLNVDQPAATCWFHPHQHGKTGRQVAMGLAGLVVIEDDEILKL

>d1kv7a2 b.6.1.3 (A:171-335) multi-copper oxidase CueO {Escherichia coli}

MLPKQWGIDDVPVIVQDKKFSADGQIDYQLDVMTAAVGWFGDTLLTNGAIYPQHAAPRGWLRLRLLNGCNARSLNFATSDNRPLYVIASDGGLLPEPVKVSELPVLMGERFEVLVEVNDNKPFDLVTLPVSQMGMAIAPFDKPHPVMRIQPIAISASGALPDTLS

>d1kv7a3 b.6.1.3 (A:336-516) multi-copper oxidase CueO {Escherichia coli}

SLPALPSLEGLTVRKLQLSMDPMLDMMGMQMLMEKYGDQAMAGMDHSQMMGHMGHGNMNHMNHGGKFDFHHANKINGQAFDMNKPMFAAAKGQYERWVISGVGDMMLHPFHIHGTQFRILSENGKPPAAHRAGWKDTVKVEGNVSEVLVKFNHDAPKEHAYMAHCHLLEHEDTGMMLGFTV

>d1aoza1 b.6.1.3 (A:1-129) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}

SQIRHYKWEVEYMFWAPNCNENIVMGINGQFPGPTIRANAGDSVVVELTNKLHTEGVVIHWHGILQRGTPWADGTASISQCAINPGETFFYNFTVDNPGTFFYHGHLGMQRSAGLYGSLIVDPPQGKKE

>d1aoza2 b.6.1.3 (A:130-338) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}

PFHYDGEINLLLSDWWHQSIHKQEVGLSSKPIRWIGEPQTILLNGRGQFDCSIAAKYDSNLEPCKLKGSESCAPYIFHVSPKKTYRIRIASTTALAALNFAIGNHQLLVVEADGNYVQPFYTSDIDIYSGESYSVLITTDQNPSENYWVSVGTRARHPNTPPGLTLLNYLPNSVSKLPTSPPPQTPAWDDFDRSKNFTYRITAAMGSPK

>d1aoza3 b.6.1.3 (A:339-552) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}

PPVKFNRRIFLLNTQNVINGYVKWAINDVSLALPPTPYLGAMKYNLLHAFDQNPPPEVFPEDYDIDTPPTNEKTRIGNGVYQFKIGEVVDVILQNANMMKENLSETHPWHLHGHDFWVLGYGDGKFSAEEESSLNLKNPPLRNTVVIFPYGWTAIRFVADNPGVWAFHCHIEPHLHMGMGVVFAEGVEKVGRIPTKALACGGTAKSLINNPKNP

>d1hfua1 b.6.1.3 (A:1-131) Laccase {Inky cap fungus (Coprinus cinereus)}

AIVNSVDTMTLTNANVSPDGFTRAGILVNGVHGPLIRGGKNDNFELNVVNDLDNPTMLRPTSIHWHGLFQRGTNWADGADGVNQCPISPGHAFLYKFTPAGHAGTFWYHSHFGTQYCDGLRGPMVIYDDND

>d1hfua2 b.6.1.3 (A:132-303) Laccase {Inky cap fungus (Coprinus cinereus)}

PHAALYDEDDENTIITLADWYHIPAPSIQGAAQPDATLINGKGRYVGGPAAELSIVNVEQGKKYRMRLISLSCDPNWQFSIDGHELTIIEVDGELTEPHTVDRLQIFTGQRYSFVLDANQPVDNYWIRAQPNKGRNGLAGTFANGVNSAILRYAGAANADPTTSANPNPAQL

>d1hfua3 b.6.1.3 (A:304-503) Laccase {Inky cap fungus (Coprinus cinereus)}

NEADLHALIDPAAPGIPTPGAADVNLRFQLGFSGGRFTINGTAYESPSVPTLLQIMSGAQSANDLLPAGSVYELPRNQVVELVVPAGVLGGPHPFHLHGHAFSVVRSAGSSTYNFVNPVKRDVVSLGVTGDEVTIRFVTDNPGPWFFHCHIEFHLMNGLAIVFAEDMANTVDANNPPVEWAQLCEIYDDLPPEATSIQTV

>d1kcw\_1 b.6.1.3 (1-192) Ceruloplasmin {Human (Homo sapiens)}

KEKHYYIGIIETTWDYASDHGEKKLISVDTEHSNIYLQNGPDRIGRLYKKALYLQYTDETFRTTIEKPVWLGFLGPIIKAETGDKVYVHLKNLASRPYTFHSHGITYYKEHEGAIYPDNTTDFQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCVTRIYHSHIDAPKDIASGLIGPLIICKKDSLDKEKEK

>d1kcw\_2 b.6.1.3 (193-338) Ceruloplasmin {Human (Homo sapiens)}

HIDREFVVMFSVVDENFSWYLEDNIKTYCSEPEKVDKDNEDFQESNRMYSVNGYTFGSLPGLSMCAEDRVKWYLFGMGNEVDVHAAFFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNHLKAGLQAFFQVQEC

>d1kcw\_3 b.6.1.3 (347-553) Ceruloplasmin {Human (Homo sapiens)}

IRGKHVRHYYIAAEEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTRIGGSYKKLVYREYTDASFTNRKERGPEEEHLGILGPVIWAEVGDTIRVTFHNKGAYPLSIEPIGVRFNKNNEGTYYSPNYNPQSRSVPPSASHVAPTETFTYEWTVPKEVGPTNADPVCLAKMYYSAVDPTKDIFTGLIGPMKICKKGSLHANGRQK

>d1kcw\_4 b.6.1.3 (554-705) Ceruloplasmin {Human (Homo sapiens)}

DVDKEFYLFPTVFDENESLLLEDNIRMFTTAPDQVDKEDEDFQESNKMHSMNGFMYGNQPGLTMCKGDSVVWYLFSAGNEADVHGIYFSGNTYLWRGERRDTANLFPQTSLTLHMWPDTEGTFNVECLTTDHYTGGMKQKYTVNQCRRQSED

>d1kcw\_5 b.6.1.3 (706-884) Ceruloplasmin {Human (Homo sapiens)}

STFYLGERTYYIAAVEVEWDYSPQREWEKELHHLQEQNVSNAFLDKGEFYIGSKYKKVVYRQYTDSTFRVPVERKAEEEHLGILGPQLHADVGDKVKIIFKNMATRPYSIHAHGVQTESSTVTPTLPGETLTYVWKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLIGPLIVCRRP

>d1kcw\_6 b.6.1.3 (892-1040) Ceruloplasmin {Human (Homo sapiens)}

RRKLEFALLFLVFDENESWYLDDNIKTYSDHPEKVNKDDEEFIESNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGHSFQYKHRGVYSSDVFDIFPGTYQTLEMFPRTPGIWLLHCHVTDHIHAGMETTYTVLQN

>d1qasa2 b.7.1.1 (A:626-756) PI-specific phospholipase C isozyme D1 (PLC-D1), C-terminal domain {Rat (Rattus norvegicus)}

WRPERLRVRIISGQQLPKVNKNKNSIVDPKVIVEIHGVGRDTGSRQTAVITNNGFNPRWDMEFEFEVTVPDLALVRFMVEDYDSSSKNDFIGQSTIPWNSLKQGYRHVHLLSKNGDQHPSATLFVKISIQD

>d1rlw\_\_ b.7.1.1 (-) Domain from cytosolic phospholipase A2 {Human (Homo sapiens)}

SSHKFTVVVLRATKVTKGAFGDMLDTPDPYVELFISTTPDSRKRTRHFNNDINPVWNETFEFILDPNQENVLEITLMDANYVMDETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMSLEVASS

>d1d5ra1 b.7.1.1 (A:188-351) Pten tumor suppressor (Phoshphoinositide phosphatase), C-terminal domain {Human (Homo sapiens)}

YRPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTRREDKFMYFEFPQPLPVCGDIKVEFFHKQNKMLKKDKMFHFWVNTFFIPGPEEVDNDKEYLVLTLTKNDLDKANKDKANRYFSPNFKVKLYFTKTV

>d1e8xa2 b.7.1.1 (A:357-522) Phoshoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}

CDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSGKTSAEMPSPESKGKAQLLYYVNLLLIDHRFLLRHGEYVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDN

>d1e8ya2 b.7.1.1 (A:357-522) Phoshoinositide 3-kinase (PI3K) {Human (Homo sapiens)}

CDRKFRVKIRGIDIPVLPRNTDLTVFVEANIQHGQQVLCQRRTSPKPFTEEVLWNVWLEFSIKIKDLPKGALLNLQIYCGKAPALSSKASAESPSSESKGKVRLLYYVNLLLIDHRFLLRRGEYVLHMWQISGKGEDQGSFNADKLTSATNPDKENSMSISILLDN

>d1bdya\_ b.7.1.1 (A:) Domain from protein kinase C delta {Rat (Rattus norvegicus)}

MAPFLRISFNSYELGSLQAEDDASQPFCAVKMKEALTTDRGKTLVQKKPTMYPEWKSTFDAHIYEGRVIQIVLMRAAEDPMSEVTVGVSVLAERCKKNNGKAEFWLDLQPQAKVLMCVQYFLE

>d1gmia\_ b.7.1.1 (A:) Domain from protein kinase C epsilon {Rat (Rattus rattus)}

MVVFNGLLKIKICEAVSLKPTAWSLRDAVGPRPQTFLLDPYIALNVDDSRIGQTATKQKTNSPAWHDEFVTDVCNGRKIELAVFHDAPIGYDDFVANCTIQFEELLQNGSRHFEDWIDLEPEGKVYVIIDLSGSSG

>d1byna\_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}

EKLGKLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVKVFLLPDKKKKFETKVHRKTLNPVFNEQFTFKVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMNTVDFGHVTEEWRDLQSAEK

>d1dqva1 b.7.1.2 (A:295-424) Synaptogamin I {Rat (Rattus norvegicus)}

GAPCGRISFALRYLYGSDQLVVRILQALDLPAKDSNGFSDPYVKIYLLPDRKKKFQTKVHRKTLNPIFNETFQFSVPLAELAQRKLHFSVYDFDRFSRHDLIGQVVLDNLLELAEQPPDRPLWRDILEGG

>d1dqva2 b.7.1.2 (A:425-569) Synaptogamin I {Rat (Rattus norvegicus)}

SEKADLGELNFSLCYLPTAGLLTVTIIKASNLKAMDLTGFSDPYVKASLISEGRRLKKRKTSIKKNTLNPTYNEALVFDVAPESVENVGLSIAVVDYDCIGHNEVIGVCRVGPEAADPHGREHWAEMLANPRKPVEHWHQLVEEK

>d1k5wa\_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}

KLGDICFSLRYVPTAGKLTVVILEAKNLKKMDVGGLSDPYVKIHLMQNGKRLKKKKTTIKKNTLNPYYNESFSFEVPFEQIQKVQVVVTVLDYDKIGKNDAIGKVFVGYNSTGAELRHWSDMLANPRRPIAQWHTLQVEEEVDAMLAV

>d1rsy\_\_ b.7.1.2 (-) Synaptogamin I {Rat (Rattus norvegicus)}

GGGILDSMVEKEEPKEEEKLGKLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVKVFLLPDKKKKFETKVHRKTLNPVFNEQFTFKVPYSELGGKTLVMAVYDFDRFSKHDIIGEFKVPMNTVDFGHVTEEWRDLQSA

>d1dsya\_ b.7.1.2 (A:) C2 domain from protein kinase c (alpha) {Rat (Rattus norvegicus)}

TEKRGRIYLKAEVTDEKLHVTVRDAKNLIPMDPNGLSDPYVKLKLIPDPKNESKQKTKTIRSTLNPQWNESFTFKLKPSDKDRRLSVEIWDWDRTTRNDFMGSLSFGVSELMKMPASGWYKLLNQEEGEYYNVPIPE

>d1a25a\_ b.7.1.2 (A:) C2 domain from protein kinase c (beta) {Rat (Rattus norvegicus)}

ERRGRIYIQAHIDREVLIVVVRDAKNLVPMDPNGLSDPYVKLKLIPDPKSESKQKTKTIKCSLNPEWNETFRFQLKESDKDRRLSVEIWDWDLTSRNDFMGSLSFGISELQKAGVDGWFKLLSQEEGEYFNV

>d3rpba\_ b.7.1.2 (A:) C2b-domain of rabphilin {Rat (Rattus norvegicus)}

RGKILVSLMYSTQQGGLIVGIIRCVHLAAMDANGYSDPFVKLWLKPDMGKKAKHKTQIKKKTLNPEFNEEFFYDIKHSDLAKKSLDISVWDYDIGKSNDYIGGCQLGISAKGERLKHWYECLKNKDKKIERWHQLQNENH

>d1qpxa2 b.7.2.1 (A:125-215) PapD {Escherichia coli}

NEVWQDQLILNKVSGGYRIENPTPYYVTVIGLGGSEKQAEEGEFETVMLSPRSEQTVKSANYNTPYLSYINDYGGRPVLSFICNGSRCSVK

>d1quna2 b.7.2.1 (A:122-205) FimC {Escherichia coli}

LPPDQAAEKLRFRRSANSLTLINPTPYYLTVTELNAGTRVLENALVPPMGESAVKLPSDAGSNITYRTINDYGALTPKMTGVME

>d1who\_\_ b.7.3.1 (-) Pollen allergen PHL P 2 {Timothy grass (Phleum pratense)}

VPKVTFTVEKGSNEKHLAVLVKYEGDTMAEVELREHGSDEWVAMTKGEGGVWTFDSEEPLQGPFNFRFLTEKGMKNVFDDVVPEKYTIGATYAP

>d1dcea2 b.7.4.1 (A:241-350) Rab geranylgeranyltransferase alpha-subunit, insert domain {Rat (Rattus norvegicus)}

PHDVLCCVHVSREEACLSVCFSRPLTVGSRMGTLLLMVDEAPLSVEWRTPDGRNRPSHVWLCDLPAASLNDQLPQHTFRVIWTGSDSQKECVLLKDRPECWCRDSATDEQ

>d1czya1 b.8.1.1 (A:350-501) TNF receptor associated factor 2 (TRAF2) {Human (Homo sapiens)}

YDGVFIWKISDFPRKRQEAVAGRIPAIFSPAFYTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVVMKGPNDALLRWPFNQKVTLMLLDQNNREHVIDAFRPDVTSSSFQRPVNDMNIASGCPLFCPVSKMEAKNSYVRDDAIFIKAIVDLTGL

>d1flka1 b.8.1.1 (A:350-504) TNF receptor associated factor 3 (TRAF3) {Human (Homo sapiens)}

YNGVLIWKIRDYKRRKQEAVMGKTLSLYSQPFYTGYFGYKMCARVYLNGDGMGKGTHLSLFFVIMRGEYDALLPWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSSFKKPTGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKVIVDTSDLPDP

>d1k2fa\_ b.8.1.2 (A:) SIAH, seven in absentia homolog {Mouse (Mus musculus)}

SVLFPCKYASSGCEITLPHTEKAEHEELCEFRPYSCPCPGASCKWQGSLDAVMPHLMHQHKSITTLQGEDIVFLATDINLPGAVDWVMMQSCFGFHFMLVLEKQEKYDGHQQFFAIVQLIGTRKQAENFAYRLELNGHRRRLTWEATPRSIHEGIATAIMNSDCLVFDTSIAQLFAENGNLGINVTISMC

>d2bn2a\_ b.9.1.1 (A:) Neurophysin II {Cow (Bos taurus)}

AMSDLELRQCLPCGPGGKGRCFGPSICCGDELGCFVGTAEALRCQEENYLPSPCQSGQKPCGSGGRCAAAGICCNDESCVTEPEC

>d1kvp\_\_ b.10.1.1 (-) Bacteriophage capsid proteins {Bacteriophage phi-X174}

SNIQTGAERMPHDLSHLGFLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPLRRGLAIDSTVDIFTFYVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKIPKHLFQGYLNIYNNYFKAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPPETELSRQMTTSTGMAPVTTKFRDVPNLSGTPLIFRDNKGRTIKTGQLGIGPVDAGFLVAQNTAQAANGERAIPSNLWADLSNATSIDIMGLQAAYANLHTDQERDYFMQRYRDVISSFGGKTSYDADNRPLLVMRSNLWASGYDVDGTDQTSLGQFSGRVQQTYKHSVPRFFVPEHGTMFTLALVRFPPTATKEIQYLNAKGALTYTDIAGDPVLYGNLPPREISMKDVFRSGDSSKKFKIAEGQWYRYAPSYVSPAYHLLEGFPFIQEPPSGDLQERVLIRHHDYDQCFQSVQLLQWNSQVKFNVTVYRNLPTTRDSIMTS

>d2bpa1\_ b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage phi-X174}

SNIQTGAERMPHDLSHLGFLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPLRRGLAIDSTVDIFTFYVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKIPKHLFQGYLNIYNNYFKAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPPETELSRQMTTSTTSIDIMGLQAAYANLHTDQERDYFMQRYRDVISSFGGKTSYDADNRPLLVMRSNLWASGYDVDGTDQTSLGQFSGRVQQTYKHSVPRFFVPEHGTMFTLALVRFPPTATKEIQYLNAKGALTYTDIAGDPVLYGNLPPREISMKDVFRSGDSSKKFKIAEGQWYRYAPSYVSPAYHLLEGFPFIQEPPSGDLQERVLIRHHDYDQCFQSVQLLQWNSQVKFNVTVYRNLPTTRDSIMTS

>d2bpa2\_ b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage phi-X174}

MFQTFISRHNSNFFSDKLVLTSVTPASSAPVLQTPKATSSTLYFDSLTVNAGNGGFLHCIQMDTSVNAANQVVSVGADIAFDADPKFFACLVRFESSSVPTTLPTAYDVYPLNGRHDGGYYTVKDCVTIDVLPRTPGNNVYVGFMVWSNFTATKCRGLVSLNQVIKEIICLQPLK

>d1gff1\_ b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage G4}

VPHDLSHLVFEAGKIGRLKTISWTPVVAGDSFECDMVGAIRLSPLRRGLAVDSRVDIFSFYIPHRHIYGQQWINFMKDGVNASPLPPVTCSSGWDSAAYLGTIPSSTLKVPKFLHQGYLNIYNNYFKPPWSDDLTYANPSNMPSEDYKWGVRVANLKSIWTAPLPPDTRTSENMTTGTSTIDIMGLQAAYAKLHTEQERDYFMTRYRDIMKEFGGHTSYDGDNRPLLLMRSEFWASGYDVDGTDQSSLGQFSGRVQQTFNHKVPRFYVPEHGVIMTLAVTRFPPTHEMEMHYLVGKENLTYTDIACDPALMANLPPREVSLKEFFHSSPDSAKFKIAEGQWYRTQPDRVAFPYNALDGFPFYSALPSTDLKDRVLVNTNNYDEIFQSMQLAHWNMQTKFNINVYRHMPTTRDSIMTS

>d1gff2\_ b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage G4}

MFQKFISKHNAPINSTQLAATKTPAVAAPVLSVPNLSRSTILINATTTAVTTHSGLCHVVRIDETNPTNHHALSIAGSLSNVPADMIAFAIRFEVADGVVPTAVPALYDVYPIETFNNGKAISFKDAVTIDSHPRTVGNDVYAGIMLWSNAWTASTISGVLSVNQVNREATVLQPLK

>d1stma\_ b.10.1.2 (A:) SPMV coat protein {Satellite panicum mosaic virus}

AAATSLVYDTCYVTLTERATTSFQRQSFPTLKGMGDRAFQVVAFTIQGVSAAPLMYNARLYNPGDTDSVHATGVQLMGTVPRTVRLTPRVGQNNWFFGNTEEAETILAIDGLVSTKGANAPSNTVIVTGCFRLAPSELQSS

>d1a34a\_ b.10.1.2 (A:) STMV coat protein {Satellite tobacco mosaic virus}

TGDNSNVVTMIRAGSYPKVNPTPTWVRAIPFEVSVQSGIAFKVPVGSLFSANFRTDSFTSVTVMSVRAWTQLTPPVNEYSFVRLKPLFKTGDSTEEFEGRASNINTRASVGYRIPTNLRQNTVAADNVCEVRSNCRQVALVISCCFN

>d2stv\_\_ b.10.1.2 (-) STNV coat protein {Satellite tobacco necrosis virus}

TMRAVKRMINTHLEHKRFALINSGNTNATAGTVQNLSNGIIQGDDINQRSGDQVRIVSHKLHVRGTAITVSQTFRFIWFRDNMNRGTTPTVLEVLNTANFMSQYNPITLQQKRFTILKDVTLNCSLTGESIKDRIINLPGQLVNYNGATAVAASNGPGAIFMLQIGDSLVGLWDSSYEAVYTDA

>d1smva\_ b.10.1.2 (A:) SMV coat potein {Sesbania mosaic virus}

GAITVLHCELTAEIGVTDSIVVSSELVMPYTVGTWLRGVADNWSKYSWLSVRYTYIPSCPSSTAGSIHMGFQYDMADTVPVSVNKLSNLRGYVSGQVWSGSAGLCFINNSRCSDTSTAISTTLDVSELGKKWYPYKTSADYATAVGVDVNIATDLVPARLVIALLDGSSSTAVAAGRIYDTYTIQMIEPTASALNL

>d1smvc\_ b.10.1.2 (C:) SMV coat potein {Sesbania mosaic virus}

QAGISMAPSAQGAMVRIRNPAVSSSRGAITVLHCELTAEIGVTDSIVVSSELVMPYTVGTWLRGVADNWSKYSWLSVRYTYIPSCPSSTAGSIHMGFQYDMADTVPVSVNKLSNLRGYVSGQVWSGSAGLCFINNSRCSDTSTAISTTLDVSELGKKWYPYKTSADYATAVGVDVNIATDLVPARLVIALLDGSSSTAVAAGRIYDTYTIQMIEPTASALNL

>d1f2na\_ b.10.1.2 (A:) RYMV capsid protein {Rice yellow mottle virus}

LSSNTWPLHSVEFLADFKRSSTSADATTYDCVPFNLPRVWSLARCYSMWKPTRWDVVYLPEVSATVAGSIEMCFLYDYADTIPRYTGKMSRTAGFVTSSVWYGAEGCHLLSGGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVVNTILPARLAVRSSIKPTVSDTPGKLYVIASMVLRDPVDPTLNT

>d1f2nc\_ b.10.1.2 (C:) RYMV capsid protein {Rice yellow mottle virus}

AEPQLQRAPVAQASRISGTVPGPLSSNTWPLHSVEFLADFKRSSTSADATTYDCVPFNLPRVWSLARCYSMWKPTRWDVVYLPEVSATVAGSIEMCFLYDYADTIPRYTGKMSRTAGFVTSSVWYGAEGCHLLSGGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVVNTILPARLAVRSSIKPTVSDTPGKLYVIASMVLRDPVDPTLNT

>d1bmv1\_ b.10.1.2 (1:) BPMV coat protein {Bean pod mottle virus}

SISQQTVWNQMATVRTPLNFDSSKQSFCQFSVDLLGGGISVDKTGDWITLVQNSPISNLLRVAAWKKGCLMVKVVMSGNAAVKRSDWASLVQVFLTNSNSTEHFDACRWTKSEPHSWELIFPIEVCGPNNGFEMWSSEWANQTSWHLSFLVDNPKQSTTFDVLLGISQNFEIAGNTLMPAFSVPQ

>d1bmv2\_ b.10.1.2 (2:) BPMV coat protein {Bean pod mottle virus}

METNLFKLSLDDVETPKGSMLDLKISQSKIALPKNTVGGTILRSDLLANFLTEGNFRASVDLQRTHRIKGMIKMVATVGIPENTGIALACAMNSSIRGRASSDIYTICSQDCELWNPACTKAMTMSFNPNPCSDAWSLEFLKRTGFHCDIICVTGWTATPMQDVQVTIDWFISSQECVPRTYCVLNPQNPFVLNRWMGKLTFPQGTSRSVKRMPLSIGGGAGAKSAILMNMPNAVLSMWRYFVGDLVFEVSKMTSPYIKCTVSFFIAFGNLADDTINFEAFPHKLVQFGEIQEKVVLKFSQEEFLTAWSTQVRPATTLLADGCPYLYAMVHDSSVSTIPGDFVIGVKLTIIENMCAYGLNPGISGSRLLGTIPQ

>d1a6ca1 b.10.1.2 (A:1-176) TRSV capsid protein {Tobacco ringspot virus}

AVTVVPDPTCCGTLSFKVPKDAKKGKHLGTFDIRQAIMDYGGLHSQEWCAKGIVNPTFTVRMHAPRNAFAGLSIACTFDDYKRIDLPALGNECPPSEMFELPTKVFMLKDADVHEWQFNYGELTGHGLCNWANVATQPTLYFFVASTNQVTMAADWQCIVTMHVDMGPVIDRFELN

>d1a6ca2 b.10.1.2 (A:177-348) TRSV capsid protein {Tobacco ringspot virus}

PTMTWPIQLGDTFAIDRYYEAKEIKLDGSTSMLSISYNFGGPVKHSKKHAISYSRAVMSRNLGWSGTISGSVKSVSSLFCTASFVIFPWECEAPPTLRQVLWGPHQIMHGDGQFEIAIKTRLHSAATTEEGFGRLGILPLSGPIAPDAHVGSYEFIVHINTWRPDSQVHPPM

>d1a6ca3 b.10.1.2 (A:349-513) TRSV capsid protein {Tobacco ringspot virus}

FSSSELYNWFTLTNLKPDANTGVVNFDIPGYIHDFASKDATVTLASNPLSWLVAATGWHYGEVDLCISWSRSKQAQAQEGSVSITTNYRDWGAYWQGQARIYDLRRTEAEIPIFLGSYAGATPSGALGKQNYVRISIVNAKDIVALRVCLRPKSIKFWGRSATLF

>d4sbva\_ b.10.1.2 (A:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}

SSMDVTILSHCELSTELAVTVTIVVTSELVMPFTVGTWLRGVAQNWSKYAWVAIRYTYLPSCPTTTSGAIHMGFQYDMADTLPVSVNQLSNLKGYVTGPVWEGQSGLCFVNNTKCPDTSRAITIALDTNEVSEKRYPFKTATDYATAVGVNANIGNILVPARLVTAMEGGSSKTAVNTGRLYASYTIRLIEPIAAALNL

>d4sbvc\_ b.10.1.2 (C:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}

QAGVSMAPIAQGTMVKLRPPMLRSSMDVTILSHCELSTELAVTVTIVVTSELVMPFTVGTWLRGVAQNWSKYAWVAIRYTYLPSCPTTTSGAIHMGFQYDMADTLPVSVNQLSNLKGYVTGPVWEGQSGLCFVNNTKCPDTSRAITIALDTNEVSEKRYPFKTATDYATAVGVNANIGNILVPARLVTAMEGGSSKTAVNTGRLYASYTIRLIEPIAAALNL

>d2tbva\_ b.10.1.2 (A:) TBSV coat protein {Tomato bushy stunt virus}

GGVTVTSHREYLTQVNNSSGFVVNGGIVGNSLQLNPSNGTLFSWLPALASNFDQYSFNSVVLDYVPLCGTTEVGRVALYFDKDSQDPEPADRVELANFGVLKETAPWAEAMLRIPTDKVKRYCNDSATVDQKLIDLGQLGIATYGGAGADAVGELFLARSVTLYFPQPTNTLLSSKRLDLTGSLADATGPGYLVLTRTPTVLTHTFRATGTFNLSGGLRCLTSLTLGATGAVVINDILAIDNVGTASDYFLNCTVSSLPATVTFTVSGVAAGILLVGRARANVVNLL

>d2tbvc\_ b.10.1.2 (C:) TBSV coat protein {Tomato bushy stunt virus}

IITHVGGVGGSIMAPVAVSRQLVGSKPKFTGRTSGGVTVTSHREYLTQVNNSSGFVVNGGIVGNSLQLNPSNGTLFSWLPALASNFDQYSFNSVVLDYVPLCGTTEVGRVALYFDKDSQDPEPADRVELANFGVLKETAPWAEAMLRIPTDKVKRYCNDSATVDQKLIDLGQLGIATYGGAGADAVGELFLARSVTLYFPQPTNTLLSSKRLDLTGSLADATGPGYLVLTRTPTVLTHTFRATGTFNLSGGLRCLTSLTLGATGAVVINDILAIDNVGTASDYFLNCTVSSLPATVTFTVSGVAAGILLVGRARANVVNLL

>d1cwpa\_ b.10.1.2 (A:) Cowpea chlorotic mottle virus {Host: cowpea (Vigna unguiculta), (L.)}

KAIKAWTGYSVSKWTASCAAAEAKVTSAITISLPNELSSERNKQLKVGRVLLWLGLLPSVSGTVKSCVTETQTTAAASFQVALAVADNSKDVVAAMYPEAFKGITLEQLAADLTIYLYSSAALTEGDVIVHLEVEHVRPTFDDSFTPVY

>d1c8na\_ b.10.1.2 (A:) TNV coat protein {Tobacco necrosis virus}

NSTVVSNSELILNLTPIALAYTVQSLPLIATQPAWLGTIADNYSKWRWVSLRIIYSPKCPTTTSGTVAMCLSYDRNDVAPGSRVQLSQTYKAINFPPYAGYDGAAILNTDVTPTSAIYVDVDVTRFDKAWYSTIGTAAFAALTAFDQNQFCPCTVHIGSDGGPAVAVPPGDIFFKYVIELIEPINPTMN

>d1c8nc\_ b.10.1.2 (C:) TNV coat protein {Tobacco necrosis virus}

GVSRAGGFVTAPVIGAMVTRPTVPRFGMRGNSTVVSNSELILNLTPIALAYTVQSLPLIATQPAWLGTIADNYSKWRWVSLRIIYSPKCPTTTSGTVAMCLSYDRNDVAPGSRVQLSQTYKAINFPPYAGYDGAAILNTDVTPTSAIYVDVDVTRFDKAWYSTIGTAAFAALTAFDQNQFCPCTVHIGSDGGPAVAVPPGDIFFKYVIELIEPINPTMN

>d1auya\_ b.10.1.2 (A:) TYMV coat protein {Turnip yellow mosaic virus}

SPLTIKQPFQSEVLFAGTKDAEASLTIANIDSVSTLTTFYRHASLESLWVTIHPTLQAPTFPTTVGVCWVPAQSPVTPAQITKTYGGQIFCIGGAIQTLSPLIVKCPLEMMQPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTLSMHSPLITDTST

>d1auyb\_ b.10.1.2 (B:) TYMV coat protein {Turnip yellow mosaic virus}

MEIDKELAPQDRTVTVATVLPAVPGPSPLTIKQPFQSEVLFAGTKDAEASLTIANIDSVSTLTTFYRHASLESLWVTIHPTLQAPTFPTTVGVCWVPAQSPVTPAQITKTYGGQIFCIGGAIQTLSPLIVKCPLEMMQPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTLSMHSPLITDTST

>d1e57a\_ b.10.1.2 (A:) PHMV coat protein {Physalis mottle virus}

SPAIVLPFQFEATTFGTAETAAQVSLQTADPITKLTAPYRHAQIVECKAILTPTDLAVSNPLTVYLAWVPANSPATPTQILRVYGGQSFVLGGAISAAKTIEVPLNLDSVNRMLKDSVTYTDTPKLLAYSRAPTNPSKIPTASIQISGRIRLSKPMLIAN

>d1e57b\_ b.10.1.2 (B:) PHMV coat protein {Physalis mottle virus}

VVKVKQASIPAPGSILSQPNTEQSPAIVLPFQFEATTFGTAETAAQVSLQTADPITKLTAPYRHAQIVECKAILTPTDLAVSNPLTVYLAWVPANSPATPTQILRVYGGQSFVLGGAISAAKTIEVPLNLDSVNRMLKDSVTYTDTPKLLAYSRAPTNPSKIPTASIQISGRIRLSKPMLIAN

>d1ddla\_ b.10.1.2 (A:) DYMV coat protein {Desmodium yellow mottle tymovirus}

MEQDKILAHQASLNTKPSLLPPPVGNPPPVISYPFQITLASLGTEDAADSVSIASNSVLATYTALYRHAQLKHLKATIHPTYMAPKYPTSVALVWVPANSTATSTQVLDTYGGLHFCIGGSVNSVKPIDVEANLTNLNPIIKASTTFTDTPKLLYYSKAQATAPTSPTCYLTIQGQIELSSPLLQASS

>d1f15a\_ b.10.1.2 (A:) CMV coat protein {Cucumber mosaic virus, strain fny}

ERCRPGYTFTSITLKPPKIDRGSYYGKRLLLPDSVTEYDKKLVSRLQIRVNPLPKFDSTVWVTVRKVPASSDLSVAAISAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIGDMRKYAVLVYSKDDALETDELVLHVDIEHQRIPTSGVLPV

>d1f15b\_ b.10.1.2 (B:) CMV coat protein {Cucumber mosaic virus, strain fny}

DANFRVLSQQLSRLNKTLAAGRPTINHPTFVGSERCRPGYTFTSITLKPPKIDRGSYYGKRLLLPDSVTEYDKKLVSRLQIRVNPLPKFDSTVWVTVRKVPASSDLSVAAISAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIGDMRKYAVLVYSKDDALETDELVLHVDIEHQRIPTSGVLPV

>d2bbva\_ b.10.1.3 (A:) Nodavirus capsid protein {Black beetle virus}

LTRLSQPGLAFLKCAFAPPDFNTDPGKGIPDRFEGKVVTRKDVLNQSINFTANRDTFILIAPTPGVAYWVADVPAGTFPISTTTFNAVNFPGFNSMFGNAAASRSDQVSSFRYASMNVGIYPTSNLMQFAGSITVWKCPVKLSNVQFPVATTPATSALVHTLVGLDGVLAVGPDNFSESFIKGVFSQSVCNEPDFEFSDILEGIQTLPPANVTVATSGQPFNLAAGAEAVSGIVGWGNMDTIVIRVSAPTGAVNSAILKTWACLEYRPNPNAMLYQFGHDSPPCDEVALQEYRTVARSLPVAVIAAQN

>d2bbvc\_ b.10.1.3 (C:) Nodavirus capsid protein {Black beetle virus}

TQTAPVPQQNVPKQPRRRRNRARRNRRQGRAMNMGALTRLSQPGLAFLKCAFAPPDFNTDPGKGIPDRFEGKVVTRKDVLNQSINFTANRDTFILIAPTPGVAYWVADVPAGTFPISTTTFNAVNFPGFNSMFGNAAASRSDQVSSFRYASMNVGIYPTSNLMQFAGSITVWKCPVKLSNVQFPVATTPATSALVHTLVGLDGVLAVGPDNFSESFIKGVFSQSVCNEPDFEFSDILEGIQTLPPANVTVATSGQPFNLAAGAEAVSGIVGWGNMDTIVIRVSAPTGAVNSAILKTWACLEYRPNPNAMLYQFGHDSPPCDEVALQEYRTVARSLPVAVIAAQN

>d1nova\_ b.10.1.3 (A:) Nodavirus capsid protein {Nodamura virus}

NMLKMSAPGLDFLKCAFASPDFSTDPGKGIPDKFQGLVLPKKHCLTQSITFTPGKQTMLLVAPIPGIACLKAEANVGASFSGVPLASVEFPGFDQLFGTSATDTAANVTAFRYASMAAGVYPTSNLMQFAGSIQVYKIPLKQVLNSYSQTVATVPPTNLAQNTIAIDGLEALDALPNNNYSGSFIEGCYSQSVCNEPEFEFHPIMEGYASVPPANVTNAQASMFTNLTFSGARYTGLGDMDAIAILVTTPTGAVNTAVLKVWACVEYRPNPNSTLYEFARESPANDEYALAAYRKIARDIPIAVACKDN

>d1novc\_ b.10.1.3 (C:) Nodavirus capsid protein {Nodamura virus}

RRRAAPRQQQRQQSNRASNQPRRRRARRTRRQQRMAATNNMLKMSAPGLDFLKCAFASPDFSTDPGKGIPDKFQGLVLPKKHCLTQSITFTPGKQTMLLVAPIPGIACLKAEANVGASFSGVPLASVEFPGFDQLFGTSATDTAANVTAFRYASMAAGVYPTSNLMQFAGSIQVYKIPLKQVLNSYSQTVATVPPTNLAQNTIAIDGLEALDALPNNNYSGSFIEGCYSQSVCNEPEFEFHPIMEGYASVPPANVTNAQASMFTNLTFSGARYTGLGDMDAIAILVTTPTGAVNTAVLKVWACVEYRPNPNSTLYEFARESPANDEYALAAYRKIARDIPIAVACKDN

>g1f8v.1 b.10.1.3 (A:,D:) Nodavirus capsid protein {Pariacoto virus}

NRRNKARKVVSRSTALVPMAPASQRTGPAPRKPRKRNQALVRNPRLTDAGLAFLKCAFAAPDFSVDPGKGIPDNFHGRTLAIKDCNTTSVVFTPNTDTYIVVAPVPGFAYFRAEVAVGAQPTTFVGVPYPTYATNFGAGSQNGLPAVNNYSKFRYASMACGLYPTSNMMQFSGSVQVWRVDLNLSEAVNPAVTAITPAPGVFANFVDKRINGLRGIRPLAPRDNYSGNFIDGAYTFAFDKSTDFEWCDFVRSLEFSESNVLGAATAMKLLAPGGGTDTTLTGLGNVNTLVYKISTPTGAVNTAILRTWNCIELQPYTDSALFQFSGVSPPFDPLALECYHNLKMRFPVAVSSRENXSKFWEGVLRVLNQISGTLSVIPGPVGTISAGVHQLTGMYM

>g1f8v.2 b.10.1.3 (B:,E:) Nodavirus capsid protein {Pariacoto virus}

NPRLTDAGLAFLKCAFAAPDFSVDPGKGIPDNFHGRTLAIKDCNTTSVVFTPNTDTYIVVAPVPGFAYFRAEVAVGAQPTTFVGVPYPTYATNFGAGSQNGLPAVNNYSKFRYASMACGLYPTSNMMQFSGSVQVWRVDLNLSEAVNPAVTAITPAPGVFANFVDKRINGLRGIRPLAPRDNYSGNFIDGAYTFAFDKSTDFEWCDFVRSLEFSESNVLGAATAMKLLAPGGGTDTTLTGLGNVNTLVYKISTPTGAVNTAILRTWNCIELQPYTDSALFQFSGVSPPFDPLALECYHNLKMRFPVAVSSRENXSKFWEGVLRVLNQISGTLSVIP

>d1dnv\_\_ b.10.1.3 (-) Galleria mellonella densovirus capsid protein {Wax moth (Galleria mellonella), densovirus}

VYIIPRPFSNFGKKLSTYTKSHKFMIFGLANNVIGPTGTGTTAVNRLLTTCLAEIPWQKLPLYMNQSEFDLLPPGSRVVECNVKVIFRTNRIAFETSSTVTKQATLNQISNVQTAIGLNKLGWGINRAFTAFQSDQPMIPTATTAPKYEPVTGDTGYRGMIADYYGADSTNDTAFGNAGNYPHHQVSSFTFLQNYYCMYQQTNQGTGGWPCLAEHLQQFDSKTVNNQCLIDVTYKPKMGLIKSPLNYKIIGQPTVKGTISVGDNLVNMRGAVVTNPPEATQNVAESTHNLTRNFPADLFNIYSDIEKSQVLHKGPWGHENPQIQPSVHIGIQAVPALTTGALLINSSPLNSWTDSMGYIDVMSSCTVMEAQPTHFPFSTEANTNPGNTIYRINLTPNSLTSAFNGLYGNGATLGN

>d1b35a\_ b.10.1.3 (A:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

VMGEDQQIPRNEAQHGVHPISIDTHRISNNWSPQAMCIGEKVVSIRQLIKRFGIFGDANTLQADGSSFVVAPFTVTSPTKTLTSTRNYTQFDYYYYLYAFWRGSMRIKMVAETQDGTGTPRKKTNFTWFVRMFNSLQDSFNSLISTSSSAVTTTVLPSGTINMGPSTQVIDPTVEGLIEVEVPYYNISHITPAVTIDDGTPSMEDYLKGHSPPCLLTFSPRDSISATNHIITASFMRALGDDFSFMYLLGVPPLVNVARA

>d1b35b\_ b.10.1.3 (B:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

ENSHIENEDKRLTSEQKEIVHFVSEGVTPSTTALPDIVNLSTNYLDKNTREDRIHSIKDFLSRPIIIATNLWSVSDPVEKQLYTANFPEVLISNAMYQDKLKGFVGLRATLVVKVQVNSQPFQQGRLMLQYIPYAQYMPNRVTLINETLQGRSGCPRTDLELSVGTEVEMRIPYVSPHLYYNLITGQGSFGSIYVVVYSQLHDQVSGTGSIEYTVWAHLEDVDVQYPTGANIFTGNEAYIKGTSRYDAAQKAHAA

>d1b35c\_ b.10.1.3 (C:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

SKPTVQGKIGECKLRGQGRMANFDGMDMSHKMALSSTNEIETNEGLAGTSLDVMDLSRVLSIPNYWDRFTWKTSDVINTVLWDNYVSPFKVKPYSATITDRFRCTHMGKVANAFTYWRGSMVYTFKFVKTQYHSGRLRISFIPYYYNTTISTGTPDVSRTQKIVVDLRTSTAVSFTVPYIGSRPWLYCIRPESSWLSKDNTDGALMYNCVSGIVRVEVLNQLVAAQNVFSEIDVICEVNGGPDLEFAGPTCPRYVPYAGDFTLADTRKIEAERTQEYSNNED

>d1sida\_ b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

KACPRPAPVPKLLIKGGMEVLDLVTGPDSVTEIEAFLNPRMGQPPTPESLTEGGQYYGWSRGINLATSDTEDSPGNNTLPTWSMAKLQLPMLNEDLTCDTLQMWEAVSVKTEVVGSGSLLDVHGFNKPTDTVNTKGISTPVEGSQYHVFAVGGEPLDLQGLVTDARTKYKEEGVVTIKTITKKDMVNKDQVLNPISKAKLDKDGMYPVEIWHPDPAKNENTRYFGNYTGGTTTPPVLQFTNTLTTVLLDENGVGPLCKGEGLYLSCVDIMGWRVTRNYDVHHWRGLPRYFKITLRKRWVKNPYPMASLISSLFNNMLPQVQGQPMEGENTQVEEVRVYDGTEPVPGDPDMTRYVDRFGKTKTVFPG

>d1vpsa\_ b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

GGMEVLDLVTGPDSVTEIEAFLNPRMGQPPTPESLTEGGQYYGWSRGINLATSDTEDSPGNNTLPTWSMAKLQLPMLNEDLTCDTLQMWEAVSVKTEVVGSGSLLDVHGFNKPTDTVNTKGISTPVEGSQYHVFAVGGEPLDLQGLVTDARTKYKEEGVVTIKTITKKDMVNKDQVLNPISKAKLDKDGMYPVEIWHPDPAKNENTRYFGNYTGGTTTPPVLQFTNTLTTVLLDENGVGPLCKGEGLYLSCVDIMGWRVTRNYDVHHWRGLPRYFKITLRKRWVK

>d1fmd1\_ b.10.1.4 (1:) Foot-and-mouth desease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTTTGESADPVTTTVENYGGETQVQRRHHTDVAFVLDRFVKVTVSDNQHTLDVMQAHKDNIVGALLRAATYYFSDLEIAVTHTGKLTWVPNGAPVSALNNTTNPTAYHKGPVTRLALPYTAPHRVLATAYTGTTTYTASARGDLAHLTTTHAAHLPTSFNFGAVKAETITELLVRMKRAELYCPRPILPIQPTGDRHKQPLVAPAKQ

>d1fmd2\_ b.10.1.4 (2:) Foot-and-mouth desease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

DKKTEETTLLEDRILTTRNGHTTSTTQSSVGVTFGYATAEDSTSGPNTSALETRVHQAERFFKMALFDWVPSQNFGHMHKVVLPHEPKGVYGGLVKSYAYMRNGWDVEVTAVGNQFNGGCLLVALVPEMGDISDREKYQLTLYPHQFINPRTNMTAHITVPYVGVNRYDQYKQHRPWTLVVMVVAPLTTNTAGAQQIKVYANIAPTNVHVAGELPSKE

>d1fmd3\_ b.10.1.4 (3:) Foot-and-mouth desease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

GIFPVACSDGYGNMVTTDPKTADPAYGKVYNPPRTALPGRFTNYLDVAEACPTFLMFENVPYVSTRTDGQRLLAKFDVSLAAKHMSNTYLAGLAQYYTQYTGTINLHFMFTGPTDAKARYMVAYVPPGMDAPDNPEEAAHCIHAEWDTGLNSKFTFSIPYISAADYTYTASHEAETTCVQGWVCVYQITHGKADADALVVSASAGKDFELRLPVDARQQ

>d1qqp1\_ b.10.1.4 (1:) Foot-and-mouth desease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTSAGESADPVTTTVENYGGETQIQRRQHTDVSFIMDRFVKVTPQNQINILDLMQVPSHTLVGALLRASTYYFSDLEIAVKHEGDLTWVPNGAPEKALDNTTNPTAYHKAPLTRLALPYTAPHRVLATVYNGECRYSRNAVPNLRGDLQVLAQKVARTLPTSFNYGAIKATRVTELLYRMKRAETYCPRPLLAIHPTEARHKQKIVAPVK

>d1qqp2\_ b.10.1.4 (2:) Foot-and-mouth desease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

DKKTEETTLLEDRILTTRNGHTTSTTQSSVGVTYGYATAEDFVSGPNTSGLETRVVQAERFFKTHLFDWVTSDSFGRCHLLELPTDHKGVYGSLTDSYAYMRNGWDVEVTAVGNQFNGGCLLVAMVPELCSIQKRELYQLTLFPHQFINPRTNMTAHITVPFVGVNRYDQYKVHKPWTLVVMVVAPLTVNTEGAPQIKVYANIAPTNVHVAGEFPSKE

>d1qqp3\_ b.10.1.4 (3:) Foot-and-mouth desease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

GIFPVACSDGYGGLVTTDPKTADPVYGKVFNPPRNQLPGRFTNLLDVAEACPTFLRFEGGVPYVTTKTDSDRVLAQFDMSLAAKHMSNTFLAGLAQYYTQYSGTINLHFMFTGPTDAKARYMVAYAPPGMEPPKTPEAAAHCIHAEWDTGLNSKFTFSIPYLSAADYTYTASDVAETTNVQGWVCLFQITHGKADGDALVVLASAGKDFELRLPVDARAE

>d1c8da\_ b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host: dog (Canis familiaris)}

GVGISTGTFNNQTEFKFLENGWVYITANSSRLVHLNMPESENYRRVVVNNMDKTAVNGNMALDDIHAEIVTPWSLVDANAWGVWFNPGDWQLIVNTMSELHLVSFEQEIFNVVLKTVSESATQPPTKVYNNDLTASLMVALDSNNTMPFTPAAMRSETLGFYPWKPTIPTPWRYYFQWDRTLIPSHTGTSGTPTNIYHGTDPDDVQFYTIENSVPVHLLRTGDEFATGTFFFDCKPCRLTHTWQTNRALGLPPFLNSLPQSEGDTNFGDIGVQQDKRRGVTQMGNTNYITEATIMRPAEVGYSAPYYSFEASTQGPFKTPIAAGRGGAQTDENQAADGNPRYAFGRQHGQKTTTTGETPERFTYIAHQDTGRYPEGDWIQNINFNLPVTNDNVLLPTDPIGGKTGINYTNIFNTYGPLTALNNVPPVYPNGQIWDKEFDTDLKPRLHVNAPFVCQNNCPGQLFVKVAPNLTNQYDPDASANMSRIVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSINVDNQFNYVPSNIGGMKIVYEKSQLAPRKLY

>d1k3va\_ b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host: pig (Sus scrofa)}

GVGVSTGTFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKRIHVLNSESGVAGQMVQDDAHTQMVTPWSLIDANAWGVWFNPADWQLISNNMTEINLVSFEQEIFNVVLKTITESATSPPTKIYNNDLTASLMVALDTNNTLPYTPAAPRSETLGFYPWLPTKPTQYRYYLSCIRNLNPPTYTGQSQQITDSIQTGLHSDIMFYTIENAVPIHLLRTGDEFSTGIYHFDTKPLKLTHSWQTNRSLGLPPKLLTEPTTEGDQHPGTLPAANTRKGYHQTINNSYTEATAIRPAQVGYNTPYMNFEYSNGGPFLTPIVPTADTQYNDDEPNGAIRFTMDYQHGHLTTSSQELERYTFNPQSKCGRAPKQQFNQQAPLNLENTNNGTLLPSDPIGGKSNMHFMNTLNTYGPLTALNNTAPVFPNGQIWDKELDTDLKPRLHVTAPFVCKNNPPGQLFVKIAPNLTDDFNADSPQQPRIITYSNFWWKGTLTFTAKMRSSNMWNPIQQHTTTAENIGNYIPTNIGGIRMFPEYSQLIPRKLY

>d1mvma\_ b.10.1.4 (A:) MVM coat protein {Murine minute virus, strain i}

GVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGNMAKDDAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSLDQEIFNVVLKTVTEQDSGGQAIKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYYFCVDRDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDTNPVKLTHTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADVTQGMDREANGSVRYSYGKQHGENWAAHGPAPERYTWDETNFGSGRDTRDGFIQSAPLVVPPPLNGILTNANPIGTKNDIHFSNVFNSYGPLTTFSHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRAKLRANTTWNPVYQVSVEDNGNSYMSVTKWLPTATGNMQSVPLITRPVARNTY

>d1hxs1\_ b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}

GSSSTDNTVRETVGAATSRDALPNTEASGPTHSKEIPALTAVETGATNPLVPSDTVQTRHVVQHRSRSESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRRKLEFFTYSRFDMELTFVVTANFTETNNGHALNQVYQIMYVPPGAPVPEKWDDYTWQTSSNPSIFYTYGTAPARISVPYVGISNAYSHFYDGFSKVPLKDQSAALGDSLYGAASLNDFGILAVRVVNDHNPTKVTSKIRVYLKPKHIRVWCPRPPRAVAYYGPGVDYKDGTLTPLSTKDLTTY

>d1hxs2\_ b.10.1.4 (2:) Poliovirus {Poliovirus type 1, strain Mahoney}

ACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEYLRDSEANPVDQPTEPDVAACRFYTLDTVSWTKESRGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSNTTTMHTSYQNANPGEKGGTFTGTFTPDNNQTSPARRFCPVDYLLGNGTLLGNAFVFPHQIINLRTNNCATLVLPYVNSLSIDSMVKHNNWGIAILPLAPLNFASESSPEIPITLTIAPMCCEFNGLRNITLPRLQ

>d1hxs3\_ b.10.1.4 (3:) Poliovirus {Poliovirus type 1, strain Mahoney}

GLPVMNTPGSNQYLTADNFQSPCALPEFDVTPPIDIPGEVKNMMELAEIDTMIPFDLSATKKNTMEMYRVRLSDKPHTDDPILCLSLSPASDPRLSHTMLGEILNYYTHWAGSLKFTFLFCGSMMATGKLLVSYAPPGADPPKKRKEAMLGTHVIWDIGLQSSCTMVVPWISNTTYRQTIDDSFTEGGYISVFYQTRIVVPLSTPREMDILGFVSACNDFSVRLLRDTTHIEQKA

>d1pov0\_ b.10.1.4 (0:) Poliovirus {Poliovirus type 1, strain Mahoney}

GAQVSSQKVGAHENSNRAYGGSTINYTTINYYRDSASNAASKQDFSQDPSKFTEPIKDVLIKTAPMLNSPNIEACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEYLRDSEANPVDQPTEPDVAACRFYTLDTVSWTKESRGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSNTTTMHTSYQNANPGEKGGTFTGTFTPDNNQTSPARRFCPVDYLLGNGTLLGNAFVFPHQIINLRTNNCATLVLPYVNSLSIDSMVKHNNWGIAILPLAPLNFASESSPEIPITLTIAPMCCEFNGLRNITLPRLQ

>d1pov1\_ b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}

QHRSRSESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRRKLEFFTYSRFDMELTFVVTANFTETNNGHALNQVYQIMYVPPGAPVPEKWDDYTWQTSSNPSIFYTYGTAPARISVPYVGISNAYSHFYDGFSKVPLKDQSAALGDSLYGAASLNDFGILAVRVVNDHNPTKVTSKIRVYLKPKHIRVWCPRPPRAVAYYGPGVDYKDGTLTPLSTKDLTTY

>d1eah1\_ b.10.1.4 (1:) Poliovirus {Poliovirus type 2, strain Lansing}

ANNLPDTQSSGPAHSKETPALTAVETGATNPLVPSDTVQTRHVIQKRTRSESTVESFFARGACVAIIEVDNDAPTKRASKLFSVWKITYKDTVQLRRKLEFFTYSRFDMEFTFVVTSNYTDANNGHALNQVYQIMYIPPGAPIPGKWNDYTWQTSSNPSVFYTYGAPPARISVPYVGIANAYSHFYDGFAKVPLAGQASTEGDSLYGAASLNDFGSLAVRVVNDHNPTKLTSKIRVYMKPKHVRVWCPRPPRAVPYYGPGVDYKDGLAPLPGKGLTTY

>d1eah2\_ b.10.1.4 (2:) Poliovirus {Poliovirus type 2, strain Lansing}

SVRVMQLTLGNSTITTQEAANSVVAYGRWPEYIKDSEANPVDQPTEPDVAACRFYTLDTVTWRKESRGWWWKLPDALKDMGLFGQNMFYHYLGRAGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSTTHMFTKYENANPGEKGGEFKGSFTLDTNATNPARNFCPVDYLFGSGVLAGNAFVYPHQIINLRTNNCATLVLPYVNSLSIDSMTKHNNWGIAILPLAPLDFATESSTEIPITLTIAPMCCEFNGLRNITVPRTQ

>d1eah3\_ b.10.1.4 (3:) Poliovirus {Poliovirus type 2, strain Lansing}

GLPVLNTPGSNQYLTADNYQSPCAIPEFDVTPPIDIPGEVRNMMELAEIDTMIPLNLTNQRKNTMDMYRVELNDAAHSDTPILCLSLSPASDPRLAHTMLGEILNYYTHWAGSLKFTFLFCGSMMATGKLLVSYAPPGAEAPKSRKEAMLGTHVIWDIGLQSSCTMVVPWISNTTYRQTINDSFTEGGYISMFYQTRVVVPLSTPRKMDILGFVSACNDFSVRLLRDTTHISQEA

>d1pvc1\_ b.10.1.4 (1:) Poliovirus {Poliovirus type 3, strain Sabin}

QDSLPDTKASGPAHSKEVPALTAVETGATNPLAPSDTVQTRHVVQRRSRSESTIESFFARGACVAIIEVDNEQPTTRAQKLFAMWRITYKDTVQLRRKLEFFTYSRFDMEFTFVVTANFTNANNGHALNQVYQIMYIPPGAPTPKSWDDYTWQTSSNPSIFYTYGAAPARISVPYVGLANAYSHFYDGFAKVPLKTDANDQIGDSLYSAMTVDDFGVLAVRVVNDHNPTKVTSKVRIYMKPKHVRVWCPRPPRAVPYYGPGVDYRNNLDPLSEKGLTTY

>d1pvc2\_ b.10.1.4 (2:) Poliovirus {Poliovirus type 3, strain Sabin}

ACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEFIRDDEANPVDQPTEPDVATCRFYTLDTVMWGKESKGWWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAIPEYCLAGDSDKQRYTSYANANPGERGGKFYSQFNKDNAVTSPKREFCPVDYLLGCGVLLGNAFVYPHQIINLRTNNSATIVLPYVNALAIDSMVKHNNWGIAILPLSPLDFAQDSSVEIPITVTIAPMCSEFNGLRNVTAPKFQ

>d1pvc3\_ b.10.1.4 (3:) Poliovirus {Poliovirus type 3, strain Sabin}

GLPVLNTPGSNQYLTSDNHQSPCAIPEFDVTPPIDIPGEVKNMMELAEIDTMIPLNLESTKRNTMDMYRVTLSDSADLSQPILCLSLSPAFDPRLSHTMLGEVLNYYTHWAGSLKFTFLFCGSMMATGKILVAYAPPGAQPPTSRKEAMLGTHVIWDLGLQSSCTMVVPWISNVTYRQTTQDSFTEGGYISMFYQTRIVVPLSTPKSMSMLGFVSACNDFSVRLLRDTTHISQSA

>d4rhv1\_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 14}

TVASISSGPKHTQKVPILTANETGATMPVLPSDSIETRTTYMHFNGSETDVECFLGRAACVHVTEIQNKDATGIDNHREAKLFNDWKINLSSLVQLRKKLELFTYVRFDSEYTILATASQPDSANYSSNLVVQAMYVPPGAPNPKEWDDYTWQSASNPSVFFKVGDTSRFSVPYVGLASAYNCFYDGYSHDDAETQYGITVLNHMGSMAFRIVNEHDEHKTLVKIRVYHRAKHVEAWIPRAPRALPYTSIGRTNYPKNTEPVIKKRKGDIKSY

>d4rhv2\_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 14}

GYSDRVQQITLGNSTITTQEAANAVVCYAEWPEYLPDVDASDVNKTSKPDTSVCRFYTLDSKTWTTGSKGWCWKLPDALKDMGVFGQNMFFHSLGRSGYTVHVQCNATKFHSGCLLVVVIPEHQLASHEGGNVSVKYTFTHPGERGIDLSSANEVGGPVKDVLYNMNGTLLGNLLIFPHQFINLRTNNTATIVIPYINSVPIDSMTRHNNVSLMVIPIAPLTVPTGATPSLPITVTIAPMCTEFSGIRSKSIVPQ

>d4rhv3\_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 14}

GLPTTTLPGSGQFLTTDDRQSPSALPNYEPTPRIHIPGKVHNLLEIIQVDTLIPMNNTHTKDEVNSYLIPLNANRQNEQVFGTNLFIGDGVFKTTLLGEIVQYYTHWSGSLRFSLMYTGPALSSAKLILAYTPPGARGPQDRREAMLGTHVVWDIGLQSTIVMTIPWTSGVQFRYTDPDTYTSAGFLSCWYQTSLILPPETTGQVYLLSFISACPDFKLRLMKDTQTISQTVALTE

>d1aym1\_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 16}

NPVERYVDEVLNEVLVVPNINQSHPTTSNAAPVLDAAETGHTNKIQPEDTIETRYVQSSQTLDEMSVESFLGRSGCIHESVLDIVDNYNDQSFTKWNINLQEMAQIRRKFEMFTYARFDSEITMVPSVAAKDGHIGHIVMQYMYVPPGAPIPTTRDDYAWQSGTNASVFWQHGQPFPRFSLPFLSIASAYYMFYDGYDGDTYKSRYGTVVTNDMGTLCSRIVTSEQLHKVKVVTRIYHKAKHTKAWCPRPPRAVQYSHTHTTNYKLSSEVHNDVAIRPRTNLTTV

>d1aym2\_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 16}

SDRIIQITRGDSTITSQDVANAVVGYGVWPHYLTPQDATAIDKPTQPDTSSNRFYTLDSKMWNSTSKGWWWKLPDALKDMGIFGENMFYHFLGRSGYTVHVQCNASKFHQGTLLVVMIPEHQLATVNKGNVNAGYKYTHPGEAGREVGTQVENEKQPSDDNWLNFDGTLLGNLLIFPHQFINLRSNNSATLIVPYVNAVPMDSMVRHNNWSLVIIPVCQLQSNNISNIVPITVSISPMCAEFSGARAKTVVQ

>d1aym3\_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 16}

GLPVYVTPGSGQFMTTDDMQSPCALPWYHPTKEIFIPGEVKNLIEMCQVDTLIPINSTQSNIGNVSMYTVTLSPQTKLAEEIFAIKVDIASHPLATTLIGEIASYFTHWTGSLRFSFMFCGTANTTLKVLLAYTPPGIGKPRSRKEAMLGTHVVWDVGLQSTVSLVVPWISASQYRFTTPDTYSSAGYITCWYQTNFVVPPNTPNTAEMLCFVSGCKDFCLRMARDTDLHKQTGPITQ

>d1r1a1\_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 1A}

NYIDEVLNEVLVVPNIKESHHTTSNSAPLLDAAETGHTSNVQPEDAIETRYVITSQTRDEMSIESFLGRSGCVHISRIKVDYTDYNGQDINFTKWKITLQEMAQIRRKFELFTYVRFDSEITLVPCIAGRGDDIGHIVMQYMYVPPGAPIPSKRNDFSWQSGTNMSIFWQHGQPFPRFSIPFLSIASAYYMFYDGYDGDNTSSKYGSVVTNDMGTICSRIVTEKQKLSVVITTHIYHKAKHTKAWCPRPPRAVPYTHSHVTNYMPETGDVTTAIVRRNTITTA

>d1r1a2\_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 1A}

DRIMQITRGDSTISSDDVANAVVGYGVWPHYLTPQDATAINKPTQPDTSSNRFYTLESKHWNGSSKGWWWKLPDALKDMGIFGENMYYHFLGRSGYTVHVQCNASKFHQGTLLVAMIPEHQLASAKHGSVTAGYKLTHPGEAGRDVSQERDASLRQPSDDSWLNFDGTLLGNLLIFPHQFINLRSNNSATLIVPYVNAVPMDSMLRHNNWCLVIIPISPLRSETTSSNIVPITVSISPMCAEFSGARAKNIKQ

>d1r1a3\_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 1A}

GLPVYITPGSGQFMTTDDMQSPCALPWYHPTKEISIPGEVKNLIEMCQVDTLIPVNNVGNNVGNVSMYTVQLGNQTGMAQKVFSIKVDITSTPLATTLIGEIASYYTHWTGSLRFSFMFCGTANTTLKLLLAYTPPGIDEPTTRKDAMLGTHVVWDVGLQSTISLVVPWVSASHFRLTADNKYSMAGYITCWYQTNLVVPPSTPQTADMLCFVSACKDFCLRMARDTDLHIQSGPIEQ

>d1fpn1\_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 2}

LVVPNINSSNPTTSNSAPALDAAETGHTSSVQPEDVIETRYVQTSQTRDEMSLESFLGRSGCIHESKLEVTLANYNKENFTVWAINLQEMAQIRRKFELFTYTRFDSEITLVPCISALSQDIGHITMQYMYVPPGAPVPNSRDDYAWQSGTNASVFWQHGQAYPRFSLPFLSVASAYYMFYDGYDEQDQNYGTANTNNMGSLCSRIVTEKHIHKVHIMTRIYHKAKHVKAWCPRPPRALEYTRAHRTNFKIEDRSIQTAIVTRPIITTA

>d1fpn2\_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 2}

RIIQITRGDSTITSQDVANAIVAYGVWPHYLSSKDASAIDKPSQPDTSSNRFYTLRSVTWSSSSKGWWWKLPDALKDMGIFGENMFYHYLGRSGYTIHVQCNASKFHQGTLIVALIPEHQIASALHGNVNVGYNYTHPGETGREVKAETRLNPDLQPTEEYWLNFDGTLLGNITIFPHQFINLRSNNSATIIAPYVNAVPMDSMRSHNNWSLVIIPICPLETSSAINTIPITISISPMCAEFSGARAKRQ

>d1fpn3\_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 2}

GLPVFITPGSGQFLTTDDFQSPCALPWYHPTKEISIPGEVKNLVEICQVDSLVPINNTDTYINSENMYSVVLQSSINAPDKIFSIRTDVASQPLATTLIGEISSYFTHWTGSLRFSFMFCGTANTTVKLLLAYTPPGIAEPTTRKDAMLGTHVIWDVGLQSTISMVVPWISASHYRNTSPGRSTSGYITCWYQTRLVIPPQTPPTARLLCFVSGCKDFCLRMARDTNLHLQSGAIAQ

>d1rhi1\_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 3}

QTLASVSSGPKHTQSVPALTANETGATLPTRPSDNVETRTTYMHFNGSETDVESFLGRAACVHVTEIKNKNAAGLDNHRKEGLFNDWKINLSSLVQLRKKLELFTYVRFDSEYTILATASQPEASSYSSNLTVQAMYVPPGAPNPKEWDDYTWQSASNPSVFFKVGETSRFSVPFVGIASAYNCFYDGYSHDDPDTPYGITVLNHMGSMAFRVVNEHDVHTTIVKIRVYHRAKHVEAWIPRAPRALPYVSIGRTNYPRDSKTIVKKRTNIKTY

>d1rhi2\_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 3}

GYSDRVQQITLGNSTITTQEARNAIVCYAEWPEYLSDNDASDVNKTSKPDISVCRFYTLDSKTWKATSKGWCWKLPDALKDMGVFGQNMFYHSLGRTGYTIHVQCNATKFHSGCLLVVVIPEHQLASHEGGTVSVKYKYTHPGDRGIDLDTVEVAGGPTSDAIYNMDGTLLGNLLIFPHQFINMRTNNTATIVVPYINSVPIDSMTRHNNVSLMVVPIAPLNAPTGSSPTLPVTVTIAPMCTEFTGIRSRSIVPQ

>d1rhi3\_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 3}

GLPTTTLPGSGQFLTTDDRQSPSALPSYEPTPRIHIPGKVRNLLEIIQVGTLIPMNNTGTNDNVTNYLIPLHADRQNEQIFGTKLYIGDGVFKTTLLGEIAQYYTHWSGSLRISLMYTGPALSSAKIILAYTPPGTRGPEDKKEAMLGTHVVWDIGLQSTIVMTIPWTSGVQFRYTDPDTYTSAGYLSCWYLTSLILPPQTSGQVYLLSFISACPDFKLRLMKDTQTISQTDALTE

>d1bev1\_ b.10.1.4 (1:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

QAAGALVAGTSTSTHSVATDSTPALQAAETGATSTARDESMIETRTIVPTHGIHETSVESFFGRSSLVGMPLLATGTSITHWRIDFREFVQLRAKMSWFTYMRFDVEFTIIATSSTGQNVTTEQHTTYQVMYVPPGAPVPSNQDSFQWQSGCNPSVFADTDGPPAQFSVPFMSSANAYSTVYDGYARFMDTDPDRYGILPSNFLGFMYFRTLEDAAHQVRFRIYAKIKHTSCWIPRAPRQAPYKKRYNLVFSGDSDRICSNRASLTSY

>d1bev2\_ b.10.1.4 (2:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

EACGYSDRVAQLTLGNSTITTQEAANICVAYGCWPAKLSDTDATSVDKPTEPGVSADRFYTLRSKPWQADSKGWYWKLPDALNNTGMFGQNAQFHYLYRGGWAVHVQCNATKFHQGTLLVLAIPEHQIATQEQPAFDRTMPGSEGGTFQEPFWLEDGTSLGNSLIYPHQWINLRTNNSATLILPYVNAIPMDSAIRHSNWTLAIIPVAPLKYAAETTPLVPITVTIAPMETEYNGLRRAIASNQ

>d1bev3\_ b.10.1.4 (3:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

GLPTKPGPGSYQFMTTDEDCSPCILPDFQPTPEIFIPGKVNNLLEIAQVESILEANNREGVEGVERYVIPVSVQDALDAQIYALRLELGGSGPLSSSLLGTLAKHYTQWSGSVEITCMFTGTFMTTGKVLLAYTPPGGDMPRNREEAMLGTHVIWDFGLQSSITLVIPWISASHFRGVSNDDVLNYQYYAAGHVTIWYQTNMVIPPGFPNTAGIIMMIAAQPNFSFRIQKDREDMTQTAILQ

>d2mev1\_ b.10.1.4 (1:) Mengo virus {Host: monkey brain; middle size plaque variant}

GVENAEKGVTENTDATADFVAQPVYLPENQTKVAFFYDRSSPIGAFAVKSGSLESGFAPFSNKACPNSVILTPGPQFDPAYDQLRPQRLTEIWGNGNEETSEVFPLKTKQDYSFCLFSPFVYYKCDLEVTLSPHTSGAHGLLVRWCPTGTPTKPTTQVLHEVSSLSEGRTPQVYSAGPGTSNQISFVVPYNSPLSVLPAVWYNGHKRFDNTGDLGIAPNSDFGTLFFAGTKPDIKFTVYLRYKNMRVFCPRPTVFFPWPTSGDKIDMT

>d2mev2\_ b.10.1.4 (2:) Mengo virus {Host: monkey brain; middle size plaque variant}

ENLSDRVSQDTAGNTVTNTQSTVGRLVGYGTVHDGEHPASCADTASEKILAVERYYTFKVNDWTSTQKPFEYIRIPLPHVLSGEDGGVFGATLRRHYLVKTGWRVQVQCNASQFHAGSLLVFMAPEYPTLDVFAMDNRWSKDNLPNGTRTQTNRKGPFAMDHQNFWQWTLYPHQFLNLRTNTTVDLEVPYVNIAPTSSWTQHASWTLVIAVVAPLTYSTGASTSLDITASIQPVRPVFNGLRHEVLSRQ

>d2mev3\_ b.10.1.4 (3:) Mengo virus {Host: monkey brain; middle size plaque variant}

SPIPVTIREHAGTWYSTLPDSTVPIYGKTPVAPANYMVGEYKDFLEIAQIPTFIGNKVPNAVPYIEASNTAVKTQPLAVYQVTLSCSCLANTFLAALSRNFAQYRGSLVYTFVFTGTAMMKGKFLIAYTPPGAGKPTSRDQAMQATYAIWDLGLNSSYSFTVPFISPTHFRMVGTDQANITNVDGWVTVWQLTPLTYPPGCPTSAKILTMVSAGKDFSLKMPISPAPWSPQ

>d1cov1\_ b.10.1.4 (1:) Coxsackievirus B3 {Host: human (Homo sapiens)}

RVADTVGTGPTNSEAIPALTAAETGHTSQVVPSDTMQTRHVKNYHSRSESTIENFLCRSACVYFTEYENSGAKRYAEWVITPRQAAQLRRKLEFFTYVRFDLELTFVITSTQQPSTTQNQDAQILTHQIMYVPPGGPVPDKVDSYVWQTSTNPSVFWTEGNAPPRMSVPFLSIGNAYSNFYDGWSEFSRNGVYGINTLNNMGTLYARHVNAGSTGPIKSTIRIYFKPKHVKAWIPRPPRLCQYEKAKNVNFQPSGVTTTRQSITTMTNT

>d1cov2\_ b.10.1.4 (2:) Coxsackievirus B3 {Host: human (Homo sapiens)}

GYSDRVRSITLGNSTITTQECANVVVGYGVWPDYLKDSEATAEDQPTQPDVATCRFYTLDSVQWQKTSPGWWWKLPDALSNLGLFGQNMQYHYLGRTGYTIHVQCNASKFHQGCLLVVCVPEAEMGCATLNNTPSSAELLGGDTAKEFADKPVASGSNKLVQRVVYNAGMGVGVGNLTIFPHQWINLRTNNSATIVMPYTNSVPMDNMFRHNNVTLMVIPFVPLDYCPGSTTYVPITVTIAPMCAEYNGLRLAGHQ

>d1cov3\_ b.10.1.4 (3:) Coxsackievirus B3 {Host: human (Homo sapiens)}

GLPTMNTPGSCQFLTSDDFQSPSAMPQYDVTPEMRIPGEVKNLMEIAEVDSVVPVQNVGEKVNSMEAYQIPVRSNEGSGTQVFGFPLQPGYSSVFSRTLLGEILNYYTHWSGSIKLTFMFCGSAMATGKFLLAYSPPGAGAPTKRVDAMLGTHVVWDVGLQSSCVLCIPWISQTHYRYVASDEYTAGGFITCWYQTNIVVPADAQSSCYIMCFVSACNDFSVRLLKDTPFISQENFFQ

>d1d4m1\_ b.10.1.4 (1:) Coxsackievirus A9 {Host: human (Homo sapiens)}

GDVEEAIERAVVHVADTMRSGPSNSASVPALTAVETGHTSQVTPSDTMQTRHVKNYHSRSESTVENFLGRSACVYMEEYKTTDNDVNKKFVAWPINTKQMVQMRRKLEMFTYLRFDMEVTFVITSRQDPGTTLAQDMPVLTHQIMYVPPGGPIPAKVDDYAWQTSTNPSIFWTEGNAPARMSIPFISIGNAYSNFYDGWSNFDQRGSYGYNTLNNLGHIYVRHVSGSSPHPITSTIRVYFKPKHTRAWVPRPPRLCQYKKAFSVDFTPTPITDTRKDINTVTTV

>d1d4m2\_ b.10.1.4 (2:) Coxsackievirus A9 {Host: human (Homo sapiens)}

SDRVRSITLGNSTITTQECANVVVGYGRWPTYLRDDEATAEDQPTQPDVATCRFYTLDSIKWEKGSVGWWWKFPEALSDMGLFGQNMQYHYLGRAGYTIHVQCNASKFHQGCLLVVCVPEAEMGGAVVGQAFSATAMANGDKAYEFTSATQSDQTKVQTAIHNAGMGVGVGNLTIYPHQWINLRTNNSATIVMPYINSVPMDNMFRHYNFTLMVIPFVKLDYADTASTYVPITVTVAPMCAEYNGLRLAQAQ

>d1d4m3\_ b.10.1.4 (3:) Coxsackievirus A9 {Host: human (Homo sapiens)}

GLPTMNTPGSTQFLTSDDFQSPCALPQFDVTPSMNIPGEVKNLMEIAEVDSVVPVNNVQDTTDQMEMFRIPVTINAPLQQQVFGLRLQPGLDSVFKHTLLGEILNYYAHWSGSMKLTFVFCGSAMATGKFLIAYSPPGANPPKTRKDAMLGTHIIWDIGLQSSCVLCVPWISQTHYRLVQQDEYTSAGYVTCWYQTGMIVPPGTPNSSSIMCFASACNDFSVRMLRDTPFISQDNKLQ

>d1ev11\_ b.10.1.4 (1:) Echovirus type 1 {Host: human (Homo sapiens)}

GDVQNAVEGAMVRVADTVQTSATNSERVPNLTAVETGHTSQAVPGDTMQTRHVINNHVRSESTIENFLARSACVFYLEYKTGTKEDSNSFNNWVITTRRVAQLRRKLEMFTYLRFDMEITVVITSSQDQSTSQNQNAPVLTHQIMYVPPGGPIPVSVDDYSWQTSTNPSIFWTEGNAPARMSIPFISIGNAYSNFYDGWSHFSQAGVYGFTTLNNMGQLFFRHVNKPNPAAITSVARIYFKPKHVRAWVPRPPRLCPYINSTNVNFEPKPVTEVRTNIITT

>d1ev12\_ b.10.1.4 (2:) Echovirus type 1 {Host: human (Homo sapiens)}

GYSDRVRSITLGNSTITTQECANVVVGYGEWPEYLSDNEATAEDQPTQPDVATCRFYTLDSVQWENGSPGWWWKFPDALRDMGLFGQNMYYHYLGRAGYTIHVQCNASKFHQGCILVVCVPEAEMGSAQTSGVVNYEHISKGEIASRFTTTTTAEDHGVQAAVWNAGMGVGVGNLTIFPHQWINLRTNNSATIVMPYVNSVPMDNMYRHHNFTLMIIPFVPLDFSAGASTYVPITVTVAPMCAEYNGLRLAGHQ

>d1ev13\_ b.10.1.4 (3:) Echovirus type 1 {Host: human (Homo sapiens)}

GLPTMNTPGSNQFLTSDDFQSPSAMPQFDVTPEMHIPGEVRNLMEIAEVDSVMPINNDSAAKVSSMEAYRVELSTNTNAGTQVFGFQLNPGAESVMNRTLMGEILNYYAHWSGSIKITFVFCGSAMTTGKFLLSYAPPGAGAPKTRKDAMLGTHVVWDVGLQSSCVLCIPWISQTHYRFVEKDPYTNAGFVTCWYQTSVVSPASNQPKCYMMCMVSACNDFSVRMLRDTKFIEQTSFYQ

>d1tme1\_ b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

GSDNAEKGKVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNIESTFVYQENDLRLNCLLLTPLPSFCPDSTSGPVKTKAPVQWRWVRSGGTTNFPLMTKQDYAFLCFSPFTYYKCDLEVTVSALGTDTVASVLRWAPTGAPADVTDQLIGYTPSLGETRNPHMWLVGAGNTQISFVVPYNSPLSVLPAAWFNGWSDFGNTKDFGVAPNADFGRLWIQGNTSASVRIRYKKMKVFCPRPTLFFPWPV

>d1tme2\_ b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

DRVASDKAGNSATNTQSTVGRLCGYGEAHHGEHPASCADTATDKVLAAERYYTIDLASWTTTQEAFSHIRIPLPHVLAGEDGGVFGATLRRHYLCKTGWRVQVQCNASQFHAGSLLVFMAPEFYTGKGTKTGDMEPTDPFTMDTTWRAPQGAPTGYRYDSRTGFFAMNHQNQWQWTVYPHQILNLRTNTTVDLEVPYVNIAPTSSWTQHANWTLVVAVFSPLQYASGSSSDVQITASIQPVNPVFNGLRHETVIA

>d1tme3\_ b.10.1.4 (3:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

SPIAVTVREHKGCFYSTNPDTTVPIYGKTISTPNDYMCGEFSDLLELCKLPTFLGNPNSNNKRYPYFSATNSVPTTSLVDYQVALSCSCMCNSMLAAVARNFNQYRGSLNFLFVFTGAAMVKGKFLIAYTPPGAGKPTTRDQAMQATYAIWDLGLNSSFVFTAPFISPTHYRQTSYTSATIASVDGWVTVWQLTPLTYPSGTPVNSDILTLVSAGDDFTLRMPISPTKWVPQ

>d1tmf1\_ b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

GVDNAEKGKVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNMETTFNYQENDYRLNCLLLTPLPSFCPDSSSGPQKTKAPVQWRWVRSGGVNGANFPLMTKQDYAFLCFSPFTFYKCDLEVTVSALGTDTVASVLRWAPTGAPADVTDQLIGYTPSLGETRNPHMWLVGAGNSQVSFVVPYNSPLSVLPAAWFNGWSDFGNTKDFGVAPNADFGRLWIQGNTSASVRIRYKKMKVFCPRPTLFFPWPTPTTTKINADNPVPILELE

>d1tmf2\_ b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

DQNTEEMENLSDRVASDKAGNSATNTQSTVGRLCGYGKSHHGEHPASCADTATDKVLAAERYYTIDLASWTTSQEAFSHIRIPLPHVLAGEDGGVFGATLRRHYLCKTGWRVQVQCNASQFHAGSLLVFMAPEFYTGKGTKTGTMEPSDPFTMDTEWRSPQGAPTGYRYDSRTGFFATNHQNQWQWTVYPHQILNLRTNTTVDLEVPYVNVAPSSSWTQHANWTLVVAVLSPLQYATGSSPDVQITASLQPVNPVFNGLRHETVIAQ

>d1sva1\_ b.10.1.4 (1:) Simian virus 40 (SV40) coat protein {Simian virus 40}

PKKPKEPVQVPKLVIKGGIEVLGVKTGVDSFTEVECFLNPQMGNPDEHQKGLSKSLAAEKQFTDDSPDKEQLPCYSVARIPLPNINEDLTCGNILMWEAVTVKTEVIGVTAMLNLHSGTQKTHENGAGKPIQGSNFHFFAVGGEPLELQGVLANYRTKYPAQTVTPKNATVDSQQMNTDHKAVLDKDNAYPVECWVPDPSKNENTRYFGTYTGGENVPPVLHITNTATTVLLDEQGVGPLCKADSLYVSAVDICGLFTNTSGTQQWKGLPRYFKITLRKRSVKNPYPISFLLSDLINRRTQRVDGQPMIGMSSQVEEVRVYEDTEELPGDPDMIRYIDEFGQTTTRMQ

>d1dzla\_ b.10.1.4 (A:) L1 protein {Human papillomavirus type 16}

KVVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIKKPNNNKILVPKVSGLQYRVFRIHLPDPNKFGFPDTSFYNPDTQRLVWACVGVEVGRGQPLGVGISGHPLLNKLDDTENASAYAANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPCTQVAVQPGDCPPLELINTVIQDGDMVDTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRREQMFVRHLFNRAGTVGENVPDDLYIKGSGSTANLASSNYFPTPSGSMVTSDAQIFNKPYWLQRAQGHNNGICWGNQLFVTVVDTTRSTNMSLCAAISTSETTYKNTNFKEYLRHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVTSQAIACQKHTPPAPKEDPLKKYTFWEVNLKEKFSADLDQFPLGRKFLLQLGL

>d1ihma\_ b.10.1.4 (A:) Calcivirus capsid protein {Norwalk virus}

DPLAMDPVAGSSTAVATAGQVNPIDPWIINNFVQAPQGEFTISPNNTPGDVLFDLSLGPHLNPFLLHLSQMYNGWVGNMRVRIMLAGNAFTAGKIIVSCIPPGFGSHNLTIAQATLFPHVIADVRTLDPIEVPLEDVRNVLFHNNDRNQQTMRLVCMLYTPLRTGGGTGDSFVVAGRVMTCPSPDFNFLFLVPPTVEQKTRPFTLPNLPLSSLSNSRAPLPISSMGISPDNVQSVQFQNGRCTLDGRLVGTTPVSLSHVAKIRGTSNGTVINLTELDGTPFHPFEGPAPIGFPDLGGCDWHINMTQFGHSSQTQYDVDTTPDTFVPHLGSIQANGIGSGNYVGVLSWISPPSHPSGSQVDLWKIPNYGSSITEATHLAPSVYPPGFGEVLVFFMSKMPGPGAYNLPCLLPQEYISHLASEQAPTVGEAALLHYVDPDTGRNLGEFKAYPDGFLTCVPNGASSGPQQLPINGVFVFVSWVSRFYQLKPVGTAS

>d1amm\_1 b.11.1.1 (1-85) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GKITFYEDRGFQGHCYECSSDCPNLQPYFSRCNSIRVDSGCWMLYERPNYQGHQYFLRRGDYPDYQQWMGFNDSIRSCRLIPQHT

>d1amm\_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GTFRMRIYERDDFRGQMSEITDDCPSLQDRFHLTEVHSLNVLEGSWVLYEMPSYRGRQYLLRPGEYRRYLDWGAMNAKVGSLRRVMDFY

>d1elpa1 b.11.1.1 (A:1-85) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}

GKITFYEDRGFQGRHYECSSDHSNLQPYLGRCNSVRVDSGCWMIYEQPNYLGPQYFLRRGDYPDYQQWMGLNDSIRSCRLIPHAG

>d1elpa2 b.11.1.1 (A:87-174) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}

SHRLRLYEREDYRGQMIEITEDCSSLQDRFHFNEIHSLNVLEGSWVLYELPNYRGRQYLLRPGEYRRYHDWGAMNAKVGSLRRVIDIY

>d1a7ha\_ b.11.1.1 (A:) gamma-Crystallin {Cow (Bos taurus), isoform S}

MYKIQIFEKGDFNGQMHETTEDCPSIMEQFHMREVHSCKVLEGAWIFYELPNYRGRQYLLDKKEYRKPVDWGAASPAVQSFRRIVE

>d1ha4a\_ b.11.1.1 (A:) gamma-Crystallin {Human (Homo sapiens)}

GQYKIQIFEKGDFSGQMYETTEDCPSIMEQFHMREIHSCKVLEGVWIFYELPNYRGRQYLLDKKEYRKPIDWGAASPAVQSFRRIVE

>d1a45\_1 b.11.1.1 (1-84) gamma-Crystallin {Cow (Bos taurus), isoform F}

GKITFYEDRGFQGRHYECSSDHSNLQPYFSRCNSIRVDSGCWMLYEQPNFQGPQYFLRRGDYPDYQQWMGLNDSIRSCRLIPHT

>d1a45\_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform F}

GSHRLRIYEREDYRGQMVEITEDCSSLHDRFHFSEIHSFNVLEGWWVLYEMTNYRGRQYLLRPGDYRRYHDWGATNARVGSLRRAVDFY

>d2bb2\_1 b.11.1.1 (-2-85) beta-Crystallin {Cow (Bos taurus)}

LNPKIIIFEQENFQGHSHELNGPCPNLKETGVEKAGSVLVQAGPWVGYEQANCKGEQFVFEKGEYPRWDSWTSSRRTDSLSSLRPIKVDS

>d2bb2\_2 b.11.1.1 (86-175) beta-Crystallin {Cow (Bos taurus)}

QEHKITLYENPNFTGKKMEVIDDDVPSFHAHGYQEKVSSVRVQSGTWVGYQYPGYRGLQYLLEKGDYKDSGDFGAPQPQVQSVRRIRDMQW

>d1a5da1 b.11.1.1 (A:1-84) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

GKITFYEDRGFQGRHYECSTDHSNLQPYFSRCNSVRVDSGCWMLYEQPNFTGCQYFLRRGDYPDYQQWMGFSDSVRSCRLIPHS

>d1a5da2 b.11.1.1 (A:85-174) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

SSHRIRIYEREDYRGQMVEITDDCPHLQDRFHFSDFHSFHVMEGYWVLYEMPNYRGRQYLLRPGEYRRYHDWGAMNARVGSLRRIMDFY

>d1bd7a\_ b.11.1.1 (A:) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

EHKIILYENPNFTGKKMEIVDDDVPSFHAHGYQEKVSSVRVQSGTWVGYQYPGYRGLQYLLEKGDYKDNSDFGAPHPQVQSVRRIRDMQGNPKIIIFEQENFQGHSHELSGPCPNLKETGMEKAGSVLVQAGPWVGYEQANCKGEQFVFEKGEYPRWDSWTSSRRTDSLSSLRPIK

>d1npsa\_ b.11.1.1 (A:) Protein S {Myxococcus xanthus}

ANITVFYNEDFQGKQVDLPPGNYTRAQLAALGIENNTISSVKVPPGVKAILYQNDGFAGDQIEVVANAEELGPLNNNVSSIRVISVPV

>d1prr\_2 b.11.1.1 (91-173) Protein S {Myxococcus xanthus}

PRARFFYKEQFDGKEVDLPPGQYTQAELERYGIDNNTISSVKPQGLAVVLFKNDNFSGDTLPVNSDAPTLGAMNNNTSSIRIS

>d1hdfa\_ b.11.1.1 (A:) Spherulin 3a (S3a) {Slime mold (Physarum polycephalum)}

SVCKGVSGNPAKGEVFLYKHVNFQGDSWKVTGNVYDFRSVSGLNDVVSSVKVGPNTKAFIFKDDRFNGNFIRLEESSQVTDLTTRNLNDAISSMIVATFE

>d1wkt\_\_ b.11.1.2 (-) Yeast killer toxin {Williopsis mrakii}

GDGYLIMCKNCDPNTGSCDWKQNWNTCVGIGANVHWMVTGGSTDGKQGCATIWEGSGCVGRSTTMCCPANTCCNINTGFYIRSYRRVE

>d1bhu\_\_ b.11.1.3 (-) Streptomyces metalloproteinase inhibitor, SMPI {Streptomyces nigrescens}

APSCPAGSLCTYSGTGLSGARTVIPASDMEKAGTDGVKLPASARSFANGTHFTLRYGPARKVTCVRFPCYQYATVGKVAPGAQLRSLPSPGATVTVGQDLGD

>d1f53a\_ b.11.1.4 (A:) Killer toxin-like protein SKLP {Streptomyces sp.}

IDHVPCRGGENFLKIWSHSGGQQSVDCYANRGRIDFGGWWVDKISTGNNDLIYYDANGDSVRVDRWHDITYPNRPPKVNSIEIL

>d1g6ea\_ b.11.1.6 (A:) Antifungal protein AFP1 {Streptomyces tendae, tu901}

MINRTDCNENSYLEIHNNEGRDTLCFANAGTMPVAIYGVNWVESGNNVVTLQFQRNLSDPRLETITLQKWGSWNPGHIHEILSIRIY

>d1c01a\_ b.11.1.5 (A:) Plant antimicrobial protein MIAMP1 {Macadamia nut (Macadamia integrifolia)}

SAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGWKSIFIQC

>d1f8na2 b.12.1.1 (A:6-149) Plant lipoxigenase {Soybean (Glycine max), isozyme L1}

HKIKGTVVLMPKNELEVNPDGSAVDNLNAFLGRSVSLQLISATKADAHGKGKVGKDTFLEGINTSLPTLGAGESAFNIHFEWDGSMGIPGAFYIKNYMQVEFFLKSLTLEAISNQGTIRFVCNSWVYNTKLYKSVRIFFANHTY

>d1ik3a2 b.12.1.1 (A:9-167) Plant lipoxigenase {Soybean (Glycine max), isozyme L3}

GHKIKGTVVLMRKNVLDVNSVTSVGGIIGQGLDLVGSTLDTLTAFLGRSVSLQLISATKADANGKGKLGKATFLEGIITSLPTLGAGQSAFKINFEWDDGSGIPGAFYIKNFMQTEFFLVSLTLEDIPNHGSIHFVCNSWIYNAKLFKSDRIFFANQTY

>d1lox\_2 b.12.1.1 (2-112) 15-Lipoxygenase {Rabbit (Oryctolagus cuniculus)}

GVYRVCVSTGASIYAGSKNKVELWLVGQHGEVELGSCLRPTRNKEEEFKVNVSKYLGSLLFVRLRKKHFLKEDAWFCNWISVQALGAAEDKYWFPCYRWVVGDGVQSLPVG

>d1hpla1 b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain {Horse (Equus caballus)}

RWRYRVDVTLSGKKVTGHVLVSLFGNKGNSRQYEIFQGTLKPDNTYSNEFDSDVEVGDLEKVKFIWYNNVINLTLPKVGASKITVERNDGSVFNFCSEETVREDVLLTLTAC

>d1etha1 b.12.1.2 (A:337-448) Pancreatic lipase, C-terminal domain {Pig (Sus scrofa)}

ARWRYKVSVTLSGKKVTGHILVSLFGNEGNSRQYEIYKGTLQPDNTHSDEFDSDVEVGDLQKVKFIWYNVINPTLPRVGASKITVERNDGKVYDFCSQETVREEVLLTLNPC

>d1gpl\_1 b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain {Guinea pig (Cavia porcellus)}

RWRYKVSVTLSGKKVTGHILVSLFGNKGNSKQYEIFKGTLKPDSTHSNEFDSDVDVGDLQMVKFIWYNNVINPTLPRVGASKIIVETNVGKQFNFCSPETVREEVLLTLTPC

>d1rp1\_1 b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain {Dog (Canis familiaris)}

RWRYGVSITLSGKRATGQAKVALFGSKGNTHQFNIFKGILKPGSTHSNEFDAKLDVGTIEKVKFLWNNNNPTFPKVGAAKITVQKGEEKTVHSFCSESTVREDVLLTLTPC

>d1bu8a1 b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain {Rat (Rattus norvegicus)}

RWRYKVSVTLSGAKKLSGYILVALYGNNGNSKQYEIFKGSLKPEARHVRDIDVDINVGEIQKVKFLWNNKVINLFRPTLGASQITVQSGVDGKEYNFCSSDTVREDVLQSLYPC

>d1ca1\_2 b.12.1.3 (250-370) Alpha-toxin, C-terminal domain {Clostridium perfringens}

SVGKNVKELVAYISTSGEKDAGTDDYMYFGIKTKDGKTQEWEMDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRKYTAFPDAYKPENIKVIANGKVVVDKDINEWISGNSTYNIK

>d1k5ja\_ b.13.3.1 (A:) Nucleoplasmin core {Xenopus laevis}

VSLIWGCELNEQNKTFEFKVEDDEEKCEHQLALRTVCLGDKAKDEFHIVEIVTQEEGAEKSVPIATLKPSILPMATMVGIELTPPVTFRLKAGSGPLYISGQHVA

>d1pgs\_1 b.13.1.1 (4-140) Peptide:N-glycosidase F, PNGase F {Flavobacterium meningosepticum}

DNTVNIKTFDKVKNAFGDGLSQSAEGTFTFPADVTTVKTIKMFIKNECPNKTCDEWDRYANVYVKNKTTGEWYEIGRFITPYWVGTEKLPRGLEIDVTDFKSLLSGNTELKIYTETWLAKGREYSVDFDIVYGTPDY

>d1pgs\_2 b.13.1.1 (141-314) Peptide:N-glycosidase F, PNGase F {Flavobacterium meningosepticum}

KYSAVVPVIQYNKSSIDGVPYGKAHTLGLKKNIQLPTNTEKAYLRTTISGWGHAKPYDAGSRGCAEWCFRTHTIAINNANTFQHQLGALGCSANPINNQSPGNWTPDRAGWCPGMAVPTRIDVLNNSLTGSTFSYEYKFQSWTNNGTNGDAFYAISSFVIAKSNTPISAPVVTN

>d1phm\_1 b.13.1.2 (45-198) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (Rattus norvegicus)}

NECLGTIGPVTPLDASDFALDIRMPGVTPKESDTYFCMSMRLPVDEEAFVIDFKPRASMDTVHHMLLFGCNMPSSTGSYWFCDEGTCTDKANILYAWARNAPPTRLPKGVGFRVGGETGSKYFVLQVHYGDISAFRDNHKDCSGVSVHLTRVPQ

>d1phm\_2 b.13.1.2 (199-354) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (Rattus norvegicus)}

PLIAGMYLMMSVDTVIPPGEKVVNADISCQYKMYPMHVFAYRVHTHHLGKVVSGYRVRNGQWTLIGRQNPQLPQAFYPVEHPVDVTFGDILAARCVFTGEGRTEATHIGGTSSDEMCNLYIMYYMEAKYALSFMTCTKNVAPDMFRTIPAEANIPI

>d1hx6a1 b.13.2.1 (A:15-244) Coat protein p3 {Bacteriophage prd1}

LRNQQAMAANLQARQIVLQQSYPVIQQVETQTFDPANRSVFDVTPANVGIVKGFLVKVTAAITNNHATEAVALTDFGPANLVQRVIYYDPDNQRHTETSGWHLHFVNTAKQGAPFLSSMVTDSPIKYGDVMNVIDAPATIAAGATGELTMYYWVPLAYSETDLTGAVLANVPQSKQRLKLEFANNNTAFAAVGANPLEAIYQGAGAADCEFEEISYTVYQSYLDQLPVGQ

>d1hx6a2 b.13.2.1 (A:245-384) Coat protein p3 {Bacteriophage prd1}

NGYILPLIDLSTLYNLENSAQAGLTPNVDFVVQYANLYRYLSTIAVFDNGGSFNAGTDINYLSQRTANFSDTRKLDPKTWAAQTRRRIATDFPKGVYYCDNRDKPIYTLQYGNVGFVVNPKTVNQNARLLMGYEYFTSRT

>d1dhx\_1 b.13.2.2 (44-650) Adenovirus hexon {Human adenovirus type 2}

FRNPTVAPTHDVTTDRSQRLTLRFIPVDREDTAYSYKARFTLAVGDNRVLDMASTYFDIRGVLDRGPTFKPYSGTAYNALAPKGAPNSCEWEQTEDSGRAVAEDEEEEDEDEEEEEEEQNARDQATKKTHVYAQAPLSGETITKSGLQIGSDNAETQAKPVYADPSYQPEPQIGESQWNEADANAAGGRVLKKTTPMKPCYGSYARPTNPFGGQSVLVPDEKGVPLPKVDLQFFSNTTSLNDRQGNATKPKVVLYSEDVNMETPDTHLSYKPGKGDENSKAMLGQQSMPNRPNYIAFRDNFIGLMYYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDPDVRIIENHGTEDELPNYCFPLGGIGVTDTYQAIKANGNGSGDNGDTTWTKDETFATRNEIGVGNNFAMEINLNANLWRNFLYSNIALYLPDKLKYNPTNVEISDNPNTYDYMNKRVVAPGLVDCYINLGARWSLDYMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMVLQSSLGNDLRVDGASIKFDSICLYATFFPMAHNTASTLEAMLR

>d1ruxa1 b.13.2.2 (A:5-636) Adenovirus hexon {Human adenovirus type 5}

MMPQWSYMHISGQDASEYLSPGLVQFARATETYFSLNNKFRNPTVAPTHDVTTDRSQRLTLRFIPVDREDTAYSYKARFTLAVGDNRVLDMASTYFDIRGVLDRGPTFKPYSGTAYNALAPKGAPNPCEWDEAATALEINLEEEDDDNEDEVDEQAEQQKTHVFGQAPYSGINITKEGIQIGVEGQTPKYADKTFQPEPQIGESQWYETEINHAAGRVLKKTTPMKPCYGSYAKPTNENGGQGILVKQQNGKLESQVEMQFFSTTEATAGNGDNLTPKVVLYSEDVDIETPDTHISYMPTIKEGNSRELMGQQSMPNRPNYIAFRDNFIGLMYYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLLDSIGDRTRYFSMWNQAVDSYDPDVRIIENHGTEDELPNYCFPLGGVINTETLTKVKPKTGQENGWEKDATEFSDKNEIRVGNNFAMEINLNANLWRNFLYSNIALYLPDKLKYSPSNVKISDNPNTYDYMNKRVVAPGLVDCYINLGARWSLDYMDNVNPFNHHRNAGLRYRSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMVLQSSLGNDLRVDGASIKFDSICLYATFFPMAHNTASTLEAMLRND

>d1ruxa2 b.13.2.2 (A:637-946) Adenovirus hexon {Human adenovirus type 5}

TNDQSFNDYLSAANMLYPIPANATNVPISIPSRNWAAFRGWAFTRLKTKETPSLGSGYDPYYTYSGSIPYLDGTFYLNHTFKKVAITFDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTKDWFLVQMLANYNIGYQGFYIPESYKDRMYSFFRNFQPMSRQVVDDTKYKDYQQVGILHQHNNSGFVGYLAPTMREGQAYPANFPYPLIGKTAVDSITQKKFLCDRTLWRIPFSSNFMSMGALTDLGQNLLYANSAHALDMTFEVDPMDEPTLLYVLFEVFDVVRVHRPHRGVIETVYLRTPFSA

>d1kful2 b.14.1.1 (L:356-514) Calpain large subunit, middle domain (domain III) {Human (Homo sapiens)}

WKLTKMDGNWRRGSTAGGCRNYPNTFWMNPQYLIKLEEEDEDEEDGESGCTFLVGLIQKHRRRQRKMGEDMHTIGFGIYEVPEELSGQTNIHLSKNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADYQAVDD

>d1df0a2 b.14.1.1 (A:356-514) Calpain large subunit, middle domain (domain III) {Rat (Rattus norvegicus)}

WKLTKMDGNWRRGSTAGGCRNYPNTFWMNPQYLIKLEEEDEDDEDGERGCTFLVGLIQKHRRRQRKMGEDMHTIGFGIYEVPEELTGQTNIHLSKNFFLTTRARERSDTFINLREVLNRFKLPPGEYVLVPSTFEPHKNGDFCIRVFSEKKADYQTVDD

>d1f35a\_ b.94.1.1 (A:) Olfactory marker protein {Mouse (Mus musculus)}

AEDGPQKQQLEMPLVLDQDLTQQMRLRVESLKQRGEKKQDGEKLIRPAESVYRLDFIQQQKLQFDHWNVVLDKPGKVTITGTSQNWTPDLTNLMTRQLLDPAAIFWRKEDSDAMDWNEADALEFGERLSDLAKIRKVMYFLITFGEGVEPANLKASVVFNQL

>d1shsa\_ b.15.1.1 (A:) Small heat shock protein {Archaeon Methanococcus jannaschii}

TGIQISGKGFMPISIIEGDQHIKVIAWLPGVNKEDIILNAVGDTLEIRAKRSPLMITESERIIYSEIPEEEEIYRTIKLPATVKEENASAKFENGVLSVILPKAESSIKKGINIE

>d1gmea\_ b.15.1.1 (A:) Small heat shock protein {Wheat (Triticum aestivum)}

SIVRRSNVFDPFADLWADPFDTFRSIVPAISGGGSETAAFANARMDWKETPEAHVFKADLPGVKKEEVKVEVEDGNVLVVSGERTKEKEDKNDKWHRVERSSGKFVRRFRLLEDAKVEEVKAGLENGVLTVTVPKAEVKKPEVKAIQISG

>d1gmeb\_ b.15.1.1 (B:) Small heat shock protein {Wheat (Triticum aestivum)}

NARMDWKETPEAHVFKADLPGVKKEEVKVEVEDGNVLVVSGERTKEKEDKNDKWHRVERSSGKFVRRFRLLEDAKVEEVKAGLENGVLTVTVPKAEVKKPEVKAIQISG

>d1ejfa\_ b.15.1.2 (A:) Co-chaperone p23 {Human (Homo sapiens)}

MQPASAKWYDRRDYVFIEFCVEDSKDVNVNFEKSKLTFSCLGGSDNFKHLNEIDLFHCIDPNDSKHKRTDRSILCCLRKGESGQSWPRLTKERAKLNWLSVDFNNWKDWE

>d1ezsa\_ b.16.1.1 (A:) Ecotin, trypsin inhibitor {Escherichia coli}

PYPQAEKGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGAAAAYYVFDKVSSPVSTRMACPDGKKEKKFVTAYLGDAGMLRYNSKLPIVVYTPDNVDVKYRVWKAEEKIDNAVVR

>d1slua\_ b.16.1.1 (A:) Ecotin, trypsin inhibitor {Escherichia coli}

IAPYPQAEKGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGYDYYVFDKVSSPVSTMMHCPDGKKEKKFVTAYLGDAGMLRYNSKLPIVVYTPDNVDVKYRVWKAEEKIDNAVVR

>g1fi8.1 b.16.1.1 (C:,D:) Ecotin, trypsin inhibitor {Escherichia coli}

PLEKIAPYPQAEKGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGYDYYVFDKVSSPIEPDXKFVTAYLGDAGMLRYNSKLPIVVYTPDNVDVKYRVWKAEEKIDNAVVR

>d1beha\_ b.17.1.1 (A:) Phosphatidylethanolamine binding protein, PEBP {Human (Homo sapiens)}

VDLSKWSGPLSLQEVDEQPQHPLHVTYAGAAVDELGKVLTPTQVKNRPTSISWDGLDSGKLYTLVLTDPDAPSRKDPKYREWHHFLVVNMKGNDISSGTVLSDYVGSGPPKGTGLHRYVWLVYEQDRPLKCDEPILSNRSGDHRGKFKVASFRKKYELRAPVAGTCYQAEWDDYVPKLYEQLSG

>d1a44\_\_ b.17.1.1 (-) Phosphatidylethanolamine binding protein, PEBP {Cow (Bos taurus)}

PVDLSKWSGPLSLQEVDERPQHPLQVKYGGAEVDELGKVLTPTQVKNRPTSITWDGLDPGKLYTLVLTDPDAPSRKDPKYREWHHFLVVNMKGNNISSGTVLSDYVGSGPPKGTGLHRYVWLVYEQEGPLKCDEPILSNRSGDHRGKFKVASFRKKYELGAPVAGTCYQAEWDDYVPKLYEQLSG

>d1qoua\_ b.17.1.1 (A:) Centroradialis protein Cen {Garden snapdragon (Antirrhinum majus)}

GRVIGDVVDHFTSTVKMSVIYNSNNSIKHVYNGHELFPSAVTSTPRVEVHGGDMRSFFTLIMTDPDVPGPSDPYLREHLHWIVTDIPGTTDSSFGKEVVSYEMPRPNIGIHRFVFLLFKQKKRGQAMLSPPVVCRDGFNTRKFTQENELGLPVAAVFFNCQRET

>d1fjja\_ b.17.1.2 (A:) Hypothetical protein YbhB {Escherichia coli}

AMKLISNDLRDGDKLPHRHVFNGMGYDGDNISPHLAWDDVPAGTKSFVVTCYDPDAPTGSGWWHWVVVNLPADTRVLPQGFGSGLVAMPDGVLQTRTDFGKTGYDGAAPPKGETHRYIFTVHALDIERIDVDEGASGAMVGFNVHFHSLASASITAMFS

>d1fuxa\_ b.17.1.2 (A:) Hypothetical protein YbcL {Escherichia coli}

EFQVTSNEIKTGEQLTTSHVFSGFGCEGGNTSPSLTWSGVPEGTKSFAVTVYDPDAPTGSGWWHWTVVNIPATVTYLPVDAGRRDGTKLPTGAVQGRNDFGYAGFGGACPPKGDKPHHYQFKVWALKTEKIPVDSNSSGALVGYMLNANKIATAEITPVYEIKLE

>d1g13a\_ b.95.1.1 (A:) Ganglioside M2 (gm2) activator {Human (Homo sapiens)}

SSFSWDNCDEGKDPAVIRSLTLEPDPIIVPGNVTLSVMGSTSVPLSSPLKVDLVLEKEVAGLWIKIPCTDYIGSCTFEHFCDVLDMLIPTGEPCPEPLRTYGLPCHCPFKEGTYSLPKSEFVVPDLELPSWLTTGNYRIESVLSSSGKRLGCIKIAASLKGI

>d1i9ba\_ b.96.1.1 (A:) Acetylcholine binding protein (ACHBP) {Great pond snail (Lymnaea stagnalis)}

FDRADILYNIRQTSRPDVIPTQRDRPVAVSVSLKFINILEVNEITNEVDVVFWQQTTWSDRTLAWNSSHSPDQVSVPISSLWVPDLAAYNAISKPEVLTPQLARVVSDGEVLYMPSIRQRFSCDVSGVDTESGATCRIKIGSWTHHSREISVDPTTENSDDSEYFSQYSRFEILDVTQKKNSVTYSCCPEAYEDVEVSLNFRKKG

>d1k3ia2 b.18.1.1 (A:-12-150) Galactose oxidase, N-terminal domain {Fungi (Fusarium spp)}

IPEGSLQFLSLRASAPIGSAISRNNWAVTCDSAQSGNECNKAIDGNKDTFWHTFYGANGDPKPPHTYTIDMKTTQNVNGLSMLPRQDGNQNGWIGRHEVYLSSDGTNWGSPVASGSWFADSTTKYSNFETRPARYVRLVAITEANGQPWTSIAEINVFQASS

>d1eut\_2 b.18.1.1 (506-647) Sialidase, C-terminal domain {Micromonospora viridifaciens}

QARMSIADVDSEETAREDGRASNVIDGNPSTFWHTEWSRADAPGYPHRISLDLGGTHTISGLQYTRRQNSANEQVADYEIYTSLNGTTWDGPVASGRFTTSLAPQRAVFPARDARYIRLVALSEQTGHKYAAVAELEVEGQR

>d1czsa\_ b.18.1.2 (A:) C2 domain of factor V {Human (Homo sapiens)}

GCSTPLGMENGKIENKQITASSFKKSWWGDYWEPFRARLNAQGRVNAWQAKANNNKQWLEIDLLKIKKITAIITQGCKSLSSEMYVKSYTIHYSEQGVEWKPYRLKSSMVDKIFEGNTNTKGHVKNFFNPPIISRFIRVIPKTWNQSITLRLELFGCDIY

>d1d7pm\_ b.18.1.2 (M:) C2 domain of factor VIII {Human (Homo sapiens)}

LNSCSMPLGMESKAISDAQITASSYFTNMFATWSPSKARLHLQGRSNAWRPQVNNPKEWLQVDFQKTMKVTGVTTQGVKSLLTSMYVKEFLISSSQDGHQWTLFFQNGKVKVFQGNQDSFTPVVNCLDPPLLTRYLRIHPQSWVHQIALRMEVLGCEAQ

>d1jhja\_ b.18.1.9 (A:) APC10/DOC1 subunit of the anaphase-promoting complex {Human (Homo sapiens)}

ATPNKTPPGADPKQLERTGTVREIGSQAVWSLSSCKPGFGVDQLRDDNLETYWQSDGSQPHLVNIQFRRKTTVKTLCIYADYKSDESYTPSKISVRVGNNFHNLQEIRQLELVEPSGWIHVPLTDNHKKPTRTFMIQIAVLANHQNGRDTHMRQIKIYTPV

>d1dlc\_1 b.18.1.3 (500-644) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}

FFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN

>d1ji6a1 b.18.1.3 (A:503-652) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis, CRY3bb1}

FFNTIDAEKITQLPVVKAYALSSGASIIEGPGFTGGNLLFLKESSNSIAKFKVTLNSAALLQRYRVRIRYASTTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPVQL

>d1ciy\_1 b.18.1.3 (462-609) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis, CRYIA (A)}

NNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVT

>d1i5pa1 b.18.1.3 (A:473-633) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

NIYAANENGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNGNSYNLYLRVSSIGNSTIRVTINGRVYTVSNVNTTTNNDGVNDNGARFSDINIGNIVASDNTNVTLDINVTLNSGTPFDLMNIMFVPTNLPPLY

>d1nuka\_ b.18.1.4 (A:) Ligand-binding domain of the ephb2 receptor tyrosine kinase {Mouse (Mus musculus)}

EETLMDSTTATAELGWMVHPPSGWEEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKFIRRRGAHRIHVEMKFSVRDCSSIPSVPGSCKETFNLYYYEADFDLATKTFPNWMENPWVKVDTIAADESFSQVDLGGRVMKINTEVRSFGPVSRNGFYLAFQDYGGCMSLIAVRVFYR

>d1jz8a3 b.18.1.5 (A:13-219) beta-Galactosidase {Escherichia coli}

RRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQLRSLNGEWRFAWFPAPEAVPESWLECDLPEADTVVVPSNWQMHGYDAPIYTNVTYPITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVNSAFHLWCNGRWVGYGQDSRLPSEFDLSAFLRAGENRLAVMVLRWSDGSYLEDQDMWRMSGIFRDVSLLHKPT

>d1bhga2 b.18.1.5 (A:22-225) beta-Glucuronidase {Human (Homo sapiens)}

GLQGGMLYPQESPSRECKELDGLWSFRADFSDNRRRGFEEQWYRRPLWESGPTVDMPVPSSFNDISQDWRLRHFVGWVWYEREVILPERWTQDLRTRVVLRIGSAHSYAIVWVNGVDTLEHEGGYLPFEADISNLVQVGPLPSRLRITIAINNTLTPTTLPPGTIQYLTDTSKYPKGYFVQNTYFDFFNYAGLQRSVLLYTTPT

>d1cx1a\_ b.18.1.6 (A:) Cellulose-binding domain {Cellulomonas fimi}

ASLDSEVELLPHTSFAESLGPWSLYGTSEPVFADGRMCVDLPGGQGNPWDAGLVYNGVPVGEGESYVLSFTASATPDMPVRVLVGEGGGAYRTAFEQGSAPLTGEPATREYAFTSNLTFPPDGDAPGQVAFHLGKAGAYEFCISQVSLTTSAT

>d1ulo\_\_ b.18.1.6 (-) Cellulose-binding domain {Cellulomonas fimi}

ASPIGEGTFDDGPEGWVAYGTDGPLDTSTGALCVAVPAGSAQYGVGVVLNGVAIEEGTTYTLRYTATASTDVTVRALVGQNGAPYGTVLDTSPALTSEPRQVTETFTASATYPATPAADDPEGQIAFQLGGFSADAWTLCLDDVALDSEVEL

>d1gmma\_ b.18.1.10 (A:) Carbohydrate binding module from xylanase U {Clostridium thermocellum}

FSKIESEEYNSLKSSTIQTIGTSDGGSGIGYIESGDYLVFNKINFGNGANSFKARVASGADTPTNIQLRLGSPTGTLIGTLTVASTGGWNNYEEKSCSITNTTGQHDLYLVFSGPVNIDYFIFDSN

>d1gnya\_ b.18.1.11 (A:) Xylan-binding module from xylanase 10c {Pseudomonas cellulosa}

GNVVIEVDMANGWRGNASGSTSHSGITYSADGVTFAALGDGVGAVFDIARPTTLEDAVIAMVVNVSAEFKASEANLQIFAQLKEDWSKGEWDCLAGSSELTADTDLTLTCTIDEDDDKFNQTARDVQVGIQAKGTPAGTITIKSVTITLAQEA

>d1j83a\_ b.18.1.12 (A:) Endo-1,4-beta glucanase EngF {Clostridium cellulovorans}

QPTAPKDFSSGFWDFNDGTTQGFGVNPDSPITAINVENANNALKISNLNSKGSNDLSEGNFWANVRISADIWGQSINIYGDTKLTMDVIAPTPVNVSIAAIPQSSTHGWGNPTRAIRVWTNNFVAQTDGTYKATLTISTNDSPNFNTIATDAADSVVTNMILFVGSNSDNISLDNIKFTK

>d1dyoa\_ b.18.1.7 (A:) Xylan-binding domain {Clostridium thermocellum}

PDAGYYYHDTFEGSVGQWTARGPAEVLLSGRTAYKGSESLLVRNRTAAWNGAQRALNPRTFVPGNTYCFSVVASFIEGASSTTFCMKLQYVDGSGTQRYDTIDMKTVGPNQWVHLYNPQYRIPSDATDMYVYVETADDTINFYIDEAIGAVAGTVI

>d1xnaa\_ b.18.1.8 (A:) N-terminal domain of xrcc1 {Human (Homo sapiens)}

MPEIRLRHVVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISVVLQLEKEEQIHSVDIGNDGSAFVEVLVGSSAGGAGEQDYEVLLVTSSFMSPSESRSGSNPNRVRMFGPDKLVRAAAEKRWDRVKIVCSQPYSKDSPFGLSFVRFHS

>d1ju3a1 b.18.1.13 (A:352-574) Bacterial cocaine esterase C-terminal domain {Rhodococcus sp. mb1}

PLPDTAYTPFYLGGSGAANTSTGGGTLSTSISGTESADTYLYDPADPVPSLGGTLLFHNGDNGPADQRPIHDRDDVLCYSTEVLTDPVEVTGTVSARLFVSSSAVDTDFTAKLVDVFPDGRAIALCDGIVRMRYRETLVNPTLIEAGEIYEVAIDMLATSNVFLPGHRIMVQVSSSNFPKYDRNSNTGGVIAREQLEEMCTAVNRIHRGPEHPSHIVLPIIKR

>d1bvp12 b.19.1.1 (1:121-254) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {Bluetongue virus}

PARQPYGFFLETEETFQPGRWFMRAAQAVTAVVCGPDMIQVSLNAGARGDVQQIFQGRNDPMMIYLVWRRIENFAMAQGNSQQTQAGVTVSVGGVDMRAGRIIAWDGQAALHVHNPTQQNAMVQIQVVFYISMD

>d1ahsa\_ b.19.1.1 (A:) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {African horse sickness virus}

TGPYAGAVEVQQSGRYYVPQGRTRGGYINSNIAEVCMDAGAAGQVNALLAPRRGDAVMIYFVWRPLRIFCDPQGASLESAPGTFVTVDGVNVAAGDVVAWNTIAPVNVGNPGARRSILQFEVLWYT

>d1qhda2 b.19.1.1 (A:149-332) vp6, the major capsid protein of group A rotavirus {Bovine rotavirus}

GFTFHKPNIFPYSASFTLNRSQPAHDNLMGTMWLNAGSEIQVAGFDYSCAINAPANTQQFEHIVQLRRVLTTATITLLPDAERFSFPRVITSADGATTWYFNPVILRPNNVEIEFLLNGQIINTYQARFGTIIARNFDTIRLSFQLMRPPNMTPAVAALFPNAQPFEHHATVGLTLRIESAVCE

>d1jsda\_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}

DKICIGYQSTNSTETVDTLTETNVPVTHAKELLHTSHNGMLCATNLGHPLILDTCTIEGLIYGNPSCDLLLGGREWSYIVERPSAVNGMCYPGNVENLEELRSLFSSASSYQRIQIFPDTIWNVSYSGTSSACSDSFYRSMRWLTQKNNAYPIQDAQYTNNRGKSILFMWGINHPPTDTVQTNLYTRTDTTTSVTTEDINRTFKPVIGPRPLVNGLHGRIDYYWSVLKPGQTLRVRSNGNLIAPWYGHILSGESHGRILKTDLNSGNCVVQCQTERGGLNTTLPFHNVSKYAFGNCPKYVGVKSLKLAVGLRNVPAR

>d1jsma\_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}

DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDLNGVKPLILRDCSVAGWLLGNPMCDEFLNVPEWSYIVEKDNPVNGLCYPENFNDYEELKHLLSSTNHFEKIRIIPRSSWSNHDASSGVSSACPYNGRSSFFRNVVWLIKKNNAYPTIKRSYNNTNQEDLLILWGIHHPNDAAEQTKLYQNPTTYVSVGTSTLNQRSVPEIATRPKVNGQSGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKGGSAIMKSGLEYGNCNTKCQTPMGAINSSMPFHNIHPLTIGECPKYVKSGRLVLATGLRNVP

>d2visc\_ b.19.1.2 (C:) Hemagglutinin {Influenza A virus, different strains}

VQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFITEGFTWTGVIQNGGSNACKRGPGSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYIWGIHHPSTNQEQTSLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYV

>d2viua\_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}

STATLCLGHHAVPNGTLVKTITDDQIEVTNATELVQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFITEGFTWTGVIQNGGSNACKRGPGSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYIWGIHHPSTNQEQTSLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKLATGMRNVPEKQT

>d1flca1 b.19.1.3 (A:151-306) Hemagglutinin domain of haemagglutinin-esterase-fusion glycoprotein HEF1 {Influenza C virus}

CMSLVNALDKTIPLQVTAGTAGNCNNSFLKNPALYTQEVKPSENKCGKENLAFFTLPTQFGTYECKLHLVASCYFIYDSKEVYNKRGCDNYFQVIYDSFGKVVGGLDNRVSPYTGNSGDTPTMQCDMLQLKPGRYSVRSSPRFLLMPERSYCFDMK

>d1aol\_\_ b.20.1.1 (-) F-MuLV receptor-binding domain {Friend murine leukemia virus}

QVYNITWEVTNGDRETVWAISGNHPLWTWWPVLTPDLCMLALSGPPHWGLEYQAPYSSPPGPPCCSGSSGSSAGCSRDCDEPLTSLTPRCNTAWNRLKLDQVTHKSSEGFYVCPGSHRPREAKSCGGPDSFYCASWGCETTGRVYWKPSSSWDYITVDNNLTTSQAVQVCKDNKWCNPLAIQFTNAGKQVTSWTTGHYWGLRLYVSGRDPGLTFGIRLRYQNLGPRVP

>d1knb\_\_ b.21.1.1 (-) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 5}

NDKLTLWTTPAPSPNCRLNAEKDAKLTLVLTKCGSQILATVSVLAVKGSLAPISGTVQSAHLIIRFDENGVLLNNSFLDPEYWNFRNGDLTEGTAYTNAVGFMPNLSAYPKSHGKTAKSNIVSQVYLNGDKTKPVTLTITLNGTQETGDTTPSAYSMSFSWDWSGHNYINEIFATSSYTFSYIAQE

>d1qhva\_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 2}

AITIGNKNDDKLTLWTTPDPSPNCRIHSDNDCKFTLVLTKCGSQVLATVAALAVSGDLSSMTGTVASVSIFLRFDQNGVLMENSSLKKHYWNFRNGNSTNANPYTNAVGFMPNLLAYPKTQSQTAKNNIVSQVYLHGDKTKPMILTITLNGTSESTETSEVSTYSMSFTWSWESGKYTTETFATNSYTFSYIAQE

>d1h7za\_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 3}

KNNTLWTGPKPEANCIIEYGKQNPDSKLTLILVKNGGIVNGYVTLMGASDYVNTLFKNKNVSINVELYFDATGHILPDSSSLKTDLELKYKQTADFSARGFMPSTTAYPFVLPNAGTHNENYIFGQCYYKASDGALFPLEVTVMLNKRLPDSRTSYVMTFLWSLNAGLAPETTQATLITSPFTFSYIREDD

>d1kaca\_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 12}

TPYDPLTLWTTPDPPPNCSLIQELDAKLTLCLTKNGSIVNGIVSLVGVKGNLLNIQSTTTTVGVHLVFDEQGRLITSTPTALVPQASWGYRQGQSVSTNTVTNGLGFMPNVSAYPRPNASEAKSQMVSLTYLQGDTSKPITMKVAFNGITSLNGYSLTFMWSGLSNYINQPFSTPSCSFSYITQE

>d1kkea1 b.21.1.2 (A:250-312) Reovirus attachment protein sigma 1 {Reovirus}

EQSYVASAVTPLRLNSSTKVLDMLIDSSTLEINSSGQLTVRSTSPNLRYPIADVSGGIGMSPN

>d1aly\_\_ b.22.1.1 (-) Extracellular domain of CD40 ligand {Human (Homo sapiens)}

GDQNPQIAAHVISEASSKTTSVLQWAEKGYYTMSNNLVTLENGKQLTVKRQGLYYIYAQVTFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFELQPGASVFVNVTDPSQVSHGTGFTSFGLLKL

>d1c28a\_ b.22.1.1 (A:) 30 kd adipocyte complement-related protein {Mouse (Mus musculus)}

MYRSAFSVGLETRVTVPNVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFKKDKAVLFTYDQYQEKNVDQASGSVLLHLEVGDQVWLQVYGDGDHNGLYADNVNDSTFTGFLLYHDT

>d1tnra\_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}

KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNNSLLVPTSGIYFVYSQVVFSGKAYSPKATSSPLYLAHEVQLFSSQYPFHVPLLSSQKMVYPGLQEPWLHSMYHGAAFQLTQGDQLSTHTDGIPHLVLSPSTVFFGAFAL

>d4tsva\_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}

DKPVAHVVANPQAEGQLQWSNRRANALLANGVELRDNQLVVPIEGLFLIYSQVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL

>d2tnfa\_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Mouse (Mus musculus)}

SDKPVAHVVANHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYSQVLFKGQGCPDYVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYLGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL

>d1dg6a\_ b.22.1.1 (A:) Apoptosis-2 ligand, apo2l/TRAIL {Human (Homo sapiens)}

QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKGFYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPAPILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG

>d1jtzx\_ b.22.1.1 (X:) TRANCE/RANKL cytokine {Mouse (Mus musculus)}

QPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGGSTKNWSGNSEFHFYSINVGGFFKLRAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID

>d1jh5a\_ b.22.1.1 (A:) Soluble part of TALL-1, sTALL-1 {Human (Homo sapiens)}

VTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLFRCIQNMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDVTFFGALKLL

>d1gr3a\_ b.22.1.1 (A:) Collagen X NC1 trimerisation domain {Human (Homo sapiens)}

MPVSAFTVILSKAYPAIGTPIPFDKILYNRQQHYDPRTGIFTCQIPGIYYFSYHVHVKGTHVWVGLYKNGTPVMYTYDEYTKGYLDQASGSAIIDLTENDQVWLQLPNAESNGLYSSEYVHSSFSGFLVAPM

>d1sfp\_\_ b.23.1.1 (-) Acidic seminal fluid protein (ASFP) {Cow (Bos taurus)}

LPRNTNCGGILKEESGVIATYYGPKTNCVWTIQMPPEYHVRVSIQYLQLNCNKESLEIIDGLPGSPVLGKICEGSLMDYRSSGSIMTVKYIREPEHPASFYEVLYFQDPQA

>d1sppa\_ b.23.1.1 (A:) Major seminal plasma glycoprotein PSP-I {Pig (Sus scrofa)}

LDYHACGGRLTDDYGTIFTYKGPKTECVWTLQVDPKYKLLVSIPTLNLTCGKEYVEVLEGAPGSKSLGKFCEGLSILNRGSSGMTVKYKRDSGHPASPYEIIFLRDSQG

>d1sppb\_ b.23.1.1 (B:) Major seminal plasma glycoprotein PSP-II {Pig (Sus scrofa)}

ARINGPDECGRVIKDTSGSISNTDRQKNLCTWTILMKPDQKVRMAIPYLNLACGKEYVEVFDGLLSGPSYGKLCAGAAIVFLSTANTMTIKYNRISGNSSSPFLIYFYGSSP

>d1cb8a2 b.24.1.1 (A:600-700) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

PKVLANTNQLQAVYHQQLDMVQAIFYTAGKLSVAGIEIETDKPCAVLIKHINGKQVIWAADPLQKEKTAVLSIRDLKTGKTNRVKIDFPQQEFAGATVELK

>d1egua2 b.24.1.1 (A:815-893) Hyaluronate lyase {Streptococcus pneumoniae}

SSLIENNETLQSVYDAKQGVWGIVKYDDSVSTISNQFQVLKRGVYTIRKEGDEYKIAYYNPETQESAPDQEVFKKLEQH

>d1f1sa3 b.24.1.1 (A:920-984) Hyaluronate lyase {Streptococcus agalactiae}

SKQQVIYDKNSQTWAVIKHDNQESLINNQFKMNKAGLYLVQKVGNDYQNVYYQPQTMTKTDQLAI

>d1iaza\_ b.97.1.1 (A:) Equinatoxin II (eqtII, tenebrosin C) {European sea anemone (Actinia equina)}

AGAVIDGASLSFDILKTVLEALGNVKRKIAVGVDNESGKTWTALNTYFRSGTSDIVLPHKVPHGKALLYNGQKDRGPVATGAVGVLAYLMSDGNTLAVLFSVPYDYNWYSNWWNVRIYKGKRRADQRMYEELYYNLSPFRGDNGWHTRNLGYGLKSRGFMNSSGHAILEIHVSKA

>d1aun\_\_ b.25.1.1 (-) Pathogenesis-related protein 5d {Common tobacco (Nicotiana tabacum)}

SGVFEVHNNCPYTVWAAATPVGGGRRLERGQSWWFWAPPGTKMARIWGRTNCNFDGAGRGWCQTGDCGGVLECKGWGKPPNTLAEYALNQFSNLDFWDISVIDGFNIPMSFGPTKPGPGKCHGIQCTANINGECPGSLRVPGGCNNPCTTFGGQQYCCTQGPCGPTELSRWFKQRCPDAYSYPQDDPTSTFTCTSWTTDYKVMFCPYG

>d1du5a\_ b.25.1.1 (A:) Zeamatin {Maize (Zea mays)}

AVFTVVNQCPFTVWAASVPVGGGRQLNRGESWRITAPAGTTAARIWARTGCKFDASGRGSCRTGDCGGVLQCTGYGRAPNTLAEYALKQFNNLDFFDISLIDGFNVPMSFLPDGGSGCSRGPRCAVDVNARCPAELRQDGVCNNACPVFKKDEYCCVGSAANDCHPTNYSRYFKGQCPDAYSYPKDDATSTFTCPAGTNYKVVFCP

>d1thw\_\_ b.25.1.1 (-) Thaumatin {Ketemfe (Thaumatococcus daniellii)}

ATFEIVNRCSYTVWAAASKGDAALDAGGRQLNSGESWTINVEPGTKGGKIWARTDCYFDDSGSGICKTGDCGGLLRCKRFGRPPTTLAEFSLNQYGKDYIDISNIKGFNVPMDFSPTTRGCRGVRCAADIVGQCPAKLKAPGGGCNDACTVFQTSEYCCTTGKCGPTEYSRFFKRLCPDAFSYVLDKPTTVTCPGSSNYRVTFCPTA

>d1dd1a\_ b.26.1.1 (A:) Smad4 tumor suppressor C-terminal domain {Human (Homo sapiens)}

NGHLQHHPPMPPHPGHYWPVHNELAFQPPISNHPAPEYWCSIAYFEMDVQVGETFKVPSSCPIVTVDGYVDPSGGDRFCLGQLSNVHRTEAIERARLHIGKGVQLECKGEGDVWVRCLSDHAVFVQSYYLDREAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQQQAATAQAAAAAQAAAVAGNIPGPGSVGGIAPAISLSAAAGIGVDDLRRLCILRMSFVKGWGPDYPRQSIKETPCWIEIHLHRALQLLDEVLHTMPI

>d1ygs\_\_ b.26.1.1 (-) Smad4 tumor suppressor C-terminal domain {Human (Homo sapiens)}

APEYWCSIAYFEMDVQVGETFKVPSSCPIVTVDGYVDPSGGDRFCLGQLSNVHRTEAIERARLHIGKGVQLECKGEGDVWVRCLSDHAVFVQSYYLDREAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQQQAATAQAAAAAQAAAVAGNIPGPGSVGGIAPAISLSAAAGIGVDDLRRLCILRMSFVKGWGPDYPRQSIKETPCWIEIHLHRALQLLDEVLHTM

>d1khxa\_ b.26.1.1 (A:) Smad2 MH2 domain {Human (Homo sapiens)}

PVTYSEPAFWCSIAYYELNQRVGETFHASQPSLTVDGFTDPSNSERFCLGLLSNVNRNATVEMTRRHIGRGVRLYYIGGEVFAECLSDSAIFVQSPNCNQRYGWHPATVCKIPPGCNLKIFNNQEFAALLAQSVNQGFEAVYQLTRMCTIRMSFVKGWGAEYRRQTVTSTPCWIELHLNGPLQWLDKVLTQMGSPSVRCSSMS

>d1khua\_ b.26.1.1 (A:) Smad1 {Human (Homo sapiens)}

PKHWCSIVYYELNNRVGEAFHASSTSVLVDGFTDPSNNKNRFCLGLLSNVNRNSTIENTRRHIGKGVHLYYVGGEVYAECLSDSSIFVQSRNCNYHHGFHPTTVCKIPSGCSLKIFNNQEFAQLLAQSVNHGFETVYELTKMCTIRMSFVKGWGAEYHRQDVTSTPCWIEIHLHGPLQWLDKVLTQMGSPHNPISSVS

>d1dmza\_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

GNGRFLTLKPLPDSIIQESLEIQQGVNPFFIGRSEDCNCKIEDNRLSRVHCFIFKKRHAVGKSMYESPAQGLDDIWYCHTGTNVSYLNNNRMIQGTKFLLQDGDEIKIIWDKNNKFVIGFKVEINDTTGLFNEGLGMLQEQRVVLKQTAEEKDLVKKL

>d1g6ga\_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

GENIVCRVICTTGQIPIRDLSADISQVLKEKRSIKKVWTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVGVGVESDILSLVIFINDKFKQCL

>d1k3ja\_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

ATQRFLIEKFSQEQIGENIVCRVICTTGQIPIRDLSADISQVLKEKRSIKKVWTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVGVGVESDILSLVIFINDKFKQCLEQNKVDRIR

>d1qu5a\_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

EAETREQKLLHSNNTENVKSSKKKGNGRFLTLKPLPDSIIQESLEIQQGVNPFFIGRSEDCNCKIEDNRLSRVHCFIFKKRHAVGKSMYESPAQGLDDIWYCHTGTNVSYLNNNRMIQGTKFLLQDGDEIKIIWDKNNKFVIGFKVEINDTTGLFNEGLGMLQEQRVVLKQTAEEKDLVKKL

>d1cq3a\_ b.27.1.1 (A:) Soluble secreted chemokine inhibitor, VCCI {Cowpox virus}

SFSSSSSCTEEENKHHMGIDVIIKVTKQDQTPTNDKICQSVTEVTESEDESEEVVKGDPTTYYTVVGGGLTMDFGFTKCPKISSISEYSDGNTVNARLSSVSPGQGKDSPAITREEALSMIKDCEMSINIKCSEEEKDSNIKTHPVLGSNISHKKVSYEDIIGSTIVDTKCVKNLEISVRIGDMCKESSELEVKDGFKYVDGSASEDAADDTSLINSAKLIACV

>d1p35a\_ b.28.1.1 (A:) Paculovirus p35 {Nuclear polyhedrosis virus (Autographa californica), ACMNPV}

CVIFPVEIDVSQTIIRDCQVDKQTRELVYINKIMNTQLTKPVLMMFNISGPIRSVTRKNNNLRDRIKSKVDEQFDQLERDYSDQMDGFHDSIKYFKDEHYSVSCQNGSVLKSKFAKILKSHDYTDKKSIEAYEKYCLPKLVDERNDYYVAVCVLKPGFENGSNQVLSFEYNPIGNKVIVPFAHEINDTGLYEYDVVAYVDSVQFDGEQFEEFVQSLILPSSFKNSEKVLYYNEASKNKSMIYKALEFTTESSWGKSEKYNWKIFCNGFIYDKKSKVLYVKLHNVTSALNKNVILNTIKA

>d1nls\_\_ b.29.1.1 (-) Concanavalin A {Jack bean (Canavalia ensiformis)}

ADTIVAVELDTYPNTDIGDPSYPHIGIDIKSVRSKKTAKWNMQNGKVGTAHIIYNSVDKRLSAVVSYPNADSATVSYDVDLDNVLPEWVRVGLSASTGLYKETNTILSWSFTSKLKSNSTHETNALHFMFNQFSKDQKDLILQGDATTGTDGNLELTRVSSNGSPQGSSVGRALFYAPVHIWESSAVVASFEATFTFLIKSPDSHPADGIAFFISNIDSSIPSGSTGRLLGLFPDAN

>d2cna\_\_ b.29.1.1 (-) Concanavalin A {Jack bean (Canavalia ensiformis)}

ADTIVAVELDTYPNTDIGDPSYPHIGIDIKSVRSKKTAKWNMQDGKVGTAHIIYNSVDKRLSAVVSYPNADATSVSYDVDLNDVLPEWVRVGLSASTGLYKETNTILSWSFTSKLKSNSTHQTDALHFMFNQFSKDQKDLILQGDATTGTDGNLELTRVSSNGSPEGSSVGRALFYAPVHIWESSATVSAFEATFAFLIKSPDSHPADGIAFFISNIDSSIPSGSTGRLLGLFPDAN

>g2ltn.1 b.29.1.1 (A:,B:) Legume lectin {Garden pea (Pisum sativum)}

TETTSFLITKFSPDQQNLIFQGDGYTTKEKLTLTKAVKNTVGRALYSSPIHIWDRETGNVANFVTSFTFVINAPNSYNVADGFTFFIAPVDTKPQTGGGYLGVFNSAEYDKTTQTVAVEFDTFYNAAWDPSNRDRHIGIDVNSIKSVNTKSWKLQNGEEANVVIAFNAATNVLTVSLTYPNXVTSYTLSDVVSLKDVVPEWVRIGFSATTGAEYAAHEVLSWSFHSELSG

>g1len.1 b.29.1.1 (A:,B:) Legume lectin {Common lentil (Lens culinaris)}

TETTSFSITKFSPDQQNLIFQGDGYTTKGKLTLTKAVKSTVGRALYSTPIHIWDRDTGNVANFVTSFTFVIDAPSSYNVADGFTFFIAPVDTKPQTGGGYLGVFNSKEYDKTSQTVAVEFDTFYNAAWDPSNKERHIGIDVNSIKSVNTKSWNLQNGERANVVIAFNAATNVLTVTLTYPNXVTSYTLNEVVPLKDVVPEWVRIGFSATTGAEFAAQEVHSWSFNSQLG

>d1led\_\_ b.29.1.1 (-) Legume lectin {West-central african legume (Griffonia simplicifolia)}

ENTVNFTYPDFWSYSLKNGTEITFLGDATRIPGALQLTKTDANGNPVRSSAGQASYSEPVFLWDSTGKAASFYTSFTFLLKNYGAPTADGLAFFLAPVDSSVKDYGGFLGLFRHETAADPSKNQVVAVEFDTWINKDWNDPPYPHIGIDVNSIVSVATTRWENDDAYGSSIATAHITYDARSKILTVLLSYEHGRDYILSHVVDLAKVLPQKVRIGFSAGVGYDEVTYILSWHFFSTLDGTNK

>d1hqla\_ b.29.1.1 (A:) Legume lectin {Griffonia simplicifolia, lectin I-b4}

SVSFTFPNFWSDVEDSIIFQGDANTTAGTLQLCKTNQYGTPLQWSAGRALYSDPVQLWDNKTESVASFYTEFTFFLKITGNGPADGLAFFLAPPDSDVKDAGEYLGLFNKSTATQPSKNQVVAVEFDTWTNPNFPEPSYRHIGINVNSIVSVATKRWEDSDIFSGKIATARISYDGSAEILTVVLSYPDGSDYILSHSVDMRQNLPESVRVGISASTGNNQFLTVYILSWRFSSNL

>d1ax0\_\_ b.29.1.1 (-) Legume lectin {Coral tree (Erythrina corallodendron)}

VETISFSFSEFEPGNDNLTLQGAALITQSGVLQLTKINQNGMPAWDSTGRTLYAKPVHIWDMTTGTVASFETRFSFSIEQPYTRPLPADGLVFFMGPTKSKPAQGYGYLGIFNNSKQDNSYQTLGVEFDTFSNPWDPPQVPHIGIDVNSIRSIKTQPFQLDNGQVANVVIKYDASSKILHAVLVYPSSGAIYTIAEIVDVKQVLPEWVDVGLSGATGAQRDAAETHDVYSWSFQASLPE

>d1wbfa\_ b.29.1.1 (A:) Legume lectin {Winged bean (Psophocarpus tetragonolobus), basic agglutinin}

KTISFNFNQFHQNEEQLKLQRDARISSNSVLELTKVVNGVPTWNSTGRALYAKPVQVWDSTTGNVASFETRFSFSIRQPFPRPHPADGLVFFIAPPNTQTGEGGGYFGIYNPLSPYPFVAVEFDTFRNTWDPQIPHIGIDVNSVISTKTVPFTLDNGGIANVVIKYDASTKILHVVLVFPSLGTIYTIADIVDLKQVLPESVNVGFSAATGDPSGKQRNATETHDILSWSFSASLPG

>d1f9ka\_ b.29.1.1 (A:) Legume lectin {Winged bean (Psophocarpus tetragonolobus), acidic lectin}

ETQSFNFDHFEENSKELNLQRQASIKSNGVLELTKLTKNGVPVWKSTGRALYAEPIKIWDSTTGNVASFETRFSFNITQPYAYPEPADGLTFFMVPPNSPQGEDGGNLGVFKPPEGDNAFAVEFDTFQNTWDPQVPHIGIDVNSIVSSKTLHFQLENGGVANVVIKYDSPTKILNVVLAFHSVGTVYTLSNIVDLKQEFPNSEWVNVGLSATTGYQKNAVETHEIISWSFTSSL

>g1loe.1 b.29.1.1 (A:,B:) Legume lectin {Lathyrus ochrus, isolectin I}

TETTSFSITKFGPDQQNLIFQGDGYTTKERLTLTKAVRNTVGRALYSSPIHIWDSKTGNVANFVTSFTFVIDAPNSYNVADGFTFFIAPVDTKPQTGGGYLGVFNSKDYDKTSQTVAVEFDTFYNTAWDPSNGDRHIGIDVNSIKSINTKSWALQNGKEANVVIAFNAATNVLTVSLTYPXTSYTLNEVVPLKEFVPEWVRIGFSATTGAEFAAHEVLSWYFHSELA

>d2pela\_ b.29.1.1 (A:) Legume lectin {Peanut (Arachis hypogaea)}

AETVSFNFNSFSEGNPAINFQGDVTVLSNGNIQLTNLNKVNSVGRVLYAMPVRIWSSATGNVASFLTSFSFEMKDIKDYDPADGIIFFIAPEDTQIPAGSIGGGTLGVSDTKGAGHFVGVEFDTYSNSEYNDPPTDHVGIDVNSVDSVKTVPWNSVSGAVVKVTVIYDSSTKTLSVAVTNDNGDITTIAQVVDLKAKLPERVKFGFSASGSLGGRQIHLIRSWSFTSTLITT

>d1g9fa\_ b.29.1.1 (A:) Legume lectin {Soybean (Glycine max)}

AETVSFSWNKFVPKQPNMILQGDAIVTSSGKLQLNKVDENGTPKPSSLGRALYSTPIHIWDKETGSVASFAASFNFTFYAPDTKRLADGLAFFLAPIDTKPQTHAGYLGLFNENESGDQVVAVEFDTFRNSWDPPNPHIGINVNSIRSIKTTSWDLANNKVAKVLITYDASTSLLVASLVYPSQRTSNILSDVVDLKTSLPEWVRIGFSAATGLDIPGESHDVLSWSFASNLPHASSNIDPLDLTSFVLHE

>g1qmo.1 b.29.1.1 (A:,E:) Legume lectin {Field bean (Dolichos lab lab), Fril}

AQSLSFSFTKFDPNQEDLIFQGHATSTNNVLQVTKLDSAGNPVSSSAGRVLYSAPLRLWEDSAVLTSFDTIINFEISTPYTSRIADGLAFFIAPPDSVISYHGGFLGLFPNANXSNVVAVEFDTYLNPDYGDPNYIHIGIDVNSIRSKVTAKWDWQNGKIATAHISYNSVSKRLSVTSYYAGSKPATLSYDIELHTVLPEWVRVGLSASTGQDKERNTVHSWSFTSSLWTN

>d1g7ya\_ b.29.1.1 (A:) Legume lectin {Horse gram (Dolichos biflorus), different isoforms}

ADIQSFSFKNFNSSSFILQGDATVSSSKLRLTKVKGNGLPTLSSLGRAFYSSPIQIYDKSTGAVASWATSFTANIFAPNKSSSADGIAFALVPVGSEPKSNSGFLGVFDSDVYDNSAQTVAVEFDTFSNTDWDPTSRHIGIDVNSIKSIRTASWGLANGQNAEILITYNAATSLLVASLVHPSRRTSYIVSERVDITNELPEYVSIGFSATTGLSEGYTETHDVLSWSFASKLPDDSTTEPLDIASYLVRNVL

>d1lu1\_\_ b.29.1.1 (-) Legume lectin {Horse gram (Dolichos biflorus), different isoforms}

ANIQSFSFKNFNSPSFILQGDATVSSGKLQLTKVKENGIPTPSSLGRAFYSSPIQIYDKSTGAVASWATSFTVKISAPSKASFADGIAFALVPVGSEPRRNGGYLGVFDSDVYNNSAQTVAVEFDTLSNSGWDPSMKHIGIDVNSIKSIATVSWDLANGENAEILITYNAATSLLVASLVHPSRRTSYILSERVDITNELPEYVSVGFSATTGLSEGYIETHDVLSWSFASKLPDDSTAEPLDLASYLVRNVL

>d1h9wa\_ b.29.1.1 (A:) Legume lectin {Duke (Dioclea guianensis)}

ADTIVAVELDSYPNTDIGDPSYPHIGIDIKSIRSKSTARWNMQTGKVGTAHISYNSVAKRLSAVVSYTGSSSTTVSYDVDLNNVLPEWVRVGLSATTGLYKETNTILSWSFTSKLKTNSIADANSLHFSFNQFSQNPKDLILQGDATTDSDGNLELTKVSSSGDPQGSSVGRALFYAPVHIWEKSAVVASFDATFTFLIKSPDRDPADGITFFIANTDTSIPSGSGGRLLGLFPDAN

>d1fx5a\_ b.29.1.1 (A:) Legume lectin {Furze (Ulex europaeus), UEA-I}

SDDLSFKFKNFSQNGKDLSFQGNASVIETGVLQLNKVGNNLPDETGGIARYIAPIHIWNCNTGELASFITSFSFFMETSANPKAATDGLTFFLAPPDSPLRRAGGYFGLFNDTKCDSSYQTVAVEFDTIGSPVNFWDPGFPHIGIDVNCVKSINAERWNKRYGLNNVANVEIIYEASSKTLTASLTYPSDQTSISVTSIVDLKEILPEWVSVGFSGSTYIGRQATHEVLNWYFTSTFINT

>d1qnwa\_ b.29.1.1 (A:) Legume lectin {Furze (Ulex europaeus), UEA-II}

SDDLSFNFDKFVPNQKNIIFQGDASVSTTGVLQVTKVSKPTTTSIGRALYAAPIQIWDSITGKVASFATSFSFVVKADKSDGVDGLAFFLAPANSQIPSGSSAGMFGLFSSSDSKSSNQIIAVEFDTYFGKAYNPWDPDFKHIGIDVNSIKSIKTVKWDWRNGEVADVVITYRAPTKSLTVCLSYPSDGTSNIITASVDLKAILPEWVSVGFSGGVGNAAEFETHDVLSWYFTSNLE

>d1dbna\_ b.29.1.1 (A:) Legume lectin {Maackia amurensis, leukoagglutinin}

SDELSFTINNFVPNEADLLFQGEASVSSTGVLQLTKVENGQPQKYSVGRALYAAPVRIWGNTTGSVASFSTSFTFVVKAPNPDITSDGLAFYLAPPDSQIPSGSVSKYLGLFNNSNSDSSNQIVAVEFDTYFAHSYDPWDPNYRHIGIDVNGIESIKTVQWDWINGGVAFATITYLAPNKTLIASLVYPSNQTTFSVAASVDLKEILPEWVRVGFSAATGYPTEVETHDVLSWSFTSTL

>d1fnya\_ b.29.1.1 (A:) Legume lectin {Black locust (Robinia pseudoacacia)}

TGSLSFSFPKFAPNQPYLINQGDALVTSTGVLQLTNVVNGVPSSKSLGRALYAAPFQIWDSTTGNVASFVTSFTFIIQAPNPATTADGLAFFLAPVDTQPLDLGGMLGIFKDGYFNKSNQIVAVEFDTFSNGDWDPKGRHLGINVNSIESIKTVPWNWTNGEVANVFISYEASTKSLTASLVYPSLETSFIIDAIVDVKIVLPEWVRFGFSATTGIDKGYVQTNDVLSWSFESNLPG

>d1avba\_ b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (Phaseolus vulgaris)}

SNDASFNVETFNKTNLILQGDATVSSEGHLLLTNVKGNEEDSMGRAFYSAPIQINDRTIDNLASFSTNFTFRINAKNIENSAYGLAFALVPVGSRPKLKGRYLGLFNTTNYDRDAHTVAVVFDTVSNRIEIDVNSIRPIATESCNFGHNNGEKAEVRITYDSPKNDLRVSLLYPSSEEKCHVSATVPLEKEVEDWVSVGFSATSGSKKETTETHNVLSWSFSSNFI

>d1dhkb\_ b.29.1.1 (B:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (Phaseolus vulgaris)}

ATETSFIIDAFNKTNLILQGDATVSSNGNLQLSYNSYDSMSRAFYSAPIQIRDSTTGNVASFDTNFTMNIRTHRQANSAVGLDFVLVPVQPESKGDTVTVEFDTFLSRISIDVNNNDIKSVPWDVHDYDGQNAEVRITYNSSTKVFSVSLSNPSTGKSNNVSTTVELEKEVYDWVSVGFSATSGAYQWSYETHDVLSWSFSSKF

>d1g8wa\_ b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (Phaseolus vulgaris)}

SNDIYFNFQRFNETNLILQRDASVSSSGQLRLTNLNGNGEPRVGSLGRAFYSAPIQIWDNTTGTVASFATSFTFNIQVPNNAGPADGLAFALVPVGSQPKDKGGFLGLFDGSNSNFHTVAVEFDTLYNKDWDPTERHIGIDVNSIRSIKTTRWDFVNGENAEVLITYDSSTNLLVASLVYPSQKTSFIVSDTVDLKSVLPEWVSVGFSATTGINKGNVETNDVLSWSFASKLS

>d1ioaa\_ b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (Phaseolus vulgaris), G02771, arcelin-5a}

ATETSFNFPNFHTDDKLILQGNATISSKGQLQLTGVGSNELPRVDSLGRAFYSDPIQIKDSNNVASFNTNFTFIIRAKNQSISAYGLAFALVPVNSPPQKKQEFLGIFNTNNPEPNARTVAVVFNTFKNRIDFDKNFIKPYVNENCDFHKYNGEKTDVQITYDSSNNDLRVFLHFTVSQVKCSVSATVHLEKEVDEWVSVGFSPTSGLTEDTTETHDVLSWSFSSKFR

>d1gbg\_\_ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus licheniformis}

QTGGSFYEPFNNYNTGLWQKADGYSNGNMFNCTWRANNVSMTSLGEMRLSLTSPSYNKFDCGENRSVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPTDGTPWDEIDIEFLGKDTTKVQFNYYTNGVGNHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQLKHTATTQIPQTPGKIMMNLWNGAGVDEWLGSYNGVTPLYAHYNWVRYTKR

>d2ayh\_\_ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Hybrid protein: residues 1-16 from Bacillus amyloliquefaciens and Bacillus macerans}

QTGGSFFEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYYTNGVGGHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTSN

>d1ajka\_ b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

NTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYYTNGVGGHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTSNQTGGSFFEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAK

>d1ajoa\_ b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

GHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTSNQTGGSFFEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYYTNG

>d1cpm\_\_ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYYTNGVGGHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTSNQTGGSFFEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNA

>d1cpn\_\_ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTYTGPAHGTQWDEIDIEFLGKDTTKVQFNYYTNGVGGHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTSNGSVFWEPKSYFNPSTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSS

>d1dypa\_ b.29.1.2 (A:) kappa-Carrageenase, catalytic {Pseudoalteromonas carrageenovora}

SMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQTENYGVWSWKNENATVSKGKLKLTTKRESHQRTFWDGCNQQQVANYPLYYTSGVAKSRATGNYGYYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRESDHDLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDPRNDFHTYGVNVTKDKITWYVDGEIVGEKDNLYWHRQMNLTLSQGLRAPHTQWKCNQFYPSANKSAEGFPTSMEVDYVRTWVKV

>d1slta\_ b.29.1.3 (A:) S-lectin, different isoforms {Cow (Bos taurus)}

CGLVASNLNLKPGECLRVRGEVAADAKSFLLNLGKDDNNLCLHFNPRFNAHGDVNTIVCNSKDAGAWGAEQRESAFPFQPGSVVEVCISFNQTDLTIKLPDGYEFKFPNRLNLEAINYLSAGGDFKIKCVAFE

>d1bkza\_ b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}

SNVPHKSSLPEGIRPGTVLRIRGLVPPNASRFHVNLLCGEEQGSDAALHFNPRLDTSEVVFNSKEQGSWGREERGPGVPFQRGQPFEVLIIASDDGFKAVVGDAQYHHFRHRLPLARVRLVEVGGDVQLDSVRIF

>d1hlca\_ b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}

ELEVKNMDMKPGSTLKITGSIADGTDGFVINLGQGTDKLNLHFNPRFSESTIVCNSLDGSNWGQEQREDHLCFSPGSEVKFTVTFESDKFKVKLPDGHELTFPNRLGHSHLSYLSVRGGFNMSSFKLKE

>d1qmja\_ b.29.1.3 (A:) S-lectin, different isoforms {Chicken (Gallus gallus)}

QGLVVTQLDVQPGECVKVKGKILSDAKGFSVNVGKDSSTLMLHFNPRFDCHGDVNTVVCNSKEDGTWGEEDRKADFPFQQGDKVEICISFDAAEVKVKVPEVEFEFPNRLGMEKIQYLAVEGDFKVKAIKFS

>d1a78a\_ b.29.1.3 (A:) S-lectin, different isoforms {Toad (Bufo arenarum)}

ASAGVAVTNLNLKPGHCVEIKGSIPPDCKGFAVNLGEDASNFLLHFNARFDLHGDVNKIVCNSKEADAWGSEQREEVFPFQQGAEVMVCFEYQTQKIIIKFSSGDQFSFPVRKVLPSIPFLSLEGLAFKSITTE

>d1hdka\_ b.29.1.3 (A:) Charcot-Leyden crystal (CLC) protein {Human (Homo sapiens)}

SLLPVPYTEAASLSTGSTVTIKGRPLVCFLNEPYLQVDFHTEMKEESDIVFHFQVCFGRRVVMNSREYGAWKQQVESKNMPFQDGQEFELSISVLPDKYQVMVNGQSSYTFDHRIKPEAVKMVQVWRDISLTKFNVSYL

>d1a3k\_\_ b.29.1.3 (-) Galectin-3 CRD {Human (Homo sapiens)}

LIVPYNLPLPGGVVPRMLITILGTVKPNANRIALDFQRGNDVAFHFNPRFNENNRRVIVCNTKLDNNWGREERQSVFPFESGKPFKIQVLVEPDHFKVAVNDAHLLQYNHRVKKLNEISKLGISGDIDLTSASYTMI

>d1c1la\_ b.29.1.3 (A:) Congerin I {Conger eel (Conger myriaster)}

GGLQVKNFDFTVGKFLTVGGFINNSPQRFSVNVGESMNSLSLHLDHRFNYGADQNTIVMNSTLKGDNGWETEQRSTNFTLSAGQYFEITLSYDINKFYIDILDGPNLEFPNRYSKEFLPFLSLAGDARLTLVKLE

>d1d2sa\_ b.29.1.4 (A:) Sex hormone-binding globulin {Human (Homo sapiens)}

PPAVHLSNGPGQEPIAVMTFDLTKITKTSSSFEVRTWDPEGVIFYGDTNPKDDWFMLGLRDGRPEIQLHNHWAQLTVGAGPRLDDGRWHQVEVKMEGDSVLLEVDGEEVLRLRQVSGHPIMRIALGGLLFPASNLRLPLVPALDGCLRRDSWLDKQAEISASAPTSLRSC

>d1dyka1 b.29.1.4 (A:2744-2932) Laminin alpha2 chain {Mouse (Mus musculus)}

HGPCVAESEPALLTGSKQFGLSRNSHIAIAFDDTKVKNRLTIELEVRTEAESGLLFYMARINHADFATVQLRNGFPYFSYDLGSGDTSTMIPTKINDGQWHKIKIVRVKQEGILYVDDASSQTISPKKADILDVVGILYVGGLPINYTTRRIGPVTYSLDGCVRNLHMEQAPVDLDQPTSSFHVGTCFA

>d1dyka2 b.29.1.4 (A:2933-3117) Laminin alpha2 chain {Mouse (Mus musculus)}

NAESGTYFDGTGFAKAVGGFKVGLDLLVEFEFRTTRPTGVLLGVSSQKMDGMGIEMIDEKLMFHVDNGAGRFTAIYDAEIPGHMCNGQWHKVTAKKIKNRLELVVDGNQVDAQSPNSASTSADTNDPVFVGGFPGGLNQFGLTTNIRFRGCIRSLKLTKGTGKPLEVNFAKALELRGVQPVSCPT

>d1c4ra\_ b.29.1.4 (A:) Ligand-binding domain of neurexin 1beta {Rat (Rattus norvegicus)}

HAGTTYIFSKGGGQITYKWPPNDRPSTRADRLAIGFSTVQKEAVLVRVDSSSGLGDYLELHIHQGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFTRSGGNATLQVDSWPVIERYPAGRQLTIFNSQATIIIGGKEQGQPFQGQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEV

>d1saca\_ b.29.1.5 (A:) Serum amyloid P component (SAP) {Human (Homo sapiens)}

HTDLSGKVFVFPRESVTDHVNLITPLEKPLQNFTLCFRAYSDLSRAYSLFSYNTQGRDNELLVYKERVGEYSLYIGRHKVTSKVIEKFPAPVHICVSWESSSGIAEFWINGTPLVKKGLRQGYFVEAQPKIVLGQEQDSYGGKFDRSQSFVGEIGDLYMWDSVLPPENILSAYQGTPLPANILDWQALNYEIRGYVIIKPLVWV

>d1b09a\_ b.29.1.5 (A:) C-reactive protein (CRP) {Human (Homo sapiens)}

QTDMSRKAFVFPKESDTSYVSLKAPLTKPLKAFTVCLHFYTELSSTRGYSIFSYATKRQDNEILIFWSKDIGYSFTVGGSEILFEVPEVTVAPVHICTSWESASGIVEFWVDGKPRVRKSLKKGYTVGAEASIILGQEQDSFGGNFEGSQSLVGDIGNVNMWDFVLSPDEINTIYLGGPFSPNVLNWRALKYEVQGEVFTKPQLWP

>d1jhna1 b.29.1.12 (A:61-262) Calnexin {Dog (Canis familiaris)}

YKAPVPSGEVYFADSFDRGTLSGWILSKAKKDDTDDEIAKYDGKWEVDEMKETKLPGDKGLVLMSRAKHHAISAKLNKPFLFDTKPLIVQYEVNFQNGIECGGAYVKLLSKTPELNLDQFHDKTPYTIMFGPDKCGEDYKLHFIFRHKNPKTGVYEEKHAKRPDADLKTYFTDKKTHLYTLILNPDNSFEILVDQSIVNSGN

>d1jhna2 b.29.1.12 (A:412-458) Calnexin {Dog (Canis familiaris)}

LEPFKMTPFSAIGLELWSMTSDIFFDNFIVCGDRRVVDDWANDGWGL

>d1a8d\_1 b.29.1.6 (1-247) Tetanus neurotoxin {Clostridium tetani}

MKNLDCWVDNEEDIDVILKKSTILNLDINNDIISDISGFNSSVITYPDAQLVPGINGKAIHLVNNESSEVIVHKAMDIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISSMKKHSLSIGSGWSVSLKGNNLIWTLKDSAGEVRQITFRDLPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNNITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLS

>d3btaa1 b.29.1.6 (A:872-1078) Botulinum neurotoxin {Clostridium botulinum, serotype A}

IINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPISNLGNIHASNNIMFKLDGCRDTHRYIWIKYFNLFDKEL

>d1epwa1 b.29.1.6 (A:862-1079) Botulinum neurotoxin {Clostridium botulinum, serotype B}

NIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRTQFIWMKYFSIFNTELSQSNIEERYKIQSY

>d1ikpa1 b.29.1.7 (A:2-251) Exotoxin A, N-terminal domain {Pseudomonas aeruginosa}

EEAFDLWNECAKACVLDLKDGVRSSRMSVDPAIADTNGQGVLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSWSLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVVMAQAQPRREKRWSEWASGKVLCLLDQLDGVYNYLAQQRCNLDDTWEGKIYRVLAGNPAKHDLDIKPTVISHRLHFP

>d1kit\_1 b.29.1.8 (25-216) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}

ALFDYNATGDTEFDSPAKQGWMQDNTNNGSGVLTNADGMPAWLVQGIGGRAQWTYSLSTNQHAQASSFGWRMTTEMKVLSGGMITNYYANGTQRVLPIISLDSSGNLVVEFEGQTGRTVLATGTAATEYHKFELVFLPGSNPSASFYFDGKLIRDNIQPTASKQNMIVWGNGSSNTDGVAAYRDIKFEIQGD

>d1kit\_2 b.29.1.8 (347-543) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}

DVTDQVKERSFQIAGWGGSELYRRNTSLNSQQDWQSNAKIRIVDGAANQIQVADGSRKYVVTLSIDESGGLVANLNGVSAPIILQSEHAKVHSFHDYELQYSALNHTTTLFVDGQQITTWAGEVSQENNIQFGNADAQIDGRLHVQKIVLTQQGHNLVEFDAFYLAQQTPEVEKDLEKLGWTKIKTGNTMSLYGNAS

>d2sli\_1 b.29.1.9 (81-276) Leech intramolecular trans-sialidase, N-terminal domain {North american leech (Macrobdella decora)}

IPEGILMEKNNVDIAEGQGYSLDQEAGAKYVKAMTQGTIILSYKSTSENGIQSLFSVGNSTAGNQDRHFHIYITNSGGIGIELRNTDGVFNYTLDRPASVRALYKGERVFNTVALKADAANKQCRLFANGELLATLDKDAFKFISDITGVDNVTLGGTKRQGKIAYPFGGTIGDIKVYSNALSDEELIQATGVTTY

>d6cel\_\_ b.29.1.10 (-) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma reesei, Cel7A}

ESACTLQSETHPPLTWQKCSSGGTCTQQTGSVVIDANWRWTHATNSSTNCYDGNTWSSTLCPDNETCAKNCCLDGAAYASTYGVTTSGNSLSIDFVTQSAQKNVGARLYLMASDTTYQEFTLLGNEFSFDVDVSQLPCGLNGALYFVSMDADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQANVEGWEPSSNNANTGIGGHGSCCSQMDIWEANSISEALTPHPCTTVGQEICEGDGCGGTYSDNRYGGTCDPDGCDWNPYRLGNTSFYGPGSSFTLDTTKKLTVVTQFETSGAINRYYVQNGVTFQQPNAELGSYSGNELNDDYCTAEEAEFGGSSFSDKGGLTQFKKATSGGMVLVMSLWDDYYANMLWLDSTYPTNETSSTPGAVRGSCSTSSGVPAQVESQSPNAKVTFSNIKFGPIGSTGNPSG

>d1eg1a\_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma reesei, Endoglucanase I}

EQPGTSTPEVHPKLTTYKCTKSGGCVAQDTSVVLDWNYRWMHDANYNSCTVNGGVNTTLCPDEATCGKNCFIEGVDYAASGVTTSGSSLTMNQYMPSSSGGYSSVSPRLYLLDSDGEYVMLKLNGQELSFDVDLSALPCGENGSLYLSQMDENGGANQYNTAGANYGSGYCDAQCPVQTWRNGTLNTSHQGFCCNEMDILEGNSRANALTPHSCTATACDSAGCGFNPYGSGYKSYYGPGDTVDTSKTFTIITQFNTDNGSPSGNLVSITRKYQQNGVDIPSAQPGGDTISSCPSASAYGGLATMGKALSSGMVLVFSIWNDNSQYMNWLDSGNAGPCSSTEGNPSNILANNPNTHVVFSNIRWGDIGSTT

>d3ovwa\_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Fusarium oxysporum}

ETPDKAKEQHPKLETYRCTKASGCKKQTNYIVADAGIHGIRQKNGAGCGDWGQKPNATACPDEASCAKNCILSGMDSNAYKNAGITTSGNKLRLQQLINNQLVSPRVYLLEENKKKYEMLHLTGTEFSFDVEMEKLPCGMNGALYLSEMPQDGGKSTSRNSKAGAYYGAGYCDAQCYVTPFINGVGNIKGQGVCCNELDIWEANSRATHIAPHPCSKPGLYGCTGDECGSSGICDKAGCGWNHNRINVTDFYGRGKQYKVDSTRKFTVTSQFVANKQGDLIELHRHYIQDNKVIESAVVNISGPPKINFINDKYCAATGANEYMRLGGTKQMGDAMSRGMVLAMSVWWSEGDFMAWLDQGVAGPCDATEGDPKNIVKVQPNPEVTFSNIRIGEIGSTSSV

>d1dyma\_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Humicola insolens, Cel7b}

EKPGETKEVHPQLTTFRCTKRGGCKPATNFIVLDSLSHPIHRAEGLGPGGCGDWGNPPPKDVCPDVESCAKNCIMEGIPDYSQYGVTTNGTSLRLQHILPDGRVPSPRVYLLDKTKRRYEMLHLTGFEFTFDVDATKLPCGMNSALYLSEMHPTGAKSKYNPGGAYYGTGYCDAQCFVTPFINGLGNIEGKGSCCNAMDIWEANSRASHVAPHTCNKKGLYLCEGEECAFEGVCDKNGCGWNNYRVNVTDYYGRGEEFKVNTLKPFTVVTQFLANRRGKLEKIHRFYVQDGKVIESFYTNKEGVPYTNMIDDEFCEATGSRKYMELGATQGMGEALTRGMVLAMSIWWDQGGNMEWLDHGEAGPCAKGEGAPSNIVQVEPFPEVTYTNLRWGEIGSTY

>d1gpia\_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Phanerochaete chrysosporium, Cel7d}

EQAGTNTAENHPQLQSQQCTTSGGCKPLSTKVVLDSNWRWVHSTSGYTNCYTGNEWDTSLCPDGKTCAANCALDGADYSGTYGITSTGTALTLKFVTGSNVGSRVYLMADDTHYQLLKLLNQEFTFDVDMSNLPCGLNGALYLSAMDADGGMSKYPGNKAGAKYGTGYCDSQCPKDIKFINGEANVGNWTETGSNTGTGSYGTCCSEMDIWEANNDAAAFTPHPCTTTGQTRCSGDDCARNTGLCDGDGCDFNSFRMGDKTFLGKGMTVDTSKPFTVVTQFLTNDNTSTGTLSEIRRIYIQNGKVIQNSVANIPGVDPVNSITDNFCAQQKTAFGDTNWFAQKGGLKQMGEALGNGMVLALSIWDDHAANMLWLDSDYPTDKDPSAPGVARGTCATTSGVPSDVESQVPNSQVVFSNIKFGDIGSTFSGTS

>d1xnb\_\_ b.29.1.11 (-) Xylanase II {Bacillus circulans}

ASTDYWQNWTDGGGIVNAVNGSGGNYSVNWSNTGNFVVGKGWTTGSPFRTINYNAGVWAPNGNGYLTLYGWTRSPLIEYYVVDSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDGDRTTFTQYWSVRQSKRPTGSNATITFTNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW

>d1qh7a\_ b.29.1.11 (A:) Xylanase II {Bacillus agaradhaerens}

EIVTDNSIGNHDGYDYEFWKDSGGSGTMILNHGGTFSAQWNNVNNILFRKGKKFNETQTHQQVGNMSINYGANFQPNGNAYLCVYGWTVDPLVEYYIVDSWGNWRPPGATPKGTITVDGGTYDIYETLRVNQPSIKGIATFKQYWSVRRSKRTSGTISVSNHFRAWENLGMNMGKMYEVALTVEGYQSSGSANVYSNTLRINGNPLS

>d1hixa\_ b.29.1.11 (A:) Xylanase II {Streptomyces sp. s38, xyl1}

ITTNQTGTNNGYYYSFWTDGGGSVSMNLASGGSYGTSWTNCGNFVAGKGWANGARRTVNYSGSFNPSGNAYLTLYGWTANPLVEYYIVDNWGTYRPTGTYKGTVTSDGGTYDVYQTTRVNAPSVEGTKTFNQYWSVRQSKRTGGSITAGNHFDAWARYGMPLGSFNYYMIMATEGYQSSGSSSIS

>d1xnd\_\_ b.29.1.11 (-) Xylanase II {Trichoderma harzianum}

QTIGPGTGYSNGYYYSYWNDGHAGVTYTNGGGGSFTVNWSNSGNFVAGKGWQPGTKNKVINFSGSYNPNGNSYLSIYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNHRSSGSVNTANHFNAWASHGLTLGTMDYQIVAVEGYFSSGSASITVS

>d1xyn\_\_ b.29.1.11 (-) Xylanase II {Trichoderma reesei, xynI}

ASINYDQNYQTGGQVSYSPSNTGFSVNWNTQDDFVVGVGWTTGSSAPINFGGSFSVNSGTGLLSVYGWSTNPLVEYYIMEDNHNYPAQGTVKGTVTSDGATYTIWENTRVNEPSIQGTATFNQYISVRNSPRTSGTVTVQNHFNAWASLGLHLGQMNYQVVAVEGWGGSGSASQSVSN

>d1enxa\_ b.29.1.11 (A:) Xylanase II {Trichoderma reesei, xynII}

ETIQPGTGYNNGYFYSYWNDGHGGVTYTNGPGGQFSVNWSNSGNFVGGKGWQPGTKNKVINFSGSYNPNGNSYLSVYGWSRNPLIEYYIVENFGTYNPSTGATKLGEVTSDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNHRSSGSVNTANHFNAWAQQGLTLGTMDYQIVAVEGYFSSGSASITVS

>d1yna\_\_ b.29.1.11 (-) Xylanase II {Thermomyces lanuginosus}

ETTPNSEGWHDGYYYSWWSDGGAQATYTNLEGGTYEISWGDGGNLVGGKGWNPGLNARAIHFEGVYQPNGNSYLAVYGWTRNPLVEYYIVENFGTYDPSSGATDLGTVECDGSIYRLGKTTRVNAPSIDGTQTFDQYWSVRQDKRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG

>d1bk1\_\_ b.29.1.11 (-) Xylanase II {Aspergillus kawachii}

AGINYVQNYNGNLGDFTYDESAGTFSMYWEDGVSSDFVVGLGWTTGSSNAITYSAEYSASGSSSYLAVYGWVNYPQAEYYIVEDYGDYNPCSSATSLGTVYSDGSTYQVCTDTRTNEPSITGTSTFTQYFSVRESTRTSGTVTVANHFNFWAQHGFGNSDFNYQVMAVEAWSGAGSASVTIS

>d1pvxa\_ b.29.1.11 (A:) Xylanase II {Paecilomyces variotii bainier}

GTTPNSEGWHDGYYYSWWSDGGGDSTYTNNSGGTYEITWGNGGNLVGGKGWNPGLNARAIHFTGVYQPNGTSYLSVYGWTRNPLVEYYIVENFGSSNPSSGSTDLGTVSCDGSTYTLGQSTRYNAPSIDGTQTFNQYWSVRQDKRSSGTVQTGCHFDAWASAGLNVTGDHYYQIVATEGYFSSGYARITVADVG

>d1f5ja\_ b.29.1.11 (A:) Xylanase II {Dictyoglomus thermophilum}

ALTSNASGTFDGYYYELWKDTGNTTMTVYTQGRFSCQWSNINNALFRTGKKYNQNWQSLGTIRITYSATYNPNGNSYLCIYGWSTNPLVEFYIVESWGNWRPPGATSLGQVTIDGGTYDIYRTTRVNQPSIVGTATFDQYWSVRTSKRTSGTVTVTDHFRAWANRGLNLGTIDQITLCVEGYQSSGSANITQNTFSQSS

>d2nlra\_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Streptomyces lividans, CelB2}

DTTICEPFGTTTIQGRYVVQNNRWGSTAPQCVTATDTGFRVTQADGSAPTNGAPKSYPSVFNGCHYTNCSPGTDLPVRLDTVSAAPSSISYGFVDGAVYNASYDIWLDPTARTDGVNQTEIMIWFNRVGPIQPIGSPVGTASVGGRTWEVWSGGNGSNDVLSFVAPSAISGWSFDVMDFVRATVARGLAENDWYLTSVQAGFEPWQNGAGLAVNSFSSTVET

>d1h8va\_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Trichoderma reesei, Cel12A}

ETSCDQWATFTGNGYTVSNNLWGASAGSGFGCVTAVSLSGGASWHADWQWSGGQNNVKSYQNSQIAIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVTYSGDYELMIWLGKYGDIGPIGSSQGTVNVGGQSWTLYYGYNGAMQVYSFVAQTNTTNYSGDVKNFFNYLRDNKGYNAAGQYVLSYQFGTEPFTGSGTLNVASWTASIN

>d1jz8a4 b.30.1.1 (A:731-1023) beta-Galactosidase, domain 5 {Escherichia coli}

PAASHAIPHLTTSEMDFCIELGNKRWQFNRQSGFLSQMWIGDKKQLLTPLRDQFTRAPLDNDIGVSEATRIDPNAWVERWKAAGHYQAEAALLQCTADTLADAVLITTAHAWQHQGKTLFISRKTYRIDGSGQMAITVDVEVASDTPHPARIGLNCQLAQVAERVNWLGLGPQENYPDRLTAACFDRWDLPLSDMYTPYVFPSENGLRCGTRELNYGPHQWRGDFQFNISRYSQQQLMETSHRHLLHAEEGTWLNIDGFHMGIGGDDSWSPSVSAEFQLSAGRYHYQLVWCQK

>d1oaca1 b.30.2.1 (A:301-724) Copper amine oxidase, domain 3 (catalytic) {Escherichia coli}

PAVKPMQIIEPEGKNYTITGDMIHWRNWDFHLSMNSRVGPMISTVTYNDNGTKRKVMYEGSLGGMIVPYGDPDIGWYFKAYLDSGDYGMGTLTSPIARGKDAPSNAVLLNETIADYTGVPMEIPRAIAVFERYAGPEYKHQEMGQPNVSTERRELVVRWISTVGNADYIFDWIFHENGTIGIDAGATGIEAVKGVKAKTMHDETAKDDTRYGTLIDHNIVGTTHQHIYNFRLDLDVDGENNSLVAMDPVVKPNTAGGPRTSTMQVNQYNIGNEQDAAQKFDPGTIRLLSNPNKENRMGNPVSYQIIPYAGGTHPVAKGAQFAPDEWIYHRLSFMDKQLWVTRYHPGERFPEGKYPNRSTHDTGLGQYSKDNESLDNTDAVVWMTTGTTHVARAEEWPIMPTEWVHTLLKPWNFFDETPTLGALK

>d1ksia1 b.30.2.1 (A:207-647) Copper amine oxidase, domain 3 (catalytic) {Pea seedling (Pisum sativum)}

VSKQSPPFGPKQHSLTSHQPQGPGFQINGHSVSWANWKFHIGFDVRAGIVISLASIYDLEKHKSRRVLYKGYISELFVPYQDPTEEFYFKTFFDSGEFGFGLSTVSLIPNRDCPPHAQFIDTYVHSANGTPILLKNAICVFEQYGNIMWRHTENGIPNESIEESRTEVNLIVRTIVTVGNADNVIDWEFKASGSIKPSIALSGILEIKGTNIKHKDEIKEDLHGKLVSANSIGIYHDHFYIYYLDFDIDGTHNSFEKTSLKTVRIKDGSSKRKSYWTTETQTAKTESDAKITIGLAPAELVVVNPNIKTAVGNEVGYRLIPAIPAHPLLTEDDYPQIRGAFTNYNVWVTAYNRTEKWAGGLYVDHSRGDDTLAVWTKQNREIVNKDIVMWHVVGIHHVPAQEDFPIMPLLSTSFELRPTNFFERNPVLKTLSPRDVAWPGC

>d1av4\_1 b.30.2.1 (212-628) Copper amine oxidase, domain 3 (catalytic) {Arthrobacter globiformis}

PLRTTQKPISITQPEGPSFTVTGGNHIEWEKWSLDVGFDVREGVVLHNIAFRDGDRLRPIINRASIAEMVVPYGDPSPIRSWQNYFDTGEYLVGQYANSLELGCDCLGDITYLSPVISDAFGNPREIRNGICMHEEDWGILAKHSDLWSGINYTRRNRRMVISFFTTIGNADYGFYWYLYLDGTIEFEAKATGVVFTSAFPEGGSDNISQLAPGLGAPFHQHIFSARLDMAIDGFTNRVEEEDVVRQTMGPGNERGNAFSRKRTVLTRESEAVREADARTGRTWIISNPESKNRLNEPVGYKLHAHNQPTLLADPGSSIARRAAFATKDLWVTRYADDERYPTGDFVNQHSGGAGLPSYIAQDRDIDGQDIVVWHTFGLTHFPRVEDWPIMPVDTVGFKLRPEGFFDRSPVLDVPAN

>d1a2va1 b.30.2.1 (A:237-672) Copper amine oxidase, domain 3 (catalytic) {Yeast (Hansenula polymorpha)}

PEAPPINVTQPEGVSFKMTGNVMEWSNFKFHIGFNYREGIVLSDVSYNDHGNVRPIFHRISLSEMIVPYGSPEFPHQRKHALDIGEYGAGYMTNPLSLGCDCKGVIHYLDAHFSDRAGDPITVKNAVCIHEEDDGLLFKHSDFRDNFATSLVTRATKLVVSQIFTAANAEYCLYWVFMQDGAIRLDIRLTGILNTYILGDDEEAGPWGTRVYPNVNAHNHQHLFSLRIDPRIDGDGNSAAACDAKSSPYPLGSPENMYGNAFYSEKTTFKTVKDSLTNYESATGRSWDIFNPNKVNPYSGKPPSYKLVSTQCPPLLAKEGSLVAKRAPWASHSVNVVPYKDNRLYPSGDHVPQWSGDGVRGMREWIGDGSENIDNTDILFFHTFGITHFPAPEDFPLMPAEPITLMLRPRHFFTENPGLDIQPSYAMTTSEAKRAV

>d1cb8a3 b.30.3.1 (A:336-599) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

IEPYHHQFWNGDYVQHLRPAYSFNVRMVSKRTRRSESGNKENLLGRYLSDGATNIQLRGPEYYNIMPVWEWDKIPGITSRDYLTDRPLTKLWGEQGSNDFAGGVSDGVYGASAYALDYDSLQAKKAWFFFDKEIVCLGAGINSNAPENITTTLNQSWLNGPVISTAGKTGRGKITTFKAQGQFWLLHDAIGYYFPEGANLSLSTQSQKGNWFHINNSHSKDEVSGDVFKLWINHGARPENAQYAYIVLPGINKPEEIKKYNGTA

>d1egua3 b.30.3.1 (A:541-814) Hyaluronate lyase {Streptococcus pneumoniae}

TSYLSAFNKMDKTAMYNAEKGFGFGLSLFSSRTLNYEHMNKENKRGWYTSDGMFYLYNGDLSHYSDGYWPTVNPYKMPGTTETDAKRADSDTGKVLPSAFVGTSKLDDANATATMDFTNWNQTLTAHKSWFMLKDKIAFLGSNIQNTSTDTAATTIDQRKLESSNPYKVYVNDKEASLTEQEKDYPETQSVFLESSDSKKNIGYFFFKKSSISMSKALQKGAWKDINEGQSDKEVENEFLTISQAHKQNGDSYGYMLIPNVDRATFNQMIKELE

>d1f1sa4 b.30.3.1 (A:620-919) Hyaluronate lyase {Streptococcus agalactiae}

LKSNLSTFNSMDRLAYYNAKKDFGFALSLHSKRTLNYEGMNDENTRGWYTGDGMFYIYNSDQSHYSNHFWPTVNPYKMAGTTEKDAKREDTTKEFMSKHSKDAKEKTGQVTGTSDFVGSVKLNDHFALAAMDFTNWDRTLTAQKGWVILNDKIVFLGSNIKNTNGIGNVSTTIDQRKDDSKTPYTTYVNGKTIDLKQASSQQFTDTKSVFLESKEPGRNIGYIFFKNSTIDIERKEQTGTWNSINRTSKNTSIVSNPFITISQKHDNKGDSYGYMMVPNIDRTSFDKLANSKEVELLENS

>d1h54a2 b.30.4.1 (A:1-268) Lactobacillus maltose phosphorylase, N-terminal domain {Lactobacillus brevis}

MKRIFEVQPWNVITHTFDPKDKRLQESMTSLGNGYMGMRGDFEEGYSGDSLQGIYLGGVWYPDKTRVGWWKNGYPKYFGKVVNAVNFIKLPIEINGEPVDLAKDKISDFTLDLDMHQGVLNRSFVVERGAVRVALNFQRFLSVAQPELSVQKVTVKNLSDAEVDVTLKPSIDADVMNEEANYDERFWDVLATDQQADRGSIVAKTTPNPFGTPRFTSGMEMRLVTDLKNVAITQPNEKEVTTAYTGKLAPQASAELEKRVIVVTSRDY

>d1hs6a2 b.98.1.1 (A:1-208) Leukotriene A4 hydrolase N-terminal domain {Human (Homo sapiens)}

PEIVDTCSLASPASVCRTKHLHLRCSVDFTRRTLTGTAALTVQSQEDNLRSLVLDTKDLTIEKVVINGQEVKYALGERQSYKGSPMEISLPIALSKNQEIVIEISFETSPKSSALQWLTPEQTSGKEHPYLFSQCQAIHCRAILPCQDTPSVKLTYTAEVSVPKELVALMSAIRDGETPDPEDPSRKIYKFIQKVPIPCYLIALVVGA

>d1es6a\_ b.31.1.1 (A:) EV matrix protein {Ebola virus}

GDTPSNPLRPIADDTIDHASHTPGSVSSAFILEAMVNVISGPKVLMKQIPIWLPLGVADQKTYSFDSTTAAIMLASYTITHFGKATNPLVRVNRLGPGIPDHPLRLLRIGNQAFLQEFVLPPVQLPQYFTFDLTALKLITQPLPAATWTDDTPTGSNGALRPGISFHPKLRPILLPNKSGKKGNSADLTSPEKIQAIMTSLQDFKIVPIDPTKNIMGIEVPETLVLKLTGKKVTSKNGQPIIPVLLPKYIGLDPVAPGDLTMVITQDCDTCHSPASLP

>d1qexa\_ b.32.1.1 (A:) gp9 {Bacteriophage T4}

MFIQEPKKLIDTGEIGNASTGDILFDGGNKINSDFNAIYNAFGDQRKMAVANGTGADGQIIHATGYYQKHSITEYATPVKVGTRHDIDTSTVGVKVIIERGELGDCVEFINSNGSISVTNPLTIQAIDSIKGVSGNLVVTSPYSKVTLRCISSDNSTSVWNYSIESMFGQKESPAEGTWNISTSGSVDIPLFHRTEYNMAKLLVTCQSVDGRKIKTAEINILVDTVNSEVISSEYAVMRVGNETEEDEIANIAFSIKENYVTATISSSTVGMRAAVKVIATQKIGVAQ

>d1rie\_\_ b.33.1.1 (-) ISP subunit of the mitochondrial cytochrome bc1-complex, watersoluble domain {Cow (Bos taurus)}

AMSKIEIKLSDIPEGKNMAFKWRGKPLFVRHRTKKEIDQEAAVEVSQLRDPQHDLERVKKPEWVILIGVCTHLGCVPIANAGDFGGYYCPCHGSHYDASGRIRKGPAPLNLEVPSYEFTSDDMVIVG

>d1ezve1 b.33.1.1 (E:87-215) ISP subunit of the mitochondrial cytochrome bc1-complex, watersoluble domain {Baker's yeast (Saccharomyces cerevisiae)}

DVLAMAKVEVNLAAIPLGKNVVVKWQGKPVFIRHRTPHEIQEANSVDMSALKDPQTDADRVKDPQWLIMLGICTHLGCVPIGEAGDFGGWFCPCHGSHYDISGRIRKGPAPLNLEIPAYEFDGDKVIVG

>d1rfs\_\_ b.33.1.1 (-) ISP subunit from chloroplast cytochrome bf complex {Spinach (Spinacia oleracea)}

TIAKDALGNDVIAAEWLKTHAPGDRTLTQGLKGDPTYLVVESDKTLATFGINAVCTHLGCVVPFNAAENKFICPCHGSQYNNQGRVVRGPAPLSLALAHCDVDDGKVVFVPWTETDFRTGEAPWWSA

>d1g8kb\_ b.33.1.1 (B:) Arsenite oxidase Rieske subunit {Alcaligenes faecalis}

RTTLAYPATAVSVAKNLAANEPVSFTYPDTSSPCVAVKLGAPVPGGVGPDDDIVAYSVLCTHMGCPTSYDSSSKTFSCPCHFTEFDAEKAGQMICGEATADLPRVLLRYDAASDALTAVGVDGLIYGRQANVI

>d1fqta\_ b.33.1.1 (A:) Rieske-type ferredoxin associated with biphenyl dioxygenase {Burkholderia cepacia}

MKFTRVCDRRDVPEGEALKVESGGTSVAIFNVDGELFATQDRCTHGDWSLSDGGYLEGDVVECSLHMGKFCVRTGKVKSPPPCEALKIFPIRIEDNDVLVDFEAGYLAP

>d1eg9a1 b.33.1.2 (A:1-154) Naphthalene 1,2-dioxygenase alpha subunit, N-domain {Pseudomonas putida}

MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQ

>d1bia\_2 b.34.1.1 (271-317) Biotin repressor/biotin holoenzyme synthetase, C-terminal domain {Escherichia coli}

FINRPVKLIIGDKEIFGISRGIDKQGALLLEQDGIIKPWMGGEISLR

>d1byma\_ b.34.1.2 (A:) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}

NPIPGLDELGVGNSDAAAPGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLSHNGKDVELLDDLAHTIRIEEL

>d1c0wa3 b.34.1.2 (A:165-223) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}

IVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLSHNGKDVELLDDLAHTIRI

>d1g3sa3 b.34.1.2 (A:148-225) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}

PGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLSHNGKDVELLDDLAHTIRIEE

>d1fx7a3 b.34.1.2 (A:145-230) Iron-dependent regulator IdeR {Mycobacterium tuberculosis}

GADDANLVRLTELPAGSPVAVVVRQLTEHVQGDIDLITRLKDAGVVPNARVTVETTPGGGVTIVIPGHENVTLPHEMAHAVKVEKV

>d1igqa\_ b.34.1.3 (A:) Transcriptional repressor protein KorB {Escherichia coli}

KKAIVQVEHDERPARLILNRRPPAEGYAWLKYEDDGQEFEANLADVKLVALIEG

>d1igub\_ b.34.1.3 (B:) Transcriptional repressor protein KorB {Escherichia coli}

PDPDKLKKAIVQVEHDERPARLILNRRPPAEGYAWLKYEDDGQEFEANLADVKLVALIEG

>d1ckaa\_ b.34.2.1 (A:) C-Crk, N-terminal SH3 domain {Mouse (Mus musculus)}

AEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYVEKY

>d1efna\_ b.34.2.1 (A:) Fyn proto-oncogene tyrosine kinase, SH3 domain {Human (Homo sapiens)}

ALFVALYDYEAITEDDLSFHKGEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPV

>d1shfa\_ b.34.2.1 (A:) Fyn proto-oncogene tyrosine kinase, SH3 domain {Human (Homo sapiens)}

VTLFVALYDYEARTEDDLSFHKGEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPVD

>d1neb\_\_ b.34.2.1 (-) SH3 domain from nebulin {Human (Homo sapiens)}

TAGKIFRAMYDYMAADADEVSFKDGDAIINVQAIDEGWMYGTVQRTGRTGMLPANYVEAI

>d1bbza\_ b.34.2.1 (A:) Abl tyrosine kinase, SH3 domain {Human (Homo sapiens)}

NLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNGQGWVPSNYITPVNS

>d2abl\_1 b.34.2.1 (75-139) Abl tyrosine kinase, SH3 domain {Human (Homo sapiens)}

MGPSENDPNLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNGQGWVPSNYITPVN

>d1pht\_\_ b.34.2.1 (-) Phosphatidylinositol 3-kinase (p85-alpha subunit, pi3k), SH3 domain {Human (Homo sapiens)}

AEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYIGRKKISPP

>d1g2ba\_ b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}

MDRQGFVPAAYVKKLDSGTGKELVLALYDYQEKSPREVTMKKGDILTLLNSTNKDWWKVEVN

>d1pwt\_\_ b.34.2.1 (-) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}

MGTGKELVLALYDYQEKSPREVTMKKGDILTLLNSTNKDWWKVEVNDRQGFVPAAYVKKLD

>d1qkwa\_ b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}

KELVLALYDYQEKSPREVTMKKGDILTLLNSTNKDWWKVEVGDRQGFVPAAYVKKLD

>d1tuc\_\_ b.34.2.1 (-) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}

MGPREVTMKKGDILTLLNSTNKDWWKVEVNDRQGFVPAAYVKKLDSGTGKELVLALYDYQE

>d1awj\_\_ b.34.2.1 (-) IL-2 inducible T-cell (Itc) kinase {Mouse (Mus musculus)}

KKPLPPTPEDNRRSFQEPEETLVIALYDYQTNDPQELALRCDEEYYLLDSSEIHWWRVQDKNGHEGYAPSSYLVEKS

>d1bu1a\_ b.34.2.1 (A:) Hemapoetic cell kinase Hck {Human (Homo sapiens)}

IIVVALYDYEAIHHEDLSFQKGDQMVVLEESGEWWKARSLATRKEGYIPSNYVARVD

>d1qcfa1 b.34.2.1 (A:80-145) Hemapoetic cell kinase Hck {Human (Homo sapiens)}

SGIRIIVVALYDYEAIHHEDLSFQKGDQMVVLEESGEWWKARSLATRKEGYIPSNYVARVDSLET

>d1cska\_ b.34.2.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}

GTECIAKYNFHGTAEQDLPFCKGDVLTIVAVTKDPNWYKAKNKVGREGIIPANYVQKR

>d1fmk\_1 b.34.2.1 (82-145) c-src tyrosine kinase {Human (Homo sapiens)}

MVTTFVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLSTGQTGYIPSNYVAPSDSIQA

>d1nloc\_ b.34.2.1 (C:) c-src tyrosine kinase {Chicken (Gallus gallus)}

TFVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQTGYIPSNYVAPS

>d1awx\_\_ b.34.2.1 (-) Bruton's tyrosine kinase {Human (Homo sapiens)}

GSMSTSELKKVVALYDYMPMNANDLQLRKGDEYFILEESNLPWWRARDKNGQEGYIPSNYVTEAEDS

>d1qlya\_ b.34.2.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}

LKKVVALYDYMPMNANDLQLRKGDEYFILEESNLPWWRARDKNGQEGYIPSNYVTEAE

>d1gl5a\_ b.34.2.1 (A:) tyrosine kinase tec {Mouse (Mus musculus)}

GSEIVVAMYDFQATEAHDLRLERGQEYIILEKNDLHWWRARDKYGSEGYIPSNYVTGKKSNNLDQYD

>d1gcqa\_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}

STYVQALFDFDPQEDGELGFRRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPV

>d1gria1 b.34.2.1 (A:1-56) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}

MEAIAKYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIPKNYIEMK

>d1gria2 b.34.2.1 (A:157-217) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}

QPTYVQALFDFDPQEDGELGFRRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPVNRNV

>d1gbra\_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Mouse (Mus musculus)}

GSRRASVGSMEAIAKYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIPKNYIEMKPHPEFIVTD

>d1sema\_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Caenorhabditis elegans, SEM-5}

ETKFVQALFDFNPQESGELAFKRGDVITLINKDDPNWWEGQLNNRRGIFPSNYVCPYN

>d2hsp\_\_ b.34.2.1 (-) Phospholipase C, SH3 domain {Human (Homo sapiens)}

GSPTFKCAVKALFDYKAQREDELTFIKSAIIQNVEKQEGGWWRGDYGGKKQLWFPSNYVEEMVNPEGIHRD

>d1h92a\_ b.34.2.1 (A:) p56-lck tyrosine kinase, SH3 domain {Human (Homo sapiens)}

GSPLQDNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQEGFIPFNFVAKAN

>d1lcka1 b.34.2.1 (A:63-116) p56-lck tyrosine kinase, SH3 domain {Human (Homo sapiens)}

DNLVIALHSYEPSHDGDLGFEKGEQLRILEQSGEWWKAQSLTTGQEGFIPFNFV

>d1ycsb2 b.34.2.1 (B:457-519) 53BP2 {Human (Homo sapiens)}

IMNKGVIYALWDYEPQNDDELPMKEGDCMTIIHREDEDEIEWWWARLNDKEGYVPRNLLGLYP

>d1bb9\_\_ b.34.2.1 (-) Amphiphysin 2 {Rat (Rattus norvegicus)}

TTGRLDLPPGFMFKVQAQHDYTATDTDELQLKAGDVVLVIPFQNPEEQDEGWLMGVKESDWNQHKELEKCRGVFPENFTERVQ

>d1i07a\_ b.34.2.1 (A:) EPS8 SH3 domain {Mouse (Mus musculus)}

KKYAKSKYDFVARNSSELSVMKDDVLEILDDRRQWWKVRNASGDSGFVPNNILDIMRTP

>d1gcqc\_ b.34.2.1 (C:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}

GSHMPKMEVFQEYYGIPPPPGAFGPFLRLNPGDIVELTKAEAEHNWWEGRNTATNEVGWFPCNRVHPYV

>d1k1za\_ b.34.2.1 (A:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}

RAQDKKRNELGLPKMEVFQEYYGIPPPPGAFGGFLRLNPGDIVELTKAEAEHNWWEGRNTATNEVGWFPCNRVHPYVH

>d1i1ja\_ b.34.2.1 (A:) Melanoma inhibitory activity protein {Human (Homo sapiens)}

GPMPKLADRKLCADQECSHPISMAVALQDYMAPDCRFLTIHRGQVVYVFSKLKGRGRLFWGGSVQGDYYGDLAARLGYFPSSIVREDQTLKPGKVDVKTDKWDFYC

>d1kjwa1 b.34.2.1 (A:430-525) Psd-95 {Rat (Rattus norvegicus)}

GFYIRALFDYDKTKDCGFLSQALSFRFGDVLHVIDAGDEEWWQARRVHSDSETDDIGFIPSKRRVERREWSRLKAKDWGSSSGSQGREDSVLSYET

>d1br2a1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain {Chicken (Gallus gallus), pectoral muscle}

LVWVPSEKHGFEAASIKEEKGDEVTVELQENGKKVTLSKDDIQKMN

>d2mysa1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain {Chicken (Gallus gallus), pectoral muscle}

AKSSVFVVHPKQSFVKGTIQSKEGGKVTVKTEGGETLTVKEDQVFS

>d1b7ta1 b.34.3.1 (A:29-76) Myosin S1 fragment, N-terminal domain {Bay scallop (Aequipecten irradians)}

DGKKNCWVPDEKEGFASAEIQSSKGDEITVKIVADSSTRTVKKDDIQS

>d1jwya1 b.34.3.1 (A:36-79) Myosin S1 fragment, N-terminal domain {Slime mold (Dictyostelium discoideum)}

FKLTVSDKRYIWYNPDPKERDSYECGEIVSETSDSFTFKTVDGQ

>d1lvk\_1 b.34.3.1 (34-79) Myosin S1 fragment, N-terminal domain {Slime mold (Dictyostelium discoideum)}

YIWYNPDPKERDSYECGEIVSETSDSFTFKTSDGQDRQVKKDDANQ

>d1g5va\_ b.34.9.1 (A:) Survival motor neuron protein 1, smn {Human (Homo sapiens)}

QQWKVGDKCSAIWSEDGCIYPATIASIDFKRETCVVVYTGYGNREEQNLSDLLSPI

>d1khca\_ b.34.9.2 (A:) DNA methyltransferase DNMT3B {Mouse (Mus musculus)}

TEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMRWVQWFGDGKFSEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLEKARVRAGKTFSSSPGESLEDQLKPMLEWAHGGFKPTGIEGLKPN

>d1vie\_\_ b.34.4.1 (-) R67 dihydrofolate reductase {Escherichia coli, plasmid PLZ1}

PSNATFGMGDRVRKKSGAAWQGQIVGWYCTNLTPEGYAVESEAHPGSVQIYPVAALERIN

>d1psf\_\_ b.34.4.2 (-) Photosystem I accessory protein E (PsaE) {Cyanobacterium (Synechococcus sp.), pcc 7002}

AIERGSKVKILRKESYWYGDVGTVASIDKSGIIYPVIVRFNKVNYNGFSGSAGGLNTNNFAEHELEVVG

>d1qp2a\_ b.34.4.2 (A:) Photosystem I accessory protein E (PsaE) {Cyanobacterium (Nostoc sp.), strain pcc8009}

MVQRGSKVRILRPESYWFQDVGTVASVDQSGIKYPVIVRFEKVNYSGINTNNFAEDELVEVEAPKAKPKK

>d1jb0e\_ b.34.4.2 (E:) Photosystem I accessory protein E (PsaE) {Synechococcus elongatus}

VQRGSKVKILRPESYWYNEVGTVASVDQTPGVKYPVIVRFDKVNYTGYSGSASGVNTNNFALHEVQEVA

>d1dj7b\_ b.34.4.3 (B:) Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain {Synechocystis sp.}

MNVGDRVRVTSSVVVYHHPEHKKTAFDLQGMEGEVAAVLTEWQGRPISANLPVLVKFEQRFKAHFRPDEVTLI

>d2ahjb\_ b.34.4.4 (B:) Nitrile hydratase beta chain {Rhodococcus erythropolis}

MDGVHDLAGVQGFGKVPHTVNADIGPTFHAEWEHLPYSLMFAGVAELGAFSVDEVRYVVERMEPRHYMMTPYYERYVIGVATLMVEKGILTQDELESLAGGPFPLSRPSESEGRPAPVETTTFEVGQRVRVRDEYVPGHIRMPAYCRGRVGTISHRTTEKWPFPDAIGHGRNDAGEEPTYHVKFAAEELFGSDTDGGSVVVDLFEGYLEPA

>d1jj2s\_ b.34.5.1 (S:) Ribosomal proteins L24 (L24p) {Archaeon Haloarcula marismortui}

SKQPDKQRKSQRRAPLHERHKQVRATLSADLREEYGQRNVRVNAGDTVEVLRGDFAGEEGEVINVDLDKAVIHVEDVTLEKTDGEEVPRPLDTSNVRVTDLDLEDEKREARLESEDDSA

>d1jj2p\_ b.34.5.1 (P:) Ribosomal proteins L21e {Archaeon Haloarcula marismortui}

PSSNGPLEGTRGKLKNKPRDRGTSPPQRAVEEFDDGEKVHLKIDPSVPNGRFHPRFDGQTGTVEGKQGDAYKVDIVDGGKEKTIIVTAAHLRRQE

>d2eifa1 b.34.5.2 (A:1-73) N-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Methanococcus jannaschii}

VIIMPGTKQVNVGSLKVGQYVMIDGVPCEIVDISVSKPGKHGGAKARVVGIGIFEKVKKEFVAPTSSKVEVPI

>d1bkb\_1 b.34.5.2 (4-74) N-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Pyrobaculum aerophilum}

KWVMSTKYVEAGELKEGSYVVIDGEPCRVVEIEKSKTGKHGSAKARIVAVGVFDGGKRTLSLPVDAQVEVP

>d1rl2a1 b.34.5.3 (A:126-195) C-terminal domain of ribosomal protein L2 {Bacillus stearothermophilus}

GNALPLENIPVGTLVHNIELKPGRGGQLVRAAGTSAQVLGKEGKYVIVRLASGEVRMILGKCRATVGEVG

>d1jj2a1 b.34.5.3 (A:91-237) C-terminal domain of ribosomal protein L2 {Archaeon Haloarcula marismortui}

GNTLPLAEIPEGVPVCNVESSPGDGGKFARASGVNAQLLTHDRNVAVVKLPSGEMKRLDPQCRATIGVVGGGGRTDKPFVKAGNKHHKMKARGTKWPNVRGVAMNAVDHPFGGGGRQHPGKPKSISRNAPPGRKVGDIASKRTGRGG

>d3vub\_\_ b.34.6.1 (-) CcdB {Escherichia coli}

MQFKVYTYKRESRYRLFVDVQSDIIDTPGRRMVIPLASARLLSDKVSRELYPVVHIGDESWRMMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI

>d1hyoa1 b.34.8.1 (A:1-118) Fumarylacetoacetate hydrolase, FAH, N-terminal domain {Mouse (Mus musculus)}

MSFIPVAEDSDFPIQNLPYGVFSTQSNPKPRIGVAIGDQILDLSVIKHLFTGPALSKHQHVFDETTLNNFMGLGQAAWKEARASLQNLLSASQARLRDDKELRQRAFTSQASATMHLP

>d1ex4a1 b.34.7.1 (A:223-270) DNA-binding domain of retroviral integrase {Human immunodeficiency virus type 1}

FRVYYRDSRNSLWKGPAKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRD

>d1ihva\_ b.34.7.1 (A:) DNA-binding domain of retroviral integrase {Human immunodeficiency virus type 1}

MIQNFRVYYRDSRDPVWKGPAKLLWKGEGAVVIQDNSDIKVVPRRKAKIIRD

>d1c0ma1 b.34.7.1 (A:217-269) DNA-binding domain of retroviral integrase {Rous sarcoma virus (RSV, avian sarcoma virus)}

VLTEGPPVKIRIETGEWEKGWNVLVWGRGYAAVKNRDTDKVIWVPSRKVKPDI

>d1c6vx\_ b.34.7.1 (X:) DNA-binding domain of retroviral integrase {Simian immunodeficiency virus}

KNSKFKNFRVYYREGRDQLWKGPGELLWKGEGAVLLKVGTDIKVVPRRKAKIIKD

>d1aono\_ b.35.1.1 (O:) Chaperonin-10 (GroES) {Escherichia coli}

MNIRPLHDRVIVKRKEVETKSAGGIVLTGSAAAKSTRGEVLAVGNGRILENGEVKPLDVKVGDIVIFNDGYGVKSEKIDNEEVLIMSESDILAIVEA

>d1jh2a\_ b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium tuberculosis}

AKVNIKPLEDKILVQANEAETTTASGLVIPDTAKEKPQEGTVVAVGPGRWDEDGEKRIPLDVAEGDTVIYSKYGGTEIKYNGEEYLILSARDVLAVVSK

>d1lepa\_ b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium leprae}

AKVKIKPLEDKILVQAGEAETMTPSGLVIPENAKEKPQEGTVVAVGPGRWDEDGAKRIPVDVSEGDIVIYSKYGGTEIKYNGEEYLILSARDVLAVVSK

>d1g31a\_ b.35.1.1 (A:) GP31 co-chaperonin {Bacteriophage T4}

QQLPIRAVGEYVILVSEPAQAGDEEVTESGLIIGKRVQGEVPELCVVHSVGPDVPEGFCEVGDLTSLPVGQIRNVPHPFVALGLKQPKEIKQKFVTCHYKAIPCLYK

>d1heta1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Horse (Equus caballus)}

STAGKVIKCKAAVLWEEKKPFSIEEVEVAPPKAHEVRIKMVATGICRSDDHVVSGTLVTPLPVIAGHEAAGIVESIGEGVTTVRPGDKVIPLFTPQCGKCRVCKHPEGNFCLKNDLSMPRGTMQDGTSRFTCRGKPIHHFLGTSTFSQYTVVDEISVAKIDAASPLEKVCLIGCXKDSVPKLVADFMAKKFALDPLITHVLPFEKINEGFDLLRSGESIRTILTF

>d1d1ta1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

GTAGKVIKCKAAVLWEQKQPFSIEEIEVAPPKTKEVRIKILATGICRTDDHVIKGTMVSKFPVIVGHEATGIVESIGEGVTTVKPGDKVIPLFLPQCRECNACRNPDGNLCIRSDITGRGVLADGTTRFTCKGKPVHHFLNTSTFTEYTVVDESSVAKIDDAAPPEKVCLIGCXRDDVPKLVTEFLAKKFDLDQLITHVLPFKKISEGFELLNSGQSIRTVLTF

>d1hsoa1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

STAGKVIKCKAAVLWELKKPFSIEEVEVAPPKAHEVRIKMVAVGICGTDDHVVSGTMVTPLPVILGHEAAGIVESVGEGVTTVKPGDKVIPLAIPQCGKCRICKNPESNYCLKNDVSNPQGTLQDGTSRFTCRRKPIHHFLGISTFSQYTVVDENAVAKIDAASPLEKVCLIGCXKECVPKLVADFMAKKFSLDALITHVLPFEKINEGFDLLHSGKSIRTILMF

>d1hsza1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

STAGKVIKCKAAVLWEVKKPFSIEDVEVAPPKAYEVRIKMVAVGICRTDDHVVSGNLVTPLPVILGHEAAGIVESVGEGVTTVKPGDKVIPLFTPQCGKCRVCKNPESNYCLKNDLGNPRGTLQDGTRRFTCRGKPIHHFLGTSTFSQYTVVDENAVAKIDAASPLEKVCLIGCXKEGIPKLVADFMAKKFSLDALITHVLPFEKINEGFDLLHSGKSIRTVLTF

>d1ht0a1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

STAGKVIKCKAAVLWELKKPFSIEEVEVAPPKAHEVRIKMVAAGICRSDEHVVSGNLVTPLPVILGHEAAGIVESVGEGVTTVKPGDKVIPLFTPQCGKCRICKNPESNYCLKNDLGNPRGTLQDGTRRFTCSGKPIHHFVGVSTFSQYTVVDENAVAKIDAASPLEKVCLIGCXKESVPKLVADFMAKKFSLDALITNVLPFEKINEGFDLLRSGKSIRTVLTF

>d1teha1 b.35.1.2 (A:3-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

ANEVIKCKAAVAWEAGKPLSIEEIEVAPPKAHEVRIKIIATAVCHTDAYTLSGADPEGCFPVILGHEGAGIVESVGEGVTKLKAGDTVIPLYIPQCGECKFCLNPKTNLCQKIRVTQGKGLMPDGTSRFTCKGKTILHYMGTSTFSEYTVVADISVAKIDPLAPLDKVCLLGCXVESVPKLVSEYMSKKIKVDEFVTHNLSFDEINKAFELMHSGKSIRTVVKI

>d1e3ia1 b.35.1.2 (A:1-174,A:325-376) Alcohol dehydrogenase {Mouse (Mus musculus), class II}

GTQGKVIKCKAAIAWKTGSPLCIEEIEVSPPKACEVRIQVIATCVCPTDINATDPKKKALFPVVLGHECAGIVESVGPGVTNFKPGDKVIPFFAPQCKRCKLCLSPLTNLCGKLRNFKYPTIDQELMEDRTSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEANLERVCXKSVDSVPNLVSDYKNKKFDLDLLVTHALPFESINDAIDLMKEGKSIRTILTF

>d1cdoa1 b.35.1.2 (A:1-175,A:325-374) Alcohol dehydrogenase {Cod (Gadus callarias)}

ATVGKVIKCKAAVAWEANKPLVIEEIEVDVPHANEIRIKIIATGVCHTDLYHLFEGKHKDGFPVVLGHEGAGIVESVGPGVTEFQPGEKVIPLFISQCGECRFCQSPKTNQCVKGWANESPDVMSPKETRFTCKGRKVLQFLGTSTFSQYTVVNQIAVAKIDPSAPLDTVCLLGCXKDGVPKMVKAYLDKKVKLDEFITHRMPLESVNDAIDLMKHGKCIRTVLSL

>d1keva1 b.35.1.2 (A:1-150,A:315-351) Bacterial secondary alcohol dehydrogenase {Clostridium beijerinckii}

MKGFAMLGINKLGWIEKERPVAGSYDAIVRPLAVSPCTSDIHTVFEGALGDRKNMILGHEAVGEVVEVGSEVKDFKPGDRVIVPCTTPDWRSLEVQAGFQQHSNGMLAGWKFSNFKDGVFGEYFHVNDADMNLAILPKDMPLENAVMITDXDLSKLVTHVYHGFDHIEEALLLMKDKPKDLIKAVVIL

>d1ykfa1 b.35.1.2 (A:1-150,A:315-352) Bacterial secondary alcohol dehydrogenase {Thermoanaerobacter brockii}

MKGFAMLSIGKVGWIEKEKPAPGPFDAIVRPLAVAPCTSDIHTVFEGAIGERHNMILGHEAVGEVVEVGSEVKDFKPGDRVVVPAITPDWRTSEVQRGYHQHSGGMLAGWKFSNVKDGVFGEFFHVNDADMNLAHLPKEIPLEAAVMIPDXDPSKLVTHVFRGFDNIEKAFMLMKDKPKDLIKPVVILA

>d1e3ja1 b.35.1.2 (A:4-150,A:314-351) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}

DNLSAVLYKQNDLRLEQRPIPEPKEDEVLLQMAYVGICGSDVHYYEHGRIADFIVKDPMVIGHEASGTVVKVGKNVKHLKKGDRVAVEPGVPCRRCQFCKEGKYNLCPDLTFCATPPDDGNLARYYVHAADFCHKLPDNVSLEEGALXNVKQLVTHSFKLEQTVDAFEAARKKADNTIKVMISCRQ

>d1qora1 b.35.1.2 (A:2-135,A:266-327) Quinone oxidoreductase {Escherichia coli}

ATRIEFHKHGGPEVLQAVEFTPADPAENEIQVENKAIGINFIDTYIRSGLYPPPSLPSGLGTEAAGIVSKVGSGVKHIKAGDRVVYAQSALGAYSSVHNIIADKAAILPAAISFEQAAASFLKGLTVYYLLRKTXLQGYITTREELTEASNELFSLIASGVIKVDVAEQQKYPLKDAQRAHEILESRATQGSSLLIP

>d1auua\_ b.35.2.1 (A:) SacY {Bacillus subtilis}

MKIKRILNHNAIVVKDQNEEKILLGAGIAFNKKKNDIVDPSKIEKTFIRKDTPDY

>d1pdr\_\_ b.36.1.1 (-) Discs large protein homolog {Human (Homo sapiens)}

ITREPRKVVLHRGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAAALKNAGQAVTIVAQYRPEEYSRQHA

>d1kwaa\_ b.36.1.1 (A:) Cask/Lin-2 {Human (Homo sapiens)}

RSRLVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMIHRQGTLHVGDEIREINGISVANQTVEQLQKMLREMRGSITFKIVPSYREF

>d1be9a\_ b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}

FLGEEDIPREPRRIVIHRGSTGLGFNIIGGEDGEGIFISFILAGGPADLSGELRKGDQILSVNGVDLRNASHEQAAIALKNAGQTVTIIAQYKPEEYSRFEANSRVNSSGRIVTN

>d1qlca\_ b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}

AEKVMEIKLIKGPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAAHKDGRLQIGDKILAVNSVGLEDVMHEDAVAALKNTYDVVYLKVAKPSNA

>d1qava\_ b.36.1.1 (A:) Syntrophin {Mouse (Mus musculus)}

GSLQRRRVTVRKADAGGLGISIKGGRENKMPILISKIFKGLAADQTEALFVGDAILSVNGEDLSSATHDEAVQALKKTGKEVVLEVKYMK

>d1b8qa\_ b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}

GSHMIEPNVISVRLFKRKVGGLGFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRPLVDLSYDSALEVLRGIASETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTQPLGPPTKAV

>d1qaua\_ b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}

NVISVRLFKRKVGGLGFLVKERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRPLVDLSYDSALEVLRGIASETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTQP

>d3pdza\_ b.36.1.1 (A:) Phosphatase hPTP1e {Human (Homo sapiens)}

PKPGDIFEVELAKNDNSLGISVTGGVNTSVRHGGIYVKAVIPQGAAESDGRIHKGDRVLAVNGVSLEGATHKQAVETLRNTGQVVHLLLEKGQSPT

>d1g9oa\_ b.36.1.1 (A:) Na+/H+ exchanger regulatory factor, NHERF {Human (Homo sapiens)}

RMLPRLCCLEKGPNGYGFHLHGEKGKLGQYIRLVEPGSPAEKAGLLAGDRLVEVNGENVEKETHQQVVSRIRAALNAVRLLVVDPETDEQL

>d1ihja\_ b.36.1.1 (A:) Inad {Fruit fly (Drosophila melanogaster)}

GELIHMVTLDKTGKKSFGICIVRGEVKDSPNTKTTGIFIKGIVPDSPAHLCGRLKVGDRILSLNGKDVRNSTEQAVIDLIKEADFKIELEIQTF

>d1fc6a3 b.36.1.3 (A:157-248) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}

AGSVTGVGLEITYDGGSGKDVVVLTPAPGGPAEKAGARAGDVIVTVDGTAVKGMSLYDVSDLLQGEADSQVEVVLHAPGAPSNTRTLQLTRQ

>d1k32a1 b.36.1.3 (A:763-853) Tricorn protease {Archaeon Thermoplasma acidophilum}

GRIACDFKLDGDHYVVAKAYAGDYSNEGEKSPIFEYGIDPTGYLIEDIDGETVGAGSNIYRVLSEKAGTSARIRLSGKGGDKRDLMIDILD

>d1i16\_\_ b.36.1.2 (-) Interleukin 16 {Human (Homo sapiens)}

MPDLNSSTDSAASASAASDVSVESTAEATVCTVTLEKMSAGLGFSLEGGKGSLHGDKPLTINRIFKGAASEQSETVQPGDEILQLGGTAMQGLTRFEAWNIIKALPDGPVTIVIRRKSLQSKETTAAGDS

>d1g3p\_1 b.37.1.1 (1-65) N-terminal domains of the minor coat protein g3p {Bacteriophage M13}

AETVESCLAKSHTENSFTNVWKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIP

>d1g3p\_2 b.37.1.1 (91-217) N-terminal domains of the minor coat protein g3p {Bacteriophage M13}

EYGDTPIPGYTYINPLDGTYPPGTEQNPANPNPSLEESQPLNTFMFQNNRFRNRQGALTVYTGTVTQGTDPVKTYYQYTPVSSKAMYDAYWNGKFRDCAFHSGFNEDIFVCEYQGQSSDLPQPPVNA

>d1fgp\_\_ b.37.1.1 (-) N-terminal domains of the minor coat protein g3p {Bacteriophage fd}

ETVESCLAKPHTENSFTNVWKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIPENAAAH

>d1b34a\_ b.38.1.1 (A:) D1 core SNRNP protein {Human (Homo sapiens)}

KLVRFLMKLSHETVTIELKNGTQVHGTITGVDVSMNTHLKAVKMTLKNREPVQLETLSIRGNNIRYFILPDSLPLDTLLV

>d1b34b\_ b.38.1.1 (B:) D2 core SNRNP protein {Human (Homo sapiens)}

TGPLSVLTQSVKNNTQVLINCRNNKKLLGRVKAFDRHCNMVLENVKEMWTEVPKSGKGKKKSKPVNKDRYISKMFLRGDSVIVVLRNPLIAGK

>d1d3ba\_ b.38.1.1 (A:) D3 core SNRNP protein {Human (Homo sapiens)}

GVPIKVLHEAEGHIVTCETNTGEVYRGKLIEAEDNMNCQMSNITVTYRDGRVAQLEQVYIRGCKIRFLILPD

>d1d3bb\_ b.38.1.1 (B:) B core SNRNP protein {Human (Homo sapiens)}

SKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFRKIKPKNSKQAEREEKRVLGLVLLRGENLVSMTVEGPPP

>d1d3bl\_ b.38.1.1 (L:) B core SNRNP protein {Human (Homo sapiens)}

TVGKSSKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFRKIKPKNSKQAEREEKRVLGLVLLRGENLVSMTVEGPPPKDTG

>d1i81a\_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium thermoautotrophicum}

RVNVQRPLDALGNSLNSPVIIKLKGDREFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGDNIVYISP

>d1jria\_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium thermoautotrophicum}

QRPLDALGNSLNSPVIIKLKGDREFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGDNIVYISRGK

>d1i8fa\_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Pyrobaculum aerophilum}

ATLGATLQDSIGKQVLVKLRDSHEIRGILRSFDQHVNLLLEDAEEIIDGNVYKRGTMVVRGENVLFISPVP

>d1i4k1\_ b.38.1.1 (1:) Archaeal homoheptameric Sm protein {Archaeon Archaeoglobus fulgidus}

PPRPLDVLNRSLKSPVIVRLKGGREFRGTLDGYDIHMNLVLLDAEEIQNGEVVRKVGSVVIRGDTVVFVSPA

>d1h5pa\_ b.99.1.1 (A:) Nuclear autoantigen Sp100b {Human (Homo sapiens)}

MDENINFKQSELPVTCGEVKGTLYKERFKQGTSKKCIQSEDKKWFTPREFEIEGDRGASKNWKLSIRCGGYTLKVLMENKFLPEPPSTRKKVTIK

>d1whi\_\_ b.39.1.1 (-) Ribosomal protein L14 {Bacillus stearothermophilus}

MIQQESRLKVADNSGAREVLVIKVLGGSGRRYANIGDVVVATVKDATPGGVVKKGQVVKAVVVRTKRGVRRPDGSYIRFDENACVIIRDDKSPRGTRIFGPVARELRDKDFMKIISLAPEVI

>d1jj2j\_ b.39.1.1 (J:) Ribosomal protein L14 {Archaeon Haloarcula marismortui}

MEALGADVTQGLEKGSLITCADNTGARELKVISVHGYSGTKNRHPKAGLGDKITVSVTKGTPEMRRQVLEAVVVRQRKPIRRPDGTRVKFEDNAAVIVDENEDPRGTELKGPIAREVAQRFGSVASAATMIV

>d1ez6a\_ b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}

LHKEPATLIKAIDGDTVKLMYKGQPMVFRLLLVDIPETKHPKKGVEKYGPEAAAFTKKMVENAKKIEVEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAYVYKGNNTHEQLLRKAEAQAKKEKLNIWS

>d1joqa\_ b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}

ATSTKKLHKEPATLIKAIDGDTVKLMYKGQPMTFRLLLVDTPETKHPKKGVEKYGPEASAFTKKMVENAKKIEVEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAYVYKPNNTHEQLLRKSEAQAKKEKLNIWSEDNADSGQ

>d1sty\_\_ b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}

KLHKEPATLIKAIDGDTVKLMYKGQPMTFRLLLVDTPETKHPKKGVEKYGPEASAFTKKMVENAKKIEVEFDKGQRTDKYGRGLAYIYADGKMVNEALVRQGLAKVAYVYKPNNTHEQHLRGKSEAQAKKEKLNIWS

>d2sob\_\_ b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}

ATSTKKLHKEPATLIKAIDGDTVKLMYKGQPMTFRLLLVDTPETKHPKKGVEKYGPEASAFTKKMLENAKKIEVEFDKGQRTDKYGRVLAYIYADGKMVNEAL

>d1djrd\_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}

APQTITELCSEYRNTQIYTINDKILSYTESMAGKREMVIITFKSGETFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETKIDKLCVWNNKTPNSIAAISMKN

>d1ltrd\_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}

APQSITELCSEYHNTQIYTINDKILSYTESMAGKREMVIITFKSGATFQVEVPGSQHIDSQKKAIERMKDTLRITYLTETKIDKLCVWNNKTPNSIAAISMEKLYAGA

>d1tiid\_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IIB}

GASQFFKDNCNRTTASLVEGVELTKYISDINNNTDGMYVVSSTGGVWRISRAKDYPDNVMTAEMRKIAMAAVLSGMRVNMCASPASSPNVIWAIELEA

>d3chbd\_ b.40.2.1 (D:) Cholera toxin {Vibrio cholerae}

TPQNITDLCAEYHNTQIHTLNDKIFSYTESLAGKREMAIITFKNGATFQVEVPGSQHIDSQKKAIERMKDTLRIAYLTEAKVEKLCVWNNKTPRAIAAISMAN

>d1c4qa\_ b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}

TPDCVTGKVEYTKYNDDDTFTVKVGDKELATNRANLQSLLLSAQITGMTVTIKTNACHNGGGFSEVIFR

>d2bosa\_ b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}

ADCAKGKIEFSKYNEDNTFTVKVSGREYWTNRWNLQPLLQSAQLTGMTVTIISNTCSSGSGFAEVQFN

>d1prtb1 b.40.2.1 (B:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain {Bordetella pertussis}

TTRNTGQPATDHYYSNVTATRLLSSTNSRLCAVFVRSGQPVIGACTSPYDGKYWSMYSRLRKMLYLIYVAGISVRVHVSKEEQYYDYEDATFETYALTGISICNPGSSLC

>d1prtc1 b.40.2.1 (C:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain {Bordetella pertussis}

TIYKTGQPAADHYYSKVTATRLLASTNSRLCAVFVRDGQSVIGACASPYEGRYRDMYDALRRLLYMIYMSGLAVRVHVSKEEQYYDYEDATFQTYALTGISLCNPAASIC

>d1prtd\_ b.40.2.1 (D:) Pertussis toxin S4 subunit {Bordetella pertussis}

DVPYVLVKTNMVVTSVAMKPYEVTPTRMLVCGIAAKLGAAASSPDAHVPFCFGKDLKRPGSSPMEVMLRAVFMQQRPLRMFLGPKQLTFEGKPALELIRMVECSGKQDCP

>d1prtf\_ b.40.2.1 (F:) Pertussis toxin S5 subunit {Bordetella pertussis}

LPTHLYKNFTVQELALKLKGKNQEFCLTAFMSGRSLVRACLSDAGHEHDTWFDTMLGFAISAYALKSRIALTVEDSPYPGTPGDLLELQICPLNGYCE

>d1esfa1 b.40.2.2 (A:1-120) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}

SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDHSWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNRLT

>d1i4pa1 b.40.2.2 (A:1-120) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}

ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYVSATKVMSVDKFLAHDLIYNISDKKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTGGKTCMYGGITKHEG

>d3tss\_1 b.40.2.2 (5-93) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}

NIKDLLDWYSSGSDTFTNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPAFTKGEKVDLNTKRIKKSQHTSEGTWIHFQISGVTNTEK

>d1sebd1 b.40.2.2 (D:2-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKKTCMYGGVTEH

>d3seb\_1 b.40.2.2 (1-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNYDNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTEH

>d1jckb1 b.40.2.2 (B:1-121) Staphylococcal enterotoxin C3, SEC3 {Staphylococcus aureus}

ESQPDPMPDDLHKSSEFTGTMGNMKYLYDDHYVSATKVKSVDKFLAHDLIYNINDKKLNNYDKVKTELLNEDLANKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTSGKTCMYGGITKHEGN

>d1enfa1 b.40.2.2 (A:2-101) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}

DLHDKSELTDLALANAYGQYNHPFIKENIKSDEISGEKDLIFRNQGDSGNDLRVKFATADLAQKFKNKNVDIYGASFYYKCEKISENISECLYGGTTLNS

>d1an8\_1 b.40.2.2 (3-95) Streptococcal superantigen Spe-C {Streptococcus pyogenes}

KKDISNVKSDLLYAYTITPYDYKDCRVNFSTTHTLNIDTQKYRGKDYYISSEMSYEASQKFKRDDHVDVFGLFYILNSHTGEYIYGGITPAQN

>d1et9a1 b.40.2.2 (A:1-95) Streptococcal superantigen Spe-H {Streptococcus pyogenes}

NSYNTTNRHNLESLYKHDSNLIEADSIKNSPDIVTSHMLKYSVKDKNLSVFFEKDWISQEFKDKEVDIYALSAQEVCECPGKRYEAFGGITLTNS

>d1eu3a1 b.40.2.2 (A:2A-96) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}

GLEVDNNSLLRNIYSTIVYEYSDIVIDFKTSHNLVTKKLDVRDARDFFINSEMDEYAANDFKTGDKIAVFSVPFDWNYLSKGKVTAYTYGGITPYQK

>d1bxta1 b.40.2.2 (A:1-119) Streptococcal superantigen SSA {Streptococcus pyogenes}

SSQPDPTPEQLNKSSQFTGVMGNLRCLYDNHFVEGTNVRSTGQLLQHDLIFPIKDLKLKNYDSVKTEFNSKDLATKYKNKDVDIFGSNYYYNCYYSEGNSCKNAKKTCMYGGVTEHHRN

>d1fnua1 b.40.2.2 (A:1-107) Streptococcal pyrogenic exotoxin A1 {Streptococcus pyogenes}

QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSHDLIYNVSGPNYDKLKTELKNQEMATLFKDKNVDIYGVEYYHLCYLCENAERSACIYGGVTNHE

>d1d2ba\_ b.40.3.1 (A:) TIMP-1 {Human (Homo sapiens)}

CTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHNRSEEFLIAGKLQDGLLHITTCSFVAPWNSLSLAQRRGFTKTYTVGCEE

>d1ueab\_ b.40.3.1 (B:) TIMP-1 {Human (Homo sapiens)}

CTCVPPHPQTAFCNSDLVIRAKFVGTPEVAQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCGYFHRSHARSEEFLIAGKLQDGLLHITTCSFVAPWNSLSLAQRRGFTKTYTVGCEECTVFPCLSIPCKLQSGTHCLWTDQLLQGSEKGFQSRHLACLPREPGLCTWQSLRS

>d1br9\_\_ b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}

CSCSPVHPQQAFCNADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIEFIYTAPSSAVCGVSLDVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSTTQKKSLNHRYQMGCECKITRCPMIPCYISSPDECLWMDWVTEKNINGHQAKFFACIKRSDGSCAWYRGAA

>d2tmp\_\_ b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}

CSCSPVHPQQAFCNADVVIRTKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIEFIYTAPSSAVCGVSLDVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDTLSTTQKKSLNHRYQMGCE

>d1bqqt\_ b.40.3.1 (T:) TIMP-2 {Cow (Bos taurus)}

CSCSPVHPQQAFCNADIVIRAKAVNKKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPDQDIEFIYTAPAAAVCGVSLDIGGKKEYLIAGKAEGNGNMHITLCDFIVPWDTLSATQKKSLNHRYQMGCECKITRCPMIPCYISSPDECLWMDWVTEKNINGHQAKFFACIKRSDGSCAWYRGAAPP

>d1jb3a\_ b.40.3.2 (A:) The laminin-binding domain of agrin {Chicken (Gallus gallus)}

ELQRREEEANVVLTGTVEEIMNVDPVHHTYSCKVRVWRYLKGKDIVTHEILLDGGNKVVIGGFGDPLICDNQVSTGDTRIFFVNPAPQYMWPAHRNELMLNSSLMRITLRNLEEVEHCVEEHRKLLA

>d1k28a1 b.40.8.1 (A:6-129) Tail-associated lysozyme gp5, N-terminal domain {Bacteriophage T4}

NNLNWFVGVVEDRMDPLKLGRVRVRVVGLHPPQRAQGDVMGIPTEKLPWMSVIQPITSAAMSGIGGSVTGPVEGTRVYGHFLDKWKTNGIVLGTYGGIVREKPNRLEGFSDPTGQYPRRLGNDT

>d1eova1 b.40.4.1 (A:71-204) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}

AKDNYGKLPLIQSRDSDRTGQKRVKFVDLDEAKDSDKEVLFRARVHNTRQQGATLAFLTLRQQASLIQGLVKANKEGTISKNMVKWAGSLNLESIVLVRGIVKKVDEPIKSATVQNLEIHITKIYTISETPEAL

>d1b8aa1 b.40.4.1 (A:1-103) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus kodakaraensis}

MYRTHYSSEITEELNGQKVKVAGWVWEVKDLGGIKFLWIRDRDGIVQITAPKKKVDPELFKLIPKLRSEDVVAVEGVVNFTPKAKLGFEILPEKIVVLNRAET

>d1c0aa1 b.40.4.1 (A:1-106) Aspartyl-tRNA synthetase (AspRS) {Escherichia coli}

MRTEYCGQLRLSHVGQQVTLCGWVNRRRDLGSLIFIDMRDREGIVQVFFDPDRADALKLASELRNEFCIQVTGTVRARDEKNINRDMATGEIEVLASSLTIINRAD

>d1g51a1 b.40.4.1 (A:1-104) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}

MRRTHYAGSLRETHVGEEVVLEGWVNRRRDLGGLIFLDLRDREGLVQLVAHPASPAYATAERVRPEWVVRAKGLVRLRPEPNPRLATGRVEVELSALEVLAEAK

>d1bbua1 b.40.4.1 (A:11-154) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}

VVDLNNELKTRREKLANLREQGIAFPNDFRRDHTSDQLHAEFDGKENEELEALNIEVAVAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDLPEGVYNEQFKKWDLGDILGAKGKLFKTKTGELSIHCTELRLLTKALRPLPD

>d1krs\_\_ b.40.4.1 (-) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}

FRRDHTSDQLHAEFDGKENEELEALNIEVAVAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDLPEGVYNEQFKKWDLGDILGAKGKLFKTKTGELSIHCTELRLLTKA

>d1e1oa1 b.40.4.1 (A:11-153) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysU}

AIDFNDELRNRREKLAALRQQGVAFPNDFRRDHTSDQLHEEFDAKDNQELESLNIEVSVAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDSLPEGVYNDQFKKWDLGDIIGARGTLFKTQTGELSIHCTELRLLTKALRPLP

>d1gm5a2 b.40.4.9 (A:106-285) RecG "wedge" domain {Thermotoga maritima}

CSGEEVDLSTDIQYAKGVGPNRKKKLKKLGIETLRDLLEFFPRDYEDRRKIFKLNDLLPGEKVTTQGKIVSVETKKFQNMNILTAVLSDGLVHVPLKWFNQDYLQTYLKQLTGKEVFVTGTVKSNAYTGQYEIHNAEVTPKEGEYVRRILPIYRLTSGISQKQMRKIFEENIPSLCCSLK

>d1cuk\_3 b.40.4.2 (1-64) DNA helicase RuvA subunit, N-terminal domain {Escherichia coli}

MIGRLRGIIIEKQPPLVLIEVGGVGYEVHMPMTCFYELPEAGQEAIVFTHFVVREDAQLLYGFN

>d1bvsa3 b.40.4.2 (A:1-63) DNA helicase RuvA subunit, N-terminal domain {Mycobacterium leprae}

MIFSVRGEVLEVALDHAVIEAAGIGYRVNATPSALATLNQGSQARLVTAMVVREDSMTLYGFS

>d3ulla\_ b.40.4.3 (A:) ssDNA-binding protein {Human (Homo sapiens), mitochondria}

LERSLNRVHLLGRVGQDPVLRQVEGKNPVTIFSLATNEMWRSGDSEVYQLGDVSQKTTWHRISVFRPGLRDVAYQYVKKGSRIYLEGKIDYGEYMDKNNVRRQATTIIADNIIFL

>d1kawa\_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}

RGVNKVILVGNLGQDPEVRYMPNGGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAEVASEYLRKGSQVYIEGQLRTRKWTDQSGQDRYTTEVVVNVGGTMQML

>d1qvca\_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}

ASRGVNKVILVGNLGQDPEVRYMPNGGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAEVASEYLRKGSQVYIEGQLRTRKWTDQSGQDRYTTEVVVNVGGTMQMLGGRQGGGAPAGGNIGGGQPQGGWGQPQQPQGGN

>d1ewia\_ b.40.4.3 (A:) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

MVGQLSEGAIAAIMQKGDTNIKPILQVINIRPITTGNSPPRYRLLMSDGLNTLSSFMLATQLNPLVEEEQLSSNCVCQIHRFIVNTLKDGRRVVILMELEVLKSAEAVGVKIGN

>d1fgua1 b.40.4.3 (A:181-298) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

MSKVVPIASLTPYQSKWTICARVTNKSQIRTWSNSRGEGKLFSLELVDESGEIRATAFNEQVDKFFPLIEVNKVYYFSKGTLKIANKQFTAVKNDYEMTFNNETSVMPCEDDHHLPTV

>d1fgua2 b.40.4.3 (A:299-426) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

QFDFTGIDDLENKSKDSLVDIIGICKSYEDATKITVRSNNREVAKRNIYLMDTSGKVVTATLWGEDADKFDGSRQPVLAIKGARVSDFGGRSLSVLSSSTIIANPDIPEAYKLRGWFDAEGQALDGVS

>d1quqa\_ b.40.4.3 (A:) Replication protein A 32 KDa subunit (RPA32) fragment {Human (Homo sapiens)}

HIVPCTISQLLSATLVDEVFRIGNVEISQVTIVGIIRHAEKAPTNIVYKIDDMTAAPMDVRQWVDTDDTSSENTVVPPETYVKVAGHLRSFQNKKSLVAFKIMPLEDMNEFTTHILEVINAHMVLSK

>d1quqb\_ b.40.4.3 (B:) Replication protein A 14 KDa (RPA14) subunit {Human (Homo sapiens)}

DMMDLPRSRINAGMLAQFIDKPVCFVGRLEKIHPTGKMFILSDGEGKNGTIELMEPLDEEISGIVEVVGRVTAKATILCTSYVQFKEDSHPFDLGLYNEAVKIIHDFPQFYPLG

>d1jb7a1 b.40.4.3 (A:36-204) Telomere end binding protein alpha subunit {Oxytricha nova}

YEYVELAKASLTSAQPQHFYAVVIDATFPYKTNQERYICSLKIVDPTLYLKQQKGAGDASDYATLVLYAKRFEDLPIIHRAGDIIRVHRATLRLYNGQRQFNANVFYSSSWALFSTDKRSVTQEINNQDAVSDTTPFSFSSKHATIEKNEISILQNLRKWANQYFSSYS

>d1jb7a2 b.40.4.3 (A:205-328) Telomere end binding protein alpha subunit {Oxytricha nova}

VISSDMYTALNKAQAQKGDFDVVAKILQVHELDEYTNELKLKDASGQVFYTLSLKLKFPHVRTGEVVRIRSATYDETSTQKKVLILSHYSNIITFIQSSKLAKELRAKIQDDHSVEVASLKKNV

>d1jb7a3 b.40.4.3 (A:329-495) Telomere end binding protein alpha subunit {Oxytricha nova}

SLNAVVLTEVDKKHAALPSTSLQDLFHHADSDKELQAQDTFRTQFYVTKIEPSDVKEWVKGYDRKTKKSSSLKGASGKGDNIFQVQFLVKDASTQLNNNTYRVLLYTQDGLGANFFNVKADNLHKNADARKKLEDSAELLTKFNSYVDAVVERRNGFYLIKDTKLIY

>d1k8ga2 b.40.4.3 (A:205-315) Telomere end binding protein alpha subunit {Oxytricha nova}

VISSDMYTALNKAQAQKGDFDVVAKILQVHELDEYTNELKLKDASGQVFYTLSLKLKFPHVRTGEVVRIRSATYDETSTQKKVLILSHYSNIITFIQSSKLAKELRAKIQD

>d1jb7b\_ b.40.4.3 (B:) Core domain of telomere end binding protein beta subunit {Oxytricha nova}

QQQSAFKQLYTELFNNEGDFSKVSSNLKKPLKCYVKESYPHFLVTDGYFFVAPYFTKEAVNEFHAKFPNVNIVDLTDKVIVINNWSLELRRVNSAEVFTSYANLEARLIVHSFKPNLQERLNPTRYPVNLFRDDEFKTTIQHFRHTALQAAINKTVKGDNLVDISKVADAAGKKGKVDAGIVKASASKGDEFSDFSFKEGNTATLKIADIFVQEKG

>d1jjcb3 b.40.4.4 (B:39-151) Domain B2 of PheRS-beta, PheT {Thermus thermophilus (Thermus aquaticus)}

FPIPRGVVFARVLEAHPIPGTRLKRLVLDAGRTVEVVSGAENARKGIGVALALPGTELPGLGQKVGERVIQGVRSFGMALSPRELGVGEYGGGLLEFPEDALPPGTPLSEAWP

>d1fl0a\_ b.40.4.4 (A:) EMAP II {Human (Homo sapiens)}

IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQNRMVILLCNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIKL

>d1gd7a\_ b.40.4.4 (A:) CsaA {Thermus thermophilus}

MTPLEAFQILDLRVGRVLRAEPHEKARKPSYKLWVDLGPLGVKQSSAQITELYRPEDLVGRLVVCAVNLGAKRVAGFLSEVLVLGVPDEAGRVVLLAPDREVPLGGKVF

>d1mjc\_\_ b.40.4.5 (-) Major cold shock protein {Escherichia coli}

SGKMTGIVKWFNADKGFGFITPDDGSKDVFVHFSAIQNDGYKSLDEGQKVSFTIESGAKGPAAGNVTSL

>d1csp\_\_ b.40.4.5 (-) Major cold shock protein {Bacillus subtilis}

MLEGKVKWFNSEKGFGFIEVEGQDDVFVHFSAIQGEGFKTLEEGQAVSFEIVEGNRGPQAANVTKEA

>d1c9oa\_ b.40.4.5 (A:) Major cold shock protein {Bacillus caldolyticus}

MQRGKVKWFNNEKGYGFIEVEGGSDVFVHFTAIQGEGFKTLEEGQEVSFEIVQGNRGPQAANVVKL

>d1g6pa\_ b.40.4.5 (A:) Major cold shock protein {Thermotoga maritima}

MRGKVKWFDSKKGYGFITKDEGGDVFVHWSAIEMEGFKTLKEGQVVEFEIQEGKKGPQAAHVKVVE

>d1h95a\_ b.40.4.5 (A:) Y-box protein 1 cold shock domain (YB1-CSD) {Human (Homo sapiens)}

MKKVIATKVLGTVKWFNVRNGYGFINRNDTKEDVFVHQTAIKKNNPRKYLRSVGDGETVEFDVVEGEKGAEAANVTGPG

>d1sro\_\_ b.40.4.5 (-) S1 RNA-binding domain of polyribonucleotide phosphorylase, PNPase {Escherichia coli}

AEIEVGRVYTGKVTRIVDFGAFVAIGGGKEGLVHISQIADKRVEKVTDYLQMGQEVPVKVLEVDRQGRIRLSIKEA

>d1e3pa2 b.40.4.5 (A:656-717) S1 RNA-binding domain of polyribonucleotide phosphorylase, PNPase {Streptomyces antibioticus}

GSVVKTTTFGAFVSLLPGKDGLLHISQIRKLAGGKRVENVEDVLGVGQKVQVEIAEIDSRGK

>d1hh2p1 b.40.4.5 (P:127-198) S1 domain of NusA {Thermotoga maritima}

FEKYSELKGTVTTAEVIRVMGEWADIRIGKLETRLPKKEWIPGEEIKAGDLVKVYIIDVVKTTKGPKILVSR

>d1k0ra1 b.40.4.5 (A:108-183) S1 domain of NusA {Mycobacterium tuberculosis}

STREGEIVAGVIQRDSRANARGLVVVRIGTETKASEGVIPAAEQVPGESYEHGNRLRCYVVGVTRGAREPLITLSR

>d1go3e\_ b.40.4.5 (E:) RNA polymerase II subunit RBP4 (RpoE) {Archaeon Methanococcus jannaschii}

MYKILEIADVVKVPPEEFGKDLKETVKKILMEKYEGRLDKDVGFVLSIVDVKDIGEGKVVHGDGSAYHPVVFETLVYIPEMYELIEGEVVDVVEFGSFVRLGPLDGLIHVSQIMDDYVSYDPKREAIIGKETGKVLEIGDYVRARIVAISLKAERKRGSKIALTMRQPYLGKLEWIEEEKAKKQ

>d1ah9\_\_ b.40.4.5 (-) Translational initiation factor 1, IF1 {Escherichia coli}

AKEDNIEMQGTVLETLPNTMFRVELENGHVVTAHISGKMRKNYIRILTGDKVTVELTPYDLSKGRIVFRSR

>d1hr0w\_ b.40.4.5 (W:) Translational initiation factor 1, IF1 {Escherichia coli}

AKEKDTIRTEGVVTEALPNATFRVKLDSGPEILAYISGKMRMHYIRILPGDRVVVEITPYDPTRGRIVYRK

>d1jt8a\_ b.40.4.5 (A:) Archaeal initiation factor-1a, aIF1a {Archaeon Methanococcus jannaschii}

MAEQQQEQQIRVRIPRKEENEILGIIEQMLGASRVRVRCLDGKTRLGRIPGRLKNRIWVREGDVVIVKPWEVQGDQKCDIIWRYTKTQVEWLKRKGYLDELL

>d1d7qa\_ b.40.4.5 (A:) Translation initiation factor-1a, eIF1a {Human (Homo sapiens)}

PKNKGKGGKNRRRGKNENESEKRELVFKEDGQEYAQVIKMLGNGRLEAMCFDGVKRLCHIRGKLRKKVWINTSDIILVGLRDYQDNKADVILKYNADEARSLKAYGELPEHAKINETDTFGPGDDDEIQFDDIGDDDEDIDDI

>d1a62\_2 b.40.4.5 (48-125) Rho termination factor, RNA-binding domain {Escherichia coli}

DIFGDGVLEILQDGFGFLRSADSSYLAGPDDIYVSPSQIRRFNLRTGDTISGKIRPPKEGERYFALLKVNEVNFDKPE

>d2eifa2 b.40.4.5 (A:74-132) C-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Methanococcus jannaschii}

IDRRKGQVLAIMGDMVQIMDLQTYETLELPIPEGIEGLEPGGEVEYIEAVGQYKITRVI

>d1bkb\_2 b.40.4.5 (75-139) C-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Pyrobaculum aerophilum}

IIEKFTAQILSVSGDVIQLMDMRDYKTIEVPMKYVEEEAKGRLAPGAEVEVWQILDRYKIIRVKG

>d1rl2a2 b.40.4.5 (A:60-125) N-terminal domain of ribosomal protein L2 {Bacillus stearothermophilus}

QYRIIDFKRDKDGIPGRVATIEYDPNRSANIALINYADGEKRYIIAPKNLKVGMEIMSGPDADIKI

>d1jj2a2 b.40.4.5 (A:1-90) N-terminal domain of ribosomal protein L2 {Archaeon Haloarcula marismortui}

GRRIQGQRRGRGTSTFRAPSHRYKADLEHRKVEDGDVIAGTVVDIEHDPARSAPVAAVEFEDGDRRLILAPEGVGVGDELQVGVDAEIAP

>d1fjgl\_ b.40.4.5 (L:) Ribosomal protein S12 {Thermus thermophilus}

PTINQLVRKGREKVRKKSKVPALKGAPFRRGVCTVVRTVTPKKPNSALRKVAKVRLTSGYEVTAYIPGEGHNLQEHSVVLIRGGRVKDLPGVRYHIVRGVYDAAGVKDRKKSRSKYGTKKPKEAA

>d1fjgq\_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}

PKKVLTGVVVSDKMQKTVTVLVERQFPHPLYGKVIKRSKKYLAHDPEEKYKLGDVVEIIESRPISKRKRFRVLRLVESGRMDLVEKYLIRRQNYQSLSKRGGKA

>d1i94q\_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}

PKKVLTGVVVSDKMQKTVTVLVERQFPHPLYGKVIKRSKKYLAHDPEERYKVGDVVEIIEARPISKRKRFRVLRLVEEGRLDLVEKYLVRRQNYASLSKRGGKA

>d1rip\_\_ b.40.4.5 (-) Ribosomal protein S17 {Bacillus stearothermophilus}

QRKVYVGRVVSDKMDKTITVLVETYKKHPLYGKRVKYSKKYKAHDEHNEAKVGDIVKIMETRPLSATKRFRLVEIVEKAVR

>d1ckma1 b.40.4.6 (A:239-327) RNA guanylyltransferase (mRNA capping enzyme) {Chlorella virus, PBCV-1}

THHTIDFIIMSEDGTIGIFDPNLRKNVPVGKLDGYYNKGSIVECGFADGTWKYIQGRSDKNQANDRLTYEKTLLNIEENITIDELLDLF

>d1a0i\_1 b.40.4.6 (241-349) ATP-dependent DNA ligase {Bacteriophage T7}

PENEADGIIQGLVWGTKGLANEGKVIGFEVLLESGRLVNATNISRALMDEFTETVKEATLSQWGFFSPYGIGDNDACTINPYDGWACQISYMEETPDGSLRHPSFVMFR

>d1fvia1 b.40.4.6 (A:190-293) ATP-dependent DNA ligase {Chlorella virus, PBCV-1}

FKDAEATIISMTALFKNTNTKTKDNFGYSKRSTHKSGKVEEDVMGSIEVDYDGVVFSIGTGFDADQRRDFWQNKESYIGKMVKFKYFEMGSKDCPRFPVFIGIR

>d1dgsa2 b.40.4.6 (A:315-400) NAD+-dependent DNA ligase {Thermus filiformis}

AEEKETRLLDVVFQVGRTGRVTPVGVLEPVFIEGSEVSRVTLHNESYIEELDIRIGDWVLVHKAGGVIPEVLRVLKERRTGKERPI

>d1gvp\_\_ b.40.4.7 (-) Gene V protein {Filamentous bacteriophage (f1, M13)}

MIKVEIKPSQAQFTTRSGVSRQGKPYSLNEQLCYVDLGNEYPVLVKITLDEGQPAYAPGLYTVHLSSFKVGQFGSLMIDRLRLVPAK

>d1pfsa\_ b.40.4.7 (A:) Gene V protein {Pseudomonas bacteriophage pf3}

MNIQITFTDSVRQGTSAKGNPYTFQEGFLHLEDKPHPLQCQFFVESVIPAGSYQVPYRINVNNGRPELAFDFKAMKRA

>d1gpc\_\_ b.40.4.7 (-) Gene 32 protein (gp32) core {Bacteriophage T4}

GFSSEDKGEWKLKLDNAGNGQAVIRFLPSKNDEQAPFAILVNHGFKKNGKWYIETCSSTHGDYDSCPVCQYISKNDLYNTDNKEYSLVKRKTSYWANILVVKDPAAPENEGKVFKYRFGKKIWDKINAMIAVDVEMGETPVDVTCPWEGANFVLKVKQVSGFSNYDESKFLNQSAIPNIDDESFQKELFEQMVDLSEMTSKDKFKSFEELNTKFGQVM

>d1je5a\_ b.40.4.7 (A:) gp2.5 {Bacteriophage T7}

MAKKIFTSALGTAEPYAYIAKPDYGNEERGFGNPRGVYKVDLTIPNKDPRCQRMVDEIVKCHEEAYAAAVEEYEANPPAVARGKKPLKPYEGDMPFFDNGDGTTTFKFKCYASFQDKKTKETKHINLVVVDSKGKKMEDVPIIGGGSKLKVKYSLVPYKWNTAVGASVKLQLESVMLVELATFGGGEDDWADEVEEN

>d1i50h\_ b.40.4.8 (H:) RNA polymerase subunit RBP8 {Baker's yeast (Saccharomyces cerevisiae)}

SNTLFDDIFQVSEVDPGRYNKVCRIEAASTTQDQCKLTLDINVELFPVAAQDSLTVTIASSLNLEDTPANDSSATRSWRPPQAGDRSLADDYDYVMYGTAYKFEEVSKDLIAVYYSFGGLLMRLEGNYRNLNNLKQENAYLLIRR

>d1e9ga\_ b.40.5.1 (A:) Inorganic pyrophosphatase {Baker's yeast (Saccharomyces cerevisiae)}

TYTTRQIGAKNTLEYKVYIEKDGKPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEITKEETLNPIIQDTKKGKLRFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPIDVLEIGETIAYTGQVKQVKALGIMALLDEGETDWKVIAIDINDPLAPKLNDIEDVEKYFPGLLRATNEWFRIYKIPDGKPENQFAFSGEAKNKKYALDIIKETHDSWKQLIAGKSSDSKGIDLTNVTLPDTPTYSKAASDAIPPASLKADAPIDKSIDKWFFISG

>d1qeza\_ b.40.5.1 (A:) Inorganic pyrophosphatase {Archaeon Sulfolobus acidocaldarius}

KLSPGKNAPDVVNVLVEIPQGSNIKYEYDDEEGVIKVDRVLYTSMNYPFNYGFIPGTLEEDGDPLDVLVITNYQLYPGSVIEVRPIGILYMKDEEGEDAKIVAVPKDKTDPSFSNIKDINDLPQATKNKIVHFFEHYKELEPGKYVKISGWGSATEAKNRIQLAIKRVSG

>d1i40a\_ b.40.5.1 (A:) Inorganic pyrophosphatase {Escherichia coli}

SLLNVPAGKDLPEDIYVVIEIPANADPIKYEIDKESGALFVDRFMSTAMFYPCNYGYINHTLSLDGDPVDVLVPTPYPLQPGSVTRCRPVGVLKMTDEAGEDAKLVAVPHSKLSKEYDHIKDVNDLPELLKAQIAHFFEHYKDLEKGKWVKVEGWENAEAAKAEIVASFERAKNK

>d2prd\_\_ b.40.5.1 (-) Inorganic pyrophosphatase {Thermus thermophilus}

ANLKSLPVGDKAPEVVHMVIEVPRGSGNKYEYDPDLGAIKLDRVLPGAQFYPGDYGFIPSTLAEDGDPLDGLVLSTYPLLPGVVVEVRVVGLLLMEDEKGGDAKVIGVVAEDQRLDHIQDIGDVPEGVKQEIQHFFETYKALEAKKGKWVKVTGWRDRKAALEEVRACIARYKG

>d1fr3a\_ b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {Sporomusa ovata}

MKISGRNKLEATVKEIVKGTVMAKIVMDYKGTELVAAITIDSVADLDLVPGDKVTALVKATEMEVLK

>d1guta\_ b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {Clostridium pasteurianum, MOP II}

SISARNQLKGKVVGLKKGVVTAEVVLEIAGGNKITSIISLDSVEELGVKEGAELTAVVKSTDVMILA

>d1h9ma1 b.40.6.2 (A:1-73) Cytoplasmic molybdate-binding protein ModG {Azotobacter vinelandii}

MKISARNVFKGTVSALKEGAVNAEVDILLGGGDKLAAVVTLESARSLQLAAGKEVVAVVKAPWVLLMTDSSGY

>d1h9ma2 b.40.6.2 (A:74-141) Cytoplasmic molybdate-binding protein ModG {Azotobacter vinelandii}

RLSARNILTGTVKTIETGAVNAEVTLALQGGTEITSMVTKEAVAELGLKPGASASAVIKASNVILGVP

>d1h9ra1 b.40.6.2 (A:123-199) C-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}

MQTSARNQWFGTITARDHDDVQQHVDVLLADGKTRLKVAITAQSGARLGLDEGKEVLILLKAPWVGITQDEAVAQNA

>d1h9ra2 b.40.6.2 (A:200-261) C-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}

DNQLPGIISHIERGAEQCEVLMALPDGQTLCATVPVNEATSLQQGQNVTAYFNADSVIIATL

>d1g2913 b.40.6.3 (1:241-301) Maltose transport protein MalK, C-terminal domain {Archaeon Thermococcus litoralis}

GSPPMNFLDAIVTEDGFVDFGEFRLKLLPDQFEVLGELGYVGREVIFGIRPEDLYDAMFAQ

>d1g2914 b.40.6.3 (1:302-372) Maltose transport protein MalK, C-terminal domain {Archaeon Thermococcus litoralis}

VRVPGENLVRAVVEIVENLGSERIVRLRVGGVTFVGSFRSESRVREGVEVDVVFDMKKIHIFDKTTGKAIF

>d1b3qa2 b.40.7.1 (A:540-671) Histidine kinase CheA, C-terminal domain {Thermotoga maritima}

TLAIICALLVKVNNLVYAIPIANIDTILSISKEDIQRVQDRDVIVIRGEVIPVYRLWEVLQIEHKEELEEMEAVIVRVGNRKYGIVVDDLLGQDDIVIKSLGKVFSEVKEFSGAAILGDGSIALIINVSGIV

>d1k0sa\_ b.40.7.1 (A:) Chemotaxis protein CheW {Thermotoga maritima}

MKTLADALKEFEVLSFEIDEQALAFDVDNIEMVIEKSDITPVPKSRHFVEGVINLRGRIIPVVNLAKILGISFDEQKMKSIIVARTKDVEVGFLVDRVLGVLRITENQLDLTNVSDKFGKKSKGLVKTDGRLIIYLDIDKIIEEITVKEGV

>d1dxrh1 b.41.1.1 (H:37-258) Photosynthetic reaction centre {Rhodopseudomonas viridis}

RREGYPLVEPLGLVKLAPEDGQVYELPYPKTFVLPHGGTVTVPRRRPETRELKLAQTDGFEGAPLQPTGNPLVDAVGPASYAERAEVVDATVDGKAKIVPLRVATDFSIAEGDVDPRGLPVVAADGVEAGTVTDLWVDRSEHYFRYLELSVAGSARTALIPLGFCDVKKDKIVVTSILSEQFANVPRLQSRDQITLREEDKVSAYYAGGLLYATPERAESLL

>d1qovh1 b.41.1.1 (H:36-250) Photosynthetic reaction centre {Rhodobacter sphaeroides}

MREGYPLENEDGTPAANQGPFPLPKPKTFILPHGRGTLTVPGPESEDRPIALARTAVSEGFPHAPTGDPMKDGVGPASWVARRDLPELDGHGHNKIKPMKAAAGFHVSAGKNPIGLPVRGCDLEIAGKVVDIWVDIPEQMARFLEVELKDGSTRLLPMQMVKVQSNRVHVNALSSDLFAGIPTIKSPTEVTLLEEDKICGYVAGGLMYAAPKRKS

>d1eysh1 b.41.1.1 (H:59-259) Photosynthetic reaction centre {Thermochromatium tepidum}

PDLPDPKTFVLPHNGGTVVAPRVEAPVAVNATPFSPAPGSPLVPNGDPMLSGFGPAASPDRPKHCDLTFEGLPKIVPMRVAKEFSIAEGDPDPRGMTVVGLDGEVAGTVSDVWVDRSEPQIRYLEVEVAANKKKVLLPIGFSRFDKKARKVKVDAIKAAHFANVPTLSNPDQVTLYEEDKVCAYYAGGKLYATAERAGPLL

>d1bfg\_\_ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}

DPKRLYCKNGGFFLRIHPDGRVDGVREKSDPHIKLQLQAEERGVVSIKGVSANRYLAMKEDGRLLASKSVTDECFFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPGQKAILFLPMSA

>d1bla\_\_ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}

MAEGEITTLPALPEDGGSGAFPPGHFKDPKRLYCKNGGFFLRIHPDGRVDGVREKSDPHIKLQLQAEERGVVSIKGVSANRYLAMKEDGRLLASKSVTDECFFFERLESNNYNTYRSRKYTSWYVALKRTGQYKLGSKTGPGQKAILFLPMSAKS

>d1bara\_ b.42.1.1 (A:) Acidic FGF (FGF1) {Cow (Bos taurus)}

PKLLYCSNGGYFLRILPDGTVDGTKDRSDQHIQLQLAAESIGEVYIKSTETGQFLAMDTDGLLYGSQTPNEECLFLERLEENGYNTYISKKHAEKHWFVGLKKNGRSKLGPRTHFGQKAILFLPLPV

>d1jqza\_ b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}

HHHHFNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTETGQYLAMDTDGLLYGSQTPNEECLFLERLEENHYNTYISKKHAEKNWFVGLKKNGSCKRGPRTHYGQKAILFLPLPV

>d2afga\_ b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}

KPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHIQLQLSAESVGEVYIKSTETGQYLAMDTDGLLYGSQTPNEECLFLERLEENHYNTYISKKHAEKNWFVGLKKNGSCKRGPRTHYGQKAILFLPLPVS

>d1fmms\_ b.42.1.1 (S:) Acidic FGF (FGF1) {Eastern newt (Notophthalmus viridescens)}

QKPKLLYCSNGGYFLRIFPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSLETGQYLAMDSDGQLYASQSPSEECLFLERLEENNYNTYKSKVHADKDWFVGIKKNGKTKPGSRTHFGQKAILFLPLPVSSD

>d1ijta\_ b.42.1.1 (A:) Fibroblast growth factor 4 (FGF4) {Human (Homo sapiens)}

GIKRLRRLYCNVGIGFHLQALPDGRIGGAHADTRDSLLELSPVERGVVSIFGVASRFFVAMSSKGKLYGSPFFTDECTFKEILLPNNYNAYESYKYPGMFIALGKNGKTKKGNRVSPTMKVTHFLPRL

>d1qqka\_ b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus norvegicus)}

DIRVRRLFCRTQWYLRIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIKGVESEYYLAMNKEGKLYAKKECNEDCNFKELILENHYNTYASAKWTHSGGEMFVALNQKGLPVKGKKTKKEQKTAHFLPMAIT

>d1qqla\_ b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus norvegicus)}

DIRVRRLFCRTQWYLRIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIKGVESEYYLAMNKEGKLYAKQTPNEECLFLERLEENHYNTYISKKHAEKNWFVGLKKNGSCKRGPRTHYGQKAILFLPLPVSS

>d1ihka\_ b.42.1.1 (A:) Fibroblast growth factor 9, FGF9 {Human (Homo sapiens)}

TDLDHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLYLGMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGTRTKRHQKFTHFLPRPVDPDKVPELYKDILSQS

>d1i1b\_\_ b.42.1.2 (-) Interleukin-1beta {Human (Homo sapiens)}

VRSLNCTLRDSQQKSLVMSGPYELKALHLQGQDMEQQVVFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDFTMQFVSS

>d8i1b\_\_ b.42.1.2 (-) Interleukin-1beta {Mouse (Mus musculus)}

QLHYRLRDEQQKSLVLSDPYELKALHLNGQNINQQVIFSMSFVQGEPSNDKIPVALGLKGKNLYLSCVMKDGTPTLQLESVDPKQYPKKKMEKRFVFNKIEVKSKVEFESAEFPNWYISTSQAEHKPVFLGNNSGQDIIDFTMESV

>d1ilr1\_ b.42.1.2 (1:) Interleukin-1 receptor antagonist protein {Human (Homo sapiens)}

SKMQAFRIWDVNQKTFYLRNNQLVAGYLQGPNVNLEEKIDVVPIEPHALFLGIHGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEADQPVSLTNMPDEGVMVTKFYFQEDE

>d2ila\_\_ b.42.1.2 (-) Interleukin-1alpha {Human (Homo sapiens)}

NVKYNFMRIIKYEFILNDALNQSIIRANAQYLTAAALHNLDEAVKFDMGAYKSSKDDAKITVILRISKTQLYVTAQDEDQPVLLKEMPEIPKTITGSETNLLFFWETHGTKNYFTSVAHPNLFIATKQDYWVCLAGGPPSITDFQILE

>d2aaib1 b.42.2.1 (B:1-135) Plant cytotoxin B-chain (lectin) {Castor bean (Ricinus communis), Ricin}

ADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTVQTNIYAVSQGWLPTN

>d2aaib2 b.42.2.1 (B:136-262) Plant cytotoxin B-chain (lectin) {Castor bean (Ricinus communis), Ricin}

NTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF

>d1abrb1 b.42.2.1 (B:1-140) Plant cytotoxin B-chain (lectin) {Abrus precatorius}

IVEKSKICSSRYEPTVRIGGRDGMCVDVYDNGYHNGNRIIMWKCKDRLEENQLWTLKSDKTIRSNGKCLTTYGYAPGSYVMIYDCTSAVAEATYWEIWDNGTIINPKSALVLSAESSSMGGTLTVQTNEYLMRQGWRTGN

>d1abrb2 b.42.2.1 (B:141-267) Plant cytotoxin B-chain (lectin) {Abrus precatorius}

NTSPFVTSISGYSDLCMQAQGSNVWMADCDSNKKEQQWALYTDGSIRSVQNTNNCLTSKDHKQGSTILLMGCSNGWASQRWVFKNDGSIYSLYDDMVMDVKGSDPSLKQIILWPYTGKPNQIWLTLF

>d1ce7b1 b.42.2.1 (B:1-133) Plant cytotoxin B-chain (lectin) {European mistletoe (Viscum album)}

CSASEPTVRIVGRNGMNVDVRDDDFHDGNQIQLWPSKSNNDPNQLWTIKRDGTIRSNGSCLTTYGYTAGVYVMIFDCATAVGEATVWQIWGNGTIINPRSNLVLAASSGIKGTTLTVQTLDYTLGQGWLAGND

>d1ce7b2 b.42.2.1 (B:134-255) Plant cytotoxin B-chain (lectin) {European mistletoe (Viscum album)}

TAPREVTIYGFNDLCMESGGGSVTVETCSSGKADKWALYGDGSIRPEQNQAQCLTSGGDSVAGVNIVSCSGAASGQRWVFTNEGAILNLKNGLAMDVANPGGGRIIIYPATGKPNQMWLPVF

>d1hwmb1 b.42.2.1 (B:3-135) Plant cytotoxin B-chain (lectin) {Sambucus ebulus, ebulin}

ETCAIPAPFTRRIVGRDGLCVDVRNGYDTDGTPIQLWPCGTQRNQQWTFYNDKTIRSMGKCMTANGLNSGSYIMITDCSTAAEDATKWEVLIDGSIINPSSGLVMTAPSGASRTTLLLENNIHAASQGWTVSN

>d1hwmb2 b.42.2.1 (B:136-266) Plant cytotoxin B-chain (lectin) {Sambucus ebulus, ebulin}

DVQPIATLIVGYNEMCLQANGENNNVWMEDCDVTSVQQQWALFDDRTIRVNNSRGLCVTSNGYVSKDLIVIRKCQGLATQRWFFNSDGSVVNLKSTRVMDVKESDVSLQEVIIFPATGNPNQQWRTQVPQI

>d1xyfa1 b.42.2.1 (A:313-436) Endo-1,4-beta-xylanase C-terminal domain {Streptomyces olivaceoviridis}

GQIKGVGSGRCLDVPNASTTDGTQVQLYDCHSATNQQWTYTDAGELRVYGDKCLDAAGTGNGTKVQIYSCWGGDNQKWRLNSDGSIVGVQSGLCLDAVGGGTANGTLIQLYSCSNGSNQRWTRT

>d1dqga\_ b.42.2.2 (A:) Mannose receptor {Mouse (Mus musculus)}

DARQFLIYNEDHKRCVDALSAISVQTATCNPEAESQKFRWVSDSQIMSVAFKLCLGVPSKTDWASVTLYACDSKSEYQKWECKNDTLFGIKGTELYFNYGNRQEKNIKLYKGSGLWSRWKVYGTTDDLCSRGYE

>d1jlxa1 b.42.3.1 (A:1-153) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}

AGLPVIMCLKSNNHQKYLRYQSDNIQQYGLLQFSADKILDPLAQFEVEPSKTYDGLVHIKSRYTNKYLVRWSPNHYWITASANEPDENKSNWACTLFKPLYVEEGNMKKVRLLHVQLGHYTQNYTVGGSFVSYLFAESSQIDTGSKDVFHVID

>d1jlxa2 b.42.3.1 (A:154-299) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}

WKSIFQFPKGYVTFKGNNGKYLGVITINQLPCLQFGYDNLNDPKVAHQMFVTSNGTICIKSNYMNKFWRLSTDDWILVDGNDPRETNEAAALFRSDVHDFNVISLLNMQKTWFIKRFTSGKPGFINCMNAATQNVDETAILEIIEL

>d1wba\_\_ b.42.4.1 (-) Winged bean albumin 1 {Goa bean (Psophocarpus tetragonolobus)}

DDPVYDAEGNKLVNRGKYTIVSFSDGAGIDVVATGNENPEDPLSIVKSTRNIMYATSISSEDKTPPQPRNILENMRLKINFATDPHKGDVWSVVDFQPDGQQLKLAGRYPNQVKGAFTIQKGSNTPRTYKLLFCPVGSPCKNIGISTDPEGKKRLVVSYQSDPLVVKFHRH

>d1tie\_\_ b.42.4.1 (-) Erythrina cafra trypsin inhibitor {Erythrina caffra}

VLLDGNGEVVQNGGTYYLLPQVWAQGGGVQLAKTGEETCPLTVVQSPNELSDGKPIRIESRLRSAFIPDDDKVRIGFAYAPKCAPSPWWTVVEDEQEGLSVKLSEDESTQFDYPFKFEQVSDQLHSYKLLYCEGKHEKCASIGINRDQKGYRRLVVTEDYPLTVVLKKDE

>d1eyla\_ b.42.4.1 (A:) chymotrypsin inhibitor WCI {Winged bean (Psophocarpus tetragonolobus)}

EFDDDLVDAEGNLVENGGTYYLLPHIWAHGGGIETAKTGNEPCPLTVVRSPNEVSKGEPIRISSQFLSLFIPRGSLVALGFANPPSCAASPWWTVVDSPQGPAVKLSQQKLPEKDILVFKFEKVSHSNIHVYKLLYCQHDEEDVKCDQYIGIHRDRNGNRRLVVTEENPLELVLLKAKS

>d1avwb\_ b.42.4.1 (B:) Soybean trypsin inhibitor {Soybean (Glycine max)}

DFVLDNEGNPLENGGTYYILSDITAFGGIRAAPTGNERCPLTVVQSRNELDKGIGTIISSPYRIRFIAEGHPLSLKFDSFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAMDGWFRLERVSEFNNYKLVFCPQDKCGDIGISIDHDDGTRRLVVSKNKPLVVQFQKLD

>d1avac\_ b.42.4.1 (C:) Amylase/subtilisin inhibitor {Barley (Hordeum vulgare), seed}

ADPPPVHDTDGHELRADANYYVLSANRAHGGGLTMAPGHGRHCPLFVSQDPNGQHDGFPVRITPYGVAPSDKIIRLSTDVRISFRAYTTCLQSTEWHIDSELAAGRRHVITGPVKDPSPSGRENAFRIEKYSGAEVHEYKLMSCGDWCQDLGVFRDLKGGAWFLGATEPYHVVVFKKAPPA

>d1a8d\_2 b.42.4.2 (248-452) Tetanus neurotoxin {Clostridium tetani}

ITFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYMYLTNAPSYTNGKLNIYYRRLYNGLKFIIKRYTPNNEIDSFVKSGDFIKLYVSYNNNEHIVGYPKDGNAFNNLDRILRVGYNAPGIPLYKKMEAVKLRDLKTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNWYFNHLKDKILGCDWYFVPTDEGWTND

>d3btaa2 b.42.4.2 (A:1079-1295) Botulinum neurotoxin {Clostridium botulinum, serotype A}

NEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYYMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL

>d1epwa2 b.42.4.2 (A:1080-1290) Botulinum neurotoxin {Clostridium botulinum, serotype B}

SEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRRKSNSQSINDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEEKLFLAPISDSDEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKLGCNWQFIPKDEGWTE

>d1dfca1 b.42.5.1 (A:1008-1140) Fascin {Human (Homo sapiens)}

EAVQIQFGLINCGNKYLTAEAFGFKVNASASSLKKKQIWTLEQPPDEAGSAAVCLRSHLGRYLAADKDGNVTCEREVPGPDCRFLIVAHDDGRWSLQSEAHRRYFGGTEDRLSCFAQTVSPAEKWSVHIAMHP

>d1dfca2 b.42.5.1 (A:1141-1259) Fascin {Human (Homo sapiens)}

QVNIYSVTRKRYAHLSARPADEIAVDRDVPWGVDSLITLAFQDQRYSVQTADHRFLRHDGRLVARPEPATGYTLEFRSGKVAFRDCEGRYLAPSGPSGTLKAGKATKVGKDELFALEQS

>d1dfca3 b.42.5.1 (A:1260-1382) Fascin {Human (Homo sapiens)}

CAQVVLQAANERNVSTRQGMDLSANQDEETDQETFQLEIDRDTKKCAFRTHTGKYWTLTATGGVQSTASSKNASCYFDIEWRDRRITLRASNGKFVTSKKNGQLAASVETAGDSELFLMKLIN

>d1dfca4 b.42.5.1 (A:1383-1493) Fascin {Human (Homo sapiens)}

RPIIVFRGEHGFIGCRKVTGTLDANRSSYDVFQLEFNDGAYNIKDSTGKYWTVGSDSAVTSSGDTPVDFFFEFCDYNKVAIKVGGRYLKGDHAGVLKASAETVDPASLWEY

>d1hcd\_\_ b.42.5.2 (-) Histidine-rich actin-binding protein (hisactophilin) {Dictyostelium discoideum}

MGNRAFKSHHGHFLSAEGEAVKTHHGHHDHHTHFHVENHGGKVALKTHCGKYLSIGDHKQVYLSHHLHGDHSLFHLEHHGGKVSIKGHHHHYISADHHGHVSTKEHHDHDTTFEEIII

>d1i8da1 b.43.4.3 (A:1-93) Riboflavin synthase {Escherichia coli}

MFTGIVQGTAKLVSIDEKPNFRTHVVELPDHMLDGLETGASVAHNGCCLTVTEINGNHVSFDLMKETLRITNLGDLKVGDWVNVERAAKFSDE

>d1i8da2 b.43.4.3 (A:94-206) Riboflavin synthase {Escherichia coli}

IGGHLMSGHIMTTAEVAKILTSENNRQIWFKVQDSQLMKYILYKGFIGIDGISLTVGEVTPTRFCVHLIPETLERTTLGKKKLGARVNIEIDPQTQAVVDTVERVLAARENAM

>d1fnc\_1 b.43.4.2 (19-154) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Spinach (Spinacia oleracea)}

HSKKMEEGITVNKFKPKTPYVGRCLLNTKITGDDAPGETWHMVFSHEGEIPYREGQSVGVIPDGEDKNGKPHKLRLYSIASSALGDFGDAKSVSLCVKRLIYTNDAGETIKGVCSNFLCDLKPGAEVKLTGPVGKE

>d1qfza1 b.43.4.2 (A:1-153) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Garden pea (Pisum sativum)}

QVTTEAPAKVVKHSKKQDENIVVNKFKPKEPYVGRCLLNTKITGDDAPGETWHMVFSTEGEVPYREGQSIGIVPDGIDKNGKPHKLRLYSIASSAIGDFGDSKTVSLCVKRLVYTNDAGEVVKGVCSNFLCDLKPGSEVKITGPVGKEMLMPK

>d1fb3a1 b.43.4.2 (A:67-207) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Paprika (Capsicum annuum)}

ISKKQDEGVVVNKFRPKEPYIGRCLLNTKITGDDAPGETWHMVFSTEGEIPYREGQSIGVIADGVDANGKPHKLRLYSIASSALGDFGDSKTVSLCVKRLVYTNDKGEEVKGVCSNFLCDLKPGADVKITGPVGKEMLMPK

>d1gawa1 b.43.4.2 (A:11-156) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Maize (Zea mays), leaf isoform}

PATAKAKKESKKQEEGVVTNLYKPKEPYVGRCLLNTKITGDDAPGETWHMVFSTEGKIPYREGQSIGVIADGVDKNGKPHKVRLYSIASSAIGDFGDSKTVSLCVKRLIYTNDAGEIVKGVCSNFLCDLQPGDNVQITGPVGKEML

>d1jb9a1 b.43.4.2 (A:6-162) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Maize (Zea mays), root isoform}

SRSKVSVAPLHLESAKEPPLNTYKPKEPFTATIVSVESLVGPKAPGETCHIVIDHGGNVPYWEGQSYGVIPPGENPKKPGAPQNVRLYSIASTRYGDNFDGRTGSLCVRRAVYYDPETGKEDPSKNGVCSNFLCNSKPGDKIQLTGPSGKIMLLPEE

>d1que\_1 b.43.4.2 (1-141) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Cyanobacterium (Anabaena sp.), pcc 7119}

TQAKAKHADVPVNLYRPNAPFIGKVISNEPLVKEGGIGIVQHIKFDLTGGNLKYIEGQSIGIIPPGVDKNGKPEKLRLYSIASTRHGDDVDDKTISLCVRQLEYKHPESGETVYGVCSTYLTHIEPGSEVKITGPVGKEML

>d1fdr\_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Escherichia coli}

ADWVTGKVTKVQNWTDALFSLTVHAPVLPFTAGQFTKLGLEIDGERVQRAYSYVNSPDNPDLEFYLVTVPDGKLSPRLAALKPGDEVQVVSEAAGFFVL

>d1a8p\_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Azotobacter vinelandii}

SNLNVERVLSVHHWNDTLFSFKTTRNPSLRFENGQFVMIGLEVDGRPLMRAYSIASPNYEEHLEFFSIKVQNGPLTSRLQHLKEGDELMVSRKPTGTLV

>d1qfja1 b.43.4.2 (A:1-97) NAD(P)H:flavin oxidoreductase {Escherichia coli}

TTLSCKVTSVEAITDTVYRVRIVPDAAFSFRAGQYLMVVMDERDKRPFSMASTPDEKGFIELHIGASEINLYAKAVMDRILKDHQIVVDIPHGEAWL

>d2cnd\_1 b.43.4.2 (11-124) Nitrate reductase core domain {Corn (Zea mays)}

GRIHCRLVAKKELSRDVRLFRFSLPSPDQVLGLPIGKHIFVCATIEGKLCMRAYTPTSMVDEIGHFDLLVKVYFKNEHPKFPNGGLMTQYLDSLPVGSYIDVKGPLGHVEYTGR

>d1ndh\_1 b.43.4.2 (3-125) cytochrome b5 reductase {Pig (Sus scrofa), liver}

PAITLENPDIKYPLRLIDKEVVNHDTRRFRFALPSPEHILGLPVGQHIYLSARIDGNLVIRPYTPVSSDDDKGFVDLVIKVYFKDTHPKFPAGGKMSQYLESMKIGDTIEFRGPNGLLVYQGK

>d1i7pa1 b.43.4.2 (A:29-153) cytochrome b5 reductase {Rat (Rattus norvegicus)}

HHHMITLENPDIKYPLRLIDKEILSHDTRRFRFALPSPQHILGLPIGQHIYLSTRIDGNLVIRPYTPVSSDDDKGFVDLVVKVYFKETHPKFPAGGKMSQYLENMNIGDTIEFRGPNGLLVYQGK

>d2pia\_1 b.43.4.2 (1-103) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}

TTPQEDGFLRLKIASKEKIARDIWSFELTDPQGAPLPPFEAGANLTVAVPNGSRRTYSLCNDSQERNRYVIAVKRDSNGRGGSISFIDDTSEGDAVEVSLPRN

>d1ep3b1 b.43.4.2 (B:2-102) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}

SQLQEMMTVVSQREVAYNIFEMVLKGTLVDEMDLPGQFLHLAVPNGAMLLRRPISISSWDKRAKTCTILYRIGDETTGTYKLSKLESGAKVDVMGPLGNGF

>d1cqxa2 b.43.4.2 (A:151-261) Flavohemoglobin, central domain {Alcaligenes eutrophus}

WKGWRTFVIREKRPESDVITSFILEPADGGPVVNFEPGQYTSVAIDVPALGLQQIRQYSLSDMPNGRTYRISVKREGGGPQPPGYVSNLLHDHVNVGDQVKLAAPYGSFHI

>d1ja1a1 b.43.4.1 (A:240-518) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}

SSIRQYELVVHEDMDVAKVYTGEMGRLKSYENQKPPFDAKNPFLAAVTANRKLNQGTERHLMHLELDISDSKIRYESGDHVAVYPANDSALVNQIGEILGADLDVIMSLNNLDEESNKKHPFPCPTTYRTALTYYLDITNPPRTNVLYELAQYASEPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDYPSLRPPIDHLCELLPRLQARYYAIASSSKVHPNSVHICAVAVEYEAKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQF

>d1ddga1 b.43.4.1 (A:226-446) Sulfite reductase flavoprotein {Escherichia coli}

IHTSPYSKDAPLVASLSVNQKITGRNSEKDVRHIEIDLGDSGLRYQPGDALGVWYQNDPALVKELVELLWLKGDEPVTVEGKTLPLNEALQWHFELTVNTANIVENYATLTRSETLLPLVGDKAKLQHYAATTPIVDMVRFSPAQLDAEALINLLRPLTPRLYSIASSQAEVENEVHVTVGVVRYDVEGRARAGGASSFLADRVEEEGEVRVFIEHNDNFR

>d1f20a1 b.43.4.1 (A:963-1232) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat (Rattus norvegicus)}

SWKRNKFRLTYVAEAPDLTQGLSNVHKKRVSAARLLSRQNLQSPKSSRSTIFVRLHTNGNQELQYQPGDHLGVFPGNHEDLVNALIERLEDAPPANHVVKVEMLEERNTALGVISNWKDESRLPPCTIFQAFKYYLDITTPPTPLQLQQFASLATNEKEKQRLLVLSKGLQEYEEWKWGKNPTMVEVLEEFPSIQMPATLLLTQLSLLQPRYYSISSSPDMYPDEVHLTVAIVSYHTRDGEGPVHHGVCSSWLNRIQADDVVPCFVRGAP

>d1fuia1 b.43.2.1 (A:356-591) L-fucose isomerase, C-terminal domain {Escherichia coli}

AQVFADVRTYWSPEAIERVTGHKLDGLAEHGIIHLINSGSAALDGSCKQRDSEGNPTMKPHWEISQQEADACLAATEWCPAIHEYFRGGGYSSRFLTEGGVPFTMTRVNIIKGLGPVLQIAEGWSVELPKDVHDILNKRTNSTWPTTWFAPRLTGKGPFTDVYSVMANWGANHGVLTIGHVGADFITLASMLRIPVCMHNVEETKVYRPSAWAAHGMDIEGQDYRACQNYGPLYKR

>d1efca1 b.43.3.1 (A:205-296) Elongation factor Tu (EF-Tu), domain 2 {Escherichia coli}

AIDKPFLLPIEDVFSISGRGTVVTGRVERGIIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGIKREEIERGQVLAKPG

>d1exma1 b.43.3.1 (A:213-312) Elongation factor Tu (EF-Tu), domain 2 {Thermus thermophilus}

PVRDVDKPFLMPVEDVFTITGRGTVATGRIERGKVKVGDEVEIVGLAPETRKTVVTGVEMHRKTLQEGIAGDNVGVLLRGVSREEVERGQVLAKPGSITP

>d1d2ea1 b.43.3.1 (A:251-348) Elongation factor Tu (EF-Tu), domain 2 {Cow (Bos taurus), mitochondrial}

TRDLEKPFLLPVESVYSIPGRGTVVTGTLERGILKKGDECEFLGHSKNIRTVVTGIEMFHKSLDRAEAGDNLGALVRGLKREDLRRGLVMAKPGSIQP

>d1f60a1 b.43.3.1 (A:241-334) Elongation factor eEF-1alpha, domain 2 {Baker's yeast (Saccharomyces cerevisiae)}

DKPLRLPLQDVYKIGGIGTVPVGRVETGVIKPGMVVTFAPAGVTTEVKSVEMHHEQLEQGVPGDNVGFNVKNVSVKEIRRGNVCGDAKNDPPKG

>d1jnya1 b.43.3.1 (A:228-322) Elongation factor eEF-1alpha, domain 2 {Archaeon Sulfolobus solfataricus}

PVDKPLRIPIQDVYSISGVGTVPVGRVESGVLKVGDKIVFMPAGKVGEVRSIETHHTKMDKAEPGDNIGFNVRGVEKKDIKRGDVVGHPNNPPTV

>d1dar\_1 b.43.3.1 (283-400) Elongation factor G (EF-G), domain II {Thermus thermophilus}

PLDIPPIKGTTPEGEVVEIHPDPNGPLAALAFKIMADPYVGRLTFIRVYSGTLTSGSYVYNTTKGRKERVARLLRMHANHREEVEELKAGDLGAVVGLKETITGDTLVGEDAPRVILE

>d1g7sa1 b.43.3.1 (A:228-328) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

EDSPARGTILEVKEETGLGMTIDAVIYDGILRKDDTIAMMTSKDVISTRIRSLLKPRPLEEMRESRKKFQKVDEVVAAAGIKIVAPGIDDVMAGSPLRVVT

>d1g7sa2 b.43.3.1 (A:460-587) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

IIKPASIRLIPKLVFRQSKPAIGGVEVLTGVIRQGYPLMNDDGETVGTVESMQDKGENLKSASRGQKVAMAIKDAVYGKTIHEGDTLYVDIPENHYHILKEQLSGDLTDEELDLMDKIAEIKRKKNPD

>d1d1na\_ b.43.3.1 (A:) Initiation factor IF2/eIF5b, domains 2 and 4 {Bacillus stearothermophilus}

YEEKVIGQAEVRQTFKVSKVGTIAGCYVTDGKITRDSKVRLIRQGIVVYEGEIDSLKRYKDDVREVAQGYECGLTIKNFNDIKEGDVIEAYVMQEVARA

>d1jj2b\_ b.43.3.2 (B:) Ribosomal protein L3 {Archaeon Haloarcula marismortui}

PQPSRPRKGSLGFGPRKRSTSETPRFNSWPSDDGQPGVQGFAGYKAGMTHVVLVNDEPNSPREGMEETVPVTVIETPPMRAVALRAYEDTPYGQRPLTEVWTDEFHSELDRTLDVPEDHDPDAAEEQIRDAHEAGDLGDLRLITHTVPDAVPSVPKKKPDVMETRVGGGSVSDRLDHALDIVEDGGEHAMNDIFRAGEYADVAGVTKGKGTQGPVKRWGVQKRKGKHARQGWRRRIGNLGPWNPSRVRSTVPQQGQTGYHQRTELNKRLIDIGEGDEPTVDGGFVNYGEVDGPYTLVKGSVPGPDKRLVRFRPAVRPNDQPRLDPEVRYVSNESNQG

>d1efca2 b.44.1.1 (A:297-393) Elongation factor Tu (EF-Tu) {Escherichia coli}

TIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGDNIKMVVTLIHPIAMDDGLRFAIREGGRTVGAGVVAKVLS

>d1exma2 b.44.1.1 (A:313-405) Elongation factor Tu (EF-Tu) {Thermus thermophilus}

HTKFEASVYVLKKEEGGRHTGFFSGYRPQFYFRTTDVTGVVQLPPGVEMVMPGDNVTFTVELIKPVALEEGLRFAIREGGRTVGAGVVTKILE

>d1d2ea2 b.44.1.1 (A:349-451) Elongation factor Tu (EF-Tu) {Cow (Bos taurus), mitochondrial}

HQKVEAQVYILTKEEGGRHKPFVSHFMPVMFSLTWDMACRIILPPGKELAMPGEDLKLTLILRQPMILEKGQRFTLRDGNRTIGTGLVTDTPAMTEEDKNIKW

>d1f60a2 b.44.1.1 (A:335-441) Elongation factor eEF-1alpha, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

CASFNATVIVLNHPGQISAGYSPVLDCHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPLGRFAVRDMRQTVAVGVIKSVDK

>d1jnya2 b.44.1.1 (A:323-429) Elongation factor eEF-1alpha, C-terminal domain {Archaeon Sulfolobus solfataricus}

ADEFTARIIVVWHPTALANGYTPVLHVHTASVACRVSELVSKLDPRTGQEAEKNPQFLKQGDVAIVKFKPIKPLCVEKYNEFPPLGRFAMRDMGKTVGVGIIVDVKP

>d1flma\_ b.45.1.1 (A:) FMN-binding protein {Desulfovibrio vulgaris, strain Miyazaki F}

MLPGTFFEVLKNEGVVAIATQGEDGPHLVNTWNSYLKVLDGNRIVVPVGGMHKTEANVARDERVLMTLGSRKVAGRNGPGTGFLIRGSAAFRTDGPEFEAIARFKWARAALVITVVSAEQTL

>d1ci0a\_ b.45.1.1 (A:) Pyridoxine 5'-phoshate oxidase (PNP oxidase) {Baker's yeast (Saccharomyces cerevisiae)}

FTLNEKQLTDDPIDLFTKWFNEAKEDPRETLPEAITFSSAELPSGRVSSRILLFKELDHRGFTIYSNWGTSRKAHDIATNPNAAIVFFWKDLQRQVRVEGITEHVNRETSERYFKTRPRGSKIGAWASRQSDVIKNREELDELTQKNTERFKDAEDIPCPDYWGGLRIVPLEIEFWQGRPSRLHDRFVYRRKTENDPWKVVRLAP

>d1dnla\_ b.45.1.1 (A:) Pyridoxine 5'-phoshate oxidase (PNP oxidase) {Escherichia coli}

GGLRRRDLPADPLTLFERWLSQACEAKLADPTAMVVATVDEHGQPYQRIVLLKHYDEKGMVFYTNLGSRKAHQIENNPRVSLLFPWHTLERQVMVIGKAERLSTLEVMKYFHSRPRDSQIGAWVSKQSSRISARGILESKFLELKQKFQQGEVPLPSFWGGFRVSLEQIEFWQGGEHRLHDRFLYQRENDAWKIDRLAP

>d1ejea\_ b.45.1.2 (A:) FMN-binding protein MTH152 {Archaeon Methanobacterium thermoautotrophicum}

GSQAAHMMSMDFEDFPVESAHRILTPRPTVMVTTVDEEGNINAAPFSFTMPVSIDPPVVAFASAPDHHTARNIESTHEFVINITPADIIERMWVTARDIPAGENELEAAGLAWTSSRRVKPPRIVEAPGHLECELLRMFEVGDHNLITGSVVSASVRSGAVKEGLLDVESVKPVLHVGGNKFVVGDHVRHVE

>d1i0ra\_ b.45.1.2 (A:) Ferric reductase {Archaeon Archaeoglobus fulgidus}

MDVEAFYKISYGLYIVTSESNGRKCGQIANTVFQLTSKPVQIAVCLNKENDTHNAVKESGAFGVSVLELETPMEFIGRFGFRKSSEFEKFDGVEYKTGKTGVPLVTQHAVAVIEAKVVKECDVGTHTLFVGEAVDAEVLKDAEVLTYADYHLMKKGKTPRT

>d1k28d1 b.106.1.1 (D:4-200) Baseplate structural protein gp27 {Bacteriophage T4}

LQRPGYPNLSVKLFDSYDAWSNNRFVELAATITTLTMRDSLYGRNEGMLQFYDSKNIHTKMDGNEIIQISVANANDINNVKTRIYGCKHFSVSVDSKGDNIIAIELGTIHSIENLKFGRPFFPDAGESIKEMLGVIYQDRTLLTPAINAINAYVPDIPWTSTFENYLSYVREVALAVGSDKFVFVWQDIMGVNMMDY

>d1k28d2 b.106.1.1 (D:201-376) Baseplate structural protein gp27 {Bacteriophage T4}

DMMINQEPYPMIVGEPSLIGQFIQELKYPLAYDFVWLTKSNPHKRDPMKNATIYAHSFLDSSIPMITTGKGENSIVVSRSGAYSEMTYRNGYEEAIRLQTMAQYDGYAKCSTIGNFNLTPGVKIIFNDSKNQFKTEFYVDEVIHELSNNNSVTHLYMFTNATKLETIDPVKVKNEF

>d1fmta1 b.46.1.1 (A:207-314) Methionyl-tRNAfmet formyltransferase, C-terminal domain {Escherichia coli}

LSKEEARIDWSLSAAQLERCIRAFNPWPMSWLEIEGQPVKVWKASVIDTATNAAPGTILEANKQGIQVATGDGILNLLSLQPAGKKAMSAQDLLNSRREWFVPGNRLV

>d1ewna\_ b.46.1.2 (A:) 3-methyladenine DNA glycosylase (AAG, ANPG, MPG) {Human (Homo sapiens)}

HLTRLGLEFFDQPAVPLARAFLGQVLVRRLPNGTELRGRIVETQAYLGPEDEAAHSRGGRQTPRNRGMFMKPGTLYVYIIYGMYFCMNISSQGDGACVLLRALEPLEGLETMRQLRSTLRKGTASRVLKDRELCSGPSKLCQALAINKSFDQRDLAQDEAVWLERGPLEPSEPAVVAAARVGVGHAGEWARKPLRFYVRGSPWVSVVDRVAEQD

>d1arb\_\_ b.47.1.1 (-) Achromobacter protease {Achromobacter lyticus, strain m497-1}

GVSGSCNIDVVCPEGDGRRDIIRAVGAYSKSGTLACTGSLVNNTANDRKMYFLTAHHCGMGTASTAASIVVYWNYQNSTCRAPNTPASGANGDGSMSQTQSGSTVKATYATSDFTLLELNNAANPAFNLFWAGWDRRDQNYPGAIAIHHPNVAEKRISNSTSPTSFVAWGGGAGTTHLNVQWQPSGGVTEPGSSGSPIYSPEKRVLGQLHGGPSSCSATGTNRSDQYGRVFTSWTGGGAAASRLSDWLDPASTGAQFIDGLDS

>d1qq4a\_ b.47.1.1 (A:) alpha-Lytic protease {Lysobacter enzymogenes, 495}

ANIVGGIEYSINNASLCSVGFSVTRGATKGFVTAGHCGTVNATARIGGAVVGTFAARVFPGNDRAWVSLTSAQTLLPRVANGSSFVTVRGSTEAAVGAAVCHSGRTTGYQCGTITAKNVTANYAEGAVRGLTQSNACMGRGDSGGSWITSAGQAQGVMSGGNVQSNGNNCGIPASQRSSLFERLQPILSQYGLSLVTG

>d2sga\_\_ b.47.1.1 (-) Protease A {Streptomyces griseus, strain k1}

IAGGEAITTGGSRCSLGFNVSVNGVAHALTAGHCTNISASWSIGTRTGTSFPNNDYGIIRHSNPAAADGRVYLYNGSYQDITTAGNAFVGQAVQRSGSTTGLRSGSVTGLNATVNYGSSGIVYGMIQTNVCAQPGDSGGSLFAGSTALGLTSGGSGNCRTGGTTFYQPVTEALSAYGATVL

>d1hpga\_ b.47.1.1 (A:) Glutamic acid-specific protease {Streptomyces griseus}

VLGGGAIYGGGSRCSAAFNVTKGGARYFVTAGHCTNISANWSASSGGSVVGVREGTSFPTNDYGIVRYTDGSSPAGTVDLYNGSTQDISSAANAVVGQAIKKSGSTTKVTSGTVTAVNVTVNYGDGPVYNMVRTTACSAGGDSGGAHFAGSVALGIHSGSSGCSGTAGSAIHQPVTEALSAYGVTVY

>d1sgt\_\_ b.47.1.1 (-) Trypsin {Streptomyces griseus, strain k1}

VVGGTRAAQGEFPFMVRLSMGCGGALYAQDIVLTAAHCVSGSGNNTSITATGGVVDLQSGAAVKVRSTKVLQAPGYNGTGKDWALIKLAQPINQPTLKIATTTAYNQGTFTVAGWGANREGGSQQRYLLKANVPFVSDAACRSAYGNELVANEEICAGYPDTGGVDTCQGDSGGPMFRKDNADEWIQVGIVSWGYGCARPGYPGVYTEVSTFASAIASAARTL

>d2sfa\_\_ b.47.1.1 (-) Serine proteinase {Streptomyces fradiae}

IAGGEAIYAAGGGRCSLGFNVRSSSGATYALTAGHCTEIASTWYTNSGQTSLLGTRAGTSFPGNDYGLIRHSNASAADGRVYLYNGSYRDITGAGNAYVGQTVQRSGSTTGLHSGRVTGLNATVNYGGGDIVSGLIQTNVCAEPGDSGGALFAGSTALGLTSGGSGNCRTGGTTFFQPVTEALSAYGVSIL

>d1sgpe\_ b.47.1.1 (E:) Protease B {Streptomyces griseus, strain k1}

ISGGDAIYSSTGRCSLGFNVRSGSTYYFLTAGHCTDGATTWWANSARTTVLGTTSGSSFPNNDYGIVRYTNTTIPKDGTVGGQDITSAANATVGMAVTRRGSTTGTHSGSVTALNATVNYGGGDVVYGMIRTNVCAEPGDSGGPLYSGTRAIGLTSGGSGNCSSGGTTFFQPVTEALVAYGVSVY

>d1agja\_ b.47.1.1 (A:) Epidermolytic (exfoliative) toxin A {Staphylococcus aureus}

EVSAEEIKKHEEKWNKYYGVNAFNLPKELFSKVDEKDRQKYPYNTIGNVFVKGQTSATGVLIGKNTVLTNRHIAKFANGDPSKVSFRPSINTDDNGNTETPYGEYEVKEILQEPFGAGVDLALIRLKPDQNGVSLGDKISPAKIGTSNDLKDGDKLELIGYPFDHKVNQMHRSEIELTTLSRGLRYYGFTVPGNSGSGIFNSNGELVGIHSSKVSHLDREHQINYGVGIGNYVKRIINEKNE

>d1qtfa\_ b.47.1.1 (A:) Exfoliative toxin B {Staphylococcus aureus}

KEYSAEEIRKLKQKFEVPPTDKELYTHITDNARSPYNSVGTVFVKGSTLATGVLIGKNTIVTNYHVAREAAKNPSNIIFTPAQNRDAEKNEFPTPYGKFEAEEIKESPYGQGLDLAIIKLKPNEKGESAGDLIQPANIPDHIDIAKGDKYSLLGYPYNYSAYSLYQSQIEMFNDSQYFGYTEVGNSGSGIFNLKGELIGIHSGKGGQHNLPIGVFFNRKISSLYSVDNTFGDTLGNDLKKRAKLDK

>d1ezxc\_ b.47.1.2 (C:) Trypsin(ogen) {Cow (Bos taurus)}

CGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSYNSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGDSGGPVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN

>d1hj9a\_ b.47.1.2 (A:) Trypsin(ogen) {Cow (Bos taurus)}

IVGGYTCGANTVPYQVSLNSGYHFCGGSLINSQWVVSAAHCYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSYNSNTLNNDIMLIKLKSAASLNSRVASISLPTSCASAGTQCLISGWGNTKSSGTSYPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGDSGGPVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN

>d1mcta\_ b.47.1.2 (A:) Trypsin(ogen) {Pig (Sus scrofa)}

IVGGYTCAANSIPYQVSLNSGSHFCGGSLINSQWVVSAAHCYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPNFNGNTLDNDIMLIKLSSPATLNSRVATVSLPRSCAAAGTECLISGWGNTKSSGSSYPSLLQCLKAPVLSNSSCKSSYPGQITGNMICVGFLQGGKDSCQGDSGGPVVCNGQLQGIVSWGYGCAQKNKPGVYTKVCNYVNWIQQTIAAN

>d1f7za\_ b.47.1.2 (A:) Trypsin(ogen) {Rat (Rattus norvegicus)}

IVGGYTCQENSVPYQVSLNSGYHFCGGSLINDQWVVSAAHCYKSRIQVRLGEHNINVLEGNEQFVNAAKIIKHPNFDRKTLNNDIMLIKLSSPVKLNARVATVALPSSCAPAGTQCLISGWGNTLSSGVNEPDLLQCLDAPLLPQADCEASYPGKITDNMVCVGFLEGGKDSCQGDSGGPVVCNGELQGIVSWGYGCALPDNPGVYTKVCNYVDWIQDTIAAN

>d1trna\_ b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens)}

IVGGYNCEENSVPYQVSLNSGYHFCGGSLINEQWVVSAGHCYKSRIQVRLGEHNIEVLEGNEQFINAAKIIRHPQYDRKTLNNDIMLIKLSSRAVINARVSTISLPTAPPATGTKCLISGWGNTASSGADYPDELQCLDAPVLSQAKCEASYPGKITSNMFCVGFLEGGKDSCQGDSGGPVVCNGQLQGVVSWGDGCAQKNKPGVYTKVYNYVKWIKNTIAANS

>d1h4wa\_ b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens), trypsin IV (brain isoform)}

IVGGYTCEENSLPYQVSLNSGSHFCGGSLISEQWVVSAAHCYKTRIQVRLGEHNIKVLEGNEQFINAVKIIRHPKYNRDTLDNDIMLIKLSSPAVINARVSTISLPTAPPAAGTECLISGWGNTLSFGADYPDELKCLDAPVLTQAECKASYPGKITNSMFCVGFLEGGKDSCQRDSGGPVVCNGQLQGVVSWGHGCAWKNRPGVYTKVYNYVDWIKDTIAANS

>d1a0ja\_ b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo salar)}

IVGGYECRKNSASYQASLQSGYHFCGGSLISSTWVVSAAHCYKSRIQVRLGEHNIAVNEGTEQFIDSVKVIMHPSYNSRNLDNDIMLIKLSKPASLNSYVSTVALPSSCASSGTRCLVSGWGNLSGSSSNYPDTLRCLDLPILSSSSCNSAYPGQITSNMFCAGFMEGGKDSCQGDSGGPVVCNGQLQGVVSWGYGCAQRNKPGVYTKVCNYRSWISSTMSSN

>d1hj8a\_ b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo salar)}

IVGGYECKAYSQPHQVSLNSGYHFCGGSLVNENWVVSAAHCYKSRVEVRLGEHNIKVTEGSEQFISSSRVIRHPNYSSYNIDNDIMLIKLSKPATLNTYVQPVALPTSCAPAGTMCTVSGWGNTMSSTADSNKLQCLNIPILSYSDCNNSYPGMITNAMFCAGYLEGGKDSCQGDSGGPVVCNGELQGVVSWGYGCAEPGNPGVYAKVCIFNDWLTSTMASY

>d1gdna\_ b.47.1.2 (A:) Trypsin(ogen) {Mold (Fusarium oxysporum)}

IVGGTSASAGDFPFIVSISRNGGPWCGGSLLNANTVLTAAHCVSGYAQSGFQIRAGSLSRTSGGITSSLSSVRVHPSYSGNNNDLAILKLSTSIPSGGNIGYARLAASGSDPVAGSSATVAGWGATSEGGSSTPVNLLKVTVPIVSRATCRAQYGTSAITNQMFCAGVSSGGKDSCQGDSGGPIVDSSNTLIGAVSWGNGCARPNYSGVYASVGALRSFIDTYA

>d1pytd\_ b.47.1.2 (D:) (alpha,gamma)-chymotrypsin(ogen) {Cow (Bos taurus)}

CGAPIFQPNLSARVVGGEDAIPHSWPWQISLQYLRDNTWRHTCGGTLITPNHVLTAAHCISNTLTYRVALGKNNLEVEDEAGSLYVGVDTIFVHEKWNSFLVRNDIALIKLAETVELGDTIQVACLPSEGSLLPQDYPCFVTGWGRLYTNGPIAAELQQGLQPVVDYATCSQRDWWGTTVKETMVCAGGDGVISACNGDSGGPLNCQADGQWDVRGIVSFGSGLSCNTFKKPTVFTRVSAYIDWINQKLQL

>g1gg6.1 b.47.1.2 (A:,B:,C:) (alpha,gamma)-chymotrypsin(ogen) {Cow (Bos taurus)}

CGVPAIQPVLXIVNGEEAVPGSWPWQVSLQDKTGFHFCGGSLINENWVVTAAHCGVTTSDVVVAGEFDQGSSSEKIQKLKIAKVFKNSKYNSLTINNDITLLKLSTAASFSQTVSAVCLPSASDDFAAGTTCVTTGWGLTRYXANTPDRLQQASLPLLSNTNCKKYWGTKIKDAMICAGASGVSSCMGDSGGPLVCKKNGAWTLVGIVSWGSSTCSTSTPGVYARVTALVNWVQQTLAAN

>d1eq9a\_ b.47.1.2 (A:) (alpha,gamma)-chymotrypsin(ogen) {Red fire ant (Solenopsis invicta)}

IVGGKDAPVGKYPYQVSLRLSGSHRCGASILDNNNVLTAAHCVDGLSNLNRLKVHVGTNYLSESGDVYDVEDAVVNKNYDDFLLRNDVALVHLTNPIKFNDLVQPIKLSTNDEDLESNPCTLTGWGSTRLGGNTPNALQEIELIVHPQKQCERDQWRVIDSHICTLTKRGEGACHGDSGGPLVANGAQIGIVSFGSPCALGEPDVYTRVSSFVSWINANLKK

>d1npma\_ b.47.1.2 (A:) Neuropsin {Mouse (Mus musculus)}

ILEGRECIPHSQPWQAALFQGERLICGGVLVGDRWVLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPCYNNSNPEDHSHDIMLIRLQNSANLGDKVKPVQLANLCPKVGQKCIISGWGTVTSPQENFPNTLNCAEVKIYSQNKCERAYPGKITEGMVCAGSSNGADTCQGDSGGPLVCDGMLQGITSWGSDPCGKPEKPGVYTKICRYTTWIKKTMD

>d1azza\_ b.47.1.2 (A:) Crab collagenase {Atlantic sand fiddler crab (Uca pugilator)}

IVGGVEAVPNSWPHQAALFIDDMYFCGGSLISPEWILTAAHCMDGAGFVDVVLGAHNIREDEATQVTIQSTDFTVHENYNSFVISNDIAVIRLPVPVTLTAAIATVGLPSTDVGVGTVVTPTGWGLPSDSALGISDVLRQVDVPIMSNADCDAVYGIVTDGNICIDSTGGKGTCNGDSGGPLNYNGLTYGITSFGAAAGCEAGYPDAFTRVTYFLDWIQTQTGITP

>d2hlca\_ b.47.1.2 (A:) HL collagenase {Common cattle grub (Hypoderma lineatum)}

IINGYEAYTGLFPYQAGLDITLQDQRRVWCGGSLIDNKWILTAAHCVHDAVSVVVYLGSAVQYEGEAVVNSERIISHSMFNPDTYLNDVALIKIPHVEYTDNIQPIRLPSGEELNNKFENIWATVSGWGQSNTDTVILQYTYNLVIDNDRCAQEYPPGIIVESTICGDTSDGKSPCFGDSGGPFVLSDKNLLIGVVSFVSGAGCESGKPVGFSRVTSYMDWIQQNTGIKF

>g1h8d.1 b.47.1.2 (L:,H:) Thrombin {Human (Homo sapiens)}

EADCGLRPLFEKKSLEDKTERELLESYISXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWIQKVIDQFGCSSVLIVVC

>g1jou.1 b.47.1.2 (A:,B:) Thrombin {Human (Homo sapiens)}

SEYQTFFNPRTFGSGEADCGLRPLFEKKSLEDKTERELLESYIDGXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDAGGPFVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWIQKVIDQFGE

>g1vr1.1 b.47.1.2 (L:,H:) Thrombin {Human (Homo sapiens)}

ADCGLRPLFEKKSLEDKTERELLESYIXIVEGSDAEIGMSPWQVMLFAKHRRSPGERFLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAYYKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWIQKVID

>g2hnt.1 b.47.1.2 (L:,C:,E:,F:) Thrombin {Human (Homo sapiens)}

ADCGLRPLFEKKSLEDKTERELLESYIDXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSXEKISMLEKIYIHPRYNWRENLDRDIALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGXPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWIQKVIDQ

>g1etr.1 b.47.1.2 (L:,H:) Thrombin {Cow (Bos taurus)}

TFGAGEADCGLRPLFEKKQVQDQTEKELFESYIEGRXIVEGQDAEVGLSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTVDDLLVRIGKHSRTRYERKVEKISMLDKIYIHPRYNWKENLDRDIALLKLKRPIELSDYIHPVCLPDKQTAAKLLHAGFKGRVTGWGNRRETWTTSVAEVQPSVLQVVNLPLVERPVCKASTRIRITDNMFCAGYKPGEGKRGDACEGDSGGPFVMKSPYNNRWYQMGIVSWGEGCDRDGKYGFYTHVFRLKKWIQKVIDRLGS

>d1fona\_ b.47.1.2 (A:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (Bos taurus)}

SWSWQVSLQYEKDGAFHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGEYDRSVLEGSEQVIPINAGDLFVHPLWNSNCVACGNDIALVKLSRSAQLGDKVQLANLPPAGDILPNEAPCYISGWGRLYTGGPLPDKLQQALLPTVDYEHCSQWDWWGITVKKTMVCAGGDTRSGCNGDSGGPLNCPAADGSWQVHGVTSFVSAFGCNTIKKPTVFTRVSAFIDWIDETIASN

>d1pytc\_ b.47.1.2 (C:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (Bos taurus)}

SRPSSRVVNGEDAVPYSWSWQVSLQYEKDGAFHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGEYDRSVLQGSEQVIPINAGDLFVHPLWNSNCVACGNDIALVKLSRSAQLGDKVQLANLPPAGDILPNEAPCYISGWGRLYTGGPLPDKLQEALLPVVDYEHCSQYDWWGITVKKTMVCAGGDTRSGCDGDSGGPLNCPAADGSWQVHGVTSFVSAFGCNTIKKPTVFTRVSAFIDWINETIASN

>d1ppfe\_ b.47.1.2 (E:) Elastase {Human (Homo sapiens)}

IVGGRRARPHAWPFMVSLQLRGGHFCGATLIAPNFVMSAAHCVANVNVRAVRVVLGAHNLSRREPTRQVFAVQRIFENGYDPVNLLNDIVILQLNGSATINANVQVAQLPAQGRRLGNGVQCLAMGWGLLGRNRGIASVLQELNVTVVTSLCRRSNVCTLVRGRQAGVCFGDSGSPLVCNGLIHGIASFVRGGCASGLYPDAFAPVAQFVNWIDSIIQ

>d1brup\_ b.47.1.2 (P:) Elastase {Pig (Sus scrofa)}

VVGGEDARPNSWPWQVSLQYDSSGQWRHTCGGTLVDQSWVLTAAHCISSSRTYRVVLGRHSLSTNEPGSLAVKVSKLVVHQDWNSNQLSNGNDIALLKLASPVSLTDKIQLGCLPAAGTILPNNYVCYVTGWGRLQTNGASPDILQQGQLLVVDYATCSKPGWWGSTVKTNMICAGGDGIISSCNGDSGGPLNCQGANGQWQVHGIVSFGSSLGCNYYHKPSVFTRVSNYIDWINSVIANN

>d1qnja\_ b.47.1.2 (A:) Elastase {Pig (Sus scrofa)}

VVGGTEAQRNSWPSQISLQYRSGSSWAHTCGGTLIRQNWVMTAAHCVDRELTFRVVVGEHNLNQNDGTEQYVGVQKIVVHPYWNTDDVAAGYDIALLRLAQSVTLNSYVQLGVLPRAGTILANNSPCYITGWGLTRTNGQLAQTLQQAYLPTVDYAICSSSSYWGSTVKNSMVCAGGDGVRSGCQGDSGGPLHCLVNGQYAVHGVTSFVSRLGCNVTRKPTVFTRVSAYISWINNVIASN

>d1elt\_\_ b.47.1.2 (-) Elastase {Salmon (Salmo salar)}

VVGGRVAQPNSWPWQISLQYKSGSSYYHTCGGSLIRQGWVMTAAHCVDSARTWRVVLGEHNLNTNEGKEQIMTVNSVFIHSGWNSDDVAGGYDIALLRLNTQASLNSAVQLAALPPSNQILPNNNPCYITGWGKTSTGGPLSDSLKQAWLPSVDHATCSSSGWWGSTVKTTMVCAGGGANSGCNGDSGGPLNCQVNGSYYVHGVTSFVSSSGCNASKKPTVFTRVSAYISWMNGIM

>d1ekbb\_ b.47.1.2 (B:) Enteropeptidase (enterokinase light chain) {Cow (Bos taurus)}

IVGGSDSREGAWPWVVALYFDDQQVCGASLVSRDWLVSAAHCVYGRNMEPSKWKAVLGLHMASNLTSPQIETRLIDQIVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGALIYQGSTADVLQEADVPLLSNEKCQQQMPEYNITENMVCAGYEAGGVDSCQGDSGGPLMCQENNRWLLAGVTSFGYQCALPNRPGVYARVPRFTEWIQSFLH

>d1a7s\_\_ b.47.1.2 (-) Heparin binding protein, HBP {Human (Homo sapiens)}

IVGGRKARPRQFPFLASIQNQGRHFCGGALIHARFVMTAASCFPGVSTVVLGAYDLRRRERQSRQTFSISSMSENGYDPQQNLNDLMLLQLDREANLTSSVTILPLPLQNATVEAGTRCQVAGWGSQRSGGRLSRFPRFVNVTVTPEDQCRPNNVCTGVLTRRGGICNGDGGTPLVCEGLAHGVASFSLGPCGRGPDFFTRVALFRDWIDGVLNNPGPGPA

>d1a0la\_ b.47.1.2 (A:) beta-Tryptase {Human (Homo sapiens)}

IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRVQLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVTLPPASETFPPGMPCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDMLCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWIHHYVPKK

>d1cgha\_ b.47.1.2 (A:) Cathepsin G {Human (Homo sapiens)}

IIGGRESRPHSRPYMAYLQIQSPAGQSRCGGFLVREDFVLTAAHCWGSNINVTLGAHNIQRRENTQQHITARRAIRHPQYNQRTIQNDIMLLQLSRRVRRNRNVNPVALPRAQEGLRPGTLCTVAGWGRVSMRRGTDTLREVQLRVQRDRQCLRIFGSYDPRRQICVGDRRERKAAFKGDSGGPLLCNNVAHGIVSYGKSSGVPPEVFTRVSSFLPWIRTTMRS

>d1danh\_ b.47.1.2 (H:) Coagulation factor VIIa {Human (Homo sapiens)}

IVGGKVCPKGECPWQVLLLVNGAQLCGGTLINTIWVVSAAHCFDKIKNWRNLIAVLGEHDLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIALLRLHQPVVLTDHVVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQSRKVGDSPNITEYMFCAGYSDGSKDSCKGDSGGPHATHYRGTWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP

>d3rp2a\_ b.47.1.2 (A:) Chymase (Proteinase II) {Rat (Rattus rattus)}

IIGGVESIPHSRPYMAHLDIVTEKGLRVICGGFLISRQFVLTAAHCKGREITVILGAHDVRKRESTQQKIKVEKQIIHESYNSVPNLHDIMLLKLEKKVELTPAVNVVPLPSPSDFIHPGAMCWAAGWGKTGVRDPTSYTLREVELRIMDEKACVDYRYYEYKFQVCVGSPTTLRAAFMGDSGGPLLCAGVAHGIVSYGHPDAKPPAIFTRVSTYVPWINAVIN

>d1klt\_\_ b.47.1.2 (-) Chymase (Proteinase II) {Human (Homo sapiens)}

IIGGTESKPHSRPYMAYLEIVTSNGPSKFCGGFLIRRNFVLTAAHCAGRSITVTLGAHNITEEEDTWQKLEVIKQFRHPKYNTSTLHHDIMLLKLKEKASLTLAVGTLPFPSQFNFVPPGRMCRVAGWGRTGVLKPGSDTLQEVKLRLMDPQACSHFRDFDHNLQLCVGNPRKTKSAFKGDSGGPLLCAGVAQGIVSYGRSDAKPPAVFTRISHYRPWINQILQAN

>g2pka.1 b.47.1.2 (A:,B:) Kallikrein A {Pig (Sus scrofa)}

IIGGRECEKNSHPWQVAIYHYSSFQCGGVLVNPKWVLTAAHCKNDNYEVWLGRHNLFENENTAQFFGVTADFPHPGFNLSXADGKDYSHDLMLLRLQSPAKITDAVKVLELPTQEPELGSTCEASGWGSIEPGPDDFEFPDEIQCVQLTLLQNTFCADAHPDKVTESMLCAGYLPGGKDTCMGDSGGPLICNGMWQGITSWGHTPCGSANKPSIYTKLIFYLDWIDDTITENP

>d1ton\_\_ b.47.1.2 (-) Tonin {Rat (Rattus rattus)}

IVGGYKCEKNSQPWQVAVINEYLCGGVLIDPSWVITAAHCYSNNYQVLLGRNNLFKDEPFAQRRLVRQSFRHPDYIPLIVTNDTEQPVHDHSNDLMLLHLSEPADITGGVKVIDLPTKEPKVGSTCLASGWGSTNPSEMVVSHDLQCVNIHLLSNEKCIETYKDNVTDVMLCAGEMEGGKDTCAGDSGGPLICDGVLQGITSGGATPCAKPKTPAIYAKLIKFTSWIKKVMKENP

>d1sgfa\_ b.47.1.2 (A:) 7S NGF protease subunits {Mouse (Mus musculus)}

NSQPWHVAVYRFNKYQCGGVLLDRNWVLTAAHCYNDKYQVWLGKNNFLEDEPSDQHRLVSKAIPHPDFNMSLLNEHTPQPEDDYSNDLMLLRLSKPADITDVVKPITLPTEEPKLGSTCLASGWGSTTPIKYPDDLQCVNLKLLPNEDCDKAHEMKVTDAMLCAGEMDGGSYTCEHDSGGPLICDGILQGITSWGPEPCGEPTEPSVYTKLIKFSSWIRETMANNP

>d1sgfg\_ b.47.1.2 (G:) 7S NGF protease subunits {Mouse (Mus musculus)}

IVGGFKCEKNSQPWHVAVYRYTQYLCGGVLLDPNWVLTAAHCYDDNYKVWLGKNNLFKDEPSAQHRFVSKAIPHPGFNMSLMRFLEYDYSNDLMLLRLSKPADITDTVKPITLPTEEPKLGSTCLASGWGSITPTKFQFTDDLYCVNLKLLPNEDCAKAHIEKVTDAMLCAGEMDGGKDTCKGDSGGPLICDGVLQGITSWGHTPCGEPDMPGVYTKLNKFTSWIKDTMAKNP

>d1dlea\_ b.47.1.2 (A:) Factor B {Human (Homo sapiens)}

ADPDESQSLSLCGMVWEHRKGTDYHKQPWQAKISVIRPSKGHESCMGAVVSEYFVLTAAHCFTVDDKEHSIKVSVGGEKRDLEIEVVLFHPNYNINGKKEAGIPEFYDYDVALIKLKNKLKYGQTIRPICLPCTEGTTRALRLPPTTTCQQQKEELLPAQDIKALFVSEEEKKLTRKEVYIKNGDKKGSCERDAQYAPGYDKVKDISEVVTPRFLCTGGVSPYADPNTCRGDSGGPLIVHKRSRFIQVGVISWGVVDVCKNQKRQKQVPAHARDFHINLFQVLPWLKEKLQDEDLGFL

>d1bio\_\_ b.47.1.2 (-) Factor D {Human (Homo sapiens)}

ILGGREAEAHARPYMASVQLNGAHLCGGVLVAEQWVLSAAHCLEDAADGKVQVLLGAHSLSQPEPSKRLYDVLRAVPHPDSQPDTIDHDLLLLQLSEKATLGPAVRPLPWQRVDRDVAPGTLCDVAGWGIVNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMCAESNRRDSCKGDSGGPLVCGGVLEGVVTSGSRVCGNRKKPGIYTRVASYAAWIDSVLA

>g1rtf.1 b.47.1.2 (A:,B:) Two-chain tissue plasminogen activator (TC)-T-PA {Human (Homo sapiens)}

TCGLRQYSXIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDDTYDNDIALLQLKSDSSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVTDNMLCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLGCGQKDVPGVYTKVTNYLDWIRDNMRP

>d1a5ia\_ b.47.1.2 (A:) Single chain tissue plasminogen activator {Vampire bat (Desmodus rotundus)}

TCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCFQESYLPDQLKVVLGRTYRVKPGEEEQTFKVKKYIVHKEFDDDTYNNDIALLQLKSDSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPKFLFNKTVTNNMLCAGDTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGCGEKDVPGVYTKVTNYLGWIRDNMHL

>d1bqya\_ b.47.1.2 (A:) Plasminogen activator from snake venom, TSV-PA {Chinese green tree viper (Trimeresurus stejnejeri)}

VFGGDECNINEHRSLVVLFNSNGFLCGGTLINQDWVVTAAHCDSNNFQLLFGVHSKKILNEDEQTRDPKEKFFCPNRKKDDEVDKDIMLIKLDSSVSNSEHIAPLSLPSSPPSVGSVCRIMGWGKTIPTKEIYPDVPHCANINILDHAVCRTAYSWRQVANTTLCAGILQGGRDTCHFDSGGPLICNGIFQGIVSWGGHPCGQPGEPGVYTKVFDYLDWIKSIIAGNKDATCPP

>d1ao5a\_ b.47.1.2 (A:) Kallikrein-13 {Mouse (Mus musculus)}

VVGGFNCEKNSQPWQVAVYYQKEHICGGVLLDRNWVLTAAHCYVDQYEVWLGKNKLFQEEPSAQHRLVSKSFPHPGFNMSLLMLQTIPPGADFSDDLMLLRLSKPADITDVVKPIALPTKEPKPGSKCLASGWGSITPTRWQKPDDLQCVFITLLPNENCAKVYLQKVTDVMLCAGEMGGGKDTCRDDSGGPLICDGILQGTTSYGPVPCGKPGVPAIYTNLIKFNSWIKDTMMKNA

>d1pfxc\_ b.47.1.2 (C:) Coagulation factor IXa, protease domain {Pig (Sus scrofa)}

IVGGENAKPGQFPWQVLLNGKIDAFCGGSIINEKWVVTAAHCIEPGVKITVVAGEYNTEETEPTEQRRNVIRAIPHHSYNATVNKYSHDIALLELDEPLTLNSYVTPICIADKEYTNIFLKFGSGYVSGWGRVFNRGRSATILQYLKVPLVDRATCLRSTKFTIYSNMFCAGFHEGGKDSCQGDSGGPHVTEVEGTSFLTGIISWGEECAVKGKYGIYTKVSRYVNWIKEKTKLT

>d1rfna\_ b.47.1.2 (A:) Coagulation factor IXa, protease domain {Human (Homo sapiens)}

VVGGEDAKPGQFPWQVVLNGKVDAFCGGSIVNEKWIVTAAHCVETGVKITVVAGEHNIEETEHTEQKRNVIRIIPHHNYNAAINKYNHDIALLELDEPLVLNSYVTPICIADKEYTNIFLKFGSGYVSGWGRVFHKGRSALVLQYLRVPLVDRATCLRSTKFTIYNNMFCAGFHEGGRDSCQGDSGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRYVNWIKEKTKLT

>d1fjsa\_ b.47.1.2 (A:) Coagulation factor Xa (Chrismas factor), protease domain {Human (Homo sapiens)}

IVGGQECKDGECPWQALLINEENEGFCGGTILSEFYILTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITFRMNVAPACLPERDWAESTLMTQKTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCKLSSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKYGIYTKVTAFLKWIDRSMKT

>d1kigh\_ b.47.1.2 (H:) Coagulation factor Xa (Chrismas factor), protease domain {Cow (Bos taurus)}

IVGGRDCAEGECPWQALLVNEENEGFCGGTILNEFYVLTAAHCLHQAKRFTVRVGDRNTEQEEGNEMAHEVEMTVKHSRFVKETYDFDIAVLRLKTPIRFRRNVAPACLPEKDWAEATLMTQKTGIVSGFGRTHEKGRLSSTLKMLEVPYVDRSTCKLSSSFTITPNMFCAGYDTQPEDACQGDSGGPHVTRFKDTYFVTGIVSWGEGCARKGKFGVYTKVSNFLKWIDKIMKARAGAAGS

>d1fxya\_ b.47.1.2 (A:) Coagulation factor Xa-trypsin chimera {Synthetic, based on Homo sapiens sequence}

IVGGYNCKDGEVPWQALLINEENEGFCGGTILSEFYILTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVLRLKTPITFRMNVAPASLPTAPPATGTKCLISGWGNTASSGADYPDELQCLDAPVLSQAKCEASYPGKITSNMFCVGFLEGGKDSCQGDSGGPVVCNGQLQGVVSWGDGCAQKNKPGVYTKVYNYVKWIKNTIAANS

>d1elva1 b.47.1.2 (A:410-668) Complement C1S protease, catalytic domain {Human (Homo sapiens)}

CGVPREPFEEKQRIIGGSDADIKNFPWQVFFDNPWAGGALINEYWVLTAAHVVEGNREPTMYVGSTSVQTSRLAKSKMLTPEHVFIHPGWKLLAVPEGRTNFDNDIALVRLKDPVKMGPTVSPICLPGTSSDYNLMDGDLGLISGWGRTEKRDRAVRLKAARLPVAPLRKCKEVKVEKPTADAEAYVFTPNMICAGGEKGMDSCKGDSGGAFAVQDPNDKTKFYAAGLVSWGPQCGTYGLYTRVKNYVDWIMKTMQENS

>d1autc\_ b.47.1.2 (C:) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}

LIDGKMTRRGDSPWQVVLLDSKKKLACGAVLIHPSWVLTAAHCMDESKKLLVRLGEYDLRRWEKWELDLDIKEVFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPDSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFVLNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLHNYGVYTKVSRYLDWIHGHIRD

>d1fuja\_ b.47.1.2 (A:) Myeloblastin, PR3 {Human (Homo sapiens)}

IVGGHEAQPHSRPYMASLQMRGNPGSHFCGGTLIHPSFVLTAAHCLRDIPQRLVNVVLGAHNVRTQEPTQQHFSVAQVFLNNYDAENKLNDILLIQLSSPANLSASVATVQLPQQDQPVPHGTQCLAMGWGRVGAHDPPAQVLQELNVTVVTFFCRPHNICTFVPRRKAGICFGDSGGPLICDGIIQGIDSFVIWGCATRLFPDFFTRVALYVDWIRSTLR

>g1c5y.1 b.47.1.2 (A:,B:) Urokinase-type plasminogen activator (LMW U-PA), catalytic domain {Human (Homo sapiens)}

LKFQCGQKTXIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLMSPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCEITGFGKEASTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGCALKDKPGVYTRVSHFLPWIRSHTKEE

>d1ddja\_ b.47.1.2 (A:) Plasmin(ogen), catalytic domain {Human (Homo sapiens)}

SFDCGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSLRTRFGMHFCGGTLISPEWVLTAAHCLEKSPRPSSYKVILGAHQEVNLEPHVQEIEVSRLFLEPTRKDIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTFGAGLLKEAQLPVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDAGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWIEGVMRNN

>d1fi8a\_ b.47.1.2 (A:) Granzyme B {Rat (Rattus norvegicus)}

IIGGHEAKPHSRPYMAYLQIMDEYSGSKKCGGFLIREDFVLTAAHCSGSKIQVTLGAHNIKEQEKMQQIIPVVKIIPHPAYNSKTISNDIMLLKLKSKAKRSSAVKPLNLPRRNVKVKPGDVCYVAGWGKLGPMGKYSDTLQEVELTVQEDQKCESYLKNYFDKANEICAGDPKIKRASFRGDSGGPLVCKKVAAGIVSYGQNDGSTPRAFTKVSTFLSWIKKTMKK

>d1iaua\_ b.47.1.2 (A:) Granzyme B {Human (Homo sapiens)}

IIGGHEAKPHSRPYMAYLMIWDQKSLKRCGGFLIRDDFVLTAAHCWGSSINVTLGAHNIKEQEPTQQFIPVKRPIPHPAYNPKNFSNDIMLLQLERKAKRTRAVQPLRLPSNKAQVKPGQTCSVAGWGQTAPLGKHSHTLQEVKMTVQEDRKCESDLRHYYDSTIELCVGDPEIKKTSFKGDSGGPLVCNKVAQGIVSYGRNNGMPPRACTKVSSFVHWIKKTMKR

>d1eufa\_ b.47.1.2 (A:) Duodenase {Cow (Bos taurus)}

IIGGHEAKPHSRPYMAFLLFKTSGKSHICGGFLVREDFVLTAAHCLGSSINVTLGAHNIMERERTQQVIPVRRPIPHPDYNDETLANDIMLLKLTRKADITDKVSPINLPRSLAEVKPGMMCSVAGWGRLGVNMPSTDKLQEVDLEVQSEEKCIARFKNYIPFTQICAGDPSKRKNSFSGDSGGPLVCNGVAQGIVSYGRNDGTTPDVYTRISSFLSWIHSTMR

>g1fiw.1 b.47.1.2 (L:,A:) Beta-acrosin {Sheep (Ovis aries)}

TTCDGPCGVRFRQNXIIGGQDAAHGAWPWMVSLQIFTYHNNRRYHVCGGSLLNSQWLLTAAHCFRIKKKVTDWRLIFGAKEVEWGTNKPVKPPLQERYVEKIIIHEKYSASSEANDIALMKITPPVTCGHFIGPGCLPQFRAGPPRVPQTCWVAGWGFLQENARRTSPMLQEARVDLIDLGLCNSTRWYNGRIRSTNVCAGYPEGKIDTCQGDSGGPLMCKDSAENSYVVVGITSWGVGCARAKRPGVYTSTWSYLNWIASKIGSTAVHMIQLPT

>g1fiz.1 b.47.1.2 (L:,A:) Beta-acrosin {Pig (Sus scrofa)}

ATCDGPCGLRFRQXVVGGMSAEPGAWPWMVSLQIFMYHNNRRYHTCGGILLNSHWVLTAAHCFKNKKKVTDWRLIFGANEVVWGSNKPVKPPLQERFVEEIIIHEKYVSGLEINDIALIKITPPVPCGPFIGPGCLPQFKAGPPRAPQTCWVTGWGYLKEKGPRTSPTLQEARVALIDLELCNSTRWYNGRIRSTNVCAGYPRGKIDTCQGDSGGPLMCRDRAENTFVVVGITSWGVGCARAKRPGVYTSTWPYLNWIASKIGSNALQMVQLGTPPR

>d1eaxa\_ b.47.1.2 (A:) Matriptase MTSP1 {Human (Homo sapiens)}

VVGGTDADEGEWPWQVSLHALGQGHICGASLISPNWLVSAAHCYIDDRGFRYSDPTQWTAFLGLHDQSQRSAPGVQERRLKRIISHPFFNDFTFDYDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLLPQQITPRMMCVGFLSGGVDSCQGDSGGPLSSVEADGRIFQAGVVSWGDGCAQRNKPGVYTRLPLFRDWIKENTGV

>d1svpa\_ b.47.1.3 (A:) Viral capsid protein {Sindbis virus}

ALKLEADRLFDVKNEDGDVIGHALAMEGKVMKPLHVKGTIDHPVLSKLKFTKSSAYDMEFAQLPVNMRSEAFTYTSEHPEGFYNWHHGAVQYSGGRFTIPRGVGGRGDAGRPIMDNSGRVVAIVLGGADEGTRTALSVVTWNSKGKTIKTTPEGTEEWSA

>d1vcpa\_ b.47.1.3 (A:) Viral capsid protein {Semliki forest virus}

CIFEVKHEGKVTGYACLVGDKVMKPAHVKGVIDNADLAKLAFKKSSKYDLECAQIPVHMRSDASKYTHEKPEGHYNWHHGAVQYSGGRFTIPTGAGKPGDSGRPIFDNKGRVVAIVLGGANEGSRTALSVVTWNKDMVTRVTPEGSEEW

>d1a1qa\_ b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

PITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRSPVF

>d1cu1a1 b.47.1.3 (A:705-720,A:3-186) NS3 protease {Human hepatitis C virus (HCV), different isolates}

GSVVIVGRIILSGSGSXITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRSPVFTD

>d1dxwa\_ b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

TGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRASKKKK

>g1a1r.1 b.47.1.3 (A:,C:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

VEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPTGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMRXGSVVIVGRIVLSGKPA

>g1a1r.2 b.47.1.3 (B:,D:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

PITAYAQQTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKGSSGGPLLCPTGHAVGLFRAAVCTRGVAKAVDFIPVENLETTMRXKGSVVIVGRIVLSGKPAIIPK

>g1dy9.1 b.47.1.3 (A:,C:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

APITAYSQQTRGLLGCIITSLTGRDKNQVDGEVQVLSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWPAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHVVGIFRAAVCTRGVAKAVDFIPVESMXGSVVIVGRIILS

>g1ns3.1 b.47.1.3 (A:,C:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

ITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPVSYLKGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRXKGSVVIVGRIILS

>d1befa\_ b.47.1.3 (A:) NS3 protease {Dengue virus serotype 2}

WDVPSPPPVGKAELEDGAYRIKQKGILGYSQIGAGVYKEGTFHTMWHVTRGAVLMHKGKRIEPSWADVKKDLVSCGGGWKLEGEWKEGEEVQVLALEPGKNPRAVQTKPGLFKTNAGTIGAVSLDFSPGTSGSPIIDKKGKVVGIYGNGVVTRSGAYVSAIAQTEKSIEDNPEIEDD

>d1cqqa\_ b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human rhinovirus type 2}

GPEEEFGMSLIKHNSCVITTENGKFTGLGVYDRFVVVPTHADPGKEIQVDGITTKVIDSYDLYNKNGIKLEITVLKLDRNEKFRDIRRYIPNNEDDYPNCNLALLANQPEPTIINVGDVVSYGNILLSGNQTARMLKYSYPTKSGYCGGVLYKIGQVLGIHVGGNGRDGFSAMLLRSYFT

>d1hava\_ b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human hepatitis A virus}

STLEIAGLVRKNLVQFGVGEKNGSVRWVMNALGVKDDWLLVPSHAYKFEKDYEMMEFYFNRGGTYYSISAGNVVIQSLDVGFQDVVLMKVPTIPKFRDITQHFIKKGDVPRALNRLATLVTTVNGTPMLISEGPLKMEEKATYVHKKNDGTTVDLTVDQAWRGKGEGLPGMCGGALVSSNQSIQNAILGIHVAGGNSILVAKLVTQEMFQNIDKKI

>d2hrva\_ b.47.1.4 (A:) 2A cysteine proteinase {Human rhinovirus 2}

GPSDMYVHVGNLIYRNLHLFNSEMHESILVSYSSDLIIYRTNTVGDDYIPSCDCTQATYYCKHKNRYFPITVTSHDWYEIQESEYYPKHIQYNLLIGEGPCEPGDCGGKLLCKHGVIGIVTAGGDNHVAFIDLRHFHCA

>d1bco\_1 b.48.1.1 (481-560) mu transposase, C-terminal domain {Bacteriophage mu}

TEEQKRMLLLPAEAVNVSRKGEFTLKVGGSLKGAKNVYYNMALMNAGVKKVVVRFDPQQLHSTVYCYTLDGRFICEAECL

>d1e79a2 b.49.1.1 (A:19-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

ADTSVDLEETGRVLSIGDGIARVHGLRNVQAEEMVEFSSGLKGMSLNLEPDNVGVVVFGNDKLIKEGDIVKRTGAI

>d1e79d2 b.49.1.1 (D:9-81) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

TTGRIVAVIGAVVDVQFDEGLPPILNALEVQGRETRLVLEVAQHLGESTVRTIAMDGTEGLVRGQKVLDSGAP

>d1maba2 b.49.1.1 (A:10-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (Rattus norvegicus)}

SSILEERILGADTSVDLEETGRVLSIGDGIARVHGLRNVQAEEMVEFSSGLKGMSLNLEPDNVGVVVFGNDKLIKEGDIVKRTGAI

>d1mabb2 b.49.1.1 (B:1-81) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (Rattus norvegicus)}

SAAPKAGTATGQIVAVIGAVVDVQFDEGLPPILNALEVQGRESRLVLEVAQHLGESTVRTIAMDGTEGLVRGQKVLDSGAP

>d1skyb2 b.49.1.1 (B:21-95) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

SQIQVSDVGTVIQVGDGIARAHGLDNVMSGEAVEFANAVMGMALNLEENNVGIVILGPYTGIKEGDEVRRTGRIM

>d1skye2 b.49.1.1 (E:1-82) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

MTRGRVIQVMGPVVDVKFENGHLPAIYNALKIQHKARNENEVDIDLTLEVALHLGDDTVRTIAMASTDGLIRGMEVIDTGAP

>d1fx0a2 b.49.1.1 (A:25-96) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

KVVNTGTVLQVGDGIARIHGLDEVMAGELVEFEEGTIGIALNLESNNVGVVLMGDGLMIQEGSSVKATGRIA

>d1fx0b2 b.49.1.1 (B:19-97) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

NLGRIAQIIGPVLNVAFPPGKMPNIYNALIVKGRDTAGQPMNVTCEVQQLLGNNRVRAVAMSATDGLTRGMEVIDTGAP

>d1bd0a1 b.49.2.1 (A:2-11,A:245-382) Alanine racemase {Bacillus stearothermophilus}

NDFHRDTWAEXFSLHSRLVHVKKLQPGEKVSYGATYTAQTEEWIGTIPIGYADGWLRRLQHFHVLVDGQKAPIVGRICMDQCMIRLPGPLPVGTKVTLIGRQGDEVISIDDVARHLETINYEVPCTISYRVPRIFFRHKRIMEVRNAIG

>d1d7ka1 b.49.2.1 (A:7-43,A:284-427) Eukaryotic ornithine decarboxylase {Human (Homo sapiens)}

EEFDCHFLDEGFTAKDILDQKINEVSSSDDKDAFYVAXFTLAVNIIAKKIVLKEQTGSDDEDESSEQTFMYYVNDGVYGSFNCILYDHAHVKPLLQKRPKPDERYYSSSIWGPTCDGLDRIVERCDLPEMHVGDWMLFENMGAYTVAAASTFNGFQRPTIYYVMSGPAWQLMQQFQNPDFPP

>d7odca1 b.49.2.1 (A:2-43,A:284-418) Eukaryotic ornithine decarboxylase {Mouse (Mus musculus)}

SSFTKDEFDCHILDEGFTAKDILDQKINEVSSSDDKDAFYVAXFTLAVNIIAKKTVWKEQPGSDDEDESNEQTFMYYVNDGVYGSFNCILYDHAHVKALLQKRPKPDEKYYSSSIWGPTCDGLDRIVERCNLPEMHVGDWMLFENMGAYTVAAASTFNGFQRPNIYYVMSRPMWQLMK

>d1f3ta1 b.49.2.1 (A:14-43,A:284-422) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}

RFLEGFNTRDALCKKISMNTCDEGDPFFVAXFTLAVNVIAKKVTPGVQTDVGAHAESNAQSFMYYVNDGVYGSFNCILYDHAVVRPLPQREPIPNEKLYPSSVWGPTCDGLDQIVERYYLPEMQVGEWLLFEDMGAYTVVGTSSFNGFQSPTIYYVVSGLPDHVVRELKS

>d2toda1 b.49.2.1 (A:37-43,A:284-410) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}

GDPFFVAXFTLAVNVIAKKVTPGVQTDVGAHAESNAQSFMYYVNDGVYGSFNCILYDHAVVRPLPQREPIPNEKLYPSSVWGPTCDGLDQIVERYYLPEMQVGEWLLFEDMGAYTVVGTSSFNGFQSPTIYYVVS

>d1b6la\_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWKRPLVTIRIGGQLKEALLDTGADDTVIEEMNLPGKWKPKMIGGIGGFIKVRQYDQIPVEIXGHKAIGTVLVGPTPVNIIGRNLLTQIGXTLNF

>d1bdqa\_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWQRPLVTIKIGGQLKEALLDTGADDSIVAGIELPGRWKPKMVGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPINIIGRNLLTQIGCTLNF

>d1c6ya\_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWQRPVVTIKIGGQLMEALIDTGADDTVLEEMDLPGRWKPKIIGGIGGFVKVRQYDQIPIEICGHKVIGTVLVGPTPTNIIGRNLLTQIGCTLNF

>d1dazc\_ b.50.1.1 (C:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWKRPLVTIKIGGQLKEALLDTGADDTVIEEMSLPGRWKPIMIGGIGGFIKVRQYDQIIIEIAGHKAIGTVLVGPTPVNIIGRNLLTQIGATLNF

>d1difa\_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF

>d1hvc\_\_ b.50.1.1 (-) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}

PQITLWQRPLVTIRIGGQLKEALLDTGADDTVLEEMNLPGKWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFGGSSGPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF

>d1idaa\_ b.50.1.1 (A:) Human immunodeficiency virus type 2 (HIV-2) protease {Human immunodeficiency virus type 2}

PQFSLWKRPVVTAYIEGQPVEVLLDTGADDSIVAGIELGNNYSPKIVGGIGGFINTKEYKNVEIEVLNKKVRATIMTGDTPINIFGRNILTALGMSLNL

>d1az5\_\_ b.50.1.1 (-) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}

PQFHLWKRPVVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVEVEVLGKRIKGTIMTGDTPINIFGRNLLTALGMSLNF

>d1k6va\_ b.50.1.1 (A:) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}

PQITLWKRPLVTIRIGGQLKEALLDTGADDTVLEEMNLPGRWKPKMIGGIGGFIKVRQYDQIPIEICGHKAIGTVLVGPTPTNVIGRNLLTQIGCTLNF

>d1siva\_ b.50.1.1 (A:) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}

PQFSLWRRPVVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVKIEVLGKRIKGTIMTGDTPINIFGRNLLTALGMSLNL

>d4fiv\_\_ b.50.1.1 (-) Feline immunodeficiency virus (FIV) protease {Feline immunodeficiency virus}

VGTTTTLEKRPEILIFVNGYPIKFLLDTGADITILNRRDFQVKNSIENGRQNMIGVGGGKRGTNYINVHLEIRDENYKTQCIFGNVCVLEDNSLIQPLLGRDNMIKFNIRLVM

>d1baia\_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}

LAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDTGADDTVISEEDWPTDWPVMEAANPQIHGIGGGIPVRKSRDMIELGVINRDGSLERPLLLFPLVAMTPVNILGRDCLQGLGLRLTNL

>d2rspa\_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}

LAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDSGADITIISEEDWPTDWPVMEAANPQIHGIGGGIPMRKSRDMIELGVINRDGSLERPLLLFPAVAMVRGSILGRDCLQGLGLRLTNL

>d1fmb\_\_ b.50.1.1 (-) EIAV protease {Equine infectious anemia virus}

VTYNLEKRPTTIVLINDTPLNVLLDTGADTSVLTTAHYNRLKYRGRKYQGTGIGGVGGNVETFSTPVTIKKKGRHIKTRMLVADIPVTILGRDILQDLGAKLVL

>d2er7e\_ b.50.1.2 (E:) Endothiapepsin {Chestnut blight fungus (Endothia parasitica)}

STGSATTTPIDSLDDAYITPVQIGTPAQTLNLDFDTGSSDLWVFSSETTASEVDGQTIYTPSKSTTAKLLSGATWSISYGDGSSSSGDVYTDTVSVGGLTVTGQAVESAKKVSSSFTEDSTIDGLLGLAFSTLNTVSPTQQKTFFDNAKASLDSPVFTADLGYHAPGTYNFGFIDTTAYTGSITYTAVSTKQGFWEWTSTGYAVGSGTFKSTSIDGIADTGTTLLYLPATVVSAYWAQVSGAKSSSSVGGYVFPCSATLPSFTFGVGSARIVIPGDYIDFGPISTGSSSCFGGIQSSAGIGINIFGDVALKAAFVVFNGATTPTLGFASK

>d1bxoa\_ b.50.1.2 (A:) Acid protease {Fungus (Penicillium janthinellum), penicillopepsin}

AASGVATNTPTANDEEYITPVTIGGTTLNLNFDTGSADLWVFSTELPASQQSGHSVYNPSATGKELSGYTWSISYGDGSSASGNVFTDSVTVGGVTAHGQAVQAAQQISAQFQQDTNNDGLLGLAFSSINTVQPQSQTTFFDTVKSSLAQPLFAVALKHQQPGVYDFGFIDSSKYTGSLTYTGVDNSQGFWSFNVDSYTAGSQSGDGFSGIADTGTTLLLLDDSVVSQYYSQVSGAQQDSNAGGYVFDCSTNLPDFSVSISGYTATVPGSLINYGPSGDGSTCLGGIQSNSGIGFSIFGDIFLKSQYVVFDSDGPQLGFAPQA

>d1ibqa\_ b.50.1.2 (A:) Acid protease {Fungus (Aspergillus phoenicis), aspergillopepsin}

SKGSAVTTPQNNDEEYLTPVTVGKSTLHLDFDTGSADLWVFSDELPSSEQTGHDLYTPSSSATKLSGYSWDISYGDGSSASGDVYRDTVTVGGVTTNKQAVEAASKISSEFVQDTANDGLLGLAFSSINTVQPKAQTTFFDTVKSQLDSPLFAVQLKHDAPGVYDFGYIDDSKYTGSITYTDADSSQGYWGFSTDGYSIGDGSSSSSGFSAIADTGTTLILLDDEIVSAYYEQVSGAQESYEAGGYVFSCSTDLPDFTVVIGDYKAVVPGKYINYAPVSTGSSTCYGGIQSNSGLGLSILGDVFLKSQYVVFNSEGPKLGFAAQA

>d2apr\_\_ b.50.1.2 (-) Acid protease {Bread mold (Rhizopus chinensis)}

AGVGTVPMTDYGNDIEYYGQVTIGTPGKKFNLDFDTGSSDLWIASTLCTNCGSGQTKYDPNQSSTYQADGRTWSISYGDGSSASGILAKDNVNLGGLLIKGQTIELAKREAASFASGPNDGLLGLGFDTITTVRGVKTPMDNLISQGLISRPIFGVYLGKAKNGGGGEYIFGGYDSTKFKGSLTTVPIDNSRGWWGITVDRATVGTSTVASSFDGILDTGTTLLILPNNIAASVARAYGASDNGDGTYTISCDTSAFKPLVFSINGASFQVSPDSLVFEEFQGQCIAGFGYGNWGFAIIGDTFLKNNYVVFNQGVPEVQIAPVAE

>d2asi\_\_ b.50.1.2 (-) Acid protease {Rhizomucor miehei}

GSVDTPGYYDFDLEEYAIPVSIGTPGQDFLLLFDTGSSDTWVPHKGCTKSEGCVGSRFFDPSASSTFKATNYNLNITYGTGANGLYFEDSIAIGDITVTKQILAYVDNVRGPTAEQSPNADIFLDGLFGAAYPDNTAMEAEYGSTYNTVHVNLYKQGLISSPLFSVYMNTNSGTGEVVFGGVNNTLLGGDIAYTDVMSRYGGYYFWDAPVTGITVDGSAAVRFSRPQAFTIDTGTNFFIMPSSAASKIVKAALPDATETQQGWVVPCASYQNSKSTISIVMQKSGSSSDTIEISVPVSKMLLPVDQSNETCMFIILPDGGNQYIVGNLFLRFFVNVYDFGNNRIGFAPLASAYENE

>d1eaga\_ b.50.1.2 (A:) Acid protease {Yeast (Candida albicans)}

QAVPVTLHNEQVTYAADITVGSNNQKLNVIVDTGSSDLWVPDVNVDCQVTYSDQTADFCKQKGTYDPSGSSASQDLNTPFKIGYGDGSSSQGTLYKDTVGFGGVSIKNQVLADVDSTSIDQGILGVGYKTNEAGGSYDNVPVTLKKQGVIAKNAYSLYLNSPDAATGQIIFGGVDNAKYSGSLIALPVTSDRELRISLGSVEVSGKTINTDNVDVLLDSGTTITYLQQDLADQIIKAFNGKLTQDSNGNSFYEVDCNLSGDVVFNFSKNAKISVPASEFAASLQGDDGQPYDKCQLLFDVNDANILGDNFLRSAYIVYDLDDNEISLAQVKYTSASSISALT

>d1j71a\_ b.50.1.2 (A:) Acid protease {Yeast (Candida tropicalis)}

SDVPTTLINEGPSYAADIVVGSNQQKQTVVIDTGSSDLWVVDTDAECQVTYSGQTNNFCKQEGTFDPSSSSSAQNLNQDFSIEYGDLTSSQGSFYKDTVGFGGISIKNQQFADVTTTSVDQGIMGIGFTADEAGYNLYDNVPVTLKKQGIINKNAYSLYLNSEDASTGKIIFGGVDNAKYTGTLTALPVTSSVELRVHLGSINFDGTSVSTNADVVLDSGTTITYFSQSTADKFARIVGATWDSRNEIYRLPSCDLSGDAVFNFDQGVKITVPLSELILKDSDSSICYFGISRNDANILGDNFLRRAYIVYDLDDKTISLAQVKYTSSSDISAL

>d1dpja\_ b.50.1.2 (A:) Acid protease {Baker's yeast (Saccharomyces cerevisiae), proteinase A}

GGHDVPLTNYLNAQYYTDITLGTPPQNFKVILDTGSSNLWVPSNECGSLACFLHSKYDHEASSSYKANGTEFAIQYGTGSLEGYISQDTLSIGDLTIPKQDFAEATSEPGLTFAFGKFDGILGLGYDTISVDKVVPPFYNAIQQDLLDEKRFAFYLGDTSKDTENGGEATFGGIDESKFKGDITWLPVRRKAYWEVKFEGIGLGDEYAELESHGAAIDTGTSLITLPSGLAEMINAEIGAKKGWTGQYTLDCNTRDNLPDLIFNFNGYNFTIGPYDYTLEVSGSCISAITPMDFPEPVGPLAIVGDAFLRKYYSIYDLGNNAVGLAKAI

>g1b5f.1 b.50.1.2 (A:,B:) Plant acid proteinase, phytepsin {Cynara cardunculus}

GSAVVALTNDRDTSYFGEIGIGTPPQKFTVIFDTGSSVLWVPSSKCINSKACRAHSMYESSDSSTYKENGTFGAIIYGTGSITGFFSQDSVTIGDLVVKEQDFIEATDEADNVFLHRLFDGILGLSFQTISVPVWYNMLNQGLVKERRFSFWLNRNVDEEEGGELVFGGLDPNHFRGDHTYVPVTYQYYWQFGIGDVLIGDKSTGFCAPGCQAFADSGTSLLSGPTAIVTQINHAIGANXEELQVDCNTLSSMPNVSFTIGGKKFGLTPEQYILKVGKGEATQCISGFTAMDATLLGPLWILGDVFMRPYHTVFDYGNLLVGFAEAA

>d1qdma2 b.50.1.2 (A:2-247,A:248-338) Plant acid proteinase, phytepsin {Barley (Hordeum vulgare)}

EEEGDIVALKNYMNAQYFGEIGVGTPPQKFTVIFDTGSSNLWVPSAKCYFSIACYLHSRYKAGASSTYKKNGKPAAIQYGTGSIAGYFSEDSVTVGDLVVKDQEFIEATKEPGITFLVAKFDGILGLGFKEISVGKAVPVWYKMIEQGLVSDPVFSFWLNRHVDEGEGGEIIFGGMDPKHYVGEHTYVPVTQKGYWQFDMGDVLVGGKSTGFCAGGCAAIADSGTSLLAGPTAIITEINEKIGAAGXSPMGESAVDCGSLGSMPDIEFTIGGKKFALKPEEYILKVGEGAAAQCISGFTAMDIPPPRGPLWILGDVFMGPYHTVFDYGKLRIGFAKAA

>d3psg\_\_ b.50.1.2 (-) Pepsin(ogen) {Pig (Sus scrofa)}

LVKVPLVRKKSLRQNLIKDGKLKDFLKTHKHNPASKYFPEAAALIGDEPLENYLDTEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDDSSTFEATSQELSITYGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISASGATPVFDNLWDQGLVSQDLFSVYLSSNDDSGSVVLLGGIDSSYYTGSLNWVPVSVEGYWQITLDSITMDGETIACSGGCQAIVDTGTSLLTGPTSAIANIQSDIGASENSDGEMVISCSSIDSLPDIVFTIDGVQYPLSPSAYILQDDDSCTSGFEGMDVPTSSGELWILGDVFIRQYYTVFDRANNKVGLAPVA

>d4pep\_\_ b.50.1.2 (-) Pepsin(ogen) {Pig (Sus scrofa)}

IGDEPLENYLDTEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDDSSTFEATSQELSITYGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISASGATPVFDNLWDQGLVSQDLFSVYLSSNDDSGSVVLLGGIDSSYYTGSLNWVPVSVEGYWQITLDSITMDGETIACSGGCQAIVDTGTSLLTGPTSAIANIQSDIGASENSDGEMVISCSSIDSLPDIVFTIDGVQYPLSPSAYILQDDDSCTSGFEGMDVPTSSGELWILGDVFIRQYYTVFDRANNKVGLAPVA

>d1psoe\_ b.50.1.2 (E:) Pepsin(ogen) {Human (Homo sapiens), 3A}

VDEQPLENYLDMEYFGTIGIGTPAQDFTVVFDTGSSNLWVPSVYCSSLACTNHNRFNPEDSSTYQSTSETVSITYGTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISSSGATPVFDNIWNQGLVSQDLFSVYLSADDQSGSVVIFGGIDSSYYTGSLNWVPVTVEGYWQITVDSITMNGEAIACAEGCQAIVDTGTSLLTGPTSPIANIQSDIGASENSDGDMVVSCSAISSLPDIVFTINGVQYPVPPSAYILQSEGSCISGFQGMNLPTESGELWILGDVFIRQYFTVFDRANNQVGLAPVA

>g1htr.1 b.50.1.2 (P:,B:) Pepsin(ogen) {Human (Homo sapiens), progastricsin (pepsinogen C)}

AVVKVPLKKFKSIRETMKEKGLLGEFLRTHKYDPAWKYRFGDLXSVTYEPMAYMDAAYFGEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHSRFNPSESSTYSTNGQTFSLQYGSGSLTGFFGYDTLTVQSIQVPNQEFGLSENEPGTNFVYAQFDGIMGLAYPALSVDEATTAMQGMVQEGALTSPVFSVYLSNQQGSSGGAVVFGGVDSSLYTGQIYWAPVTQELYWQIGIEEFLIGGQASGWCSEGCQAIVDTGTSLLTVPQQYMSALLQATGAQEDEYGQFLVNCNSIQNLPSLTFIINGVEFPLPPSSYILSNNGYCTVGVEPTYLSSQNGQPLWILGDVFLRSYYSVYDLGNNRVGFATAA

>d1am5\_\_ b.50.1.2 (-) Pepsin(ogen) {Atlantic cod (Gadus morhua)}

RVTEQMKNEADTEYYGVISIGTPPESFKVIFDTGSSNLWVSSSHCSAQACSNHNKFKPRQSSTYVETGKTVDLTYGTGGMRGILGQDTVSVGGGSDPNQELGESQTEPGPFQAAAPFDGILGLAYPSIAAAGAVPVFDNMGSQSLVEKDLFSFYLSGGGANGSEVMLGGVDNSHYTGSIHWIPVTAEKYWQVALDGITVNGQTAACEGCQAIVDTGTSKIVAPVSALANIMKDIGASENQGEMMGNCASVQSLPDITFTINGVKQPLPPSAYIEGDQAFCTSGLGSSGVPSNTSELWIFGDVFLRNYYTIYDRTNNKVGFAPAA

>d1mpp\_\_ b.50.1.2 (-) Pepsin {Mucor pusillus}

GSVDTPGLYDFDLEEYAIPVSIGTPGQDFYLLFDTGSSDTWVPHKGCDNSEGCVGKRFFDPSSSSTFKETDYNLNITYGTGGANGIYFRDSITVGGATVKQQTLAYVDNVSGPTAEQSPDSELFLDGIFGAAYPDNTAMEAEYGDTYNTVHVNLYKQGLISSPVFSVYMNTNDGGGQVVFGGVNNTLLGGDIQYTDVLKSRGGYFFWDAPVTGVKIDGSDAVSFDGAQAFTIDTGTNFFIAPSSFAEKVVKAALPDATESQQGYTVPCSKYQDSKTTFSLVLQKSGSSSDTIDVSVPISKMLLPVDKSGETCMFIVLPDGGNQFIVGNLFLRFFVNVYDFGKNRIGFAPLASGYEND

>g1lyb.1 b.50.1.2 (A:,B:) Cathepsin D {Human (Homo sapiens)}

GPIPEVLKNYMDAQYYGEIGIGTPPQCFTVVFDTGSSNLWVPSIHCKLLDIACWIHHKYNSDKSSTYVKNGTSFDIHYGSGSLSGYLSQDTVSVPCQXGGVKVERQVFGEATKQPGITFIAAKFDGILGMAYPRISVNNVLPVFDNLMQQKLVDQNIFSFYLSRDPDAQPGGELMLGGTDSKYYKGSLSYLNVTRKAYWQVHLDQVEVASGLTLCKEGCEAIVDTGTSLMVGPVDEVRELQKAIGAVPLIQGEYMIPCEKVSTLPAITLKLGGKGYKLSPEDYTLKVSQAGKTLCLSGFMGMDIPPPSGPLWILGDVFIGRYYTVFDRDNNRVGFAEAA

>d3cms\_\_ b.50.1.2 (-) Chymosin (synonim: renin) {Cow (Bos taurus)}

GEVASVPLTNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGTGSMQGILGYDTVTVSNIVDIQQTVGLSTQEPGDFFTYAEFDGILGMAYPSLASEYSIPVFDNMMNRHLVAQDLFSVYMDRNGQESMLTLGAIDPSYYTGSLHWVPVTVQQYWQFTVDSVTISGVVVACEGGCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPTVVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREYYSVFDRANNLVGLAKAI

>d1hrna\_ b.50.1.2 (A:) Chymosin (synonim: renin) {Human (Homo sapiens)}

GNTTSSVILTNYMDTQYYGEIGIGTPPQTFKVVFDTGSSNVWVPSSKCSRLYTACVYHKLFDASDSSSYKHNGTELTLRYSTGTVSGFLSQDIITVGGITVTQMFGEVTEMPALPFMLAEFDGVVGMGFIEQAIGRVTPIFDNIISQGVLKEDVFSFYYNRDSENSQSLGGQIVLGGSDPQHYEGNFHYINLIKTGVWQIQMKGVSVGSSTLLCEDGCLALVDTGASYISGSTSSIEKLMEALGAKKRLFDYVVKCNEGPTLPDISFHLGGKEYTLTSADYVFQESYSSKKLCTLAIHAMDIPPPTGPTWALGATFIRKFYTEFDRRNNRIGFALAR

>d1smra\_ b.50.1.2 (A:) Chymosin (synonim: renin) {Mouse (Mus musculus)}

TDLISPVVLTNYLNSQYYGEIGIGTPPQTFKVIFDTGSANLWVPSTKCSRLYLACGIHSLYESSDSSSYMENGDDFTIHYGSGRVKGFLSQDSVTVGGITVTQTFGEVTQLPLIPFMLAQFDGVLGMGFPAQAVGGVTPVFDHILSQGVLKEKVFSVYYNRGPHLLGGEVVLGGSDPQHYQGDFHYVSLSKTDSWQITMKGVSVGSSTLLCEEGCEVVVDTGSSFISAPTSSLKLIMQALGAKEKRLHEYVVSCSQVPTLPDISFNLGGRAYTLSSTDYVLQYPNRRDKLCTVALHAMDIPPPTGPVWVLGATFIRKFYTEFDRHNNRIGFALAR

>d1fkna\_ b.50.1.2 (A:) beta-secretase (memapsin) {Human (Homo sapiens)}

RRGSFVEMVDNLRGKSGQGYYVEMTVGSPPQTLNILVDTGSSNFAVGAAPHPFLHRYYQRQLSSTYRDLRKGVYVPYTQGKWEGELGTDLVSIPHGPNVTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLEPFFDSLVKQTHVPNLFSLQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYTGSLWYTPIRREWYYEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRLPKKVFEAAVKSIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSACHVHDEFRTAAVEGPFVTLDMEDCGYN

>d1pfza\_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}

HLTIGFKVENAHDRILKTIKTHKLKNYIKESVNFLNSGLTKTNYLGSSNDNIELVDFQNIMFYGDAEVGDNQQPFTFILDTGSANLWVPSVKCTTAGCLTKHLYDSSKSRTYEKDGTKVEMNYVSGTVSGFFSKDLVTVGNLSLPYKFIEVIDTNGFEPTYTASTFDGILGLGWKDLSIGSVDPIVVELKNQNKIENALFTFYLPVHDKHTGFLTIGGIEERFYEGPLTYEKLNHDLYWQITLDAHVGNIMLEKANCIVDSGTSAITVPTDFLNKMLQNLDVIKVPFLPFYVTLCNNSKLPTFEFTSENGKYTLEPEYYLQHIEDVGPGLCMLNIIGLDFPVPTFILGDPFMRKYFTVFDYDNHSVGIALAKKNL

>d1smea\_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}

SSNDNIELVDFQNIMFYGDAEVGDNQQPFTFILDTGSANLWVPSVKCTTAGCLTKHLYDSSKSRTYEKDGTKVEMNYVSGTVSGFFSKDLVTVGNLSLPYKFIEVIDTNGFEPTYTASTFDGILGLGWKDLSIGSVDPIVVELKNQNKIENALFTFYLPVHDKHTGFLTIGGIEERFYEGPLTYEKLNHDLYWQITLDAHVGNIMLEKANCIVDSGTSAITVPTDFLNKMLQNLDVIKVPFLPFYVTLCNNSKLPTFEFTSENGKYTLEPEYYLQHIEDVGPGLCMLNIIGLDFPVPTFILGDPFMRKYFTVFDYDNHSVGIALAKKNL

>d1qs8a\_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium vivax}

SENDVIELDDVANIMFYGEGEVGDNHQKFMLIFDTGSANLWVPSKKCNSSGCSIKNLYDSSKSKSYEKDGTKVDITYGSGTVKGFFSKDLVTLGHLSMPYKFIEVIDTDDLEPIYSSVEFDGILGLGWKDLSIGSIDPIVVELKNQNKIDNALFTFYLPVHDVHAGYLTIGGIEEKFYEGNITYEKLNHDLYWQIDLDVHFGKQTMEKANVIVDSGTTTITAPSEFLNKFFANLNVIKVPFLPFYVTTCDNKEMPTLEFKSANNTYTLEPEYYMNPILEVDDTLCMITMLPVDIDSNTFILGDPFMRKYFTVFDYDKESVGFAIAKN

>d1ile\_2 b.51.1.1 (198-386) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}

KEIQDPSVYVRFPLKEPKKLGLEKASLLIWTTTPWTLPGNVAAAVHPEYTYAAFQVGDEALILEEGLGRKLLGEGTQVLKTFPGKALEGLPYTPPYPQALEKGYFVVLADYVSQEDGTGIVHQAPAFGAEDLETARVYGLPLLKTVDEEGKLLVEPFKGLYFREANRAILRDLRGRGLLFKEESYLHSY

>d1ffya2 b.51.1.1 (A:201-394) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

HDKRSASIYVAFNVKDDKGVVDADAKFIIWTTTPWTIPSNVAITVHPELKYGQYNVNGEKYIIAEALSDAVAEALDWDKASIKLEKEYTGKELEWVVAQHPFLDRESLVINGDHVTTDAGTGCVHTAPGHGEDDYIVGQQYELPVISPIDDKGVFTEEGGQFEGMFYDKANKAVTDLLTEKGALLKLDFITHSY

>d1gaxa2 b.51.1.1 (A:190-342) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}

TEPTPGKLYTLRYEVEGGGFIEIATVRPETVFADQAIAVHPEDERYRHLLGKRARIPLTEVWIPILADPAVEKDFGTGALKVTPAHDPLDYEIGERHGLKPVSVINLEGRMEGERVPEALRGLDRFEARRKAVELFREAGHLVKEEDYTIALA

>d1gmua1 b.107.1.1 (A:1-70) Urease metallochaperone UreE, N-terminal domain {Klebsiella aerogenes}

MLYLTQRLEIPAAATASVTLPIDVRVKSRVKVTLNDGRDAGLLLPRGLLLRGGDVLSNEEGTEFVQVIAA

>d1eara1 b.107.1.1 (A:1-74) Urease metallochaperone UreE, N-terminal domain {Bacillus pasteurii}

MVITKIVGHIDDLSHQIKKVDWLEVEWEDLNKRILRKETENGTDIAIKLENSGTLRYGDVLYESDDTLIAIRTK

>d2eng\_\_ b.52.1.1 (-) Endoglucanase V {Humicola insolens}

ADGRSTRYWDCCKPSCGWAKKAPVNQPVFSCNANFQRITDFDAKSGCEPGGVAYSCADQTPWAVNDDFALGFAATSIAGSNEAGWCCACYELTFTSGPVAGKKMVVQSTSTGGDLGSNHFDLNIPGGGVGIFDGCTPQFGGLPGQRYGGISSRNECDRFPDALKPGCYWRFDWFKNADNPSFSFRQVQCPAELVARTGCRRNDDGNFPAV

>d1bw3\_\_ b.52.1.2 (-) Barwin {Barley (Hordeum vulgare)}

EQANDVRATYHYYRPAQNNWDLGAPAVSAYCATWDASKPLSWRSKYGWTAFCGPAGPRGQAACGKCLRVTNPATGAQITARIVDQCANGGLDLDWDTVFTKIDTNGIGYQQGHLNVNYQFVDCRD

>g1aw8.1 b.52.2.1 (A:,B:) Pyruvoyl dependent aspartate decarboxylase, ADC {Escherichia coli}

MIRTMLQGKLHRVKVTHADLHYEGXSCAIDQDFLDAAGILENEAIDIWNVTNGKRFSTYAIAAERGSRIISVNGAAAHCASVGDIVIIASFVTMPDEEARTWRPNVAYFEGDNEMK

>d1eu1a1 b.52.2.2 (A:626-780) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter sphaeroides}

ERLGGAGAKYPLHVVASHPKSRLHSQLNGTSLRDLYAVAGHEPCLINPADAAARGIADGDVLRVFNDRGQILVGAKVSDAVMPGAIQIYEGGWYDPLDPSEEGTLDKYGDVNVLSLDVGTSKLAQGNCGQTILADVEKYAGAPVTVTVFDTPKGA

>d1dmr\_1 b.52.2.2 (626-781) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter capsulatus}

ERLDGPGAKYPLHIAASHPFNRLHSQLNGTVLREGYAVQGHEPCLMHPDDAAARGIADGDVVRVHNDRGQILTGVKVTDAVMKGVIQIYEGGWYDPSDVTEPGTLDKYGDVNVLSADIGTSKLAQGNCGQTVLAEVEKYTGPAVTLTGFVAPKAAE

>d1aa6\_1 b.52.2.2 (565-715) Formate dehydrogenase H {Escherichia coli}

PIDKLTDEYPMVLSTVREVGHYSCRSMTGNCAALAALADEPGYAQINTEDAKRLGIEDEALVWVHSRKGKIITRAQVSDRPNKGAIYMTYQWWIGACNELVTENLSPITKTPEYKYCAVRVEPIADQRAAEQYVIDEYNKLKTRLREAALA

>d1tmo\_1 b.52.2.2 (632-798) Trimethylamine N-oxide reductase {Shewanella massilia}

ERSHGGPGSDKHPIWLQSCHPDKRLHSQMCESREYRETYAVNGREPVYISPVDAKARGIKDGDIVRVFNDRGQLLAGAVVSDNFPKGIVRIHEGAWYGPVGKDGSTEGGAEVGALCSYGDPNTLTLDIGTSKLAQACSAYTCLVEFEKYQGKVPKVSSFDGPIEVEI

>d1g8ka1 b.52.2.2 (A:683-825) Arsenite oxidase large subunit {Alcaligenes faecalis}

LPATVQQQKDKYRFWLNNGRNNEVWQTAYHDQYNSLMQERYPMAYIEMNPDDCKQLDVTGGDIVEVYNDFGSTFAMVYPVAEIKRGQTFMLFGYVNGIQGDVTTDWTDRDIIPYYKGTWGDIRKVGSMSEFKRTVSFKSRRFG

>d2napa1 b.52.2.2 (A:601-723) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}

AAEEPDAEYPLYLTSMRVIDHWHTATMTGKVPELQKANPIAFVEINEEDAARTGIKHGDSVIVETRRDAMELPARVSDVCRPGLIAVPFFDPKKLVNKLFLDATDPVSREPEYKICAARVRKA

>d1qcsa1 b.52.2.3 (A:0-85) N-terminal domain of NSF-N, NSF-Nn {Hamster (Cricetulus griseus)}

NMAGRSMQAARCPTDELSLSNCAVVSEKDYQSGQHVIVRTSPNHKYIFTLRTHPSVVPGSVAFSLPQRKWAGLSIGQEIEVALYSF

>d1cr5a1 b.52.2.3 (A:26-107) N-terminal domain of NSF-N, NSF-Nn {Baker's yeast (Saccharomyces cerevisiae), sec18p}

TRHLKVSNCPNNSYALANVAAVSPNDFPNNIYIIIDNLFVFTTRHSNDIPPGTIGFNGNQRTWGGWSLNQDVQAKAFDLFKY

>d1cz4a1 b.52.2.3 (A:1-91) N-terminal domain of VAT-N, VAT-Nn {Archaeon Thermoplasma acidophilum}

MESNNGIILRVAEANSTDPGMSRVRLDESSRRLLDAEIGDVVEIEKVRKTVGRVYRARPEDENKGIVRIDSVMRNNCGASIGDKVKVRKVR

>d1e32a1 b.52.2.3 (A:21-106) Membrane fusion atpase p97 N-terminal domain , P97-Nn {Mouse (Mus musculus)}

NRPNRLIVDEAINEDNSVVSLSQPKMDELQLFRGDTVLLKGKKRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVISIQPCP

>d1dfup\_ b.53.1.1 (P:) Ribosomal protein L25 {Escherichia coli}

MFTINAEVRKEQGKGASRRLRAANKFPAIIYGGKEAPLAIELDHDKVMNMQAKAEFYSEVLTIVVDGKEIKVKAQDVQRHPYKPKLQHIDFVRA

>d1feua\_ b.53.1.1 (A:) Ribosomal protein TL5 (general stress protein CTC) {Thermus thermophilus}

MEYRLKAYYREGEKPSALRRAGKLPGLMYNRHLNRKVYVDLVEFDKVFRQASIHHVIVLELPDGQSLPTLVRQVNLDKRRRRPEHVDFFVLSDEPVEMYVPLRFVGTPAGVRAGGVLQEIHRDILVKVSPRNIPEFIEVDVSGLEIGDSLHASDLKLPPGVELAVSPEETIAAVVPPEDVEKLAE

>d1gtra1 b.53.1.2 (A:339-547) Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain {Escherichia coli}

APRAMAVIDPVKLVIENYQGEGEMVTMPNHPNKPEMGSRQVPFSGEIWIDRADFREEANKQYKRLVLGKEVRLRNAYVIKAERVEKDAEGNITTIFCTYDADTLSKDPADGRKVKGVIHWVSAAHALPVEIRLYDRLFSVPNPGAADDFLSVINPESLVIKQGFAEPSLKDAVAGKAFQFEREGYFCLDSRHSTAEKPVFNRTVGLRDT

>d1h9db\_ b.54.1.1 (B:) Core binding factor beta, CBF {Human (Homo sapiens)}

PRVVPDQRSKFENEEFFRKLSRECEIKYTGFRDRPHEERQARFQNACRDGRSEIAFVATGTNLSLQFFPASWQGEQRQTPSREYVDLEREAGKVYLKAPMILNGVCVIWKGWIDLQRLDGMGCLEFDEERAQQE

>d1mai\_\_ b.55.1.1 (-) Phospholipase C delta-1 {Rat (Rattus norvegicus)}

GLQDDPDLQALLKGSQLLKVKSSSWRRERFYKLQEDCKTIWQESRKVMRSPESQLFSIEDIQEVRMGHRTEGLEKFARDIPEDRCFSIVFKDQRNTLDLIAPSPADAQHWVQGLRKIIH

>d1btn\_\_ b.55.1.1 (-) beta-spectrin {Mouse (Mus musculus), brain}

MEGFLNRKHEWEAHNKKASSRSWHNVYCVINNQEMGFYKDAKSAASGIPYHSEVPVSLKEAICEVALDYKKKKHVFKLRLSDGNEYLFQAKDDEEMNTWIQAISSA

>d1dro\_\_ b.55.1.1 (-) beta-spectrin {Fruit fly (Drosophila melanogaster)}

GSGTGAGEGHEGYVTRKHEWDSTTKKASNRSWDKVYMAAKAGRISFYKDQKGYKSNPELTFRGEPSYDLQNAAIEIASDYTKKKHVLRVKLANGALFLLQAHDDTEMSQWVTSLKAQSDSTA

>d1dyna\_ b.55.1.1 (A:) Dynamin {Human (Homo sapiens)}

ILVIRKGWLTINNIGIMKGGSKEYWFVLTAENLSWYKDDEEKEKKYMLSVDNLKLRDVEKGFMSSKHIFALFNTEQRNVYKDYRQLELACETQEEVDSWKASFLRAGVYPERV

>d1btka\_ b.55.1.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}

AAVILESIFLKRSQQKKKTSPLNFKKCLFLLTVHKLSYYEYDFERGRRGSKKGSIDVEKITCVETVVPEKNPPPERQIPRRGEESSEMEQISIIERFPYPFQVVYDEGPLYVFSPTEELRKRWIHQLKNVIRYNSDLVQKYHPCFWIDGQYLCCSQTAKNAMGCQILEN

>d1pls\_\_ b.55.1.1 (-) Pleckstrin, N-terminal domain {Human (Homo sapiens)}

MEPKRIREGYLVKKGSVFNTWKPMWVVLLEDGIEFYKKKSDNSPKGMIPLKGSTLTSPCQDFGKRMFVFKITTTKQQDHFFQAAFLEERDAWVRDINKAIKCIEGLEHHHHHH

>d1dbha2 b.55.1.1 (A:418-550) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}

AIKKMNEIQKNIDGWEGKDIGQCCNEFIMEGTLTRVGAKHERHIFLFDGLMICCKSNHGQPRLPGASNAEYRLKEKFFMRKVQINDKDDTNEYKHAFEIILKDENSVIFSAKSAEEKNNWMAALISLQYRSTL

>d1foea2 b.55.1.1 (A:1240-1401) GEF of TIAM1 (T-Lymphoma invasion and metastasis indusing protein 1) {Mouse (Mus musculus)}

EFGAVFDQLIAEQTGEKKEVADLSMGDLLLHTSVIWLNPPASLGKWKKEPELAAFVFKTAVVLVYKDGSKQKKKLVGSHRLSIYEEWDPFRFRHMIPTEALQVRALPSADAEANAVCEIVHVKSESEGRPERVFHLCCSSPESRKDFLKSVHSILRDKHRRQ

>d1bak\_\_ b.55.1.1 (-) G-protein coupled receptor kinase 2 (beta-adrenergic receptor kinase 1) {Human (Homo sapiens)}

GSHMGKDCIMHGYMSKMGNPFLTQWQRRYFYLFPNRLEWRGEGEAPQSLLTMEEIQSVEETQIKERKCLLLKIRGGKQFILQCDSDPELVQWKKELRDAYREAQQLVQRVPKMKNKPRS

>d1faoa\_ b.55.1.1 (A:) Dual adaptor of phosphotyrosine and 3-phosphoinositides DAPP1/PHISH {Human (Homo sapiens)}

PSLGTKEGYLTKQGGLVKTWKTRWFTLHRNELKYFKDQMSPEPIRILDLTECSAVQFDYSQERVNCFCLVFPFRTFYLCAKTGVEADEWIKILRWKLSQI

>d1fgya\_ b.55.1.1 (A:) Grp1 {Mouse (Mus musculus)}

TFFNPDREGWLLKLGGRVKTWKRRWFILTDNCLYYFEYTTDKEPRGIIPLENLSIREVLDPRKPNCFELYNPSHKGQVIKACKTEADGRVVEGNHVVYRISAPSPEEKEEWMKSIKASISRDPFYDM

>d1fhoa\_ b.55.1.1 (A:) UNC-89 {Nematode (Caenorhabditis elegans)}

MGDTGKLGRIIRHDAFQVWEGDEPPKLRYVFLFRNKIMFTEQDASTSPPSYTHYSSIRLDKYNIRQHTTDEDTIVLQPQEPGLPSFRIKPKDFETSEYVRKAWLRDIAEEQEKYAAERD

>d1aqca\_ b.55.1.2 (A:) X11 {Human (Homo sapiens)}

MEDLIDGIIFAANYLGSTQLLSDKTPSKNVRMMQAQEAVSRIKMAQKLAKSRKKAPEGESQPMTEVDLFILTQRIKVLNADTQETMMDHPLRTISYIADIGNIVVLMARRRIPRSNSQENVEASHPSQDGKRQYKMICHVFESEDAQLIAQSIGQAFSVAYQEFLR

>d1qqga1 b.55.1.2 (A:12-114) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

DVRKVGYLRKPKSMHKRFFVLRAASEAGGPARLEYYENEKKWRHKSSAPKRSIPLESCFNINKRADSKNKHLVALYTRDEHFAIAADSEAEQDSWYQALLQLH

>d1qqga2 b.55.1.2 (A:159-262) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

AFKEVWQVILKPKGLGQTKNLIGIYRLCLTSKTISFVKLNSEAAAVVLQLMNIRRCGHSENFFFIEVGRSAVTGPGEFWMQVDDSVVAQNMHETILEAMRAMSD

>d1shca\_ b.55.1.2 (A:) Shc adaptor protein {Human (Homo sapiens)}

GSHMGQLGGEEWTRHGSFVNKPTRGWLHPNDKVMGPGVSYLVRYMGCVEVLQSMRALDFNTRTQVTREAISLVCEAVPGAKGATRRRKPCSRPLSSILGRSNLKFAGMPITLTVSTSSLNLMAADCKQIIANHHMQSISFASGGDPDTAEYVAYVAKDPVNQRACHILECPEGLAQDVISTIGQAFELRFKQYLR

>d1ddma\_ b.55.1.2 (A:) Numb {Fruit fly (Drosophila melanogaster)}

HQWQADEEAVRSATCSFSVKYLGCVEVFESRGMQVCEEALKVLRQSRRRPVRGLLHVSGDGLRVVDDETKGLIVDQTIEKVSFCAPDRNHERGFSYICRDGTTRRWMCHGFLACKDSGERLSHAVGCAFAVCLER

>d1rrpb\_ b.55.1.3 (B:) Nuclear pore complex protein Nup358 {Human (Homo sapiens)}

HFEPVVPLPDKIEVKTGEEDEEEFFCNRAKLFRFDVESKEWKERGIGNVKILRHKTSGKIRLLMRREQVLKICANHYISPDMKLTPNAGSDRSFVWHALDYADELPKPEQLAIRFKTPEEAALFKCKFEEAQSI

>d1k5db\_ b.55.1.3 (B:) Ran-binding protein 1, Ranbp1 {Human (Homo sapiens)}

NHDPQFEPIVSLPEQEIKTLEEDEEELFKMRAKLFRFASENDLPEWKERGTGDVKLLKHKEKGAIRLLMRRDKTLKICANHYITPMMELKPNAGSDRAWVWNTHADFADECPKPELLAIRFLNAENAQKFKTKFEECRKEIEEREK

>d1evha\_ b.55.1.4 (A:) Enabled {Mouse (Mus musculus)}

SEQSICQARAAVMVYDDANKKWVPAGGSTGFSRVHIYHHTGNNTFRVVGRKIQDHQVVINCAIPKGLKYNQATQTFHQWRDARQVYGLNFGSKEDANVFASAMMHALEVLN

>d1qc6a\_ b.55.1.4 (A:) Ena/vasp-like protein {Mouse (Mus musculus)}

MSEQSICQARASVMVYDDTSKKWVPIKPGQQGFSRINIYHNTASSTFRVVGVKLQDQQVVINYSIVKGLKYNQATPTFHQWRDARQVYGLNFASKEEATTFSNAMLFALNIMN

>d1egxa\_ b.55.1.4 (A:) Vasodilator-stimulated phosphoprotein (VASP) {Human (Homo sapiens)}

MSETVICSSRATVMLYDDGNKRWLPAGTGPQAFSRVQIYHNPTANSFRVVGRKMQPDQQVVINCAIVRGVKYNQATPNFHQWRDARQVWGLNFGSKEDAAQFAAGMASALEALEG

>d1ddwa\_ b.55.1.4 (A:) Homer {Rat (Rattus norvegicus)}

MGEQPIFSTRAHVFQIDPNTKKNWVPTSKHAVTVSYFYDSTRNVYRIISLDGSKAIINSTITPNMTFTKTSQKFGQWADSRANTVYGLGFSSEHHLSKFAEKFQEFKEAAR

>d1i7aa\_ b.55.1.4 (A:) Homer {Mouse (Mus musculus), 2b/vesl 2}

EQPIFTTRAHVFQIDPSTKKNWVPASKQAVTVSYFYDVTRNSYRIISVDGAKVIINSTITPNMTFTKTSQKFGQWADSRANTVFGLGFSSELQLTKFAEKFQEVREAAR

>d1e5wa2 b.55.1.5 (A:199-346) Moesin {Human (Homo sapiens)}

EMYGVNYFSIKNKKGSELWLGVDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVFYAPRLRINKRILALCMGNHELYMRRRKPDTIEVQQMKAQAREEKHQKQMERAMLENEKKKREMAEKEKEKIEREKEE

>d1ef1a2 b.55.1.5 (A:199-297) Moesin {Human (Homo sapiens)}

EMYGVNYFSIKNKKGSELWLGVDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVFYAPRLRINKRILALCMGNHELYMRRRKP

>d1gc7a2 b.55.1.5 (A:199-297) Radixin {Mouse (Mus musculus)}

EMYGVNYFEIKNKKGTELWLGVDALGLNIYEHDDKLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVFYAPRLRINKRILALCMGNHELYMRRRKP

>d1gg3a2 b.55.1.5 (A:188-279) Erythroid membrane protein 4.1R {Human (Homo sapiens)}

GVDLHKAKDLEGVDIILGVCSSGLLVYKDKLRINRFPWPKVLKISYKRSSFFIKIRPGEQEQYESTIGFKLPSYRAAKKLWKVCVEHHTFFR

>d1h4ra2 b.55.1.5 (A:215-313) Merlin {Human (Homo sapiens)}

EMYGVNYFAIRNKKGTELLLGVDALGLHIYDPENRLTPKISFPWNEIRNISYSDKEFTIKPLDKKIDVFKFNSSKLRVNKLILQLCIGNHDLFMRRRKA

>d1ytfc1 b.56.1.1 (C:) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

ENLMLCLYDKVTRTKARWKCSLKDGVVTINRNDYTFQKAQVEAEWV

>d1ytfd2 b.56.1.1 (D:55-119) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

NTQSKLTVKGNLDTYGFCDDVWTFIVKNCQVTVEDSHRDASQNGSGDSQSVISVDKLRIVACNSK

>d1iega\_ b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}

QAVAPVYVGGFLARYDQSPDEAELLLPRDVVEHWLHAQGQGQPSLSVALPLNINHDDTAVVGHVAAMQSVRDGLFCLGCVTSPRFLEIVRRASEKSELVSRGPVSPLQPDKVVEFLSGSYAGLSLASRRCDDVEQATSLSGSETTPFKAVALCSVGRRRGTLAVYGRDPEWVTQRFPDLTAADRDGLRAQWQRCGSTAVDASGDPFRSDSYGLLGNSVDALYIRERLPKLRYDKQLVGVTERESYVKA

>d1jq6a\_ b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}

VAPVYVGGFLARYDQSPDEAELLLPRDVVEHWLHAQGQGQPSLSVALPLNINHDDTAVVGHVAAMQSVRDGLFCLGCVTSPRFLEIVRRASEKSELVSRGPVSPLQPDKVVEFLSGSYAGLSLSSRRCDDVEQATSLSGSETTPFKHVALCSVGRRRGTLAVYGRDPEWVTQRFPDLTAADRDGLRAQWQRCGSTAVDASGDPFRSDSYGLLGNYVDALY

>d1at3a\_ b.57.1.1 (A:) HSV-2 protease {Herpes simplex virus type 2}

RAVPIYVAGFLALYDSGDPGELALDPDTVRAALPPENPLPINVDHRARCEVGRVLAVVNDPRGPFFVGLIACVQLERVLETAASAAIFERRGPALSREERLLYLITNYLPSVSLSTKRRGDEVPPDRTLFAHVALCAIGRRLGTIVTYDTSLDAAIAPFRHLDPATREGVRREAAEAELALAGRTWAPGVEALTHTLLSTAVNNMMLRDRWSLVAERRRQAGIAGHTYLQA

>d1fl1a\_ b.57.1.1 (A:) KSHV protease {Kaposi's sarcoma-associated herpes virus}

AQGLYVGGFVDVVSCPKLEQELYLDPDQVTDYLPVTEPLPITIEHLPETEVGWTLGLFQVSHGIFCTGAITSPAFLELASRLADTSHVARAPVKNLPKEPLLEILHTWLPGLSLSSIHPRELSQTPSGPVFQHVSLCALGRRRGTVAVYGHDAEWVVSRFSSVSKSERAHILQHVSSCRLEDLSTPNFVSPLETLMAKAIDAGFIRDRLDLLKTDRGVASILSPVYLKA

>d1vzv\_\_ b.57.1.1 (-) VZV protease {Varicella-Zoster virus}

EALYVAGYLALYSKDEGELNITPEIVRSALPPTSKIPINIDHRKDCVVGEVIAIIEDIRGPFFLGIVRCPQLHAVLFEAAHSNFFGNRDSVLSPLERALYLVTNYLPSVSLSSKRLFTHVALCVVGRRVGTVVNYDCTPESSIEPFRVLSMESKARLLSLVKDYAGLNKVWKVSEDKLAKVLLSTAVNNMLLRDRWDVVAKRRREAGIMGH

>d1a49a1 b.58.1.1 (A:116-217) Pyruvate kinase (PK) {Rabbit (Oryctolagus cuniculus)}

PEIRTGLIKGSGTAEVELKKGATLKITLDNAYMEKCDENILWLDYKNICKVVDVGSKVYVDDGLISLQVKQKGPDFLVTEVENGGFLGSKKGVNLPGAAVDL

>d1pkm\_1 b.58.1.1 (116-217) Pyruvate kinase (PK) {Cat (Felis domestica)}

PEIRTGLIKGSGTAEVELKKGATLKITLDNAYMEKCDENVLWLDYKNICKVVEVGSKVYVDDGLISLLVKEKGADFLVTEVENGGSLGSKKGVNLPGAAVDL

>d1pkla1 b.58.1.1 (A:88-186) Pyruvate kinase (PK) {Leishmania mexicana}

EIRTGQFVGGDAVMERGATCYVTTDPAFADKGTKDKFYIDYQNLSKVVRPGNYIYIDDGILILQVQSHEDEQTLECTVTNSHTISDRRGVNLPGCDVDL

>d1a3wa1 b.58.1.1 (A:88-188) Pyruvate kinase (PK) {Baker's yeast (Saccharomyces cerevisiae)}

PEIRTGTTTNDVDYPIPPNHEMIFTTDDKYAKACDDKIMYVDYKNITKVISAGRIIYVDDGVLSFQVLEVVDDKTLKVKALNAGKICSHKGVNLPGTDVDL

>d1e0ta1 b.58.1.1 (A:70-167) Pyruvate kinase (PK) {Escherichia coli}

PEIRTMKLEGGNDVSLKAGQTFTFTTDKSVIGNSEMVAVTYEGFTTDLSVGNTVLVDDGLIGMEVTAIEGNKVICKVLNNGDLGENKGVNLPGVSIAL

>d1g8fa1 b.58.1.2 (A:2-168) ATP sulfurylase N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

PAPHGGILQDLIARDALKKNELLSEAQSSDILVWNLTPRQLCDIELILNGGFSPLTGFLNENDYSSVVTDSRLADGTLWTIPITLDVDEAFANQIKPDTRIALFQDDEIPIAILTVQDVYKPNKTIEAERVFRGDPEHPAISYLFNVAGDYYVGGSLEAIQLPQHYD

>d1i2da1 b.58.1.2 (A:2-170) ATP sulfurylase N-terminal domain {Fungus (Penicillium chrysogenum)}

ANAPHGGVLKDLLARDAPRQAELAAEAESLPAVTLTERQLCDLELIMNGGFSPLEGFMNQADYDRVCEDNRLADGNVFSMPITLDASQEVIDEKKLQAGSRITLRDFRDDRNLAILTIDDIYRPDKTKEAKLVFGGDPEHPAIVYLNNTVKEFYIGGKIEAVNKLNHYD

>d1jhda1 b.58.1.2 (A:1-173) ATP sulfurylase N-terminal domain {unnamed symbiont of Riftia pachyptila}

MIKPVGSDELKPLFVYDPEEHHKLSHEAESLPSVVISSQAAGNAVMMGAGYFSPLQGFMNVADAMGAAEKMTLSDGSFFPVPVLCLLENTDAIGDAKRIALRDPNVEGNPVLAVMDIEAIEEVSDEQMAVMTDKVYRTTDMDHIGVKTFNSQGRVAVSGPIQVLNFSYFQADF

>d1ik9a1 b.59.1.1 (A:1-117) XRCC4, N-terminal domain {Human (Homo sapiens)}

MERKISRIHLVSEPSITHFLQVSWEKTLESGFVITLTDGHSAWTGTVSESEISQEADDMAMEKGKYVGELRKALLSGAGPADVYTFNFSKESAYFFFEKNLKDVSFRLGSFNLEKVE

>d1hbq\_\_ b.60.1.1 (-) Retinol binding protein {Cow (Bos taurus)}

ERDCRVSSFRVKENFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGQMSATAKGRVRLLNNWDVCADMVGTFTDTEDPAKFKMKYWGVASFLQKGNDDHWIIDTDYETFAVQYSCRLLNLDGTCADSYSFVFARDPSGFSPEVQKIVRQRQEELCLARQYRLIPHNGYCNGK

>d1aqb\_\_ b.60.1.1 (-) Retinol binding protein {Pig (Sus scrofa domestica)}

ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDENGHMSATAKGRVRLLNNWDVCADMVGTFTDTEDPAKFKMKYWGVASFLQKGNDDHWIIDTDYDTYAVQYSCRLQNLDGTCADSYSFVFARDPHGFSPEVQKIVRQRQEELCLARQYRIITHNGYCD

>d1rbp\_\_ b.60.1.1 (-) Retinol binding protein {Human (Homo sapiens)}

ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDETGQMSATAKGRVRLLNNWDVCADMVGTFTDTEDPAKFKMKYWGVASFLQKGNDDHWIVDTDYDTYAVQYSCRLLNLDGTCADSYSFVFSRDPNGLPPEAQKIVRQRQEELCLARQYRLIVHNGYCD

>d1iiua\_ b.60.1.1 (A:) Retinol binding protein {Chicken (Gallus gallus), plasma isoform}

MDCRVSSFKVKENFDKNRYSGTWYAMAKKDPEGLFLQDNVVAQFTVDENGQMSATAKGRVRLFNNWDVCADMIGSFTDTEDPAKFKMKYWGVASFLQKGNDDHWVVDTDYDTYALHYSCRELNEDGTCADSYSFVFSRDPKGLPPEAQKIVRQRQIDLCLDRKYRVIVHNGFCS

>d1hn2a\_ b.60.1.1 (A:) Odorant-binding protein {Cow (Bos taurus)}

AQEEEAEQNLSELSGPWRTVYIGSTNPEKIQENGPFRTYFRELVFDDEKGTVDFYFSVKRDGKWKNVHVKATKQDDGTYVADYEGQNVFKIVSLSRTHLVAHNINVDKHGQTTELTELFVKLNVEDEDLEKFWKLTEDKGIDKKNVVNFLENENHPHPE

>d1dzka\_ b.60.1.1 (A:) Odorant-binding protein {Pig (Sus scrofa)}

FELSGKWITSYIGSSDLEKIGENAPFQVFMRSIEFDDKESKVYLNFFSKENGICEEFSLIGTKQEGNTYDVNYAGNNKFVVSYASETALIISNINVDEEGDKTIMTGLLGKGTDIEDQDLEKFKEVTRENGIPEENIVNIIERDDCPA

>d1bj7\_\_ b.60.1.1 (-) Lipocalin allergen {Cow (Bos taurus), bos d 2}

IDPSKIPGEWRIIYAAADNKDKIVEGGPLRNYYRRIECINDCESLSITFYLKDQGTCLLLTEVAKRQEGYVYVLEFYGTNTLEVIHVSENMLVTYVENYDGERITKMTEGLAKGTSFTPEELEKYQQLNSERGVPNENIENLIKTDNCPP

>d1ew3a\_ b.60.1.1 (A:) Lipocalin allergen {Horse (Equus caballus), equ c 1}

VAIRNFDISKISGEWYSIFLASDVKEKIEENGSMRVFVDVIRALDNSSLYAEYQTKVNGECTEFPMVFDKTEEDGVYSLNYDGYNVFRISEFENDEHIILYLVNFDKDRPFQLFEFYAREPDVSPEIKEEFVKIVQKRGIVKENIIDLTKIDRCFQLRG

>d1e5pa\_ b.60.1.1 (A:) Aphrodisin, a sex pheromone {Golden hamster (Mesocricetus auratus)}

FAELQGKWYTIVIAADNLEKIEEGGPLRFYFRHIDCYKNCSEMEITFYVITNNQCSKTTVIGYLKGNGTYETQFEGNNIFQPLYITSDKIFFTNKNMDRAGQETNMIVVAGKGNALTPEENEILVQFAHEKKIPVENILNILATDTCPE

>d1beba\_ b.60.1.1 (A:) beta-Lactoglobulin {Cow (Bos taurus)}

QTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVEELKPTPEGDLEILLQKWENGECAQKKIIAEKTKIPAVFKIDALNENKVLVLDTDYKKYLLFCMENSAEPEQSLVCQCLVRTPEVDDEALEKFDKALKALPMHIRLSFNPTQLEEQC

>d1exsa\_ b.60.1.1 (A:) beta-Lactoglobulin {Pig (Sus scrofa)}

VEVTPIMTELDTQKVAGTWHTVAMAVSDVSLLDAKSSPLKAYVEGLKPTPEGDLEILLQKRENDKCAQEVLLAKKTDIPAVFKINALDENQLFLLDTDYDSHLLLCMENSASPEHSLVCQSLARTLEVDDQIREKFEDALKTLSVPMRILPAQLEEQCRV

>d1epba\_ b.60.1.1 (A:) Retinoic acid-binding protein {Rat (Rattus norvegicus), albino}

VKDFDISKFLGFWYEIAFASKMGTPGLAHKEEKMGAMVVELKENLLALTTTYYSEDHCVLEKVTATEGDGPAKFQVTRLSGKKEVVVEATDYLTYAIIDITSLVAGAVHRTMKLYSRSLDDNGEALYNFRKITSDHGFSETDLYILKHDLTCVKVLQSAA

>d1jv4a\_ b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Mouse (Mus musculus)}

EEASSTGRNFNVEKINGEWHTIILASDKREKIEDNGNFRLFLEQIHVLEKSLVLKFHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNFLMAHLINEKDGETFQLMGLYGREPDLSSDIKERFAQLCEEHGILRENIIDLSNANRC

>d2a2ua\_ b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Rat (Rattus norvegicus)}

EEASSTRGNLDVAKLNGDWFSIVVASNKREKIEENGSMRVFMQHIDVLENSLGFKFRIKENGECRELYLVAYKTPEDGEYFVEYDGGNTFTILKTDYDRYVMFHLINFKNGETFQLMVLYGRTKDLSSDIKEKFAKLCEAHGITRDNIIDLTKTDRCL

>d1qqsa\_ b.60.1.1 (A:) Neutrophil gelatinase-associated lipocalin (NGAL) {Human (Homo sapiens)}

TSDLIPAPPLSKVPLQQNFQDNQFQGKWYVVGLAGNAILREDKDPQKMYATIYEEKEDASYNVTSVLFRKKKCDYAIRTFVPGCQPGEFTLGNIKSYPGLTSYLVRVVSTNYNQHAMVFFKKVSQNREYFKITLYGRTKELTSELKNNFIRFSKSLGLPENHIVFPVPIDQCID

>d1bbpa\_ b.60.1.1 (A:) Bilin-binding protein {Cabbage butterfly (Pieris brassicae)}

NVYHDGACPEVKPVDNFDWSNYHGKWWEVAKYPNSVEKYGKCGWAEYTPEGKSVKVSNYHVIHGKEYFIEGTAYPVGDSKIGKIYHKLTYGGVTKENVFNVLSTDNKNYIIGYYCKYDEDKKGHQDFVWVLSRSKVLTGEAKTAVENYLIGSPVVDSQKLVYSDFSEAACKVN

>d1i4ua\_ b.60.1.1 (A:) Alpha-crustacyanin {European lobster (Homarus gammarus)}

DKIPDFVVPGKCASVDRNKLWAEQTPNRNSYAGVWYQFALTNNPYQLIEKCVRNEYSFDGKQFVIESTGIAYDGNLLKRNGKLYPNPFGEPHLSIDYENSFAAPLVILETDYSNYACLYSCIDYNFGYHSDFSFIFSRSANLADQYVKKCEAAFKNINVDTTRFVKTVQGSSCPYDTQKTL

>d1qfta\_ b.60.1.1 (A:) Histamine binding protein {Brown ear tick (Rhipicephalus appendiculatus)}

NQPDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCDVIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLEIAAA

>d1np1a\_ b.60.1.1 (A:) Nitrophorin 1 {Rhodnius prolixus}

KCTKNALAQTGFNKDKYFNGDVWYVTDYLDLEPDDVPKRYCAALAAGTASGKLKEALYHYDPKTQDTFYDVSELQEESPGKYTANFKKVEKNGNVKVDVTSGNYYTFTVMYADDSSALIHTCLHKGNKDLGDLYAVLNRNKDTNAGDKVKGAVTAASLKFSDFISTKDNKCEYDNVSLKSLLTK

>d1euoa\_ b.60.1.1 (A:) Nitrophorin 2 (prolixin-s) {Rhodnius prolixus}

MDCSTNISPKQGLDKAKYFSGKWYVTHFLDKDPQVTDQYCSSFTPRESDGTVKEALYHYNANKKTSFYNIGEGKLESSGLQYTAKYKTVDKKKAVLKEADEKNSYTLTVLEADDSSALVHICLREGSKDLGDLYTVLTHQKDAEPSAKVKSAVTQAGLQLSQFVGTKDLGCQYDDQFTSL

>d1koia\_ b.60.1.1 (A:) Nitrophorin 4 {Rhodnius prolixus}

ACTKNAIAQTGFNKDKYFNGDVWYVTDYLDLEPDDVPKRYCAALAAGTASGKLKEALYHYDPKTQDTFYDVSELQVESLGKYTANFKKVDKNGNVKVAVTAGNYYTFTVMYADDSSALIHTCLHKGNKDLGDLYAVLNRNKDAAAGDKVKSAVSAATLEFSKFISTKENNCAYDNDSLKSLLTK

>d1hms\_\_ b.60.1.2 (-) Muscle fatty acid binding protein (m-fabp) {Human (Homo sapiens)}

VDAFLGTWKLVDSKNFDDYMKSLGVGFATRQVASMTKPTTIIEKNGDILTLKTHSTFKNTEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHLQKWDGQETTLVRELIDGKLILTLTHGTAVCTRTYEKE

>d1bwya\_ b.60.1.2 (A:) Muscle fatty acid binding protein (m-fabp) {Cow (Bos taurus)}

VDAFVGTWKLVDSKNFDDYMKSLGVGFATRQVGNMTKPTTIIEVNGDTVIIKTQSTFKNTEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHVQKWNGQETSLVREMVDGKLILTLTHGTAVCTRTYEKQA

>d1a57\_\_ b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}

AFDGTWKVDRNENYSGAHDNLKLTITQEGNKFTVKESSNFRNIDVVFELGVDFAYSLADGTELTGTWTMEGNKLVGKFKRVDNGKELIAVREISGNELIQTYTYEGVEAKRIFKKE

>d1ifc\_\_ b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}

AFDGTWKVDRNENYEKFMEKMGINVVKRKLGAHDNLKLTITQEGNKFTVKESSNFRNIDVVFELGVDFAYSLADGTELTGTWTMEGNKLVGKFKRVDNGKELIAVREISGNELIQTYTYEGVEAKRIFKKE

>d3ifba\_ b.60.1.2 (A:) Intestinal fatty acid binding protein {Human (Homo sapiens)}

AFDSTWKVDRSENYDKFMEKMGVNIVKRKLAAHDNLKLTITQEGNKFTVKESSAFRNIEVVFELGVTFNYNLADGTELRGTWSLEGNKLIGKFKRTDNGNELNTVREIIGDELVQTYVYEGVEAKRIFKKD

>d1fdqa\_ b.60.1.2 (A:) Brain fatty acid binding protein {Human (Homo sapiens)}

VEAFCATWKLTNSQNFDEYMKALGVGFATRQVGNVTKPTVIISQEGDKVVIRTLSTFKNTEISFQLGEEFDETTADDRNCKSVVSLDGDKLVHIQKWDGKETNFVREIKDGKMVMTLTFGDVVAVRHYEKA

>d1b56\_\_ b.60.1.2 (-) Epidermal fatty acid binding protein {Human (Homo sapiens)}

TVQQLEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKTTQFSCTLGEKFEETTADGRKTQTVCNFTDGALVQHQEWDGKESTITRKLKDGKLVVECVMNNVTCTRIYEKVE

>d1lid\_\_ b.60.1.2 (-) Adipocyte lipid-binding protein, ALBP {Mouse (Mus musculus)}

CDAFVGTWKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDLVTIRSESTFKNTEISFKLGVEFDEITADDRKVKSIITLDGGALVQVQKWDGKSTTIKRKRDGDKLVVECVMKGVTSTRVYERA

>d1mdc\_\_ b.60.1.2 (-) Fatty acid-binding protein {Tobacco hornworm (Manduca sexta)}

SYLGKVYSLVKQENFDGFLKSAGLSDDKIQALVSDKPTQKMEANGDSYSNTSTGGGGAKTVSFKSGVEFDDVIGAGDSVKSMYTVDGNVVTHVVKGDAGVATFKKEYNGDDLVVTITSSNWDGVARRYYKA

>d1ftpa\_ b.60.1.2 (A:) Fatty acid-binding protein {Desert locust (Schistocerca gregaria)}

VKEFAGIKYKLDSQTNFEEYMKAIGVGAIERKAGLALSPVIELEILDGDKFKLTSKTAIKNTEFTFKLGEEFDEETLDGRKVKSTITQDGPNKLVHEQKGDHPTIIIREFSKEQCVITIKLGDLVATRIYKAQ

>d1cbs\_\_ b.60.1.2 (-) Cellular retinoic-acid-binding protein (CRABP) {Human (Homo sapiens), CRABP-II}

PNFSGNWKIIRSENFEELLKVLGVNVMLRKIAVAAASKPAVEIKQEGDTFYIKTSTTVRTTEINFKVGEEFEEQTVDGRPCKSLVKWESENKMVCEQKLLKGEGPKTSWTRELTNDGELILTMTADDVVCTRVYVRE

>d1cbia\_ b.60.1.2 (A:) Cellular retinoic-acid-binding protein (CRABP) {Cow and mouse (Bos taurus) and (Mus musculus), CRABP-I, identical sequences}

PNFAGTWKMRSSENFDELLKALGVNAMLRKVAVAAASKPHVEIRQDGDQFYIKTSTTVRTTEINFKVGEGFEEETVDGRKCRSLPTWENENKIHCTQTLLEGDGPKTYWTRELANDELILTFGADDVVCTRIYVRE

>d1crb\_\_ b.60.1.2 (-) Cellular retinol-binding protein II (CRBP) {Rat (Rattus norvegicus)}

PVDFNGYWKMLSNENFEEYLRALDVNVALRKIANLLKPDKEIVQDGDHMIIRTLSTFRNYIMDFQVGKEFEEDLTGIDDRKCMTTVSWDGDKLQCVQKGEKEGRGWTQWIEGDELHLEMRAEGVTCKQVFKKVH

>d1opaa\_ b.60.1.2 (A:) Cellular retinol-binding protein II (CRBP) {Rat (Rattus norvegicus)}

TKDQNGTWEMESNENFEGYMKALDIDFATRKIAVRLTQTKIIVQDGDNFKTKTNSTFRNYDLDFTVGVEFDEHTKGLDGRNVKTLVTWEGNTLVCVQKGEKENRGWKQWVEGDKLYLELTCGDQVCRQVFKKK

>d1ggla\_ b.60.1.2 (A:) Cellular retinol-binding protein III {Human (Homo sapiens)}

PPNLTGYYRFVSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVCVQKGEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVH

>d1lfo\_\_ b.60.1.2 (-) Liver fatty acid binding protein {Rat (Rattus norvegicus)}

MNFSGKYQVQSQENFEPFMKAMGLPEDLIQKGKDIKGVSEIVHEGKKVKLTITYGSKVIHNEFTLGEECELETMTGEKVKAVVKMEGDNKMVTTFKGIKSVTEFNGDTITNTMTLGDIVYKRVSKRI

>d1pmpa\_ b.60.1.2 (A:) P2 myelin protein {Cow (Bos taurus), caudal spinal root myelin}

SNKFLGTWKLVSSENFDEYMKALGVGLATRKLGNLAKPRVIISKKGDIITIRTESPFKNTEISFKLGQEFEETTADNRKTKSTVTLARGSLNQVQKWNGNETTIKRKLVDGKMVVECKMKDVVCTRIYEKV

>d1eal\_\_ b.60.1.2 (-) Ileal lipid binding protein {Pig (Sus scrofa)}

AFTGKYEIESEKNYDEFMKRLALPSDAIDKARNLKIISEVKQDGQNFTWSQQYPGGHSITNTFTIGKECDIETIGGKKFKATVQMEGGKVVVNSPNYHHTAEIVDGKLVEVSTVGGVSYERVSKKLA

>d1avgi\_ b.60.1.3 (I:) Thrombin inhibitor {Triatomine bug (Triatoma pallidipennis)}

AEGDDCSIEKAMGDFKPEEFFNGTWYLAHGPGVTSPAVCQKFTTSGSKGFTQIVEIGYNKFESNVKFQCNQVDNKNGEQYSFKCKSSDNTEFEADFTFISVSYDNFALVCRSITFTSQPKEDRYLVFERTKSDTDPDAKEIC

>d1swga\_ b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}

SRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKPSAASGGGSAEAGITGTWYNQLGSTFIVTAGADGALTGTYESA

>d1swua\_ b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}

GITGTWYNQLGSTFIVTAGADGALTGTFESAVGNAESRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLLTSGTTEANAWKSTLVGHDTFTKVKP

>d1ij8a\_ b.61.1.1 (A:) Avidin {Chicken (Gallus gallus)}

KCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYTTAVTATSNEIKESPLHGTENTINKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGINIFTRL

>d1smpi\_ b.61.2.1 (I:) Metalloprotease inhibitor {Erwinia chrysanthemi}

SSLRLPSAAELSGQWVLSGAEQHCDIRLNTDVLDGTTWKLAGDTACLQKLLPEAPVGWRPTPDGLTLTQADGSAVAFFSRNRDRYEHKLVDGSVRTLKKK

>d1jiwi\_ b.61.2.1 (I:) Metalloprotease inhibitor {Pseudomonas aeruginosa, aprin}

SSLILLSASDLAGQWTLQQDEAPAICHLELRDSEVAEASGYDLGGDTACLTRWLPSEPRAWRPTPAGIALLERGGLTLMLLGRQGEGDYRVQKGDGGQLVLRRAT

>d1ei5a1 b.61.3.1 (A:336-417) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum anthropi}

EVSRVEADSAWFGSWLDDETGLVLSLEDAGHGRMKARFGTSPEMMDVVSANEARSAVTTIRRDGETIELVRASENLRLSMKR

>d1ei5a2 b.61.3.1 (A:418-520) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum anthropi}

VKGEAKHDIIGRYHSDELDADLLLVSEGGAIYGAFEGFLGKSDMYPLYSVGSDVWLLPVQRSMDAPSPGEWKLVFRRDDKGEITGLSVGCWLARGVEYRRVQP

>d1jjua5 b.61.4.1 (A:166-273) Quinohemoprotein amine dehydrogenase A chain, domain 3 {Paracoccus denitrificans}

PDAYADDASGAYVLAGRQPGRGDYTGRLVLKKAGEDYEVTMTLDFADGSRSFSGTGRILGAGEWRATLSDGTVTIRQIFALQDGRFSGRWHDADSDVIGGRLAAVKAD

>d1jmxa5 b.61.4.1 (A:163-281) Quinohemoprotein amine dehydrogenase A chain, domain 3 {Pseudomonas putida}

ESAAWAEWQKARPKADALPGQWAFSGHMLAKGDVRGVMSVTPDQGDTFKVEVKGAYADGTPFNGSGSAILYNGYEWRGNVKVGDANLRQVFAALDGEMKGRMFEAEHDERGLDFTAVKE

>d2cpl\_\_ b.62.1.1 (-) Cyclophilin (eukaryotic) {Human (Homo sapiens), variant A}

VNPTVFFDIAVDGEPLGRVSFELFADKVPKTAENFRALSTGEKGFGYKGSCFHRIIPGFMCQGGDFTRHNGTGGKSIYGEKFEDENFILKHTGPGILSMANAGPNTNGSQFFICTAKTEWLDGKHVVFGKVKEGMNIVEAMERFGSRNGKTSKKITIADCGQLE

>d1cyna\_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens), variant B}

GPKVTVKVYFDLRIGDEDVGRVIFGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENFKLKHYGPGWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKVLEGMEVVRKVESTKTDSRDKPLKDVIIADCGKIEVEKPFAIAKE

>d1qoia\_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens), U4/U6 snRNP-specific cyclophilin snucyp-20}

NSSPVNPVVFFDVSIGGQEVGRMKIELFADVVPKTAENFRQFCTGEFRKDGVPIGYKGSTFHRVIKDFMIQGGDFVNGDGTGVASIYRGPFADENFKLRHSAPGLLSMANSGPSTNGCQFFITCSKCDWLDGKHVVFGKIIDGLLVMRKIENVPTGPNNKPKLPVVISQCGEM

>d2rmca\_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Mouse (Mus musculus), variant C}

KRGPSVTDKVFFDVRIGDKDVGRIVIGLFGNVVPKTVENFVALATGEKGYGYKGSIFHRVIKDFMIQGGDFTARDGTGGMSIYGETFPDENFKLKHYGIGWVSMANAGPDTNGSQFFITLTKPTWLDGKHVVFGKVLDGMTVVHSIELQATDGHDRPLTDCTIVNSGKIDVKTPFVVEVPDW

>d1a33\_\_ b.62.1.1 (-) Cyclophilin (eukaryotic) {Nematode (Brugia malayi)}

KDRRRVFLDVTIDGNLAGRIVMELYNDIAPRTCNNFLMLCTGMAGTGKISGKPLHYKGSTFHRVIKNFMIQGGDFTKGDGTGGESIYGGMFDDEEFVMKHDEPFVVSMANKGPNTNGSQFFITTTPAPHLNNIHVVFGKVVSGQEVVTKIEYLKTNSKNRPLADVVILNCGELV

>d1dywa\_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Caenorhabditis elegans, isoform 3}

MSRSKVFFDITIGGKASGRIVMELYDDVVPKTAGNFRALCTGENGIGKSGKPLHFKGSKFHRIIPNFMIQGGDFTRGNGTGGESIYGEKFPDENFKEKHTGPGVLSMANAGPNTNGSQFFLCTVKTEWLDGKHVVFGRVVEGLDVVKAVESNGSQSGKPVKDCMIADCGQLK

>d1qnga\_ b.62.1.1 (A:) Cyclophilin (eukaryotic) {Plasmodium falciparum}

SKRSKVFFDISIDNSNAGRIIFELFSDITPRTCENFRALCTGEKIGSRGKNLHYKNSIFHRIIPQFMCQGGDITNGNGSGGESIYGRSFTDENFNMKHDQPGLLSMANAGPNTNSSQFFITLVPCPWLDGKHVVFGKVIEGMNVVREMEKEGAKSGYVKRSVVITDCGEL

>d1ihga2 b.62.1.1 (A:2-196) Cyclophilin 40 isomerase domain {Cow (Bos taurus)}

SHPSPQAKPSNPSNPRVFFDVDIGGERVGRIVLELFADIVPKTAENFRALCTGEKGIGPTTGKPLHFKGCPFHRIIKKFMIQGGDFSNQNGTGGESIYGEKFEDENFHYKHDKEGLLSMANAGSNTNGSQFFITTVPTPHLDGKHVVFGQVIKGMGVAKILENVEVKGEKPAKLCVIAECGELKEGDDWGIFPKD

>d1clh\_\_ b.62.1.1 (-) Bacterial cyclophilin {Escherichia coli}

AKGDPHVLLTTSAGNIELELDKQKAPVSVQNFVDYVNSGFYNNTTFHRVIPGFMIQGGGFTEQMQQKKPNPPIKNEADNGLRNTRGTIAMARTADKDSATSQFFINVADNAFLDHGQRDFGYAVFGKVVKGMDVADKISQVPTHDVGPYQNVPSKPVVILSAKVLP

>d1lopa\_ b.62.1.1 (A:) Bacterial cyclophilin {Escherichia coli}

MVTFHTNHGDIVIKTFDDKAPETVKNFLDYCREGFYNNTIFHRVINGFMIQGGGFEPGMKQKATKEPIKNEANNGLKNTRGTLAMARTQAPHSATAQFFINVVDNDFLNFSGESLQGWGYCVFAEVVDGMDEVDKIKGVATGRSGMHQDVPKEDVIIESVTVSE

>d1jsg\_\_ b.63.1.1 (-) p14-TCL1 {Human (Homo sapiens)}

CPTLGEAVTDHPDRLWAWEKFVYLDEKQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD

>d1jnpa\_ b.63.1.1 (A:) p14-TCL1 {Mouse (Mus musculus)}

RAETPAHPNRLWIWEKHVYLDEFRRSWLPVVIKSNEKFQVILRQEDVTLGEAMSPSQLVPYELPLMWQLYPKDRYRSADSMYWQILYHIKFRDVEDMLLEL

>d1a1x\_\_ b.63.1.1 (-) p13-MTCP1 {Human (Homo sapiens)}

AGEDVGAPPDHLWVHQEGIYRDEYQRTWVAVVEEETSFLRARVQQIQVPLGDAARPSHLLTSQLPLMWQLYPEERYMDNNSRLWQIQHHLMVRGVQELLLKLLPDD

>d1ijaa\_ b.100.1.1 (A:) Sortase {Staphylococcus aureus}

MQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVSFAEENESLDDQNISIAGHTFIDRPNYQFTNLKAAKKGSMVYFKVGNETRKYKMTSIRDVKPTDVGVLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEVK

>d1c39a\_ b.64.1.1 (A:) Cation-dependent mannose 6-phosphate receptor, extracytoplasmic domain {Cow (Bos taurus)}

EKTCDLVGEKGKESEKELALLKRLTPLFQKSFESTVGQSPDMYSYVFRVCREAGQHSSGAGLVQIQKSNGKETVVGRFNETQIFQGSNWIMLIYKGGDEYDNHCGREQRRAVVMISCNRHTLADNFNPVSEERGKVQDCFYLFEMDSSLACS

>d1e6fa\_ b.64.1.1 (A:) Cation-independent mannose-6-phosphate receptor (MIR-receptor) {Human (Homo sapiens)}

DDCQVTNPSTGHLFDLSSLSGRAGFTAAYSEKGLVYMSICGENENCPPGVGACFGQTRISVGKANKRLRYVDQVLQLVYKDGSPCPSKSGLSYKSVISFVCRPEAGPTNRPMLISLDKQTCTLFFSWHTPLACE

>d1f3ua\_ b.65.1.1 (A:) TFIIF beta subunit, Rap30 {Human (Homo sapiens)}

AERGELDLTGAKQNTGVWLVKVPKYLSQQWAKASGRGEVGKLRIAKTQGRTEVSFTLNEDLANIHDIGGKPASVSAPREHPFVLQSVGGQTLTVFTESSSDKLSLEGIVVQRAECRPA

>d1f3ub\_ b.65.1.1 (B:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}

GPSSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHR

>d1f3ud\_ b.65.1.1 (D:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}

SSQNVTEYVVRVPKNTTKKYNIMAFNAADKVNFATWNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQCPDGAFEAFPVHNWYNFTPLARHRTLTAEEAEEEWERRN

>d1hxn\_\_ b.66.1.1 (-) Hemopexin {Rabbit (Oryctolagus cuniculus)}

ESTRCDPDLVLSAMVSDNHGATYVFSGSHYWRLDTNRDGWHSWPIAHQWPQGPSTVDAAFSWEDKLYLIQDTKVYVFLTKGGYTLVNGYPKRLEKELGSPPVISLEAVDAAFVCPGSSRLHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKPLGPNSCSTSGPNLYLIHGPNLYCYRHVDKLNAAKNLPQPQRVSRLLGCTH

>d1qhua1 b.66.1.1 (A:24-215) Hemopexin {Rabbit (Oryctolagus cuniculus)}

IEQCSDGWSFDATTLDDNGTMLFFKDEFVWKSHRGIRELISERWKNFIGPVDAAFRHGHTSVYLIKGDKVWVYTSEKNEKVYPKSLQDEFPGIPFPLDAAVECHRGECQDEGILFFQGNRKWFWDLTTGTKKERSWPAVGNCTSALRWLGRYYCFQGNQFLRFNPVSGEVPPGYPLDVRDYFLSCPGRGHRS

>d1gen\_\_ b.66.1.1 (-) Gelatinase A (MMP-2), C-terminal domain {Human (Homo sapiens)}

LGPVTPEICKQDIVFDGIAQIRGEIFFFKDRFIWRTVTPRDKPMGPLLVATFWPELPEKIDAVYEAPQEEKAVFFAGNEYWIYSASTLERGYPKPLTSLGLPPDVQRVDAAFNWSKNKKTYIFAGDKFWRYNEVKKKMDPGFPKLIADAWNAIPDNLDAVVDLQGGGHSYFFKGAYYLKLENQSLKSVKFGSIKSDWLGC

>d1fbl\_1 b.66.1.1 (272-466) Collagenase, C-terminal domain {Pig (Sus scrofa)}

PQTPQVCDSKLTFDAITTLRGELMFFKDRFYMRTNSFYPEVELNFISVFWPQVPNGLQAAYEIADRDEVRFFKGNKYWAVRGQDVLYGYPKDIHRSFGFPSTVKNIDAAVFEEDTGKTYFFVAHECWRYDEYKQSMDTGYPKMIAEEFPGIGNKVDAVFQKDGFLYFFHGTRQYQFDFKTKRILTLQKANSWFNC

>d1pex\_\_ b.66.1.1 (-) Collagenase-3 (MMP-13), C-terminal domain {Human (Homo sapiens)}

TPDKCDPSLSLDAITSLRGETMIFKDRFFWRLHPQQVDAELFLTKSFWPELPNRIDAAYEHPSHDLIFIFRGRKFWALNGYDILEGYPKKISELGLPKEVKKISAAVHFEDTGKTLLFSGNQVWRYDDTNHIMDKDYPRLIEEDFPGIGDKVDAVYEKNGYIYFFNGPIQFEYSIWSNRIVRVMPANSILWC

>d1tl2a\_ b.67.1.1 (A:) Tachylectin-2 {Japanese horseshoe crab (Tachypleus tridentatus)}

GGESMLRGVYQDKFYQGTYPQNKNDNWLARATLIGKGGWSNFKFLFLSPGGELYGVLNDKIYKGTPPTHDNDNWMGRAKKIGNGGWNQFQFLFFDPNGYLYAVSKDKLYKASPPQSDTDNWIARATEVGSGGWSGFKFLFFHPNGYLYAVHGQQFYKALPPVSNQDNWLARATKIGQGGWDTFKFLFFSSVGTLFGVQGGKFYEDYPPSYAYDNWLARAKLIGNGGWDDFRFLFF

>d3sil\_\_ b.68.1.1 (-) Salmonella sialidase {Salmonella typhimurium, strain lt2}

EKSVVFKAEGEHFTDQKGNTIVGSGSGGTTKYFRIPAMCTTSKGTIVVFADARHNTASDQSFIDTAAARSTDGGKTWNKKIAIYNDRVNSKLSRVMDPTCIVANIQGRETILVMVGKWNNNDKTWGAYRDKAPDTDWDLVLYKSTDDGVTFSKVETNIHDIVTKNGTISAMLGGVGSGLQLNDGKLVFPVQMVRTKNITTVLNTSFIYSTDGITWSLPSGYCEGFGSENNIIEFNASLVNNIRNSGLRRSFETKDFGKTWTEFPPMDKKVDNRNHGVQGSTITIPSGNKLVAAHSSAQNKNNDYTRSDISLYAHNLYSGEVKLIDDFYPKVGNASGAGYSCLSYRKNVDKETLYVVYEANGSIEFQDLSRHLPVIKSYN

>d1f8ea\_ b.68.1.1 (A:) Influenza neuraminidase {Influenza A virus, different strains}

RDFNNLTKGLCTINSWHIYGKDNAVRIGEDSDVLVTREPYVSCDPDECRFYALSQGTTIRGKHSNGTIHDRSQYRALISWPLSSPPTVYNSRVECIGWSSTSCHDGKTRMSICISGPNNNASAVIWYNRRPVTEINTWARNILRTQESECVCHNGVCPVVFTDGSATGPAETRIYYFKEGKILKWEPLAGTAKHIEECSCYGERAEITCTCRDNWQGSNRPVIRIDPVAMTHTSQYICSPVLTDNPRPNDPTVGKCNDPYPGNNNNGVKGFSYLDGVNTWLGRTISIASRSGYEMLKVPNALTDDKSKPTQGQTIVLNTDWSGYSGSFMDYWAEGECYRACFYVELIRGRPKEDKVWWTSNSIVSMCSSTEFLGQWDWPDGAKIEYFL

>d2bat\_\_ b.68.1.1 (-) Influenza neuraminidase {Influenza A virus, different strains}

VEYRNWSKPQCQITGFAPFSKDNSIRLSAGGDIWVTREPYVSCDPVKCYQFALGQGTTLDNKHSNDTVHDRIPHRTLLMNELGVPFHLGTRQVCIAWSSSSCHDGKAWLHVCITGDDKNATASFIYDGRLVDSIGSWSQNILRTQESECVCINGTCTVVMTDGSASGRADTRILFIEEGKIVHISPLAGSAQHVEECSCYPRYPGVRCICRDNWKGSNRPVVDINMEDYSIDSSYVCSGLVGDTPRNDDRSSNSNCRNPNNERGTQGVKGWAFDNGNDLWMGRTISKDLRSGYETFKVIGGWSTPNSKSQINRQVIVDSDNRSGYSGIFSVEGKSCINRCFYVELIRGRKQETRVWWTSNSIVVFCGTSGTYGTGSWPDGANINFMPI

>d1inv\_\_ b.68.1.1 (-) Influenza neuraminidase {Influenza B virus, different strains}

EPEWTYPRLSCQGSTFQKALLISPHRFGEIKGNSAPLIIREPFVACGPKECRHFALTHYAAQPGGYYNGTRKDRNKLRHLVSVKLGKIPTVENSIFHMAAWSGSACHDGREWTYIGVDGPDNDALVKIKYGEAYTDTYHSYAHNILRTQESACNCIGGDCYLMITDGSASGISKCRFLKIREGRIIKEILPTGRVEHTEECTCGFASNKTIECACRDNSYTAKRPFVKLNVETDTAEIRLMCTKTYLDTPRPDDGSIAGPCESNGDKWLGGIKGGFVHQRMASKIGRWYSRTMSKTNRMGMELYVRYDGDPWTDSDALTLSGVMVSIEEPGWYSFGFEIKDKKCDVPCIGIEMVHDGGKDTWHSAATAIYCLMGSGQLLWDTVTGVDMAL

>d1nsca\_ b.68.1.1 (A:) Influenza neuraminidase {Influenza B virus, different strains}

EPEWTYPRLSCQGSTFQKALLISPHRFGEARGNSAPLIIREPFIACGPKECKHFALTHYAAQPGGYYNGTREDRNKLRHLISVKLGKIPTVENSIFHMAAWSGSACHDGREWTYIGVDGPDSNALIKIKYGEAYTDTYHSYANNILRTQESACNCIGGDCYLMITDGSASGISKCRFLKIREGRIIKEIFPTGRVEHTEECTCGFASNKTIECACRDNSYTAKRPFVKLNVETDTAEIRLMCTETYLDTPRPDDGSITGPCESNGDKGRGGIKGGFVHQRMASKIGRWYSRTMSKTERMGMELYVRYDGDPWTDSDALAHSGVMVSMKEPGWYSFGFEIKDKKCDVPCIGIEMVHDGGKKTWHSAATAIYCLMGSGQLLWDTVTGVDMAL

>d1e8ua\_ b.68.1.1 (A:) Paramyxovirus hemagglutinin-neuraminidase head domain {Newcastle disease virus}

GAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDMSATHYCYTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSVSATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYPGVGGGSFIDGRVWFSVYGGLKPNSPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKPGRFGGKRIQQAILSIKVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSYFSPALLYPMTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPYPLIFYRNHTLRGVFGTMLDSEQARLNPASAVFDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKTYCLSIAEISNTLFGEFRIVPLLVEILKND

>d1eur\_\_ b.68.1.1 (-) Micromonospora sialidase, N-terminal domain {Micromonospora viridifaciens}

GEPLYTEQDLAVNGREGFPNYRIPALTVTPDGDLLASYDGRPTGIDAPGPNSILQRRSTDGGRTWGEQQVVSAGQTTAPIKGFSDPSYLVDRETGTIFNFHVYSQRQGFAGSRPGTDPADPNVLHANVATSTDGGLTWSHRTITADITPDPGWRSRFAASGEGIQLRYGPHAGRLIQQYTIINAAGAFQAVSVYSDDHGRTWRAGEAVGVGMDENKTVELSDGRVLLNSRDSARSGYRKVAVSTDGGHSYGPVTIDRDLPDPTNNASIIRAFPDAPAGSARAKVLLFSNAASQTSRSQGTIRMSCDDGQTWPVSKVFQPGSMSYSTLTALPDGTYGLLYEPGTGIRYANFNLAWLGGICAP

>d2sli\_2 b.68.1.1 (277-759) Leech intramolecular trans-sialidase, C-terminal domain {North american leech (Macrobdella decora)}

GENIFYAGDVTESNYFRIPSLLTLSTGTVISAADARYGGTHDSKSKINIAFAKSTDGGNTWSEPTLPLKFDDYIAKNIDWPRDSVGKNVQIQGSASYIDPVLLEDKLTKRIFLFADLMPAGIGSSNASVGSGFKEVNGKKYLKLRWHKDAGRAYDYTIREKGVIYNDATNQPTEFRVDGEYNLYQHDTNLTCKQYDYNFSGNNLIESKTDVDVNMNIFYKNSVFKAFPTNYLAMRYSDDEGASWSDLDIVSSFKPEVSKFLVVGPGIGKQISTGENAGRLLVPLYSKSSAELGFMYSDDHGDNWTYVEADNLTGGATAEAQIVEMPDGSLKTYLRTGSNCIAEVTSIDGGETWSDRVPLQGISTTSYGTQLSVINYSQPIDGKPAIILSSPNATNGRKNGKIWIGLVNDTGNTGIDKYSVEWKYSYAVDTPQMGYSYSCLAELPDGQVGLLYEKYDSWSRNELHLKDILKFEKYSISELTGQA

>d1kit\_3 b.68.1.1 (217-346,544-781) Vibrio cholerae sialidase {Vibrio cholerae}

VIFRGPDRIPSIVASSVTPGVVTAFAEKRVGGGDPGALSNTNDIITRTSRDGGITWDTELNLTEQINVSDEFDFSDPRPIYDPSSNTVLVSYARWPTDAAQNGDRIKPWMPNGIFYSVYDVASGNWQAPIXVNPGPGHGITLTRQQNISGSQNGRLIYPAIVLDRFFLNVMSIYSDDGGSNWQTGSTLPIPFRWKSSSILETLEPSEADMVELQNGDLLLTARLDFNQIVNGVNYSPRQQFLSKDGGITWSLLEANNANVFSNISTGTVDASITRFEQSDGSHFLLFTNPQGNPAGTNGRQNLGLWFSFDEGVTWKGPIQLVNGASAYSDIYQLDSENAIVIVETDNSNMRILRMPITLLKQKLTLSQN

>d1crua\_ b.68.2.1 (A:) Soluble quinoprotein glucose dehydrogenase {Acinetobacter calcoaceticus}

DVPLTPSQFAKAKSENFDKKVILSNLNKPHALLWGPDNQIWLTERATGKILRVNPESGSVKTVFQVPEIVNDADGQNGLLGFAFHPDFKNNPYIYISGTFKNPKSTDKELPNQTIIRRYTYNKSTDTLEKPVDLLAGLPSSKDHQSGRLVIGPDQKIYYTIGDQGRNQLAYLFLPNQAQHTPTQQELNGKDYHTYMGKVLRLNLDGSIPKDNPSFNGVVSHIYTLGHRNPQGLAFTPNGKLLQSEQGPNSDDEINLIVKGGNYGWPNVAGYKDDSGYAYANYSAAANKSIKDLAQNGVKVAAGVPVTKESEWTGKNFVPPLKTLYTVQDTYNYNDPTCGEMTYICWPTVAPSSAYVYKGGKKAITGWENTLLVPSLKRGVIFRIKLDPTYSTTYDDAVPMFKSNNRYRDVIASPDGNVLYVLTDTAGNVQKDDGSVTNTLENPGSLIKFT

>d1h6la\_ b.68.3.1 (A:) Thermostable phytase (3-phytase) {Bacillus amyloliquefaciens}

KLSDPYHFTVNAAAETEPVDTAGDAADDPAIWLDPKNPQNSKLITTNKKSGLAVYSLEGKMLHSYHTGKLNNVDIRYDFPLNGKKVDIAAASNRSEGKNTIEIYAIDGKNGTLQSITDPNRPIASAIDEVYGFSLYHSQKTGKYYAMVTGKEGEFEQYELNADKNGYISGKKVRAFKMNSQTEGMAADDEYGSLYIAEEDEAIWKFSAEPDGGSNGTVIDRADGRHLTPDIEGLTIYYAADGKGYLLASSQGNSSYAIYERQGQNKYVADFQITDGPETDGTSDTDGIDVLGFGLGPEYPFGLFVAQNGENIDHGQKANQNFKMVPWERIADKIGFHPQVNKQVDPRKMTDRS

>d1crza1 b.68.4.1 (A:141-409) TolB, C-terminal domain {Escherichia coli}

AFRTRIAYVVQTNGGQFPYELRVSDYDGYNQFVVHRSPQPLMSPAWSPDGSKLAYVTFESGRSALVIQTLANGAVRQVASFPRHNGAPAFSPDGSKLAFALSKTGSLNLYVMDLASGQIRQVTDGRSNNTEPTWFPDSQNLAFTSDQAGRPQVYKVNINGGAPQRITWEGSQNQDADVSSDGKFMVMVSSNGGQQHIAKQDLATGGVQVLSSTFLDETPSLAPNGTMVIYSSSQGMGSVLNLVSTDGRFKARLPATDGQVKFPAWSPYL

>d1ijqa1 b.68.5.1 (A:377-642) Low density lipoprotein (LDL) reseptor YWTD domain {Human (Homo sapiens)}

IAYLFFTNRHEVRKMTLDRSEYTSLIPNLRNVVALDTEVASNRIYWSDLSQRMICSTQLDRAHGVSSYDTVISRDIQAPDGLAVDWIHSNIYWTDSVLGTVSVADTKGVKRKTLFRENGSKPRAIVVDPVHGFMYWTDWGTPAKIKKGGLNGVDIYSLVTENIQWPNGITLDLLSGRLYWVDSKLHSISSIDVNGGNRKTILEDEKRLAHPFSLAVFEDKVFWTDIINEAIFSANRLTGSDVNLLAENLLSPEDMVLFHNLTQPRG

>d1e1aa\_ b.68.6.1 (A:) Diisopropylfluorophosphatase (phosphotriesterase, DFP) {Squid (Loligo vulgaris)}

IPVIEPLFTKVTEDIPGAEGPVFDKNGDFYIVAPEVEVNGKPAGEILRIDLKTGKKTVICKPEVNGYGGIPAGCQCDRDANQLFVADMRLGLLVVQTDGTFEEIAKKDSEGRRMQGCNDCAFDYEGNLWITAPAGEVAPADYTRSMQEKFGSIYCFTTDGQMIQVDTAFQFPNGIAVRHMNDGRPYQLIVAETPTKKLWSYDIKGPAKIENKKVWGHIPGTHEGGADGMDFDEDNNLLVANWGSSHIEVFGPDGGQPKMRIRCPFEKPSNLHFKPQTKTIFVTEHENNAVWKFEWQRNGKKQYCETLKFGIF

>d1k32a2 b.68.7.1 (A:39-319) Tricorn protease N-terminal domain {Archaeon Thermoplasma acidophilum}

MPNLLLNPDIHGDRIIFVCCDDLWEHDLKSGSTRKIVSNLGVINNARFFPDGRKIAIRVMRGSSLNTADLYFYNGENGEIKRITYFSGKSTGRRMFTDVAGFDPDGNLIISTDAMQPFSSMTCLYRVENDGINFVPLNLGPATHILFADGRRVIGRNTFELPHWKGYRGGTRGKIWIEVNSGAFKKIVDMSTHVSSPVIVGHRIYFITDIDGFGQIYSTDLDGKDLRKHTSFTDYYPRHLNTDGRRILFSKGGSIYIFNPDTEKIEKIEIGDLESPEDRII

>d1k3ia3 b.69.1.1 (A:151-537) Galactose oxidase, central domain {Fungi (Fusarium spp)}

YTAPQPGLGRWGPTIDLPIVPAAAAIEPTSGRVLMWSSYRNDAFGGSPGGITLTSSWDPSTGIVSDRTVTVTKHDMFCPGISMDGNGQIVVTGGNDAKKTSLYDSSSDSWIPGPDMQVARGYQSSATMSDGRVFTIGGSWSGGVFEKNGEVYSPSSKTWTSLPNAKVNPMLTADKQGLYRSDNHAWLFGWKKGSVFQAGPSTAMNWYYTSGSGDVKSAGKRQSNRGVAPDAMCGNAVMYDAVKGKILTFGGSPDYQDSDATTNAHIITLGEPGTSPNTVFASNGLYFARTFHTSVVLPDGSTFITGGQRRGIPFEDSTPVFTPEIYVPEQDTFYKQNPNSIVRVYHSISLLLPDGRVFNGGGGLCGDCTTNHFDAQIFTPNYLYNSN

>d1mdah\_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}

EKSKVAGSAAAASAAAASDGSSCDHGPGAISRRSHITLPAYFAGTTENWVSCAGCGVTLGHSLGAFLSLAVAGHSGSDFALASTSFARSAKGKRTDYVEVFDPVTFLPIADIELPDAPRFSVGPRVHIIGNCASSACLLFFLFGSSAAAGLSVPGASDDQLTKSASCFHIHPGAAATHYLGSCPASLAASDLAAAPAAAGIVGAQCTGAQNCSSQAAQANYPGMLVWAVASSILQGDIPAAGATMKAAIDGNESGRKADNFRSAGFQMVAKLKNTDGIMILTVEHSRSCLAAAENTSSVTASVGQTSGPISNGHDSDAIIAAQDGASDNYANSAGTEVLDIYDAASDQDQSSVELDKGPESLSVQNEA

>d2bbkh\_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}

DEPRILEAPAPDARRVYVNDPAHFAAVTQQFVIDGEAGRVIGMIDGGFLPNPVVADDGSFIAHASTVFSRIARGERTDYVEVFDPVTLLPTADIELPDAPRFLVGTYPWMTSLTPDGKTLLFYQFSPAPAVGVVDLEGKAFKRMLDVPDCYHIFPTAPDTFFMHCRDGSLAKVAFGTEGTPEITHTEVFHPEDEFLINHPAYSQKAGRLVWPTYTGKIHQIDLSSGDAKFLPAVEALTEAERADGWRPGGWQQVAYHRALDRIYLLVDQRDEWRHKTASRFVVVLDAKTGERLAKFEMGHEIDSINVSQDEKPLLYALSTGDKTLYIHDAESGEELRSVNQLGHGPQVITTADMG

>d2madh\_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Gram negative methylotrophic bacteria (Thiobacillus versutus)}

SSASAAAAAAAAALAAGAADGPTNDEAPGADGRRSYINLPAHHSAIIQQWVLDAGSGSILGHVNGGFLPNPVAAHSGSEFALASTSFSRIAKGKRTDYVEVFDPVTFLPIADIELPDAPRFDVGPYSWMNANTPNNADLLFFQFAAGPAVGLVVQGGSSDDQLLSSPTCYHIHPGAPSTFYLLCAQGGLAKTDHAGGAAGAGLVGAMLTAAQNLLTQPAQANKSGRIVWPVYSGKILQADISAAGATNKAPIDALSGGRKADTWRPGGWQQVAYLKSSDGIYLLTSEQSAWKLHAAAKEVTSVTGLVGQTSSQISLGHDVDAISVAQDGGPDLYALSAGTEVLHIYDAGAGDQDQSTVELGSGPQVLSVMNEA

>d1jjub\_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Paracoccus denitrificans}

RDYILAPARPDKLVVIDTEKMAVDKVITIADAGPTPMVPMVAPGGRIAYATVNKSESLVKIDLVTGETLGRIDLSTPEERVKSLFGAALSPDGKTLAIYESPVRLELTHFEVQPTRVALYDAETLSRRKAFEAPRQITMLAWARDGSKLYGLGRDLHVMDPEAGTLVEDKPIQSWEAETYAQPDVLAVWNQHESSGVMATPFYTARKDIDPADPTAYRTGLLTMDLETGEMAMREVRIMDVFYFSTAVNPAKTRAFGAYNVLESFDLEKNASIKRVPLPHSYYSVNVSTDGSTVWLGGALGDLAAYDAETLEKKGQVDLPGNASMSLASVRLFTRDE

>d1jmxb\_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Pseudomonas putida}

GPALKAGHEYMIVTNYPNNLHVVDVASDTVYKSCVMPDKFGPGTAMMAPDNRTAYVLNNHYGDIYGIDLDTCKNTFHANLSSVPGEVGRSMYSFAISPDGKEVYATVNPTQRLNDHYVVKPPRLEVFSTADGLEAKPVRTFPMPRQVYLMRAADDGSLYVAGPDIYKMDVKTGKYTVALPLRNWNRKGYSAPDVLYFWPHQSPRHEFSMLYTIARFKDDKQDPATADLLYGYLSVDLKTGKTHTQEFADLTELYFTGLRSPKDPNQIYGVLNRLAKYDLKQRKLIKAANLDHTYYCVAFDKKGDKLYLGGTFNDLAVFNPDTLEKVKNIKLPGGDMSTTTPQVFIR

>d1qnia2 b.69.3.1 (A:10-450) Nitrous oxide reductase, N-terminal domain {Pseudomonas nautica}

AHVAPGELDEYYGFWSGGHQGEVRVLGVPSMRELMRIPVFNVDSATGWGITNESKEILGGDQQYLNGDCHHPHISMTDGRYDGKYLFINDKANTRVARIRLDIMKTDKITHIPNVQAIHGLRLQKVPKTNYVFCNAEFVIPQPNDGTDFSLDNSYTMFTAIDAETMDVAWQVIVDGNLDNTDADYTGKYATSTCYNSERAVDLAGTMRNDRDWVVVFNVERIAAAVKAGNFKTIGDSKVPVVDGRGESEFTRYIPVPKNPHGLNTSPDGKYFIANGKLSPTVSVIAIDKLDDLFEDKIELRDTIVAEPELGLGPLHTTFDGRGNAYTTLFIDSQVCKWNIADAIKHYNGDRVNYIRQKLDVQYQPGHNHASLTESRDADGKWLVVLSKFSKDRFLPVGPLHPENDQLIDISGEEMKLVHDGPTYAEPHDCILVRRDQIKTK

>d1fwxa2 b.69.3.1 (A:8-451) Nitrous oxide reductase, N-terminal domain {Paracoccus denitrificans}

ADGSVAPGQLDDYYGFWSSGQSGEMRILGIPSMRELMRVPVFNRCSATGWGQTNESVRIHERTMSERTKKFLAANGKRIHDNGDLHHVHMSFTEGKYDGRFLFMNDKANTRVARVRCDVMKCDAILEIPNAKGIHGLRPQKWPRSNYVFCNGEDETPLVNDGTNMEDVANYVNVFTAVDADKWEVAWQVLVSGNLDNCDADYEGKWAFSTSYNSEKGMTLPEMTAAEMDHIVVFNIAEIEKAIAAGDYQELNGVKVVDGRKEASSLFTRYIPIANNPHGCNMAPDKKHLCVAGKLSPTVTVLDVTRFDAVFYENADPRSAVVAEPELGLGPLHTAFDGRGNAYTSLFLDSQVVKWNIEDAIRAYAGEKVDPIKDKLDVHYQPGHLKTVMGETLDATNDWLVCLSKFSKDRFLNVGPLKPENDQLIDISGDKMVLVHDGPTFAEPHDAIAVHPSILSDIK

>d1tbga\_ b.69.4.1 (A:) beta1-subunit of the signal-transducing G protein heterotrimer {Cow (Bos taurus)}

MSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVGRIQMRTRRTLRGHLAKIYAMHWGTDSRLLVSASQDGKLIIWDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDNICSIYNLKTREGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIETGQQTTTFTGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGMCRQTFTGHESDINAICFFPNGNAFATGSDDATCRLFDLRADQELMTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDALKADRAGVLAGHDNRVSCLGVTDDGMAVATGSWDSFLKIWN

>d1erja\_ b.69.4.1 (A:) Tup1, C-therminal domain {Baker's yeast (Saccharomyces cerevisiae)}

HYLVPYNQRANHSKPIPPFLLDLDSQSVPDALKKQTNDYYILYNPALPREIDVELHKSLDHTSVVCCVKFSNDGEYLATGCNKTTQVYRVSDGSLVARLSDDSAANKDPENLNTSSSPSSDLYIRSVCFSPDGKFLATGAEDRLIRIWDIENRKIVMILQGHEQDIYSLDYFPSGDKLVSGSGDRTVRIWDLRTGQCSLTLSIEDGVTTVAVSPGDGKYIAAGSLDRAVRVWDSETGFLVERLDSENESGTGHKDSVYSVVFTRDGQSVVSGSLDRSVKLWNLQNANNKSDSKTPNSGTCEVTYIGHKDFVLSVATTQNDEYILSGSKDRGVLFWDKKSGNPLLMLQGHRNSVISVAVANGSSLGPEYNVFATGSGDCKARIWKYKKI

>d1k8kc\_ b.69.4.1 (C:) Arp2/3 complex 41 kDa subunit ARPC1 {Cow (Bos taurus)}

AYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKSGNKWVQVHELKEHNGQVTGVDWAPDSNRIVTCGTDRNAYVWTLKGRTWKPTLVILRINRAARCVRWAPNEKKFAVGSGSRVISICYFEQENDWWVCKHIKKPIRSTVLSLDWHPNSVLLAAGSCDFKCRIFSAYIKEVEERPAPTPWGSKMPFGELMFESSSSCGWVHGVCFSANGSRVAWVSHDSTVCLADADKKMAVATLASETLPLLAVTFITESSLVAAGHDCFPVLFTYDSAAGKLSFGGRLDVPKQSSQRGLTARERFQNLDKKASSEGSAAAGAGLDSLHKNSVSQISVLSGGKAKCSQFCTTGMDGGMSIWDVRSLESALKDLKIV

>d1a12a\_ b.69.5.1 (A:) Regulator of chromosome condensation RCC1 {Human (Homo sapiens)}

KKVKVSHRSHSTEPGLVLTLGQGDVGQLGLGENVMERKKPALVSIPEDVVQAEAGGMHTVCLSKSGQVYSFGCNDEGALGRDTSVEGSEMVPGKVELQEKVVQVSAGDSHTAALTDDGRVFLWGSFRDNNGVIGLLEPMKKSMVPVQVQLDVPVVKVASGNDHLVMLTADGDLYTLGCGEQGQLGRVPELFANRGGRQGLERLLVPKCVMLKSRGSRGHVRFQDAFCGAYFTFAISHEGHVYGFGLSNYHQLGTPGTESCFIPQNLTSFKNSTKSWVGFSGGQHHTVCMDSEGKAYSLGRAEYGRLGLGEGAEEKSIPTLISRLPAVSSVACGASVGYAVTKDGRVFAWGMGTNYQLGTGQDEDAWSPVEMMGKQLENRVVLSVSSGGQHTVLLVKDKEQS

>d1jtdb\_ b.69.5.2 (B:) of beta-lactamase inhibitor protein-II, BLIP-II {Streptomyces exfoliatus}

VAATSVVAWGGNNDWGEATVPAEAQSGVDAIAGGYFHGLALKGGKVLGWGANLNGQLTMPAATQSGVDAIAAGNYHSLALKDGEVIAWGGNEDGQTTVPAEARSGVDAIAAGAWASYALKDGKVIAWGDDSDGQTTVPAEAQSGVTALDGGVYTALAVKNGGVIAWGDNYFGQTTVPAEAQSGVDDVAGGIFHSLALKDGKVIAWGDNRYKQTTVPTEALSGVSAIASGEWYSLALKNGKVIAWGSSRTAPSSVQSGVSSIEAGPNAAYALKG

>d1c9la2 b.69.6.1 (A:3-330) Clathrin heavy-chain terminal domain {Rat (Rattus norvegicus)}

QILPIRFQEHLQLQNLGINPANIGFSTLTMESDKFICIREKVGEQAQVVIIDMNDPSNPIRRPISADSAIMNPASKVIALKAGKTLQIFNIEMKSKMKAHTMTDDVTFWKWISLNTVALVTDNAVYHWSMEGESQPVKMFDRHSSLAGCQIINYRTDAKQKWLLLTGISAQQNRVVGAMQLYSVDRKVSQPIEGHAASFAQFKMEGNAEESTLFCFAVRGQAGGKLHIIEVGTPPTGNQPFPKKAVDVFFPPEAQNDFPVAMQISEKHDVVFLITKYGYIHLYDLETGTCIYMNRISGETIFVTAPHEATAGIIGVNRKGQVLSVCVE

>d1jv2a4 b.69.8.1 (A:1-438) Integrin alpha N-terminal domain {Human (Homo sapiens)}

FNLDVDSPAEYSGPEGSYFGFAVDFFVPSASSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRRCQPIEFDATGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQEREPVGTCFLQDGTKTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADRVLLGGPGSFYWQGQLISDQVAEIVSKYDPNVYSIKYNNQLATRTAQAIFDDSYLGYSVAVGDFNGDGIDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGEQMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRASGDFQTTKLNGFEVFARFGSAIAPLGDLDQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQILEGQWAARSMPPSFGYSMKGATDIDKNGYPDLIVGAFGVDRAILYRAR

>d1qfma1 b.69.7.1 (A:1-430) Prolyl oligopeptidase, N-terminal domain {Pig (Sus scrofa)}

MLSFQYPDVYRDETAIQDYHGHKVCDPYAWLEDPDSEQTKAFVEAQNKITVPFLEQCPIRGLYKERMTELYDYPKYSCHFKKGKRYFYFYNTGLQNQRVLYVQDSLEGEARVFLDPNILSDDGTVALRGYAFSEDGEYFAYGLSASGSDWVTIKFMKVDGAKELPDVLERVKFSCMAWTHDGKGMFYNAYPQQDGKSDGTETSTNLHQKLYYHVLGTDQSEDILCAEFPDEPKWMGGAELSDDGRYVLLSIREGCDPVNRLWYCDLQQESNGITGILKWVKLIDNFEGEYDYVTNEGTVFTFKTNRHSPNYRLINIDFTDPEESKWKVLVPEHEKDVLEWVACVRSNFLVLCYLHDVKNTLQLHDLATGALLKIFPLEVGSVVGYSGQKKDTEIFYQFTSFLSPGIIYHCDLTKEELEPRVFREVTVKGI

>d1k32a3 b.69.9.1 (A:320-679) Tricorn protease N-terminal domain {Archaeon Thermoplasma acidophilum}

SIPSKFAEDFSPLDGDLIAFVSRGQAFIQDVSGTYVLKVPEPLRIRYVRRGGDTKVAFIHGTREGDFLGIYDYRTGKAEKFEENLGNVFAMGVDRNGKFAVVANDRFEIMTVDLETGKPTVIERSREAMITDFTISDNSRFIAYGFPLKHGETDGYVMQAIHVYDMEGRKIFAATTENSHDYAPAFDADSKNLYYLSYRSLDPSPDRVVLNFSFEVVSKPFVIPLIPGSPNPTKLVPRSMTSEAGEYDLNDMYKRSSPINVDPGDYRMIIPLESSILIYSVPVHGEFAAYYQGAPEKGVLLKYDVKTRKVTEVKNNLTDLRLSADRKTVMVRKDDGKIYTFPLEKPEDERTVETDKRPLV

>d1g72a\_ b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylophilus methylotrophus, w3a1}

DADLDKQVNTAGAWPIATGGYYSQHNSPLAQINKSNVKNVKAAWSFSTGVLNGHEGAPLVIGDMMYVHSAFPNNTYALNLNDPGKIVWQHKPKQDASTKAVMCCDVVDRGLAYGAGQIVKKQANGHLLALDAKTGKINWEVEVCDPKVGSTLTQAPFVAKDTVLMGCSGAELGVRGAVNAFDLKTGELKWRAFATGSDDSVRLAKDFNSANPHYGQFGLGTKTWEGDAWKIGGGTNWGWYAYDPKLNLFYYGSGNPAPWNETMRPGDNKWTMTIWGRDLDTGMAKWGYQKTPHDEWDFAGVNQMVLTDQPVNGKMTPLLSHIDRNGILYTLNRENGNLIVAEKVDPAVNVFKKVDLKTGTPVRDPEFATRMDHKGTNICPSAMGFHNQGVDSYDPESRTLYAGLNHICMDWEPFMLPYRAGQFFVGATLAMYPGPNGPTKKEMGQIRAFDLTTGKAKWTKWEKFAAWGGTLYTKGGLVWYATLDGYLKALDNKDGKELWNFKMPSGGIGSPMTYSFKGKQYIGSMYGVGGWPGVGLVFDLTDPSAGLGAVGAFRELQNHTQMGGGLMVFSL

>d1h4ia\_ b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylobacterium extorquens}

NDKLVELSKSDDNWVMPGKNYDSNNFSDLKQINKGNVKQLRPAWTFSTGLLNGHEGAPLVVDGKMYIHTSFPNNTFALGLDDPGTILWQDKPKQNPAARAVACCDLVNRGLAYWPGDGKTPALILKTQLDGNVAALNAETGETVWKVENSDIKVGSTLTIAPYVVKDKVIIGSSGAELGVRGYLTAYDVKTGEQVWRAYATGPDKDLLLASDFNIKNPHYGQKGLGTGTWEGDAWKIGGGTNWGWYAYDPGTNLIYFGTGNPAPWNETMRPGDNKWTMTIFGRDADTGEAKFGYQKTPHDEWDYAGVNVMMLSEQKDKDGKARKLLTHPDRNGIVYTLDRTDGALVSANKLDDTVNVFKSVDLKTGQPVRDPEYGTRMDHLAKDICPSAMGYHNQGHDSYDPKRELFFMGINHICMDWEPFMLPYRAGQFFVGATLNMYPGPKGDRQNYEGLGQIKAYNAITGDYKWEKMERFAVWGGTMATAGDLVFYGTLDGYLKARDSDTGDLLWKFKIPSGAIGYPMTYTHKGTQYVAIYYGVGGWPGVGLVFDLADPTAGLGAVGAFKKLANYTQMGGGVVVFSLDGKGPYDDPNVGEWK

>d1flga\_ b.70.1.1 (A:) Ethanol dehydrogenase {Pseudomonas aeruginosa}

KDVTWEDIANDDKTTGDVLQYGMGTHAQRWSPLKQVNADNVFKLTPAWSYSFGDEKQRGQESQAIVSDGVIYVTASYSRLFALDAKTGKRLWTYNHRLPDDIRPCCDVVNRGAAIYGDKVFFGTLDASVVALNKNTGKVVWKKKFADHGAGYTMTGAPTIVKDGKTGKVLLIHGSSGDEFGVVGRLFARDPDTGEEIWMRPFVEGHMGRLNGKDSTVTGDVKAPSWPDDRNSPTGKVESWSHGGGAPWQSASFDAETNTIIVGAGNPGPWNTWARTAKGGNPHDYDSLYTSGQVGVDPSSGEVKWFYQHTPNDAWDFSGNNELVLFDYKAKDGKIVKATAHADRNGFFYVVDRSNGKLQNAFPFVDNITWASHIDLKTGRPVEREGQRPPLPEPGQKHGKAVEVSPPFLGGKNWNPMAYSQDTGLFYVPANHWKEDYWTEEVSYTKGSAYLGMGFRIKRMYDDHVGSLRAMDPVSGKVVWEHKEHLPLWAGVLATAGNLVFTGTGDGYFKAFDAKSGKELWKFQTGSGIVSPPITWEQDGEQYLGVTVGYGGAVPLWGGDMADLTRPVAQGGSFWVFKLPSW

>d1kb0a2 b.70.1.1 (A:1-573) Quinoprotein alcohol dehydrogenase, N-terminal domain {Comamonas testosteroni}

TGPAAQAAAAVQRVDGDFIRANAARTPDWPTIGVDYAETRYSRLDQINAANVKDLGLAWSYNLESTRGVEATPVVVDGIMYVSASWSVVHAIDTRTGNRIWTYDPQIDRSTGFKGCCDVVNRGVALWKGKVYVGAWDGRLIALDAATGKEVWHQNTFEGQKGSLTITGAPRVFKGKVIIGNGGAEYGVRGYITAYDAETGERKWRWFSVPGDPSKPFEDESMKRAARTWDPSGKWWEAGGGGTMWDSMTFDAELNTMYVGTGNGSPWSHKVRSPKGGDNLYLASIVALDPDTGKYKWHYQETPGDNWDYTSTQPMILADIKIAGKPRKVILHAPKNGFFFVLDRTNGKFISAKNFVPVNWASGYDKHGKPIGIAAARDGSKPQDAVPGPYGAHNWHPMSFNPQTGLVYLPAQNVPVNLMDDKKWEFNQAGPGKPQSGTGWNTAKFFNAEPPKSKPFGRLLAWDPVAQKAAWSVEHVSPWNGGTLTTAGNVVFQGTADGRLVAYHAATGEKLWEAPTGTGVVAAPSTYMVDGRQYVSVAVGWGGVYGLAARATERQGPGTVYTFVVGGKARMPE

>d1nira2 b.70.2.1 (A:118-543) C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase {Pseudomonas aeruginosa}

EWGMPEMRESWKVLVKPEDRPKKQLNDLDLPNLFSVTLRDAGQIALVDGDSKKIVKVIDTGYAVHISRMSASGRYLLVIGRDARIDMIDLWAKEPTKVAEIKIGIEARSVESSKFKGYEDRYTIAGAYWPPQFAIMDGETLEPKQIVSTRGMTVDTQTYHPEPRVAAIIASHEHPEFIVNVKETGKVLLVNYKDIDNLTVTSIGAAPFLHDGGWDSSHRYFMTAANNSNKVAVIDSKDRRLSALVDVGKTPHPGRGANFVHPKYGPVWSTSHLGDGSISLIGTDPKNHPQYAWKKVAELQGQGGGSLFIKTHPKSSHLYVDTTFNPDARISQSVAVFDLKNLDAKYQVLPIAEWADLGEGAKRVVQPEYNKRGDEVWFSVWNGKNDSSALVVVDDKTLKLKAVVKDPRLITPTGKFNVYNTQHDVY

>d1qksa2 b.70.2.1 (A:136-567) C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase {Paracoccus denitrificans}

EFGMKEMRESWKVHVAPEDRPTQQMNDWDLENLFSVTLRDAGQIALIDGSTYEIKTVLDTGYAVHISRLSASGRYLFVIGRDGKVNMIDLWMKEPTTVAEIKIGSEARSIETSKMEGWEDKYAIAGAYWPPQYVIMDGETLEPKKIQSTRGMTYDEQEYHPEPRVAAILASHYRPEFIVNVKETGKILLVDYTDLNNLKTTEISAERFLHDGGLDGSHRYFITAANARNKLVVIDTKEGKLVAIEDTGGQTPHPGRGANFVHPTFGPVWATSHMGDDSVALIGTDPEGHPDNAWKILDSFPALGGGSLFIKTHPNSQYLYVDATLNPEAEISGSVAVFDIKAMTGDGSDPEFKTLPIAEWAGITEGQPRVVQGEFNKDGTEVWFSVWNGKDQESALVVVDDKTLELKHVIKDERLVTPTGKFNVYNTMTDTY

>d1e43a1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus licheniformis}

YAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWHDITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR

>d1g94a1 b.71.1.1 (A:355-448) Bacterial alpha-Amylase {Pseudoalteromonas haloplanctis (Alteromonas haloplanctis)}

NWAVTNWWDNTNNQISFGRGSSGHMAINKEDSTLTATVQTDMASGQYCNVLKGELSADAKSCSGEVITVNSDGTINLNIGAWDAMAIHKNAKLN

>d1bag\_1 b.71.1.1 (348-425) Bacterial alpha-Amylase {Bacillus subtilis}

QPEELSNPNGNNQIFMNQRGSHGVVLANAGSSSVSINTATKLPDGRYDNKAGAGSFQVNDGKLTGTINARSVAVLYPD

>d1hvxa1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus stearothermophilus}

YAYGTQHDYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFYDLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPR

>d1gjwa1 b.71.1.1 (A:573-636) Maltosyltransferase {Thermotoga maritima}

GKFENLTTKDLVMYSYEKNGQKIVIAANVGKEPKEITGGRVWNGKWSDEEKVVLKPLEFALVVQ

>d1cgt\_3 b.71.1.1 (407-494) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

GSTQQRWINNDVYVYERKFGKSVAVVAVNRNLSTSASITGLSTSLPTGSYTDVLGGVLNGNNITSTNGSINNFTLAAGATAVWQYTTA

>d1kcla3 b.71.1.1 (A:407-495) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

GSTQERWINNDVLIYERKFGSNVAVVAVNRNLNAPASISGLVTSLPQGSYNDVLGGLLNGNTLSVGSGGAASNFTLAAGGTAVWQYTAA

>d1cyg\_3 b.71.1.1 (403-491) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus}

GDTEQRWINGDVYVYERQFGKDVVLVAVNRSSSSNYSITGLFTALPAGTYTDQLGGLLDGNTIQVGSNGSVNAFDLGPGEVGVWAYSAT

>d1qhoa3 b.71.1.1 (A:408-495) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}

GTTTQRWINNDVYIYERKFFNDVVLVAINRNTQSSYSISGLQTALPNGSYADYLSGLLGGNGISVSNGSVASFTLAPGAVSVWQYSTS

>d1pama3 b.71.1.1 (A:407-496) Cyclodextrin glycosyltransferase {Bacillus sp., strain 1011}

GSTHERWINNDVIIYERKFGNNVAVVAINRNMNTPASITGLVTSLPRGSYNDVLGGILNGNTLTVGAGGAASNFTLAPGGTAVWQYTTDA

>d1ciu\_3 b.71.1.1 (407-495) Cyclodextrin glycosyltransferase {Thermoanaerobacterium thermosulfurigenes, EM1}

GTTQQRWINNDVYIYERKFGNNVALVAINRNLSTSYNITGLYTALPAGTYTDVLGGLLNGNSISVASDGSVTPFTLSAGEVAVWQYVSS

>d1hx0a1 b.71.1.1 (A:404-496) Animal alpha-amylase {Pig (Sus scrofa)}

QPFANWWDNGSNQVAFGRGNRGFIVFNNDDWQLSSTLQTGLPGGTYCDVISGDKVGNSCTGIKVYVSSDGTAQFSISNSAEDPFIAIHAESKL

>d1smd\_1 b.71.1.1 (404-496) Animal alpha-amylase {Human (Homo sapiens)}

QPFTNWYDNGSNQVAFGRGNRGFIVFNNDDWTFSLTLQTGLPAGTYCDVISGDKINGNCTGIKIYVSDDGKAHFSISNSAEDPFIAIHAESKL

>d1jae\_1 b.71.1.1 (379-471) Animal alpha-amylase {Yellow mealworm (Tenebrio molitor), larva}

GTQVENWWSNDDNQIAFSRGSQGFVAFTNGGDLNQNLNTGLPAGTYCDVISGELSGGSCTGKSVTVGDNGSADISLGSAEDDGVLAIHVNAKL

>d2aaa\_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus niger, acid amylase}

YANDAFYTDSNTIAMAKGTSGSQVITVLSNKGSSGSSYTLTLSGSGYTSGTKLIEAYTCTSVTVDSSGDIPVPMASGLPRVLLPASVVDSSSLCG

>d2taaa1 b.71.1.1 (A:382-478) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}

YKNPYIKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSLSGASYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICSDSS

>d7taa\_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}

YKNWPIYKDDTTIAMRKGTDGSQIVTILSNKGASGDSYTLSLSGAGYTAGQQLTEVIGCTTVTVGSDGNVPVPMAGGLPRVLYPTEKLAGSKICS

>d1smaa2 b.71.1.1 (A:506-588) Maltogenic amylase {Thermus sp.}

GDVAFLTADDEVNHLVYAKTDGNETVMIIINRSNEAAEIPMPIDARGKWLVNLLTGERFAAEAETLCVSLPPYGFVLYAVESW

>d1bvza2 b.71.1.1 (A:503-585) Maltogenic amylase {Thermoactinomyces vulgaris, TVAII}

GNVRSWHADKQANLYAFVRTVQDQHVGVVLNNRGEKQTVLLQVPESGGKTWLDCLTGEEVHGKQGQLKLTLRPYQGMILWNGR

>d1eh9a2 b.71.1.1 (A:491-557) Glycosyltrehalose trehalohydrolase {Archaeon Sulfolobus solfataricus, km1}

CDRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLLSSNNSFPQHIEEGKYEFDKGFALYK

>d1bf2\_2 b.71.1.1 (638-750) Isoamylase {Pseudomonas amyloderamosa}

YSGSQLTWYQPSGAVADSNYWNNTSNYAIAYAINGPSLGDSNSIYVAYNGWSSSVTFTLPAPPSGTQWYRVTDTCDWNDGASTFVAPGSETLIGGAGTTYGQCGQSLLLLISK

>d1gcya1 b.71.1.1 (A:358-418) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase) {Pseudomonas stutzeri}

RADSAISFHSGYSGLVATVSGSQQTLVVALNSDLGNPGQVASGSFSEAVNASNGQVRVWRS

>d1avaa1 b.71.1.1 (A:347-403) Plant alpha-amylase {Barley (Hordeum vulgare), seeds, AMY2 isozyme}

HNESKLQIIEADADLYLAEIDGKVIVKLGPRYDVGNLIPGGFKVAAHGNDYAVWEKI

>d1uok\_1 b.71.1.1 (480-558) Oligo-1,6-glucosidase {Bacillus cereus}

GSYDLILENNPSIFAYVRTYGVEKLLVIANFTAEECIFELPEDISYSEVELLIHNYDVENGPIENITLRPYEAMVFKLK

>d1g5aa1 b.71.1.1 (A:555-628) Amylosucrase {Neisseria polysaccharea}

RLVTFNTNNKHIIGYIRNNALLAFGNFSEYPQTVTAHTLQAMPFKAHDLIGGKTVSLNQDLTLQPYQVMWLEIA

>d1f8ab1 b.72.1.1 (B:1-42) Mitotic rotamase PIN1 {Human (Homo sapiens)}

GSHGMADEEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPS

>d1i8hb\_ b.72.1.1 (B:) Mitotic rotamase PIN1 {Human (Homo sapiens)}

KLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSSG

>d1pina1 b.72.1.1 (A:6-39) Mitotic rotamase PIN1 {Human (Homo sapiens)}

KLPPGWEKRMSRSSGRVYYFNHITNASQWERPSG

>d1e0la\_ b.72.1.1 (A:) Formin binding protein FBP28 domain {Domestic mouse (Mus musculus)}

GATAVSEWTEYKTADGKTYYYNNRTLESTWEKPQELK

>d1eg3a3 b.72.1.1 (A:47-84) Dystrophin {Human (Homo sapiens)}

PASQHFLSTSVQGPWERAISPNKVPYYINHETQTTCWD

>d1i5hw\_ b.72.1.1 (W:) Ubiquitin ligase NEDD4 WWIII domain {Rat (Rattus norvegicus)}

GSPVDSNDLGPLPPGWEERTHTDGRVFFINHNIKKTQWEDPRMQNVAITG

>d1e0na\_ b.72.1.1 (A:) Hypothetical protein Yjq8 (Set2p) {Baker's yeast (Saccharomyces cerevisiae)}

PGWEIIHENGRPLYYNAEQKTKLHYPP

>d1jmqa\_ b.72.1.1 (A:) Yap65 ww domain {Human (Homo sapiens)}

FEIPDDVPLPAGWEMAKTSSGQRYFKNHIDQTTTWQDPRKAMLSQM

>d1k9ra\_ b.72.1.1 (A:) Yap65 ww domain {Human (Homo sapiens)}

FEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTTWQDPRK

>d1aiw\_\_ b.72.2.1 (-) Cellulose-binding domain of endoglucanase Z {Erwinia chrysanthemi}

MGDCANANVYPNWVSKDWAGGQPTHNEAGQSIVYKGNLYTANWYTASVPGSDSSWTQVGSCN

>d1ed7a\_ b.72.2.1 (A:) Chitin-binding domain of chitinase A1 {Bacillus circulans}

AWQVNTAYTAGQLVTYNGKTYKCLQPHTSLAGWEPSNVPALWQLQ

>d1goia1 b.72.2.1 (A:447-498) Chitinase B, C-terminal domain {Serratia marcescens}

NLPIMTAPAYVPGTTYAQGALVSYQGYVWQTKWGYITSAPGSDSAWLKVGRV

>d1dkga1 b.73.1.1 (A:139-197) Head domain of nucleotide exchange factor GrpE {Escherichia coli}

VEVIAETNVPLDPNVHQAIAMVESDDVAPGNVLGIMQKGYTLNGRTIRAAMVTVAKAKA

>d1e44b\_ b.101.1.1 (B:) Ribonuclease domain of colicin E3 {Escherichia coli}

GFKDYGHDYHPAPKTENIKGLGDLKPGIPKTPKQNGGGKRKRWTGDKGRKIYEWDSQHGELEGYRASDGQHLGSFDPKTGNQLKGPDPKRNIKKYL

>d1hcb\_\_ b.74.1.1 (-) Carbonic anhydrase {Human (Homo sapiens), erythrocytes, isozyme I}

PDWGYDDKNGPEQWSKLYPIANGNNQSPVDIKTSETKHDTSLKPISVSYNPATAKEIINVGHSFHVNFEDNDNRSVLKGGPFSDSYRLFQFHFHWGSTNEHGSEHTVDGVKYSAELHVAHWNSAKYSSLAEAASKADGLAVIGVLMKVGEANPKLQKVLDALQAIKTKGKRAPFTNFDPSTLLPSSLDFWTYPGSLTHPPLYESVTWIICKESISVSSEQLAQFRSLLSNVEGDNAVPMQHNNRPTQPLKGRTVRASF

>d2cba\_\_ b.74.1.1 (-) Carbonic anhydrase {Human (Homo sapiens), erythrocytes, isozyme II}

HHWGYGKHNGPEHWHKDFPIAKGERQSPVDIDTHTAKYDPSLKPLSVSYDQATSLRILNNGHAFNVEFDDSQDKAVLKGGPLDGTYRLIQFHFHWGSLDGQGSEHTVDKKKYAAELHLVHWNTKYGDFGKAVQQPDGLAVLGIFLKVGSAKPGLQKVVDVLDSIKTKGKSADFTNFDPRGLLPESLDYWTYPGSLTTPPLLECVTWIVLKEPISVSSEQVLKFRKLNFNGEGEPEELMVDNWRPAQPLKNRQIKASFK

>d1flja\_ b.74.1.1 (A:) Carbonic anhydrase {Rat (Rattus norvegicus), isozyme III}

AKEWGYASHNGPEHWHELYPIAKGDNQSPIELHTKDIRHDPSLQPWSVSYDPGSAKTILNNGKTCRVVFDDTFDRSMLRGGPLSGPYRLRQFHLHWGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTFGEALKQPDGIAVVGIFLKIGREKGEFQILLDALDKIKTKGKEAPFNHFDPSCLFPACRDYWTYHGSFTTPPCEECIVWLLLKEPMTVSSDQMAKLRSLFASAENEPPVPLVGNWRPPQPIKGRVVRASFK

>d1znca\_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme IV}

WCYEVQAESSNYPCLVPVKWGGNCQKDRQSPINIVTTKAKVDKKLGRFFFSGYDKKQTWTVQNNGHSVMMLLENKASISGGGLPAPYQAKQLHLHWSDLPYKGSEHSLDGEHFAMEMHIVHEKEKGTSRNVKEAQDPEDEIAVLAFLVEAGTQVNEGFQPLVEALSNIPKPEMSTTMAESSLLDLLPKEEKLRHYFRYLGSLTTPTCDEKVVWTVFREPIQLHREQILAFSQKLYYDKEQTVSMKDNVRPLQQLGQRTVIKS

>d2znc\_\_ b.74.1.1 (-) Carbonic anhydrase {Mouse (Mus musculus), isozyme IV}

WCYEIQTEDPRSSCLGPEKWPGACKENQQSPINIVTARTKVNPRLTPFILVGYDQKQQWPIKNNQHTVEMTLGGGACIIGGDLPARYEAVQLHLHWSNGNDNGSEHSIDGRHFAMEMHIVHKKLTSSKEDSKDKFAVLAFMIEVGDKVNKGFQPLVEALPSISKPHSTSTVRESSLQDMLPPSTKMYTYFRYNGSLTTPNCDETVIWTVYKQPIKIHKNQFLEFSKNLYYDEDQKLNMKDNVRPLQPLGKRQVFKSHA

>d1dmxa\_ b.74.1.1 (A:) Carbonic anhydrase {Mouse (Mus musculus), liver, isozyme V}

GTRQSPINIQWKDSVYDPQLAPLRVSYDAASCRYLWNTGYFFQVEFDDSCEDSGISGGPLGNHYRLKQFHFHWGATDEWGSEHAVDGHTYPAELHLVHWNSTKYENYKKASVGENGLAVIGVFLKLGAHHQALQKLVDVLPEVRHKDTQVAMGPFDPSCLMPACRDYWTYPGSLTTPPLAESVTWIVQKTPVEVSPSQLSMFRTLLFSGRGEEEDVMVNNYRPLQPLRDRKLRSSFR

>d1jd0a\_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme XII}

KWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLTNNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHYNSDLYPDASTASNKSEGLAVLAVLIEMGSFNPSYDKIFSHLQHVKYKGQEAFVPGFNIEELLPERTAEYYRYRGSLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREMINNFRQVQKFDERLVYTSFS

>d1kopa\_ b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}

HTHWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPAIKVNYKPSMVDVENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFHVPSENQIKGRTFPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLNQPFDASTLLPKRLKYYRFAGSLTTPPCTEGVSWLVLKTYDHIDQAQAEKFTRAVGSENNRPVQPLNARVVIE

>d1koqa\_ b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}

THWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPAIKVNYKPSMVDVENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFLTVNGRTYTLKQFHFHVPSENQIKGRTFPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSLAVLYEAGKTNGRLSSIWNVMPMTAGKVKLNQPFDASTLLPKRLKYYRFAGSLTTPPCTEGVSWLVLKTYDHIDQAQAEKFTRAVGSENNRPVQPLNARVVIE

>d4bcl\_\_ b.75.1.1 (-) Bacteriochlorophyll A protein {Prosthecochloris aestuarii, strain 2k}

TTTAHSDYEIILEGGSSSWGQVKGRAKVNVPAAIPLLPTDCNIRIDAKPLDAQKGVVRFTTKIESVVDSVKNTLNVEVDIANETKDRRIAVGEGSLSVGDFSHSFSFEGSVVNMYYYRSDAVRRNIPNPIYMQGRQFHDILMKVPLDNNDLVDTWEGFQQSISGGGANFGDWIREFWFIGPAFAAINEGGQRISPIVVNSSNVEGGEKGPVGVTRWKFSHAGSGVVDSISRWTELFPVEQLNKPASIEGGFRSDSQGIEVKVDGNLPGVSRDAGGGLRRILNHPLIPLVHHGMVGKFNDFTVDTQLKIVLPKGYKIRYAAPQFRSQNLEEYRWSGGAYARWVEHVCKGGTGQFEVLYAQ

>d1ksaa\_ b.75.1.1 (A:) Bacteriochlorophyll A protein {Green sulfur bacterium (Chlorobium tepidum)}

TTAHSDYEIVLEGGSSSWGKVKARAKVNAPPASPLLPADCDVKLNVKPLDPAKGFVRISAVFESIVDSTKNKLTIEADIANETKERRISVGEGMVSVGDFSHTFSFEGSVVNLFYYRSDAVRRNVPNPIYMQGRQFHDILMKVPLDNNDLIDTWEGTVKAIGSTGAFNDWIRDFWFIGPAFTALNEGGQRISRIEVNGLNTESGPKGPVGVSRWRFSHGGSGMVDSISRWAELFPSDKLNRPAQVEAGFRSDSQGIEVKVDGEFPGVSVDAGGGLRRILNHPLIPLVHHGMVGKFNNFNVDAQLKVVLPKGYKIRYAAPQYRSQNLEEYRWSGGAYARWVEHVCKGGVGQFEILYAQ

>d1ospo\_ b.76.1.1 (O:) Outer surface protein A {Lyme disease spirochete (Borrelia burgdorferi)}

SLDEKNSVSVDLPGEMKVLVSKEKNKDGKYDLIATVDKLELKGTSDKNNGSGVLEGVKADKCKVKLTISDDLGQTTLEVFKEDGKTLVSKKVTSKDKSSTEEKFNEKGEVSEKIITRADGTRLEYTGIKSDGSGKAKEVLKGYVLEGTLTAEKTTLVVKEGTVTLSKNISKSGEVSVELNDTDSSAATKKTAAWNSGTSTLTITVNSKKTKDLVFTKENTITVQQYDSNGTKLEGSAVEITKLDEIKNALK

>d1vmoa\_ b.77.1.1 (A:) Vitelline membrane outer protein-I (VMO-I) {Hen (Gallus gallus)}

RTREYTSVITVPNGGHWGKWGIRQFCHSGYANGFALKVEPSQFGRDDTALNGIRLRCLDGSVIESLVGKWGTWTSFLVCPTGYLVSFSLRSEKSQGGGDDTAANNIQFRCSDEAVLVGDGLSWGRFGPWSKRCKICGLQTKVESPQGLRDDTALNNVRFFCCK

>d1dlc\_2 b.77.2.1 (290-499) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}

LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSFNYWSGNYVSTRPSIGSNDIITSPFYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVTKVEFSQYNDQTDEASTQTYDSKRNVGAVSWDSIDQLPPETTDEPLEKGYSHQLNYVMCFLMQGSRGTIPVLTWTHKSVD

>d1ji6a2 b.77.2.1 (A:291-502) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis, CRY3bb1}

LYSKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLQGIEFHTRLQPGYFGKDSFNYWSGNYVETRPSIGSSKTITSPFYGDKSTEPVQKLSFDGQKVYRTIANTDVAAWPNGKVYLGVTKVDFSQYDDQKNETSTQTYDSKRNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRRGTIPFFTWTHRSVD

>d1ciy\_2 b.77.2.1 (256-461) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis, CRYIA (A)}

PIRTVSQLTREIYTNPVLENFDGSFRGMAQRIEQNIRQPHLMDILNSITIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTNLPSTIYRQRGTVDSLDVIPPQDNSVPPRAGFSHRLSHVTMLSQAAGAVYTLRAPTFSWQHRSAEF

>d1i5pa2 b.77.2.1 (A:264-472) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

YQSLMVSSGANLYASGSGPQQTQSFTAQNWPFLYSLFQVNSNYILSGISGTRLSITFPNIGGLPGSTTTHSLNSARVNYSGGVSSGLIGATNLNHNFNCSTVLPPLSTPFVRSWLDSGTDRAGVATSTNWQTESFQTTLSLRCGAFSARGNSNYFPDYFIRNISGVPLVIRNEDLTRPLHYNQIRNIESPSGTPGGARAYLVSVHNRKN

>g1jac.5 b.77.3.1 (B:,A:) Jacalin {Jackfruit (Artocarpus integrifolia)}

SGKSQTVIVGSWGAKXGKAFDDGAFTGIREINLSYNKETAIGDFQVVYDLNGSPYVGQNHKSFITGFTPVKISLDFPSEYIMEVSGYTGNVSGYVVVRSLTFKTNKKTYGPYGVTSGTPFNLPIENGLIVGFKGSIGYWLDYFSMYLSL

>g1jot.2 b.77.3.1 (B:,A:) Lectin MPA {Osage orange (Maclura pomifera)}

RNGKSQSIIVGPWGDRXGVTFDDGAYTGIREINFEYNSETAIGGLRVTYDLNGMPFVAEDHKSFITGFKPVKISLEFPSEYIVEVSGYVGKVEGYTVIRSLTFKTNKQTYGPYGVTNGTPFSLPIENGLIVGFKGSIGYWLDYFSIYLSL

>d1c3ma\_ b.77.3.1 (A:) Heltuba lectin {Jerusalem artishoke (Helianthus tuberosus)}

ASDIAVQAGPWGGNGGKRWLQTAHGGKITSIIIKGGTCIFSIQFVYKDKDNIEYHSGKFGVLGDKAETITFAEDEDITAISGTFGAYYHMTVVTSLTFQTNKKVYGPFGTVASSSFSLPLTKGKFAGFFGNSGDVLDSIGGVVVP

>d1jpc\_\_ b.78.1.1 (-) Lectin (agglutinin) {Snowdrop (Galanthus nivalis)}

DNILYSGETLSTGEFLNYGSFVFIMQEDCNLVLYDVDKPIWATNTGGLSRSCFLSMQTDGNLVVYNPSNKPIWASNTGGQNGNYVCILQKDRNVVIYGTDRWATGTHT

>d1bwua\_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (Allium sativum)}

RNILRNDEGLYGGQSLDVNPYHFIMQEDCNLVLYDHSTSVWASNTGILGKKGCRAVLQSDGNFVVYDAEGRSLWASHSVRGNGNYVLVLQEDGNVVIYRSDIWSTN

>d1bwud\_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (Allium sativum)}

RNILTNDEGLYGGQSLDVNPYHLIMQEDCNLVLYDHSTAVWSSNTDIPGKKGCKAVLQSDGNFVVYDAEGASLWASHSVRGNGNYVLVLQEDGNVVIYRSDIWSTNTYR

>d1kj1a\_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (Allium sativum)}

RNLLTNGEGLYAGQSLDVEPYHFIMQEDCNLVLYDHSTSVWASNTGILGKKGCKAVLQSDGNFVVYDAEGRSLWASHSVRGNGNYVLVLQEDGNVVIYGSDIWSTGTYK

>d1kj1d\_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (Allium sativum)}

RNILMNDEGLYAGQSLDVEPYHLIMQEDCNLVLYDHSTAVWTTNTDIPGKKGCKAVLQSDGNFVVYDAEGRSLWASHSVRGNGNYVLVLQEDGNVVIYGSDIWSTNTYK

>d1npla\_ b.78.1.1 (A:) Lectin (agglutinin) {Daffodil (Narcissus pseudonarcissus)}

DNILYSGETLSPGEFLNNGRYVFIMQEDCNLVLYDVDKPIWATNTGGLDRRCHLSMQSDGNLVVYSPRNNPIWASNTGGENGNYVCVLQKDRNVVIYGTARWATGTNIH

>d1b2pa\_ b.78.1.1 (A:) Lectin (agglutinin) {Bluebell (Scilla campanulata)}

NNIIFSKQPDDNHPQILHATESLEILFGTHVYRFIMQTDCNLVLYDNNNPIWATNTGGLGNGCRAVLQPDGVLVVITNENVTVWQSPVAGKAGHYVLVLQPDRNVVIYGDALWATQTVR

>d1dlpa1 b.78.1.1 (A:1-115) Fetuin-binding protein Scafet precursor {Bluebell (Scilla campanulata)}

NNILFGLSHEGSHPQTLHAAQSLELSSFRFTMQSDCNLVLFDSDVRVWASNTAGATGCRAVLQSDGLLVILTAQNTIRWSSGTKGSIGNYVLVLQPDRTVTIYGPGLWDSGTSNK

>d1dlpa2 b.78.1.1 (A:116-235) Fetuin-binding protein Scafet precursor {Bluebell (Scilla campanulata)}

GSVVVANNGNSILYSTQGNDNHPQTLHATQSLQLSPYRLSMETDCNLVLFDRDDRVWSTNTAGKGTGCRAVLQPNGRMDVLTNQNIAVWTSGNSRSAGRYVFVLQPDRNLAIYGGALWTT

>d1kapp1 b.79.1.1 (P:247-470) Metalloprotease, C-terminal domain {Pseudomonas aeruginosa, alkaline protease}

GANLTTRTGDTVYGFNSNTERDFYSATSSSSKLVFSVWDAGGNDTLDFSGFSQNQKINLNEKALSDVGGLKGNVSIAAGVTVENAIGGSGSDLLIGNDVANVLKGGAGNDILYGGLGADQLWGGAGADTFVYGDIAESSAAAPDTLRDFVSGQDKIDLSGLDAFVNGGLVLQYVDAFAGKAGQAILSYDAASKAGSLAIDFSGDAHADFAINLIGQATQADIVV

>d1sat\_1 b.79.1.1 (247-471) Metalloprotease, C-terminal domain {Serratia marcescens}

GANLSTRTGDTVYGFNSNTGRDFLSTTSNSQKVIFAAWDAGGNDTFDFSGYTANQRINLNEKSFSDVGGLKGNVSIAAGVTIENAIGGSGNDVIVGNAANNVLKGGAGNDVLFGGGGADELWGGAGKDIFVFSAASDSAPGASDWIRDFQKGIDKIDLSFFDKEANSSSFIHFVDHFSGTAGEALLSYNASSNVTDLSVNIGGHAAPDFLVKIVGQVDVATDFIV

>d1air\_\_ b.80.1.1 (-) Pectate lyase {Erwinia chrysanthemi, type C}

ATDTGGYAATAGGNVTGAVSKTATSMQDIVNIIDAARLDANGKKVKGGAYPLVITYTGNEDSLINAAAANICGQWSKDPRGVEIKEFTKGITIIGANGSSANFGIWIKKSSDVVVQNMRIGYLPGGAKDGDMIRVDDSPNVWVDHNELFAANHECDGTPDNDTTFESAVDIKGASNTVTVSYNYIHGVKKVGLDGSSSSDTGRNITYHHNYYNDVNARLPLQRGGLVHAYNNLYTNITGSGLNVRQNGQALIENNWFEKAINPVTSRYDGKNFGTWVLKGNNITKPADFSTYSITWTADTKPYVNADSWTSTGTFPTVAYNYSPVSAQCVKDKLPGYAGVGKNLATLTSTAC

>d1pcl\_\_ b.80.1.1 (-) Pectate lyase {Erwinia chrysanthemi, type E}

AVETDAATTGWATQNGGTTGGAKAAKAVEVKNISDFKKALNGTDSSAKIIKVTGPIDISGGKAYTSFDDQKARSQISIPSNTTIIGVGSNGKFTNGSLVIKGVKNVILRNLYIETPVDVAPHYESGDGWNAEWDAAVIDNSTNVWVDHVTISDGSFTDDKYTTKDGEKYVQHDGALDIKKGSDYVTISYSRFELHDKTILIGHSDSNGSQDSGKLRVTFHNNVFDRVTERAPRVRFGSIHAYNNVYLGDVKHSVYPYLYSFGLGTSGSILSESNSFTLSNLKSIDGKNPECSIVKQFNSKVFSDKGSLVNGSTTTKLDTCGLTAYKPTLPYKYSAQTMTSSLATSINNNAGYGKL

>d1bn8a\_ b.80.1.1 (A:) Pectate lyase {Bacillus subtilis}

ADLGHQTLGSNDGWGAYSTGTTGGSKASSSNVYTVSNRNQLVSALGKETNTTPKIIYIKGTIDMNVDDNLKPLGLNDYKDPEYDLDKYLKAYDPSTWGKKEPSGTQEEARARSQKNQKARVMVDIPANTTIVGSGTNAKVVGGNFQIKSDNVIIRNIEFQDAYDYFPQWDPTDGSSGNWNSQYDNITINGGTHIWIDHCTFNDGSRPDSTSPKYYGRKYQHHDGQTDASNGANYITMSYNYYHDHDKSSIFGSSDSKTSDDGKLKITLHHNRYKNIVQRAPRVRFGQVHVYNNYYEGSTSSSSYPFSYAWGIGKSSKIYAQNNVIDVPGLSAAKTISVFSGGTALYDSGTLLNGTQINASAANGLSSSVGWTPSLHGSIDASANVKSNVINQAGAGKLN

>d1ee6a\_ b.80.1.1 (A:) Pectate lyase {Bacillus sp., strain ksmp15}

APTVVHETIRVPAGQTFDGKGQTYVANPNTLGDGSQAENQKPIFRLEAGASLKNVVIGAPAADGVHCYGDCTITNVIWEDVGEDALTLKSSGTVNISGGAAYKAYDKVFQINAAGTINIRNFRADDIGKLVRQNGGTTYKVVMNVENCNISRVKDAILRTDSSTSTGRIVNTRYSNVPTLFKGFKSGNTTASGNTQY

>d1idk\_\_ b.80.1.2 (-) Pectin lyase {Aspergillus niger, type A}

VGVSGSAEGFAKGVTGGGSATPVYPDTIDELVSYLGDDEARVIVLTKTFDFTDSEGTTTGTGCAPWGTASACQVAIDQDDWCENYEPDAPSVSVEYYNAGTLGITVTSNKSLIGEGSSGAIKGKGLRIVSGAENIIIQNIAVTDINPKYVWGGDAITLDDCDLVWIDHVTTARIGRQHYVLGTSADNRVSLTNNYIDGVSDYSATCDGYHYWAIYLDGDADLVTMKGNYIYHTSGRSPKVQDNTLLHAVNNYWYDISGHAFEIGEGGYVLAEGNVFQNVDTVLETYEGEAFTVPSSTAGEVCSTYLGRDCVINGFGSSGTFSEDSTSFLSDFEGKNIASASAYTSVASRVVANAGQGNL

>d1qcxa\_ b.80.1.2 (A:) Pectin lyase {Aspergillus niger, type B}

AGVVGAAEGFAHGVTGGGSASPVYPTTTDELVSYLGDNEPRVIILDQTFDFTGTEGTETTTGCAPWGTASQCQVAINLHSWCDNYQASAPKVSVTYDKAGILPITVNSNKSIVGQGTKGVIKGKGLRVVSGAKNVIIQNIAVTDINPKYVWGGDAITVDDSDLVWIDHVTTARIGRQHIVLGTSADNRVTISYSLIDGRSDYSATCNGHHYWGVYLDGSNDMVTLKGNYFYNLSGRMPKVQGNTLLHAVNNLFHNFDGHAFEIGTGGYVLAEGNVFQDVNVVVETPISGQLFSSPDANTNQQCASVFGRSCQLNAFGNSGSMSGSDTSIISKFAGKTIAAAHPPGAIAQWTMKNAGQGK

>d1rmg\_\_ b.80.1.3 (-) Rhamnogalacturonase A {Aspergillus aculeatus}

QLSGSVGPLTSASTKGATKTCNILSYGAVADNSTDVGPAITSAWAACKSGGLVYIPSGNYALNTWVTLTGGSATAIQLDGIIYRTGTASGNMIAVTDTTDFELFSSTSKGAVQGFGYVYHAEGTYGARILRLTDVTHFSVHDIILVDAPAFHFTMDTCSDGEVYNMAIRGGNEGGLDGIDVWGSNIWVHDVEVTNKDECVTVKSPANNILVESIYCNWSGGCAMGSLGADTDVTDIVYRNVYTWSSNQMYMIKSNGGSGTVSNVLLENFIGHGNAYSLDIDGYWSSMTAVAGDGVQLNNITVKNWKGTEANGATRPPIRVVCSDTAPCTDLTLEDIAIWTESGSSELYLCRSAYGSGYCLKDSSSHTSYTTTSTVTAAPSGYSATTMAADLATAFGLTASIPIPTIPTSFYPGLTPYSALAG

>d1bhe\_\_ b.80.1.3 (-) Polygalacturonase {Erwinia carotovora, subsp. carotovora}

SDSRTVSEPKTPSSCTTLKADSSTATSTIQKALNNCDQGKAVRLSAGSTSVFLSGPLSLPSGVSLLIDKGVTLRAVNNAKSFENAPSSCGVVDKNGKGCDAFITAVSTTNSGIYGPGTIDGQGGVKLQDKKVSWWELAADAKVKKLKQNTPRLIQINKSKNFTLYNVSLINSPNFHVVFSDGDGFTAWKTTIKTPSTARNTDGIDPMSSKNITIAYSNIATGDDNVAIKAYKGRAETRNISILHNDFGTGHGMSIGSETMGVYNVTVDDLKMNGTTNGLRIKSDKSAAGVVNGVRYSNVVMKNVAKPIVIDTVYEKKEGSNVPDWSDITFKDVTSETKGVVVLNGENAKKPIEVTMKNVKLTSDSTWQIKNVNVKK

>d1ia5a\_ b.80.1.3 (A:) Polygalacturonase {Fungus (Aspergillus aculeatus)}

ATTCTFSGSNGASSASKSKTSCSTIVLSNVAVPSGTTLDLTKLNDGTHVIFSGETTFGYKEWSGPLISVSGSDLTITGASGHSINGDGSRWWDGEGGNGGKTKPKFFAAHSLTNSVISGLKIVNSPVQVFSVAGSDYLTLKDITIDNSDGDDNGGHNTDAFDIGTSTYVTISGATVYNQDDCVAVNSGENIYFSGGYCSGGHGLSIGSVGGRSDNTVKNVTFVDSTIINSDNGVRIKTNIDTTGSVSDVTYKDITLTSIAKYGIVVQQNYGDTSSTPTTGVPITDFVLDNVHGSVVSSGTNILISCGSGSCSDWTWTDVSVSGGKTSSKCTNVPSGASC

>d1czfa\_ b.80.1.3 (A:) Polygalacturonase {Fungus (Aspergillus niger), endo-polygalacturonase II}

DSCTFTTAAAAKAGKAKCSTITLNNIEVPAGTTLDLTGLTSGTKVIFEGTTTFQYEEWAGPLISMSGEHITVTGASGHLINCDGARWWDGKGTSGKKKPKFFYAHGLDSSSITGLNIKNTPLMAFSVQANDITFTDVTINNADGDTQGGHNTDAFDVGNSVGVNIIKPWVHNQDDCLAVNSGENIWFTGGTCIGGHGLSIGSVGDRSNNVVKNVTIEHSTVSNSENAVRIKTISGATGSVSEITYSNIVMSGISDYGVVIQQDYEDGKPTGKPTNGVTIQDVKLESVTGSVDSGATEIYLLCGSGSCSDWTWDDVKVTGGKKSTACKNFPSVASC

>d1hg8a\_ b.80.1.3 (A:) Polygalacturonase {Fusarium moniliforme}

DPCSVTEYSGLATAVSSCKNIVLNGFQVPTGKQLDLSSLQNDSTVTFKGTTTFATTADNDFNPIVISGSNITITGASGHVIDGNGQAYWDGKGSNSNSNQKPDHFIVVQKTTGNSKITNLNIQNWPVHCFDITGSSQLTISGLILDNRAGDKPNAKSGSLPAAHNTDGFDISSSDHVTLDNNHVYNQDDCVAVTSGTNIVVSNMYCSGGHGLSIGSVGGKSDNVVDGVQFLSSQVVNSQNGCRIKSNSGATGTINNVTYQNIALTNISTYGVDVQQDYLNGGPTGKPTNGVKISNIKFIKVTGTVASSAQDWFILCGDGSCSGFTFSGNAITGGGKTSSCNYPTNTCPS

>d1dbga\_ b.80.1.4 (A:) Chondroitinase B {Flavobacterium heparinum}

QVVASNETLYQVVKEVKPGGLVQIADGTYKDVQLIVSNSGKSGLPITIKALNPGKVFFTGDAKVELRGEHLILEGIWFKDGNRAIQAWKSHGPGLVAIYGSYNRITACVFDCFDEANSAYITTSLTEDGKVPQHCRIDHCSFTDKITFDQVINLNNTARAIKDGSVGGPGMYHRVDHCFFSNPQKPGNAGGGIRIGYYRNDIGRCLVDSNLFMRQDSEAEIITSKSQENVYYGNTYLNCQGTMNFRHGDHQVAINNFYIGNDQRFGYGGMFVWGSRHVIACNYFELSETIKSRGNAALYLNPGAMASEHALAFDMLIANNAFINVNGYAIHFNPLDERRKEYCAANRLKFETPHQLMLKGNLFFKDKPYVYPFFKDDYFIAGKNSWTGNVALGVEKGIPVNISANRSAYKPVKIKDIQPIEGIALDLNALISKGITGKPLSWDEVRPYWLKEMPGTYALTARLSADRAAKFKAVIKRNKEH

>d1h80a\_ b.80.1.8 (A:) iota-carrageenase {Alteromonas sp., atcc 43554}

VSPKTYKDADFYVAPTQQDVNYDLVDDFGANGNDTSDDSNALQRAINAISRKPNGGTLLIPNGTYHFLGIQMKSNVHIRVESDVIIKPTWNGDGKNHRLFEVGVNNIVRNFSFQGLGNGFLVDFKDSRDKNLAVFKLGDVRNYKISNFTIDDNKTIFASILVDVTERNGRLHWSRNGIIERIKQNNALFGYGLIQTYGADNILFRNLHSEGGIALRMETDNLLMKNYKQGGIRNIFADNIRCSKGLAAVMFGPHFMKNGDVQVTNVSSVSCGSAVRSDSGFVELFSPTDEVHTRQSWKQAVESKLGRGCAQTPYARGNGGTRWAARVTQKDACLDKAKLEYGIEPGSFGTVKVFDVTARFGYNADLKQDQLDYFSTSNPMCKRVCLPTKEQWSKQGQIYIGPSLAAVIDTTPETSKYDYDVKTFNVKRINFPVNSHKTIDTNTESSRVCNYYGMSECSSSRWER

>d1qjva\_ b.80.1.5 (A:) Pectin methylesterase PemA {Erwinia chrysanthemi}

ATTYNAVVSKSSSDGKTFKTIADAIASAPAGSTPFVILIKNGVYNERLTITRNNLHLKGESRNGAVIAAATAAGTLKSDGSKWGTAGSSTITISAKDFSAQSLTIRNDFDFPANQAKSDSDSSKIKDTQAVALYVTKSGDRAYFKDVSLVGYQDTLYVSGGRSFFSDCRISGTVDFIFGDGTALFNNCDLVSRYRADVKSGNVSGYLTAPSTNINQKYGLVITNSRVIRESDSVPAKSYGLGRPWHPTTTFSDGRYADPNAIGQTVFLNTSMDNHIYGWDKMSGKDKNGNTIWFNPEDSRFFEYKSYGAGAAVSKDRRQLTDAQAAEYTQSKVLGDWTPTLP

>d1qq1a\_ b.80.1.6 (A:) P22 tailspike protein {Salmonella phage P22}

YSIEADKKFKYSVKLSDYPTLQDAASAAVDGLLIDRDYNFYGGETVDFGGKVLTIECKAKFIGDGNLIFTKLGKGSRIAGVFMESTTTPWVIKPWTDDNQWLTDAAAVVATLKQSKTDGYQPTVSDYVKFPGIETLLPPNAKGQNITSTLEIRECIGVEVHRASGLMAGFLFRGCHFCKMVDANNPSGGKDGIITFENLSGDWGKGNYVIGGRTSYGSVSSAQFLRNNGGFERDGGVIGFTSYRAGGSGVKTWQGTVGSTTSRNYNLQFRDSVVIYPVWDGFDLGADTDMNPELDRPGDYPITQYPLHQLPLNHLIDNLLVRGALGVGFGMDGKGMYVSNITVEDCAGSGAYLLTHESVFTNIAIIDTNTKDFQANQIYISGACRVNGLRLIGIRSTDGQSLTIDAPNSTVSGITGMVDPSRINVANLAEEGLGNIRANSFGYDSAAIKLRIHKLSKTLDSGALYSHINGGAGSGSAYTQLTAISGSTPDAVSLKVNHKDCRGAEIPFVPDIASDDFIKDSSCFLPYWENNSTSLKALVKKPNGELVRLTLATL

>d1daba\_ b.80.1.7 (A:) Virulence factor P.69 pertactin {Bordetella pertussis}

DWNNQSIVKTGERQHGIHIQGSDPGGVRTASGTTIKVSGRQAQGILLENPAAELQFRNGSVTSSGQLSDDGIRRFLGTVTVKAGKLVADHATLANVGDTWDDDGIALYVAGEQAQASIADSTLQGAGGVQIERGANVTVQRSAIVDGGLHIGALQSLQPEDLPPSRVVLRDTNVTAVPASGAPAAVSVLGASELTLDGGHITGGRAAGVAAMQGAVVHLQRATIRRGDALAGGAVPGGAVPGGAVPGGFGPGGFGPVLDGWYGVDVSGSSVELAQSIVEAPELGAAIRVGRGARVTVPGGSLSAPHGNVIETGGARRFAPQAAPLSITLQAGAHAQGKALLYRVLPEPVKLTLTGGADAQGDIVATELPSIPGTSIGPLDVALASQARWTGATRAVDSLSIDNATWVMTDNSNVGALRLASDGSVDFQQPAEAGRFKVLTVNTLAGSGLFRMNVFADLGLSDKLVVMQDASGQHRLWVRNSGSEPASANTLLLVQTPLGSAATFTLANKDGKVDIGTYRYRLAANGNGQWSLVGAKAPP

>d1ezga\_ b.80.2.1 (A:) Insect cysteine-rich antifreeze protein {Yellow mealworm (Tenebrio molitor)}

QCTGGADCTSCTGACTGCGNCPNAVTCTNSQHCVKANTCTGSTDCNTAQTCTNSKDCFEANTCTDSTNCYKATACTNSSGCP

>d1hf2a1 b.80.3.1 (A:100-206) Cell-division inhibitor MinC, C-terminal domain {Thermotoga maritima}

TGKVIKRNIRSGQTVVHSGDVIVFGNVNKGAEILAGGSVVVFGKAQGNIRAGLNEGGQAVVAALDLQTSLIQIAGFITHSKGEENVPSIAHVKGNRIVIEPFDKVSF

>d1ea0a1 b.80.4.1 (A:1203-1472) Alpha subunit of glutamate synthase, C-terminal domain {Azospirillum brasilense}

GRNEVPDTLDARIVADARPLFEEGEKMQLAYNARNTQRAIGTRLSSMVTRKFGMFGLQPGHITIRLRGTAGQSLGAFAVQGIKLEVMGDANDYVGKGLSGGTIVVRPTTSSPLETNKNTIIGNTVLYGATAGKLFAAGQAGERFAVRNSGATVVVEGCGSNGCEYMTGGTAVILGRVGDNFAAGMTGGMAYVYDLDDSLPLYINDESVIFQRIEVGHYESQLKHLIEEHVTETQSRFAAEILNDWAREVTKFWQVVPKEMLNRLEVPVHL

>d1kq5a\_ b.80.5.1 (A:) C-terminal domain of adenylylcyclase associated protein {Baker's yeast (Saccharomyces cerevisiae)}

MPPRKELVGNKWFIENYENETESLVIDANKDESIFIGKCSQVLVQIKGKVNAISLSETESCSVVLDSSISGMDVIKSNKFGIQVNHSLPQISIDKSDGGNIYLSKESLNTEIYTSCSTAINVNLPIGEDDDYVEFPISEQMKHSFADGKFKSAVFE

>d1lxa\_\_ b.81.1.1 (-) UDP N-acetylglucosamine acyltransferase {Escherichia coli, gene lpxA}

MIDKSAFVHPTAIVEEGASIGANAHIGPFCIVGPHVEIGEGTVLKSHVVVNGHTKIGRDNEIYQFASIGEVNQDLKYAGEPTRVEIGDRNRIRESVTIHRGTVQGGGLTKVGSDNLLMINAHIAHDCTVGNRCILANNATLAGHVSVDDFAIIGGMTAVHQFCIIGAHVMVGGCSGVAQDVPPYVIAQGNHATPFGVNIEGLKRRGFSREAITAIRNAYKLIYRSGKTLDEVKPEIAELAETYPEVKAFTDFFARSTRGLIR

>d3tdt\_\_ b.81.1.2 (-) Tetrahydrodipicolinate-N-succinlytransferase, THDP-succinlytransferase, DapD {Mycobacterium bovis}

MQQLQNVIESAFERRADITPANVDTVTREAVNQVIGLLDSGALRVAEKIDGQWVTHQWLKKAVLLSFRINDNKVMDGAETRYYDKVPMKFADYDEARFQKEGFRVVPPATVRQGAFIARNTVLMPSYVNIGAYVDEGTMVDTWATVGSCAQIGKNVHLSGGVGIGGVLEPLQANPTIIEDNCFIGARSEVVEGVIVEEGSVISMGVYLGQSTRIYDRETGEIHYGRVPAGSVVVSGNLPSKDGSYSLYCAVIVKKVDAKTRGKVGINELLRTID

>d1xat\_\_ b.81.1.3 (-) Xenobiotic acetyltransferase {Pseudomonas aeruginosa}

NYFESPFRGKLLSEQVSNPNIRVGRYSYYSGYYHGHSFDDCARYLMPDRDDVDKLVIGSFCSIGSGAAFIMAGNQGHRAEWASTFPFHFMHEEPAFAGAVNGYQPAGDTLIGHEVWIGTEAMFMPGVRVGHGAIIGSRALVTGDVEPYAIVGGNPARTIRKRFSDGDIQNLLEMAWWDWPLADIEAAMPLLCTGDIPALYQHWKQRQA

>d1kk6a\_ b.81.1.3 (A:) Xenobiotic acetyltransferase {Enterococcus faecium, VAT(D)}

MGPNPMKMYPIEGNKSVQFIKPILEKLENVEVGEYSYYDSKNGETFDKQILYHYPILNDKLKIGKFCSIGPGVTIIMNGANHRMDGSTYPFNLFGNGWEKHMPKLDQLPIKGDTIIGNDVWIGKDVVIMPGVKIGDGAIVAANSVVVKDIAPYMLAGGNPANEIKQRFDQDTINQLLDIKWWNWPIDIINENIDKILDNSIIREVIW

>d1fxja1 b.81.1.4 (A:252-329) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Escherichia coli}

VMLRDPARFDLRGTLTHGRDVEIDTNVIIEGNVTLGHRVKIGTGCVIKNSVIGDDCEISPYTVVEDANLAAACTIGPF

>d1hv9a1 b.81.1.4 (A:252-452) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Escherichia coli}

VMLRDPARFDLRGTLTHGRDVEIDTNVIIEGNVTLGHRVKIGTGCVIKNSVIGDDCEISPYTVVEDANLAAACTIGPFARLRPGAELLEGAHVGNFVEMKKARLGKGSKAGHLTYLGDAEIGDNVNIGAGTITCNYDGANKFKTIIGDDVFVGSDTQLVAPVTVGKGATIAAGTTVTRNVGENALAISRVPQTQKEGWRRP

>d1hm9a1 b.81.1.4 (A:252-459) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Streptococcus pneumoniae}

VSFVNPEATYIDIDVEIAPEVQIEANVILKGQTKIGAETVLTNGTYVVDSTIGAGAVITNSMIEESSVADGVTVGPYAHIRPNSSLGAQVHIGNFVEVKGSSIGENTKAGHLTYIGNCEVGSNVNFGAGTITVNYDGKNKYKTVIGDNVFVGSNSTIIAPVELGDNSLVGAGSTITKDVPADAIAIGRGRQINKDEYATRLPHHPKNQ

>d1qrea\_ b.81.1.5 (A:) Carbonic anhydrase {Archaeon Methanosarcina thermophila}

TVDEFSNIRENPVTPWNPEPSAPVIDPTAYIDPQASVIGEVTIGANVMVSPMASIRSDEGMPIFVGDRSNVQDGVVLHALETINEEGEPIEDNIVEVDGKEYAVYIGNNVSLAHQSQVHGPAAVGDDTFIGMQAFVFKSKVGNNCVLEPRSAAIGVTIPDGRYIPAGMVVTSQAEADKLPEVTDDYAYSHTNEAVVYVNVHLAEGYKETS

>d1ewwa\_ b.81.2.1 (A:) An insect antifreeze protein {Spruce budworm (Choristoneura fumiferana)}

DGSCTNTNSQLSANSKCEKSTLTNCYVDKSEVYGTTCTGSRFDGVTITTSTSTGSRISGPGCKISTCIITGGVPAPSAACKISGCTFSAN

>d1dzra\_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC {Salmonella typhimurium}

MMIVIKTAIPDVLILEPKVFGDERGFFFESYNQQTFEELIGRKVTFVQDNHSKSKKNVLRGLHFQRGENAQGKLVRCAVGEVFDVAVDIRKESPTFGQWVGVNLSAENKRQLWIPEGFAHGFVTLSEYAEFLYKATNYYSPSSEGSILWNDEAIGIEWPFSQLPELSAKDAAAPLLDQALLTE

>d1ep0a\_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC {Archaeon Methanobacterium thermoautotrophicum}

EFRFIKTSLDGAIIIEPEVYTDERGYFMETFNEAIFQENGLEVRFVQDNESMSVRGVLRGLHFQREKPQGKLVRVIRGEIFDVAVDLRKNSDTYGEWTGVRLSDENRREFFIPEGFAHGFLALSDECIVNYKCTELYHPEYDSGIPWDDPDIGIDWPLEMVDDLIISEKDRNWKPLRENPVYL

>d1fi2a\_ b.82.1.2 (A:) Germin {Barley (Hordeum vulgare)}

TDPDPLQDFCVADLDGKAVSVNGHTCKPMSEAGDDFLFSSKLTKAGNTSTPNGSAVTELDVAEWPGTNTLGVSMNRVDFAPGGTNPPHIHPRATEIGMVMKGELLVGILGSLDSGNKLYSRVVRAGETFVIPRGLMHFQFNVGKTEAYMVVSFNSQNPGIVFVPLTLFGSDPPIPTPVLTKALRVEAGVVELLKSKFAGGS

>d2phla1 b.82.1.2 (A:11-210) Seed storage 7S protein {French bean (Phaseolus vulgaris), phaseolin}

DNPFYFNSDNSWNTLFKNQYGHIRVLQRFDQQSKRLQNLEDYRLVEFRSKPETLLLPQQADAELLLVVRSGSAILVLVKPDDRREYFFLTSDNPIFSDHQKIPAGTIFYLVNPDPKEDLRIIQLAMPVNNPQIHEFFLSSTEAQQSYLQEFSKHILEASFNSKFEEINRVLFEEEGQQEGVIVNIDSEQIKELSKHAKSS

>d2phla2 b.82.1.2 (A:220-381) Seed storage 7S protein {French bean (Phaseolus vulgaris), phaseolin}

NTIGNEFGNLTERTDNSLNVLISSIEMEEGALFVPHYYSKAIVILVVNEGEAHVELVGPKGNKETLEYESYRAELSKDDVFVIPAAYPVAIKATSNVNFTGFGINANNNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSGSGDEVMKLINKQSGSYFVDAH

>d1dgwa\_ b.82.1.2 (A:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}

NNPYLFRSNKFLTLFKNQHGSLRLLQRFNEDTEKLENLRDYRVLEYCSKPNTLLLPHHSDSDLLVLVLEGQAILVLVNPDGRDTYKLDQGDAIKIQAGTPFYLINPDNNQNLRILKFAITFRRPGTVEDFFLSSTKRLPSYLSAFSKNFLEASYDSPYDEIEQTLLQEEQEGVIVKMP

>g1dgr.3 b.82.1.2 (M:,N:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}

QLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQVSDLTFPGSGEEVEELLENQKESYFVDGQPXDKPFNLRSRDPIYSNNYGKLYEITPEKNSQLRDLDILLNCLQMNEGALFVPHYNSRATVILVANEGRAEVELVGLE

>g1dgw.1 b.82.1.2 (X:,Y:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}

DKPFNLRSRDPIYSNNYGKLYEITPEKNSQLRDLDILLNCLQMNEGALFVPHYNSRATVILVANEGRAEVELVGLEXQLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQVSDLTFPGSGEEVEELLENQKESYFVDGQP

>d1fxza1 b.82.1.2 (A:10-248) Seed storage 7S protein {Soybean (Glycine max), proglycinin}

NECQIQKLNALKPDNRIESEGGLIETWNPNNKPFQCAGVALSRCTLNRNALRRPSYTNGPQEIYIQQGKGIFGMIYPGCPSTFEEPQQPQQRGQSSRPQDRHQKIYNFREGDLIAVPTGVAWWMYNNEDTPVVAVSIIDTNSLENQLDQMPRRFYLAGNQEQEFLKYQQEQGGHQSQKGKHQQEEENEGGSILSGFTLEFLEHAFSVDKQIAKNLQGENEGEDKGAIVTVKGGLSVIKP

>d1fxza2 b.82.1.2 (A:297-470) Seed storage 7S protein {Soybean (Glycine max), proglycinin}

ICTMRLRHNIGQTSSPDIYNPQAGSVTTATSLDFPALSWLRLSAEFGSLRKNAMFVPHYNLNANSIIYALNGRALIQVVNCNGERVFDGELQEGRVLIVPQNFVVAARSQSDNFEYVSFKTNDTPMIGTLAGANSLLNALPEEVIQHTFNLKSQQARQIKNNNPFKFLVPPQES

>d1pmi\_\_ b.82.1.3 (-) Phosphomannose isomerase {Yeast (Candida albicans)}

SSEKLFRIQCGYQNYDWGKIGSSSAVAQFVHNSDPSITIDETKPYAELWMGTHPSVPSKAIDLNNQTLRDLVTAKPQEYLGESIITKFGSSKELPFLFKVLSIEKVLSIQAHPDKKLGAQLHAADPKNYPDDNHKPEMAIAVTDFEGFCGFKPLDQLAKTLATVPELNEIIGQELVDEFISGIKLPAEVGSQDDVNNRKLLQKVFGKLMNTDDDVIKQQTAKLLERTDREPQVFKDIDSRLPELIQRLNKQFPNDIGLFCGCLLLNHVGLNKGEAMFLQAKDPHAYISGDIIECMAASDNVVRAGFTPKFKDVKNLVEMLTYSYESVEKQKMPLQEFPRSKGDAVKSVLYDPPIAEFSVLQTIFDKSKGGKQVIEGLNGPSIVIATNGKGTIQITGDDSTKQKIDTGYVFFVAPGSSIELTADSANQDQDFTTYRAFVEA

>d1eyba\_ b.82.1.4 (A:) Homogentisate dioxygenase {Human (Homo sapiens)}

AELKYISGFGNECSSEDPRCPGSLPEGQNNPQVCPYNLYAEQLSGSAFTCPRSTNKRSWLYRILPSVSHKPFESIDEGHVTHNWDEVDPDPNQLRWKPFEIPKASQKKVDFVSGLHTLCGAGDIKSNNGLAIHIFLCNTSMENRCFYNSDGDFLIVPQKGNLLIYTEFGKMLVQPNEICVIQRGMRFSIDVFEETRGYILEVYGVHFELPDLGPIGANGLANPRDFLIPIAWYEDRQVPGGYTVINKYQGKLFAAKQDVSPFNVVAWHGNYTPYKYNLKNFMVINSVAFDHADPSIFTVLTAKSVRPGVAIADFVIFPPRWGVADKTFRPPYYHRNCMSEFMGLIRGHYEAKQGGFLPGGGSLHSTMTPHGPDADCFEKASKVKLAPERIADGTMAFMFESSLSLAVTKWGLKASRCLDENYHKCWEPLKSHFTPNSRN

>d1qjea\_ b.82.2.1 (A:) Isopenicillin N synthase {Emericella nidulans}

SKANVPKIDVSPLFGDDQAAKMRVAQQIDAASRDTGFFYAVNHGINVQRLSQKTKEFHMSITPEEKWDLAIRAYNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNFTPDHPRIQAKTPTHEVNVWPDETKHPGFQDFAEQYYWDVFGLSSALLKGYALALGKEENFFARHFKPDDTLASVVLIRYPYLDPYPEAAIKTAADGTKLSFEWHEDVSLITVLYQSNVQNLQVETAAGYQDIEADDTGYLINCGSYMAHLTNNYYKAPIHRVKWVNAERQSLPFFVNLGYDSVIDPFDPREPNGKSDREPLSYGDYLQNGLVSLINKNGQT

>d1dcs\_\_ b.82.2.1 (-) Deacetoxycephalosporin C synthase {Streptomyces clavuligerus}

MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRRGFTGLESESTAQITNTGSYSDYSMCYSMGTADNLFPSGDFERIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFRYFPQVPEHRSAEEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGGNYVNIRRTSKA

>d1gp6a\_ b.82.2.1 (A:) Anthocyanidin synthase {Mouse-ear cress (Arabidopsis thaliana)}

VAVERVESLAKSGIISIPKEYIRPKEELESINDVFLEEKKEDGPQVPTIDLKNIESDDEKIRENCIEELKKASLDWGVMHLINHGIPADLMERVKKAGEEFFSLSVEEKEKYANDQATGKIQGYGSKLANNASGQLEWEDYFFHLAYPEEKRDLSIWPKTPSDYIEATSEYAKCLRLLATKVFKALSVGLGLEPDRLEKEVGGLEELLLQMKINYYPKCPQPELALGVEAHTDVSALTFILHNMVPGLQLFYEGKWVTAKCVPDSIVMHIGDTLEILSNGKYKSILHRGLVNKEKVRISWAVFCEPPKDKIVLKPLPEMVSVESPAKFPPRTFAQHIEHKLFGKEQEEL

>d1ds1a\_ b.82.2.2 (A:) Clavaminate synthase {Streptomyces clavuligerus}

TSVDCTAYGPELRALAARLPRTPRADLYAFLDAAHTAAASLPGALATALDTFNAEGSEDGHLLLRGLPVEADADLPTTPSSTPAPEDRSLLTMEAMLGLVGRRLGLHTGYRELRSGTVYHDVYPSPGAHHLSSETSETLLEFHTEMAYHRLQPNYVMLACSRADHERTAATLVASVRKALPLLDERTRARLLDRRMPCCVDVAFRGGVDDPGAIAQVKPLYGDADDPFLGYDRELLAPEDPADKEAVAALSKALDEVTEAVYLEPGDLLIVDNFRTTHARTPFSPRWDGKDRWLHRVYIRTDRNGQLSGGERAGDVVAFTPRG

>d1jr7a\_ b.82.2.3 (A:) Gab protein (hypothetical protein YgaT) {Escherichia coli}

GQDYSGFTLTPSAQSPRLLELTFTEQTTKQFLEQVAEWPVQALEYKSFLRFRVAKILDDLCANQLQPLLLKTLLNRAEGALLINAVGVDDVKQADEMVKLATAVAHLIGRSNFDAMSGQYYARFVVKNVDNSDSYLRQPHRVMELHNDGTYVEEITDYVLMMKIDEQNMQGGNSLLLHLDDWEHLDNYFRHPLARRPMRFAAPPSKNVSKDVFHPVFDVDQQGRPVMRYIDQFVQPKDFEEGVWLSELSDAIETSKGILSVPVPVGKFLLINNLFWLHGRDRFTPHPDLRRELMRQRGYFAYASNHYQTHQ

>d1e5sa\_ b.82.2.4 (A:) Type II Proline 3-hydroxylase (proline oxidase) {Streptomyces sp.}

MRSHILGKIELDQTRLAPDLAYLAAVPTVEEEYDEFSNGFWKHVPLWNASGDSEDRLYRDLKDAAAQPTAHVEHVPYLKEIVTTVFDGTHLQMARSRNLKNAIVIPHRDFVELDREVDRYFRTFMVLEDSPLAFHSNEDTVIHMRPGEIWFLDAATVHSAVNFSEISRQSLCVDFAFDGPFDEKEIFADATLYAPGSTPDLPERRPFTAEHRRRILSLGQVIERENFRDILFLLSKVHYKYDVHPSETYDWLIEISKQAGDEKMVVKAEQIRDFAVEARALSERFSLTSW

>d1ft9a2 b.82.3.1 (A:2-133) CO-sensing protein CooA, N-terminal domain {Rhodospirillum rubrum}

PPRFNIANVLLSPDGETFFRGFRSKIHAKGSLVCTGEGDENGVFVVVDGRLRVYLVGEEREISLFYLTSGDMFCMHSGCLVEATERTEVRFADIRTFEQKLQTCPSMAWGLIAILGRALTSCMRTIEDLMFH

>d1hw5a2 b.82.3.2 (A:1-137) Catabolite gene activator protein, N-terminal domain {Escherichia coli}

VLGKPQTDPTLEWFLSHCHIHKYPSKSTLIHQGEKAETLYYIVKGSVAVLIKDEEGKEMILSYLNQGDFIGELGLFEEGQERSAWVRAKTACEVAEISYKKFRQLIQVNPDILMRLSAQMARRLQVLAEKVGNLAFL

>d1rgs\_1 b.82.3.2 (113-244) Regulatory subunit of Protein kinase A {Cow (Bos taurus)}

RKVIPKDYKTMAALAKAIEKNVLFSHLDDNERSDIFDAMFPVSFIAGETVIQQGDEGDNFYVIDQGEMDVYVNNEWATSVGEGGSFGELALIYGTPRAATVKAKTNVKLWGIDRDSYRRILMGSTLRKRKMY

>d1rgs\_2 b.82.3.2 (245-376) Regulatory subunit of Protein kinase A {Cow (Bos taurus)}

EEFLSKVSILESLDKWERLTVADALEPVQFEDGQKIVVQGEPGDEFFIILEGSAAVLQRRSENEEFVEVGRLGPSDYFGEIALLMNRPRAATVVARGPLKCVKLDRPRFERVLGPCSDILKRNIQQYNSFVS

>d1cx4a1 b.82.3.2 (A:130-265) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}

RIIHPKTDDQRNRLQEACKDILLFKNLDPEQMSQVLDAMFEKLVKEGEHVIDQGDDGDNFYVIDRGTFDIYVKCDGVGRCVGNYDNRGSFGELALMYNTPRAATITATSPGALWGLDRVTFRRIIVKNNAKKRKMY

>d1cx4a2 b.82.3.2 (A:266-412) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}

ESFIESLPFLKSLEVSERLKVVDVIGTKVYNDGEQIIAQGDSADSFFIVESGEVRITMKRKGKSDIEENGAVEIARCLRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCMEIMKRNIATYEEQLVALFGTNMDIV

>d2arca\_ b.82.4.1 (A:) Regulatory protein AraC {Escherichia coli}

DPLLPGYSFNAHLVAGLTPIEANGYLDFFIDRPLGMKGYILNLTIRGQGVVKNQGREFVCRPGDILLFPPGEIHHYGRHPEAREWYHQWVYFRPRAYWHEWLNWPSIFANTGFFRPDEAHQPHFSDLFGQIINAGQGEGRYSELLAINLLEQLLLRRMEAI

>d1ig3a1 b.82.6.1 (A:179-263) Thiamin pyrophosphokinase, substrate-binding domain {Mouse (Mus musculus)}

DSLIYLLQPGKHRLHVDTGMEGSWCGLIPVGQPCNQVTTTGLKWNLTNDVLGFGTLVSTSNTYDGSGLVTVETDHPLLWTMAIKS

>d1ig0a1 b.82.6.1 (A:224-319) Thiamin pyrophosphokinase, substrate-binding domain {Baker's yeast (Saccharomyces cerevisiae)}

TDLIFLIKKNGTLIEYDPQFRNTCIGNCGLLPIGEATLVKETRGLKWDVKNWPTSVVTGRVSSSNRFVGDNCCFIDTKDDIILNVEIFVDKLIDFL

>d1wapa\_ b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP) {Bacillus subtilis}

DFVVIKAVEDGVNVIGLTRGTDTKFHHSEKLDKGEVIIAQFTEHTSAIKVRGEALIQTAYGEMKSEKK

>d1c9sa\_ b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP) {Bacillus stearothermophilus}

SDFVVIKALEDGVNVIGLTRGADTRFHHSEKLDKGEVLIAQFTEHTSAIKVRGKAYIQTRHGVIESEGK

>g1h6w.1 b.108.1.1 (A:,B:) Heat- and protease-stable fragment of the short fibre {Bacteriophage T4}

TGATLNGRGSTTSMRGVVKLTTTAGSQSGGDASSALAWNADVIHQRGGQTINGTLRINNTLTIASGGANITGTVNMTGGYIQGKRVVTQNEIDRTIPVGAIMMWAADSLPSDAWRFCHGGTVSASDCPLYASRIGTRYGGSSSNPGLPDMRXSLNYIIKVKE

>d1k28a2 b.108.1.2 (A:362-584) Tail-associated lysozyme gp5, C-terminal domain {Bacteriophage T4}

DPADPPIPNDSRILFKEPVSSYKGEYPYVHTMETESGHIQEFDDTPGQERYRLVHPTGTYEEVSPSGRRTRKTVDNLYDITNADGNFLVAGDKKTNVGGSEIYYNMDNRLHQIDGSNTIFVRGDETKTVEGNGTILVKGNVTIIVEGNADITVKGDATTLVEGNQTNTVNGNLSWKVAGTVDWDVGGDWTEKMASMSSISSGQYTIDGSRIDIGSVDHHHHHH

>d1qiua2 b.83.1.1 (A:319-395) Adenovirus {Human adenovirus type 2}

VSIKKSSGLNFDNTAIAINAGKGLEFDTNTSESPDINPIKTKIGSGIDYNENGAMITKLGAGLSFDNSGAITIGNKN

>d1kkea2 b.83.1.2 (A:313-455) Reovirus attachment protein sigma 1 {Reovirus}

YRFRQSMWIGIVSYSGSGLNWRVQVNSDIFIVDDYIHICLPAFDGFSIADGGDLSLNFVTGLLPPLLTGDTEPAFHNDVVTYGAQTVAIGLSSGGAPQYMSKNLWVEQWQDGVLRLRVEGGGSITHSNSKWPAMTVSYPRSFT

>d1h8ga\_ b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}

TDGNWYWFDNSGEMATGWKKIADKWYYFNEEGAMKTGWVKYKDTWYYLDAKEGAMVSNAFIQSADGTGWYYLKPDGTLADRPEFTVEPDGLITVK

>d1hcxa\_ b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}

GSYPKDKFEKINGTWYYFDSSGYMLADRWRKHTDGNWYWFDNSGEMATGWKKIADKWYYFNEEGAMKTGWVKYKDTWYYLDAKEGAMVSNAFIQSADGTGWYYLKPDGTLADRPEFTVEPDGLITVK

>d1bdo\_\_ b.84.1.1 (-) Biotinyl domain of acetyl-CoA carboxylase {Escherichia coli}

EISGHIVRSPMVGTFYRTPSPDAKAFIEVGQKVNVGDTLCIVEAMKMMNQIEADKSGTVKAILVESGQPVEFDEPLVVIE

>d1dd2a\_ b.84.1.1 (A:) Biotin carboxyl carrier domain of transcarboxylase (TC 1.3S) {Propionibacterium freudenreichii, subsp. shermanii}

AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGLIKIG

>d1htp\_\_ b.84.1.1 (-) Protein H of glycine cleavage system {Pea (Pisum sativum)}

SNVLDGLKYAPSHEWVKHEGSVATIGITDHAQDHLGEVVFVELPEPGVSVTKGKGFGAVESVKATSDVNSPISGEVIEVNTGLTGKPGLINSSPYEDGWMIKIKPTSPDELESLLGAKEYTKFCEEEDAAH

>d1lac\_\_ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Bacillus stearothermophilus}

AFEFKLPDIGEGIHEGEIVKWFVKPGDEVNEDDVLCEVQNDKAVVEIPSPVKGKVLEILVPEGTVATVGQTLITLDAPGY

>d1iyu\_\_ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Azotobacter vinelandii}

SEIIRVPDIGGDGEVIELLVKTGDLIEVEQGLVVLESAKASMEVPSPKAGVVKSVSVKLGDKLKEGDAIIELEPAAGAR

>d1qjoa\_ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Escherichia coli}

MVKEVNVPDIGGDEVEVTEVMVKVGDKVAAEQSLITVEGDKASMEVPAPFAGVVKELKVNVGDKVKTGSLIMIFEVEGAA

>d1gjxa\_ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Neisseria meningitidis}

ALVELKVPDIGGHENVDIIAVEVNVGDTIAVDDTLITLETDKATMDVPAEVAGVVKEVKVKVGDKISEGGLIVVVEAEGTA

>d1fyc\_\_ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Human (Homo sapiens)}

GSNMSYPPHMQVLLPALSPTMTMGTVQRWEKKVGEKLSEGDLLAEIETDKATIGFEVQEEGYLAKILVPEGTRDVPLGTPLCIIVEKEADISAFADYRPTEVTDLK

>d1ghk\_\_ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Azotobacter vinelandii}

AIDIKAPTFPESIADGTVATWHKKPGEAVKRDELIVDIETDKVVMEVLAEADGVIAEIVKNEGDTVLSGELLGKLTEGG

>d1pmr\_\_ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Escherichia coli}

SSVDILVPDLPESVADATVATWHKKPGDAVVRDEVLVEIETDKVVLEVPASADGILDAVLEDEGTTVTSRQILGRLREGN

>d1k8ma\_ b.84.1.1 (A:) Lipoyl domain of the mitochondrial branched-chain alpha-ketoacid dehydrogenase {Human (Homo sapiens)}

MGQVVQFKLSDIGEGIREVTVKEWYVKEGDTVSQFDSICEVQSDKASVTITSRYDGVIKKLYYNLDDIAYVGKPLVDIETEALKDLE

>d1dv1a1 b.84.2.1 (A:331-446) Biotin carboxylase subunit of acetyl-CoA carboxylase, C-terminal domain {Escherichia coli}

RGHAVECRINAEDPNTFLPSPGKITRFHAPGGFGVRWESHIYAGYTVPPYYDSMIGKLICYGENRDVAIARMKNALQELIIDGIKTNVDLQIRIMNDENFQHGGTNIHYLEKKLGL

>d1gsoa1 b.84.2.1 (A:328-426) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}

ERASLGVVMAAGGYPGDYRTGDVIHGLPLEEVAGGKVFHAGTKLADDEQVVTNGGRVLCVTALGHTVAEAQKRAYALMTDIHWDDCFCRKDIGWRAIER

>d1b6ra1 b.84.2.1 (A:277-355) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

NNPSVMINLIGSDVNYDWLKLPLVHLHWYDKEVRPGRKVGHLNLTDSDTSRLTATLEALIPLLPPEYASGVIWAQSKFG

>d1eyza1 b.84.2.1 (A:319-392) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

GPAASAVILPQLTSQNVTFDNVQNAVGADLQIRLFGKPEIDGSRRLGVALATAESVVDAIERAKHAAGQVKVQG

>d1hcz\_2 b.84.2.2 (168-230) Cytochrome f, small domain {Turnip (Brassica rapa)}

NTVYNATAGGIISKILRKEKGGYEITIVDASNERQVIDIIPRGLELLVSEGESIKLDQPLTSN

>d1e2wa2 b.84.2.2 (A:169-232) Cytochrome f, small domain {Chlamydomonas reinhardtii}

TIYNASAAGKIVAITALSEKKGGFEVSIEKANGEVVVDKIPAGPDLIVKEGQTVQADQPLTNNP

>d1ci3m2 b.84.2.2 (M:170-231) Cytochrome f, small domain {Phormidium laminosum}

AVYNASAAGVITAIAKADDGSAEVKIRTEDGTTIVDKIPAGPELIVSEGEEVAAGAALTNNP

>d1gpr\_\_ b.84.3.1 (-) Glucose permease IIa domain, IIa-glc {Bacillus subtilis}

EPLQNEIGEEVFVSPITGEIHPITDVPDQVFSGKMMGDGFAILPSEGIVVSPVRGKILNVFPTKHAIGLQSDGGREILIHFGIDTVSLKGEGFTSFVSEGDRVEPGQKLLEVDLDAVKPNVPSLMTPIVFTNLAEGETVSIKASGSVNREQEDIVKIE

>d2gpr\_\_ b.84.3.1 (-) Glucose permease IIa domain, IIa-glc {Mycoplasma capricolum}

MWFFNKNLKVLAPCDGTIITLDEVEDEVFKERMLGDGFAINPKSNDFHAPVSGKLVTAFPTKHAFGIQTKSGVEILLHIGLDTVSLDGNGFESFVTQDQEVNAGDKLVTVDLKSVAKKVPSIKSPIIFTNNGGKTLEIVKMGEVKQGDVVAILK

>d1glaf\_ b.84.3.1 (F:) Glucose-specific factor III (glsIII) {Escherichia coli}

GLFDKLKSLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEKIVGDGIAIKPTGNKMVAPVDGTIGKIFETNHAFSIESDSGVELFVHFGIDTVELKGEGFKRIAEEGQRVKVGDTVIEFDLPLLEEKAKSTLTPVVISNMDEIKELIKLSGSVTVGETPVIRIKK

>d2f3ga\_ b.84.3.1 (A:) Glucose-specific factor III (glsIII) {Escherichia coli}

TIEIIAPLSGEIVNIEDVPDVVFAEKIVGDGIAIKPTGNKMVAPVDGTIGKIFETNHAFSIESDSGVELFVHFGIDTVELKGEGFKRIAEEGQRVKVGDTVIEFDLPLLEEKAKSTLTPVVISNMDEIKELIKLSGSVTVGETPVIRIKK

>d1hg7a\_ b.85.1.1 (A:) Type III antifreeze protein {Ocean pout (Macrozoarces americanus), different isoforms}

MNQASVVANQLIPINTALTLVMMRSEVVTPVGIPAEDIPRLVSMQVNRAVPLGTTLMPDMVKGYAA

>d1ops\_\_ b.85.1.1 (-) Type III antifreeze protein {Ocean pout (Macrozoarces americanus), different isoforms}

SQSVVATQLIPMNTALTPAMMEGKVTNPIGIPFAEMSQLVGKQVNTPVAKGQTLMPNMVKTYAA

>d1c8aa2 b.85.1.1 (A:69-134) Type III antifreeze protein {Antarctic eel pout (Austrolycichthys brachycephalus) and (Lycodichthys dearborni)}

SPGLKSVVANQLIPINTALTLVMMKAEEVSPKGIPSEEISKLVGMQVNRAVYLDQTLMPDMVKNYE

>d3rdn\_\_ b.85.1.1 (-) Type III antifreeze protein {Antarctic eel pout (Austrolycichthys brachycephalus) and (Lycodichthys dearborni)}

NKASVVANQLIPINTALTLIMMKAEVVTPMGIPAEEIPNLVGMQVNRAVPLGTTLMPDMVKNYEDGTTSPGLK

>d1c5ea\_ b.85.2.1 (A:) Head decoration protein D (gpD, major capsid protein D) {Bacteriophage lambda}

SDPAHTATAPGGLSAKAPAMTPLMLDTSSRKLVAWDGTTDGAAVGILAVAADQTSTTLTFYKSGTFRYEDVLWPEAASDETKKRTAFAGTAISIV

>d1ejrb\_ b.85.3.1 (B:) Urease, beta-subunit {Klebsiella aerogenes}

MIPGEYHVKPGQIALNTGRATCRVVVENHGDRPIQVGSHYHFAEVNPALKFDRQQAAGYRLNIPAGTAVRFEPGQKREVELVAFAGHRAVFGFRGEVMGPL

>d4ubpb\_ b.85.3.1 (B:) Urease, beta-subunit {Bacillus pasteurii}

NYIVPGEYRVAEGEIEINAGREKTTIRVSNTGDRPIQVGSHIHFVEVNKELLFDRAEGIGRRLNIPSGTAARFEPGEEMEVELTELGGNREVFGISDLTNGSVDNKELILQRAKELGYKGVE

>d1e9ya1 b.85.3.1 (A:106-238) Urease, beta-subunit {Helicobacter pylori}

LVPGELFLKNEDITINEGKKAVSVKVKNVGDRPVQIGSHFHFFEVNRCLDFDREKTFGKRLDIAAGTAVRFEPGEEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGFHGAKSDDNYVKTIKE

>d1g8la1 b.85.6.1 (A:327-409) Molybdenum cofactor biosynthesis protein MoeA, C-terminal domain {Escherichia coli}

LPARQRVRTASRLKKTPGRLDFQRGVLQRNADGELEVTTTGHQGSHIFSSFSLGNCFIVLERDRGNVEVGEWVEVEPFNALFG

>d1euwa\_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Escherichia coli}

MMKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIADPSLAAMMLPRSGLGHKHGIVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMIFVPVVQAEFNLVEDF

>d1f7da\_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline immunodeficiency virus}

MIIEGDGILDKRSEDAGYDLLAAKEIHLLPGEVKVIPTGVKLMLPKGYWGLIIGKSSIGSKGLDVLGGVIDEGYRGEIGVIMINVSRKSITLMERQKIAQLIILPCKHEVLEQGKVVM

>d1f7ra\_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline immunodeficiency virus}

MIIEGDGILDKRSEDAGYDLLAAKEIHLLPGEVKVIPTGVKLMLPKGYWGLIIGKSSIGSKGLDVLGGVIDEGYRGEIGVIMINVSRKSITLMERQKIAQLIILPCKHEVLEQGKVVMDSERGDNGYGSTGVF

>d1dun\_\_ b.85.4.1 (-) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Equine infectious anemia virus}

MLAYQGTQIKEKRDEDAGFDLCVPYDIMIPVSDTKIIPTDVKIQVPPNSFGWVTGKSSMAKQGLLINGGIIDEGYTGEIQVICTNIGKSNIKLIEGQKFAQLIILQHHSNSRQPWDENKI

>d1tul\_\_ b.85.5.1 (-) ACMNPV telokin-like protein {Baculovirus (Autographa californica), nuclear polyhedrosis virus}

GTPDIIVNAQINSEDENVLDFIIEDEYYLKKRGVGAHIIKVASSPQLRLLYKNAYSTVSCGNYGVLCNLVQNGEYDLNAIMFNCAEIKLNKGQMLFQTKIWR

>d1at0\_\_ b.86.1.1 (-) Hedgehog {Fruit fly (Drosophila melanogaster)}

CFTPESTALLESGVRKPLGELSIGDRVLSMTANGQAVYSEVILFMDRNLEQMQNFVQLHTDGGAVLTVTPAHLVSVWQPESQKLTFVFADRIEEKNQVLVRDVETGELRPQRVVKVGSVRSKGVVAPLTREGTIVVNSVAASCYA

>d1dfaa1 b.86.1.2 (A:1-180,A:416-454) PI-Scei intein {Baker's yeast (Saccharomyces cerevisiae)}

CFAKGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPRGRETMYSVVQKSQHRAHKSDSSREVPELLKFTCNATHELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELVKEVSKSYPISEGPERANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAXCRGFYFELQELKEDDYYGITLSDDSDHQFLLANQVVVHN

>d1dq3a1 b.86.1.2 (A:1-128,A:415-454) PI-Pfui intein {Archaeon Pyrococcus furiosus}

CIDGKAKIIFENEGEEHLTTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPESKRVVKGKVNVIWKYELGKDVTKYEIITNKGTKILTSPWHPFFVLTPDFKIVEKRADELKEGDILIGGMXGLEVVRHITTTNEPRTFYDLTVENYQNYLAGENGMIFVHN

>d1am2\_\_ b.86.1.2 (-) GyrA intein {Mycobacterium xenopi}

ASITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNPVLADRLFHSGEHPVYAVRTVEGLRVTGTANHPLLCLVDVAGVPTLLWKLIDEIKPGDYAVIQRSAFSVDCAGFARGKPEFAPTTYTVGVPGLVRFLEAHHRDPDAKAIADELTDGRFYYAKVASVTDAGVQPVYSLRVDTADHAFITNGFVSHN

>d1umua\_ b.87.1.1 (A:) UmuD' {Escherichia coli}

DYVEQRIDLNQLLIQHPSATYFVKASGDSMIDGGISDGDLLIVDSAITASHGDIVIAAVDGEFTVKKLQLRPTVQLIPMNSAYSPITISSEDTLDVFGVVIHVVK

>d1jhfa2 b.87.1.1 (A:73-198) LexA C-terminal domain {Escherichia coli}

EEGLPLVGRVAADEPLLAQQHIEGHYQVDPSLFKPNADFLLRVSGMSMKDIGIMDGDLLAVHKTQDVRNGQVVVARIDDEVTVKRLKKQGNKVELLPENSEFKPIVVDLRQQSFTIEGLAVGVIRN

>d1f39a\_ b.87.1.1 (A:) lambda repressor C-terminal domain {Bacteriophage lambda virus}

ASASAFWLEVEGNSMTAPTGSKPSFPDGMLILVDPEQAVEPGDFCIARLGGDEFTFKKLIRDSGQVFLQPLNPQYPMIPCNESCSVVGKVIASQWPEETFG

>d1b12a\_ b.87.1.2 (A:) Type 1 signal peptidase {Escherichia coli}

RSFIYEPFQIPSGSMMPTLLIGDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKNETKENGIRLSERKETLGDVTHRILTVPIAQDQVGMYYQQPGQQLATWIVPPGQYFMMGDNRDNSADSRYWGFVPEANLVGRATAIWMSFDKQEGEWPTGLRLSRIGGIH

>d1jcha2 b.110.1.1 (A:84-315) Colicin E3 translocation domain {Escherichia coli}

VAAPVAFGFPALSTPGAGGLAVSISAGALSAAIADIMAALKGPFKFGLWGVALYGVLPSQIAKDDPNMMSKIVTSLPADDITESPVSSLPLDKATVNVNVRVVDDVKDERQNISVVSGVPMSVPVVDAKPTERPGVFTASIPGAPVLNISVNNSTPAVQTLSPGVTNNTDKDVRPAFGTQGGNTRDAVIRFPKDSGHNAVYVSVSDVLSPDQVKQRQDEENRRQQEWDATHP

>d1hxra\_ b.88.1.1 (A:) RabGEF Mss4 {Rat (Rattus norvegicus)}

ELVSAEGRNRKAVLCQRCGSRVLQPGTALFSRRQLFLPSMRKKPDLVDGSNPDGDVLEEHWLVNDMFIFENVGFTKDVGNVKFLVCADCEIGPIGWHCLDDKNSFYVALERVSHE

>d1fwqa\_ b.88.1.1 (A:) RabGEF Mss4 {Human (Homo sapiens)}

ELVSAEGRNRKAVLCQRCGSRVLQPGTALFSRRQLFLPSMRKKPALSDGSNPDGDLLQEHWLVEDMFIFENVGFTKDVGNIKFLVCADCEIGPIGWHCLDDKNSFYVALERVSHE

>d1h6qa\_ b.88.1.2 (A:) Translationally controlled tumor-associated protein tctp, p23fyp {Fission yeast (Schizosaccharomyces pombe)}

MLLYKDVISGDELVSDAYDLKEVDDIVYEADCQMVTVKQGGDVDIGANPSAEDAEENAEEGTETVNNLVYSFRLSPTSFDKKSYMSYIKGYMKAIKARLQESNPERVPVFEKNAIGFVKKILANFKDYDFYIGESMDPDAMVVLMNYREDGITPYMIFFKDGLVSEKF

>d3ezma\_ b.89.1.1 (A:) Cyanovirin-N {Cyanobacterium (Nostoc ellipsosporum)}

LGKFSQTCYNSAIQGSVLTSTCERTNGGYNTSSIDLNSVIENVDGSLKWQPSNFIETCRNTQLAGSSELAAECKTRAQQFVSTKINLDDHIANIDGTLKYE

>d1fjra\_ b.102.1.1 (A:) Methuselah ectodomain {Fruit fly (Drosophila melanogaster)}

DILECDYFDTVDISAAQKLQNGSYLFEGLLVPAILTGEYDFRILPDDSKQKVARHIRGCVCKLKPCVRFCCPHDHIMDNGVCYDNMSDEELAELDPFLNVTLDDGSVSRRHFKNELIVQWDLPMPCDGMFYLDNREEQDKYTLFENGTFFRHFDRVTLRKREYCLQHLTFADGNATSIRIAPHNCLIV

>d1lkta\_ b.90.1.1 (A:) Head-binding domain of phage P22 tailspike protein {Salmonella bacteriophage P22}

ANVVVSNPRPIFTESRSFKAVANGKIYIGQIDTDPVNPANQIPVYIENEDGSHVQITQPLIINAAGKIVYNGQLVKIVTVQGHSMAIYDANGSQVDYIANVLKY

>d1qqha\_ b.91.1.1 (A:) E2 regulatory, transactivation domain {Human papillomavirus type 18}

KSKAHKAIELQMALQGLAQSAYKTEDWTLQDTCEELWNTEPTHCFKKGGQTVQVYFDGNKDNCMTYVAWDSVYYMTDAGTWDKTATCVSHRGLYYVKEGYNTFYIEFKSECEKYGNTGTWEVHFGNNVIDCNDSMCSTSDDTVS

>d1dtoa\_ b.91.1.1 (A:) E2 regulatory, transactivation domain {Human papillomavirus type 16}

HMETLCQRLNVCQDKILTHYENDSTDLRDHIDYWKHMRLECAIYYKAREMGFKHINHQVVPTLAVSKNKALQAIELQLTLETIYNSQYSNEKWTLQDVSLEVYLTAPTGCIKKHGYTVEVQFDGDICNTMHYTNWTHIYICEEASVTVVEGQVDYYGLYYVHEGIRTYFVQFKDDAEKYSKNKVWEVHAGGQVILCPTSVFS

>d1g8la2 b.103.1.1 (A:7-177) Molybdenum cofactor biosynthesis protein MoeA, N-terminal and linker domains {Escherichia coli}

LMSLDTALNEMLSRVTPLTAQETLPLVQCFGRILASDVVSPLDVPGFDNSAMDGYAVRLADIASGQPLPVAGKSFAGQPYHGEWPAGTCIRIMTGAPVPEGCEAVVMQEQTEQMDNGVRFTAEVRSGQNIRRRGEDISAGAVVFPAGTRLTTAELPVIASLGIAEVPVIRK

>d1k6wa1 b.92.1.2 (A:4-55,A:376-426) Cytosine deaminase {Escherichia coli}

ALQTIINARLPGEEGLWQIHLQDGKISAIDAQSGVMPITENSLDAEQGLVIPXLIILPAENGFDALRRQVPVRYSVRGGKVIASTQPAQTTVYLEQPEAIDYKR

>d1ejrc1 b.92.1.1 (C:1002-1129,C:1423-1475) alpha-Subunit of urease {Klebsiella aerogenes}

SNISRQAYADMFGPTVGDKVRLADTELWIEVEDDLTTYGEEVKFGGGKVIRDGMGQGQMLAADCVDLVLTNALIVDHWGIVKADIGVKDGRIFAIGKAGNPDIQPNVTIPIGAATEVIAAEGKIVTAGXSIEVGKLADLVVWSPAFFGVKPATVIKGGMIAIAPMGDINASIPTPQPVHYRP

>d4ubpc1 b.92.1.1 (C:1-131,C:435-483) alpha-Subunit of urease {Bacillus pasteurii}

MKINRQQYAESYGPTVGDEVRLADTDLWIEVEKDYTTYGDEVNFGGGKVLREGMGENGTYTRTENVLDLLLTNALILDYTGIYKADIGVKDGYIVGIGKGGNPDIMDGVTPNMIVGTATEVIAAEGKIVTAXLVLWEPKFFGVKADRVIKGGIIAYAQIGDPSASIPTPQPVMGRRMYGTV

>d1e9yb1 b.92.1.1 (B:1-131,B:432-480) alpha-Subunit of urease {Helicobacter pylori}

MKKISRKEYVSMYGPTTGDKVRLGDTDLIAEVEHDYTIYGEELKFGGGKTLREGMSQSNNPSKEELDLIITNALIVDYTGIYKADIGIKDGKIAGIGKGGNKDMQDGVKNNLSVGPATEALAGEGLIVTAGXADLVLWSPAFFGVKPNMIIKGGFIALSQMGDANASIPTPQPVYYREMFA

>d1aqt\_2 b.93.1.1 (2-86) Epsilon subunit of F1F0-ATP synthase N-terminal domain {Escherichia coli}

STYHLDVVSAEQQMFSGLVEKIQVTGSEGELGIYPGHAPLLTAIKPGMIRIVKQHGHEEFIYLSGGILEVQPGNVTVLADTAIRG

>d1e79h2 b.93.1.1 (H:15-100) Epsilon subunit of F1F0-ATP synthase N-terminal domain {Cow (Bos taurus)}

QMSFTFASPTQVFFNSANVRQVDVPTQTGAFGILAAHVPTLQVLRPGLVVVHAEDGTTSKYFVSSGSVTVNADSSVQLLAEEAVTL

>d1hhna\_ b.104.1.1 (A:) Calreticulin {Rat (Rattus norvegicus)}

SKKIKDPDAAKPEDWDERAKIDDPTDSKPEDWDKPEHIPDPDAKKPEDWDEEMDGEWEPPVIQNPEYKGEWKPRQIDNPDYKGTWIHPEIDNPEYSPDANI

>d1jhna3 b.104.1.1 (A:270-411) Calnexin {Dog (Canis familiaris)}

PVNPSREIEDPEDQKPEDWDERPKIPDPDAVKPDDWNEDAPAKIPDEEATKPDGWLDDEPEYVPDPDAEKPEDWDEDMDGEWEAPQIANPKCESAPGCGVWQRPMIDNPNYKGKWKPPMIDNPNYQGIWKPRKIPNPDFFED

>d1tph1\_ c.1.1.1 (1:) Triosephosphate isomerase {Chicken (Gallus gallus)}

RKFFVGGNWKMNGDKKSLGELIHTLNGAKLSADTEVVCGAPSIYLDFARQKLDAKIGVAAQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKLDEREAGITEKVVFEQTKAIADNVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKTHVSDAVAQSTRIIYGGSVTGGNCKELASQHDVDGFLVGGASLKPEFVDIINAKH

>d1htia\_ c.1.1.1 (A:) Triosephosphate isomerase {Human (Homo sapiens)}

APSRKFFVGGNWKMNGRKQSLGELIGTLNAAKVPADTEVVCAPPTAYIDFARQKLDPKIAVAAQNCYKVTNGAFTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKLDEREAGITEKVVFEQTKVIADNVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKSNVSDAVAQSTRIIYGGSVTGATCKELASQPDVDGFLVGGASLKPEFVDIINAKQ

>d1i45a\_ c.1.1.1 (A:) Triosephosphate isomerase {Baker's yeast (Saccharomyces cerevisiae)}

ARTFFVGGNFKLNGSKQSIKEIVERLNTASIPENVEVVICPPATYLDYSVSLVKKPQVTVGAQNAYLKASGAFTGENSVDQIKDVGAKYVILGHSERRSYFHEDDKFIADKTKFALGQGVGVILCIGETLEEKKAGKTLDVVERQLNAVLEEVKDFTNVVVAYEPVWAIGTGLAATPEDAQDIHASIRKFLASKLGDKAASELRILYGGSANGSNAVTFKDKADVDGFLVGGASLKPEFVDIINSRN

>d1ttj\_\_ c.1.1.1 (-) Triosephosphate isomerase {Trypanosoma brucei}

SKPQPIAAANWKCNGSQQSLSELIDLFNSTSINHDVQCVVASTSSHLAMTKERLSHPKFVIAAQNAGNADALASLKDFGVNWIVLGHSERRAYYGETNEIVADKVAAAVASGFMVIACIGETLQERESGRTAVVVLTQIAAIAKKLKKADWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSKIGADVAGELRILYGGSVNGKNARTLYQQRDVNGFLVGGASLKPEFVDIIKATQ

>d5tima\_ c.1.1.1 (A:) Triosephosphate isomerase {Trypanosoma brucei}

SKPQPIAAANWKCNGSQQSLSELIDLFNSTSINHDVQCVVASTFVHLAMTKERLSHPKFVIAAQNAIAKSGAFTGEVSLPILKDFGVNWIVLGHSERRAYYGETNEIVADKVAAAVASGFMVIACIGETLQERESGRTAVVVLTQIAAIAKKLKKADWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSKIGADVAGELRILYGGSVNGKNARTLYQQRDVNGFLVGGASLKPEFVDIIKATQ

>d1tcda\_ c.1.1.1 (A:) Triosephosphate isomerase {Trypanosoma cruzi}

KPQPIAAANWKCNGSESLLVPLIETLNAATFDHDVQCVVAPTFLHIPMTKARLTNPKFQIAAQNAITRSGAFTGEVSLQILKDYGISWVVLGHSERRLYYGETNEIVAEKVAQACAAGFHVIVCVGETNEEREAGRTAAVVLTQLAAVAQKLSKEAWSRVVIAYEPVWAIGTGKVATPQQAQEVHELLRRWVRSKLGTDIAAQLRILYGGSVTAKNARTLYQMRDINGFLVGGASLKPEFVEIIEATK

>d1ydva\_ c.1.1.1 (A:) Triosephosphate isomerase {Plasmodium falciparum}

RKYFVAANWKCNGTLESIKSLTNSFNNLDFDPSKLDVVVFPVSVHYDHTRKLLQSKFSTGIQNVSKFGNGSYTGEVSAEIAKDLNIEYVIIGHFERRKYFHETDEDVREKLQASLKNNLKAVVCFGESLEQREQNKTIEVITKQVKAFVDLIDNFDNVILVYEPLWAIGTGKTATPEQAQLVHKEIRKIVKDTCGEKQANQIRILYGGSVNTENCSSLIQQEDIDGFLVGNASLKESFVDIIKSAM

>d1amk\_\_ c.1.1.1 (-) Triosephosphate isomerase {Leishmania mexicana}

SAKPQPIAAANWKCNGTTASIEKLVQVFNEHTISHDVQCVVAPTFVHIPLVQAKLRNPKYVISAENAIAKSGAFTGEVSMPILKDIGVHWVILGHSERRTYYGETDEIVAQKVSEACKQGFMVIACIGETLQQREANQTAKVVLSQTSAIAAKLTKDAWNQVVLAYEPVWAIGTGKVATPEQAQEVHLLLRKWVSENIGTDVAAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPEFRDIIDATR

>d1trea\_ c.1.1.1 (A:) Triosephosphate isomerase {Escherichia coli}

MRHPLVMGNWKLNGSRHMVHELVSNLRKELAGVAGCAVAIAPPEMYIDMAKREAEGSHIMLGAQNVNLNLSGAFTGETSAAMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETEAENEAGKTEEVCARQIDAVLKTQGAAAFEGAVIAYEPVWAIGTGKSATPAQAQAVHKFIRDHIAKVDANIAEQVIIQYGGSVNASNAAELFAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA

>d2btma\_ c.1.1.1 (A:) Triosephosphate isomerase {Bacillus stearothermophilus}

RKPIIAGNWKMNGTLAEAVQFVEDVKGHVPPADEVISVVCAPFLFLDRLVQAADGTDLKIGAQTMHFADQGAYTGEVSPVMLKDLGVTYVILGHSERRQMFAETDETVNKKVLAAFTRGLIPIICCGESLEEREAGQTNAVVASQVEKALAGLTPEQVKQAVIAYEPIWAIGTGKSSTPEDANSVCGHIRSVVSRLFGPEAAEAIRIQYGGSVKPDNIRDFLAQQQIDGALVGGASLEPASFLQLVEAGRH

>d1aw1a\_ c.1.1.1 (A:) Triosephosphate isomerase {Vibrio marinus}

RHPVVMGNWKLNGSKEMVVDLLNGLNAELEGVTGVDVAVAPPALFVDLAERTLTEAGSAIILGAQNTDLNNSGAFTGDMSPAMLKEFGATHIIIGHSERREYHAESDEFVAKKFAFLKENGLTPVLCIGESDAQNEAGETMAVCARQLDAVINTQGVEALEGAIIAYEPIWAIGTGKAATAEDAQRIHAQIRAHIAEKSEAVAKNVVIQYGGSVKPENAAAYFAQPDIDGALVGGAALDAKSFAAIAKAAAEAKA

>d1b9ba\_ c.1.1.1 (A:) Triosephosphate isomerase {Thermotoga maritima}

TRKLILAGNWKMHKTISEAKKFVSLLVNELHDVKEFEIVVCPPFTALSEVGEILSGRNIKLGAQNVFYEDQGAFTGEISPLMLQEIGVEYVIVGHSERRRIFKEDDEFINRKVKAVLEKGMTPILCVGETLEEREKGLTFCVVEKQVREGFYGLDKEEAKRVVIAYEPVWAIGTGRVATPQQAQEVHAFIRKLLSEMYDEETAGSIRILYGGSIKPDNFLGLIVQKDIDGGLVGGASLKESFIELARIMRGV

>d1hg3a\_ c.1.1.1 (A:) Triosephosphate isomerase {Archaeon Pyrococcus woesei}

AKLKEPIIAINFKTYIEATGKRALEIAKAAEKVYKETGVTIVVAPQLVDLRMIAESVEIPVFAQHIDPIKPGSHTGHVLPEAVKEAGAVGTLLNHSENRMILADLEAAIRRAEEVGLMTMVCSNNPAVSAAVAALNPDYVAVEPPELIGTGIPVSKAKPEVITNTVELVKKVNPEVKVLCGAGISTGEDVKKAIELGTVGVLLASGVTKAKDPEKAIWDLVSGI

>d1qo2a\_ c.1.2.1 (A:) Phosphoribosylformimino-5-aminoimidazole carboxamide ribotite isomerase HisA {Thermotoga maritima}

MLVVPAIDLFRGKVARMIKGRKENTIFYEKDPVELVEKLIEEGFTLIHVVDLSNAIENSGENLPVLEKLSEFAEHIQIGGGIRSLDYAEKLRKLGYRRQIVSSKVLEDPSFLKSLREIDVEPVFSLDTRGGRVAFKGWLAEEEIDPVSLLKRLKEYGLEEIVHTEIEKDGTLQEHDFSLTKKIAIEAEVKVLAAGGISSENSLKTAQKVHTETNGLLKGVIVGRAFLEGILTVEVMKRYAR

>d1thfd\_ c.1.2.1 (D:) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}

MLAKRIIACLDVKDGRVVKGSNFENLRDSGDPVELGKFYSEIGIDELVFLDITASVEKRKTMLELVEKVAEQIDIPFTVGGGIHDFETASELILRGADKVSINTAAVENPSLITQIAQTFGSQAVVVAIDAKRVDGEFMVFTYSGKKNTGILLRDWVVEVEKRGAGEILLTSIDRDGTKSGYDTEMIRFVRPLTTLPIIASGGAGKMEHFLEAFLAGADAALAASVFHFREIDVRELKEYLKKHGVNVRLEGL

>d1jvna1 c.1.2.1 (A:230-552) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}

DYSNYGLTRRIIACLDVRTNDQGDLVVTKGDQYDVREKSDGKGVRNLGKPVQLAQKYYQQGADEVTFLNITSFRDCPLKDTPMLEVLKQAAKTVFVPLTVGGGIKDIVDVDGTKIPALEVASLYFRSGADKVSIGTDAVYAAEKYYELGNRGDGTSPIETISKAYGAQAVVISVDPKRVYVNSQADTKNKVFETEYPGPNGEKYCWYQCTIKGGRESRDLGVWELTRACEALGAGEILLNCIDKDGSNSGYDLELIEHVKDAVKIPVIASSGAGVPEHFEEAFLKTRADACLGAGMFHRGEFTVNDVKEYLLEHGLKVRMDEE

>d1h5ya\_ c.1.2.1 (A:) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Archaeon Pyrobaculum aerophilum}

HMALRIIPCLDIDGGAKVVVKGVNFQGIREVGDPVEMAVRYEEEGADEIAILDITAAPEGRATFIDSVKRVAEAVSIPVLVGGGVRSLEDATTLFRAGADKVSVNTAAVRNPQLVALLAREFGSQSTVVAIDAKWNGEYYEVYVKGGREATGLDAVKWAKEVEELGAGEILLTSIDRDGTGLGYDVELIRRVADSVRIPVIASGGAGRVEHFYEAAAAGADAVLAASLFHFRVLSIAQVKRYLKERGVEVRI

>d1rpxa\_ c.1.2.2 (A:) D-ribulose-5-phosphate 3-epimerase {Potato (Solanum tuberosum)}

SRVDKFSKSDIIVSPSILSANFSKLGEQVKAIEQAGCDWIHVDVMDGRFVPNITIGPLVVDSLRPITDLPLDVHLMIVEPDQRVPDFIKAGADIVSVHCEQSSTIHLHRTINQIKSLGAKAGVVLNPGTPLTAIEYVLDAVDLVLIMSVNPGFGGQSFIESQVKKISDLRKICAERGLNPWIEVDGGVGPKNAYKVIEAGANALVAGSAVFGAPDYAEAIKGIKTSKRPE

>d1dbta\_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Bacillus subtilis}

MKNNLPIIALDFASAEETLAFLAPFQQEPLFVKVGMELFYQEGPSIVKQLKERNCELFLDLKLHDIPTTVNKAMKRLASLGVDLVNVHAAGGKKMMQAALEGLEEGTPAGKKRPSLIAVTQLTSTSEQIMKDELLIEKSLIDTVVHYSKQAEESGLDGVVCSVHEAKAIYQAVSPSFLTVTPGIRMSEDAANDQVRVATPAIAREKGSSAIVVGRSITKAEDPVKAYKAVRLEWEGI

>d1eixa\_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Escherichia coli}

VTNSPVVVALDYHNRDDALAFVDKIDPRDCRLKVGKEMFTLFGPQFVRELQQRGFDIFLDLKFHDIPNTAAHAVAAAADLGVWMVNVHASGGARMMTAAREALVPFGKDAPLLIAVTVLTSMEASDLVDLGMTLSPADYAERLAALTQKCGLDGVVCSAQEAVRFKQVFGQEFKLVTPGIRPQGSEAGDQRRIMTPEQALSAGVDYMVIGRPVTQSVDPAQTLKAINASLQ

>d1dvja\_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Archaeon Methanobacterium thermoautotrophicum}

MDVMNRLILAMDLMNRDDALRVTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRFGCRIIADFKVADIPETNEKICRATFKAGADAIIVHGFPGADSVRACLNVAEEMGREVFLLTEMSHPGAEMFIQGAADEIARMGVDLGVKNYVGPSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSIYLADNPAAAAAGIIESIKDLLIPEDPAANKARKEAELAAATA

>d1dvjb\_ c.1.2.3 (B:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Archaeon Methanobacterium thermoautotrophicum}

RLILAMDLMNRDDALRVTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRFGCRIIADFKVADIPETNEKICRATFKAGADAIIVHGFPGADSVRACLNVAEEMGREVFLLTEMSHPGAEMFIQGAADEIARMGVDLGVKNYVGPSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSIYLADNPAAAAAGIIESIKD

>d1dqwa\_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Baker's yeast (Saccharomyces cerevisiae)}

MHKATYKERAATHPSPVAAKLFNIMHEKQTNLCASLDVRTTKELLELVEALGPKICLLKTHVDILTDFSMEGTVKPLKALSAKYNFLLFEDRKFADIGNTVKLQYSAGVYRIAEWADITNAHGVVGPGIVSGLKQAAEEVTKEPRGLLMLAELSCKGSLSTGEYTKGTVDIAKSDKDFVIGFIAQRDMGGRDEGYDWLIMTPGVGLDDKGDALGQQYRTVDDVVSTGSDIIIVGRGLFAKGRDAKVEGERYRKAGWEAYLRRCGQQD

>d1pii\_2 c.1.2.4 (255-452) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Escherichia coli}

GENKVCGLTRGQDAKAAYDAGAIYGGLIFVATSPRCVNVEQAQEVMAAAPLQYVGVFRNHDIADVVDKAKVLSLAAVQLHGNEEQLYIDTLREALPAHVAIWKALSVGETLPAREFQHVDKYVLDNGQGGSGQRFDWSLLNGQSLGNVLLAGGLGADNCVEAAQTGCAGLDFNSAVESQPGIKDARLLASVFQTLRAY

>d1nsj\_\_ c.1.2.4 (-) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Thermotoga maritima}

MVRVKICGITNLEDALFSVESGADAVGFVFYPKSKRYISPEDARRISVELPPFVFRVGVFVNEEPEKILDVASYVQLNAVQLHGEEPIELCRKIAERILVIKAVGVSNERDMERALNYREFPILLDTKTPEYGGSGKTFDWSLILPYRDRFRYLVLSGGLNPENVRSAIDVVRPFAVDVSSGVEAFPGKKDHDSIKMFIKNAKGL

>d1pii\_1 c.1.2.4 (1-254) Indole-3-glycerophosphate synthase, IPGS {Escherichia coli}

MQTVLAKIVADKAIWVEARKQQQPLASFQNEVQPSTRHFYDALQGARTAFILECKKASPSKGVIRDDFDPARIAAIYKHYASAISVLTDEKYFQGSFNFLPIVSQIAPQPILCKDFIIDPYQIYLARYYQADACLLMLSVLDDDQYRQLAAVAHSLEMGVLTEVSNEEEQERAIALGAKVVGINNRDLRDLSIDLNRTRELAPKLGHNVTVISESGINTYAQVRELSHFANGFLIGSALMAHDDLHAAVRRVLL

>d1a53\_\_ c.1.2.4 (-) Indole-3-glycerophosphate synthase, IPGS {Archaeon Sulfolobus solfataricus}

PRYLKGWLKDVVQLSLRRPSFRASRQRPIISLNERILEFNKRNITAIIAEYKRKSPSGLDVERDPIEYSKFMERYAVGLSILTEEKYFNGSYETLRKIASSVSIPILMKDFIVKESQIDDAYNLGADTVLLIVKILTERELESLLEYARSYGMEPLIEINDENDLDIALRIGARFIGINSRDLETLEINKENQRKLISMIPSNVVKVAESGISERNEIEELRKLGVNAFLIGSSLMRNPEKIKEFIL

>d1qopa\_ c.1.2.4 (A:) Trp synthase alpha-subunit {Salmonella typhimurium}

MERYENLFAQLNDRREGAFVPFVTLGDPGIEQSLKIIDTLIDAGADALELGVPFSDPLADGPTIQNANLRAFAAGVTPAQCFEMLAIIREKHPTIPIGLLMYANLVFNNGIDAFYARCEQVGVDSVLVADVPVEESAPFRQAALRHNIAPIFICPPNADDDLLRQVASYGRGYTYLLSRSGVTGAENRGALPLHHLIEKLKEYHAAPALQGFGISSPEQVSAAVRAGAAGAISGSAIVKIIEKNLASPKQMLAELRSFVSAMKAASR

>d1geqa\_ c.1.2.4 (A:) Trp synthase alpha-subunit {Archaeon Pyrococcus furiosus}

MFKDGSLIPYLTAGDPDKQSTLNFLLALDEYAGAIELGIPFSDPIADGKTIQESHYRALKNGFKLREAFWIVKEFRRHSSTPIVLMTYYNPIYRAGVRNFLAEAKASGVDGILVVDLPVFHAKEFTEIAREEGIKTVFLAAPNTPDERLKVIDDMTTGFVYLVSLYGTTGAREEIPKTAYDLLRRAKRICRNKVAVGFGVSKREHVVSLLKEGANGVVVGSALVKIIGEKGREATEFLKKKVEELLGI

>d2tpsa\_ c.1.3.1 (A:) Thiamin phosphate synthase {Bacillus subtilis}

HGIRMTRISREMMKELLSVYFIMGSNNTKADPVTVVQKALKGGATLYQFREKGGDALTGEARIKFAEKAQAACREAGVPFIVNDDVELALNLKADGIHIGQEDANAKEVRAAIGDMILGVSAHTMSEVKQAEEDGADYVGLGPIYPTETKKDTRAVQGVSLIEAVRRQGISIPIVGIGGITIDNAAPVIQAGADGVSMISAISQAEDPESAARKFREEIQTYKTGR

>d1ho1a\_ c.1.24.1 (A:) Pyridoxine 5'-phosphate synthase {Escherichia coli}

AELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRILRQTLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACKRLADAGIQVSLFIDADEEQIKAAAEVGAPFIEIHTGCYADAKTDAEQAQELARIAKAATFAASLGLKVNAGHGLTYHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEARG

>d2dora\_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme A}

MLNTTFANAKFANPFMNASGVHCMTIEDLEELKASQAGAYITKSSTLEKREGNPLPRYVDLELGSINSMGLPNLGFDYYLDYVLKNQKENAQEGPIFFSIAGMSAAENIAMLKKIQESDFSGITELNLSCPNVPGKPQLAYDFEATEKLLKEVFTFFTKPLGVKLPPYFDLVHFDIMAEILNQFPLTYVNSVNSIGNGLFIDPEAESVVIKPKDGFGGIGGAYIKPTALANVRAFYTRLKPEIQIIGTGGIETGQDAFEHLLCGATMLQIGTALHKEGPAIFDRIIKELEEIMNQKGYQSIADFHGKLKSL

>d1ep3a\_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme B}

MTENNRLSVKLPGLDLKNPIIPASGCFGFGEEYAKYYDLNKLGSIMVKATTLHPRFGNPTPRVAETASGMLNAIGLQNPGLEVIMTEKLPWLNENFPELPIIANVAGSEEADYVAVCAKIGDAANVKAIELNISCPNVKHGGQAFGTDPEVAAALVKACKAVSKVPLYVKLSPNVTDIVPIAKAVEAAGADGLTMINTLMGVRFDLKTRQPILANITGGLSGPAIKPVALKLIHQVAQDVDIPIIGMGGVANAQDVLEMYMAGASAVAVGTANFADPFVCPKIIDKLPELMDQYRIESLESLIQEVKEGKK

>d1d3ga\_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Human (Homo sapiens)}

MATGDERFYAEHLMPTLQGLLDPESAHRLAVRFTSLGLLPRARFQDSDMLEVRVLGHKFRNPVGIAAGFDKHGEAVDGLYKMGFGFVEIGSVTPKPQEGNPRPRVFRLPEDQAVINRYGFNSHGLSVVEHRLRARQQKQAKLTEDGLPLGVNLGKNKTSVDAAEDYAEGVRVLGPLADYLVVNVSSPNTAGLRSLQGKAELRRLLTKVLQERDGLRRVHRPAVLVKIAPDLTSQDKEDIASVVKELGIDGLIVTNTTVSRPAGLQGALRSETGGLSGKPLRDLSTQTIREMYALTQGRVPIIGVGGVSSGQDALEKIRAGASLVQLYTALTFWGPPVVGKVKRELEALLKEQGFGGVTDAIGADHRR

>d1oyb\_\_ c.1.4.1 (-) Old yellow enzyme (OYE) {Brewer's yeast (Saccharomyces carlsbergensis)}

SFVKDFKPQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRALHPGNIPNRDWAVEYYTQRAQRPGTMIITEGAFISPQAGGYDNAPGVWSEEQMVEWTKIFNAIHEKKSFVWVQLWVLGWAAFPDNLARDGLRYDSASDNVFMDAEQEAKAKKANNPQHSLTKDEIKQYIKEYVQAAKNSIAAGADGVEIHSANGYLLNQFLDPHSNTRTDEYGGSIENRARFTLEVVDALVEAIGHEKVGLRLSPYGVFNSMSGGAETGIVAQYAYVAGELEKRAKAGKRLAFVHLVEPRVTNPFLTEGEGEYEGGSNDFVYSIWKGPVIRAGNFALHPEVVREEVKDKRTLIGYGRFFISNPDLVDRLEKGLPLNKYDRDTFYQMSAHGYIDYPTYEEALKLGWDKK

>d1icpa\_ c.1.4.1 (A:) 12-oxophytodienoate reductase 1 (OYE homolog) {Tomato (Lycopersicon esculentum)}

QVDKIPLMSPCKMGKFELCHRVVLAPLTRQRSYGYIPQPHAILHYSQRSTNGGLLIGEATVISETGIGYKDVPGIWTKEQVEAWKPIVDAVHAKGGIFFCQIWHVGRVSNKDFQPNGEDPISCTDRGLTPQIMSNGIDIAHFTRPRRLTTDEIPQIVNEFRVAARNAIEAGFDGVEIHGAHGYLIDQFMKDQVNDRSDKYGGSLENRCRFALEIVEAVANEIGSDRVGIRISPFAHYNEAGDTNPTALGLYMVESLNKYDLAYCHVVEPRMKTAWEKIECTESLVPMRKAYKGTFIVAGGYDREDGNRALIEDRADLVAYGRLFISNPDLPKRFELNAPLNKYNRDTFYTSDPIVGYTDYPFLE

>d1gox\_\_ c.1.4.1 (-) Glycolate oxidase {Spinach (Spinacia oleracea)}

MEITNVNEYEAIAKQKLPKMVYDYYASGAEDQWTLAENRNAFSRILFRPRILIDVTNIDMTTTILGFKISMPIMIAPTAMQKMAHPEGEYATARAASAAGTIMTLSSWATSSVEEVASTGPGIRFFQLYVYKDRNVVAQLVRRAERAGFKAIALTVDTPRLGRREADIKNRFVLPPFLTLKNFEGIDLGKMDKANDSGLSSYVAGQIDRSLSWKDVAWLQTITSLPILVKGVITAEDARLAVQHGAAGIIVSNHGARQLDYVPATIMALEEVVKAAQGRIPVFLDGGVRRGTDVFKALALGAAGVFIGRPVVFSLAAEGEAGVKKVLQMMRDEFELTMALSGCRSLKEISRSHIAADWD

>d1huva\_ c.1.4.1 (A:) Membrane-associated (S)-mandelate dehydrogenase {Pseudomonas putida}

NLFNVEDYRKLAQKRLPKMVYDYLEGGAEDEYGVKHNRDVFQQWRFKPKRLVDVSRRSLQAEVLGKRQSMPLLIGPTGLNGALWPKGDLALARAATKAGIPFVLSTASNMSIEDLARQCDGDLWFQLYVIHREIAQGMVLKALHTGYTTLVLTTDVAVNGYRERDLHNRFKIPPFLTLKNFEGIDLGKMDKANLEMQAALMSRQMDASFNWEALRWLRDLWPHKLLVKGLLSAEDADRCIAEGADGVILSNHGGRQLDCAISPMEVLAQSVAKTGKPVLIDSGFRRGSDIVKALALGAEAVLLGRATLYGLAARGETGVDEVLTLLKADIDRTLAQIGCPDITSLSPDYLQNE

>d1h61a\_ c.1.4.1 (A:) Pentaerythritol tetranirate reductase {Enterobacter cloacae}

SAEKLFTPLKVGAVTAPNRVFMAPLTRLRSIEPGDIPTPLMGEYYRQRASAGLIISEATQISAQAKGYAGAPGLHSPEQIAAWKKITAGVHAEDGRIAVQLWHTGRISHSSIQPGGQAPVSASALNANTRTSLRDENGNAIRVDTTTPRALELDEIPGIVNDFRQAVANAREAGFDLVELHSAHGYLLHQFLSPSSNQRTDQYGGSVENRARLVLEVVDAVCNEWSADRIGIRVSPIGTFQNVDNGPNEEADALYLIEELAKRGIAYLHMSETDLAGGKPYSEAFRQKVRERFHGVIIGAGAYTAEKAEDLIGKGLIDAVAFGRDYIANPDLVARLQKKAELNPQRPESFYGGGAEGYTDYPSL

>d1djna1 c.1.4.1 (A:1-340) Trimethylamine dehydrogenase, N-terminal domain {Methylophilus methylotrophus, w3a1}

ARDPKHDILFEPIQIGPKTLRNRFYQVPHCIGAGSDKPGFQSAHRSVKAEGGWAALNTEYCSINPESDDTHRLSARIWDEGDVRNLKAMTDEVHKYGALAGVELWYGGAHAPNMESRATPRGPSQYASEFETLSYCKEMDLSDIAQVQQFYVDAAKRSRDAGFDIVYVYGAHSYLPLQFLNPYYNKRTDKYGGSLENRARFWLETLEKVKHAVGSDCAIATRFGVDTVYGPGQIEAEVDGQKFVEMADSLVDMWDITIGDIAEWGEDAGPSRFYQQGHTIPWVKLVKQVSKKPVLGVGRYTDPEKMIEIVTKGYADIIGCARPSIADPFLPQKVEQGRYD

>d1ltda1 c.1.4.1 (A:98-511) Flavocytochrome b2, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

APGETKEDIARKEQLKSLLPPLDNIINLYDFEYLASQTLTKQAWAYYSSGANDEVTHRENHNAYHRIFFKPKILVDVRKVDISTDMLGSHVDVPFYVSATALCKLGNPLEGEKDVARGCGQGVTKVPQMISTLASCSPEEIIEAAPSDKQIQWYQLYVNSDRKITDDLVKNVEKLGVKALFVTVDAPSLGQREKDMKLKFSNTKAGPKAMKKTNVEESQGASRALSKFIDPSLTWKDIEELKKKTKLPIVIKGVQRTEDVIKAAEIGVSGVVLSNHGGRQLDFSRAPIEVLAETMPILEQRNLKDKLEVFVDGGVRRGTDVLKALCLGAKGVGLGRPFLYANSCYGRNGVEKAIEILRDEIEMSMRLLGVTSIAELKPDLLDLSTLKARTVGVPNDVLYNEVYEGPTLTEFEDA

>d1h7wa2 c.1.4.1 (A:533-844) Dihydropyrimidine dehydrogenase, domain 4 {Pig (Sus scrofa)}

ISVEMAGLKFINPFGLASAAPTTSSSMIRRAFEAGWGFALTKTFSLDKDIVTNVSPRIVRGTTSGPMYGPGQSSFLNIELISEKTAAYWCQSVTELKADFPDNIVIASIMCSYNKNDWMELSRKAEASGADALELNLSCPHGMGERGMGLACGQDPELVRNICRWVRQAVQIPFFAKLTPNVTDIVSIARAAKEGGADGVTATNTVSGLMGLKADGTPWPAVGAGKRTTYGGVSGTAIRPIALRAVTTIARALPGFPILATGGIDSAESGLQFLHSGASVLQVCSAVQNQDFTVIQDYCTGLKALLYLKSIE

>d1ea0a2 c.1.4.1 (A:423-1193) Alpha subunit of glutamate synthase, central and FMN domains {Azospirillum brasilense}

TTHLDELVKTASLKGEPSDMDKAELRRRQQAFGLTMEDMELILHPMVEDGKEAIGSMGDDSPIAVLSDKYRGLHHFFRQNFSQVTNPPIDSLRERRVMSLKTRLGNLGNILDEDETQTRLLQLESPVLTTAEFRAMRDYMGDTAAEIDATFPVDGGPEALRDALRRIRQETEDAVRGGATHVILTDEAMGPARAAIPAILATGAVHTHLIRSNLRTFTSLNVRTAEGLDTHYFAVLIGVGATTVNAYLAQEAIAERHRRGLFGSMPLEKGMANYKKAIDDGLLKIMSKMGISVISSYRGGGNFEAIGLSRALVAEHFPAMVSRISGIGLNGIQKKVLEQHATAYNEEVVALPVGGFYRFRKSGDRHGWEGGVIHTLQQAVTNDSYTTFKKYSEQVNKRPPMQLRDLLELRSTKAPVPVDEVESITAIRKRFITPGMSMGALSPEAHGTLNVAMNRIGAKSDSGEGGEDPARFRPDKNGDNWNSAIKQVASGRFGVTAEYLNQCRELEIKVAQGAKPGEGGQLPGFKVTEMIARLRHSTPGVMLISPPPHHDIYSIEDLAQLIYDLKQINPDAKVTVKLVSRSGIGTIAAGVAKANADIILISGNSGGTGASPQTSIKFAGLPWEMGLSEVHQVLTLNRLRHRVRLRTDGGLKTGRDIVIAAMLGAEEFGIGTASLIAMGCIMVRQCHSNTCPVGVCVQDDKLRQKFVGTPEKVVNLFTFLAEEVREILAGLGFRSLNEVIGRTDLLHQVSRGAEHLDDLDLNPRLAQVDPG

>d1eepa\_ c.1.5.1 (A:) Inosine monophosphate dehydrogenase (IMPDH) {Lyme disease spirochete (Borrelia burgdorferi)}

NKITKEALTFDDVSLIPRKSSVLPSEVSLKTQLTKNISLNIPFLSSAMDTVTESQMAIAIAKEGGIGIIHKNMSIEAQRKEIEKVKTYKFQKTINTNGDTNEQKPEIFTAKQHLEKSDAYKNAEHKEDFPNACKDLNNKLRVGAAVSIDIDTIERVEELVKAHVDILVIDSAHGHSTRIIELIKKIKTKYPNLDLIAGNIVTKEAALDLISVGADCLKVGIGPGSICTTRIVAGVGVPQITAICDVYEACNNTNICIIADGGIRFSGDVVKAIAAGADSVMIGNLFAGTKESPSEEIIYNGKKFKSYVGMGSISAMKRGSKSRYFQLENNEPKKLVPEGIEGMVPYSGKLKDILTQLKGGLMSGMGYLGAATISDLKINSKFVKISHS

>d1zfja1 c.1.5.1 (A:2-94,A:221-492) Inosine monophosphate dehydrogenase (IMPDH) {Streptococcus pyogenes}

SNWDTKFLKKGYTFDDVLLIPAESHVLPNEVDLKTKLADNLTLNIPIITAAMDTVTGSKMAIAIARAGGLGVIHKNMSITEQAEEVRKVKRSEXGRLLVAAAVGVTSDTFERAEALFEAGADAIVIDTAHGHSAGVLRKIAEIRAHFPNRTLIAGNIATAEGARALYDAGVDVVKVGIGPGSICTTRVVAGVGVPQVTAIYDAAAVAREYGKTIIADGGIKYSGDIVKALAAGGNAVMLGSMFAGTDEAPGETEIYQGRKYKTYRGMGSIAAMKKGSSDRYFQGSVNEANKLVPEGIEGRVAYKGAASDIVFQMLGGIRSGMGYVGAGDIQELHENAQFVEMSGAGLIESHPHDVQITNEAPNYSV

>d1ak5\_1 c.1.5.1 (2-101,222-483) Inosine monophosphate dehydrogenase (IMPDH) {Tritrichomonas foetus}

AKYYNEPCHTFNEYLLIPGLSTVDCIPSNVNLSTPLVKFQKGQQSEINLKIPLVSAIMQSVSGEKMAIALAREGGISFIFGSQSIESQAAMVHAVKNFKAXHNELVDSQKRYLVGAGINTRDFRERVPALVEAGADVLCIDSSDGFSEWQKITIGWIREKYGDKVKVGAGNIVDGEGFRYLADAGADFIKIGIGGGSICITREQKGIGRGQATAVIDVVAERNKYFEETGIYIPVCSDGGIVYDYHMTLALAMGADFIMLGRYFARFEESPTRKVTINGSVMKEYWGEGSSRARNWQRYDLGGKQKLSFEEGVDSYVPYAGKLKDNVEASLNKVKSTMCNCGALTIPQLQSKAKITLVSSVSI

>d1jr1a1 c.1.5.1 (A:17-112,A:233-514) Inosine monophosphate dehydrogenase (IMPDH) {Chinese hamster (Cricetulus griseus)}

GLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKITLKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQXYPLASKDAKKQLLCGAAIGTHEDDKYRLDLLALAGVDVVVLDSSQGNSIFQINMIKYMKEKYPNLQVIGGNVVTAAQAKNLIDAGVDALRVGMGCGSICITQEVLACGRPQATAVYKVSEYARRFGVPVIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVRAMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF

>d1bd0a2 c.1.6.1 (A:12-244) Alanine racemase {Bacillus stearothermophilus}

VDLDAIYDNVENLRRLLPDDTHIMAVVKANAYGHGDVQVARTALEAGASRLAVAFLDEALALREKGIEAPILVLGASRPADAALAAQQRIALTVFRSDWLEEASALYSGPFPIHFHLKMDTGMGRLGVKDEEETKRIVALIERHPHFVLEGLYTHFATADEVNTDYFSYQYTRFLHMLEWLPSRPPLVHCANSAASLRFPDRTFNMVRFGIAMYGLAPSPGIKPLLPYPLKEA

>d1d7ka2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Human (Homo sapiens)}

DLGDILKKHLRWLKALPRVTPFYAVKCNDSKAIVKTLAATGTGFDCASKTEIQLVQSLGVPPERIIYANPCKQVSQIKYAANNGVQMMTFDSEVELMKVARAHPKAKLVLRIATDDSKAVCRLSVKFGATLRTSRLLLERAKELNIDVVGVSFHVGSGCTDPETFVQAISDARCVFDMGAEVGFSMYLLDIGGGFPGSEDVKLKFEEITGVINPALDKYFPSDSGVRIIAEPGRYYVASA

>d7odca2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Mouse (Mus musculus)}

DLGDILKKHLRWLKALPRVTPFYAVKCNDSRAIVSTLAAIGTGFDCASKTEIQLVQGLGVPAERVIYANPCKQVSQIKYAASNGVQMMTFDSEIELMKVARAHPKAKLVLRIATDDSKAVCRLSVKFGATLKTSRLLLERAKELNIDVIGVSFHVGSGCTDPDTFVQAVSDARCVFDMATEVGFSMHLLDIGGGFPGSEDTKLKFEEITSVINPALDKYFPSDSGVRIIAEPGRYYVASA

>d2toda2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}

DLGDIVRKHETWKKCLPRVTPFYAVACNDDWRVLGTLAALGTGFDCASNTEIQRVRGIGVPPEKIIYANPCKQISHIRYARDSGVDVMTFDCVDELEKVAKTHPKAKMVLRISTDDSLARCRLSVKFGAKVEDCRFILEQAKKLNIDVTGVSFHVGSGSTDASTFAQAISDSRFVFDMGTELGFNMHILDIGGGFPGTRDAPLKFEEIAGVINNALEKHFPPDLKLTIVAEPGRYYVASA

>d1ct5a\_ c.1.6.2 (A:) "Hypothetical" protein ybl036c {Baker's yeast (Saccharomyces cerevisiae)}

TGITYDEDRKTQLIAQYESVREVVNAEAKNVHVNENASKILLLVVSKLKPASDIQILYDHGVREFGENYVQELIEKAKLLPDDIKWHFIGGLQTNKCKDLAKVPNLYSVETIDSLKKAKKLNESRAKFQPDCNPILCNVQINTSHEDQKSGLNNEAEIFEVIDFFLSEECKYIKLNGLMTIGSWNVSHEDSKENRDFATLVEWKKKIDAKFGTSLKLSMGMSADFREAIRQGTAEVRIGTDIFG

>d1frb\_\_ c.1.7.1 (-) FR-1 (fibroblast growth factor-induced) protein {Mouse (Mus musculus)}

ATFVELSTKAKMPIVGLGTWKSPPNQVKEAVKAAIDAGYRHIDCAYAYCNENEVGEAIQEKIKEKAVQREDLFIVSKLWPTCFEKKLLKEAFQKTLTDLKLDYLDLYLIHWPQGLQPGKELFPKDDQGRILTSKTTFLEAWEGMEELVDQGLVKALGVSNFNHFQIERLLNKPGLKHKPVTNQVECHPYLTQEKLIQYCHSKGISVTAYSPLGSPDRPSAKPEDPSLLEDPKIKEIAAKHEKTSAQVLIRFHIQRNVVVIPKSVTPSRIQENIQVFDFQLSDEEMATILSFNRNWRACLLPETVNMEEYPYDAEY

>d1exba\_ c.1.7.1 (A:) Voltage-dependent K+ channel beta subunit {Rat (Rattus norvegicus)}

LQFYRNLGKSGLRVSCLGLGTWVTFGGQITDEMAEHLMTLAYDNGINLFDTAEVYAAGKAEVVLGNIIKKKGWRRSSLVITTKIFWGGKAETERGLSRKHIIEGLKASLERLQLEYVDVVFANRPDPNTPMEETVRAMTHVINQGMAMYWGTSRWSSMEIMEAYSVARQFNLIPPICEQAEYHMFQREKVEVQLPELFHKIGVGAMTWSPLACGIVSGKYDSGIPPYSRASLKGYQWLKDKILSEEGRRQQAKLKELQAIAERLGCTLPQLAIAWCLRNEGVSSVLLGASNAEQLMENIGAIQVLPKLSSSIVHEIDSILGNKPYS

>d1ads\_\_ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (Homo sapiens)}

ASRLLLNNGAKMPILGLGTWKSPPGQVTEAVKVAIDVGYRHIDCAHVYQNENEVGVAIQEKLREQVVKREELFIVSKLWCTYHEKGLVKGACQKTLSDLKLDYLDLYLIHWPTGFKPGKEFFPLDESGNVVPSDTNILDTWAAMEELVDEGLVKAIGISNFNHLQVEMILNKPGLKYKPAVNQIECHPYLTQEKLIQYCQSKGIVVTAYSPLGSPDRPWAKPEDPSLLEDPRIKAIAAKHNKTTAQVLIRFPMQRNLVVIPKSVTPERIAENFKVFDFELSSQDMTTLLSYNRNWRVCALLSCTSHKDYPFHEEF

>d2alr\_\_ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (Homo sapiens)}

AASCVLLHTGQKMPLIGLGTWKSEPGQVKAAVKYALSVGYRHIDCAAIYGNEPEIGEALKEDVGPGKAVPREELFVTSKLWNTKHHPEDVEPALRKTLADLQLEYLDLYLMHWPYAFERGDNPFPKNADGTICYDSTHYKETWKALEALVAKGLVQALGLSNFNSRQIDDILSVASVRPAVLQVECHPYLAQNELIAHCQARGLEVTAYSPLGSSDRAWRDPDEPVLLEEPVVLALAEKYGRSPAQILLRWQVQRKVICIPKSITPSRILQNIKVFDFTFSPEEMKQLNALNKNWRYIVPMLTVDGKRVPRDAGHPLYPFNDPY

>d1ah4\_\_ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Pig (Sus scrofa)}

ASHLVLYTGAKMPILGLGTWKSPPGKVTEAVKVAIDLGYRHIDCAHVYQNENEVGLGLQEKLQGQVVKREDLFIVSKLWCTDHEKNLVKGACQTTLRDLKLDYLDLYLIHWPTGFKPGKDPFPLDGDGNVVPDESDFVETWEAMEELVDEGLVKAIGVSNFNHLQVEKILNKPGLKYKPAVNQIEVHPYLTQEKLIEYCKSKGIVVTAYSPLGSPDRPWAKPEDPSLLEDPRIKAIAAKYNKTTAQVLIRFPMQRNLIVIPKSVTPERIAENFQVFDFELSPEDMNTLLSYNRNWRVCALMSCASHKDYPFHEEY

>d1hqta\_ c.1.7.1 (A:) Aldose reductase (aldehyde reductase) {Pig (Sus scrofa)}

AASCVLLHTGQKMPLIGLGTWKSEPGQVKAAIKYALTVGYRHIDCAAIFGNELEIGEALQETVGPGKAVPREELFVTSKLWNTKHHPEDVEPALRKTLADLQLEYLDLYLMHWPYAFERGDNPFPKNADGTIRYDATHYKDTWKALEALVAKGLVRALGLSNFSSRQIDDVLSVASVRPAVLQVECHPYLAQNELIAHCQARGLEVTAYSPLGSSDRAWRDPNEPVLLEEPVVQALAEKYNRSPAQILLRWQVQRKVICIPKSVTPSRIPQNIQVFDFTFSPEEMKQLDALNKNLRFIVPMLTVDGKRVPRDAGHPLYPFNDPY

>d1afsa\_ c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Rat (Rattus norvegicus)}

MDSISLRVALNDGNFIPVLGFGTTVPEKVAKDEVIKATKIAIDNGFRHFDSAYLYEVEEEVGQAIRSKIEDGTVKREDIFYTSKLWSTFHRPELVRTCLEKTLKSTQLDYVDLYIIHFPMALQPGDIFFPRDEHGKLLFETVDICDTWEAMEKCKDAGLAKSIGVSNFNCRQLERILNKPGLKYKPVCNQVECHLYLNQSKMLDYCKSKDIILVSYCTLGSSRDKTWVDQKSPVLLDDPVLCAIAKKYKQTPALVALRYQLQRGVVPLIRSFNAKRIKELTQVFEFQLASEDMKALDGLNRNFRYNNAKYFDDHPNHPF

>d1ihia\_ c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Human (Homo sapiens), type III}

SKYQCVKLNDGHFMPVLGFGTYAPAEVPKSKALEAVKLAIEAGFHHIDSAHVYNNEEQVGLAIRSKIADGSVKREDIFYTSKLWSNSHRPELVRPALERSLKNLQLDYVDLYLIHFPVSVKPGEEVIPKDENGKILFDTVDLCATWEAMEKCKDAGLAKSIGVSNFNHRLLEMILNKPGLKYKPVCNQVECHPYFNQRKLLDFCKSKDIVLVAYSALGSHREEPWVDPNSPVLLEDPVLCALAKKHKRTPALIALRYQLQRGVVVLAKSYNEQRIRQNVQVFEFQLTSEEMKAIDGLNRNVRYLTLDIFAGPPNYPFSDE

>d1c9wa\_ c.1.7.1 (A:) CHO reductase {Chinese hampster (Cricetulus griseus)}

STFVELSTKAKMPIVGLGTWQSPPGQVKEAVKVAIDAGYRHIDCAYAYYNEHEVGEAIQEKIKEKAVRREDLFIVSKLWPTCFERKLLKEAFQKTLTDLKLDYLDLYLIHWPQGLQPGKELFPKDDQGNVLTSKITFLDAWEVMEELVDEGLVKALGVSNFNHFQIERILNKPGLKHKPVTNQVECHPYLTQEKLIEYCHSKGITVTAYSPLGSPNRPWAKPEDPSLLEDPKIKEIAAKHKKTSAQVLIRFHIQRNVVVIPKSVTPARIHENFQVFDFQLSDQEMATILGFNRNWRACLLPETVNMEEYPYDAEY

>d1hw6a\_ c.1.7.1 (A:) 2,5-diketo-D-gluconic acid reductase A {Corynebacterium sp.}

TVPSIVLNDGNSIPQLGYGVFKVPPADTQRAVEEALEVGYRHIDTAAIYGNEEGVGAAIAASGIARDDLFITTKLWNDRHDGDEPAAAIAESLAKLALDQVDLYLVHWPTPAADNYVHAWEKMIELRAAGLTRSIGVSNHLVPHLERIVAATGVVPAVNQIELHPAYQQREITDWAAAHDVKIESWGPLGQGKYDLFGAEPVTAAAAAHGKTPAQAVLRWHLQKGFVVFPKSVRRERLEENLDVFDFDLTDTEIAAIDAMDP

>d1bli\_2 c.1.8.1 (3-393) Bacterial alpha-amylase {Bacillus licheniformis}

LNGTLMQYFEWYMPNDGQHWKRLQNDSAYLAEHGITAVWIPPAYKGTSQADVGYGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINVYGDVVINHKGGADATEDVTAVEVDPADRNRVISGEHLIKAWTHFHFPGRGSTYSDFKWHWYHFDGTDWDESRKLNRIYKFQGKAWDWEVSNEFGNYDYLMYADIDYDHPDVAAEIKRWGTWYANELQLDGFRLDAVKHIKFSFLRDWVNHVREKTGKEMFTVAEYWSYDLGALENYLNKTNFNHSVFDVPLHYQFHAASTQGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKARKQ

>d1e43a2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus amyloliquefaciens/Bacillus licheniformis chimera}

VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDLYDLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHKAGADATEDVTAVEVNPANRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFRGEGKAWDWEVSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIDAAKHIKFSFLRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNLQAASSQGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTQPGQSLESTVQTWFKPLAYAFILTRESGYPQVFYGDMYGTKGDSQREIPALKHKIEPILKARKQ

>d1g94a2 c.1.8.1 (A:1-354) Bacterial alpha-amylase {Pseudoalteromonas haloplanctis (Alteromonas haloplanctis)}

TPTTFVHLFEWNWQDVAQECEQYLGPKGYAAVQVSPPNEHITGSQWWTRYQPVSYELQSRGGNRAQFIDMVNRCSAAGVDIYVDTLINHMAAGSGTGTAGNSFGNKSFPIYSPQDFHESCTINNSDYGNDRYRVQNCELVGLADLDTASNYVQNTIAAYINDLQAIGVKGFRFDASKHVAASDIQSLMAKVNGSPVVFQEVIDQGGEAVGASEYLSTGLVTEFKYSTELGNTFRNGSLAWLSNFGEGWGFMPSSSAVVFVDNHDNQRGHGGAGNVITFEDGRLYDLANVFMLAYPYGYPKVMSSYDFHGDTDAGGPNVPVHNNGNLECFASNWKCEHRWSYIAGGVDFRNNTAD

>d1bag\_2 c.1.8.1 (1-347) Bacterial alpha-amylase {Bacillus subtilis}

LTAPSIKSGTILHAWNWSFNTLKHNMKDIHDAGYTAIQTSPINQVKEGNQGDKSMSNWYWLYQPTSYQIGNRYLGTEQEFKEMCAAAEEYGIKVIVDAVINHTTFDYAAISNEVKSIPNWTHGNTQIKNWSDRWDVTQNSLLGLYDWNTQNTQVQSYLKRFLERALNDGADGFRFDAAKHIELPDDGSYGSQFWPNITNTSAEFQYGQILQDSASRDAAYANYMDVTASNYGHSIRSALKNRNLGVSNISHYASDVSADKLVTWVESHDTYANDDEESTWMSDDDIRLGWAVIASRSGSTPLFFSRPEGGGNGVRFPGKSQIGDRGSALFEDQAITAVNRFHNVMAG

>d1hvxa2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus stearothermophilus}

AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGTSRSDVGYGVYDLYDLGEFNQKGAVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKAWDWEVDTENGNYDYLMYADLDMDHPEVVTELKSWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYIMKTNGTMSLFDAPLHNKFYTASKSGGTFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLAYAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRD

>d1gjwa2 c.1.8.1 (A:1-572) Maltosyltransferase {Thermotoga maritima}

MLLREINRYCKEKATGKRIYAVPKLWIPGFFKKFDEKSGRCFVDPYELGAEITDWILNQSREWDYSQPLSFLKGEKTPDWIKRSVVYGSLPRTTAAYNHKGSGYYEENDVLGFREAGTFFKMMLLLPFVKSLGADAIYLLPVSRMSDLFKKGDAPSPYSVKNPMELDERYHDPLLEPFKVDEEFKAFVEACHILGIRVILDFIPRTAARDSDLIREHPDWFYWIKVEELADYTPPRAEELPFKVPDEDELEIIYNKENVKRHLKKFTLPPNLIDPQKWEKIKREEGNILELIVKEFGIITPPGFSDLINDPQPTWDDVTFLRLYLDHPEASKRFLDPNQPPYVLYDVIKASKFPGKEPNRELWEYLAGVIPHYQKKYGIDGARLDMGHALPKELLDLIIKNVKEYDPAFVMIAEELDMEKDKASKEAGYDVILGSSWYFAGRVEEIGKLPDIAEELVLPFLASVETPDTPRIATRKYASKMKKLAPFVTYFLPNSIPYVNTGQEIGEKQPMNLGLDTDPNLRKVLSPTDEFFGKLAFFDHYVLHWDSPDRGVLNFIKKLIKVRHEFLDFVLN

>d1cgt\_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

DPDTAVTNKQSFSTDVIYQVFTDRFLDGNPSNNPTGAAYDATCSNLKLYCGGDWQGLINKINDNYFSDLGVTALWISQPVENIFATINYSGVTNTAYHGYWARDFKKTNPYFGTMADFQNLITTAHAKGIKIVIDFAPNHTSPAMETDTSFAENGRLYDNGTLVGGYTNDTNGYFHHNGGSDFSSLENGIYKNLYDLADFNHNNATIDKYFKDAIKLWLDMGVDGIRVDAVKHMPLGWQKSWMSSIYAHKPVFTFGEWFLGSAASDADNTDFANKSGMSLLDFRFNSAVRNVFRDNTSNMYALDSMINSTATDYNQVNDQVTFIDNHDMDRFKTSAVNNRRLEQALAFTLTSRGVPAIYYGTEQYLTGNGDPDNRAKMPSFSKSTTAFNVISKLAPLRKSNPAIAY

>d1kcla4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

APDTSVSNKQNFSTDVIYQIFTDRFSDGNPANNPTGAAFDGTCTNLRLYCGGDWQGIINKINDGYLTGMGVTAIWISQPVENIYSIINYSGVNNTAYHGYWARDFKKTNPAYGTIADFQNLIAAAHAKNIKVIIDFAPNHTSPASSDQPSFAENGRLYDNGTLLGGYTNDTQNLFHHNLGTDFSTTENGIYKNLYDLADLNHNNSTVDVYLKDAIKMWLDLGIDGIRMDAVKHMPFGWQKSFMAAVNNYKPVFTFGEWFLGVNEVSPENHKFANESGMSLLDFRFAQKVRQVFRDNTDNMYGLKAMLEGSAADYAQVDDQVTFIDNHDMERFHASNANRRKLEQALAFTLTSRGVPAIYYGTEQYMSGGTDPDNRARIPSFSTSTTAYQVIQKLAPLRKCNPAIAY

>d1cyg\_4 c.1.8.1 (1-402) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus}

AGNLNKVNFTSDVVYQIVVDRFVDGNTSNNPSGALFSSGCTNLRKYCGGDWQGIINKINDGYLTDMGVTAIWISQPVENVFSVMNDASGSASYHGYWARDFKKPNPFFGTLSDFQRLVDAAHAKGIKVIIDFAPNHTSPASETNPSYMENGRLYDNGTLLGGYTNDANMYFHHNGGTTFSSLEDGIYRNLFDLADLNHQNPVIDRYLKDAVKMWIDMGIDGIRMDAVKHMPFGWQKSLMDEIDNYRPVFTFGEWFLSENEVDANNHYFANESGMSLLDFRFGQKLRQVLRNNSDNWYGFNQMIQDTASAYDEVLDQVTFIDNHDMDRFMIDGGDPRKVDMALAVLLTSRGVPNIYYGTEQYMTGNGDPNNRKMMSSFNKNTRAYQVIQKLSSLRRNNPALAY

>d1qhoa4 c.1.8.1 (A:1-407) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}

SSSASVKGDVIYQIIIDRFYDGDTTNNNPAKSYGLYDPTKSKWKMYWGGDLEGVRQKLPYLKQLGVTTIWLSPVLDNLDTLAGTDNTGYHGYWTRDFKQIEEHFGNWTTFDTLVNDAHQNGIKVIVDFVPNHSTPFKANDSTFAEGGALYNNGTYMGNYFDDATKGYFHHNGDISNWDDRYEAQWKNFTDPAGFSLADLSQENGTIAQYLTDAAVQLVAHGADGLRIDAVKHFNSGFSKSLADKLYQKKDIFLVGEWYGDDPGTANHLEKVRYANNSGVNVLDFDLNTVIRNVFGTFTQTMYDLNNMVNQTGNEYKYKENLITFIDNHDMSRFLSVNSNKANLHQALAFILTSRGTPSIYYGTEQYMAGGNDPYNRGMMPAFDTTTTAFKEVSTLAGLRRNNAAIQY

>d1pama4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Alkalophilic bacillus sp., strain 1011}

APDTSVSNKQNFSTDVIYQIFTDRFSDGNPANNPTGAAFDGSCTNLRLYCGGDWQGIINKINDGYLTGMGITAIWISQPVENIYSVINYSGVNNTAYHGYWARDFKKTNPAYGTMQDFKNLIDTAHAHNIKVIIDFAPNHTSPASSDDPSFAENGRLYDNGNLLGGYTNDTQNLFHHYGGTDFSTIENGIYKNLYDLADLNHNNSSVDVYLKDAIKMWLDLGVDGIRVDAVKHMPFGWQKSFMATINNYKPVFTFGEWFLGVNEISPEYHQFANESGMSLLDFRFAQKARQVFRDNTDNMYGLKAMLEGSEVDYAQVNDQVTFIDNHDMERFHTSNGDRRKLEQALAFTLTSRGVPAIYYGSEQYMSGGNDPDNRARLPSFSTTTTAYQVIQKLAPLRKSNPAIAY

>d1ciu\_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Thermoanaerobacterium thermosulfurigenes, EM1}

ASDTAVSNVVNYSTDVIYQIVTDRFVDGNTSNNPTGDLYDPTHTSLKKYFGGDWQGIINKINDGYLTGMGVTAIWISQPVENIYAVLPDSTFGGSTSYHGYWARDFKRTNPYFGSFTDFQNLINTAHAHNIKVIIDFAPNHTSPASETDPTYAENGRLYDNGTLLGGYTNDTNGYFHHYGGTDFSSYEDGIYRNLFDLADLNQQNSTIDSYLKSAIKVWLDMGIDGIRLDAVKHMPFGWQKNFMDSILSYRPVFTFGEWFLGTNEIDVNNTYFANESGMSLLDFRFSQKVRQVFRDNTDTMYGLDSMIQSTASDYNFINDMVTFIDNHDMDRFYNGGSTRPVEQALAFTLTSRGVPAIYYGTEQYMTGNGDPYNRAMMTSFNTSTTAYNVIKKLAPLRKSNPAIAY

>d1hx0a2 c.1.8.1 (A:1-403) Animal alpha-amylase {Pig (Sus scrofa)}

EYAPQTQSGRTSIVHLFEWRWVDIALECERYLGPKGFGGVQVSPPNENIVVTNPSRPWWERYQPVSYKLCTRSGNENEFRDMVTRCNNVGVRIYVDAVINHMCGSGAAAGTGTTCGSYCNPGNREFPAVPYSAWDFNDGKCKTASGGIESYNDPYQVRDCQLVGLLDLALEKDYVRSMIADYLNKLIDIGVAGFRIDASKHMWPGDIKAVLDKLHNLNTNWFPAGSRPFIFQEVIDLGGEAIKSSEYFGNGRVTEFKYGAKLGTVVRKWSGEKMSYLKNWGEGWGFMPSDRALVFVDNHDNQRGHGAGGSSILTFWDARLYKIAVGFMLAHPYGFTRVMSSYRWARNFVNGEDVNDWIGPPNNNGVIKEVTINADTTCGNDWVCEHRWREIRNMVWFRNVVDG

>d1smd\_2 c.1.8.1 (1-403) Animal alpha-amylase {Human (Homo sapiens)}

EYSSNTQQGRTSIVHLFEWRWVDIALECERYLAPKGFGGVQVSPPNENVAIHNPFRPWWERYQPVSYKLCTRSGNEDEFRNMVTRCNNVGVRIYVDAVINHMCGNAVSAGTSSTCGSYFNPGSRDFPAVPYSGWDFNDGKCKTGSGDIENYNDATQVRDCRLSGLLDLALGKDYVRSKIAEYMNHLIDIGVAGFRIDASKHMWPGDIKAILDKLHNLNSNWFPEGSKPFIYQEVIDLGGEPIKSSDYFGNGRVTEFKYGAKLGTVIRKWNGEKMSYLKNWGEGWGFMPSDRALVFVDNHDNQRGHGAGGASILTFWDARLYKMAVGFMLAHPYGFTRVMSSYRWPRYFENGKDVNDWVGPPNDNGVTKEVTINPDTTCGNDWVCEHRWRQIRNMVNFRNVVDG

>d1jae\_2 c.1.8.1 (1-378) Animal alpha-amylase {Yellow mealworm (Tenebrio molitor), larva}

EKDANFASGRNSIVHLFEWKWNDIADECERFLQPQGFGGVQISPPNEYLVADGRPWWERYQPVSYIINTRSGDESAFTDMTRRCNDAGVRIYVDAVINHMTGMNGVGTSGSSADHDGMNYPAVPYGSGDFHSPCEVNNYQDADNVRNCELVGLRDLNQGSDYVRGVLIDYMNHMIDLGVAGFRVDAAKHMSPGDLSVIFSGLKNLNTDYGFADGARPFIYQEVIDLGGEAISKNEYTGFGCVLEFQFGVSLGNAFQGGNQLKNLANWGPEWGLLEGLDAVVFVDNHDNQRTGGSQILTYKNPKPYKMAIAFMLAHPYGTTRIMSSFDFTDNDQGPPQDGSGNLISPGINDDNTCSNGYVCEHRWRQVYGMVGFRNAVE

>d2aaa\_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus niger, acid amylase}

LSAASWRTQSIYFLLTDRFGRTDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAIWISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVPDHMGYAGNGNDVDYSVFDPFDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTTETAVRTIWYDWVADLVSNYSVDGLRIDSVLEVQPDFFPGYNKASGVYCVGEIDNGNPASDCPYQKVLDGVLNYPIYWQLLYAFESSSGSISNLYNMIKSVASDCSDPTLLGNFIENHDNPRFAKYTSDYSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAELYTWIATTNAIRKLAIAADSAYIT

>d7taa\_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus oryzae, Taka-amylase}

ATPADWRSQSIYFLLTDRFARTDGSTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAYGDAYHGYWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVVANHMGYDGAGSSVDYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGDNTVSLPDLDTTKDVVKNEWYDWVGSLVSNYSIDGLRIDTVKHVQKDFWPGYNKAAGVYCIGEVLDGDPAYTCPYQNVMDGVLNYPIYYPLLNAFKSTSGSMDDLYNMINTVKSDCPDSTLLGTFVENHDNPRFASYTNDIALAKNVAAFIILNDGIPIIYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVT

>d1smaa3 c.1.8.1 (A:124-505) Maltogenic amylase, central domain {Thermus sp.}

DLFQAPDWVKDTVWYQIFPERFANGNPAISPKGARPWGSEDPTPTSFFGGDLQGIIDHLDYLADLGITGIYLTPIFRAPSNHKYDTADYFEIDPHFGDKETLKTLVKRCHEKGIRVMLDAVFNHCGYEFAPFQDVLKNGAASRYKDWFHIREFPLQTEPRPNYDTFAFVPHMPKLNTAHPEVKRYLLDVATYWIREFDIDGWRLDVANEIDHQFWREFRQAVKALKPDVYILGEIWHDAMPWLRGDQFDAVMNYPLADAALRFFAKEDMSASEFADRLMHVLHSYPKQVNEAAFNLLGSHDTPRLLTVCGGDVRKVKLLFLFQLTFTGSPCIYYGDEIGMTGGNDPECRKCMVWDPEKQNKELYEHVKQLIALRKQYRALRR

>d1bvza3 c.1.8.1 (A:121-502) Maltogenic amylase, central domain {Thermoactinomyces vulgaris, TVAII}

VFTTPEWAKEAVIYQIFPERFANGDPSNDPPGTEQWAKDARPRHDSFYGGDLKGVIDRLPYLEELGVTALYFTPIFASPSHHKYDTADYLAIDPQFGDLPTFRRLVDEAHRRGIKIILDAVFNHAGDQFFAFRDVLQKGEQSRYKDWFFIEDFPVSKTSRTNYETFAVQVPAMPKLRTENPEVKEYLFDVARFWMEQGIDGWRLDVANEVDHAFWREFRRLVKSLNPDALIVGEIWHDASGWLMGDQFDSVMNYLFRESVIRFFATGEIHAERFDAELTRARMLYPEQAAQGLWNLLDSHDTERFLTSCGGNEAKFRLAVLFQMTYLGTPLIYYGDEIGMAGATDPDCRRPMIWEEKEQNRGLFEFYKELIRLRHRLASLTR

>d1eh9a3 c.1.8.1 (A:91-490) Glycosyltrehalose trehalohydrolase, central domain {Archaeon Sulfolobus solfataricus, km1}

FNNETFLKKEDLIIYEIHVGTFTPEGTFEGVIRKLDYLKDLGITAIEIMPIAQFPGKRDWGYDGVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYWIKEYNVDGFRLDAVHAIIDTSPKHILEEIADVVHKYNRIVIAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRRKTHGEPVGELDGCNFVVYIQNHDQVGNRGKGERIIKLVDRESYKIAAALYLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKENGQDTDPQDESTFNASKLSWKIDEEIFSFYKILIKMRKELSIA

>d1bf2\_3 c.1.8.1 (163-637) Isoamylase, central domain {Pseudomonas amyloderamosa}

PSTQSTGTKPTRAQKDDVIYEVHVRGFTEQDTSIPAQYRGTYYGAGLKASYLASLGVTAVEFLPVQETQNDANDVVPNSDANQNYWGYMTENYFSPDRRYAYNKAAGGPTAEFQAMVQAFHNAGIKVYMDVVYNHTAEGGTWTSSDPTTATIYSWRGLDNATYYELTSGNQYFYDNTGIGANFNTYNTVAQNLIVDSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCPNGGYNFDAADSNVAINRILREFTVRPAAGGSGLDLFAEPWAIGGNSYQLGGFPQGWSEWNGLFRDSLRQAQNELGSMTIYVTQDANDFSGSSNLFQSSGRSPWNSINFIDVHDGMTLKDVYSCNGANNSQAWPYGPSDGGTSTNYSWDQGMSAGTGAAVDQRRAARTGMAFEMLSAGTPLMQGGDEYLRTLQCNNNAYNLDSSANWLTYSWTTDQSNFYTFAQRLIAFRKAHPALRPSSW

>d1gcya2 c.1.8.1 (A:1-357) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase) {Pseudomonas stutzeri}

DQAGKSPNAVRYHGGDEIILQGFHWNVVREAPNDWYNILRQQAATIAADGFSAIWMPVPWRDFSSWSDGSKSGGGEGYFWHDFNKNGRYGSDAQLRQAASALGGAGVKVLYDVVPNHMNRGYPDKEINLPAGQGFWRNDCADPGNYPNDCDDGDRFIGGDADLNTGHPQVYGMFRDEFTNLRSQYGAGGFRFDFVRGYAPERVNSWMTDSADNSFCVGELWKGPSEYPNWDWRNTASWQQIIKDWSDRAKCPVFDFALKERMQNGSIADWKHGLNGNPDPRWREVAVTFVDNHDTGYSPGQNGGQHHWALQDGLIRQAYAYILTSPGTPVVYWDHMYDWGYGDFIRQLIQVRRAAGV

>d1avaa2 c.1.8.1 (A:1-346) Plant alpha-amylase {Barley (Hordeum vulgare), seeds, AMY2 isozyme}

QVLFQGFNWESWKHNGGWYNFLMGKVDDIAAAGITHVWLPPASQSVAEQGYMPGRLYDLDASKYGNKAQLKSLIGALHGKGVKAIADIVINHRTAEHKDGRGIYCIFEGGTPDARLDWGPHMICRDDRPYADGTGNPDTGADFGAAPDIDHLNLRVQKELVEWLNWLKADIGFDGWRFDFAKGYSADVAKIYIDRSEPSFAVAEIWTSLAYGGDGKPNLNQDQHRQELVNWVDKVGGKGPATTFDFTTKGILNVAVEGELWRLRGTDGKAPGMIGWWPAKAVTFVDNHDTGSTQHMWPFPSDRVMQGYAYILTHPGTPCIFYDHFFDWGLKEEIDRLVSVRTRHGI

>d1uok\_2 c.1.8.1 (1-479) Oligo-1,6, glucosidase {Bacillus cereus}

MEKQWWKESVVYQIYPRSFMDSNGDGIGDLRGIISKLDYLKELGIDVIWLSPVYESPNDDNGYDISDYCKIMNEFGTMEDWDELLHEMHERNMKLMMDLVVNHTSDEHNWFIESRKSKDNKYRDYYIWRPGKEGKEPNNWGAAFSGSAWQYDEMTDEYYLHLFSKKQPDLNWDNEKVRQDVYEMMKFWLEKGIDGFRMDVINFISKEEGLPTVETEEEGYVSGHKHFMNGPNIHKYLHEMNEEVLSHYDIMTVGEMPGVTTEEAKLYTGEERKELQMVFQFEHMDLDSGEGGKWDVKPCSLLTLKENLTKWQKALEHTGWNSLYWNNHDQPRVVSRFGNDGMYRIESAKMLATVLHMMKGTPYIYQGEEIGMTNVRFESIDEYRDIETLNMYKEKVMERGEDIEKVMQSIYIKGRDNARTPMQWDDQNHAGFTTGEPWITVNPNYKEINVKQAIQNKDSIFYYYKKLIELRKNNEIVVY

>d1g5aa2 c.1.8.1 (A:1-554) Amylosucrase {Neisseria polysaccharea}

SPNSQYLKTRILDIYTPEQRAGIEKSEDWRQFSRRMDTHFPKLMNELDSVYGNNEALLPMLEMLLAQAWQSYSQRNSSLKDIDIARENNPDWILSNKQVGGVCYVDLFAGDLKGLKDKIPYFQELGLTYLHLMPLFKCPEGKSDGGYAVSSYRDVNPALGTIGDLREVIAALHEAGISAVVDFIFNHTSNEHEWAQRCAAGDPLFDNFYYIFPDRRMPDQYDRTLREIFPDQHPGGFSQLEDGRWVWTTFNSFQWDLNYSNPWVFRAMAGEMLFLANLGVDILRMDAVAFIWKQMGTSCENLPQAHALIRAFNAVMRIAAPAVFFKSEAIVHPDQVVQYIGQDECQIGYNPLQMALLWNTLATREVNLLHQALTYRHNLPEHTAWVNYVRSHDDIGWTFADEDAAYLGISGYDHRQFLNRFFVNRFDGSFARGVPFQYNPSTGDCRVSGTAAALVGLAQDDPHAVDRIKLLYSIALSTGGLPLIYLGDEVGTLNDDDWSQDSNKSDDSRWAHRPRYNEALYAQRNDPSTAAGQIYQDLRHMIAVRQSNPRFDGG

>d1eswa\_ c.1.8.1 (A:) Amylomaltase MalQ {Thermus aquaticus}

MELPRAFGLLLHPTSLPGPYGVGVLGREARDFLRFLKEAGGRYWQVLPLGPTGYGDSPYQSFSAFAGNPYLIDLRPLAERGYVRLEDPGFPQGRVDYGLLYAWKWPALKEAFRGFKEKASPEEREAFAAFREREAWWLEDYALFMALKGAHGGLPWNRWPLPLRKREEKALREAKSALAEEVAFHAFTQWLFFRQWGALKAEAEALGIRIIGDMPIFVAEDSAEVWAHPEWFHLDEEGRPTVVAGVPPDYFSETGQRWGNPLYRWDVLEREGFSFWIRRLEKALELFHLVRIDHFRGFEAYWEIPASCPTAVEGRWVKAPGEKLFQKIQEVFGEVPVLAEDLGVITPEVEALRDRFGLPGMKVLQFAFDDGMENPFLPHNYPAHGRVVVYTGTHDNDTTLGWYRTATPHEKAFMARYLADWGITFREEEEVPWALMHLGMKSVARLAVYPVQDVLALGSEARMNYPGRPSGNWAWRLLPGELSPEHGARLRAMAEATERL

>d1byb\_\_ c.1.8.2 (-) beta-Amylase {Soybean (Glycine max)}

SNMLLNYVPVYVMLPLGVVNVDNVFEDPDGLKEQLLQLRAAGVDGVMVDVWWGIIELKGPKQYDWRAYRSLFQLVQECGLTLQAIMSFHQCGGNVGDIVNIPIPQWVLDIGESNHDIFYTNRSGTRNKEYLTVGVDNEPIFHGRTAIEIYSDYMKSFRENMSDFLESGLIIDIEVGLGPAGELRYPSYPQSQGWEFPRIGEFQCYDKYLKADFKAAVARAGHPEWELPDDAGKYNDVPESTGFFKSNGTYVTEKGKFFLTWYSNKLLNHGDQILDEANKAFLGCKVKLAIKVSGIHWWYKVENHAAELTAGYYNLNDRDGYRPIARMLSRHHAILNFTCLEMRDSEQPSDAKSGPQELVQQVLSGGWREDIRVAGENALPRYDATAYNQIILNAKPQGVNNNGPPKLSMFGVTYLRLSDDLLQKSNFNIFKKFVLKMHADQDYCANPQKYNHAITPLKPSAPKIPIEVLLEATKPTLPFPWLPETDMKVDG

>d1b1ya\_ c.1.8.2 (A:) beta-Amylase {Barley (Hordeum vulgare)}

MKGNYVQVYVMLPLDAVSVNNRFEKGDELRAQLRKLVEAGVDGVMVDVWWGLVEGKGPKAYDWSAYKQLFELVQKAGLKLQAIMSFHQCGGNVGDAVNIPIPQWVRDVGTRDPDIFYTDGHGTRNIEYLTLGVDNQPLFHGRSAVQMYADYMTSFRENMKDFLDAGVIVDIEVGLGPAGELRYPSYPQSHGWSFPGIGEFICYDKYLQADFKAAAAAVGHPEWEFPNDAGQYNDTPERTQFFRDNGTYLSEKGRFFLAWYSNNLIKHGDRILDEANKVFLGYKVQLAIKIAGVHWWYKVPSHAAELTAGYYNLHDRDGYRTIARMLKRHRASINFTCAEMRDSEQPPDAMSAPEELVQQVLSAGWREGLNVSCENALPRYDPTAYNTILRNARPHGINQSGPPEHKLFGFTYLRLSNQLVEGQNYVNFKTFVDRMHANLPRDPYVDPMAPLPRSGPEISIEMILQAAQPKIQPFPFQEHTDLPVGPTGGMGGQAEGPTCG

>d1fa2a\_ c.1.8.2 (A:) beta-Amylase {Sweet potato (Ipomoea batatas)}

APIPGVMPIGNYVSLYVMLPLGVVNADNVFPDKEKVEDELKQVKAGGCDGVMVDVWWGIIEAKGPKQYDWSAYRELFQLVKKCGLKIQAIMSFHQCGGNVGDAVFIPIPQWILQIGDKNPDIFYTNRAGNRNQEYLSLGVDNQRLFQGRTALEMYRDFMESFRDNMADFLKAGDIVDIEVGCGAAGELRYPSYPETQGWVFPGIGEFQCYDKYMVADWKEAVKQAGNADWEMPGKGAGTYNDTPDKTEFFRPNGTYKTDMGKFFLTWYSNKLIIHGDQVLEEANKVFVGLRVNIAAKVSGIHWWYNHVSHAAELTAGFYNVAGRDGYRPIARMLARHHATLNFTCLEMRDSEQPAEAKSAPQELVQQVLSSGWKEYIDVAGENALPRYDATAYNQMLLKLRPNGVNLNGPPKLKMSGLTYLRLSDDLLQTDNFELFKKFVKKMHADLDPSPNAISPAVLERSNSAITIDELMEATKGSRPFPWYDVTDMPVDGSNPFD

>d1b9za2 c.1.8.2 (A:1-417) Bacterial beta-amylase, catalytic domain {Bacillus cereus}

AVNGKGMNPDYKAYLMAPLKKIPEVTNWETFENDLRWAKQNGFYAITVDFWWGDMEKNGDQQFDFSYAQRFAQSVKNAGMKMIPIISTHQCGGNVGDDCNVPIPSWVWNQKSDDSLYFKSETGTVNKETLNPLASDVIRKEYGELYTAFAAAMKPYKDVIAKIYLSGGPAGELRYPSYTTSDGTGYPSRGKFQAYTEFAKSKFRLWVLNKYGSLNEVNKAWGTKLISELAILPPSDGEQFLMNGYLSMYGKDYLEWYQGILENHTKLIGELAHNAFDTTFQVPIGAKIAGVHWQYNNPTIPHGAEKPAGYNDYSHLLDAFKSAKLDVTFTCLEMTDKGSYPEYSMPKTLVQNIATLANEKGIVLNGENALSIGNEEEYKRVAEMAFNYNFAGFTLLRYQDVMYNNSLMGKFKDLLGV

>d1xyza\_ c.1.8.3 (A:) Xylanase {Clostridium thermocellum, XynZ}

NALRDYAEARGIKIGTCVNYPFYNNSDPTYNSILQREFSMVVCENEMKFDALQPRQNVFDFSKGDQLLAFAERNGMQMRGHTLIWHNQNPSWLTNGNWNRDSLLAVMKNHITTVMTHYKGKIVEWDVANECMDDSGNGLRSSIWRNVIGQDYLDYAFRYAREADPDALLFYNDYNIEDLGPKSNAVFNMIKSMKERGVPIDGVGFQCHFINGMSPEYLASIDQNIKRYAEIGVIVSFTEIDIRIPQSENPATAFQVQANNYKELMKICLANPNCNTFVMWGFTDKYTWIPGTFPGYGNPLIYDSNYNPKPAYNAIKEALM

>d1hiza\_ c.1.8.3 (A:) Xylanase {Bacillus stearothermophilus, Xt6}

SYAKKPHISALNAPQLDQRYKNEFTIGAAVEPYQLQNEKDVQMLKRHFNSIVAENVMKPISIQPEEGKFNFEQADRIVKFAKANGMDIRFHTLVWHSQVPQWFFLDKEGKPMVNETDPVKREQNKQLLLKRLETHIKTIVERYKDDIKYWDVVNEVVGDDGKLRNSPWYQIAGIDYIKVAFQAARKYGGDNIKLYMNDYNTEVEPKRTALYNLVKQLKEEGVPIDGIGHQSHIQIGWPSEAEIEKTINMFAALGLDNQITELDVSMYGWPPRAYPTYDAIPKQKFLDQAARYDRLFKLYEKLSDKISNVTFWGIADNHTWLDSRADVYYDANGNVVVDPNAPYAKVEKGKGKDAPFVFGPDYKVKPAYWAIIDHK

>d1bg4\_\_ c.1.8.3 (-) Xylanase {Penicillium simplicissimum}

EASVSIDAKFKAHGKKYLGTIGDQYTLTKNTKNPAIIKADFGQLTPENSMKWDATEPNRGQFTFSGSDYLVNFAQSNGKLIRGHTLVWHSQLPGWVSSITDKNTLISVLKNHITTVMTRYKGKIYAWDVLNEIFNEDGSLRNSVFYNVIGEDYVRIAFETARSVDPNAKLYINDYNLDSAGYSKVNGMVSHVKKWLAAGIPIDGIGSQTHLGAGAGSAVAGALNALASAGTKEIAITELDIAGASSTDYVNVVNACLNQAKCVGITVWGVADPDSWRSSSSPLLFDGNYNPKAAYNAIANAL

>d1edg\_\_ c.1.8.3 (-) Endoglucanase CelA {Clostridium cellulolyticum}

MYDASLIPNLQIPQKNIPNNDGMNFVKGLRLGWNLGNTFDAFNGTNITNELDYETSWSGIKTTKQMIDAIKQKGFNTVRIPVSWHPHVSGSDYKISDVWMNRVQEVVNYCIDNKMYVILNTHHDVDKVKGYFPSSQYMASSKKYITSVWAQIAARFANYDEHLIFEGMNEPRLVGHANEWWPELTNSDVVDSINCINQLNQDFVNTVRATGGKNASRYLMCPGYVASPDGATNDYFRMPNDISGNNNKIIVSVHAYCPWNFAGLAMADGGTNAWNINDSKDQSEVTWFMDNIYNKYTSRGIPVIIGECGAVDKNNLKTRVEYMSYYVAQAKARGILCILWDNNNFSGTGELFGFFDRRSCQFKFPEIIDGMVKYAFGLIN

>d1ceo\_\_ c.1.8.3 (-) Endoglucanase CelC {Clostridium thermocellum}

MVSFKAGINLGGWISQYQVFSKEHFDTFITEKDIETIAEAGFDHVRLPFDYPIIESDDNVGEYKEDGLSYIDRCLEWCKKYNLGLVLDMHHAPGYRFQDFKTSTLFEDPNQQKRFVDIWRFLAKRYINEREHIAFELLNQVVEPDSTRWNKLMLECIKAIREIDSTMWLYIGGNNYNSPDELKNLADIDDDYIVYNFHFYNPFFFTHQKAHWSESAMAYNRTVKYPGQYEGIEEFVKNNPKYSFMMELNNLKLNKELLRKDLKPAIEFREKKKCKLYCGEFGVIAIADLESRIKWHEDYISLLEEYDIGGAVWNYKKMDFEIYNEDRKPVSQELVNILAR

>d1cz1a\_ c.1.8.3 (A:) Exo-beta-(1,3)-glucanase {Yeast (Candida albicans)}

AWDYDNNVIRGVNLGGWFVLEPYMTPSLFEPFQNGNDQSGVPVDEYHWTQTLGKEAALRILQKHWSTWITEQDFKQISNLGLNFVRIPIGYWAFQLLDNDPYVQGQVQYLEKALGWARKNNIRVWIDLHGAPGSQNGFDNSGLRDSYNFQNGDNTQVTLNVLNTIFKKYGGNEYSDVVIGIELLNEPLGPVLNMDKLKQFFLDGYNSLRQTGSVTPVIIHDAFQVFGYWNNFLTVAEGQWNVVVDHHHYQVFSGGELSRNINDHISVACNWGWDAKKESHWNVAGEWSAALTDCAKWLNGVNRGARYEGAYDNAPYIGSCQPLLDISQWSDEHKTDTRRYIEAQLDAFEYTGGWVFWSWKTENAPEWSFQTLTYNGLFPQPVTDRQFPNQCGFH

>d1ecea\_ c.1.8.3 (A:) Endocellulase E1 {Acidothermus cellulolyticus}

AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNYVVHGLWSRDYRSMLDQIKSLGYNTIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIGLRIILDRHRPDCSGQSALWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEPHDPACWGCGDPSIDWRLAAERAGNAVLSVNPNLLIFVEGVQSYNGDSYWWGGNLQGAGQYPVVLNVPNRLVYSAHDYATSVYPQTWFSDPTFPNNMPGIWNKNWGYLFNQNIAPVWLGEFGTTLQSTTDQTWLKTLVQYLRPTAQYGADSFQWTFWSWNPDSGDTGGILKDDWQTVDTVKDGYLAPIKSSIFDPV

>d7a3ha\_ c.1.8.3 (A:) Endoglucanase Cel5a {Bacillus agaradhaerens}

SVVEEHGQLSISNGELVNERGEQVQLKGMSSHGLQWYGQFVNYESMKWLRDDWGINVFRAAMYTSSGGYIDDPSVKEKVKEAVEAAIDLDIYVIIDWHILSDNDPNIYKEEAKDFFDEMSELYGDYPNVIYEIANEPNGSDVTWGNQIKPYAEEVIPIIRNNDPNNIIIVGTGTWSQDVHHAADNQLADPNVMYAFHFYAGTHGQNLRDQVDYALDQGAAIFVSEWGTSAATGDGGVFLDEAQVWIDFMDERNLSWANWSLTHKDESSAALMPGANPTGGWTEAELSPSGTFVREKIRES

>d1egza\_ c.1.8.3 (A:) Endoglucanase Cel5a {Erwinia chrysanthemi}

SVEPLSVNGNKIYAGEKAKSFAGNSLFWSNNGWGGEKFYTADTVASLKKDWKSSIVRAAMGVQESGGYLQDPAGNKAKVERVVDAAIANDMYAIIGWHSHSAENNRSEAIRFFQEMARKYGNKPNVIYEIYNEPLQVSWSNTIKPYAEAVISAIRAIDPDNLIIVGTPSWSQNVDEASRDPINAKNIAYTLHFYAGTHGESLRNKARQALNNGIALFVTEWGTVNADGNGGVNQTETDAWVTFMRDNNISNANWALNDKNEGASTYYPDSKNLTESGKKVKSIIQSWPYKA

>d1g0ca\_ c.1.8.3 (A:) Alkaline cellulase K catalytic domain {Bacillus sp.}

PAGMQAVKSPSEAGALQLVELNGQLTLAGEDGTPVQLRGMSTHGLQWFGEIVNENAFVALSNDWGSNMIRLAMYIGENGYATNPEVKDLVYEGIELAFEHDMYVIVDWHVHAPGDPRADVYSGAYDFFEEIADHYKDHPKNHYIIWELANEPSPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMILVGNPNWSQRPDLSADNPIDAENIMYSVHFYTGSHGASHIGYPEGTPSSERSNVMANVRYALDNGVAVFATEWGTSQANGDGGPYFDEADVWLNFLNKHNISWANWSLTNKNEISGAFTPFELGRTDATDLDPGANQVWAPEELSLSGEYVRARIKGIEYTPIDRTK

>d1bqca\_ c.1.8.3 (A:) Beta-mannanase {Thermomonospora fusca}

ATGLHVKNGRLYEANGQEFIIRGVSHPHNWYPQHTQAFADIKSHGANTVRVVLSNGVRWSKNGPSDVANVISLCKQNRLICMLEVHDTTGYGEQSGASTLDQAVDYWIELKSVLQGEEDYVLINIGNEPYGNDSATVAAWATDTSAAIQRLRAAGFEHTLVVDAPNWGQDWTNTMRNNADQVYASDPTGNTVFSIHMYGVYSQASTITSYLEHFVNAGLPLIIGEFGHDHSDGNPDEDTIMAEAERLKLGYIGWSWSGNGGGVEYLDMVYNFDGDNLSPWGERIFYGPNGIASTAKEAVIFG

>d1qnra\_ c.1.8.3 (A:) Beta-mannanase {Trichoderma reesei}

ASSFVTISGTQFNIDGKVGYFAGTNCYWCSFLTNHADVDSTFSHISSSGLKVVRVWGFNDVNTQPSPGQIWFQKLSATGSTINTGADGLQTLDYVVQSAEQHNLKLIIPFVNNWSDYGGINAYVNAFGGNATTWYTNTAAQTQYRKYVQAVVSRYANSTAIFAWELGNEPRCNGCSTDVIVQWATSVSQYVKSLDSNHLVTLGDEGLGLSTGDGAYPYTYGEGTDFAKNVQIKSLDFGTFHLYPDSWGTNYTWGNGWIQTHAAACLAAGKPCVFEEYGAQQNPCTNEAPWQTTSLTTRGMGGDMFWQWGDTFANGAQSNSDPYTVWYNSSNWQCLVKNHVDAIN

>d1j9ya\_ c.1.8.3 (A:) Mannanase 26A {Pseudomonas fluorescens, subsp. cellulosa}

PVTVKLVDSQATMETRSLFAFMQEQRRHSIMFGHQHETTQGLTITRTDGTQSDTFNAVGDFAAVYGWDTLSIVAPKAEGDIVAQVKKAYARGGIITVSSHFDNPKTDTQKGVWPVGTSWDQTPAVVDSLPGGAYNPVLNGYLDQVAEWANNLKDEQGRLIPVIFRLYHENTGSWFWWGDKQSTPEQYKQLFRYSVEYLRDVKGVRNFLYAYSPNNFWDVTEANYLERYPGDEWVDVLGFDTYGPVADNADWFRNVVANAALVARMAEARGKIPVISEIGIRAPDIEAGLYDNQWYRKLISGLKADPDAREIAFLLVWRNAPQGVPGPNGTQVPHYWVPANRPENINNGTLEDFQAFYADEFTAFNRDIEQVYQRPT

>d1ghsa\_ c.1.8.3 (A:) Plant beta-glucanases {Barley (Hordeum vulgare), 1,3-beta-glucanase}

IGVCYGVIGNNLPSRSDVVQLYRSKGINGMRIYFADGQALSALRNSGIGLILDIGNDQLANIAASTSNAASWVQNNVRPYYPAVNIKYIAAGNEVQGGATQSILPAMRNLNAALSAAGLGAIKVSTSIRFDEVANSFPPSAGVFKNAYMTDVARLLASTGAPLLANVYPYFAYRDNPGSISLNYATFQPGTTVRDQNNGLTYTSLFDAMVDAVYAALEKAGAPAVKVVVSESGWPSAGGFAASAGNARTYNQGLINHVGGGTPKKREALETYIFAMFNENQKTGDATERSFGLFNPDKSPAYNIQF

>d1aq0a\_ c.1.8.3 (A:) Plant beta-glucanases {Barley (Hordeum vulgare), 1,3-1,4-beta-glucanase}

IGVCYGMSANNLPAASTVVSMFKSNGIKSMRLYAPNQAALQAVGGTGINVVVGAPNDVLSNLAASPAAAASWVKSNIQAYPKVSFRYVCVGNEVAGGATRNLVPAMKNVHGALVAAGLGHIKVTTSVSQAILGVFSPPSAGSFTGEAAAFMGPVVQFLARTNAPLMANIYPYLAWAYNPSAMDMGYALFNASGTVVRDGAYGYQNLFDTTVDAFYTAMGKHGGSSVKLVVSESGWPSGGGTAATPANARFYNQHLINHVGRGTPRHPGAIETYIFAMFNENQKDSGVEQNWGLFYPNMQHVYPINF

>d1jz8a5 c.1.8.3 (A:334-625) beta-Galactosidase, domain 3 {Escherichia coli}

EVRIENGLLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRCSHYPNHPLWYTLCDRYGLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRMVQRDRNHPSVIIWSLGNESGHGANHDALYRWIKSVDPSRPVQYEGGGADTTATDIICPMYARVDEDQPFPAVPKWSIKKWLSLPGETRPLILCQYAHAMGNSLGGFAKYWQAFRQYPRLQGGFVWDWVDQSLIKYDENGNPWSAYGGDFGDTPNDRQFCMNGLVFADRTPHPALTEAKHQQQ

>d1bhga3 c.1.8.3 (A:329-632) beta-Glucuronidase, domain 3 {Human (Homo sapiens)}

VAVTKSQFLINGKPFYFHGVNKHEDADIRGKGFDWPLLVKDFNLLRWLGANAFRTSHYPYAEEVMQMCDRYGIVVIDECPGVGLALPQFFNNVSLHHHMQVMEEVVRRDKNHPAVVMWSVANEPASHLESAGYYLKMVIAHTKSLDPSRPVTFVSNSNYAADKGAPYVDVICLNSYYSWYHDYGHLELIQLQLATQFENWYKKYQKPIIQSEYGAETIAGFHQDPPLMFTEEYQKSLLEQYHLGLDQKRRKYVVGELIWNFADFMTEQSPTRVLGNKKGIFTRQRQPKSAAFLLRERYWKIANE

>d1e0wa\_ c.1.8.3 (A:) Xylanase A, catalytic core {Streptomyces lividans}

AESTLGAAAAQSGRYFGTAIASGRLSDSTYTSIAGREFNMVTAENEMKIDATEPQRGQFNFSSADRVYNWAVQNGKQVRGHTLAWHSQQPGWMQSLSGSALRQAMIDHINGVMAHYKGKIVQWDVVNEAFADGSSGARRDSNLQRSGNDWIEVAFRTARAADPSAKLCYNDYNVENWTWAKTQAMYNMVRDFKQRGVPIDCVGFQSHFNSGSPYNSNFRTTLQNFAALGVDVAITELDIQGAPASTYANVTNDCLAVSRCLGITVWGVRDSDSWRSEQTPLLFNNDGSKKAAYTAVLDALNG

>d1clxa\_ c.1.8.3 (A:) Xylanase A, catalytic core {Pseudomonas fluorescens}

GLASLADFPIGVAVAASGGNADIFTSSARQNIVRAEFNQITAENIMKMSYMYSGSNFSFTNSDRLVSWAAQNGQTVHGHALVWHPSYQLPNWASDSNANFRQDFARHIDTVAAHFAGQVKSWDVVNEALFDSADDPDGRGSANGYRQSVFYRQFGGPEYIDEAFRRARAADPTAELYYNDFNTEENGAKTTALVNLVQRLLNNGVPIDGVGFQMHVMNDYPSIANIRQAMQKIVALSPTLKIKITELDVRLNNPYDGNSSNDYTNRNDCAVSCAGLDRQKARYKEIVQAYLEVVPPGRRGGITVWGIADPDSWLYTHQNLPDWPLLFNDNLQPKPAYQGVVEALS

>d1fxma\_ c.1.8.3 (A:) Xylanase A, catalytic core {Thermoascus aurantiacus}

QAAQSVDQLIKARGKVYFGVATDQNRLTTGKNAAIIQADFGQVTPENSMKWDATEPSQGNFNFAGADYLVNWAQQNGKLIRGHTLVWHSQLPSWVSSITDKNTLTNVMKNHITTLMTRYKGKIRAWDVVNEAFNEDGSLRQTVFLNVIGEDYIPIAFQTARAADPNAKLYINDYNLDSASYPKTQAIVNRVKQWRAAGVPIDGIGSQTHLSAGQGAGVLQALPLLASAGTPEVAITELDVAGASPTDYVNVVNACLNVQSCVGITVWGVADPDSWRASTTPLLFDGNFNPKPAYNAIVQDLQ

>d1tux\_\_ c.1.8.3 (-) Xylanase A, catalytic core {Thermoascus aurantiacus}

AAAQSVDQLIDARGKVYFGVATDQNRLTTGKNAAIIQADFGQVTPENSMKWDATEPSQGNFNFAGADYLVNWAQQNGKLIRGHTLVWHSQLPSWVVSITDKNTLTNVMKNHITTIMTRYIGKIRAWDVVNEAFNEDGSLRQTVFNNVIGEDYIPIAFRTARAADPNAKLYINDYNLDSASKPKTSAIVKRVKKWRAAGVPIDGIGSQTHLSAGQGASIDAALPNLASAGTPEVAITELDIAGATSTDYVDVVNACLDVDSCIGITVWGVADPDSWRASTTPLLFDGNFNPKPAYNAIVQLL

>d1xyfa2 c.1.8.3 (A:1-303) Xylanase A, catalytic core {Streptomyces olivaceoviridis}

AESTLGAAAAQSGRYFGTAIASGKLGDSAYTTIASREFNMVTAENEMKIDATEPQRGQFNFSAGDRVYNWAVQNGKQVRGHTLAWHSQQPGWMQSLSGSTLRQAMIDHINGVMGHYKGKIAQWDVVNEAFSDDGSGGRRDSNLQRTGNDWIEVAFRTARAADPAAKLCYNDYNIENWTWAKTQGVYNMVRDFKQRGVPIDCVGFQSHFNSGSPYNSNFRTTLQNFAALGVDVAITELDIQGASSSTYAAVTNDCLAVSRCLGITVWGVRDTDSWRSGDTPLLFNGDGSKKAAYTAVLNALNGG

>d1fh9a\_ c.1.8.3 (A:) Xylanase A, catalytic core {Cellulomonas fimi}

ATTLKEAADGAGRDFGFALDPNRLSEAQYKAIADSEFNLVVAENAMKWDATEPSQNSFSFGAGDRVASYAADTGKELYGHTLVWHSQLPDWAKNLNGSAFESAMVNHVTKVADHFEGKVASWDVVNEAFADGGGRRQDSAFQQKLGNGYIETAFRAARAADPTAKLCINDYNVEGINAKSNSLYDLVKDFKARGVPLDCVGFQSHLIVGQVPGDFRQNLQRFADLGVDVRITELDIRMRTPSDATKLATQAADYKKVVQACMQVTRCQGVTVWGITDKYSWVPDVFPGEGAALVWDASYAKKPAYAAVMEAF

>d1e4mm\_ c.1.8.4 (M:) Plant beta-glucosidase (myrosinase) {White mustard (Sinapis alba)}

EITCQENLPFTCGNTDALNSSSFSSDFIFGVASSAYQIEGTIGRGLNIWDGFTHRYPNKSGPDHGNGDTTCDSFSYWQKDIDVLDELNATGYRFSIAWSRIIPRGKRSRGVNEKGIDYYHGLISGLIKKGITPFVTLFHWDLPQTLQDEYEGFLDPQIIDDFKDYADLCFEEFGDSVKYWLTINQLYSVPTRGYGSALDAPGRCSPTVDPSCYAGNSSTEPYIVAHHQLLAHAKVVDLYRKNYTHQGGKIGPTMITRWFLPYNDTDRHSIAATERMKEFFLGWFMGPLTNGTYPQIMIDTVGERLPSFSPEESNLVKGSYDFLGLNYYFTQYAQPSPNPVNSTNHTAMMDAGAKLTYINASGHYIGPLFEKDKADSTDNIYYYPKGIYSVMDYFKNKYYNPLIYVTENGISTPGDENRNQSMLDYTRIDYLCSHLCFLNKVIKEKDVNVKGYLAWALGDNYEFNKGFTVRFGLSYIDWNNVTDRDLKKSGQWYQSFISP

>d1cbg\_\_ c.1.8.4 (-) Plant beta-glucosidase (myrosinase) {Creeping white clover (Trifolium repens)}

FKPLPISFDDFSDLNRSCFAPGFVFGTASSAFQYEGAAFEDGKGPSIWDTFTHKYPEKIKDRTNGDVAIDEYHRYKEDIGIMKDMNLDAYRFSISWPRVLPKGKLSGGVNREGINYYNNLINEVLANGMQPYVTLFHWDVPQALEDEYRGFLGRNIVDDFRDYAELCFKEFGDRVKHWITLNEPWGVSMNAYAYGTFAPGRCSDWLKLNCTGGDSGREPYLAAHYQLLAHAAAARLYKTKYQASQNGIIGITLVSHWFEPASKEKADVDAAKRGLDFMLGWFMHPLTKGRYPESMRYLVRKRLPKFSTEESKELTGSFDFLGLNYYSSYYAAKAPRIPNARPAIQTDSLINATFEHNGKPLGPMAASSWLCIYPQGIRKLLLYVKNHYNNPVIYITENGRNEFNDPTLSLQESLLDTPRIDYYYRHLYYVLTAIGDGVNVKGYFAWSLFDNMEWDSGYTVRFGLVFVDFKNNLKRHPKLSAHWFKSFLKK

>d1e55a\_ c.1.8.4 (A:) Plant beta-glucosidase (myrosinase) {Maize (Zea mays), zmglu1}

VQMLSPSEIPQRDWFPSDFTFGAATSAYQIEGAWNEDGKGESNWDHFCHNHPERILDGSNSDIGANSYHMYKTDVRLLKEMGMDAYRFSISWPRILPKGTKEGGINPDGIKYYRNLINLLLENGIEPYVTIFHWDVPQALEEKYGGFLDKSHKSIVEDYTYFAKVCFDNFGDKVKNWLTFNDPQTFTSFSYGTGVFAPGRCSPGLDCAYPTGNSLVEPYTAGHNILLAHAEAVDLYNKHYKRDDTRIGLAFDVMGRVPYGTSFLDKQAEERSWDINLGWFLEPVVRGDYPFSMRSLARERLPFFKDEQKEKLAGSYNMLGLNYYTSRFSKNIDISPNYSPVLNTDDAYASQEVNGPDGKPIGPPMGNPWIYMYPEGLKDLLMIMKNKYGNPPIYITENGIGDVDTKETPLPMEAALNDYKRLDYIQRHIATLKESIDLGSNVQGYFAWSLLDNFEWFAGFTERYGIVYVDRNNNCTRYMKESAKWLKEFNTA

>d1pbga\_ c.1.8.4 (A:) 6-phospho-beta-D-galactosidase, PGAL {Lactococcus lactis}

MTKTLPKDFIFGGATAAYQAEGATHTDGKGPVAWDKYLEDNYWYTAEPASDFYHKYPVDLELAEEYGVNGIRISIAWSRIFPTGYGEVNEKGVEFYHKLFAECHKRHVEPFVTLHHFDTPEALHSNGDFLNRENIEHFIDYAAFCFEEFPEVNYWTTFNEIGPIGDGQYLVGKFPPGIKYDLAKVFQSHHNMMVSHARAVKLYKDKGYKGEIGVVHALPTKYPYDPENPADVRAAELEDIIHNKFILDATYLGHYSDKTMEGVNHILAENGGELDLRDEDFQALDAAKDLNDFLGINYYMSDWMQAFDGETEIIHNGKGEKGSSKYQIKGVGRRVAPDYVPRTDWDWIIYPEGLYDQIMRVKNDYPNYKKIYITENGLGYKDEFVDNTVYDDGRIDYVKQHLEVLSDAIADGANVKGYFIWSLMDVFSWSNGYEKRYGLFYVDFDTQERYPKKSAHWYKKLAETQVIE

>d1e4ia\_ c.1.8.4 (A:) Beta-glucosidase A {Bacillus polymyxa}

TIFQFPQDFMWGTATAAYQIEGAYQEDGRGLSIWDTFAHTPGKVFNGDNGNVACDSYHRYEEDIRLMKELGIRTYRFSVSWPRIFPNGDGEVNQKGLDYYHRVVDLLNDNGIEPFCTLYHWDLPQALQDAGGWGNRRTIQAFVQFAETMFREFHGKIQHWLTFNEPWCIAFLSNMLGVHAPGLTNLQTAIDVGHHLLVAHGLSVRRFRELGTSGQIGIAPNVSWAVPYSTSEEDKAACARTISLHSDWFLQPIYQGSYPQFLVDWFAEQGATVPIQDGDMDIIGEPIDMIGINYYSMSVNRFNPEAGFLQSEEINMGLPVTDIGWPVESRGLYEVLHYLQKYGNIDIYITENGACINDEVVNGKVQDDRRISYMQQHLVQVHRTIHDGLHVKGYMAWSLLDNFEWAEGYNMRFGMIHVDFRTQVRTPKQSYYWYRNVVSNNWLETRR

>d1qoxa\_ c.1.8.4 (A:) Beta-glucosidase A {Bacillus circulans, subsp. alkalophilus}

SIHMFPSDFKWGVATAAYQIEGAYNEDGRGMSIWDTFAHTPGKVKNGDNGNVACDSYHRVEEDVQLLKDLGVKVYRFSISWPRVLPQGTGEVNRAGLDYYHRLVDELLANGIEPFCTLYHWDLPQALQDQGGWGSRITIDAFAEYAELMFKELGGKIKQWITFNEPWCMAFLSNYLGVHAPGNKDLQLAIDVSHHLLVAHGRAVTLFRELGISGEIGIAPNTSWAVPYRRTKEDMEACLRVNGWSGDWYLDPIYFGEYPKFMLDWYENLGYKPPIVDGDMELIHQPIDFIGINYYTSSMNRYNPGEAGGMLSSEAISMGAPKTDIGWEIYAEGLYDLLRYTADKYGNPTLYITENGACYNDGLSLDGRIHDQRRIDYLAMHLIQASRAIEDGINLKGYMEWSLMDNFEWAEGYGMRFGLVHVDYDTLVRTPKDSFYWYKGVISRGWLDL

>d1gowa\_ c.1.8.4 (A:) beta-Glycosidase {Archaeon Sulfolobus solfataricus}

MYSFPNSFRFGWSQAGFQSEMGTPGSEDPNTDWYKWVHDPENMAAGLVSGDLPENGPGYWGNYKTFHDNAQKMGLKIARLNSEWSRQFPNPLPRPQNFDESKQDVTEVEINENELKRLDEYANKDALNHYREIFKDLKSRGLYFIQNMYHWPLPLWLHDPIRVRRGDFTGPSGWLSTRTVYEFARFSAYTAWKFDDLVDEYSTMNEPNVVGGLGYVGVKSGFPPGYLSFELSRRAMYNIIQAHARAYDGIKSVSKKPVGIIYANSSFQPLTDKDMEAVEMAENDNRWWFFDAIIRGEITRGNEKIVRDDLKGRLDWIGVNYYTRTVVKRTEKGYVSLGGYGHGCERNSVSLAGLPTSDFGWEFFPEGLYDVLTKYWNRYHLYMYVTENGIADDADYQRPYYLVSHVYQVHRAINSGADVRGYLHWSLADNYEWASGFSMRFGLLKVDYNTKRLYWRPSALVYREIATNGAITDEIEHLNSVPPVKPLRH

>d1qvba\_ c.1.8.4 (A:) beta-Glycosidase {Archaeon Thermosphaera aggregans}

MKFPKDFMIGYSSSPFQFEAGIPGSEDPNSDWWVWVHDPENTAAGLVSGDFPENGPGYWNLNQNDHDLAEKLGVNTIRVGVEWSRIFPKPTFNVKVPVERDENGSIVHVDVDDKAVERLDELANKEAVNHYVEMYKDWVERGRKLILNLYHWPLPLWLHNPIMVRRMGPDRAPSGWLNEESVVEFAKYAAYIAWKMGELPVMWSTMNEPNVVYEQGYMFVKGGFPPGYLSLEAADKARRNMIQAHARAYDNIKRFSKKPVGLIYAFQWFELLEGPAEVFDKFKSSKLYYFTDIVSKGSSIINVEYRRDLANRLDWLGVNYYSRLVYKIVDDKPIILHGYGFLCTPGGISPAENPCSDFGWEVYPEGLYLLLKELYNRYGVDLIVTENGVSDSRDALRPAYLVSHVYSVWKAANEGIPVKGYLHWSLTDNYEWAQGFRQKFGLVMVDFKTKKRYLRPSALVFREIATHNGIPDELQHLTLIQ

>d2hvm\_\_ c.1.8.5 (-) Hevamine A (chitinase/lysozyme) {Para rubber tree (Hevea brasiliensis)}

GGIAIYWGQNGNEGTLTQTCSTRKYSYVNIAFLNKFGNGQTPQINLAGHCNPAAGGCTIVSNGIRSCQIQGIKVMLSLGGGIGSYTLASQADAKNVADYLWNNFLGGKSSSRPLGDAVLDGIDFDIEHGSTLYWDDLARYLSAYSKQGKKVYLTAAPQCPFPDRYLGTALNTGLFDYVWVQFYNNPPCQYSSGNINNIINSWNRWTTSINAGKIFLGLPAAPEAAGSGYVPPDVLISRILPEIKKSPKYGGVMLWSKFYDDKNGYSSSILDSV

>d1nar\_\_ c.1.8.5 (-) Seed storage protein {Vicia narbonensis, Narbonin}

PKPIFREYIGVKPNSTTLHDFPTEIINTETLEFHYILGFAIESYYESGKGTGTFEESWDVELFGPEKVKNLKRRHPEVKVVISIGGRGVNTPFDPAEENVWVSNAKESLKLIIQKYSDDSGNLIDGIDIHYEHIRSDEPFATLMGQLITELKKDDDLNINVVSIAPSENNSSHYQKLYNAKKDYINWVDYQFSNQQKPVSTDDAFVEIFKSLEKDYHPHKVLPGFSTDPLDTKHNKITRDIFIGGCTRLVQTFSLPGVFFWNANDSVIPKRDGDKPFIVELTLQQLLAA

>d1cnv\_\_ c.1.8.5 (-) Seed storage protein {Jack bean (Canavalia ensiformis), Concanavalin B}

DISSTEIAVYWGQREDGLLRDTCKTNNYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVALDGIHFDIQKPVDELNWDNLLEELYQIKDVYQSTFLLSAAPGCLSPDEYLDNAIQTRHFDYIFVRFYNDRSCQYSTGNIQRIRNAWLSWTKSVYPRDKNLFLELPASQATAPGGGYIPPSALIGQVLPYLPDLQTRYAGIALWNRQADKETGYSTNIIRYL

>d2ebn\_\_ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {Flavobacterium meningosepticum, endoglycosidase F1}

TTKANIKLFSFTEVNDTNPLNNLNFTLKNSGKPLVDMVVLFSANINYDAANDKVFVSNNPNVQHLLTNRAKYLKPLQDKGIKVILSILGNHDRSGIANLSTARAKAFAQELKNTCDLYNLDGVFFDDEYSAYQTPPPSGFVTPSNNAAARLAYETKQAMPNKLVTVYVYSRTSSFPTAVDGVNAGSYVDYAIHDYGGSYDLATNYPGLAKSGMVMSSQEFNQGRYATAQALRNIVTKGYGGHMIFAMDPNRSNFTSGQLPALKLIAKELYGDELVYSNTPYSKDW

>d1eoka\_ c.1.8.5 (A:) Endo-beta-N-acetylglucosaminidase {Flavobacterium meningosepticum, endoglycosidase F3}

NGVCIAYYITDGRNPTFKLKDIPDKVDMVILFGLKYWSLQDTTKLPGGTGMMGSFKSYKDLDTQIRSLQSRGIKVLQNIDDDVSWQSSKPGGFASAAAYGDAIKSIVIDKWKLDGISLDIEHSGAKPNPIPTFPGYAATGYNGWYSGSMAATPAFLNVISELTKYFGTTAPNNKQLQIASGIDVYAWNKIMENFRNNFNYIQLQSYGANVSRTQLMMNYATGTNKIPASKMVFGAYAEGGTNQANDVEVAKWTPTQGAKGGMMIYTYNSNVSYANAVRDAVK

>d1edt\_\_ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {Streptomyces plicatus, endoglycosidase H}

KQGPTSVAYVEVNNNSMLNVGKYTLADGGGNAFDVAVIFAANINYDTGTKTAYLHFNENVQRVLDNAVTQIRPLQQQGIKVLLSVLGNHQGAGFANFPSQQAASAFAKQLSDAVAKYGLDGVDFDDEYAEYGNNGTAQPNDSSFVHLVTALRANMPDKIISLYNIGPAASRLSYGGVDVSDKFDYAWNPYYGTWQVPGIALPKAQLSPAAVEIGRTSRSTVADLARRTVDEGYGVYLTYNLDGGDRTADVSAFTRELYGSEAVRT

>d1edqa2 c.1.8.5 (A:133-443,A:517-563) Chitinase A, catalytic domain {Serratia marcescens}

TDGSHLAPLKEPLLEKNKPYKQNSGKVVGSYFVEWGVYGRNFTVDKIPAQNLTHLLYGFIPICGGNGINDSLKEIEGSFQALQRSCQGREDFKVSIHDPFAALQKAQKGVTAWDDPYKGNFGQLMALKQAHPDLKILPSIGGWTLSDPFFFMGDKVKRDRFVGSVKEFLQTWKFFDGVDIDWEFPGGKGANPNLGSPQDGETYVLLMKELRAMLDQLSVETGRKYELTSAISAGKDKIDKVAYNVAQNSMDHIFLMSYDFYGAFDLKNLGHQTALNAPAWKPDTAYTTVNGVNALLAQGVKPGKIVVGTAMXDARSVQAKGKYVLDKQLGGLFSWEIDADNGDILNSMNASLGNSAGVQ

>d1goia2 c.1.8.5 (A:3-291,A:380-446) Chitinase B, catalytic domain {Serratia marcescens}

TRKAVIGYYFIPTNQINNYTETDTSVVPFPVSNITPAKAKQLTHINFSFLDINSNLECAWDPATNDAKARDVVNRLTALKAHNPSLRIMFSIGGWYYSNDLGVSHANYVNAVKTPASRAKFAQSCVRIMKDYGFDGVNIDWEYPQAAEVDGFIAALQEIRTLLNQQTITDGRQALPYQLTIAGAGGAFFLSRYYSKLAQIVAPLDYINLMTYDLAGPWEKVTNHQAALFGDAAGPTFYNALREANLGWSWEELTRAFPSPFSLTVDAAVQQHLMMEGVPSAKIVMGVPFXDDAESFKYKAKYIKQQQLGGVMFWHLGQDNRNGDLLAALDRYFNAADYDDSQLDMGTGLRYTGVGPG

>d1d2ka1 c.1.8.5 (A:36-292,A:355-427) Chitinase 1 {Fungus (Coccidioides immitis)}

GGFRSVVYFVNWAIYGRGHNPQDLKADQFTHILYAFANIRPSGEVYLSDTWADTDKHYPGDKWDEPGNNVYGCIKQMYLLKKNNRNLKTLLSIGGWTYSPNFKTPASTEEGRKKFADTSLKLMKDLGFDGIDIDWEYPEDEKQANDFVLLLKACREALDAYSAKHPNGKKFLLTIASPAGPQNYNKLKLAEMDKYLDFWNLMAYDFSGSWDKVSGHMSNVFPSTTKPESTPFSSDKAVKDYIKAGVPANKIVLGMPLXDTVKIAGKKAEYITKNGMGGGMWWESSSDKTGNESLVGTVVNGLGGTGKLEQRENELSYPESVYDNLKNGMPS

>d1e9la1 c.1.8.5 (A:22-266,A:337-393) Chitinase-like lectin ym1, saccharide binding domain {Mouse (Mus musculus)}

YQLMCYYTSWAKDRPIEGSFKPGNIDPCLCTHLIYAFAGMQNNEITYTHEQDLRDYEALNGLKDKNTELKTLLAIGGWKFGPAPFSAMVSTPQNRQIFIQSVIRFLRQYNFDGLNLDWQYPGSRGSPPKDKHLFSVLVKEMRKAFEEESVEKDIPRLLLTSTGAGIIDVIKSGYKIPELSQSLDYIQVMTYDLHDPKDGYTGENSPLYKSPYDIGKSADLNVDSIISYWKDHGAASEKLIVGFPAXDNVRSFKLKAQWLKDNNLGGAVVWPLDMDDFSGSFCHQRHFPLTSTLKGDLNIHSAS

>d1jfxa\_ c.1.8.8 (A:) Streptomyces lysozyme {Streptomyces coelicolor, "mueller" dsm3030}

DTSGVQGIDVSHWQGSINWSSVKSAGMSFAYIKATEGTNYKDDRFSANYTNAYNAGIIRGAYHFARPNASSGTAQADYFASNGGGWSRDNRTLPGVLDIEHNPSGAMCYGLSTTQMRTWINDFHARYKARTTRDVVIYTTASWWNTCTGSWNGMAAKSPFWVAHWGVSAPTVPSGFPTWTFWQYSATGRVGGVSGDVDRNKFNGSAARLLALANNTA

>d1qba\_3 c.1.8.6 (338-780) Bacterial chitobiase (beta-N-acetylhexosaminidase) {Serratia marcescens}

FPYRGIFLDVARNFHKKDAVLRLLDQMAAYKLNKFHFHLSDDEGWRIEIPGLPELTEVGGQRCHDLSETTCLLPQYGQGPDVYGGFFSRQDYIDIIKYAQARQIEVIPEIDMPAHARAAVVSMEARYKKLHAAGKEQEANEFRLVDPTDTSNTTSVQFFNRQSYLNPCLDSSQRFVDKVIGEIAQMHKEAGQPIKTWHFGGDEAKNIRLGAGYTDKAKPEPGKGIIDQGNEDKPWAKSQVCQTMIKEGKVADMEHLPSYFGQEVSKLVKAHGIDRMQAWQDGLKDAESSKAFATSRVGVNFWDTLYWGGFDSVNDWANKGYEVVVSNPDYVYMDFPYEVNPDERGYYWGTRFSDERKVFSFAPDNMPQNAETSVDRDGNHFNAKSDKPWPGAYGLSAQLWSETQRTDPQMEYMIFPRALSVAERSWHRAGWEQDYRAGREYKG

>d1jaka1 c.1.8.6 (A:151-506) beta-N-acetylhexosaminidase {Streptomyces plicatus}

YAWRSAMLDVSRHFFGVDEVKRYIDRVARYKYNKLHLHLSDDQGWRIAIDSWPRLATYGGSTEVGGGPGGYYTKAEYKEIVRYAASRHLEVVPEIDMPGHTNAALASYAELNCDGVAPPLYTGTKVGFSSLCVDKDVTYDFVDDVIGELAALTPGRYLHIGGDEAHSTPKADFVAFMKRVQPIVAKYGKTVVGWHQLAGAEPVEGALVQYWGLDRTGDAEKAEVAEAARNGTGLILSPADRTYLDMKYTKDTPLGLSWAGYVEVQRSYDWDPAGYLPGAPADAVRGVEAPLWTETLSDPDQLDYMAFPRLPGVAELGWSPASTHDWDTYKVRLAAQAPYWEAAGIDFYRSPQVPWT

>d1iexa1 c.1.8.7 (A:1-388) Beta-D-glucan exohydrolase, N-terminal domain {Barley (Hordeum vulgare)}

DYVLYKDATKPVEDRVADLLGRMTLAEKIGQMTQIERLVATPDVLRDNFIGSLLSGGGSVPRKGATAKEWQDMVDGFQKACMSTRLGIPMIYGIDAVHGQNNVYGATIFPHNVGLGATRDPYLVKRIGEATALEVRATGIQYAFAPCIAVCRDPRWGRCYESYSEDRRIVQSMTELIPGLQGDVPKDFTSGMPFVAGKNKVAACAKHFVGDGGTVDGINENNTIINREGLMNIHMPAYKNAMDKGVSTVMISYSSWNGVKMHANQDLVTGYLKDTLKFKGFVISDWEGIDRITTPAGSDYSYSVKASILAGLDMIMVPNKYQQFISILTGHVNGGVIPMSRIDDAVTRILRVKFTMGLFENPYADPAMAEQLGKQEHRDLAREAARKS

>d1fcqa\_ c.1.8.9 (A:) Bee venom hyaluronidase {Honeybee (Apis mellifera)}

EFNVYWNVPTFMCHKYGLRFEEVSEKYGILQNWMDKFRGEEIAILYDPGMFPALLKDPNGNVVARNGGVPQLGNLTKHLQVFRDHLINQIPDKSFPGVGVIDFESWRPIFRQNWASLQPYKKLSVEVVRREHPFWDDQRVEQEAKRRFEKYGQLFMEETLKAAKRMRPAANWGYYAYPYCYNLTPNQPSAQCEATTMQENDKMSWLFESEDVLLPSVYLRWNLTSGERVGLVGGRVKEALRIARQMTTSRKKVLPYYWYKYQDRRDTDLSRADLEATLRKITDLGADGFIIWGSSDDINTKAKCLQFREYLNNELGPAVKR

>d1a4ma\_ c.1.9.1 (A:) Adenosine deaminase (ADA) {Mouse (Mus musculus)}

TPAFNKPKVELHVHLDGAIKPETILYFGKKRGIALPADTVEELRNIIGMDKPLSLPGFLAKFDYYMPVIAGCREAIKRIAYEFVEMKAKEGVVYVEVRYSPHLLANSKVDPMPWNQTEGDVTPDDVVDLVNQGLQEGEQAFGIKVRSILCCMRHQPSWSLEVLELCKKYNQKTVVAMDLAGDETIEGSSLFPGHVEAYEGAVKNGIHRTVHAGEVGSPEVVREAVDILKTERVGHGYHTIEDEALYNRLLKENMHFEVCPWSSYLTGAWDPKTTHAVVRFKNDKANYSLNTDDPLIFKSTLDTDYQMTKKDMGFTEEEFKRLNINAAKSSFLPEEEKKELLERLYREYQ

>d1j79a\_ c.1.9.4 (A:) Dihydroorotase {Escherichia coli}

SQVLKIRRPDDWHLHLRDGDMLKTVVPYTSEIYGRAIVMPNLAPPVTTVEAAVAYRQRILDAVPAPHDFTPLMTCYLTDSLDPNELERGFNEGVFTAAKLYPANATTNSSHGVTSVDAIMPVLERMEKIGMPLLVHGEVTHADIDIFDREARFIESVMEPLRQRLTALKVVFEHITTKDAADYVRDGNERLAATITPQHLMFNRNHMLVGGVRPHLYCLPILKRNIHQQALRELVASGFQRVFLGTDSAPHARHRKESSCGCAGCFNAPTALGSYATVFEEMNALQHFEAFCSVNGPQFYGLPVNDTFIELVREEQQVAESIALTDDTLVPFLAGETVRWSVK

>d1k6wa2 c.1.9.5 (A:56-375) Cytosine deaminase catalytic domain {Escherichia coli}

PFVEPHIHLDTTQTAGQPNWNQSGTLFEGIERWAERKALLTHDDVKQRAWQTLKWQIANGIQHVRTHVDVSDATLTALKAMLEVKQEVAPWIDLQIVAFPQEGILSYPNGEALLEEALRLGADVVGAIPHFEFTREYGVESLHKTFALAQKYDRLIDVHCDEIDDEQSRFVETVAALAHHEGMGARVTASHTTAMHSYNGAYTSRLFRLLKMSGINFVANPLVNIHLQGRFDTYPKRRGITRVKEMLESGINVCFGHDDVFDPWYPLGTANMLQVLHMGLHVCQLMGYGQINDGLNLITHHSARTLNLQDYGIAAGNSAN

>d1ejrc2 c.1.9.2 (C:1130-1422,C:1476-1567) alpha-subunit of urease, catalytic domain {Klebsiella aerogenes}

GIDTHIHWICPQQAEEALVSGVTTMVGGGTGPAAGTHATTCTPGPWYISRMLQAADSLPVNIGLLGKGNVSQPDALREQVAAGVIGLKIHEAWGATPAAIDCALTVADEMDIQVALHSDTLNESGFVEDTLAAIGGRTIHTFHTEGAGGGHAPDIITACAHPNILPSSTNPTLPYTLNTIDEHLDMLMVCHHLDPDIAEDVAFAESRIRRETIAAEDVLHDLGAFSLTSSDSQAMGRVGEVILRTWQVAHRMKVQRGALAEETGDNDNFRVKRYIAKYTINPALTHGIAHEVGXMFGALGSARHHCRLTFLSQAAAANGVAERLNLRSAIAVVKGCRTVQKADMVHNSLQPNITVDAQTYEVRVDGELITSEPADVLPMAQRYFLF

>d4ubpc2 c.1.9.2 (C:132-434,C:484-570) alpha-subunit of urease, catalytic domain {Bacillus pasteurii}

GGIDTHVHFINPDQVDVALANGITTLFGGGTGPAEGSKATTVTPGPWNIEKMLKSTEGLPINVGILGKGHGSSIAPIMEQIDAGAAGLKIHEDWGATPASIDRSLTVADEADVQVAIHSDTLNEAGFLEDTLRAINGRVIHSFHVEGAGGGHAPDIMAMAGHPNVLPSSTNPTRPFTVNTIDEHLDMLMVCHHLKQNIPEDVAFADSRIRPETIAAEDILHDLGIISMMSTDALAMGRAGEMVLRTWQTADKMKKQRGPLAEEKNGSDNFRLKRYVSKYTINPAIAQGIAHEVGSIEEGKFADXGDLIHDTNITFMSKSSIQQGVPAKLGLKRRIGTVKNCRNIGKKDMKWNDVTTDIDINPETYEVKVDGEVLTCEPVKELPMAQRYFLF

>d1e9yb2 c.1.9.2 (B:132-431,B:481-569) alpha-subunit of urease, catalytic domain {Helicobacter pylori}

GIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRRNLKWMLRAAEEYSMNLGFLAKGNASNDASLADQIEAGAIGFKIHEDWGTTPSAINHALDVADKYDVQVAIHTDTLNEAGCVEDTMAAIAGRTMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNPTIPFTVNTEAEHMDMLMVCHHLDKSIKEDVQFADSRIRPQTIAAEDTLHDMGAFSITSSDSQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEYVGSVEVGKVXHHGKAKYDANITFVSQAAYDKGIKEELGLERQVLPVKNCRNVTKKDMQFNNTTAHIEVNPETYHVFVDGKEVTSKPANKVSLAQLFSIF

>d1i0da\_ c.1.9.3 (A:) Phosphotriesterase {Pseudomonas diminuta}

DRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFDPPLSMRLRSVEELTQFFLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGEQQAAIFESEGLSPSRVCIGHSDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASASALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIPLRVIPFLREKGVPQETLAGITVTNPARFLSPTLRAS

>d1bf6a\_ c.1.9.3 (A:) Phosphotriesterase homology protein {Escherichia coli}

SFDPTGYTLAHEHLHIDLSGFKNNVDCRLDQYAFICQEMNDLMTRGVRNVIEMTNRYMGRNAQFMLDVMRETGINVVACTGYYQDAFFPEHVATRSVQELAQEMVDEIEQGIDGTELKAGIIAEIGTSEGKITPLEEKVFIAAALAHNQTGRPISTHTSFSTMGLEQLALLQAHGVDLSRVTVGHCDLKDNLDNILKMIDLGAYVQFDTIGKNSYYPDEKRIAMLHALRDRGLLNRVMLSMDITRRSHLKANGGYGYDYLLTTFIPQLRQSGFSQADVDVMLRENPSQFFQ

>d1jcla\_ c.1.10.1 (A:) Deoxyribose-phosphate aldolase DeoC {Escherichia coli}

HMTDLKASSLRALKLMDLTTLNDDDTDEKVIALCHQAKTPVGNTAAICIYPRFIPIARKTLKEQGTPEIRIATVTNFPHGNDDIDIALAETRAAIAYGADEVDVVFPYRALMAGNEQVGFDLVKACKEACAAANVLLKVIIETGELKDEALIRKASEISIKAGADFIKTSTGKVAVNATPESARIMMEVIRDMGVEKTVGFKPAGGVRTAEDAQKYLAIADELFGADWADARHYRFGASSLLASLLKALGHG

>d1nal1\_ c.1.10.1 (1:) N-acetylneuraminate lyase {Escherichia coli}

NLRGVMAALLTPFDQQQALDKASLRRLVQFNIQQGIDGLYVGGSTGEAFVQSLSEREQVLEIVAEEGKGKIKLIAHVGCVTTAESQQLAASAKRYGFDAVSAVTPFYYPFSFEEHCDHYRAIIDSADGLPMVVYNIPALSGVKLTLDQINTLVTLPGVGALKQTSGDLYQMEQIRREHPDLVLYNGYDEIFASGLLAGADGGIGSTYNIMGWRYQGIVKALKEGDIQTAQKLQTECNKVIDLLIKTGVFRGLKTVLHYMDVVSVPLCRKPFGPVDEKYQPELKALAQQLMQ

>d1f74a\_ c.1.10.1 (A:) N-acetylneuraminate lyase {Haemophilus influenzae}

MRDLKGIFSALLVSFNEDGTINEKGLRQIIRHNIDKMKVDGLYVGGSTGENFMLSTEEKKEIFRIAKDEAKDQIALIAQVGSVNLKEAVELGKYATELGYDCLSAVTPFYYKFSFPEIKHYYDTIIAETGSNMIVYSIPFLTGVNMGIEQFGELYKNPKVLGVKFTAGDFYLLERLKKAYPNHLIWAGFDEMMLPAASLGVDGAIGSTFNVNGVRARQIFELTKAGKLKEALEIQHVTNDLIEGILANGLYLTIKELLKLEGVDAGYCREPMTSKATAEQVAKAKDLKAKFLS

>d1dhpa\_ c.1.10.1 (A:) Dihydrodipicolinate synthase {Escherichia coli}

MFTGSIVAIVTPMDEKGNVCRASLKKLIDYHVASGTSAIVSVGTTGESATLNHDEHADVVMMTLDLADGRIPVIAGTGANATAEAISLTQRFNDSGIVGCLTVTPYYNRPSQEGLYQHFKAIAEHTDLPQILYNVPSRTGCDLLPETVGRLAKVKNIIGIKEATGNLTRVNQIKELVSDDFVLLSGDDASALDFMQLGGHGVISVTANVAARDMAQMCKLAAEGHFAEARVINQRLMPLHNKLFVEPNPIPVKWACKELGLVATDTLRLPMTPITDSGRETVRAALKHAGLL

>d1qo5b\_ c.1.10.1 (B:) Fructose-1,6-bisphosphate aldolase {Human (Homo sapiens), liver isozyme}

AHRFPALTQEQKKELSEIAQSIVANGKGILAADESVGTMGNRLQRIKVENTEENRRQFREILFSVDSSINQSIGGVILFHETLYQKDSQGKLFRNILKEKGIVVGIKLDQGGAPLAGTNKETTIQGLDGLSERCAQYKKDGVDFGKWRAVLRIADQCPSSLAIQENANALARYASICQQNGLVPIVEPEVIPDGDHDLEHCQYVTEKVLAAVYKALNDHHVYLEGTLLKPNMVTAGHACTKKYTPEQVAMATVTALHRTVPAAVPGICFLSGGMSEEDATLNLNAINLCPLPKPWKLSFSYGRALQASALAAWGGKAANKEATQEAFMKRAMANCQAAKGQYVHTGSS

>d1adoa\_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus), muscle isozyme}

PHSHPALTPEQKKELSDIAHRIVAPGKGILAADESTGSIAKRLQSIGTENTEENRRFYRQLLLTADDRVNPCIGGVILFHETLYQKADDGRPFPQVIKSKGGVVGIKVDKGVVPLAGTNGETTTQGLDGLSERCAQYKKDGADFAKWRCVLKIGEHTPSALAIMENANVLARYASICQQNGIVPIVEPEILPDGDHDLKRCQYVTEKVLAAVYKALSDHHIYLEGTLLKPNMVTPGHACTQKYSHEEIAMATVTALRRTVPPAVTGVTFLSGGQSEEEASINLNAINKCPLLKPWALTFSYGRALQASALKAWGGKKENLKAAQEEYVKRALANSLACQGKYTSSGQAGAAASESLFISNHAY

>d1fdja\_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus), liver isozyme}

AHRFPALTPEQKKELSDIAQRIVANGKGILAADESVGTMGNRLQRIKVENSEENRRQFREILFTVDNSINQSIGGVILFHETLYQKDSQGKLFRNILKEKGIVVGIKLDQGGAPLAGTNKETTIQGLDGLSERCAQYKKDGVDFGKWRAVLRIADQCPSSLAIQENANTLARYASICQQNGLVPIVEPEVIPDGDHDLEHCQYVTEKVLAAVYKALNDHHVYLEGTLLKPNMVTAGHACTKKYTPEQVAMATVTALHRTVPAAVPGICFLSGGMSEEDATLNLNAINLCPLPKPWKLSFSYGRALQASALAAWGGKAENKKATQEAFMKRAVVNCQAAKGQYVHTGSSGAASTQSLFTASYTY

>d1fbaa\_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Drosophila melanogaster}

TTYFNYPSKELQDELREIAQKIVAPGKGILAADESGPTMGKRLQDIGVENTEDNRRAYRQLLFSTDPKLAENISGVILFHETLYQKADDGTPFAEILKKKGIILGIKVDKGVVPLFGSEDEVTTQGLDDLAARCAQYKKDGCDFAKWRCVLKIGKNTPSYQSILENANVLARYASICQSQRIVPIVEPEVLPDGDHDLDRAQKVTETVLAAVYKALSDHHVYLEGTLLKPNMVTAGQSAKKNTPEEIALATVQALRRTVPAAVTGVTFLSGGQSEEEATVNLSAINNVPLIRPWALTFSYGRALQASVLRAWAGKKENIAAGQNELLKRAKANGDAAQGKYVAGSAGAGSGSLFVANHAY

>d1a5ca\_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Plasmodium falciparum}

LPADVAEELATTAQKLVQAGKGILAADESTQTIKKRFDNIKLENTIENRASYRDLLFGTKGLGKFISGAILFEETLFQKNEAGVPMVNLLHNENIIPGIKVDKGLVNIPCTDEEKSTQGLDGLAERCKEYYKAGARFAKWRTVLVIDTAKGKPTDLSIHETAWGLARYASICQQNRLVPIVEPEILADGPHSIEVCAVVTQKVLSCVFKALQENGVLLEGALLKPNMVTAGYECTAKTTTQDVGFLTVRTLRRTVPPALPGVVFLSGGQSEEEASVNLNSINALGPHPWALTFSYGRALQASVLNTWQGKKENVAKAREVLLQRAEANSLATYGKYKGGAGG

>d1epxa\_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (Leishmania mexicana)}

MSRVTVLQSQLPAYNRLKTPYESELIATVKKLTTPGKGLLAADESIGSCTKRFQPIGLSNTEEHRRQYRALMLEAEGFEQYISGVILHDETVGQKASNGQTFPEYLTARGVVPGIKTDMGLCPLLEGAEGEQMTEGLDGYVKRASAYYKKGCRFCKWRNVYKIQNGTVSESAVRFNAETLARYAILSQMSGLVPIVEPEVMIDGKHDIDTCQRVSEHVWREVVAALQRHGVIWEGCLLKPNMVVPGAESGKTAAPEQVAHYTVMTLARTMPAMLPGVMFLSGGLSEVQASEYLNAINNSPLPRPYFLSFSYARALQSSALKAWGGKESGLAAGRRAFLHRARMNSMAQLGKYKRSDD

>d1f2ja\_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (Trypanosoma brucei)}

SKRVEVLLTQLPAYNRLKTPYEAELIETAKKMTAPGKGLLAADESTGSCSKRFAGIGLSNTAEHRRQYRALMLECEGFEQYISGVILHDETVYQKAKTGETFPQYLRRRGVVPGIKTDCGLEPLVEGAKGEQMTAGLDGYIKRAKKYYAMGCRFCKWRNVYKIQNGTVSEAVVRFNAETLARYAILSQLCGLVPIVEPEVMIDGTHDIETCQRVSQHVWSEVVSALHRHGVVWEGCLLKPNMVVPGAESGLKGHAEQVAEYTVKTLARVIPPALPGVTFLSGGLSEVMASEYLNAMNNCPLPRPWKLTFSYARALQSSAIKRWGGKESGVEAGRRAFMHRAKMNSLAQLGKYNRADD

>d1euaa\_ c.1.10.1 (A:) KDPG aldolase {Escherichia coli}

MKNWKTSAESILTTGPVVPVIVVKKLEHAVPMAKALVAGGVRVLEVTLRTECAVDAIRAIAKEVPEAIVGAGTVLNPQQLAEVTEAGAQFAISPGLTEPLLKAATEGTIPLIPGISTVSELMLGMDYGLKEFKFFPAEANGGVKALQAIAGPFSQVRFCPTGGISPANYRDYLALKSVLCIGGSWLVPADALEAGDYDRITKLAREAVEGAKL

>d1qfea\_ c.1.10.1 (A:) Type I 3-dehydroquinate dehydratase {Salmonella typhi}

MKTVTVKNLIIGEGMPKIIVSLMGRDINSVKAEALAYREATFDILEWRVDHFMDIASTQSVLTAARVIRDAMPDIPLLFTFRSAKEGGEQTITTQHYLTLNRAAIDSGLVDMIDLELFTGDADVKATVDYAHAHNVYVVMSNHDFHQTPSAEEMVSRLRKMQALGADIPKIAVMPQSKHDVLTLLTATLEMQQHYADRPVITMSMAKEGVISRLAGEVFGSAATFGAVKQASAPGQIAVNDLRSVLMILHNA

>d1i2oa\_ c.1.10.1 (A:) Transaldolase {Escherichia coli}

TDKLTSLRQYTTVVADTGDIAAMKLYQPQDATTNPSLILNAAQIPEYRKLIDDAVAWAKQQSNDRAQQIVDATDKLAVNIGLEILKLVPGRISTAVDARLSYDTEASIAKAKRLIKLYNDAGISNDRILIKLASTWQGIRAAEQLEKEGINCNLTLLFSFAQARACAEAGVFLISPFVGRILDWYKANTDKKEYAPAEDPGVVSVSEIYQYYKEHGYETVVMGASFRNIGEILELAGCDRLTIAPALLKELAESEGAIERKLSYTGEVKARPARITESEFLWQHNQDPMAVDKLAEGIRKFAIDQEKLEKMIGDLL

>d1f05a\_ c.1.10.1 (A:) Transaldolase {Human (Homo sapiens)}

MESALDQLKQFTTVVADTGDFHAIDEYKPQDATTNPSLILAAAQMPAYQELVEEAIAYGRKLGGSQEDQIKNAIDKLFVLFGAEILKKIPGRVSTEVDARLSFDKDAMVARARRLIELYKEAGISKDRILIKLSSTWEGIQAGKELEEQHGIHCNMTLLFSFAQAVACAEAGVTLISPFVGRILDWHVANTDKKSYEPLEDPGVKSVTKIYNYYKKFSYKTIVMGASFRNTGEIKALAGCDFLTISPKLLGELLQDNAKLVPVLSAKAAQASDLEKIHLDEKSFRWLHNEDQMAVEKLSDGIRKFAADAVKLERMLTERMFN

>d1dosa\_ c.1.10.2 (A:) Fructose-bisphosphate aldolase {Escherichia coli}

SKIFDFVKPGVITGDDVQKVFQVAKENNFALPAVNCVGTDSINAVLETAAKVKAPVIVQFSNGGASFIAGKGVKSDVPQGAAILGAISGAHHVHQMAEHYGVPVILHTDHCAKKLLPWIDGLLDAGEKHFAATGKPLFSSHMIDLSEESLQENIEICSKYLERMSKIGMTLEIELGCTGGEEDGVDNSHMDASALYTQPEDVDYAYTELSKISPRFTIAASFGNVHGVYKAGNVVLTPTILRDSQEYVSKKHNLPHNSLNFVFHGGSGSTAQEIKDSVSYGVVKMNIDTDTQWATWEGVLNYYKANEAYLQGQLGNPKGEDQPNKKYYDPRVWLRAGQTSMIARLEKAFQELNAIDVL

>d1h7na\_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Baker's yeast (Saccharomyces cerevisiae)}

MHTAEFLETEPTEISSVLAGGYNHPLLRQWQSERQLTKNMLIFPLFISDNPDDFTEIDSLPNINRIGVNRLKDYLKPLVAKGLRSVILFGVPLIPGTKDPVGTAADDPAGPVIQGIKFIREYFPELYIICDVCLCEYTSHGHCGVLYDDGTINRERSVSRLAAVAVNYAKAGAHCVAPSDMIDGRIRDIKRGLINANLAHKTFVLSYAAKFSGNLYGPFRDAACSAPSNGDRKCYQLPPAGRGLARRALERDMSEGADGIIVKPSTFYLDIMRDASEICKDLPICAYHVSGEYAMLHAAAEKGVVDLKTIAFESHQGFLRAGARLIITYLAPEFLDWLDE

>d1e51a\_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Human (Homo sapiens)}

MQPQSVLHSGYFHPLLRAWQTATTTLNASNLIYPIFVTDVPDDIQPITSLPGVARYGVKRLEEMLRPLVEEGLRCVLIFGVPSRVPKDERGSAADSEESPAIEAIHLLRKTFPNLLVACDVCLCPYTSHGHCGLLSENGAFRAEESRQRLAEVALAYAKAGCQVVAPSDMMDGRVEAIKEALMAHGLGNRVSVMSYSAKFASCFYGPFRDAAKSSPAFGDRRCYQLPPGARGLALRAVDRDVREGADMLMVKPGMPYLDIVREVKDKHPDLPLAVYHVSGEFAMLWHGAQAGAFDLKAAVLEAMTAFRRAGADIIITYYTPQLLQWLK

>d1b4ka\_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Pseudomonas aeruginosa}

YPYTRLRRNRRDDFSRRLVRENVLTVDDLILPVFVLDGVNQRESIPSMPGVERLSIDQLLIEAEEWVALGIPALALFPVTPVEKKSLDAAEAYNPEGIAQRATRALRERFPELGIITDVALDPFTTHGQDGILDDDGYVLNDVSIDVLVRQALSHAEAGAQVVAPSDMMDGRIGAIREALESAGHTNVRIMAYSAKYASAYYGPFRDAVGSASNLGKGNKATYQMDPANSDEALHEVAADLAEGADMVMVKPGMPYLDIVRRVKDEFRAPTFVYQVSGEYAMHMGAIQNGWLAESVILESLTAFKRAGADGILTYFAKQAAEQLRR

>d1b4ea\_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Escherichia coli}

TDLSQRPRRLRKSPALRAMFEETTLSLNDLVLPIFVEEEIDDYKAVEAMPGVMRIPEKHLAREIERIANAGIRSVMTFGISHHTDETGSDAWREDGLVARMSRICKQTVPEMIVMSDTCFCEYTSHGHCGVLKEHGVDNDATLENLGKQAVVAAAAGADFIAPSAAMDGQVQAIRQALDAAGFKDTAIMSYSTKFASSFYGPFREAAGSALKGDRKSYQMNPMNRREAIRESLLDEAQGADCLMVKPAGAYLDIVRELRERTELPIGAYQVSGEYAMIKFAALAGAIDEEKVVLESLGSIKRAGADLIFSYFALDLAEKKILR

>d1gg1a\_ c.1.10.4 (A:) 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (DAHP synthase, AroG) {Escherichia coli}

DLRIKEIKELLPPVALLEKFPATENAANTVAHARKAIHKILKGNDDRLLVVIGPCSIHDPVAAKEYATRLLALREELKDELEIVMRVYFEKPRTTVGWKGLINDPHMDNSFQINDGLRIARKLLLDINDSGLPAAGEFLDMITPQYLADLMSWGAIGARTTESQVHRELASGLSCPVGFKNGTDGTIKVAIDAINAAGAPHCFLSVTKWGHSAIVNTSGNGDCHIILRGGKEPNYSAKHVAEVKEGLNKAGLPAQVMIDFSHANSSKQFKKQMDVCADVCQQIAGGEKAIIGVMVESHLVEGNQSLESGEPLAYGKSITDACIGWEDTDALLRQLANAVKARR

>d1d9ea\_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P synthase) {Escherichia coli}

MKQKVVSIGDINVANDLPFVLFGGMNVLESRDLAMRICEHYVTVTQKLGIPYVFKASFDKANRSSIHSYRGPGLEEGMKIFQELKQTFGVKIITDVHEPSQAQPVADVVDVIQLPAFLARQTDLVEAMAKTGAVINVKKPQFVSPGQMGNIVDKFKEGGNEKVILCDRGANFGYDNLVVDMLGFSIMKKVSGNSPVIFDVTHALQCRDPFGAASGGRRAQVAELARAGMAVGLAGLFIEAHPDPEHAKCDGPSALPLAKLEPFLKQMKAIDDLVKGFEELDTSK

>d1jcxa\_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P synthase) {Aquifex aeolicus}

EKFLVIAGPCAIESEELLLKVGEEIKRLSEKFKEVEFVFKSSFDKANRSSIHSFRGHGLEYGVKALRKVKEEFGLKITTDIHESWQAEPVAEVADIIQIPAFLCRQTDLLLAAAKTGRAVNVKKGQFLAPWDTKNVVEKLKFGGAKEIYLTERGTTFGYNNLVVDFRSLPIMKQWAKVIYDATHSVQLPGGLGDKSGGMREFIFPLIRAAVAVGCDGVFMETHPEPEKALSDASTQLPLSQLEGIIEAILEIREVASKYYETI

>d1onea1 c.1.11.1 (A:142-436) Enolase {Baker's yeast (Saccharomyces cerevisiae)}

SPYVLPVPFLNVLNGGSHAGGALALQEFMIAPTGAKTFAEALRIGSEVYHNLKSLTKKRYGASAGNVGDEGGVAPNIQTAEEALDLIVDAIKAAGHDGKVKIGLDCASSEFFKDGKYDLDFKNPNSDKSKWLTGPQLADLYHSLMKRYPIVSIEDPFAEDDWEAWSHFFKTAGIQIVADDLTVTNPKRIATAIEKKAADALLLKVNQIGTLSESIKAAQDSFAAGWGVMVSHRSGETEDTFIADLVVGLRTGQIKTGAPARSERLAKLNQLLRIEEELGDNAVFAGENFHHGDKL

>d1pdz\_1 c.1.11.1 (140-433) Enolase {Lobster (Homarus vulgaris)}

DEVILPVPAFNVINGGSHAGNKLAMQEFMILPTGATSFTEAMRMGTEVYHHLKAVIKARFGLDATAVGDEGGFAPNILNNKDALDLIQEAIKKAGYTGKIEIGMDVAASEFYKQNNIYDLDFKTANNDGSQKISGDQLRDMYMEFCKDFPIVSIEDPFDQDDWETWSKMTSGTTIQIVGDDLTVTNPKRITTAVEKKACKCLLLKVNQIGSVTESIDAHLLAKKNGWGTMVSHRSGETEDCFIADLVVGLCTGQIKTGAPCRSERLAKYNQILRIEEELGSGAKFAGKNFRAPS

>d1e9ia1 c.1.11.1 (A:140-430) Enolase {Escherichia coli}

PGKYSMPVPMMNIINGGEHADNNVDIQEFMIQPVGAKTVKEAIRMGSEVFHHLAKVLKAKGMNTAVGDEGGYAPNLGSNAEALAVIAEAVKAAGYELGKDITLAMDCAASEFYKDGKYVLAGEGNKAFTSEEFTHFLEELTKQYPIVSIEDGLDESDWDGFAYQTKVLGDKIQLVGDDLFVTNTKILKEGIEKGIANSILIKFNQIGSLTETLAAIKMAKDAGYTAVISHRSGETEDATIADLAVGTAAGQIKTGSMSRSDRVAKYNQLIRIEEALGEKAPYNGRKEIKGQ

>d1bqg\_1 c.1.11.2 (144-422) D-glucarate dehydratase {Pseudomonas putida}

EGQQRDAVEMLGYLFYVGDRNKTDLGYRSEHEADNEWFRLRNKEALTPESVVALAEAAYDRYGFKDFKLKGGVLRGEDEIAAVTALSERFPDARITLDPNGAWSLKEAVALCRDQHHVLAYAEDPCGAENGYSGREVMAEFRRSTGLRTATNMIATDWRQMGHAIQLQSVDIPLADPHFWTMQGSVRVAQMCNEWGLTWGSHSNNHFDISLAMFTHVAAAAPGNITAIDTHWIWQDGQRLTKEPLQIKGGLVEVPKKPGLGVELDWDALMKAHEVYKSM

>d1ec7a1 c.1.11.2 (A:138-446) D-glucarate dehydratase {Escherichia coli}

DGQQRSEVEMLGYLFFVGNRKATPLPYQSQPDDSCDWYRLRHEEAMTPDAVVRLAEAAYEKYGFNDFKLKGGVLAGEEEAESIVALAQRFPQARITLDPNGAWSLNEAIKIGKYLKGSLAYAEDPCGAEQGFSGREVMAEFRRATGLPTATNMIATDWRQMGHTLSLQSVDIPLADPHFWTMQGSVRVAQMCHEFGLTWGSHSNNHFDISLAMFTHVAAAAPGKITAIDTHWIWQEGNQRLTKEPFEIKGGLVQVPEKPGLGVEIDMDQVMKAHELYQKHGLGARDDAMGMQYLIPGWTFDNKRPCMVR

>d1fhua1 c.1.11.2 (A:100-320) O-succinylbenzoate synthase {Escherichia coli}

QAANYRAAPLCNGDPDDLILKLADMPGEKVAKVKVGLYEAVRDGMVVNLLLEAIPDLHLRLDANRAWTPLKGQQFAKYVNPDYRDRIAFLEEPCKTRDDSRAFARETGIAIAWDESLREPDFAFVAEEGVRAVVIKPTLTGSLEKVREQVQAAHALGLTAVISSSIESSLGLTQLARIAAWLTPDTIPGLDTLDLMQAQQVRRWPGSTLPVVEVDALERLL

>d1muca1 c.1.11.2 (A:131-372) Muconate-lactonizing enzyme {Pseudomonas putida}

RVRDSLEVAWTLASGDTARDIAEARHMLEIRRHRVFKLKIGANPVEQDLKHVVTIKRELGDSASVRVDVNQYWDESQAIRACQVLGDNGIDLIEQPISRINRGGQVRLNQRTPAPIMADESIESVEDAFSLAADGAASIFALKIAKNGGPRAVLRTAQIAEAAGIGLYGGTMLEGSIGTLASAHAFLTLRQLTWGTELFGPLLLTEEIVNEPPQYRDFQLHIPRTPGLGLTLDEQRLARFAR

>d2mnr\_1 c.1.11.2 (133-359) Mandelate racemase {Pseudomonas putida}

PVQAYDSHSLDGVKLATERAVTAAELGFRAVKTKIGYPALDQDLAVVRSIRQAVGDDFGIMVDYNQSLDVPAAIKRSQALQQEGVTWIEEPTLQHDYEGHQRIQSKLNVPVQMGENWLGPEEMFKALSIGACRLAMPDAMKIGGVTGWIRASALAQQFGIPMSSHLFQEISAHLLAATPTAHWLERLDLAGSVIEPTLTFEGGNAVIPDLPGVGIIWREKEIGKYLV

>d2chr\_1 c.1.11.2 (127-370) Chlormuconate cycloisomerase {Alcaligenes eutrophus}

PLRSAIPIAWTLASGDTKRDLDSAVEMIERRRHNRFKVKLGFRSPQDDLIHMEALSNSLGSKAYLRVDVNQAWDEQVASVYIPELEALGVELIEQPVGRENTQALRRLSDNNRVAIMADESLSTLASAFDLARDRSVDVFSLKLCNMGGVSATQKIAAVAEASGIASYGGTMLDSTIGTSVALQLYSTVPSLPFGCELIGPFVLADTLSHEPLEIRDYELQVPTGVGHGMTLDEDKVRQYARVS

>d1jpdx1 c.1.11.2 (X:114-321) L-Ala-D/L-Glu epimerase {Escherichia coli}

TLPETVITAQTVVIGTPDQMANSASTLWQAGAKLLKVKLDNHLISERMVAIRTAVPDATLIVDANESWRAEGLAARCQLLADLGVAMLEQPLPAQDDAALENFIHPLPICADESCHTRSNLKALKGRYEMVNIKLDKTGGLTEALALATEARAQGFSLMLGCMLCTSRAISAALPLVPQVSFADLDGPTWLAVDVEPALQFTTGELHL

>d1jpma1 c.1.11.2 (A:126-359) L-Ala-D/L-Glu epimerase {Bacillus subtilis}

YRDTLETDYTVSVNSPEEMAADAENYLKQGFQTLKIKVGKDDIATDIARIQEIRKRVGSAVKLRLDANQGWRPKEAVTAIRKMEDAGLGIELVEQPVHKDDLAGLKKVTDATDTPIMADESVFTPRQAFEVLQTRSADLINIKLMKAGGISGAEKINAMAEACGVECMVGSMIETKLGITAAAHFAASKRNITRFDFDAPLMLKTDVFNGGITYSGSTISMPGKPGLGIIGAAL

>d1kcza1 c.1.11.2 (A:161-413) beta-Methylaspartase {Clostridium tetanomorphum}

GAEINAVPVFAQSGDDRYDNVDKMIIKEADVLPHALINNVEEKLGLKGEKLLEYVKWLRDRIIKLRVREDYAPIFHIDVYGTIGAAFDVDIKAMADYIQTLAEAAKPFHLRIEGPMDVEDRQKQMEAMRDLRAELDGRGVDAELVADEWCNTVEDVKFFTDNKAGHMVQIKTPDLGGVNNIADAIMYCKANGMGAYCGGTCNETNRSAEVTTNIGMACGARQVLAKPGMGVDEGMMIVKNEMNRVLALVGRRK

>d1kkoa1 c.1.11.2 (A:161-411) beta-Methylaspartase {Citrobacter amalonaticus}

PCVPEAIPLFGQSGDDRYIAVDKMILKGVDVLPHALINNVEEKLGFKGEKLREYVRWLSDRILSLRSSPRYHPTLHIDVYGTIGLIFDMDPVRCAEYIASLEKEAQGLPLYIEGPVDAGNKPDQIRMLTAITKELTRLGSGVKIVADEWCNTYQDIVDFTDAGSCHMVQIKTPDLGGIHNIVDAVLYCNKHGMEAYQGGTCNETEISARTCVHVALAARPMRMLIKPGMGFDEGLNIVFNEMNRTIALLQT

>d1a49a2 c.1.12.1 (A:12-115,A:218-395) Pyruvate kinase, N-terminal domain {Rabbit (Oryctolagus cuniculus)}

IQTQQLHAAMADTFLEHMCRLDIDSAPITARNTGIICTIGPASRSVETLKEMIKSGMNVARMNFSHGTHEYHAETIKNVRTATESFASDPILYRPVAVALDTKGXPAVSEKDIQDLKFGVEQDVDMVFASFIRKAADVHEVRKILGEKGKNIKIISKIENHEGVRRFDEILEASDGIMVARGDLGIEIPAEKVFLAQKMIIGRCNRAGKPVICATQMLESMIKKPRPTRAEGSDVANAVLDGADCIMLSGETAKGDYPLEAVRMQHLIAREAEAAMFHRKLFE

>d1pkla2 c.1.12.1 (A:1-87,A:187-357) Pyruvate kinase, N-terminal domain {Leishmania mexicana}

SQLAHNLTLSIFDPVANYRAARIICTIGPSTQSVEALKGLIQSGMSVARMNFSHGSHEYHQTTINNVRQAAAELGVNIAIALDTKGPXPAVSAKDRVDLQFGVEQGVDMIFASFIRSAEQVGDVRKALGPKGRDIMIICKIENHQGVQNIDSIIEESDGIMVARGDLGVEIPAEKVVVAQKILISKCNVAGKPVICATQMLESMTYNPRPTRAEVSDVANAVFNGADCVMLSGETAKGKYPNEVVQYMARICLEAQSAL

>d1a3wa2 c.1.12.1 (A:2-87,A:189-366) Pyruvate kinase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

SRLERLTSLNVVAGSDLRRTSIIGTIGPKTNNPETLVALRKAGLNIVRMNFSHGSYEYHKSVIDNARKSEELYPGRPLAIALDTKGXPALSEKDKEDLRFGVKNGVHMVFASFIRTANDVLTIREVLGEQGKDVKIIVKIENQQGVNNFDEILKVTDGVMVARGDLGIEIPAPEVLAVQKKLIAKSNLAGKPVICATQMLESMTYNPRPTRAEVSDVGNAILDGADCVMLSGETAKGNYPINAVTTMAETAVIAEQAIAYLPNYD

>d1e0ta2 c.1.12.1 (A:1-69,A:168-344) Pyruvate kinase, N-terminal domain {Escherichia coli}

MKKTKIVCTIGPKTESEEMLAKMLDAGMNVMRLNFSHGDYAEHGQRIQNLRNVMSKTGKTAAILLDTKGXPALAEKDKQDLIFGCEQGVDFVAASFIRKRSDVIEIREHLKAHGGENIHIISKIENQEGLNNFDEILEASDGIMVARGDLGVEIPVEEVIFAQKMMIEKCIRARKVVITATMMLDSMIKNPRPTDAEAGDVANAILDGTDAVMLSGESAKGKYPLEAVSIMATICERTDRVMNSRLE

>d1kbla1 c.1.12.2 (A:510-873) Pyruvate phosphate dikinase, C-terminal domain {Clostridium symbiosum}

IETQEASVSGSFERIMVWADKFRTLKVRTNADTPEDTLNAVKLGAEGIGLCRTEHMFFEADRIMKIRKMILSDSVEAREEALNELIPFQKGDFKAMYKALEGRPMTVRYLDPPLHEFVPHTEEEQAELAKNMGLTLAEVKAKVDELHEFNPMMGHRGCRLAVTYPEIAKMQTRAVMEAAIEVKEETGIDIVPEIMIPLVGEKKELKFVKDVVVEVAEQVKKEKGSDMQYHIGTMIEIPRAALTADAIAEEAEFFSFGTNDLTQMTFGFSRDDAGKFLDSYYKAKIYESDPFARLDQTGVGQLVEMAVKKGRQTRPGLKCGICGEHGGDPSSVEFCHKVGLNYVSCSPFRVPIARLAAAQAALNN

>d1fiy\_\_ c.1.12.3 (-) Phosphoenolpyruvate carboxylase {Escherichia coli}

QYSALRSNVSMLGKVLGETIKDALGEHILERVETIRKLSKSSRAGNDANRQELLTTLQNLSNDELLPVARAFSQFLNLANTAEQYHSISPKGEAASNPEVIARTLRKLKNQPELSEDTIKKAVESLSLELVLTAHPTEITRRTLIHKMVEVNACLKQLDNKDIADYEHNQLMRRLRQLIAQSWHTDEIRKLRPSPVDEAKWGFAVVENSLWQGVPNYLRELNEQLEENLGYKLPVEFVPVRFTSWMGGDRDGNPNVTADITRHVLLLSRWKATDLFLKDIQVLVSELSMVEATPELLALVGEEGAAEPYRYLMKNLRSRLMATQAWLEARLKGEELPKPEGLLTQNEELWEPLYACYQSLQACGMGIIANGDLLDTLRRVKCFGVPLVRIDIRQESTRHTEALGELTRYLGIGDYESWSEADKQAFLIRELNSKRPLLPRNWQPSAETREVLDTCQVIAEAPQGSIAAYVISMAKTPSDVLAVHLLLKEAGIGFAMPVAPLFETLDDLNNANDVMTQLLNIDWYRGLIQGKQMVMIGYSDSAKDAGVMAASWAQYQAQDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALLSQPPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPPEPKESWRRIMDELSVISCDVYRGYVRENKDFVPYFRSATPEQELGKLPLGSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGTALQKVVEDGKQSELEAMCRDWPFFSTRLGMLEMVFAKADLWLAEYYDQRLVDKALWPLGKELRNLQEEDIKVVLAIANDSHLMADLPWIAESIQLRNIYTDPLNVLQAELLHRSRQAEKEGQEPDPRVEQALMVTIAGIAAGMRNTG

>d1pyma\_ c.1.12.4 (A:) Phosphoenolpyruvate mutase {Blue mussel (Mytilus edulis)}

VKKTTQLKQMLNSKDLEFIMEAHNGLSARIVQEAGFKGIWGSGLSVSAQLGVRDSNEASWTQVVEVLEFMSDASDVPILLDADTGYGNFNNARRLVRKLEDRGVAGACLEDKLFPKTNSLHDGRAQPLADIEEFALKIKACKDSQTDPDFCIVARVEAFIAGWGLDEALKRAEAYRNAGADAILMHSKKADPSDIEAFMKAWNNQGPVVIVPTKYYKTPTDHFRDMGVSMVIWANHNLRASVSAIQQTTKQIYDDQSLVNVEDKIVSVKEIFRLQRDDELVQAEDKYLPKN

>d1dxea\_ c.1.12.5 (A:) 2-dehydro-3-deoxy-galactarate aldolase {Escherichia coli}

DVFPNKFKAALAAKQVQIGCWSALSNPISTEVLGLAGFDWLVLDGEHAPNDISTFIPQLMALKGSASAPVVRVPTNEPVIIKRLLDIGFYNFLIPFVETKEEAELAVASTRYPPEGIRGVSVSHRANMFGTVADYFAQSNKNITILVQIESQQGVDNVDAIAATEGVDGIFVGPSDLAAALGHLGNASHPDVQKAIQHIFNRASAHGKPSGILAPVEADARRYLEWGATFVAVGSDLGVFRSATQKLADTFKK

>d1dqua\_ c.1.12.6 (A:) Isocitrate lyase {Aspergillus nidulans}

SYIEEEDQRYWDEVAAVKNWWKDSRWRYTKRPFTAEQIVAKRGNLKIEYPSNVQAKKLWGILERNFKNKEASFTYGCLDPTMVTQMAKYLDTVYVSGWQSSSTASSTDEPSPDLADYPMNTVPNKVNHLWMAQLFHDRKQREERMTTPKDQRHKVANVDYLRPIIADADTGHGGLTAVMKLTKLFVERGAAGIHIEDQAPGTKKCGHMAGKVLVPISEHINRLVAIRAQADIMGTDLLAIARTDSEAATLITSTIDHRDHPFIIGSTNPDIQPLNDLMVMAEQAGKNGAELQAIEDEWLAKAGLKLFNDAVVDAINNSPLPNKKAAIEKYLTQSKGKSNLEARAIAKEIAGTDIYFDWEAPRTREGYYRYQGGTQCAINRAVAYAPFADLIWMESKLPDYKQAKEFADGVHAVWPEQKLAYNLSPSFNWKKAMPRDEQETYIKRLGALGYAWQFITLAGLHTTALISDTFAKAYAKQGMRAYGELVQEPEMANGVDVVTHQKWSGANYVDNMLKMITGG

>d1f8ma\_ c.1.12.6 (A:) Isocitrate lyase {Mycobacterium tuberculosis}

ASVVGTPKSAEQIQQEWDTNPRWKDVTRTYSAEDVVALQGSVVEEHTLARRGAEVLWEQLHDLEWVNALGALTGNMAVQQVRAGLKAIYLSGWQVAGDANLSGHTYPDQSLYPANSVPQVVRRINNALQRADQIAKIEGDTSVENWLAPIVADGEAGFGGALNVYELQKALIAAGVAGSHWEDQLASEKKCGHLGGKVLIPTQQHIRTLTSARLAADVADVPTVVIARTDAEAATLITSDVDERDQPFITGERTREGFYRTKNGIEPCIARAKAYAPFADLIWMETGTPDLEAARQFSEAVKAEYPDQMLAYNCSPSFNWKKHLDDATIAKFQKELAAMGFKFQFITLAGFHALNYSMFDLAYGYAQNQMSAYVELQEREFAAEERGYTATKHQREVGAGYFDRIATTVDPNSSTTALTGSTEEGQF

>d1igwa\_ c.1.12.6 (A:) Isocitrate lyase {Escherichia coli}

KTRTQQIEELQKEWTQPRWEGITRPYSAEDVVKLRGSVNPECTLAQLGAAKMWRLLHGESKKGYINSLGALTGGQALQQAKAGIEAVYLSGWQVAADANLAASMYPDQSLYPANSVPAVVERINNTFRRADQIQWSAGIEPGDPRYVDYFLPIVADAEAGFGGVLNAFELMKAMIEAGAAAVHFEDQLASVKKCGHMGGKVLVPTQEAIQKLVAARLCADVTGVPTLLVARTDADAADLITSDCDPYDSEFITGERTSEGFFRTHAGIEQAISRGLAYAPYADLVWCETSTPDLELARRFAQAIHAKYPGKLLAYNCSPSFNWQKNLDDKTIASFQQQLSDMGYKFQFITLAGIHSMWFNMFDLANAYAQGEGMKHYVEKVQQPEFAAAKDGYTFVSHQQEVGTGYFDKVTTIIQG

>d1d8ca\_ c.1.13.1 (A:) Malate synthase G {Escherichia coli}

QTITQSRLRIDANFKRFVDEEVLPGTGLDAAAFWRNFDEIVHDLAPENRQLLAERDRIQAALDEWHRSNPGPVKDKAAYKSFLRELGYLVPQPERVTVETTGIDSEITSQAGPQLVVPAMNARYALNAANARWGSLYDALYGSDIIPQEGAMVSGYDPQRGEQVIAWVRRFLDESLPLENGSYQDVVAFKVVDKQLRIQLKNGKETTLRTPAQFVGYRGDAAAPTCILLKNNGLHIELQIDANGRIGKDDPAHINDVIVEAAISTILDCEDSVAAVDAEDKILLYRNLLGLMQGTLQEKMEKNGRQIVRKLNDDRHYTAADGSEISLHGRSLLFIRNVGHLMTIPVIWDSEGNEIPEGILDGVMTGAIALYDLKVQKNSRTGSVYIVKPKMHGPQEVAFANKLFTRIETMLGMAPNTLKMGIMDEERRTSLNLRSCIAQARNRVAFINTGFLDRTGDEMHSVMEAGPMLRKNQMKSTPWIKAYERNNVLSGLFCGLRGKAQIGKGMWAMPDLMADMYSQKGDQLRAGANTAWVPSPTAATLHALHYHQTNVQSVQANIAQTEFNAEFEPLLDDLLTIPVAENANWSAQEIQQELDNNVQGILGYVVRWVEQGIGCSKVPDIHNVALMEDRATLRISSQHIANWLRHGILTKEQVQASLENMAKVVDQQNAGDPAYRPMAGNFANSCAFKAASDLIFLGVKQPNGYTEPLLHAWRLREKES

>d3rubl1 c.1.14.1 (L:148-467) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}

FQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEALYKAQAETGEIKGHYLNATAGTCEEMIKRAVFARELGVPIVMHDYLTGGFTANTSLAHYCRDNGLLLHIHRAMHAVIDRQKNHGIHFRVLAKALRMSGGDHIHSGTVVGKLEGERDITLGFVDLLRDDFVEQDRSRGIYFTQDWVSLPGVLPVASGGIHVWHMPALTEIFGDDSVLQFGGMTLGHPWGNAPGAVANRVALEACVKARNEGRDLAQEGNEIIREACKWSPELAAACEVWKEIVF

>d1bura1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

FQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFCAEALYKAQAETGEIKGHYLNATAGTCEDMMKRAVFARELGVPIVMHDYLTGGFTANTTLSHYCRDNGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRLSGGDHIHSGTVVGKLEGERDITLGFVDLLRDDYTEKDRSRGIYFTQSWVSTPGVLPVASGGIHVWHMPALTEIFGDDSVLQFGGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAREGNTIIREATKWSPELAAACEVWKEIKFEFPAMDTV

>d1bwva1 c.1.14.1 (A:150-478) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

GPATGVILERERLDKFGRPLLGCTTKPKLGLSGKNYGRVVYEALKGGLDFVKDDENINSQPFMRWRERYLFTMEAVNKASAATGEVKGHYLNVTAATMEEMYARANFAKELGSVIIMIDLVIGYTAIQTMAKWARDNDMILHLHRAGNSTYSRQKNHGMNFRVICKWMRMAGVDHIHAGTVVGKLEGDPIITRGFYKTLLLPKLERNLQEGLFFDMEWASLRKVMPVASGGIHAGQMHQLIHYLGEDVVLQFGGGTIGHPDGIQAGATANRVALEAMILARNENRDYLTEGPEILREAAKTCGALRTALDLWKDITFNYTSTDTSDFV

>d1gk8a1 c.1.14.1 (A:150-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}

GPPHGIQVERDKLNKYGRGLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFVAEAIYKAQAETGEVKGHYLNATAGTCEEMMKRAVCAKELGVPIIMHDYLTGGFTANTSLAIYCRDNGLLLHIHRAMHAVIDRQRNHGIHFRVLAKALRMSGGDHLHSGTVVGKLEGEREVTLGFVDLMRDDYVEKDRSRGIYFTQDWCSMPGVMPVASGGIHVWHMPALVEIFGDDACLQFGGGTLGHPWGNAPGAAANRVALEACTQARNEGRDLAREGGDVIRSACKWSPELAAACEVWKEIKFEFDTIDKL

>d1bxna1 c.1.14.1 (A:151-467) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}

FAGPSTGIIVERERLDKFGRPLLGATTKPKLGLSGRNYGRVVYEGLKGGLDFMKDDENINSQPFMHWRDRFLFVMDAVNKASAATGEVKGSYLNVTAGTMEEMYRRAEFAKSLGSVIIMVDLIVGWTCIQSMSNWCRQNDMILHLHRAGHGTYTRQKNHGVSFRVIAKWLRLAGVDHMHTGTAVGKLEGDPLTVQGYYNVCRDAYTQTDLTRGLFFDQDWASLRKVMPVASGGIHAGQMHQLIHLFGDDVVLQFGGGTIGHPQGIQAGATANRVALEAMVLARNEGRDILNEGPEILRDAARWCGPLRAALDTWGDI

>d1rbla1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}

FQGPPHGIQVERDLLNKYGRPMLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENINSQPFQRWRDRFLFVADAIHKSQAETGEIKGHYLNVTAPTCEEMMKRAEFAKELGMPIIMHDFLTAGFTANTTLAKWCRDNGVLLHIHRAMHAVIDRQRNHGIHFRVLAKCLRLSGGDHLHSGTVVGKLEGDKASTLGFVDLMREDHIEADRSRGVFFTQDWASMPGVLPVASGGIHVWHMPALVEIFGDDSVLQFGGGTLGHPWGNAPGATANRVALEACVQARNEGRDLYREGGDILREAGKWSPELAAALDLWKEIKFEFETMDKL

>d5ruba1 c.1.14.1 (A:138-457) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Rhodospirillum rubrum}

GPSVNISALWKVLGRPEVDGGLVVGTIIKPKLGLRPKPFAEACHAFWLGGDFIKNDEPQGNQPFAPLRDTIALVADAMRRAQDETGEAKLFSANITADDPFEIIARGEYVLETFGENASHVALLVDGYVAGAAAITTARRRFPDNFLHYHRAGHGAVTSPQSKRGYTAFVHCKMARLQGASGIHTGTMGFGKMEGESSDRAIAYMLTQDEAQGPFYRQSWGGMKACTPIISGGMNALRMPGFFENLGNANVILTAGGGAFGHIDGPVAGARSLRQAWQAWRDGVPVLDYAREHKELARAFESFPGDADQIYPGWRKALGV

>d1geha1 c.1.14.1 (A:137-443) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Archaeon Thermococcus kodakaraensis}

DGPAFGIEGVRKMLEIKDRPIYGVVPKPKVGYSPEEFEKLAYDLLSNGADYMKDDENLTSPWYNRFEERAEIMAKIIDKVENETGEKKTWFANITADLLEMEQRLEVLADLGLKHAMVDVVITGWGALRYIRDLAADYGLAIHGHRAMHAAFTRNPYHGISMFVLAKLYRLIGIDQLHVGTAGAGKLEGGKWDVIQNARILRESHYKPDENDVFHLEQKFYSIKAAFPTSSGGLHPGNIQPVIEALGTDIVLQLGGGTLGHPDGPAAGARAVRQAIDAIMQGIPLDEYAKTHKELARALEKWGHVTP

>d1qtwa\_ c.1.15.1 (A:) Endonuclease IV {Escherichia coli}

MKYIGAHVSAAGGLANAAIRAAEIDATAFALFTKNQRQWRAAPLTTQTIDEFKAACEKYHYTSAQILPHDSYLINLGHPVTEALEKSRDAFIDEMQRCEQLGLSLLNFHPGSHLMQISEEDCLARIAESINIALDKTQGVTAVIENTAGQGSNLGFKFEHLAAIIDGVEDKSRVGVCIDTCHAFAAGYDLRTPAECEKTFADFARTVGFKYLRGMHLNDAKSTFGSRVDRHHSLGEGNIGHDAFRWIMQDDRFDGIPLILETINPDIWAEEIAWLKAQQTEKAVA

>d1d8wa\_ c.1.15.2 (A:) L-rhamnose isomerase {Escherichia coli}

TQLEQAWELAKQRFAAVGIDVEEALRQLDRLPVSMHCWQGDDVSGFENPEGSLTGGIQATGNYPGKARNASELRADLEQAMRLIPGPKRLNLHAIYLESDTPVSRDQIKPEHFKNWVEWAKANQLGLDFNPSCFSHPLSADGFTLSHADDSIRQFWIDHCKASRRVSAYFGEQLGTPSVMNIWIPDGMKDITVDRLAPRQRLLAALDEVISEKLNPAHHIDAVESKLFGIGAESYTVGSNEFYMGYATSRQTALCLDAGHFHPTEVISDKISAAMLYVPQLLLHVSRPVRWDSDHVVLLDDETQAIASEIVRHDLFDRVHIGLDFFDASINRIAAWVIGTRNMKKALLRALLEPTAELRKLEAPGDYTARLALLEEQKSLPWQAVWEMYCQRHDTPAGSEWLESVRAYEKEILSRR

>d1dxia\_ c.1.15.3 (A:) D-xylose isomerase {Streptomyces murinus}

MSFQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVETVQRLAELGAYGVTFHDDDLIPFGSSDTERESHIKRFRQALDATGMTVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIGNIDLAAELGAKTYVAWGGREGAESGGAKDVRDALDRMKEAFDLLGEYVTAQGYDLRFAIEPKPNEPRGDILLPTVGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLETAGYEGPRHFDFKPPRTEDFDGVWASAAGCMRNYLILKDRAAAFRADPEVQEALRAARLDQLAQPTAADGLDALLADRAAFEDFDVDAAAARGMAFEHLDQLAMDHLLGARG

>d2gyia\_ c.1.15.3 (A:) D-xylose isomerase {Streptomyces olivochromogenes}

YQPTPEDRFTFGLWTVGWQGRDPFGDATRPALDPVETVQRLAELGAHGVTFHDDDLIPFGSSDTERESHIKRFRQALDATGMTVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIRNIDLAVELGAKTYVAWGGREGAESGAAKDVRVALDRMKEAFDLLGEYVTSQGYDTRFAIEPKPNEPRGDILLPTVGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGYEGPRHFDFKPPRTEDIDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRASRLDELAQPTAADGVQELLADRTAFEDFDVDAAAARGMAFERLDQLAMDHLLGAR

>d1xis\_\_ c.1.15.3 (-) D-xylose isomerase {Streptomyces rubiginosus}

NYQPTPEDRFTFGLWTVGWQGRDPFGDATRRALDPVESVRRLAELGAHGVTFHDDDLIPFGSSDSEREEHVKRFRQALDDTGMKVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIRNIDLAVELGAETYVAWGGREGAESGGAKDVRDALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEPRGDILLPTVGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQNGIKYDQDLRFGAGDLRAAFWLVDLLESAGYSGPRHFDFKPPRTEDFDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRASRLDELARPTAADGLQALLDDRSAFEEFDVDAAAARGMAFERLDQLAMDHLLGARG

>d1qt1a\_ c.1.15.3 (A:) D-xylose isomerase {Streptomyces diastaticus, M1033}

SYQPTPEDKFTFGLWTVGWQGRDPFGDATRGALDPAESVRRLAELGAHGVTFHDDDLIPFGATDSERAEHIKRFRQGLDETGMKVPMATTNLFTHPVFKDGGFTANDRDVRRYALRKTIRNIDLAVELGAQTYVAWGGREGAESGAAKDVRVALDRMKEAFDLLGEYVTSQGYDTPFAIEPKPNEPRGDILLPTIGHALAFIDGLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGPGDLRAAFWLVDLLESAGYEGPRHFDFKPPRTEDFDGVWASAAGCMRNYLILKERAAAFRADPEVQEALRAARLDELAQPTAGDGLQALLPDRSAFEDFDPDAAAARGMAFERLDQLAMDHLLGARG

>d4xiaa\_ c.1.15.3 (A:) D-xylose isomerase {Arthrobacter, strain b3728}

VQPTPADHFTFGLWTVGWTGADPFGVATRANLDPVEAVHKLAELGAYGITFHDNDLIPFDATAAEREKILGDFNQALADTGLKVPMVTTNLFSHPVFKDGGFTSNDRSIRRFALAKVLHNIDLAAEMGAETFVMWGGREGSEYDGSKDLAAALDRMREGVDTAAGYIKDKGYNLRIALEPKPNEPRGDIFLPTVGHGLAFIEQLEHGDIVGLNPETGHEQMAGLNFTHGIAQALWAEKLFHIDLNGQRGIKYDQDLVFGHGDLTSAFFTVDLLENGFPNGGPKYTGPRHFDYKPSRTDGYDGVWDSAKANMSMYLLLKERALAFRADPEVQEAMKTSGVFELGETTLNAGESAADLMNDSASFAGFDAEAAAERNFAFIRLNQLAIEHLLGSR

>d1xima\_ c.1.15.3 (A:) D-xylose isomerase {Actinoplanes missouriensis}

VQATREDKFSFGLWTVGWQARDAFGDATRTALDPVEAVHKLAEIGAYGITFHDDDLVPFGSDAQTRDGIIAGFKKALDETGLIVPMVTTNLFTHPVFKDGGFTSNDRSVRRYAIRKVLRQMDLGAELGAKTLVLWGGREGAEYDSAKDVSAALDRYREALNLLAQYSEDRGYGLRFAIEPKPNEPRGDILLPTAGHAIAFVQELERPELFGINPETGHEQMSNLNFTQGIAQALWHKKLFHIDLNGQHGPKFDQDLVFGHGDLLNAFSLVDLLENGPDGAPAYDGPRHFDYKPSRTEDYDGVWESAKANIRMYLLLKERAKAFRADPEVQEALAASKVAELKTPTLNPGEGYAELLADRSAFEDYDADAVGAKGFGFVKLNQLAIEHLLGAR

>d1a0ca\_ c.1.15.3 (A:) D-xylose isomerase {Clostridium thermosulfurogenes, also known as Thermoanaerobacter thermosulfurigenes}

NKYFENVSKIKYEGPKSNNPYSFKFYNPEEVIDGKTMEEHLRFSIAYWHTFTADGTDQFGKATMQRPWNHYTDPMDIAKARVEAAFEFFDKINAPYFCFHDRDIAPEGDTLRETNKNLDTIVAMIKDYLKTSKTKVLWGTANLFSNPRFVHGASTSCNADVFAYSAAQVKKALEITKELGGENYVFWGGREGYETLLNTDMEFELDNFARFLHMAVDYAKEIGFEGQFLIEPKPKEPTKHQYDFDVANVLAFLRKYDLDKYFKVNIEANHATLAFHDFQHELRYARINGVLGSIDANTGDMLLGWDTDQFPTDIRMTTLAMYEVIKMGGFDKGGLNFDAKVRRASFEPEDLFLGHIAGMDAFAKGFKVAYKLVKDRVFDKFIEERYASYKDGIGADIVSGKADFRSLEKYALERSQIVNKSGRQELLESILNQYLFA

>d1a0da\_ c.1.15.3 (A:) D-xylose isomerase {Bacillus stearothermophilus}

PYFDNISTIAYEGPASKNPLAFKFYNPEEKVGDKTMEEHLRFSVAYWHTFTGDGSDPFGAGNMIRPWNKYSGMDLAKARVEAAFEFFEKLNIPFFCFHDVDIAPEGETLKETYKNLDIIVDMIEEYMKTSKTKLLWNTANLFTHPRFVHGAATSCNADVFAYAAAKVKKGLEIAKRLGAENYVFWGGREGYETLLNTDMKLELDNLARFLHMAVDYAKEIGFDGQFLIEPKPKEPTKHQYDFDVATALAFLQTYGLKDYFKFNIEANHATLAGHTFEHELRVARIHGMLGSVDANQGDMLLGWDTDEFPTDLYSTTLAMYEILKNGGLGRGGLNFDAKVRRGSFEPEDLFYAHIAGMDSFAVGLKVAHRLIEDRVFDEFIEERYKSYTEGIGREIVEGTADFHKLEAHALQLGEIQNQSGRQERLKTLLNQYLLEVC

>d1a0ea\_ c.1.15.3 (A:) D-xylose isomerase {Thermotoga neapolitana}

AEFFPEIPKVQFEGKESTNPLAFKFYDPEEIIDGKPLKDHLKFSVAFWHTFVNEGRDPFGDPTADRPWNRYTDPMDKAFARVDALFEFCEKLNIEYFCFHDRDIAPEGKTLRETNKILDKVVERIKERMKDSNVKLLWGTANLFSHPRYMHGAATTCSADVFAYAAAQVKKALEITKELGGEGYVFWGGREGYETLLNTDLGFELENLARFLRMAVDYAKRIGFTGQFLIEPKPKEPTKHQYDFDVATAYAFLKSHGLDEYFKFNIEANHATLAGHTFQHELRMARILGKLGSIDANQGDLLLGWDTDQFPTNVYDTTLAMYEVIKAGGFTKGGLNFDAKVRRASYKVEDLFIGHIAGMDTFALGFKVAYKLVKDGVLDKFIEEKYRSFREGIGRDIVEGKVDFEKLEEYIIDKETIELPSGKQEYLESLINSYIVKTILELR

>d1bxca\_ c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp. Caldophilus}

MYEPKPEHRFTFGLWTVGNVGRDPFGDAVRERLDPVYVGHKLAELGVHGVNLHDEDLIPRGTPPQERDQIVRRFKRALDETGLKVPMVTGNLFSDPGFKDGGFTSRDPWVRAYAFRKSLETMDLGAELGAEIYVVWPGREGAEVEATGKARKVWDWVREPLNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFATVGSMLALIHTLERPERFGLNPEFAHETMAGLNFVHAVAQALDAGKLLHIDLNGQRMNRFDQDLRFGSENLKAAFLLVDLLESSGYQGPRHFDAHALRTEDEEGVWAFARGCMRTYLILKERAEAFREDPEVKELLAAYYQEDPAALPLMDPYSHEKAEALKRAELPLEAKRHRGYALERLDQLAVEYLLGVRG

>d1bxba\_ c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp. Thermophilus}

MYEPKPEHRFTFGLWTVGNVGRDPFGDAVRERLDPVYVVHKLAELGAYGVNLHDEDLIPRGTPPQERDQIVRRFKKALDETGLKVPMVTANLFSDPAFKDGAFTSPDPWVRAYALRKSLETMDLGAELGAEIYVVWPGREGAEVEATGKARKVWDWVREALNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFATVGSMLAFIHTLDRPERFGLNPEFAHETMAGLNFVHAVAQALDAGKLFHIDLNDQRMSRFDQDLRFGSENLKAAFFLVDLLESSGYQGPRHFDAHALRTEDEEGVWAFARGCMRTYLILKERAEAFREDPEVKELLAAYYQEDPAALALLGPYSREKAEALKRAELPLEAKRRRGYALERLDQLAVEYLLGVRG

>d1luca\_ c.1.16.1 (A:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}

MKFGNFLLTYQPPELSQTEVMKRLVNLGKASEGCGFDTVWLLEHHFTEFGLLGNPYVAAAHLLGATETLNVGTAAIVLPTAHPVRQAEDVNLLDQMSKGRFRFGICRGLYDKDFRVFGTDMDNSRALMDCWYDLMKEGFNEGYIAADNEHIKFPKIQLNPSAYTQGGAPVYVVAESASTTEWAAERGLPMILSWIINTHEKKAQLDLYNEVATEHGYDVTKIDHCLSYITSVDHDSNRAKDICRNFLGHWYDSYVNATKIFDDSDQTKGYDFNKGQWRDFVLKGHKDTNRRIDYSYEINPVGTPEECIAIIQQDIDATGIDNICCGFEANGSEEEIIASMKLFQSDVMPYLKEKQ

>d1lucb\_ c.1.16.1 (B:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}

MKFGLFFLNFMNSKRSSDQVIEEMLDTAHYVDQLKFDTLAVYENHFSNNGVVGAPLTVAGFLLGMTKNAKVASLNHVITTHHPVRVAEEACLLDQMSEGRFAFGFSDCEKSADMRFFNRPTDSQFQLFSECHKIINDAFTTGYCHPNNDFYSFPKISVNPHAFTEGGPAQFVNATSKEVVEWAAKLGLPLVFRWDDSNAQRKEYAGLYHEVAQAHGVDVSQVRHKLTLLVNQNVDGEAARAEARVYLEEFVRESYSNTDFEQKMGELLSENAIGTYEESTQAARVAIECCGAADLLMSFESMEDKAQQRAVIDVVNANIV

>d1nfp\_\_ c.1.16.2 (-) Non-fluorescent flavoprotein (luxF, FP390) {Photobacterium leiognathi}

MTKWNYGVFFLNFYHVGQQEPSLTMSNALETLRIIDEDTSIYDVVAFSEHHIDKSYNDETKLAPFVSLGKQIHVLATSPETVVKAAKYGMPLLFKWDDSQQKRIELLNHYQAAAAKFNVDIANVRHRLMLFVNVNDNPTQAKAELSIYLEDYLSYTQAETSIDEIINSNAAGNFDTCLHHVAEMAQGLNNKVDFLFCFESMKDQENKKSLMINFDKRVINYRKEHNLN

>d1fvpa\_ c.1.16.2 (A:) Non-fluorescent flavoprotein (luxF, FP390) {Photobacterium phosphoreum}

MNKWNYGVFFVNFYNKGQQEPSKTMNNALETLRIIDEDTSIYDVINIDDHYLVKKDSEDKKLAPFITLGEKLYVLATSENTVDIAAKYALPLVFKWDDINEERLKLLSFYNASASKYNKNIDLVRHQLMLHVNVNEAETVAKEELKLYIENYVACTQPSNFNGSIDSIIQSNVTGSYKDCLSYVANLAGKFDNTVDFLLCFESMQDQNKKKSVMIDLNNQVIKFRQDNNLI

>d1ezwa\_ c.1.16.3 (A:) Coenzyme F420 dependent tetrahydromethanopterin reductase {Archaeon Methanopyrus kandleri}

AEVSFGIELLPDDKPTKIAHLIKVAEDNGFEYAWICDHYNNYSYMGVLTLAAVITSKIKLGPGITNPYTRHPLITASNIATLDWISGGRAIIGMGPGDKATFDKMGLPFPCKIPIWNPEAEDEVGPATAIREVKEVIYQYLEGGPVEYEGKYVKTGTADVKARSIQGSDIPFYMGAQGPIMLKTAGEIANGVLVNASNPKDFEVAVPKIEEGAKEAGRSLDEIDVAAYTCFSIDKDEDKAIEATKIVVAFIVMGSPDVVLERHGIDTEKAEQIAEAIGKGDFGTAIGLVDEDMIEAFSIAGDPDTVVDKIEELLKAGVTQVVVGSPIGPDKEKAIELVGQEVIPHFK

>d1f07a\_ c.1.16.3 (A:) Coenzyme F420 dependent tetrahydromethanopterin reductase {Archaeon Methanobacterium thermoautotrophicum}

MKFGIEFVPNEPIEKIVKLVKLAEDVGFEYAWITDHYNNKNVYETLALIAEGTETIKLGPGVTNPYVRSPAITASAIATLDELSNGRATLGIGPGDKATFDALGIEWVKPVSTIRDAIAMMRTLLAGEKTESGAQLMGVKAVQEKIPIYMGAQGPMMLKTAGEISDGALINASNPKDFEAAVPLIKEGAEAAGKSIADIDVAAYTCCSIDEDAAAAANAAKIVVAFIAAGSPPPVFERHGLPADTGKKFGELLGKGDFGGAIGAVDDALMEAFSVVGTPDEFIPKIEALGEMGVTQYVAGSPIGPDKEKSIKLLGEVIASF

>d1qapa1 c.1.17.1 (A:130-296) Quinolinic acid phosphoribosyltransferase, C-terminal domain {Salmonella typhimurium}

VASEVRRYVGLLAGTQTQLLDTRKTLPGLRTALKYAVLCGGGANHRLGLTDAFLIKENHIIASGSVRQAVEKAFWLHPDVPVEVEVENLDELDDALKAGADIIMLDNFNTDQMREAVKRVNGQARLEVSGNVTAETLREFAETGVDFISVGALTKHVRALDLSMRFC

>d1qpoa1 c.1.17.1 (A:117-285) Quinolinic acid phosphoribosyltransferase, C-terminal domain {Mycobacterium tuberculosis}

IATATAAWVDAVRGTKAKIRDTRKTLPGLRALQKYAVRTGGGVNHRLGLGDAALIKDNHVAAAGSVVDALRAVRNAAPDLPCEVEVDSLEQLDAVLPEKPELILLDNFAVWQTQTAVQRRDSRAPTVMLESSGGLSLQTAATYAETGVDYLAVGALTHSVRVLDIGLDM

>d1qasa3 c.1.18.1 (A:299-625) Phospholipase C isozyme D1 (PLC-D1) {Rat (Rattus norvegicus)}

DQPLSHYLVSSSHNTYLLEDQLTGPSSTEAYIRALCKGCRCLELDCWDGPNQEPIIYHGYTFTSKILFCDVLRAIRDYAFKASPYPVILSLENHCSLEQQRVMARHLRAILGPILLDQPLDGVTTSLPSPEQLKGKILLKGKKLGGLLPAGGENGSEATDVSDEVEAAEMEDEAVRSQVQHKPKEDKLKLVPELSDMIIYCKSVHFGGFSSPGTSGQAFYEMASFSESRALRLLQESGNGFVRHNVSCLSRIYPAGWRTDSSNYSPVEMWNGGCQIVALNFQTPGPEMDVYLGCFQDNGGCGYVLKPAFLRDPNTTFNSRALTQGPW

>d2ptd\_\_ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Bacillus cereus}

ASSVNELENWSKWMQPIPDSIPLARISIPGTHDSGTFKLQNPIKQVWGMTQEYDFRYQMDHGARIFDIRGRLTDDNTIVLHHGPLYLYVTLHEFINEAKQFLKDNPSETIIMSLKKEYEDMKGAEDSFSSTFEKKYFVDPIFLKTEGNIKLGDARGKIVLLKRYSGSNEPGGYNNFYWPDNETFTTTVNQNANVTVQEKYKVSYDEKVKSIKDTMDETMNNSEDLNHLYINFTSLSSGGTAWNSPYYYASYINPEIANYIKQKNPARVGWVIQDYINEKWSPLLYQEVIRANKSLI

>d2plc\_\_ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Listeria monocytogenes}

VTTKQWMSALPDTTNLAALSIPGTHDTMSYNGDITWTLTKPLAQTQTMSLYQQLEAGIRYIDIRAKDNLNIYHGPIFLNASLSGVLETITQFLKKNPKETIIMRLKDEQNSNDSFDYRIQPLINIYKDYFYTTPRTDTSNKIPTLKDVRGKILLLSENHTKKPLVINSRKFGMQFGAPNQVIQDDYNGPSVKTKFKEIVQTAYQASKADNKLFLNHISATSLTFTPRQYAAALNNKVEQFVLNLTSEKVRGLGILIMDFPEKQTIKNIIKNNKF

>d7reqa1 c.1.19.1 (A:4-560) Methylmalonyl-CoA mutase, alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

LPRFDSVDLGNAPVPADAARRFEELAAKAGTGEAWETAEQIPVGTLFNEDVYKDMDWLDTYAGIPPFVHGPYATMYAFRPWTIRQYAGFSTAKESNAFYRRNLAAGQKGLSVAFDLPTHRGYDSDNPRVAGDVGMAGVAIDSIYDMRELFAGIPLDQMSVSMTMNGAVLPILALYVVTAEEQGVKPEQLAGTIQNDILKEFMVRNTYIYPPQPSMRIISEIFAYTSANMPKWNSISISGYHMQEAGATADIEMAYTLADGVDYIRAGESVGLNVDQFAPRLSFFWGIGMNFFMEVAKLRAARMLWAKLVHQFGPKNPKSMSLRTHSQTSGWSLTAQDVYNNVVRTCIEAMAATQGHTQSLHTNSLDEAIALPTDFSARIARNTQLFLQQESGTTRVIDPWSGSAYVEELTWDLARKAWGHIQEVEKVGGMAKAIEKGIPKMRIEEAAARTQARIDSGRQPLIGVNKYRLEHEPPLDVLKVDNSTVLAEQKAKLVKLRAERDPEKVKAALDKITWAAGNPDDKDPDRNLLKLCIDAGRAMATVGEMSDALEKVFGRYT

>d7reqb1 c.1.19.1 (B:16-475) Methylmalonyl-CoA mutase, alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

LTPTTLSLAGDFPKATEEQWEREVEKVLNRGRPPEKQLTFAECLKRLTVHTVDGIDIVPMYRPKDAPKKLGYPGVAPFTRGTTVRNGDMDAWDVRALHEDPDEKFTRKAILEGLERGVTSLLLRVDPDAIAPEHLDEVLSDVLLEMTKVEVFSRYDQGAAAEALVSVYERSDKPAKDLALNLGLDPIGFAALQGTEPDLTVLGDWVRRLAKFSPDSRAVTIDANIYHNAGAGDVAELAWALATGAEYVRALVEQGFTATEAFDTINFRVTATHDQFLTIARLRALREAWARIGEVFGVDEDKRGARQNAITSWRELTREDPYVNILRGSIATFSASVGGAESITTLPFTQALGLPEDDFPLRIARNTGIVLAEEVNIGRVNDPAGGSYYVESLTRSLADAAWKEFQEVEKLGGMSKAVMTEHVTKVLDACNAERAKRLANRKQPITAVSEFPMIGARSIE

>d1ccwb\_ c.1.19.2 (B:) Glutamate mutase, large subunit {Clostridium cochlearium}

MELKNKKWTDEEFHKQREEVLQQWPTGKEVDLQEAVDYLKKIPAEKNFAEKLVLAKKKGITMAQPRAGVALLDEHIELLRYLQDEGGADFLPSTIDAYTRQNRYDECENGIKESEKAGRSLLNGFPGVNFGVKGCRKVLEAVNLPLQARHGTPDSRLLAEIIHAGGWTSNEGGGISYNVPYAKNVTIEKSLLDWQYCDRLVGFYEEQGVHINREPFGPLTGTLVPPSMSNAVGITEALLAAEQGVKNITVGYGECGNMIQDIAALRCLEEQTNEYLKAYGYNDVFVTTVFHQWMGGFPQDESKAFGVIVTATTIAALAGATKVIVKTPHEAIGIPTKEANAAGIKATKMALNMLEGQRMPMSKELETEMAVIKAETKCILDKMFELGKGDLAIGTVKAFETGVMDIPFGPSKYNAGKMMPVRDNLGCVRYLEFGNVPFTEEIKNYNRERLQERAKFEGRDVSFQMVIDDIFAVGKGRLIGRPE

>d1eexa\_ c.1.19.3 (A:) Diol dehydratase, alpha subunit {Klebsiella oxytoca}

MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPSIKIVNGAVTELDGKPVSDFDLIDHFIARYGINLNRAEEVMAMDSVKLANMLCDPNVKRSEIVPLTTAMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQQAHVTNVKDNPVQIAADAAEGAWRGFDEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQCSLEEATELKLGMLGHTCYAETISVYGTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLEARCIYITKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDLECASSNDQTFTHSDMRRTARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREEDVIAIRNKAARALQAVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINKNRNGLEVVKALAQGGFTDVAQDMLNIQKAKLTGDYLHTSAIIVGDGQVLSAVNDVNDYAGPATGYRLQGERWEEIKNIPGALDPN

>d1f3ea\_ c.1.20.1 (A:) tRNA-guanine transglycosylase {Zymomonas mobilis}

RPRFSFSIAAREGKARTGTIEMKRGVIRTPAFMPVGTAATVKALKPETVRATGADIILGNTYHLMLRPGAERIAKLGGLHSFMGWDRPILTDSGGYQVMSLSSLTKQSEEGVTFKSHLDGSRHMLSPERSIEIQHLLGSDIVMAFDECTPYPATPSRAASSMERSMRWAKRSRDAFDSRKEQAENAALFGIQQGSVFENLRQQSADALAEIGFDGYAVGGLAVGEGQDEMFRVLDFSVPMLPDDKPHYLMGVGKPDDIVGAVERGIDMFDCVLPTRSGRNGQAFTWDGPINIRNARFSEDLKPLDSECHCAVCQKWSRAYIHHLIRAGEILGAMLMTEHNIAFYQQLMQKIRDSISEGRFSQFAQDFRARYF

>d1aj2\_\_ c.1.21.1 (-) Dihydropteroate synthetase {Escherichia coli}

MKLFAQGTSLDLSHPHVMGILNVTPDSFSDGGTHNSLIDAVKHANLMINAGATIIDVGGESTRPGAAEVSVEEELQRVIPVVEAIAQRFEVWISVDTSKPEVIRESAKVGAHIINDIRSLSEPGALEAAAETGLPVCLMHMQGNPKTMQEAPKYDDVFAEVNRYFIEQIARCEQAGIAKEKLLLDPGFGFGKNLSHNYSLLARLAEFHHFNLPLLVGMSRKSMIGQLLNVGPSERLSGSLACAVIAAMQGAHIIRVHDVKETVEAMRVVEATLSAKENKRYE

>d1ad1a\_ c.1.21.1 (A:) Dihydropteroate synthetase {Staphylococcus aureus}

TKTKIMGILNVTPDSFSDGGKFNNVESAVTRVKAMMDEGADIIDVGGVSTRPGHEMITVEEELNRVLPVVEAIVGFDVKISVDTFRSEVAEACLKLGVDIINDQWAGLYDHRMFQVVAKYDAEIVLMHNGNGNRDEPVVEEMLTSLLAQAHQAKIAGIPSNKIWLDPGIGFAKTRNEEAEVMARLDELVATEYPVLLATSRKRFTKEMMGYDTTPVERDEVTAATTAYGIMKGVRAVRVHNVELNAKLAKGIDFLKENENARHN

>d1eyea\_ c.1.21.1 (A:) Dihydropteroate synthetase {Mycobacterium tuberculosis}

PVQVMGVLNVTDDSFSDGGCYLDLDDAVKHGLAMAAAGAGIVDVGGESSRPGATRVDPAVETSRVIPVVKELAAQGITVSIDTMRADVARAALQNGAQMVNDVSGGRADPAMGPLLAEADVPWVLMHWRAVSADTPHVPVRYGNVVAEVRADLLASVADAVAAGVDPARLVLDPGLGFAKTAQHNWAILHALPELVATGIPVLVGASRKRFLGALLAGPDGVMRPTDGRDTATAVISALAALHGAWGVRVHDVRASVDAIKVVEAWMGAE

>d1f6ya\_ c.1.21.2 (A:) Methyltetrahydrofolate: corrinoid/iron-sulfur protein methyltransferase MetR {Moorella thermoacetica}

MLIIGERINGMFGDIKRAIQERDPAPVQEWARRQEEGGARALDLNVGPAVQDKVSAMEWLVEVTQEVSNLTLCLDSTNIKAIEAGLKKCKNRAMINSTNAEREKVEKLFPLAVEHGAALIGLTMNKTGIPKDSDTRLAFAMELVAAADEFGLPMEDLYIDPLILPANVAQDHAPEVLKTLQQIKMLADPAPKTVLGLSNVSQNCQNRPLINRTFLAMAMACGLMSAIADACDEALIETAATAEILLNQTVYCDSFVKMFKTR

>d1uroa\_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Human (Homo sapiens)}

GFPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAAQDFFSTCRSPEACCELTLQPLRRFPLDAAIIFSDILVVPQALGMEVTMVPGKGPSFPEPLREEQDLERLRDPEVVASELGYVFQAITLTRQRLAGRVPLIGFAGAPWTLMTYMVEGGGSSTMAQAKRWLYQRPQASHQLLRILTDALVPYLVGQVVAGAQALQLFESHAGHLGPQLFNKFALPYIRDVAKQVKARLREAGLAPVPMIIFAKDGHFALEELAQAGYEVVGLDWTVAPKKARECVGKTVTLQGNLDPCALYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYPDMDPEHVGAFVDAVHKHSRLLRQ

>d1j93a\_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Tobacco (Nicotiana tabacum), UROD-III}

TQPLLLDAVRGKEVERPPVWLMRQAGRYMKSYQLLCEKYPLFRDRSENVDLVVEISLQPWKVFRPDGVILFSDILTPLSGMNIPFDIIKGKGPVIFDPLRTAADVEKVREFIPEKSVPYVGEALTILRKEVNNQAAVLGFVGAPFTLASYVVEGGSSKNFTKIKRLAFAEPKVLHALLQKFATSMAKYIRYQADSGAQAVQIFDSWATELSPVDFEEFSLPYLKQIVDSVKLTHPNLPLILYASGSGGLLERLPLTGVDVVSLDWTVDMADGRRRLGPNVAIQGNVDPGVLFGSKEFITNRINDTVKKAGKGKHILNLGHGIKVGTPEENFAHFFEIAKGLRY

>d1b5ta\_ c.1.23.1 (A:) Methylenetetrahydrofolate reductase {Escherichia coli}

GQINVSFEFFPPRTSEMEQTLWNSIDRLSSLKPKFVSVTYGANSGERDRTHSIIKGIKDRTGLEAAPHLTCIDATPDELRTIARDYWNNGIRHIVALRGDLPPGSGKPEMYASDLVTLLKEVADFDISVAAYPEVHPEAKSAQADLLNLKRKVDAGANRAITQFFFDVESYLRFRDRCVSAGIDVEIIPGILPVSNFKQAKKFADMTNVRIPAWMAQMFDGLDDDAETRKLVGANIAMDMVKILSREGVKDFHFYTLNRAEMSYAICHTLGVRPA

>d1heta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Horse (Equus caballus)}

GFSTGYGSAVKVAKVTQGSTCAVFGLGGVGLSVIMGCKAAGAARIIGVDINKDKFAKAKEVGATECVNPQDYKKPIQEVLTEMSNGGVDFSFEVIGRLDTMVTALSCCQEAYGVSVIVGVPPDSQNLSMNPMLLLSGRTWKGAIFGGFKS

>d1d1ta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

GFSTGYGAAVKTGKVKPGSTCVVFGLGGVGLSVIMGCKSAGASRIIGIDLNKDKFEKAMAVGATECISPKDSTKPISEVLSEMTGNNVGYTFEVIGHLETMIDALASCHMNYGTSVVVGVPPSAKMLTYDPMLLFTGRTWKGCVFGGLKS

>d1ht0a2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

GFSTGYGSAVKVAKVTPGSTCAVFGLGGVGLSVVMGCKAAGAARIIAVDINKDKFAKAKELGATECINPQDYKKPIQEVLKEMTDGGVDFSFEVIGQLDTMMASLLCCHEACGTSVIVGVPPDSQNLSINPMLLLTGRTWKGAIFGGFKS

>d1teha2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

GISTGYGAAVNTAKLEPGSVCAVFGLGGVGLAVIMGCKVAGASRIIGVDINKDKFARAKEFGATECINPQDFSKPIQEVLIEMTDGGVDYSFECIGNVKVMRAALEACHKGWGVSVVVGVAASGEEIATRPFQLVTGRTWKGTAFGGWKS

>d1e3ia2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Mouse (Mus musculus), class II}

LIGCGFSSGYGAAINTAKVTPGSTCAVFGLGCVGLSAIIGCKIAGASRIIAIDINGEKFPKAKALGATDCLNPRELDKPVQDVITELTAGGVDYSLDCAGTAQTLKAAVDCTVLGWGSCTVVGAKVDEMTIPTVDVILGRSINGTFFGGW

>d1cdoa2 c.2.1.1 (A:176-324) Alcohol dehydrogenase {Cod (Gadus callarias)}

GVSTGFGAAVNTAKVEPGSTCAVFGLGAVGLAAVMGCHSAGAKRIIAVDLNPDKFEKAKVFGATDFVNPNDHSEPISQVLSKMTNGGVDFSLECVGNVGVMRNALESCLKGWGVSVLVGWTDLHDVATRPIQLIAGRTWKGSMFGGFKG

>d1keva2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase {Clostridium beijerinckii}

MMTTGFHGAELADIQMGSSVVVIGIGAVGLMGIAGAKLRGAGRIIGVGSRPICVEAAKFYGATDILNYKNGHIVDQVMKLTNGKGVDRVIMAGGGSETLSQAVSMVKPGGIISNINYHGSGDALLIPRVEWGCGMAHKTIKGGLCPGGRLRAEMLRDMVVYNRV

>d1ykfa2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase {Thermoanaerobacter brockii}

MMTTGFHGAELADIELGATVAVLGIGPVGLMAVAGAKLRGAGRIIAVGSRPVCVDAAKYYGATDIVNYKDGPIESQIMNLTEGKGVDAAIIAGGNADIMATAVKIVKPGGTIANVNYFGEGEVLPVPRLEWGCGMAHKTIKGGLCPGGRLRMERLIDLVFYKRV

>d1e3ja2 c.2.1.1 (A:151-313) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}

LEPLSVGVHACRRAGVQLGTTVLVIGAGPIGLVSVLAAKAYGAFVVCTARSPRRLEVAKNCGADVTLVVDPAKEEESSIIERIRSAIGDLPNVTIDCSGNEKCITIGINITRTGGTLMLVGMGSQMVTVPLVNACAREIDIKSVFRYCNDYPIALEMVASGRC

>d1qora2 c.2.1.1 (A:136-265) Quinone oxidoreductase {Escherichia coli}

YEIKPDEQFLFHAAAGGVGLIACQWAKALGAKLIGTVGTAQKAQSALKAGAWQVINYREEDLVERLKEITGGKKVRVVYDSVGRDTWERSLDCLQRRGLMVSFGNSSGAVTGVNLGILNQKGSLYVTRPS

>d1udc\_\_ c.2.1.2 (-) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase) {Escherichia coli}

MRVLVTGGSGYIGSHTCVQLLQNGHDVIILDNLCNSKRSVLPVIERLGGKHPTFVEGDIRNEALMTEILHDHAIDTVIHFAGLKAVGESVQKPLEYYDNNVNGTLRLISAMRAANVKNFIFSSSATVYGDQPKIPYVESFPTGTPQSPYGKSKLMVEQILTDLQKAQPDWSIALLRYFNPVGAHPSGDMGEDPQGIPNNLMPYIAQVAVGRRDSLAIFGNDYPTEDGTGVRDYIHVMDLADGHVVAMEKLANKPGVHIYNLGAGVGNSVLDVVNAFSKACGKPVNYHFAPRREGDLPAYWADASKADRELNWRVTRTLDEMAQDTWHWQSRHPQGYPD

>d1ek6a\_ c.2.1.2 (A:) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase) {Human (Homo sapiens)}

MAEKVLVTGGAGYIGSHTVLELLEAGYLPVVIDNFHNAFRGGGSLPESLRRVQELTGRSVEFEEMDILDQGALQRLFKKYSFMAVIHFAGLKAVGESVQKPLDYYRVNLTGTIQLLEIMKAHGVKNLVFSSSATVYGNPQYLPLDEAHPTGGCTNPYGKSKFFIEEMIRDLCQADKTWNAVLLRYFNPTGAHASGCIGEDPQGIPNNLMPYVSQVAIGRREALNVFGNDYDTEDGTGVRDYIHVVDLAKGHIAALRKLKEQCGCRIYNLGTGTGYSVLQMVQAMEKASGKKIPYKVVARREGDVAACYANPSLAQEELGWTAALGLDRMCEDLWRWQKQNPSGFGT

>d1bxka\_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Escherichia coli}

MRKILITGGAGFIGSALVRYIINETSDAVVVVDKLTYAGNLMSLAPVAQSERFAFEKVDICDRAELARVFTEHQPDCVMHLAAESHVDRSIDGPAAFIETNIVGTYTLLEAARAYWNALTEDKKSAFRFHHISTDEVYGDLHSTDDFFTETTPYAPSSPYSASKASSDHLVRAWLRTYGLPTLITNCSNNYGPYHFPEKLIPLMILNALAGKSLPVYGNGQQIRDWLYVEDHARALYCVATTGKVGETYNIGGHNERKNLDVVETICELLEELAPNKPHGVAHYRDLITFVADRPGHDLRYAIDASKIARELGCVPQETFESGMRKTVQWYLANESWWKQVQDGSYQGER

>d1kepa\_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Streptococcus suis, serotype 2}

QFKNIIVTGGAGFIGSNFVHYVYNNHPDVHVTVLDKLTYAGNKANLEAILGDRVELVVGDIADAELVDKLAAKADAIVHYAAESHNDNSLNDPSPFIHTNFIGTYTLLEAARKYDIRFHHVSTDEVYGDLPLREDLPGHGEGPGEKFTAETNYNPSSPYSSTKAASDLIVKAWVRSFGVKATISNCSNNYGPYQHIEKFIPRQITNILAGIKPKLYGEGKNVRDWIHTNDHSTGVWAILTKGRMGETYLIGADGEKNNKEVLELILEKMGQPKDAYDHVTDRAGHDLRYAIDASKLRDELGWTPQFTDFSEGLEETIQWYTDNQDWWKAEKEAVEANYAKTQEVIK

>d1kewa\_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Streptococcus suis, serotype 2}

MKILITGGAGFIGSAVVRHIIKNTQDTVVNIDKLTYAGNLESLSDISESNRYNFEHADICDSAEITRIFEQYQPDAVMHLAAESHVDRSITGPAAFIETNIVGTYALLEVARKYWSALGEDKKNNFRFHHISTDEVYGDLPHPDEVENSVTLPLFTETTAYAPSSPYSASKASSDHLVRAWRRTYGLPTIVTNCSNNYGPYHFPEKLIPLVILNALEGKPLPIYGKGDQIRDWLYVEDHARALHMVVTEGKAGETYNIGGHNEKKNLDVVFTICDLLDEIVPKATSYREQITYVADRPGHDRRYAIDAGKISRELGWKPLETFESGIRKTVEWYLANTQWVNNVKSGAYQSWIEQNYEGRQ

>d1e6ua\_ c.2.1.2 (A:) GDP-4-keto-6-deoxy-d-mannose epimerase/reductase (GDP-fucose synthetase) {Escherichia coli}

AKQRVFIAGHRGMVGSAIRRQLEQRGDVELVLRTRDELNLLDSRAVHDFFASERIDQVYLAAAKVGGIVANNTYPADFIYQNMMIESNIIHAAHQNDVNKLLFLGSSCIYPKLAKQPMAESELLQGTLEPTNEPYAIAKIAGIKLCESYNRQYGRDYRSVMPTNLYGPHDNFHPSNSHVIPALLRRFHEATAQKAPDVVVWGSGTPMREFLHVDDMAAASIHVMELAHEVWLENTQPMLSHINVGTGVDCTIRELAQTIAKVVGYKGRVVFDASKPDGTPRKLLDVTRLHQLGWYHEISLEAGLASTYQWFLENQ

>d1db3a\_ c.2.1.2 (A:) GDP-mannose 4,6-dehydratase {Escherichia coli}

SKVALITGVTGQDGSYLAEFLLEKGYEVHGIKRRASSFNTERVDHIYQDPHTCNPKFHLHYGDLSDTSNLTRILREVQPDEVYNLGAMSHVAVSFESPEYTADVDAMGTLRLLEAIRFLGLEKKTRFYQASTSELYGLVQEIPQKETTPFYPRSPYAVAKLYAYWITVNYRESYGMYACNGILFNHESPRRGETFVTRKITRAIANIAQGLESCLYLGNMDSLRDWGHAKDYVKMQWMMLQQEQPEDFVIATGVQYSVRQFVEMAAAQLGIKLRFEGTGVEEKGIVVSVTGHDAPGVKPGDVIIAVDPRYFRPAEVETLLGDPTKAHEKLGWKPEITLREMVSEMVANDLEAAKKHS

>d1eq2a\_ c.2.1.2 (A:) ADP-L-glycero-D-mannoheptose 6-epimerase {Escherichia coli}

MIIVTGGAGFIGSNIVKALNDKGITDILVVDNLKDGTKFVNLVDLNIADYMDKEDFLIQIMAGEEFGDVEAIFHEGACSSTTEWDGKYMMDNNYQYSKELLHYCLEREIPFLYASSAATYGGRTSDFIESREYEKPLNVYGYSKFLFDEYVRQILPEANSQIVGFRYFNVYGPREGHKGSMASVAFHLNTQLNNGESPKLFEGSENFKRDFVYVGDVADVNLWFLENGVSGIFNLGTGRAESFQAVADATLAYHKKGQIEYIPFPDKLKGRYQAFTQADLTNLRAAGYDKPFKTVAEGVTEYMAWLN

>d1qrra\_ c.2.1.2 (A:) Sulfolipid biosynthesis protein SQD1 {Thale cress (Arabidopsis thaliana)}

KRVMVIGGDGYCGWATALHLSKKNYEVCIVDNLVRRLFDHQLGLESLTPIASIHDRISRWKALTGKSIELYVGDICDFEFLAESFKSFEPDSVVHFGEQRSAPYSMIDRSRAVYTQHNNVIGTLNVLFAIKEFGEECHLVKLGTMGEYGTPNIDIEEGYITITHNGRTDTLPYPKQASSFYHLSKVHDSHNIAFTCKAWGIRATDLNQGVVYGVKTDETEMHEELRNRLDYDAVFGTALNRFCVQAAVGHPLTVYGKGGQTRGYLDIRDTVQCVEIAIANPAKAGEFRVFNQFTEQFSVNELASLVTKAGSKLGLDVKKMTVPNPRVEAEEHYYNAKHTKLMELGLEPHYLSDSLLDSLLNFAVQFKDRVDTKQIMPSVSWKKIGVKTKS

>d1k6xa\_ c.2.1.2 (A:) Negative transcriptional regulator NmrA {Aspergillus nidulans}

QQKKTIAVVNATGRQAASLIRVAAAVGHHVRAQVHSLKGLIAEELQAIPNVTLFQGPLLNNVPLMDTLFEGAHLAFINTTSQAGDEIAIGKDLADAAKRAGTIQHYIYSSMPDHSLYGPWPAVPMWAPKFTVENYVRQLGLPSTFVYAGIYNNNFTSLPYPLFQMELMPDGTFEWHAPFDPDIPLPWLDAEHDVGPALLQIFKDGPQKWNGHRIALTFETLSPVQVCAAFSRALNRRVTYVQVPKVEIKVNIPVGYREQLEAIEVVFGEHKAPYFPLPEFSRPAAGSPKGLGPANGKGAGAGMMQGPGGVISQRVTDEARKLWSGWRDMEEYAREVFPIEEEANGLDWML

>d1cyda\_ c.2.1.2 (A:) Carbonyl reductase {Mouse (Mus musculus)}

LNFSGLRALVTGAGKGIGRDTVKALHASGAKVVAVTRTNSDLVSLAKECPGIEPVCVDLGDWDATEKALGGIGPVDLLVNNAALVIMQPFLEVTKEAFDRSFSVNLRSVFQVSQMVARDMINRGVPGSIVNVSSMVAHVTFPNLITYSSTKGAMTMLTKAMAMELGPHKIRVNSVNPTVVLTDMGKKVSADPEFARKLKERHPLRKFAEVEDVVNSILFLLSDRSASTSGGGILVDAGYLAS

>d1oaa\_\_ c.2.1.2 (-) Sepiapterin reductase {Mouse (Mus musculus)}

ADGLGCAVCVLTGASRGFGRALAPQLARLLSPGSVMLVSARSESMLRQLKEELGAQQPDLKVVLAAADLGTEAGVQRLLSAVRELPRPEGLQRLLLINNAATLGDVSKGFLNVNDLAEVNNYWALNLTSMLCLTSGTLNAFQDSPGLSKTVVNISSLCALQPYKGWGLYCAGKAARDMLYQVLAAEEPSVRVLSYAPGPLDNDMQQLARETSKDPELRSKLQKLKSDGALVDCGTSAQKLLGLLQKDTFQSGAHVDFYD

>d1hdr\_\_ c.2.1.2 (-) Dihydropteridin reductase (pteridine reductase) {Human (Homo sapiens)}

EARRVLVYGGRGALGSRCVQAFRARNWWVASVDVVENEEASASIIVKMTDSFTEQADQVTAEVGKLLGEEKVDAILCVAGGWAGGNAKSKSLFKNCDLMWKQSIWTSTISSHLATKHLKEGGLLTLAGAKAALDGTPGMIGYGMAKGAVHQLCQSLAGKNSGMPPGAAAIAVLPVTLDTPMNRKSMPEADFSSWTPLEFLVETFHDWITGKNRPSSGSLIQVVTTEGRTELTPAYF

>d1e7wa\_ c.2.1.2 (A:) Dihydropteridin reductase (pteridine reductase) {Leishmania major}

TVPVALVTGAAKRLGRSIAEGLHAEGYAVCLHYHRSAAEANALSATLNARRPNSAITVQADLSNVATAPVSGADGSAPVTLFTRCAELVAACYTHWGRCDVLVNNASSFYPTPLLRNDEDGHEPCVGDREAMETATADLFGSNAIAPYFLIKAFAHRVAGTPAKHRGTNYSIINMVDAMTNQPLLGYTIYTMAKGALEGLTRSAALELAPLQIRVNGVGPGLSVLVDDMPPAVWEGHRSKVPLYQRDSSAAEVSDVVIFLCSSKAKYITGTCVKVDGGYSLTRA

>d1fds\_\_ c.2.1.2 (-) Human estrogenic 17beta-hydroxysteroid dehydrogenase {Human (Homo sapiens)}

ARTVVLITGCSSGIGLHLAVRLASDPSQSFKVYATLRDLKTQGRLWEAARALACPPGSLETLQLDVRDSKSVAAARERVTEGRVDVLVCNAGLGLLGPLEALGEDAVASVLDVNVVGTVRMLQAFLPDMKRRGSGRVLVTGSVGGLMGLPFNDVYCASKFALEGLCESLAVLLLPFGVHLSLIECGPVHTAFMEKVLGSPEEVLDRTDIHTFHRFYQYLAHSKQVFREAAQNPEEVAEVFLTALRAPKPTLRYFTTERFLPLLRMRLDDPSGSNYVTAMHREVFGDV

>d1fmca\_ c.2.1.2 (A:) 7-alpha-hydroxysteroid dehydrogenase {Escherichia coli}

MFNSDNLRLDGKCAIITGAGAGIGKEIAITFATAGASVVVSDINADAANHVVDEIQQLGGQAFACRCDITSEQELSALADFAISKLGKVDILVNNAGGGGPKPFDMPMADFRRAYELNVFSFFHLSQLVAPEMEKNGGGVILTITSMAAENKNINMTSYASSKAAASHLVRNMAFDLGEKNIRVNGIAPGAILTDALKSVITPEIEQKMLQHTPIRRLGQPQDIANAALFLCSPAASWVSGQILTVSGGGVQELN

>d1hdca\_ c.2.1.2 (A:) 3-alpha,20-beta-hydroxysteroid dehydrogenase {Streptomyces hydrogenans}

NDLSGKTVIITGGARGLGAEAARQAVAAGARVVLADVLDEEGAATARELGDAARYQHLDVTIEEDWQRVVAYAREEFGSVDGLVNNAGISTGMFLETESVERFRKVVEINLTGVFIGMKTVIPAMKDAGGGSIVNISSAAGLMGLALTSSYGASKWGVRGLSKLAAVELGTDRIRVNSVHPGMTYTPMTAETGIRQGEGNYPNTPMGRVGEPGEIAGAVVKLLSDTSSYVTGAELAVDGGWTTGPTVKYVMGQ

>d1fjha\_ c.2.1.2 (A:) 3-alpha-hydroxysteroid dehydrogenase {Comamonas testosteroni}

MSIIVISGCATGIGAATRKVLEAAGHQIVGIDIRDAEVIADLSTAEGRKQAIADVLAKCSKGMDGLVLCAGLGPQTKVLGNVVSVNYFGATELMDAFLPALKKGHQPAAVVISSVASAHLAFDKNPLALALEAGEEAKARAIVEHAGEQGGNLAYAGSKNALTVAVRKRAAAWGEAGVRLNTIAPGATETPLLQAGLQDPRYGESIAKFVPPMGRRAEPSEMASVIAFLMSPAASYVHGAQIVIDGGIDAVMRPTQF

>d1bdb\_\_ c.2.1.2 (-) Cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase {Pseudomonas sp., lb400}

MKLKGEAVLITGGASGLGRALVDRFVAEGAKVAVLDKSAERLAELETDHGDNVLGIVGDVRSLEDQKQAASRCVARFGKIDTLIPNAGIWDYSTALVDLPEESLDAAFDEVFHINVKGYIHAVKACLPALVASRGNVIFTISNAGFYPNGGGPLYTAAKHAIVGLVRELAFELAPYVRVNGVGSGGINSDLRGPSSLGMGSKAISTVPLADMLKSVLPIGRMPEVEEYTGAYVFFATRGDAAPATGALLNYDGGLGVRGFFSGAGGNDLLEQLNIH

>d1b16a\_ c.2.1.2 (A:) Drosophila alcohol dehydrogenase {Fruit fly (Drosophila lebanonensis)}

MDLTNKNVIFVAALGGIGLDTSRELVKRNLKNFVILDRVENPTALAELKAINPKVNITFHTYDVTVPVAESKKLLKKIFDQLKTVDILINGAGILDDHQIERTIAINFTGLVNTTTAILDFWDKRKGGPGGIIANICSVTGFNAIHQVPVYSASKAAVVSFTNSLAKLAPITGVTAYSINPGITRTPLVHTFNSWLDVEPRVAELLLSHPTQTSEQCGQNFVKAIEANKNGAIWKLDLGTLEAIEWTKHWDSHI

>d1gcoa\_ c.2.1.2 (A:) Glucose dehydrogenase {Bacillus megaterium}

MYKDLEGKVVVITGSSTGLGKSMAIRFATEKAKVVVNYRSKEDEANSVLEEIKKVGGEAIAVKGDVTVESDVINLVQSAIKEFGKLDVMINNAGLENPVSSHEMSLSDWNKVIDTNLTGAFLGSREAIKYFVENDIKGTVINMSSVHEKIPWPLFVHYAASKGGMKLMTETLALEYAPKGIRVNNIGPGAINTPINAEKFADPEQRADVESMIPMGYIGEPEEIAAVAAWLASSEASYVTGITLFADGGMTQYPSFQAGRG

>d1gega\_ c.2.1.2 (A:) meso-2,3-butanediol dehydrogenase {Klebsiella pneumoniae}

KKVALVTGAGQGIGKAIALRLVKDGFAVAIADYNDATAKAVASEINQAGGHAVAVKVDVSDRDQVFAAVEQARKTLGGFDVIVNNAGVAPSTPIESITPEIVDKVYNINVKGVIWGIQAAVEAFKKEGHGGKIINACSQAGHVGNPELAVYSSSKFAVRGLTQTAARDLAPLGITVNGYCPGIVKTPMWAEIDRQVSEAAGKPLGYGTAEFAKRITLGRLSEPEDVAACVSYLASPDSDYMTGQSLLIDGGMVFN

>d1h5qa\_ c.2.1.2 (A:) Mannitol dehydrogenase {Mushroom (Agaricus bisporus)}

PGFTISFVNKTIIVTGGNRGIGLAFTRAVAAAGANVAVIYRSAADAVEVTEKVGKEFGVKTKAYQCDVSNTDIVTKTIQQIDADLGPISGLIANAGVSVVKPATELTHEDFAFVYDVNVFGVFNTCRAVAKLWLQKQQKGSIVVTSSMSSQIINQSSLNGSLTQVFYNSSKAACSNLVKGLAAEWASAGIRVNALSPGYVNTDQTAHMDKKIRDHQASNIPLNRFAQPEEMTGQAILLLSDHATYMTGGEYFIDGGQLIW

>d1edoa\_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Oil seed rape (Brassica napus)}

SPVVVVTGASRGIGKAIALSLGKAGCKVLVNYARSAKAAEEVSKQIEAYGGQAITFGGDVSKEADVEAMMKTAIDAWGTIDVVVNNAGITRDTLLIRMKKSQWDEVIDLNLTGVFLCTQAATKIMMKKRKGRIINIASVVGLIGNIGQANYAAAKAGVIGFSKTAAREGASRNINVNVVCPGFIASDMTAKLGEDMEKKILGTIPLGRTGQPENVAGLVEFLALSPAASYITGQAFTIDGGIAI

>d1i01a\_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Escherichia coli}

MNFEGKIALVTGASRGIGRAIAETLAARGAKVIGTATSENGAQAISDYLGANGKGLMLNVTDPASIESVLEKIRAEFGEVDILVNNAGITRDNLLMRMKDEEWNDIIETNLSSVFRLSKAVMRAMMKKRHGRIITIGSVVGTMGNGGQANYAAAKAGLIGFSKSLAREVASRGITVNVVAPGFIETDMTRALSDDQRAGILAQVPAGRLGGAQEIANAVAFLASDEAAYITGETLHVNGGM

>d1eno\_\_ c.2.1.2 (-) Enoyl-ACP reductase {Oil seed rape (Brassica napus)}

LPIDLRGKRAFIAGIADDNGYGWAVAKSLAAAGAEILVGTWVPALNIFETSLRRGKFDQSRVLPDGSLMEIKKVYPLDAVFDNPEDVPEDVKANKRYAGSSNWTVQEAAECVRQDFGSIDILVHSLANGPEVSKPLLETSRKGYLAAISASSYSFVSLLSHFLPIMNPGGASISLTYIASERIIPGYGGGMSSAKAALESDTRVLAFEAGRKQNIRVNTISAGPLGSRAAKAIGFIDTMIEYSYNNAPIQKTLTADEVGNAAAFLVSPLASAITGATIYVDNGLNSMGVALDSPVFK

>d1eny\_\_ c.2.1.2 (-) Enoyl-ACP reductase {Mycobacterium tuberculosis, TB, gene InhA}

AGLLDGKRILVSGIITDSSIAFHIARVAQEQGAQLVLTGFDRLRLIQRITDRLPAKAPLLELDVQNEEHLASLAGRVTEAIGAGNKLDGVVHSIGFMPQTGMGINPFFDAPYADVSKGIHISAYSYASMAKALLPIMNPGGSIVGMDFDPSRAMPAYNWMTVAKSALESVNRFVAREAGKYGVRSNLVAAGPIRTLAMSAIVGGALGEEAGAQIQLLEEGWDQRAPIGWNMKDATPVAKTVCALLSDWLPATTGDIIYADGGAHTQLL

>d1qg6a\_ c.2.1.2 (A:) Enoyl-ACP reductase {Escherichia coli}

GFLSGKRILVTGVASKLSIAYGIAQAMHREGAELAFTYQNDKLKGRVEEFAAQLGSDIVLQCDVAEDASIDTMFAELGKVWPKFDGFVHSIGFAPGDQLDGDYVNAVTREGFKIAHDISSYSFVAMAKACRSMLNPGSALLTLSYLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEGVRVNAISAGPIRTLAASGIKDFRKMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLSAGISGEVVHVDGGFSIAAMNE

>d1ae1a\_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (Datura stramonium), I}

RWSLKGTTALVTGGSKGIGYAIVEELAGLGARVYTCSRNEKELDECLEIWREKGLNVEGSVCDLLSRTERDKLMQTVAHVFDGKLNILVNNAGVVIHKEAKDFTEKDYNIIMGTNFEAAYHLSQIAYPLLKASQNGNVIFLSSIAGFSALPSVSLYSASKGAINQMTKSLACEWAKDNIRVNSVAPGVILTPLVETAIKKNPHQKEEIDNFIVKTPMGRAGKPQEVSALIAFLCFPAASYITGQIIWADGGFTANGGF

>d2ae2a\_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (Datura stramonium), II}

AGRWNLEGCTALVTGGSRGIGYGIVEELASLGASVYTCSRNQKELNDCLTQWRSKGFKVEASVCDLSSRSERQELMNTVANHFHGKLNILVNNAGIVIYKEAKDYTVEDYSLIMSINFEAAYHLSVLAHPFLKASERGNVVFISSVSGALAVPYEAVYGATKGAMDQLTRCLAFEWAKDNIRVNGVGPGVIATSLVEMTIQDPEQKENLNKLIDRCALRRMGEPKELAAMVAFLCFPAASYVTGQIIYVDGGLMANCGF

>d1g0oa\_ c.2.1.2 (A:) 1,3,8-trihydroxynaphtalene reductase (THNR, naphtol reductase) {Rice blast fungus (Magnaporthe grisea)}

KYDAIPGPLGPQSASLEGKVALVTGAGRGIGREMAMELGRRGCKVIVNYANSTESAEEVVAAIKKNGSDAACVKANVGVVEDIVRMFEEAVKIFGKLDIVCSNSGVVSFGHVKDVTPEEFDRVFTINTRGQFFVAREAYKHLEIGGRLILMGSITGQAKAVPKHAVYSGSKGAIETFARCMAIDMADKKITVNVVAPGGIKTDMYHAVCREYIPNGENLSNEEVDEYAAVQWSPLRRVGLPIDIARVVCFLASNDGGWVTGKVIGIDGGACM

>d1ja9a\_ c.2.1.2 (A:) 1,3,6,8-tetrahydroxynaphthalene reductase {Rice blast fungus (Magnaporthe grisea)}

SKPLAGKVALTTGAGRGIGRGIAIELGRRGASVVVNYGSSSKAAEEVVAELKKLGAQGVAIQADISKPSEVVALFDKAVSHFGGLDFVMSNSGMEVWCDELEVTQELFDKVFNLNTRGQFFVAQQGLKHCRRGGRIILTSSIAAVMTGIPNHALYAGSKAAVEGFCRAFAVDCGAKGVTVNCIAPGGVKTDMFDENSWHYAPGGYKGMPQEKIDEGLANMNPLKRIGYPADIGRAVSALCQEESEWINGQVIKLTGGGI

>d1hdoa\_ c.2.1.2 (A:) Biliverdin IX beta reductase {Human (Homo sapiens)}

MAVKKIAIFGATGQTGLTTLAQAVQAGYEVTVLVRDSSRLPSEGPRPAHVVVGDVLQAADVDKTVAGQDAVIVLLGTRNDLSPTTVMSEGARNIVAAMKAHGVDKVVACTSAFLLWDPTKVPPRLQAVTDDHIRMHKVLRESGLKYVAVMPPHIGDQPLTGAYTVTLDGRGPSRVISKHDLGHFMLRCLTTDEYDGHSTYPSHQY

>d1e6wa\_ c.2.1.2 (A:) 3-hydroxyacyl-CoA dehydrogenase {Rat (Rattus norvegicus)}

SVKGLVAVITGGASGLGLSTAKRLVGQGATAVLLDVPNSEGETEAKKLGGNCIFAPANVTSEKEVQAALTLAKEKFGRIDVAVNCAGIAVAIKTYHEKKNQVHTLEDFQRVINVNLIGTFNVIRLVAGVMGQNEPDQGGQRGVIINTASVAAFEGQVGQAAYSASKGGIVGMTLPIARDLAPIGIRVVTIAPGLFATPLLTTLPDKVRNFLASQVPFPSRLGDPAEYAHLVQMVIENPFLNGEVIRLDGAIRMQP

>d1hu4a\_ c.2.1.2 (A:) Carbonyl reductase/20beta-hydroxysteroid dehydrogenase {Pig (Sus scrofa)}

SSNTRVALVTGANKGIGFAIVRDLCRQFAGDVVLTARDVARGQAAVKQLQAEGLSPRFHQLDIIDLQSIRALCDFLRKEYGGLDVLVNNAAIAFQLDNPTPFHIQAELTMKTNFMGTRNVCTELLPLIKPQGRVVNVSSTEGVRALNECSPELQQKFKSETITEEELVGLMNKFVEDTKNGVHRKEGWSDSTYGVTKIGVSVLSRIYARKLREQRAGDKILLNACCPGWVRTDMGGPKAPKSPEVGAETPVYLALLPSDAEGPHGQFVTDKKVVEWGVPPESYPWVNA

>d1gado1 c.2.1.3 (O:0-148,O:313-330) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Escherichia coli}

TIKVGINGFGRIGRIVFRAAQKRSDIEIVAINDLLDADYMAYMLKYDSTHGRFDGTVEVKDGHLIVNGKKIRVTAERDPANLKWDEVGVDVVAEATGLFLTDETARKHITAGAKKVVMTGPSKDNTPMFVKGANFDKYAGQDIVSNASXNETGYSNKVLDLIAHISK

>d1gd1o1 c.2.1.3 (O:0-148,O:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Bacillus stearothermophilus, nca 1503}

AVKVGINGFGRIGRNVFRAALKNPDIEVVAVNDLTDANTLAHLLKYDSVHGRLDAEVSVNGNNLVVNGKEIIVKAERDPENLAWGEIGVDIVVESTGRFTKREDAAKHLEAGAKKVIISAPAKNEDITIVMGVNQDKYDPKAHHVISNASXNETGYSHRVVDLAAYIASKGL

>d1cero1 c.2.1.3 (O:1-148,O:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermus aquaticus}

MKVGINGFGRIGRQVFRILHSRGVEVALINDLTDNKTLAHLLKYDSIYHRFPGEVAYDDQYLYVDGKAIRATAVKDPKEIPWAEAGVGVVIESTGVFTDADKAKAHLEGGAKKVIITAPAKGEDITIVMGVNHEAYDPSRHHIISNASXNEWGYANRVADLVELVLRKGV

>d1hdgo1 c.2.1.3 (O:1-148,O:313-331) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermotoga maritima}

ARVAINGFGRIGRLVYRIIYERKNPDIEVVAINDLTDTKTLAHLLKYDSVHKKFPGKVEYTENSLIVDGKEIKVFAEPDPSKLPWKDLGVDFVIESTGVFRNREKAELHLQAGAKKVIITAPAKGEDITVVIGCNEDQLKPEHTIISCASXNEYGYSNRVVDTLELLLKM

>d1b7go1 c.2.1.3 (O:1-138,O:301-340) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Sulfolobus solfataricus}

MVNVAVNGYGTIGKRVADAIIKQPDMKLVGVAKTSPNYEAFIAHRRGIRIYVPQQSIKKFEESGIPVAGTVEDLIKTSDIVVDTTPNGVGAQYKPIYLQLQRNAIFQGGEKAEVADISFSALCNYNEALGKKYIRVVSXESIVVPENIDAIRASMKLMSAEDSMRITNESLGILKGYLI

>d1cf2o1 c.2.1.3 (O:1-138,O:304-336) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Methanothermus fervidus}

MKAVAINGYGTVGKRVADAIAQQDDMKVIGVSKTRPDFEARMALKKGYDLYVAIPERVKLFEKAGIEVAGTVDDMLDEADIVIDCTPEGIGAKNLKMYKEKGIKAIFQGGEKHEDIGLSFNSLSNYEESYGKDYTRVVXIVPENVDAVRAILEMEEDKYKSINKTNKAMNIL

>d1ggaa1 c.2.1.3 (A:1-164,A:334-358) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Trypanosoma brucei brucei, glycosome}

TIKVGINGFGRIGRMVFQALCDDGLLGNEIDVVAVVDMNTDARYFAYQMKYDSVHGKFKHSVSTTKSKPSVAKDDTLVVNGHRILCVKAQRNPADLPWGKLGVEYVIESTGLFTVKSAAEGHLRGGARKVVISAPASGGAKTFVMGVNHNNYNPREQHVVSNASXNEWGYSHRVVDLVRHMAARDRAAKL

>d1i32a1 c.2.1.3 (A:1-165,A:335-358) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Leishmania mexicana}

APIKVGINGFGRIGRMVFQAICDQGLIGTEIDVVAVVDMSTNAEYFAYQMKHDTVHGRPKYTVEAVKSSPSVETADVLVVNGHRIKCVKAQRNPADLPWGKLGVDYVIESTGLFTDKLKAEGHIKGGAKKVVISAPASGGAKTIVMGVNQHEYSPASHHVVSNASXNEWAYSHRVVDLVRYMAAKDAASS

>d1dssg1 c.2.1.3 (G:1-148,G:313-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Lobster (Palinurus versicolor)}

SKIGINGFGRIGRLVLRAALEMGAQVVAVNDPFIALEYMVYMFKYDSTHGMFKGEVKAEDGALVVDGKKITVFNEMKPENIPWSKAGAEYIVESTGVFTTIEKASAHFKGGAKKVIISAPSADAPMFVCGVNLEKYSKDMKVVSNASXNEFGYSQRVIDLIKHMQKVDSA

>d3gpdg1 c.2.1.3 (G:1-150,G:315-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Human (Homo sapiens)}

GKVKVGVDGFGRIGRLVTRAAFNSGKVDIVAINDPFIDLHYMVYMFQYDSTHGKFHGTVKAEDGKLVIDGKAITIFQERDPENIKWGDAGTAYVVESTGVFTTMEKAGAHLKGGAKRIVISAPSADAPMFVMGVNHFKYANSLKIISNASXNEFGYSERVVDLMAHMASKE

>d1jn0a1 c.2.1.3 (A:0-148,A:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Spinach (Spinacia oleracea)}

KLKVAINGFGRIGRNFLRCWHGKDSPLDVVVINDTGGVKQASHLLKYDSILGTFDADVKTAGDSAISVGKVIKVVSDRNPVNLPWGDMGIDLVIEGTGVFVDRDGAGKHLQAGAKKVLITAPGKGDIPTYVVGVNEEGYTHADTIISNASXNEWGYSQRVVDLADIVANKWQ

>d1gl3a1 c.2.1.3 (A:1-133,A:355-367) Aspartate beta-semialdehyde dehydrogenase {Escherichia coli}

MKNVGFIGWRGMVGSVLMQRMVEERDFDAIRPVFFSTSQLGQAAPSFGGTTGTLQDAFDLEALKALDIIVTCQGGDYTNEIYPKLRESGWQGYWIDAASSLRMKDDAIIILDPVNQDVITDGLNNGIRTFVGGXAAEPLRRMLRQLA

>d1ebfa1 c.2.1.3 (A:2-150,A:341-359) Homoserine dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

STKVVNVAVIGAGVVGSAFLDQLLAMKSTITYNLVLLAEAERSLISKDFSPLNVGSDWKAALAASTTKTLPLDDLIAHLKTSPKPVILVDNTSSAYIAGFYTKFVENGISIATPNKKAFSSDLATWKALFSNKPTNGFVYHEATVGAGLXAAVTAAGVLGDVIKIAQRL

>d1e5qa1 c.2.1.3 (A:2-124,A:392-450) Saccharopine reductase {Rice blast fungus (Magnaporthe grisea)}

ATKSVLMLGSGFVTRPTLDVLTDSGIKVTVACRTLESAKKLSAGVQHSTPISLDVNDDAALDAEVAKHDLVISLIPYTFHATVIKSAIRQKKHVVTTSYVSPAMMELDQAAKDAGITVMNEIGXYSAMAKLVGVPCAVAVKFVLDGTISDRGVLAPMNSKINDPLMKELKEKYGIECKEKVVA

>d1f06a1 c.2.1.3 (A:1-118,A:269-320) Diaminopimelic acid dehydrogenase (DAPDH) {Corynebacterium glutamicum}

MTNIRVAIVGYGNLGRSVEKLIAKQPDMDLVGIFSRRATLDTKTPVFDVADVDKHADDVDVLFLCMGSATDIPEQAPKFAQFACTVDTYDNHRDIPRHRQVMNEAATAAGNVALVSTGXRNPDFTASSQIAFGRAAHRMKQQGQSGAFTVLEVAPYLLSPENLDDLIARDV

>d1dih\_1 c.2.1.3 (2-130,241-273) Dihydrodipicolinate reductase {Escherichia coli}

HDANIRVAIAGAGGRMGRQLIQAALALEGVQLGAALEREGSSLLGSDAGELAGAGKTGVTVQSSLDAVKDDFDVFIDFTRPEGTLNHLAFCRQHGKGMVIGTTGFDEAGKQAIRDAAADIAIVFAANFSXMTFANGAVRSALWLSGKESGLFDMRDVLDLNNL

>d1k5ha2 c.2.1.3 (A:1-125,A:275-300) 1-deoxy-D-xylulose-5-phosphate reductoisomerase {Escherichia coli}

MKQLTILGSTGSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLEFSPRYAVMDDEASAKLLKTMLQQQGSRTEVLSGQQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGKTILLANKXDMRTPIAHTMAWPNRVNSGVKPLDFC

>d1gcua1 c.2.1.3 (A:1-128,A:247-292) Biliverdin reductase {Rat (Rattus norvegicus)}

MDAEPKRKFGVVVVGVGRAGSVRLRDLKDPRSAAFLNLIGFVSRRELGSLDEVRQISLEDALRSQEIDVAYICSESSSHEDYIRQFLQAGKHVLVEYPMTLSFAAAQELWELAAQKGRVLHEEHVELLXKNIFLKDQDIFVQKLLDQVSAEDLAAEKKRIMHCLGLASDIQKLCH

>d1evja1 c.2.1.3 (A:30-160,A:323-381) Glucose-fructose oxidoreductase, N-terminal domain {Zymomonas mobilis}

RRFGYAIVGLGKYALNQILPGFAGCQHSRIEALVDGNAEKAKIVAAEYGVDPRKIYDYSNFDKIAKDPKIDAVYIILPNSLHAEFAIRAFKAGKHVMCEKPMATSVADCQRMIDAAKAANKKLMIGYRCHYXNQFSAQLDHLAEAVINNKPVRSPGEEGMQDVRLIQAIYEAARTGRPVNTDWGYVRQGGY

>d1h6da1 c.2.1.3 (A:51-212,A:375-433) Glucose-fructose oxidoreductase, N-terminal domain {Zymomonas mobilis}

QAATLPAGASQVPTTPAGRPMPYAIRPMPEDRRFGYAIVGLGKYALNQILPGFAGCQHSRIEALVSGNAEKAKIVAAEYGVDPRKIYDYSNFDKIAKDPKIDAVYIILPNSLHAEFAIRAFKAGKHVMCEKPMATSVADCQRMIDAAKAANKKLMIGYRCHYXNQFSAQLDHLAEAVINNKPVRSPGEEGMQDVRLIQAIYEAARTGRPVNTDWGYVRQGGY

>d1dpga1 c.2.1.3 (A:1-181,A:413-426) Glucose 6-phosphate dehydrogenase, N-terminal domain {Leuconostoc mesenteroides}

VSEIKTLVTFFGGTGDLAKRKLYPSVFNLYKKGYLQKHFAIVGTARQALNDDEFKQLVRDCIKDFTDDQAQAEAFIEHFSYRAHDVTDAASYAVLKEAIEEAADKFDIDGNRIFYMSVAPRFFGTIAKYLKSEGLLADTGYNRLMIEKPFGTSYDTAAELQNDLENAFDDNQLFRIDHYLGXEPYERMIHDTMNGD

>d1qkia1 c.2.1.3 (A:12-199,A:435-449) Glucose 6-phosphate dehydrogenase, N-terminal domain {Human (Homo sapiens)}

VCGILREELFQGDAFHQSDTHIFIIMGASGDLAKKKIYPTIWWLFRDGLLPENTFIVGYARSRLTVADIRKQSEPFFKATPEEKLKLEDFFARNSYVAGQYDDAASYQRLNSHMNALHLGSQANRLFYLALPPTVYEAVTKNIHESCMSQIGWNRIIVEKPFGRDLQSSDRLSNHISSLFREDQIYRIXDAYERLILDVFCGSQ

>d2naca1 c.2.1.4 (A:148-335) Formate dehydrogenase {Pseudomonas sp., strain 101}

ISVAEHVVMMILSLVRNYLPSHEWARKGGWNIADCVSHAYDLEAMHVGTVAAGRIGLAVLRRLAPFDVHLHYTDRHRLPESVEKELNLTWHATREDMYPVCDVVTLNCPLHPETEHMINDETLKLFKRGAYIVNTARGKLCDRDAVARALESGRLAGYAGDVWFPQPAPKDHPWRTMPYNGMTPHISG

>d1qp8a1 c.2.1.4 (A:83-263) Putative formate dehydrogenase {Archaeon Pyrobaculum aerophilum}

ADAVAEFALALLLAPYKRIIQYGEKMKRGDYGRDVEIPLIQGEKVAVLGLGEIGTRVGKILAALGAQVRGFSRTPKEGPWRFTNSLEEALREARAAVCALPLNKHTRGLVKYQHLALMAEDAVFVNVGRAEVLDRDGVLRILKERPQFIFASDVWWGRNDFAKDAEFFSLPNVVATPWVAG

>d1dxy\_1 c.2.1.4 (101-299) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}

SPAAIAEFALTDTLYLLRNMGKVQAQLQAGDYEKAGTFIGKELGQQTVGVMGTGHIGQVAIKLFKGFGAKVIAYDPYPMKGDHPDFDYVSLEDLFKQSDVIDLHVPGIEQNTHIINEAAFNLMKPGAIVINTARPNLIDTQAMLSNLKSGKLAGVGIDTYEYETEDLLNLAKHGSFKDPLWDELLGMPNVVLSPHIAYY

>d1gdha1 c.2.1.4 (A:101-291) D-glycerate dehydrogenase {Hyphomicrobium methylovorum}

VTVATAEIAMLLLLGSARRAGEGEKMIRTRSWPGWEPLELVGEKLDNKTLGIYGFGSIGQALAKRAQGFDMDIDYFDTHRASSSDEASYQATFHDSLDSLLSVSQFFSLNAPSTPETRYFFNKATIKSLPQGAIVVNTARGDLVDNELVVAALEAGRLAYAGFDVFAGEPNINEGYYDLPNTFLFPHIGSA

>d1psda1 c.2.1.4 (A:108-295) Phosphoglycerate dehydrogenase {Escherichia coli}

NTRSVAELVIGELLLLLRGVPEANAKAHRGVWNKLAAGSFEARGKKLGIIGYGHIGTQLGILAESLGMYVYFYDIENKLPLGNATQVQHLSDLLNMSDVVSLHVPENPSTKNMMGAKEISLMKPGSLLINASRGTVVDIPALCDALASKHLAGAAIDVFPTEPATNSDPFTSPLCEFDNVLLTPHIGG

>d2dlda1 c.2.1.4 (A:104-300) D-lactate dehydrogenase {Lactobacillus helveticus}

PNAIAEHAAIQAARVLRQDKRMDEKMAKRDLRWAPTIGREVRDQVVGVVGTGHIGQVFMRIMEGFGAKVIAYDIFKNPELEKKGYYVDSLDDLYKQADVISLHVPDVPANVHMINDKSIAEMKDGVVIVNCSRGRLVDTDAVIRGLDSGKIFGFVMDTYEDEVGVFNKDWEGKEFPDKRLADLIDRPNVLVTPHTAF

>d1pjca1 c.2.1.4 (A:136-303) L-alanine dehydrogenase {Phormidium lapideum}

AGRLSVQFGARFLERQQGGRGVLLGGVPGVKPGKVVILGGGVVGTEAAKMAVGLGAQVQIFDINVERLSYLETLFGSRVELLYSNSAEIETAVAEADLLIGAVLVPGRRAPILVPASLVEQMRTGSVIVDVAVDQGGCVETLHPTSHTQPTYEVFGVVHYGVPNMPGA

>d1f8ga1 c.2.1.4 (A:144-326) Nicotinamide nucleotide transhydrogenase dI component {Rhodospirillum rubrum}

AGYRAVIDGAYEFARAFPMMMTAAGTVPPARVLVFGVGVAGLQAIATAKRLGAVVMATDVRAATKEQVESLGGKFITVDDEAMKTAETAGGYAKEMGEEFRKKQAEAVLKELVKTDIAITTALIPGKPAPVLITEEMVTKMKPGSVIIDLAVEAGGNCPLSEPGKIVVKHGVKIVGHTNVPSR

>d1b3ra1 c.2.1.4 (A:190-352) S-adenosylhomocystein hydrolase {Rat (Rattus norvegicus)}

NLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVGKGCAQALRGFGARVIITEIDPINALQAAMEGYEVTTMDEACKEGNIFVTTTGCVDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWLNENAVEKVNIKPQVDRYLLKNGHRIILLAEGRLVNLGCAMGH

>d1gpja2 c.2.1.10 (A:144-302) Glutamyl tRNA-reductase middle domain {Archaeon Methanopyrus kandleri}

SEGAVSIGSAAVELAERELGSLHDKTVLVVGAGEMGKTVAKSLVDRGVRAVLVANRTYERAVELARDLGGEAVRFDELVDHLARSDVVVSATAAPHPVIHVDDVREALRKRDRRSPILIIDIANPRDVEEGVENIEDVEVRTIDDLRVIARENLERRRK

>d1mlda1 c.2.1.5 (A:1-144) Malate dehydrogenase {Pig (Sus scrofa)}

AKVAVLGASGGIGQPLSLLLKNSPLVSRLTLYDIAHTPGVAADLSHIETRATVKGYLGPEQLPDCLKGCDVVVIPAGVPRKPGMTRDDLFNTNATIVATLTAACAQHCPDAMICIISNPVNSTIPITAEVFKKHGVYNPNKIFG

>d5mdha1 c.2.1.5 (A:1-154) Malate dehydrogenase {Pig (Sus scrofa)}

SEPIRVLVTGAAGQIAYSLLYSIGNGSVFGKDQPIILVLLDITPMMGVLDGVLMELQDCALPLLKDVIATDKEEIAFKDLDVAILVGSMPRRDGMERKDLLKANVKIFKCQGAALDKYAKKSVKVIVVGNPANTNCLTASKSAPSIPKENFSCL

>d7mdha1 c.2.1.5 (A:23-197) Malate dehydrogenase {Sorghum (Sorghum vulgare), chloroplast}

DCFGVFCTTYDLKAEDKTKSWKKLVNIAVSGAAGMISNHLLFKLASGEVFGQDQPIALKLLGSERSFQALEGVAMELEDSLYPLLREVSIGIDPYEVFEDVDWALLIGAKPRGPGMERAALLDINGQIFADQGKALNAVASKNVKVLVVGNPCNTNALICLKNAPDIPAKNFHAL

>d1civa1 c.2.1.5 (A:12-193) Malate dehydrogenase {Flaveria bidentis, chloroplast}

LPAKQKPECFGVFCLTYDLKAEEETKSWKKIINVAVSGAAGMISNHLLFKLASGEVFGPDQPISLKLLGSERSFAALEGVAMELEDSLYPLLRQVSIGIDPYEIFQDAEWALLIGAKPRGPGMERADLLDINGQIFAEQGKALNAVASPNVKVMVVGNPCNTNALICLKNAPNIPPKNFHAL

>d2cmd\_1 c.2.1.5 (1-145) Malate dehydrogenase {Escherichia coli}

MKVAVLGAAGGIGQALALLLKTQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVKIKGFSGEDATPALEGADVVLISAGVRRKPGMDRSDLFNVNAGIVKNLVQQVAKTCPKACIGIITNPVNTTVAIAAEVLKKAGVYDKNKLFG

>d1bdma1 c.2.1.5 (A:0-154) Malate dehydrogenase {Thermus flavus}

MKAPVRVAVTGAAGQIGYSLLFRIAAGEMLGKDQPVILQLLEIPQAMKALEGVVMELEDCAFPLLAGLEATDDPDVAFKDADYALLVGAAPRKAGMERRDLLQVNGKIFTEQGRALAEVAKKDVKVLVVGNPANTNALIAYKNAPGLNPRNFTAM

>d2hlpa1 c.2.1.5 (A:22-162) Malate dehydrogenase {Archaeon Haloarcula marismortui}

TKVSVVGAAGTVGAAAGYNIALRDIADEVVFVDIPDKEDDTVGQAADTNHGIAYDSNTRVRQGGYEDTAGSDVVVITAGIPRQPGQTRIDLAGDNAPIMEDIQSSLDEHNDDYISLTTSNPVDLLNRHLYEAGDRSREQVIG

>d1b8pa1 c.2.1.5 (A:3-158) Malate dehydrogenase {Aquaspirillum arcticum}

KTPMRVAVTGAAGQICYSLLFRIANGDMLGKDQPVILQLLEIPNEKAQKALQGVMMEIDDCAFPLLAGMTAHADPMTAFKDADVALLVGARPRGPGMERKDLLEANAQIFTVQGKAIDAVASRNIKVLVVGNPANTNAYIAMKSAPSLPAKNFTAM

>d1guya1 c.2.1.5 (A:1-143) Malate dehydrogenase {Chloroflexus aurantiacus}

MRKKISIIGAGFVGSTTAHWLAAKELGDIVLLDIVEGVPQGKALDLYEASPIEGFDVRVTGTNNYADTANSDVIVVTSGAPRKPGMSREDLIKVNADITRACISQAAPLSPNAVIIMVNNPLDAMTYLAAEVSGFPKERVIGQ

>d1gv0a1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium tepidum}

MKITVIGAGNVGATTAFRLAEKQLARELVLLDVVEGIPQGKALDMYESGPVGLFDTKVTGSNDYADTANSDIVVITAGLPRKPGMTREDLLSMNAGIVREVTGRIMEHSKNPIIVVVSNPLDIMTHVAWQKSGLPKERVIGM

>d1guza1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium vibrioforme}

MKITVIGAGNVGATTAFRLAEKQLARELVLLDVVEGIPQGKALDMYESGPVGLFDTKVTGSNDYADTANSDIVIITAGLPRKPGMTREDLLMKNAGIVKEVTDNIMKHSKNPIIIVVSNPLDIMTHVAWVRSGLPKERVIGM

>d1hyha1 c.2.1.5 (A:21-166) L-2-hydroxyisocapronate dehydrogenase, L-HICDH {Lactobacillus confusus}

ARKIGIIGLGNVGAAVAHGLIAQGVADDYVFIDANEAKVKADQIDFQDAMANLEAHGNIVINDWAALADADVVISTLGNIKLQQDNPTGDRFAELKFTSSMVQSVGTNLKESGFHGVLVVISNPVDVITALFQHVTGFPAHKVIGT

>d5ldh\_1 c.2.1.5 (1-162) Lactate dehydrogenase {Pig (Sus scrofa)}

ATLKEKLIAPVAQQETTIPDNKITVVGVGQVGMACAISILGKSLTDELALVDVLEDKLKGEMMDLQHGSLFLQTPKIVANKDYSVTANSKIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPNCIIIVVSNPVDILTYVAWKLSGLPKHRVIG

>d9ldta1 c.2.1.5 (A:1-162) Lactate dehydrogenase {Pig (Sus scrofa)}

ATLKDQLIHNLLKEEHVPHNKITVVGVGAVGMACAISILMKELADEIALVDVMEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSRLVVITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSPNCKLLVVSNPVDILTYVAWKISGFPKNRVIG

>d1i0za1 c.2.1.5 (A:1-160) Lactate dehydrogenase {Human (Homo sapiens), heart isoform (H chain)}

ATLKEKLIAPVAEEEATVPNNKITVVGVGQVGMACAISILGKSLADELALVDVLEDKLKGEMMDLQHGSLFLQTPKIVADKDYSVTANSKIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPDCIIIVVSNPVDILTYVTWKLSGLPKHRVIG

>d1i10a1 c.2.1.5 (A:1-159) Lactate dehydrogenase {Human (Homo sapiens), muscle isoform (M chain)}

ATLKDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKGEMMDLQHGSLFLRTPKIVSGKDYNVTANSKLVIITAGARQQEGESRLNLVQRNVNIFKFIIPNVVKYSPNCKLLIVSNPVDILTYVAWKISGFPKNRVIG

>d2ldx\_1 c.2.1.5 (1-159) Lactate dehydrogenase {Mouse (Mus musculus)}

STVKEQLIQNLVPEDKLSRCKITVVGVGDVGMACAISILLKGLADELALVDADTDKLRGEALDLQHGSLFLSTPKIVFGKDYNVSANSKLVIITAGARMVSGQTRLDLLQRNVAIMKAIVPGVIQNSPDCKIIVVTNPVDILTYVVWKISGFPVGRVIG

>d1ldm\_1 c.2.1.5 (1-160) Lactate dehydrogenase {Dogfish (Squalus acanthias)}

ATLKDKLIGHLATSQEPRSYNKITVVGVGAVGMACAISILMKDLADEVALVDVMEDKLKGEMMDLQHGSLFLHTAKIVSGKDYSVSAGSKLVVITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKHSPDCIILVVSNPVDVLTYVAWKLSGLPMHRIIG

>d1ceqa1 c.2.1.5 (A:19-163) Lactate dehydrogenase {Malaria parasite (Plasmodium falciparum)}

PKAKIVLVGSGMIGGVMATLIVQKNLGDVVLFDIVKNMPHGKALDTSHTNVMAYSNCKVSGSNTYDDLAGSDVVIVTAGFTKAPGKSDKEWNRDDLLPLNNKIMIEIGGHIKKNCPNAFIIVVTNPVDVMVQLLHQHSGVPKNKIIGL

>d1ldna1 c.2.1.5 (A:15-162) Lactate dehydrogenase {Bacillus stearothermophilus}

MKNNGGARVVVIGAGFVGASYVFALMNQGIADEIVLIDANESKAIGDAMDFNHGKVFAPKPVDIWHGDYDDCRDADLVVICAGANQKPGETRLDLVDKNIAIFRSIVESVMASGFQGLFLVATNPVDILTYATWKFSGLPHERVIGSG

>d1llc\_1 c.2.1.5 (13-164) Lactate dehydrogenase {Lactobacillus casei}

ASITDKDHQKVILVGDGAVGSSYAFAMVLQGIAQEIGIVDIFKDKTKGDAIDLSNALPFTSPKKIYSAEYSDAKDADLVVITAGAPKQPGETRLDLVNKNLKILKSIVDPIVDSGFNLIFLVAANPVDILTYATWKLSGFPKNRVVGSG

>d1ez4a1 c.2.1.5 (A:16-162) Lactate dehydrogenase {Lactobacillus pentosus}

SMPNHQKVVLVGDGAVGSSYAFAMAQQGIAEEFVIVDVVKDRTKGDALDLEDAQAFTAPKKIYSGEYSDCKDADLVVITAGAPQKPGESRLDLVNKNLNILSSIVKPVVDSGFDGIFLVAANPVDILTYATWKFSGFPKERVIGSG

>d1llda1 c.2.1.5 (A:7-149) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}

PTKLAVIGAGAVGSTLAFAAAQRGIAREIVLEDIAKERVEAEVLDMQHGSSFYPTVSIDGSDDPEICRDADMVVITAGPRQKPGQSRLELVGATVNILKAIMPNLVKVAPNAIYMLITNPVDIATHVAQKLTGLPENQIFGSG

>d1a5z\_1 c.2.1.5 (22-163) Lactate dehydrogenase {Thermotoga maritima}

MKIGIVGLGRVGSSTAFALLMKGFAREMVLIDVDKKRAEGDALDLIHGTPFTRRANIYAGDYADLKGSDVVIVAAGVPQKPGETRLQLLGRNARVMKEIARNVSKYAPDSIVIVVTNPVDVLTYFFLKESGMDPRKVFGS

>d1hyea1 c.2.1.5 (A:1-145) MJ0490, lactate/malate dehydrogenase {Archaeon Methanococcus jannaschii}

MKVTIIGASGRVGSATALLLAKEPFMKDLVLIGREHSINKLEGLREDIYDALAGTRSDANIYVESDENLRIIDESDVVIITSGVPRKEGMSRMDLAKTNAKIVGKYAKKIAEICDTKIFVITNPVDVMTYKALVDSKFERNQVFG

>d1qmga2 c.2.1.6 (A:82-307) Acetohydroxy acid isomeroreductase, ketoacid reductoisomerase (KARI) {Spinach (Spinacia oleracea)}

SATTFDFDSSVFKKEKVTLSGHDEYIVRGGRNLFPLLPDAFKGIKQIGVIGWGSQAPAQAQNLKDSLTEAKSDVVVKIGLRKGSNSFAEARAAGFSEENGTLGDMWETISGSDLVLLLISDSAQADNYEKVFSHMKPNSILGLSHGFLLGHLQSLGQDFPKNISVIAVCPKGMGPSVRRLYVQGKEVNGAGINSSFAVHQDVDGRATDVALGWSIALGSPFTFATT

>d2pgd\_2 c.2.1.6 (1-176) 6-phosphogluconate dehydrogenase {Sheep (Ovis orientalis aries)}

AQADIALIGLAVMGQNLILNMNDHGFVVCAFNRTVSKVDDFLANEAKGTKVLGAHSLEEMVSKLKKPRRIILLVKAGQAVDNFIEKLVPLLDIGDIIIDGGNSEYRDTMRRCRDLKDKGILFVGSGVSGGEDGARYGPSLMPGGNKEAWPHIKAIFQGIAAKVGTGEPCCDWVGDD

>d1pgja2 c.2.1.6 (A:1-178) 6-phosphogluconate dehydrogenase {Trypanosoma brucei}

SMDVGVVGLGVMGANLALNIAEKGFKVAVFNRTYSKSEEFMKANASAPFAGNLKAFETMEAFAASLKKPRKALILVQAGAATDSTIEQLKKVFEKGDILVDTGNAHFKDQGRRAQQLEAAGLRFLGMGISGGEEGARKGPAFFPGGTLSVWEEIRPIVEAAAAKADDGRPCVTMNGSG

>d1f0ya2 c.2.1.6 (A:12-203) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (Homo sapiens)}

KIIVKHVTVIGGGLMGAGIAQVAAATGHTVVLVDQTEDILAKSKKGIEESLRKVAKKKFAENPKAGDEFVEKTLSTIATSTDAASVVHSTDLVVEAIVENLKVKNELFKRLDKFAAEHTIFASNTSSLQITSIANATTRQDRFAGLHFFNPVPVMKLVEVIKTPMTSQKTFESLVDFSKALGKHPVSCKDTP

>d1dlja2 c.2.1.6 (A:1-196) UDP-glucose dehydrogenase (UDPGDH) {Streptococcus pyogenes}

MKIAVAGSGYVGLSLGVLLSLQNEVTIVDILPSKVDKINNGLSPIQDEYIEYYLKSKQLSIKATLDSKAAYKEAELVIIATPTNYNSRINYFDTQHVETVIKEVLSVNSHATLIIKSTIPIGFITEMRQKFQTDRIIFSPEFLRESKALYDNLYPSRIIVSCEENDSPKVKADAEKFALLLKSAAKKNNVPVLIMG

>d1bg6\_2 c.2.1.6 (4-187) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}

SKTYAVLGLGNGGHAFAAYLALKGQSVLAWDIDAQRIKEIQDRGAIIAEGPGLAGTAHPDLLTSDIGLAVKDADVILIVVPAIHHASIAANIASYISEGQLIILNPGATGGALEFRKILRENGAPEVTIGETSSMLFTCRSERPGQVTVNAIKGAMDFACLPAAKAGWALEQIGSVLPQYVAVE

>d1evya2 c.2.1.6 (A:9-188) Glycerol-3- phosphate dehydrogenase {Trypanosome (Leishmania mexicana)}

KDELLYLNKAVVFGSGAFGTALAMVLSKKCREVCVWHMNEEEVRLVNEKRENVLFLKGVQLASNITFTSDVEKAYNGAEIILFVIPTQFLRGFFEKSGGNLIAYAKEKQVPVLVCTKGIERSTLKFPAEIIGEFLPSPLLSVLAGPSFAIEVATGVFTCVSIASADINVARRLQRIMSTG

>d1ks9a2 c.2.1.6 (A:1-167) Ketopantoate reductase PanE {Escherichia coli}

MKITVLGCGALGQLWLTALCKQGHEVQGWLRVPQPYCSVNLVETDGSIFNESLTANDPDFLATSDLLLVTLKAWQVSDAVKSLASTLPVTTPILLIHNGMGTIEELQNIQQPLLMGTTTHAARRDGNVIIHVANGITHIGPARQQDGDYSYLADILQTVLPDVAWHN

>d1jaya\_ c.2.1.6 (A:) Coenzyme F420H2:NADP+ oxidoreductase (FNO) {Archaeon Archaeoglobus fulgidus}

MRVALLGGTGNLGKGLALRLATLGHEIVVGSRREEKAEAKAAEYRRIAGDASITGMKNEDAAEACDIAVLTIPWEHAIDTARDLKNILREKIVVSPLVPVSRGAKGFTYSSERSAAEIVAEVLESEKVVSALHTIPAARFANLDEKFDWDVPVCGDDDESKKVVMSLISEIDGLRPLDAGPLSNSRLVESLTPLILNIMRFNGMGELGIKFL

>d1bgva1 c.2.1.7 (A:195-449) Glutamate dehydrogenase {Clostridium symbiosum}

KARSFGGSLVRPEATGYGSVYYVEAVMKHENDTLVGKTVALAGFGNVAWGAAKKLAELGAKAVTLSGPDGYIYDPEGITTEEKINYMLEMRASGRNKVQDYADKFGVQFFPGEKPWGQKVDIIMPCATQNDVDLEQAKKIVANNVKYYIEVANMPTTNEALRFLMQQPNMVVAPSKAVNAGGVLVSGFEMSQNSERLSWTAEEVDSKLHQVMTDIHDGSAAAAERYGLGYNLVAGANIVGFQKIADAMMAQGIAW

>d1gtma1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}

GGSLGRIEATARGASYTIREAAKVLGWDTLKGKTIAIQGYGNAGYYLAKIMSEDFGMKVVAVSDSKGGIYNPDGLNADEVLKWKNEHGSVKDFPGATNITNEELLELEVDVLAPAAIEEVITKKNADNIKAKIVAEVANGPVTPEADEILFEKGILQIPDFLCNAGGVTVSYFEWVQNITGYYWTIEEVRERLDKKMTKAFYDVYNIAKEKNIHMRDAAYVVAVQRVYQAMLDRGWVKH

>d1euza1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Thermococcus profundus}

IGGSLGRGTATAQGAIFTIREAAKALGIDLKGKKIAVQGYGNAGYYTAKLAKEQLGMTVVAVSDSRGGIYNPDGLDPDEVLKWKREHGSVKDFPGATNITNEELLELEVDVLAPAAIEEVITEKNADNIKAKIVAEVANGPVTPEADDILREKGILQIPDFLCNAGGVTVSYFEWVQNINGYYWTEEEVREKLDKKMTKAFWEVYNTHKDKNIHMRDAAYVVAVSRVYQAMKDRGWVKK

>d1bvua1 c.2.1.7 (A:181-418) Glutamate dehydrogenase {Archaeon Thermococcus litoralis}

GGIVARMDATARGASYTVREAAKALGMDLKGKTIAIQGYGNAGYYMAKIMSEEYGMKVVAVSDTKGGIYNPDGLNADEVLAWKKKTGSVKDFPGATNITNEELLELEVDVLAPSAIEEVITKKNADNIKAKIVAELANGPTTPEADEILYEKGILIIPDFLCNAGGVTVSYFEWVQNITGDYWTVEETRAKLDKKMTKAFWDVYNTHKEKNINMRDAAYVVAVSRVYQAMKDRGWIKK

>d1b26a1 c.2.1.7 (A:179-412) Glutamate dehydrogenase {Thermotoga maritima}

GGSKGREEATGRGVKVCAGLAMDVLGIDPKKATVAVQGFGNVGQFAALLISQELGSKVVAVSDSRGGIYNPEGFDVEELIRYKKEHGTVVTYPKGERITNEELLELDVDILVPAALEGAIHAGNAERIKAKAVVEGANGPTTPEADEILSRRGILVVPDILANAGGVTVSYFEWVQDLQSFFWDLDQVRNALEKMMKGAFNDVMKVKEKYNVDMRTAAYILAIDRVAYATKKRG

>d1hwxa1 c.2.1.7 (A:209-501) Glutamate dehydrogenase {Cow (Bos taurus)}

HGRISATGRGVFHGIENFIENASYMSILGMTPGFGDKTFAVQGFGNVGLHSMRYLHRFGAKCVAVGESDGSIWNPDGIDPKELEDFKLQHGTILGFPKAKIYEGSILEVDCDILIPAASEKQLTKSNAPRVKAKIIAEGANGPTTPQADKIFLERNIMVIPDLYLNAGGVTVSYFQILKNLNHVSYGRLTFKYERDSNYHLLMSVQESLERKFGKHGGTIPIVPTAEFQDRISGASEKDIVHSGLAYTMERSARQIMRTAMKYNLGLDLRTAAYVNAIEKVFRVYNEAGVTFT

>d1leha1 c.2.1.7 (A:135-364) Leucine dehydrogenase {Bacillus sphaericus}

GISPAFGSSGNPSPVTAYGVYRGMKAAAKEAFGSDSLEGLAVSVQGLGNVAKALCKKLNTEGAKLVVTDVNKAAVSAAVAEEGADAVAPNAIYGVTCDIFAPCALGAVLNDFTIPQLKAKVIAGSADNQLKDPRHGKYLHELGIVYAPDYVINAGGVINVADELYGYNRTRAMKRVDGIYDSIEKIFAISKRDGVPSYVAADRMAEERIAKVAKARSQFLQDQRNILNGR

>d1c1da1 c.2.1.7 (A:149-349) Phenylalanine dehydrogenase {Rhodococcus sp., M4}

SAFTTAVGVFEAMKATVAHRGLGSLDGLTVLVQGLGAVGGSLASLAAEAGAQLLVADTDTERVAHAVALGHTAVALEDVLSTPCDVFAPCAMGGVITTEVARTLDCSVVAGAANNVIADEAASDILHARGILYAPDFVANAGGAIHLVGREVLGWSESVVHERAVAIGDTLNQVFEISDNDGVTPDEAARTLAGRRAREAS

>d1a4ia1 c.2.1.7 (A:127-296) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Human (Homo sapiens)}

LTSINAGRLARGDLNDCFIPCTPKGCLELIKETGVPIAGRHAVVVGRSKIVGAPMHDLLLWNNATVTTCHSKTAHLDEEVNKGDILVVATGQPEMVKGEWIKPGAIVIDCGINYVPDDKKPNGRKVVGDVAYDEAKERASFITPVPGGVGPMTVAMLMQSTVESAKRFLE

>d1b0aa1 c.2.1.7 (A:123-288) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Escherichia coli}

FHPYNVGRLCQRAPRLRPCTPRGIVTLLERYNIDTFGLNAVVIGASNIVGRPMSMELLLAGCTTTVTHRFTKNLRHHVENADLLIVAVGKPGFIPGDWIKEGAIVIDVGINRLENGKVVGDVVFEDAAKRASYITPVPGGVGPMTVATLIENTLQACVEYHDPQDE

>d1edza1 c.2.1.7 (A:149-319) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}

PCTPLAIVKILEFLKIYNNLLPEGNRLYGKKCIVINRSEIVGRPLAALLANDGATVYSVDVNNIQKFTRGESLKLNKHHVEDLGEYSEDLLKKCSLDSDVVITGVPSENYKFPTEYIKEGAVCINFACTKNFSDDVKEKASLYVPMTGKVTIAMLLRNMLRLVRNVELSKE

>d1do8a1 c.2.1.7 (A:280-573) Mitochondrial NAD(P)-dependenent malic enzyme {Human (Homo sapiens)}

IQGTAAVALAGLLAAQKVISKPISEHKILFLGAGEAALGIANLIVMSMVENGLSEQEAQKKIWMFDKYGLLVKGRKAKIDSYQEPFTHSAPESIPDTFEDAVNILKPSTIIGVAGAGRLFTPDVIRAMASINERPVIFALSNPTAQAECTAEEAYTLTEGRCLFASGSPFGPVKLTDGRVFTPGQGNNVYIFPGVALAVILCNTRHISDSVFLEAAKALTSQLTDEELAQGRLYPPLANIQEVSINIAIKVTEYLYANKMAFRYPEPEDKAKYVKERTWRSEYDSLLPDVYEWP

>d1id1a\_ c.2.1.9 (A:) Rck domain from putative potassium channel Kch {Escherichia coli}

HRKDHFIVCGHSILAINTILQLNQRGQNVTVISNLPEDDIKQLEQRLGDNADVIPGDSNDSSVLKKAGIDRCRAILALSDNDADNAFVVLSAKDMSSDVKTVLAVSDSKNLNKIKMVHPDIILSPQLFGSEILARVLNGEEINNDMLVSMLLN

>d1jkja1 c.2.1.8 (A:1-121) Succinyl-CoA synthetase, alpha-chain, N-terminal (CoA-binding) domain {Escherichia coli}

SILIDKNTKVICQGFTGSQGTFHSEQAIAYGTKMVGGVTPGKGGTTHLGLPVFNTVREAVAATGATASVIYVPAPFCKDSILEAIDAGIKLIITITEGIPTLDMLTVKVKLDEAGVRMIGP

>d1euca1 c.2.1.8 (A:1-130) Succinyl-CoA synthetase, alpha-chain, N-terminal (CoA-binding) domain {Pig (Sus scrofa)}

CSYTASRKHLYVDKNTKVICQGFTGKQGTFHSQQALEYGTNLVGGTTPGKGGKTHLGLPVFNTVKEAKEQTGATASVIYVPPPFAAAAINEAIDAEVPLVVCITEGIPQQDMVRVKHRLLRQGKTRLIGP

>d1djna2 c.3.1.1 (A:490-645) Trimethylamine dehydrogenase, C-terminal domain {Methylophilus methylotrophus, w3a1}

RWNTDGTNCLTHDPIPGADASLPDQLTPEQVMDGKKKIGKRVVILNADTYFMAPSLAEKLATAGHEVTIVSGVHLANYMHFTLEYPNMMRRLHELHVEELGDHFCSRIEPGRMEIYNIWGDGSKRTYRGPGVSPRDANTSHRWIEFDSLVLVTGRH

>d1cjca1 c.3.1.1 (A:107-331) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos taurus)}

HQALDIPGEELPGVFSARAFVGWYNGLPENRELAPDLSCDTAVILGQGNVALDVARILLTPPDHLEKTDITEAALGALRQSRVKTVWIVGRRGPLQVAFTIKELREMIQLPGTRPMLDPADFLGLQDRIKEAARPRKRLMELLLRTATEKPGVEEAARRASASRAWGLRFFRSPQQVLPSPDGRRAAGIRLAVTRLEGIGEATRAVPTGDVEDLPCGLVLSSIGY

>d1h7wa3 c.3.1.1 (A:288-440) Dihydropyrimidine dehydrogenase, domain 3 {Pig (Sus scrofa)}

PKTDDIFQGLTQDQGFYTSKDFLPLVAKSSKAGMCACHSPLPSIRGAVIVLGAGDTAFDCATSALRCGARRVFLVFRKGFVNIRAVPEEVELAKEEKCEFLPFLSPRKVIVKGGRIVAVQFVRTEQDETGKWNEDEDQIVHLKADVVISAFGS

>d1coy\_1 c.3.1.2 (4-318,451-506) Cholesterol oxidase {Brevibacterium sterolicum}

RTLADGDRVPALVIGSGYGGAVAALRLTQAGIPTQIVEMGRSWDTPGSDGKIFCGMLNPDKRSMWLADKTDQPVSNFMGFGINKSIDRYVGVLDSERFSGIKVYQGRGVGGGSLVNGGMAVTPKRNYFEEILPSVDSNEMYNKYFPRANTGLGVNNIDQAWFESTEWYKFARTGRKTAQRSGFTTAFVPNVYDFEYMKKEAAGQVTKSGLGGEVIYGNNAGKKSLDKTYLAQAAATGKLTITTLHRVTKVAPATGSGYSVTMEQIDEQGNVVATKVVTADRVFFAAGSVGTSKLLVSMKAQGHLPNLSSQVGEGWXGVLLNKATDNFGRLPEYPGLYVVDGSLVPGNVGVNPFVTITALAERNMDKIISSDI

>d1ijha1 c.3.1.2 (A:9-318,A:451-506) Cholesterol oxidase {Streptomyces sp.}

GYVPAVVIGTGYGAAVSALRLGEAGVQTLMLEMGQLWNQPGPDGNIFCGMLNPDKRSSWFKNRTEAPLGSFLWLDVVNRNIDPYAGVLDRVNYDQMSVYVGRGVGGGSLVNGGMAVEPKRSYFEEILPRVDSSEMYDRYFPRANSMLRVNHIDTKWFEDTEWYKFARVSREQAGKAGLGTVFVPNVYDFGYMQREAAGEVPKSALATEVIYGNNHGKQSLDKTYLAAALGTGKVTIQTLHQVKTIRQTKDGGYALTVEQKDTDGKLLATKEISCRYLFLGAGSLGSTELLVRARDTGTLPNLNSEVGAGWXGCVLGKATDDYGRVAGYKNLYVTDGSLIPGSVGVLPFVTITALAERNVERIIKQDV

>d1k0ia1 c.3.1.2 (A:1-173,A:276-394) p-Hydroxybenzoate hydroxylase, PHBH {Pseudomonas aeruginosa}

MKTQVAIIGAGPSGLLLGQLLHKAGIDNVILERQTPDYVLGRIRAGVLEQGMVDLLREAGVDRRMARDGLVHEGVEIAFAGQRRRIDLKRLSGGKTVTVYGQTEVTRDLMEAREACGATTVYQAAEVRLHDLQGERPYVTFERDGERLRLDCDYIAGCDGFHGISRQSIPAERXMQHGRLFLAGDAAHIVPPTGAKGLNLAASDVSTLYRLLLKAYREGRGELLERYSAICLRRIWKAERFSWWMTSVLHRFPDTDAFSQRIQQTELEYYLGSEAGLATIAENYVGLPYEEIE

>d1el8a1 c.3.1.2 (A:1-217,A:322-385) Sarcosine oxidase {Bacillus sp., strain b0618}

STHFDVIVVGAGSMGMAAGYQLAKQGVKTLLVDAFDPPHTNGSHHGDTRIIRHAYGEGREYVPLALRSQELWYELEKETHHKIFTKTGVLVFGPKGESAFVAETMEAAKEHSLTVDLLEGDEINKRWPGITVPENYNAIFEPNSGVLFSENCIRAYRELAEARGAKVLTHTRVEDFDISPDSVKIETANGSYTADKLIVSMGAWNSKLLSKLNLDIPXDEHFIIDLHPEHSNVVIAAGFSGHGFKFSSGVGEVLSQLALTGKTEHDISIFSINRPALKESLQ

>d1foha5 c.3.1.2 (A:1-240,A:342-461) Phenol hydroxylase {Soil-living yeast (Trichosporon cutaneum)}

TKYSESYCDVLIVGAGPAGLMAARVLSEYVRQKPDLKVRIIDKRSTKVYNGQADGLQCRTLESLKNLGLADKILSEANDMSTIALYNPDENGHIRRTDRIPDTLPGISRYHQVVLHQGRIERHILDSIAEISDTRIKVERPLIPEKMEIDSSKAEDPEAYPVTMTLRYMSDHESTPLQFGHKTENSLFHSNLQTQEEEDANYRLPEGKEAGEIETVHCKYVIGCDGGHSWVRRTLGFEMIXVTEKFSKDERVFIAGDACHTHSPKAGQGMNTSMMDTYNLGWKLGLVLTGRAKRDILKTYEEERHAFAQALIDFDHQFSRLFSGRPAKDVADEMGVSMDVFKEAFVKGNEFASGTAINYDE

>d1cf3a1 c.3.1.2 (A:3-324,A:521-583) Glucose oxidase {Aspergillus niger}

GIEASLLTDPKDVSGRTVDYIIAGGGLTGLTTAARLTENPNISVLVIESGSYESDRGPIIEDLNAYGDIFGSSVDHAYETVELATNNQTALIRSGNGLGGSTLVNGGTWTRPHKAQVDSWETVFGNEGWNWDNVAAYSLQAERARAPNAKQIAAGHYFNASCHGVNGTVHAGPRDTGDDYSPIVKALMSAVEDRGVPTKKDFGCGDPHGVSMFPNTLHEDQVRSDAAREWLLPNYQRPNLQVLTGQYVGKVLLSQNGTTPRAVGVEFGTHKGNTHNVYAKHEVLLAAGSAVSPTILEYSGIGMKSILEPLGIDTVVDLPVGLXCSMMPKEMGGVVDNAARVYGVQGLRVIDGSIPPTQMSSHVMTVFYAMALKISDAILEDYASMQ

>d1gpea1 c.3.1.2 (A:1-328,A:525-587) Glucose oxidase {Penicillium amagasakiense}

YLPAQQIDVQSSLLSDPSKVAGKTYDYIIAGGGLTGLTVAAKLTENPKIKVLVIEKGFYESNDGAIIEDPNAYGQIFGTTVDQNYLTVPLINNRTNNIKAGKGLGGSTLINGDSWTRPDKVQIDSWEKVFGMEGWNWDNMFEYMKKAEAARTPTAAQLAAGHSFNATCHGTNGTVQSGARDNGQPWSPIMKALMNTVSALGVPVQQDFLCGHPRGVSMIMNNLDENQVRVDAARAWLLPNYQRSNLEILTGQMVGKVLFKQTASGPQAVGVNFGTNKAVNFDVFAKHEVLLAAGSAISPLILEYSGIGLKSVLDQANVTQLLDLPVGIXCSMMSRELGGVVDATAKVYGTQGLRVIDGSIPPTQVSSHVMTIFYGMALKVADAILDDYAKSA

>d1b5qa1 c.3.1.2 (A:5-293,A:406-463) Polyamine oxidase {Maize (Zea mays)}

PRVIVVGAGMSGISAAKRLSEAGITDLLILEATDHIGGRMHKTNFAGINVELGANWVEGVNGGKMNPIWPIVNSTLKLRNFRSDFDYLAQNVYKEDGGVYDEDYVQKRIELADSVEEMGEKLSATLHASGRDDMSILAMQRLNEHQPNGPATPVDMVVDYYKFDYEFAEPPRVTSLQNTVPLATFSDFGDDVYFVADQRGYEAVVYYLAGQYLKTDDKSGKIVDPRLQLNKVVREIKYSPGGVTVKTEDNSVYSADYVMVSASLGVLQSDLIQFKPKLPTWKVRAIYQFXWPVGVNRYEYDQLRAPVGRVYFTGEHTSEHYNGYVHGAYLSGIDSAEILINCAQKKMC

>d1f8ra1 c.3.1.2 (A:4-319,A:433-486) L-amino acid oxidase {Malayan pit viper (Calloselasma rhodostoma)}

RNPLAECFQENDYEEFLEIARNGLKATSNPKHVVIVGAGMAGLSAAYVLAGAGHQVTVLEASERPGGRVRTYRNEEAGWYANLGPMRLPEKHRIVREYIRKFDLRLNEFSQENDNAWYFIKNIRKKVGEVKKDPGLLKYPVKPSEAGKSAGQLYEESLGKVVEELKRTNCSYILNKYDTYSTKEYLIKEGDLSPGAVDMIGDLLNEDSGYYVSFIESLKHDDIFAYEKRFDEIVDGMDKLPTAMYRDIQDKVHFNAQVIKIQQNDQKVTVVYETLSKETPSVTADYVIVCTTSRAVRLIKFNPPLLPKKAHALRSVXFTPYQFQHFSDPLTASQGRIYFAGEYTAQAHGWIDSTIKSGLRAARDVNLASEN

>d1gosa1 c.3.1.2 (A:4-289,A:402-500) Monoamine oxidase B {Human (Homo sapiens)}

KCDVVVVGGGISGMAAAKLLHDSGLNVVVLEARDRVGGRTYTLRNQKVKYVDLGGSYVGPTQNRILRLAKELGLETYKVNEVERLIHHVKGKSYPFRGPFPPVWNPITYLDHNNFWRTMDDMGREIPSDAPWKAPLAEEWDNMTMKELLDKLCWTESAKQLATLFVNLCVTAETHEVSALWFLWYVKQCGGTTRIISTTNGGQERKFVGGSGQVSERIMDLLGDRVKLERPVIYIDQTRENVLVETLNHEMYEAKYVISAIPPTLGMKIHFNPPLPMMRNQMITRVXFPPGILTQYGRVLRQPVDRIYFAGTETATHWSGYMEGAVEAGERAAREILHAMGKIPEDEIWQSEPESVDVPAQPITTTFLERHLPSVPGLLRLIGLTT

>d1d5ta1 c.3.1.3 (A:-2-291,A:389-431) Guanine nucleotide dissosiation inhibitor, GDI {Cow (Bos taurus)}

HHMDEEYDVIVLGTGLTECILSGIMSVNGKKVLHMDRNPYYGGESSSITPLEELYKRFQLLEGPPETMGRGRDWNVDLIPKFLMANGQLVKMLLYTEVTRYLDFKVVEGSFVYKGGKIYKVPSTETEALASNLMGMFEKRRFRKFLVFVANFDENDPKTFEGVDPQNTSMRDVYRKFDLGQDVIDFTGHALALYRTDDYLDQPCLETINRIKLYSESLARYGKSPYLYPLYGLGELPQGFARLSAIYGGTYMLNKPVDDIIMENGKVVGVKSEGEVARCKQLICDPSYVPDRVXPIDDGSESQVFCSCSYDATTHFETTCNDIKDIYKRMAGSAFDF

>d1chua2 c.3.1.4 (A:2-237,A:354-422) L-aspartate oxidase {Escherichia coli}

NTLPEHSCDVLIIGSGAAGLSLALRLADQHQVIVLSKGPVTEGSTFYAQGGIAAVFDETDSIDSHVEDTLIAGAGICDRHAVEFVASNARSCVQWLIDQGVLFDTHIQPNGEESYHLTREGGHSHRRILHAADATGREVETTLVSKALNHPNIRVLERTNAVDLIVSDKIGLPGTRRVVGAWVWNRNKETVETCHAKAVVLATGGASKVYQYTTNPDISSGDGIAMAWRAGCRVANXCGGVMVDDHGRTDVEGLYAIGEVSYTGLHGANRMASNSLLECLVYGWSAAEDITRRMPYAHDISTLPPW

>d1fuma2 c.3.1.4 (A:1-225,A:358-442) Fumarate reductase flavoprotein subunit {Escherichia coli}

QTFQADLAIVGAGGAGLRAAIAAAQANPNAKIALISKVYPMRSHTVAAEGGSAAVAQDHDSFEYHFHDTVAGGDWLCEQDVVDYFVHHCPTEMTQLELWGCPWSRRPDGSVNVRRFGGMKIERTWFAADKTGFHMLHTLFQTSLQFPQIQRFDEHFVLDILVDDGHVRGLVAMNMMEGTLVQIRANAVVMATGGAGRVYRYNTNGGIVTGDGMGMALSHGVPLRDXMGGIETDQNCETRIKGLFAVGECSSVGLHGANRLGSNSLAELVVFGRLAGEQATERAATAGNGNEAAIEAQAAGVEQRLKDLVNQ

>d1qlaa2 c.3.1.4 (A:1-250,A:372-457) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}

MKVQYCDSLVIGGGLAGLRAAVATQQKGLSTIVLSLIPVKRSHSAAAQGGMQASLGNSKMSDGDNEDLHFMDTVKGSDWGCDQKVARMFVNTAPKAIRELAAWGVPWTRIHKGDRMAIINAQKTTITEEDFRHGLIHSRDFGGTKKWRTCYTADATGHTMLFAVANECLKLGVSIQDRKEAIALIHQDGKCYGAVVRDLVTGDIIAYVAKGTLIATGGYGRIYKNTTNAVVCEGTGTAIALETGIAQLGNXMGGIRTDYRGEAKLKGLFSAGEAACWDMHGFNRLGGNSVSEAVVAGMIVGEYFAEHCANTQVDLETKTLEKFVKGQEAYMKSLVES

>d1e39a2 c.3.1.4 (A:103-359,A:506-568) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

PTIAELAKDKSERQAALASAPHDTVDVVVVGSGGAGFSAAISATDSGAKVILIEKEPVIGGNAKLAAGGMNAAWTDQQKAKKITDSPELMFEDTMKGGQNINDPALVKVLSSHSKDSVDWMTAMGADLTDVGMMGGASVNRAHRPTGGAGVGAHVVQVLYDNAVKRNIDLRMNTRGIEVLKDDKGTVKGILVKGMYKGYYWVKADAVILATGGFAKNNERVAKLDPSLKGFISTNQPGAVGDGLDVAENAGGALKDMXTMGGVMIDTKAEVMNAKKQVIPGLYGAGEVTGGVHGANRLGGNAISDIITFGRLAGEEAAKYS

>d1qo8a2 c.3.1.4 (A:103-359,A:506-565) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

DGWDQDKIQKAIAAGPSETTQVLVVGAGSAGFNASLAAKKAGANVILVDKAPFSGGNSMISAGGMNAVGTKQQTAHGVEDKVEWFIEDAMKGGRQQNDIKLVTILAEQSADGVQWLESLGANLDDLKRSGGARVDRTHRPHGGKSSGPEIIDTLRKAAKEQGIDTRLNSRVVKLVVNDDHSVVGAVVHGKHTGYYMIGAKSVVLATGGYGMNKEMIAYYRPTMKDMTSSNNITATGDGVLMAKEIGASMTDIDWVQAXAINTTASVLDLQSKPIDGLFAAGEVTGGVHGYNRLGGNAIADTVVFGRIAGDNAAKHALD

>d1d4ca2 c.3.1.4 (A:103-359,A:506-570) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella putrefaciens}

KFVPVDADKAAQDKAIAAGVKETTDVVIIGSGGAGLAAAVSARDAGAKVILLEKEPIPGGNTKLAAGGMNAAETKPQAKLGIEDKKQIMIDDTMKGGRNINDPELVKVLANNSSDSIDWLTSMGADMTDVGRMGGASVNRSHRPTGGAGVGAHVAQVLWDNAVKRGTDIRLNSRVVRILEDASGKVTGVLVKGEYTGYYVIKADAVVIAAGGFAKNNERVSKYDPKLKGFKATNHPGATGDGLDVALQAGAATRDLEXMGGLVIDTKAEVKSEKTGKPITGLYAAGEVTGGVHGANRLGGNAISDIVTYGRIAGASAAKFAKD

>d1jnra2 c.3.1.4 (A:2-256,A:402-502) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

VYYPKKYELYKADEVPTEVVETDILIIGGGFSGCGAAYEAAYWAKLGGLKVTLVEKAAVERSGAVAQGLSAINTYIDLTGRSERQNTLEDYVRYVTLDMMGLAREDLVADYARHVDGTVHLFEKWGLPIWKTPDGKYVREGQWQIMIHGESYKPIIAEAAKMAVGEENIYERVFIFELLKDNNDPNAVAGAVGFSVREPKFYVFKAKAVILATGGATLLFRPRSTGEAAGRTWYAIFDTGSGYYMGLKAGAMLTQXAGFWVCGPEDLMPEEYAKLFPLKYNRMTTVKGLFAIGDCAGANPHKFSSGSFTEGRIAAKAAVRFILEQKPNPEIDDAVVEELKKKAYAPMERFMQYKDLS

>d3grs\_1 c.3.1.5 (18-165,291-363) Glutathione reductase {Human (Homo sapiens)}

VASYDYLVIGGGSGGLASARRAAELGARAAVVESHKLGGTCVNVGCVPKKVMWNTAVHSEFMHDHADYGFPSCEGKFNWRVIKEKRDAYVSRLNAIYQNNLTKSHIEIIRGHAAFTSDPKPTIEVSGKKYTAPHILIATGGMPSTPHEXRVPNTKDLSLNKLGIQTDDKGHIIVDEFQNTNVKGIYAVGDVCGKALLTPVAIAAGRKLAHRLFEYKEDSKLD

>d3grs\_2 c.3.1.5 (166-290) Glutathione reductase {Human (Homo sapiens)}

SQIPGASLGITSDGFFQLEELPGRSVIVGAGYIAVEMAGILSALGSKTSLMIRHDKVLRSFDSMISTNCTEELENAGVEVLKFSQVKEVKKTLSGLEVSMVTAVPGRLPVMTMIPDVDCLLWAIG

>d1gera2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}

DIPGVEYGIDSDGFFALPALPERVAVVGAGYIAVELAGVINGLGAKTHLFVRKHAPLRSFDPMISETLVEVMNAEGPQLHTNAIPKAVVKNTDGSLTLELEDGRSETVDCLIWAIG

>d1gesa1 c.3.1.5 (A:3-146,A:263-335) Glutathione reductase {Escherichia coli}

KHYDYIAIGGGSGGIASINRAAMYGQKCALIEAKELGGTCVNVGCVPKKVMWHAAQIREAIHMYGPDYGFDTTINKFNWETLIASRTAYIDRIHTSYENVLGKNNVDVIKGFARFVDAKTLEVNGETITADHILIATGGRPSHPXREPANDNINLEAAGVKTNEKGYIVVDKYQNTNIEGIYAVGDNTGAVELTPVAVAAGRRLSERLFNNKPDEHLD

>d1gesa2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}

DIPGVEYGIDSDGFFALPALPERVAVVGAGYIGVELGGVINGLGAKTHLFEMFDAPLPSFDPMISETLVEVMNAEGPQLHTNAIPKAVVKNTDGSLTLELEDGRSETVDCLIWAIG

>d1feca1 c.3.1.5 (A:1-169,A:287-357) Trypanothione reductase {Crithidia fasciculata}

SRAYDLVVIGAGSGGLEAGWNAASLHKKRVAVIDLQKHHGPPHYAALGGTCVNVGCVPKKLMVTGANYMDTIRESAGFGWELDRESVRPNWKALIAAKNKAVSGINDSYEGMFADTEGLTFHQGFGALQDNHTVLVRESADPNSAVLETLDTEYILLATGSWPQHLGIEXVPRSQTLQLEKAGVEVAKNGAIKVDAYSKTNVDNIYAIGDVTDRVMLTPVAINEGAAFVDTVFANKPRATD

>d1feca2 c.3.1.5 (A:170-286) Trypanothione reductase {Crithidia fasciculata}

GDDLCITSNEAFYLDEAPKRALCVGGGYISIEFAGIFNAYKARGGQVDLAYRGDMILRGFDSELRKQLTEQLRANGINVRTHENPAKVTKNADGTRHVVFESGAEADYDVVMLAIGR

>d1aoga1 c.3.1.5 (A:3-169,A:287-357) Trypanothione reductase {Trypanosoma cruzi}

SKIFDLVVIGAGSGGLEAAWNAATLYKKRVAVIDVQMVHGPPFFSALGGTCVNVGCVPKKLMVTGAQYMEHLRESAGFGWEFDRTTLRAEWKNLIAVKDEAVLNINKSYDEMFRDTEGLEFFLGWGSLESKNVVNVRESADPASAVKERLETEHILLASGSWPHMPNXGRSPRTKDLQLQNAGVMIKNGGVQVDEYSRTNVSNIYAIGDVTNRVMLTPVAINEAAALVDTVFGTTPRKT

>d1aoga2 c.3.1.5 (A:170-286) Trypanothione reductase {Trypanosoma cruzi}

IPGIEHCISSNEAFYLPEPPRRVLTVGGGFISVEFAGIFNAYKPKDGQVTLCYRGEMILRGFDHTLREELTKQLTANGIQILTKENPAKVELNADGSKSVTFESGKKMDFDLVMMAI

>d1h6va1 c.3.1.5 (A:10-170,A:293-366) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}

SYDFDLIIIGGGSGGLAAAKEAAKFDKKVMVLDFVTPTPLGTNWGLGGTCVNVGCIPKKLMHQAALLGQALKDSRNYGWKLEDTVKHDWEKMTESVQNHIGSLNWGYRVALREKKVVYENAYGKFIGPHKIMATNNKGKEKVYSAERFLIATGERPRYLGIXRDSCTRTIGLETVGVKINEKTGKIPVTDEEQTNVPYIYAIGDILEGKLELTPVAIQAGRLLAQRLYGGSTVKCD

>d1h6va2 c.3.1.5 (A:171-292) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}

PGDKEYCISSDDLFSLPYCPGKTLVVGASYVALECAGFLAGIGLDVTVMVRSILLRGFDQDMANKIGEHMEEHGIKFIRQFVPTKIEQIEAGTPGRLKVTAKSTNSEETIEDEFNTVLLAVG

>d1trb\_1 c.3.1.5 (1-118,245-316) Thioredoxin reductase {Escherichia coli}

GTTKHSKLLILGSGPAGYTAAVYAARANLQPVLITGMEKGGQLTTTTEVENWPGDPNDLTGPLLMERMHEHATKFETEIIFDHINKVDLQNRPFRLNGDNGEYTCDALIIATGASARYXHSPNTAIFEGQLELENGYIKVQSGIHGNATQTSIPGVFAAGDVMDHIYRQAITSAGTGCMAALDAERYLDGL

>d1trb\_2 c.3.1.5 (119-244) Thioredoxin reductase {Escherichia coli}

LGLPSEEAFKGRGVSACATSDGFFYRNQKVAVIGGGNTAVEEALYLSNIASEVHLIHRRDGFRAEKILIKRLMDKVENGNIILHTNRTLEEVTGDQMGVTGVRLRDTQNSDNIESLDVAGLFVAIG

>d1vdc\_1 c.3.1.5 (1-117,244-316) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}

LETHNTRLCIVGSGPAAHTAAIYAARAELKPLLFEGWMANDIAPGGQLTTTTDVENFPGFPEGILGVELTDKFRKQSERFGTTIFTETVTKVDFSSKPFKLFTDSKAILADAVILAIGAVAKXGHEPATKFLDGGVELDSDGYVVTKPGTTQTSVPGVFAAGDVQDKKYRQAITAAGTGCMAALDAEHYLQEI

>d1vdc\_2 c.3.1.5 (118-243) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}

RLSFVGSGEVLGGFWNRGISACAVCDGAAPIFRNKPLAVIGGGDSAMEEANFLTKYGSKVYIIHRRDAFRASKIMQQRALSNPKIDVIWNSSVVEAYGDGERDVLGGLKVKNVVTGDVSDLKVSGLFFAI

>d1hyua1 c.3.1.5 (A:199-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Salmonella typhimurium}

AEKRAAEALNKRDAYDVLIVGSGPAGAAAAVYSARKGIRTGLMGERFGGQVLDTVDIENYISVPKTEGQKLAGALKAHVSDYDVDVIDSQSASKLVPAATEGGLHQIETASGAVLKARSIIIATGAKXLPNTHWLEGALERNRMGEIIIDAKCETSVKGVFAAGDCTTVPYKQIIIATGEGAKASLSAFDYLIRTKIA

>d1fl2a1 c.3.1.5 (A:212-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Escherichia coli}

AYDVLIVGSGPAGAAAAIYSARKGIRTGLMGERFGGQILDTVDIENYISVPKTEGQKLAGALKVHVDEYDVDVIDSQSASKLIPAAVEGGLHQIETASGAVLKARSIIVATGAKXLPNTNWLEGAVERNRMGEIIIDAKCETNVKGVFAAGDCTTVPYKQIIIATGEGAKASLSAFDYLIRTKTA

>d1fl2a2 c.3.1.5 (A:326-451) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Escherichia coli}

WRNMNVPGEDQYRTKGVTYCPHCDGPLFKGKRVAVIGGGNSGVEAAIDLAGIVEHVTLLEFAPEMKADQVLQDKLRSLKNVDIILNAQTTEVKGDGSKVVGLEYRDRVSGDIHNIELAGIFVQIGL

>d1nhp\_1 c.3.1.5 (1-119,243-321) NADH peroxidase {Enterococcus faecalis}

MKVIVLGSSHGGYEAVEELLNLHPDAEIQWYEKGDFISFLSAGMQLYLEGKVKDVNSVRYMTGEKMESRGVNVFSNTEITAIQPKEHQVTVKDLVSGEERVENYDKLIISPGAVPFELDXGVRPNTAWLKGTLELHPNGLIKTDEYMRTSEPDVFAVGDATLIKYNPADTEVNIALATNARKQGRFAVKNLEEPVKPFP

>d1nhp\_2 c.3.1.5 (120-242) NADH peroxidase {Enterococcus faecalis}

IPGKDLDNIYLMRGRQWAIKLKQKTVDPEVNNVVVIGSGYIGIEAAEAFAKAGKKVTVIDILDRPLGVYLDKEFTDVLTEEMEANNITIATGETVERYEGDGRVQKVVTDKNAYDADLVVVAV

>d1d7ya1 c.3.1.5 (A:5-115,A:237-308) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}

ALKAPVVVLGAGLASVSFVAELRQAGYQGLITVVGDEAERPYDRPPLSKDFMAHGDAEKIRLDCKRAPEVEWLLGVTAQSFDPQAHTVALSDGRTLPYGTLVLATGAAPRAXVLANDALARAAGLACDDGIFVDAYGRTTCPDVYALGDVTRQRNPLSGRFERIETWSNAQNQGIAVARHLVDP

>d1d7ya2 c.3.1.5 (A:116-236) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}

LPTLQGATMPVHTLRTLEDARRIQAGLRPQSRLLIVGGGVIGLELAATARTAGVHVSLVETQPRLMSRAAPATLADFVARYHAAQGVDLRFERSVTGSVDGVVLLDDGTRIAADMVVVGIG

>d1lvl\_1 c.3.1.5 (1-150,266-335) Dihydrolipoamide dehydrogenase {Pseudomonas putida}

QQTIQTTLLIIGGGPGGYVAAIRAGQLGIPTVLVEGQALGGTCLNIGCIPSKALIHVAEQFHQASRFTEPSPLGISVASPRLDIGQSVAWKDGIVDRLTTGVAALLKKHGVKVVHGWAKVLDGKQVEVDGQRIQCEHLLLATGSSSVELPXRRPRTKGFNLECLDLKMNGAAIAIDERCQTSMHNVWAIGDVAGEPMLAHRAMAQGEMVAEIIAGKARRFE

>d1lvl\_2 c.3.1.5 (151-265) Dihydrolipoamide dehydrogenase {Pseudomonas putida}

MLPLGGPVISSTEALAPKALPQHLVVVGGGYIGLELGIAYRKLGAQVSVVEARERILPTYDSELTAPVAESLKKLGIALHLGHSVEGYENGCLLANDGKGGQLRLEADRVLVAVG

>d1lpfa1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}

SQKFDVVVIGAGPGGYVAAIRAAQLGLKTACIEKYIGKEGKVALGGTCLNVGCIPSKALLDSSYKYHEAKEAFKVHGIEAKGVTIDVPAMVARKANIVKNLTGGIATLFKANGVTSFEGHGKLLANKQVEVTGLDGKTQVLEAENVIIASGSRPVEIPXRRPVTTDLLAADSGVTLDERGFIYVDDHCKTSVPGVFAIGDVVRGAMLAHKASEEGVMVAERIAGHKAQMN

>d1lpfa2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}

PAPLSDDIIVDSTGALEFQAVPKKLGVIGAGVIGLELGSVWARLGAEVTVLEALDKFLPAADEQIAKEALKVLTKQGLNIRLGARVTASEVKKKQVTVTFTDANGEQKETFDKLIVAVG

>d3lada1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}

SQKFDVIVIGAGPGGYVAAIKSAQLGLKTALIEKYKGKEGKTALGGTCLNVGCIPSKALLDSSYKFHEAHESFKLHGISTGEVAIDVPTMIARKDQIVRNLTGGVASLIKANGVTLFEGHGKLLAGKKVEVTAADGSSQVLDTENVILASGSKPVEIPXRRPVTTDLLAADSGVTLDERGFIYVDDYCATSVPGVYAIGDVVRGAMLAHKASEEGVVVAERIAGHKAQMN

>d3lada2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}

PAPVDQDVIVDSTGALDFQNVPGKLGVIGAGVIGLELGSVWARLGAEVTVLEAMDKFLPAVDEQVAKEAQKILTKQGLKILLGARVTGTEVKNKQVTVKFVDAEGEKSQAFDKLIVAVG

>d1ebda1 c.3.1.5 (A:7-154,A:272-346) Dihydrolipoamide dehydrogenase {Bacillus stearothermophilus}

AIETETLVVGAGPGGYVAAIRAAQLGQKVTIVEKGNLGGVCLNVGCIPSKALISASHRYEQAKHSEEMGIKAENVTIDFAKVQEWKASVVKKLTGGVEGLLKGNKVEIVKGEAYFVDANTVRVVNGDSAQTYTFKNAIIATGSRPIELXVGRRPNTDELGLEQIGIKMTNRGLIEVDQQCRTSVPNIFAIGDIVPGPALAHKASYEGKVAAEAIAGHPSAVDYV

>d1ebda2 c.3.1.5 (A:155-271) Dihydrolipoamide dehydrogenase {Bacillus stearothermophilus}

PNFKFSNRILDSTGALNLGEVPKSLVVIGGGYIGIELGTAYANFGTKVTILEGAGEILSGFEKQMAAIIKKRLKKKGVEVVTNALAKGAEEREDGVTVTYEANGETKTIDADYVLVT

>d1ojt\_1 c.3.1.5 (117-275,401-470) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

GSADAEYDVVVLGGGPGGYSAAFAAADEGLKVAIVERYKTLGGVCLNVGCIPSKALLHNAAVIDEVRHLAANGIKYPEPELDIDMLRAYKDGVVSRLTGGLAGMAKSRKVDVIQGDGQFLDPHHLEVSLTAGDAYEQAAPTGEKKIVAFKNCIIAAGSRXAPNGKLISAEKAGVAVTDRGFIEVDKQMRTNVPHIYAIGDIVGQPMLAHKAVHEGHVAAENCAGHKAYFD

>d1ojt\_2 c.3.1.5 (276-400) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

VTKLPFIPEDPRIIDSSGALALKEVPGKLLIIGGGIIGLEMGTVYSTLGSRLDVVEMMDGLMQGADRDLVKVWQKQNEYRFDNIMVNTKTVAVEPKEDGVYVTFEGANAPKEPQRYDAVLVAAGR

>d1jeha1 c.3.1.5 (A:1-160,A:283-355) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

TINKSHDVVIIGGGPAGYVAAIKAAQLGFNTACVEKRGKLGGTCLNVGCIPSKALLNNSHLFHQMHTEAQKRGIDVNGDIKINVANFQKAKDDAVKQLTGGIELLFKKNKVTYYKGNGSFEDETKIRVTPVDGLEGTVKEDHILDVKNIIVATGSEVTPFXVGRRPYIAGLGAEKIGLEVDKRGRLVIDDQFNSKFPHIKVVGDVTFGPMLAHKAEEEGIAAVEMLKTGHGHVN

>d1jeha2 c.3.1.5 (A:161-282) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

PGIEIDEEKIVSSTGALSLKEIPKRLTIIGGGIIGLEMGSVYSRLGSKVTVVEFQPQIGASMDGEVAKATQKFLKKQGLDFKLSTKVISAKRNDDKNVVEIVVEDTKTNKQENLEAEVLLVA

>d1dxla1 c.3.1.5 (A:4-152,A:276-347) Dihydrolipoamide dehydrogenase {Garden pea (Pisum sativum)}

SDENDVVIIGGGPGGYVAAIKAAQLGFKTTCIEKRGALGGTCLNVGCIPSKALLHSSHMYHEAKHSFANHGVKVSNVEIDLAAMMGQKDKAVSNLTRGIEGLFKKNKVTYVKGYGKFVSPSEISVDTIEGENTVVKGKHIIIATGSDVKXGRTPFTSGLNLDKIGVETDKLGRILVNERFSTNVSGVYAIGDVIPGPMLAHKAEEDGVACVEYLAGKVGHVD

>d1dxla2 c.3.1.5 (A:153-275) Dihydrolipoamide dehydrogenase {Garden pea (Pisum sativum)}

SLPGVTIDEKKIVSSTGALALSEIPKKLVVIGAGYIGLEMGSVWGRIGSEVTVVEFASEIVPTMDAEIRKQFQRSLEKQGMKFKLKTKVVGVDTSGDGVKLTVEPSAGGEQTIIEADVVLVSA

>d1fcda1 c.3.1.5 (A:1-114,A:256-327) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (Chromatium vinosum)}

AGRKVVVVGGGTGGATAAKYIKLADPSIEVTLIEPNTDYYTCYLSNEVIGGDRKLESIKHGYDGLRAHGIQVVHDSATGIDPDKKLVKTAGGAEFGYDRCVVAPGIELIYDKIEXQRAGKIAQIAGLTNDAGWCPVDIKTFESSIHKGIHVIGDASIANPMPKSGYSANSQGKVAAAAVVVLLKGEE

>d1fcda2 c.3.1.5 (A:115-255) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (Chromatium vinosum)}

GYSEEAAAKLPHAWKAGEQTAILRKQLEDMADGGTVVIAPPAAPFRCPPGPYERASQVAYYLKAHKPMSKVIILDSSQTFSKQSQFSKGWERLYGFGTENAMIEWHPGPDSAVVKVDGGEMMVETAFGDEFKADVINLIPP

>d1djna3 c.4.1.1 (A:341-489,A:646-729) Trimethylamine dehydrogenase, middle domain {Methylophilus methylotrophus, w3a1}

DIRVCIGCNVCISRWEIGGPPMICTQNATAGEEYRRGWHPEKFRQTKNKDSVLIVGAGPSGSEAARVLMESGYTVHLTDTAEKIGGHLNQVAALPGLGEWSYHRDYRETQITKLLKKNKESQLALGQKPMTADDVLQYGADKVIIATGAXSECTLWNELKARESEWAENDIKGIYLIGDAEAPRLIADATFTGHRVAREIEEANPQIAIPYKRETIAWGTPHMPGGNFKIEYKV

>d1cjca2 c.4.1.1 (A:6-106,A:332-460) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos taurus)}

TPQICVVGSGPAGFYTAQHLLKHHSRAHVDIYEKQLVPFGLVRFGVAPDHPEVKNVINTFTQTARSDRCAFYGNVEVGRDVTVQELQDAYHAVVLSYGAEDXKSRPIDPSVPFDPKLGVVPNMEGRVVDVPGLYCSGWVKRGPTGVITTTMTDSFLTGQILLQDLKAGHLPSGPRPGSAFIKALLDSRGVWPVSFSDWEKLDAEEVSRGQASGKPREKLLDPQEMLRLLGH

>d1h7wa4 c.4.1.1 (A:184-287,A:441-532) Dihydropyrimidine dehydrogenase, domain 2 {Pig (Sus scrofa)}

EAYSAKIALLGAGPASISCASFLARLGYSDITIFEKQEYVGGLSTSEIPQFRLPYDVVNFEIELMKDLGVKIICGKSLSENEITLNTLKEEGYKAAFIGIGLPEXVLRDPKVKEALSPIKFNRWDLPEVDPETMQTSEPWVFAGGDIVGMANTTVESVNDGKQASWYIHKYIQAQYGASVSAKPELPLFYTPVDLVD

>d1an9a1 c.4.1.2 (A:1-194,A:288-340) D-amino acid oxidase, N-terminal domain {Pig (Sus scrofa)}

MRVVVIGAGVIGLSTALCIHERYHSVLQPLDVKVYADRFTPFTTTDVAAGLWQPYTSEPSNPQEANWNQQTFNYLLSHIGSPNAANMGLTPVSGYNLFREAVPDPYWKDMVLGFRKLTPRELDMFPDYRYGWFNTSLILEGRKYLQWLTERLTERGVKFFLRKVESFEEVARGGADVIINCTGVWAGVLQPDPLXQVRLEREQLRFGSSNTEVIHNYGHGGYGLTIHWGCALEVAKLFGKVLEERNLL

>d1c0pa1 c.4.1.2 (A:999-1193,A:1289-1361) D-amino acid oxidase, N-terminal domain {Yeast (Rhodotorula gracilis)}

LMMHSQKRVVVLGSGVIGLSSALILARKGYSVHILARDLPEDVSSQTFASPWAGANWTPFMTLTDGPRQAKWEESTFKKWVELVPTGHAMWLKGTRRFAQNEDGLLGHWYKDITPNYRPLPSSECPPGAIGVTYDTLSVHAPKYCQYLARELQKLGATFERRTVTSLEQAFDGADLVVNATGLGAKSIAGIDDQAXRGGPRVEAERIVLPLDRTKSPLSLGRGSARAAKEKEVTLVHAYGFSSAGYQQSWGAAEDVAQLVDEAFQRYHG

>d1i8ta1 c.4.1.3 (A:1-244,A:314-367) UDP-galactopyranose mutase, N-terminal domain {Escherichia coli}

MYDYIIVGSGLFGAVCANELKKLNKKVLVIEKRNHIGGNAYTEDCEGIQIHKYGAHIFHTNDKYIWDYVNDLVEFNRFTNSPLAIYKDKLFNLPFNMNTFHQMWGVKDPQEAQNIINAQKKKYGDKVPENLEEQAISLVGEDLYQALIKGYTEKQWGRSAKELPAFIIKRIPVRFTFDNNYFSDRYQGIPVGGYTKLIEKMLEGVDVKLGIDFLKDKDSLASKAHRIIYTGPIDQYFDYRFGALXNDNKNMELFKKYRELASREDKVIFGGRLAEYKYYDMHQVISAALYQVKNIMSTD

>d2uaga1 c.5.1.1 (A:1-93) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD, N-terminal domain {Escherichia coli}

ADYQGKNVVIIGLGLTGLSCVDFFLARGVTPRVMDTRMTPPGLDKLPEAVERHTGSLNDEWLMAADLIVASPGIALAHPSLSAAADAGIEIVG

>d1tml\_\_ c.6.1.1 (-) Cellulase E2 {Thermomonospora fusca, strain yx}

NDSPFYVNPNMSSAEWVRNNPNDPRTPVIRDRIASVPQGTWFAHHNPGQITGQVDALMSAAQAAGKIPILVVYNAPGRDCGNHSSGGAPSHSAYRSWIDEFAAGLKNRPAYIIVEPDLISLMSSCMQHVQQEVLETMAYAGKALKAGSSQARIYFDAGHSAWHSPAQMASWLQQADISNSAHGIATNTSNYRWTADEVAYAKAVLSAIGNPSLRAVIDTSRNGNGPAGNEWCDPSGRAIGTPSTTNTGDPMIDAFLWIKLPGEADGCIAGAGQFVPQAAYEMAIAA

>d1qjwa\_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Trichoderma reesei, Cel6a}

ATYSGNPFVGVTPWANAYYASEVSSLAIPSLTGAMATAAAAVAKVPSFMWLDTLDKTPLMEQTLADIRTANKNGGNYAGQFVVFDLPDRDCAALASNGEYSIADGGVAKYKNYIDTIRQIVVEYSDIRTLLVIEPDSLANLVTNLGTPKCANAQSAYLECINYAVTQLNLPNVAMYLDAGHAGWLGWPANQDPAAQLFANVYKNASSPRALRGLATNVANYNGWNITSPPSYTQGNAVYNEKLYIHAIGPLLANHGWSNAFFITDQGRSGKQPTGQQQWGDWCNVIGTGFGIRPSANTGDSLLDSFVWVKPGGECDGTSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNANPSFL

>d2bvwa\_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6a}

NGNPFEGVQLWANNYYRSEVHTLAIPQITDPALRAAASAVAEVPSFQWLDRNVTVDTLLVQTLSEIREANQAGANPQYAAQIVVYDLPDRDCAAAASNGEWAIANNGVNNYKAYINRIREILISFSDVRTILVIEPDSLANMVTNMNVPKCSGAASTYRELTIYALKQLDLPHVAMYMDAGHAGWLGWPANIQPAAELFAKIYEDAGKPRAVRGLATNVANYNAWSVSSPPPYTSPNPNYDEKHYIEAFRPLLEARGFPAQFIVDQGRSGKQPTGQKEWGHWCNAIGTGFGMRPTANTGHQYVDAFVWVKPGGECDGTSDTTAARYDYHCGLEDALKPAPEAGQWFNEYFIQLLRNANPPF

>d1dysa\_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6b}

GNPFSGRTLLVNSDYSSKLDQTRQAFLSRGDQTNAAKVKYVQEKVGTFYWISNIFLLRDIDVAIQNARAAKARGENPIVGLVLYNLPDRDCSAGESSGELKLSQNGLNRYKNEYVNPFAQKLKAASDVQFAVILEPDAIGNMVTGTSAFCRNARGPQQEAIGYAISQLQASHIHLYLDVANGGWLGWADKLEPTAQEVATILQKAGNNAKIRGFSSNVSNYNPYSTSNPPPYTSGSPSPDESRYATNIANAMRQRGLPTQFIIDQSRVALSGARSEWGQWCNVNPAGFGQPFTTNTNNPNVDAIVWVKPGGESDGQCGMGGAPAAGMWFDAYAQMLTQNAHDEIA

>d1cm5a\_ c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}

SELNEKLATAWEGFTKGDWQNEVNVRDFIQKNYTPYEGDESFLAGATEATTTLWDKVMEGVKLENRTHAPVDFDTAVASTITSHDAGYINKQLEKIVGLQTEAPLKRALIPFGGIKMIEGSCKAYNRELDPMIKKIFTEYRKTHNQGVFDVYTPDILRCRKSGVLTGLPDAYGRGRIIGDYRRVALYGIDYLMKDKLAQFTSLQADLENGVNLEQTIRLREEIAEQHRALGQMKEMAAKYGYDISGPATNAQEAIQWTYFGYLAAVKSQNGAAMSFGRTSTFLDVYIERDLKAGKITEQEAQEMVDHLVMKLRMVRFLRTPEYDELFSGDPIWATESIGGMGLDGRTLVTKNSFRFLNTLYTMGPSPEPNMTILWSEKLPLNFKKFAAKVSIDTSSLQYENDDLMRPDFNNDDYAIAAAVSPMIVGKQMQFFGARANLAKTMLYAINGGVDEKLKMQVGPKSEPIKGDVLNYDEVMERMDHFMDWLAKQYITALNIIHYMHDKYSYEASLMALHDRDVIRTMACGIAGLSVAADSLSAIKYAKVKPIRDEDGLAIDFEIEGEYPQFGNNDPRVDDLAVDLVERFMKKIQKLHTYRDAIPTQSVLTITSNVVYGKKTGNTPDGRRAGAPFGPGANPMHGRDQKGAVASLTSVAKLPFAYAKDGISYTFSIVPNALGKDDEVRKTNLAGLMDGYFHHEASIEGGQHLNVNVMNREMLLDAMENPEKYPQLTIRVSGYAVRFNSLTKEQQQDVITRTFTQSM

>d1qhma\_ c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}

NEKLATAWEGFTKGDWQNEVNVRDFIQKNYTPYEGDESFLAGATEATTTLWDKVMEGVKLENRTHAPVDFDTAVASTITSHDAGYINKQLEKIVGLQTEAPLKRALIPFGGIKMIEGSCKAYNRELDPMIKKIFTEYRKTHNQGVFDVYTPDILRCRKSGVLTGLPDAYGRGRIIGDYRRVALYGIDYLMKDKLAQFTSLQADLENGVNLEQTIRLREEIAEQHRALGQMKEMAAKYGYDISGPATNAQEAIQWTYFGYLAAVKSQNGAAMSFGRTSTFLDVYIERDLKAGKITEQEAQEMVDHLVMKLRMVRFLRTPEYDELFSGDPIWATESIGGMGLDGRTLVTKNSFRFLNTLYTMGPSPEPNMTILWSEKLPLNFKKFAAKVSIDTSSLQYENDDLMRPDFNNDDYAIACCVSPMIVGKQMQFFGARANLAKTMLYAINGGVDEKLKMQVGPKSEPIKGDVLNYDEVMERMDHFMDWLAKQYITALNIIHYMHDKYSYEASLMALHDRDVIRTMACGIAGLSVAADSLSAIKYAKVKPIRDEDGLAIDFEIEGEYPQFGNNDPRVDDLAVDLVERFMKKIQKLHTYRDAIPTQSVLTITSNVVYGKK

>d1rlr\_2 c.7.1.2 (222-748) R1 subunit of ribonucleotide reductase, C-terminal domain {Escherichia coli}

FSSCVLIECGDSLDSINATSSAIVKYVSQRAGIGINAGRIRALGSPIRGGEAFHTGCIPFYKHFQTAVKSCSQGGVRGGAATLFYPMWHLEVESLLVLKNNRGVEGNRVRHMDYGVQINKLMYTRLLKGEDITLFSPSDVPGLYDAFFADQEEFERLYTKYEKDDSIRKQRVKAVELFSLMMQERASTGRIYIQNVDHCNTHSPFDPAIAPVRQSNLCLEIALPTKPLNDVNDENGEIALCTLSAFNLGAINNLDELDELAILAVRALDALLDYQDYPIPAAKRGAMGRRTLGIGVINFAYYLAKHGKRYSDGSANNLTHKTFEAIQYYLLKASNELAKEQGACPWFNETTYAKGILPIDTYKKDLDTIANEPLHYDWEALRESIKTHGLRNSTLSALMPSETSSQISNATNGIEPPRGYVSIKASKDGILRQVVPDYEHLHDAYELLWEMPGNDGYLQLVGIMQKFIDQSISANTNYDPSRFPSGKVPMQQLLKDLLTAYKFGVKTLYYQNTRDDIDDLSNFQL

>d1b8ba\_ c.7.1.3 (A:) Class III anaerobic ribonucleotide triphosphate reductase NRDD subunit {Bacteriophage T4}

SRVFPTQRDLMAGIVSKHIAKNMVPSFIMKAHESGIIHVHDIDYSPALPFTNCCLVDLKGMLENGFKLGNAQIETPKSIGVATAIMAQITAQVASHQYGGTTFANVDKVLSPYVKRTYAKHIEDAEKWQIADALNYAQSKTEKDVYDAFQAYEYEVNTLFSSNGQTPFVTLTFGTGTDWTERMIQKAILKNRIKGLGRDGITPIFPKLVMFVEEGVNLYKDDPNYDIKQLALECASKRMYPDIISAKNNKAITGSSVPVSPMGCRSFLSVWKDSTGNEILDGRNNLGVVTLNLPRIALDSYIGTQFNEQKFVELFNERMDLCFEALMCRISSLKGVKATVAPILYQEGAFGVRLKPDDDIIELFKNGRSSVSLGYIGIHELNILVGRDIGREILTKMNAHLKQWTERTGFAFSLYSTPAENLCYRFCKLDTEKYGSVKDVTDKGWYTNSFHVSVEENITPFEKISREAPYHFIATGGHISYVELPDMKNNLKGLEAVWDYAAQHLDYFGVNMPVDKCFTCGSTHEMTPTENGFVCSICGETDPKKMNTIRRTCAYLGNPNERG

>d1kbla2 c.8.1.1 (A:377-509) Pyruvate phosphate dikinase, central domain {Clostridium symbiosum}

LHPTFNPAALKAGEVIGSALPASPGAAAGKVYFTADEAKAAHEKGERVILVRLETSPEDIEGMHAAEGILTVRGGMTSHAAVVARGMGTCCVSGCGEIKINEEAKTFELGGHTFAEGDYISLDGSTGKIYKGD

>d1zyma2 c.8.1.2 (A:3-21,A:145-249) N-terminal domain of enzyme I of the PEP:sugar phosphotransferase system {Escherichia coli}

SGILASPGIAFGKALLLKEXKIIDLSAIQDEVILVAADLTPSETAQLNLKKVLGFITDAGGRTSHTSIMARSLELPAIVGTGSVTSQVKNDDYLILDAVNNQVYVNPTNEVIDKMRAVQEQVASE

>d1aco\_1 c.8.2.1 (529-754) Aconitase, C-terminal domain {Cow (Bos taurus)}

VDVSPTSQRLQLLEPFDKWDGKDLEDLQILIKVKGKCTTDHISAAGPWLKFRGHLDNISNNLLIGAINSENRKANSVRNAVTQEFGPVPDTARYYKQHGIRWVVIGDENYGEGSSREHSALEPRFLGGRAIITKSFARIHETNLKKQGLLPLTFADPADYNKIHPVDKLTIQGLKDFAPGKPLTCIIKHPNGTQETILLNHTFNETQIEWFRAGSALNRMKELQQK

>d1a9xb1 c.8.3.1 (B:1502-1652) Carbamoyl phosphate synthetase, small subunit N-terminal domain {Escherichia coli}

IKSALLVLEDGTQFHGRAIGATGSAVGEVVFNTSMTGYQEILTDPSYSRQIVTLTYPHIGNVGTNDADEESSQVHAQGLVIRDLPLIASNFRNTEDLSSYLKRHNIVAIADIDTRKLTRLLREKGAQNGCIIAGDNPDAALALEKARAFPG

>d1de4c2 c.8.4.1 (C:190-382) Transferrin receptor ectodomain, apical domain {Human (Homo sapiens)}

IQVKDSAQNSVIIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKKDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNAIGVLIYMDQTKFPIVNAELSFFGHAHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAAAEKLFGNMEGDCPSDWKTDSTCRMVTSESKNVKLTVSNVLK

>d1dk7a\_ c.8.5.1 (A:) GroEL {Escherichia coli}

EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVVINKDTTTIIDGV

>d1kid\_\_ c.8.5.1 (-) GroEL {Escherichia coli}

GLVPRGSEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVVINKDTTTIIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQERVAKLAGGV

>d1oela2 c.8.5.1 (A:191-366) GroEL {Escherichia coli}

EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLLIIAEDVEGEALATAVVNTIRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVVINKDTTTIIDGVGEEAAIQGRVAQIRQQIEEATSDYDREKLQ

>d1ioka2 c.8.5.1 (A:191-366) GroEL {Paracoccus denitrificans}

EGMQFDRGYLSPYFVTNADKMIAELEDAYILLHEKKLSSLQPMVPLLESVIQSQKPLLIVAEDVEGEALATLVVNKLRGGLKIAAVKAPGFGDRRKAMLQDIAILTGGQVISEDLGMKLENVTIDMLGRAKKVSINKDNTTIVDGAGEKAEIEARVSQIRQQIEETTSDYDREKLQ

>d1srva\_ c.8.5.1 (A:) GroEL {Thermus thermophilus}

GYQFDKGYISPYFVTNPETMEAVLEDAFILIVEKKVSNVRELLPILEQVAQTGKPLLIIAEDVEGEALATLVVNKLRGTLSVAAVKAPGFGDRRKEMLKDIAAVTGGTVISEELGFKLENATLSMLGRAERVRITKDETTIVGGK

>d1a6db2 c.8.5.2 (B:216-367) Thermosome {Archaeon Thermoplasma acidophilum}

GIIVDKEKVHPGMPDVVKDAKIALLDAPLEIKKPEFDTNLRIEDPSMIQKFLAQEENMLREMVDKIKSVGANVVITQKGIDDMAQHYLSRAGIYAVRRVKKSDMDKLAKATGASIVSTIDEISSSDLGTAERVEQVKVGEDYMTFVTGCKNP

>d1ass\_\_ c.8.5.2 (-) Thermosome {Archaeon Thermoplasma acidophilum}

MSGIVIDKEKVHSKMPDVVKNAKIALIDSALEIKKTEIEAKVQISDPSKIQDFLNQETNTFKQMVEKIKKSGANVVLCQKGIDDVAQHYLAKEGIYAVRRVKKSDMEKLAKATGAKIVTDLDDLTPSVLGEAETVEERKIGDDRMTFVMGCK

>d1ay7b\_ c.9.1.1 (B:) Barstar (barnase inhibitor) {Bacillus amyloliquefaciens}

KKAVINGEQIRSISDLHQTLKKELALPEYYGENLDALWDCLTGWVEYPLVLEWRQFEQSKQLTENGAESVLQVFREAKAEGCDITIILS

>d1jj2x\_ c.9.2.1 (X:) Ribosomal protein L32e {Archaeon Haloarcula marismortui}

TELQARGLTEKTPDLSDEDARLLTQRHRVGKPQFNRQDHHKKKRVSTSWRKPRGQLSKQRRGIKGKGDTVEAGFRSPTAVRGKHPSGFEEVRVHNVDDLEGVDGDTEAVRIASKVGARKRERIEEEAEDAGIRVLNPTYVEV

>d1e8ca1 c.98.1.1 (A:3-87) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}

RNLRDLLAPWVPDAPSRALREMTLDSRVAAAGDLFVAVVGHQADGRRYIPQAIAQGVAAIIAEAKDEATDGEIREMHGVPVIYLS

>d1gg4a3 c.98.1.1 (A:1-81) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

MISVTLSQLTDILNGELQGADITLDAVTTDTRKLTPGCLFVALKGERFDAHDFADQAKAGGAGALLVSRPLDIDLPQLIVK

>d2bnh\_\_ c.10.1.1 (-) Ribonuclease inhibitor {Pig (Sus scrofa)}

MNLDIHCEQLSDARWTELLPLLQQYEVVRLDDCGLTEEHCKDIGSALRANPSLTELCLRTNELGDAGVHLVLQGLQSPTCKIQKLSLQNCSLTEAGCGVLPSTLRSLPTLRELHLSDNPLGDAGLRLLCEGLLDPQCHLEKLQLEYCRLTAASCEPLASVLRATRALKELTVSNNDIGEAGARVLGQGLADSACQLETLRLENCGLTPANCKDLCGIVASQASLRELDLGSNGLGDAGIAELCPGLLSPASRLKTLWLWECDITASGCRDLCRVLQAKETLKELSLAGNKLGDEGARLLCESLLQPGCQLESLWVKSCSLTAACCQHVSLMLTQNKHLLELQLSSNKLGDSGIQELCQALSQPGTTLRVLCLGDCEVTNSGCSSLASLLLANRSLRELDLSNNCVGDPGVLQLLGSLEQPGCALEQLVLYDTYWTEEVEDRLQALEGSKPGLRVIS

>d1a4ya\_ c.10.1.1 (A:) Ribonuclease inhibitor {Human (Homo sapiens)}

SLDIQSLDIQCEELSDARWAELLPLLQQCQVVRLDDCGLTEARCKDISSALRVNPALAELNLRSNELGDVGVHCVLQGLQTPSCKIQKLSLQNCCLTGAGCGVLSSTLRTLPTLQELHLSDNLLGDAGLQLLCEGLLDPQCRLEKLQLEYCSLSAASCEPLASVLRAKPDFKELTVSNNDINEAGVRVLCQGLKDSPCQLEALKLESCGVTSDNCRDLCGIVASKASLRELALGSNKLGDVGMAELCPGLLHPSSRLRTLWIWECGITAKGCGDLCRVLRAKESLKELSLAGNELGDEGARLLCETLLEPGCQLESLWVKSCSFTAACCSHFSSVLAQNRFLLELQISNNRLEDAGVRELCQGLGQPGSVLRVLWLADCDVSDSSCSSLAATLLANHSLRELDLSNNCLGDAGILQLVESVRQPGCLLEQLVLYDIYWSEEMEDRLQALEKDKPSLRVIS

>d1yrga\_ c.10.1.2 (A:) Rna1p (RanGAP1), N-terminal domain {Fission yeast (Schizosaccharomyces pombe)}

ARFSIEGKSLKLDAITTEDEKSVFAVLLEDDSVKEIVLSGNTIGTEAARWLSENIASKKDLEIAEFSDIFTGRVKDEIPEALRLLLQALLKCPKLHTVRLSDNAFGPTAQEPLIDFLSKHTPLEHLYLHNNGLGPQAGAKIARALQELAVNKKAKNAPPLRSIICGRNRLENGSMKEWAKTFQSHRLLHTVKMVQNGIRPEGIEHLLLEGLAYCQELKVLDLQDNTFTHLGSSALAIALKSWPNLRELGLNDCLLSARGAAAVVDAFSKLENIGLQTLRLQYNEIELDAVRTLKTVIDEKMPDLLFLELNGNRFSEEDDVVDEIREVFSTRGRGELDELDDME

>d1fqva2 c.10.1.3 (A:146-431) Cyclin A/CDK2-associated p19, Skp2 {Human (Homo sapiens)}

ESLWQTLDLTGKNLHPDVTGRLLSQGVIAFRCPRSFMDQPLAEHFSPFRVQHMDLSNSVIEVSTLHGILSQCSKLQNLSLEGLRLSDPIVNTLAKNSNLVRLNLSGCSGFSEFALQTLLSSCSRLDELNLSWCFDFTEKHVQVAVAHVSETITQLNLSGYRKNLQKSDLSTLVRRCPNLVHLDLSDSVMLKNDCFQEFFQLNYLQHLSLSRCYDIIPETLLELGEIPTLKTLQVFGIVPDGTLQLLKEALPHLQINCSHFTTIARPTIGNKKNQEIWGIKCRLTLQ

>d1fs2a2 c.10.1.3 (A:146-401) Cyclin A/CDK2-associated p19, Skp2 {Human (Homo sapiens)}

ESLWQTLDEFRVQHMDLSNSVIEVSTLHGILSQCSKLQNLSLEGLRLSDPIVNTLAKNSNLVRLNLSGCSGFSEFALQTLLSSCSRLDELNLSWCFDFTEKHVQVAVAHVSETITQLNLSGYRKNLQKSDLSTLVRRCPNLVHLDLSDSVMLKNDCFQEFFQLNYLQHLSLSRCYDIIPETLLELGEIPTLKTLQVFGIVPDGTLQLLKEALPHLQIN

>d1h6ta2 c.10.2.1 (A:31-240) Internalin B {Listeria monocytogenes}

GPLGSETITVPTPIKQIFSDDAFAETIKDNLKKKSVTDAVTQNELNSIDQIIANNSDIKSVQGIQYLPNVTKLFLNGNKLTDIKPLANLKNLGWLFLDENKVKDLSSLKDLKKLKSLSLEHNGISDINGLVHLPQLESLYLGNNKITDITVLSRLTKLDTLSLEDNQISDIVPLAGLTKLQNLYLSKNHISDLRALAGLKNLDVLELFSQ

>d1h6ua2 c.10.2.1 (A:36-262) Internalin H {Listeria monocytogenes}

GSITQPTAINVIFPDPALANAIKIAAGKSNVTDTVTQADLDGITTLSAFGTGVTTIEGVQYLNNLIGLELKDNQITDLAPLKNLTKITELELSGNPLKNVSAIAGLQSIKTLDLTSTQITDVTPLAGLSNLQVLYLDLNQITNISPLAGLTNLQYLSIGNAQVSDLTPLANLSKLTTLKADDNKISDISPLASLPNLIEVHLKNNQISDVSPLANTSNLFIVTLTNQ

>d1jl5a\_ c.10.2.6 (A:) Leucine rich effector protein YopM {Yersinia pestis}

KSKTEYYNAWSEWERNAPPGNGEQREMAVSRLRDCLDRQAHELELNNLGLSSLPELPPHLESLVASCNSLTELPELPQSLKSLLVDNNNLKALSDLPPLLEYLGVSNNQLEKLPELQNSSFLKIIDVDNNSLKKLPDLPPSLEFIAAGNNQLEELPELQNLPFLTAIYADNNSLKKLPDLPLSLESIVAGNNILEELPELQNLPFLTTIYADNNLLKTLPDLPPSLEALNVRDNYLTDLPELPQSLTFLDVSENIFSGLSELPPNLYYLNASSNEIRSLCDLPPSLEELNVSNNKLIELPALPPRLERLIASFNHLAEVPELPQNLKQLHVEYNPLREFPDIPESVEDLRMNS

>d1dcea3 c.10.2.2 (A:444-567) Rab geranylgeranyltransferase alpha-subunit, C-terminal domain {Rat (Rattus norvegicus)}

RVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRALPPALAALRCLEVLQASDNALENVDGVANLPRLQELLLCNNRLQQSAAIQPLVSCPRLVLLNLQGNSLCQEEGIQERLAEMLPSVSSILT

>d1koha1 c.10.2.3 (A:201-362) mRNA export factor tap {Human (Homo sapiens)}

LNELKPEQVEQLKLIMSKRYDGSQQALDLKGLRSDPDLVAQNIDVVLNRRSSMAATLRIIEENIPELLSLNLSNNRLYRLDDMSSIVQKAPNLKILNLSGNELKSERELDKIKGLKLEELWLDGNSLSDTFRDQSTYISAIRERFPKLLRLDGHELPPPIAF

>d1a9na\_ c.10.2.4 (A:) Splicesomal U2A' protein {Human (Homo sapiens)}

VKLTAELIEQAAQYTNAVRDRELDLRGYKIPVIENLGATLDQFDAIDFSDNEIRKLDGFPLLRRLKTLLVNNNRICRIGEGLDQALPDLTELILTNNSLVELGDLDPLASLKSLTYLCILRNPVTNKKHYRLYVIYKVPQVRVLDFQKVKLKERQEAEKMFK

>d1igra1 c.10.2.5 (A:1-149) L1 and L2 domains of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

EICGPGIDIRNDYQQLKRLENCTVIEGYLHILLISKAEDYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGWKLFYNYALVIFEMTNLKDIGLYNLRNITRGAIRIEKNADLCYLSTVDWSLILDAVSNNYIVGNKPPKECG

>d1igra2 c.10.2.5 (A:300-478) L1 and L2 domains of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

KVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIRHSHALVSLSFLKNLRLILGEEQLEGNYSFYVLDNQNLQQLWDWDHRNLTIKAGKMYFAFNPKLCVSEIYRMEEVTGTKGRQSKGDINTRNNGERASCESDVDDDDKEQKLISEEDLN

>d1ds9a\_ c.11.1.1 (A:) Outer arm dynein light chain 1 {Green algae (Chlamydomonas reinhardtii)}

MAKATTIKDAIRIFEERKSVVATEAEKVELHGMIPPIEKMDATLSTLKACKHLALSTNNIEKISSLSGMENLRILSLGRNLIKKIENLDAVADTLEELWISYNQIASLSGIEKLVNLRVLYMSNNKITNWGEIDKLAALDKLEDLLLAGNPLYNDYKENNATSEYRIEVVKRLPNLKKLDGMPVDVDEREQANVARGG

>d1jj2k\_ c.12.1.1 (K:) Ribosomal protein L15 (L15p) {Archaeon Haloarcula marismortui}

TSKKKRQRGSRTHGGGSHKNRRGAGHRGGRGDAGRDKHEFHNHEPLGKSGFKRPQKVQEEAATIDVREIDENVTLLAADDVAEVEDGGFRVDVRDVVEEADDADYVKVLGAGQVRHELTLIADDFSEGAREKVEGAGGSVELTDLGEERQ

>d1jj2n\_ c.12.1.1 (N:) Ribosomal protein L18e {Archaeon Haloarcula marismortui}

SKTNPRLSSLIADLKSAARSSGGAVWGDVAERLEKPRRTHAEVNLGRIERYAQEDETVVVPGKVLGSGVLQKDVTVAAVDFSGTAETKIDQVGEAVSLEQAIENNPEGSHVRVIR

>d1aua\_2 c.13.1.1 (97-299) C-terminal domain of phosphatidylinositol transfer protein sec14p {Baker's yeast (Saccharomyces cerevisiae)}

YDEKPLIAKFYPQYYHKTDKDGRPVYFEELGAVNLHEMNKVTSEERMLKNLVWEYESVVQYRLPACSRAAGHLVETSCTIMDLKGISISSAYSVMSYVREASYISQNYYPERMGKFYIINAPFGFSTAFRLFKPFLDPVTVSKIFILGSSYQKELLKQIPAENLPVKFGGKSEVDESKGGLYLSDIGPWRDPKYIGPEGEAPE

>d1h4xa\_ c.13.2.1 (A:) Anti-sigma factor antagonist SpoIIaa {Bacillus sphaericus}

AFQLEMVTRETVVIRLFGELDHHAVEQIRAKISTAIFQGAVTTIIWNFERLSFMDSSGVGLVLGRMRELEAVAGRTILLNPSPTMRKVFQFSGLGPWMMDATEEEAIDRVR

>d1auz\_\_ c.13.2.1 (-) Anti-sigma factor antagonist SpoIIaa {Bacillus subtilis}

SLGIDMNVKESVLCIRLTGELDHHTAETLKQKVTQSLEKDDIRHIVLNLEDLSFMDSSGLGVILGRYKQIKQIGGEMVVCAISPAVKRLFDMSGLFKIIRFEQSEQQALLTLGVAS

>d1tyfa\_ c.14.1.1 (A:) Clp protease, ClpP subunit {Escherichia coli}

SRGERSFDIYSRLLKERVIFLTGQVEDHMANLIVAQMLFLEAENPEKDIYLYINSPGGVITAGMSIYDTMQFIKPDVSTICMGQAASMGAFLLTAGAKGKRFCLPNSRVMIHQPLGGYQGQATDIEIHAREILKVKGRMNELMALHTGQSLEQIERDTERDRFLSAPEAVEYGLVDSILTHRN

>d1fc6a4 c.14.1.2 (A:78-156,A:249-463) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}

VTSEQLLFLEAWRAVDRAYVDKSFNGQSWFKLRETYLKKEPMDRRAQTYDAIRKMLAVLDDPFTRFLEPSRLAALRRGTXKVTINPVTFTTCSNVAAAALPPGAAKQQLGYVRLATFNSNTTAAAQQAFTELSKQGVAGLVLDIRNNGGGLFPAGVNVARMLVDRGDLVLIADSQGIRDIYSADGNSIDSATPLVVLVNRGTASASEVLAGALKDSKRGLIAGERTFGKGLIQTVVDLSDGSGVAVTVARYQTPAGVDINKIGVSPDVQLDPEVLPTDLEGVCRVLGSDAAPRLF

>d1k32a4 c.14.1.2 (A:680-762,A:854-1061) Tricorn protease {Archaeon Thermoplasma acidophilum}

SSIHEEFLQMYDEAWKLARDNYWNEAVAKEISERIYEKYRNLVPLCKTRYDLSNVIVEMQGEYRTSHSYEMGGTFTDKDPFRSXDDRFIRYRSWVEANRRYVHERSKGTIGYIHIPDMGMMGLNEFYRLFINESSYQGLIVDVRFNGGGFVSQLIIEKLMNKRIGYDNPRRGTLSPYPTNSVRGKIIAITNEYAGSDGDIFSFSFKKLGLGKLIGTRTWGGVVGITPKRRLIDGTVLTQPEFAFWFRDAGFGVENYGVDPDVEIEYAPHDYLSGKDPQIDYAIDALIEELRN

>d1j7xa\_ c.14.1.2 (A:) Interphotoreceptor retinoid-binding protein IRBP {African clawed frog (Xenopus laevis)}

DPSVTHVLHQLCDILANNYAFSERIPTLLQHLPNLDYSTVISEEDIAAKLNYELQSLTEDPRLVLKSKTDTLVMPGDSIQAENIPEDEAMLQALVNTVFKVSILPGNIGYLRFDQFADVSVIAKLAPFIVNTVWEPITITENLIIDLRYNVGGSSTAVPLLLSYFLDPETKIHLFTLHNRQQNSTDEVYSHPKVLGKPYGSKKGVYVLTSHQTATAAEEFAYLMQSLSRATIIGEITSGNLMHSKVFPFGDTQLSVTVPIINFIDSNGDYWLGGGVVPDAIVLADEALDKAKEIIAFHPPLA

>d1nzya\_ c.14.1.3 (A:) 4-Chlorobenzoyl-CoA dehalogenase {Pseudomonas sp., strain CBS-3}

MYEAIGHRVEDGVAEITIKLPRHRNALSVKAMQEVTDALNRAEEDDSVGAVMITGAEDAFCAGFYLREIPLDKGVAGVRDHFRIAALWWHQMIHKIIRVKRPVLAAINGVAAGGGLGISLASDMAICADSAKFVCAWHTIGIGNDTATSYSLARIVGMRRAMELMLTNRTLYPEEAKDWGLVSRVYPKDEFREVAWKVARELAAAPTHLQVMAKERFHAGWMQPVEECTEFEIQNVIASVTHPHFMPCLTRFLDGHRADRPQVELPAGV

>d1ey3a\_ c.14.1.3 (A:) Enoyl-CoA hydratase (crotonase) {Rat (Rattus norvegicus)}

FQYIITEKKGKNSSVGLIQLNRPKALNALCNGLIEELNQALETFEEDPAVGAIVLTGGEKAFAAGADIKEMQNRTFQDCYSGKFLSHWDHITRIKKPVIAAVNGYALGGGCELAMMCDIIYAGEKAQFGQPEILLGTIPGAGGTQRLTRAVGKSLAMEMVLTGDRISAQDAKQAGLVSKIFPVETLVEEAIQCAEKIANNSKIIVAMAKESVNAAFEMTLTEGNKLEKKLFYSTFATDDRREGMSAFVEKRKANFKDH

>d1dcia\_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Rat (Rattus norvegicus)}

AYESIQVTSAQKHVLHVQLNRPEKRNAMNRAFWRELVECFQKISKDSDCRAVVVSGAGKMFTSGIDLMDMASDILQPPGDDVARIAWYLRDLISRYQKTFTVIEKCPKPVIAAIHGGCIGGGVDLISACDIRYCTQDAFFQVKEVDVGLAADVGTLQRLPKVIGNRSLVNELTFTARKMMADEALDSGLVSRVFPDKDVMLNAAFALAADISSKSPVAVQGSKINLIYSRDHSVDESLDYMATWNMSMLQTQDIIKSVQAAMEKKDSKSITFSKL

>d1hnua\_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Baker's yeast (Saccharomyces cerevisiae)}

NEKISYRIEGPFFIIHLINPDNLNALEGEDYIYLGELLELADRNRDVYFTIIQSSGRFFSSGADFKGIAKAQGDDTNKYPSETSKWVSNFVARNVYVTDAFIKHSKVLICCLNGPAIGLSAALVALCDIVYSINDKVYLLYPFANLGLITEGGTTVSLPLKFGTNTTYECLMFNKPFKYDIMCENGFISKNFNMPSSNAEAFNAKVLEELREKVKGLYLPSCLGMKKLLKSNHIDAFNKANSVEVNESLKYWVDGEPLKRFRQ

>d1hzda\_ c.14.1.3 (A:) AUH protein {Human (Homo sapiens)}

EDELRVRHLEEENRGIVVLGINRAYGKNSLSKNLIKMLSKAVDALKSDKKVRTIIIRSEVPGIFCAGADLKERAKMSSSEVGPFVSKIRAVINDIANLPVPTIAAIDGLALGGGLELALACDIRVAASSAKMGLVETKLAIIPGGGGTQRLPRAIGMSLAKELIFSARVLDGKEAKAVGLISHVLEQNQEGDAAYRKALDLAREFLPQGPVAMRVAKLAINQGMEVDLVTGLAIEEACYAQTIPTKDRLEGLLAFKEKRPPRYKGE

>d1ef8a\_ c.14.1.3 (A:) Methylmalonyl CoA decarboxylase {Escherichia coli}

MSYQYVNVVTINKVAVIEFNYGRKLNALSKVFIDDLMQALSDLNRPEIRCIILRAPSGSKVFSAGHDIHELPSGGRDPLSYDDPLRQITRMIQKFPKPIISMVEGSVWGGAFEMIMSSDLIIAASTSTFSMTPVNLGVPYNLVGIHNLTRDAGFHIVKELIFTASPITAQRALAVGILNHVVEVEELEDFTLQMAHHISEKAPLAIAVIKEELRVLGEAHTMNSDEFERIQGMRRAVYDSEDYQEGMNAFLEKRKPNFVGH

>d1jnxx1 c.15.1.3 (X:1649-1757) Breast cancer associated protein, BRCA1 {Human (Homo sapiens)}

RMSMVVSGLTPEEFMLVYKFARKHHITLTNLITEETTHVVMKTDAEFVCERTLKYFLGIAGGKWVVSYFWVTQSIKERKMLNEHDFEVRGDVVNGRNHQGPKRARESQD

>d1jnxx2 c.15.1.3 (X:1758-1859) Breast cancer associated protein, BRCA1 {Human (Homo sapiens)}

RKIFRGLEICCYGPFTNMPTDQLEWMVQLCGASVVKELSSFTLGTGVHPIVVVQPDAWTEDNGFHAIGQMCEAPVVTREWVLDSVALYQCQELDTYLIPQIP

>d1cdza\_ c.15.1.1 (A:) DNA-repair protein XRCC1 {Human (Homo sapiens)}

ELPDFFQGKHFFLYGEFPGDERRKLIRYVTAFNGELEDYMSDRVQFVITAQEWDPSFEEALMDNPSLAFVRPRWIYSCNEKQKLLPHQLYGVVPQA

>d1in1a\_ c.15.1.2 (A:) DNA ligase III alpha {Human (Homo sapiens)}

GSADETLCQTKVLLDIFTGVRLYLPPSTPDFSRLRRYFVAFDGDLVQEFDMTSATHVLGSRDKNPAAQQVSPEWIWACIRKRRLVAPC

>d1dgtb3 c.15.1.2 (B:2582-2660) NAD+-dependent DNA ligase, domain 4 {Thermus filiformis}

EEVSDLLSGLTFVLTGELSRPREEVKALLGRLGAKVTDSVSRKTSYLVVGENPGSKLEKARALGVAVLTEEEFWRFLKE

>d1rvv1\_ c.16.1.1 (1:) Lumazine synthase {Bacillus subtilis}

MNIIQGNLVGTGLKIGIVVGRFNDFITSKLLSGAEDALLRHGVDTNDIDVAWVPGAFEIPFAAKKMAETKKYDAIITLGTVIRGATTHYDYVCNEAAKGIAQAANTTGVPVIFGIVTTENIEQAIERAGTKAGNKGVDCAVSAIEMANLNRSFE

>d1di0a\_ c.16.1.1 (A:) Lumazine synthase {Brucella abortus}

TSFKIAFIQARWHADIVDEARKSFVAELAAKTGGSVEVEIFDVPGAYEIPLHAKTLARTGRYAAIVGAAFVIDGGIYDHDFVATAVINGMMQVQLETEVPVLSVVLTPHHFHESKEHHDFFHAHFKVKGVEAAHAALQIVSERSRIAA

>d1hqka\_ c.16.1.1 (A:) Lumazine synthase {Aquifex aeolicus}

MQIYEGKLTAEGLRFGIVASRFNHALVDRLVEGAIDCIVRHGGREEDITLVRVPGSWEIPVAAGELARKEDIDAVIAIGVLIRGATPHFDYIASEVSKGLANLSLELRKPITFGVITADTLEQAIERAGTKHGNKGWEAALSAIEMANLFKSLR

>d1c41a\_ c.16.1.1 (A:) Lumazine synthase {Rice blast fungus (Magnaporthe grisea)}

GPTPQQHDGSALRIGIVHARWNETIIEPLLAGTKAKLLACGVKESNIVVQSVPGSWELPIAVQRLYSASQLQTPSSGPSLSAGDLLGSSTTDLTALPTTTASSTGPFDALIAIGVLIKGETMHFEYIADSVSHGLMRVQLDTGVPVIFGVLTVLTDDQAKARAGVIEGSHNHGEDWGLAAVEMGVRRRDWAAGKT

>d1c2ya\_ c.16.1.1 (A:) Lumazine synthase {Spinach (Spinacia oleracea)}

MNELEGYVTKAQSFRFAIVVARFNEFVTRRLMEGALDTFKKYSVNEDIDVVWVPGAYELGVTAQALGKSGKYHAIVCLGAVVKGDTSHYDAVVNSASSGVLSAGLNSGVPCVFGVLTCDNMDQAINRAGGKAGNKGAESALTAIEMASLFEHHLK

>d1ejba\_ c.16.1.1 (A:) Lumazine synthase {Baker's yeast (Saccharomyces cerevisiae)}

AVKGLGKPDQVYDGSKIRVGIIHARWNRVIIDALVKGAIERMASLGVEENNIIIETVPGSYELPWGTKRFVDRQAKLGKPLDVVIPIGVLIKGSTMHFEYISDSTTHALMNLQEKVDMPVIFGLLTCMTEEQALARAGIDEAHSMHNHGEDWGAAAVEMAVKFGKNAF

>d1cp3a\_ c.17.1.1 (A:) Apopain (caspase-3, cpp32) {Human (Homo sapiens)}

NSYKMDYPEMGLCIIINNKNFHKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEDHSKRSSFVCVLLSHGEEGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPKLFIIQACRGTELDCGIETDSGVDDDMACHKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQSLCAMLKQYADKLEFMHILTRVNRKVATEFESFSFDATFHAKKQIPCIVSMLTKELYFYH

>g1ibc.1 c.17.1.1 (A:,B:) Interleukin-1beta converting enzyme (a cysteine protease) {Human (Homo sapiens)}

GNVKLCSLEEAQRIWKQKSAEIYPIMDKSSRTRLALIICNEEFDSIPRRTGAEVDITGMTMLLQNLGYSVDVKKNLTASDMTTELEAFAHRPEHKTSDSTFLVFMSHGIREGICGKKHSEQVPDILQLNAIFNMLNTKNCPSLKDKPKVIIIQACRGDSPGVVWFKDXAIKKAHIEKDFIAFCSSTPDNVSWRHPTMGSVFIGRLIEHMQEYACSCDVEEIFRKVRFSFEQPAGRAQMPTTERVTLTRCFYLFPGH

>d1f1ja\_ c.17.1.1 (A:) Caspase-7 {Human (Homo sapiens)}

YQYNMNFEKLGKCIIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSCAKMQDLLKKASEEDHTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRSKTLLEKPKLFFIQACRGTELDDGIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKDLEIMQILTRVNDRVARHFESQSDDPHFHEKKQIPCVVSMLTKELYFS

>g1qtn.1 c.17.1.1 (A:,B:) Caspase-8 {Human (Homo sapiens)}

DKVYQMKSKPRGYCLIINNHNFAKAREKVPKLHSIRDRNGTHLDAGALTTTFEELHFEIKPHDDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKGIIYGTDGQEAPIYELTSQFTGLKCPSLAGKPKVFFIQACQGDNYQKGIPVETDXTRYIPDEADFLLGMATVNNCVSYRNPAEGTWYIQSLCQSLRERCPRGDDILTILTEVNYEVSNKDDKKNMGKQMPQPTFTLRKKLVFPSD

>d1jxqa\_ c.17.1.1 (A:) Caspase-9 {Human (Homo sapiens)}

MGALESLRGNADLAYILSMEPCGHCLIINNVNFCRESGLRTRTGSNIDCEKLRRRFSSLHFMVEVKGDLTAKKMVLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTDGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDLQSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS

>d1cvra2 c.17.1.2 (A:1-350) Gingipain R (RgpB), N-terminal domain {Porphyromonas gingivalis}

YTPVEEKENGRMIVIVAKKYEGDIKDFVDWKNQRGLRTEVKVAEDIASPVTANAIQQFVKQEYEKEGNDLTYVLLVGDHKDIPAKITPGIKSDQVYGQIVGNDHYNEVFIGRFSCESKEDLKTQIDRTIHYERNITTEDKWLGQALCIASAEGGPSADNGESDIQHENVIANLLTQYGYTKIIKCYDPGVTPKNIIDAFNGGISLVNYTGHGSETAWGTSHFGTTHVKQLTNSNQLPFIFDVACVNGDFLFSMPCFAEALMRAQKDGKPTGTVAIIASTIDQYWAPPMRGQDEMNEILCEKHPNNIKRTFGGVTMNGMFAMVEKYKKDGENMLDTWTVFGDPSLLVRTLV

>d1akz\_\_ c.18.1.1 (-) Uracil-DNA glycosylase {Human (Homo sapiens)}

MEFFGESWKKHLSGEFGKPYFIKLMGFVAEERKHYTVYPPPHQVFTWTQMCDIKDVKVVILGQDPYHGPNQAHGLCFSVQRPVPPPPSLENIYKELSTDIEDFVHPGHGDLSGWAKQGVLLLNAVLTVRAHQANSHKERGWEQFTDAVVSWLNQNSNGLVFLLWGSYAQKKGSAIDRKRHHVLQTAHPSPLSVYRGFFGCRHFSKTNELLQKSGKKPIDWKEL

>d1laue\_ c.18.1.1 (E:) Uracil-DNA glycosylase {Herpes simplex virus type 1}

LDWTTFRRVFLIDDAWRPLMEPELANPLTAHLLAEYNRRCQTEEVLPPREDVFSWTRYCTPDEVRVVIIGQDPYHHPGQAHGLAFSVRANVPPPPSLRNVLAAVKNCYPEARMSGHGCLEKWARDGVLLLNTTLTVKRGAAASHSRIGWDRFVGGVIRRLAARRPGLVFMLWGTHAQNAIRPDPRVHCVLKFSHPSPLSKVPFGTCQHFLVANRYLETRSISPIDWSV

>d3euga\_ c.18.1.1 (A:) Uracil-DNA glycosylase {Escherichia coli}

LTWHDVLAEEKQQPHFLNTLQTVASERQSGVTIYPPQKDVFNAFRFTELGDVKVVILGQDPYHGPGQAHGLAFSVRPGIAIPPSLLNMYKELENTIPGFTRPNHGYLESWARQGVLLLNTVLTVRAGQAHSHASLGWETFTDKVISLINQHREGVVFLLWGSHAQKKGAIIDKQRHHVLKAPHPSPLSAHRGFFGCNHFVLANQWLEQHGETPIDWMPVLPAESE

>d1muga\_ c.18.1.2 (A:) G:T/U mismatch-specific DNA glycosylase {Escherichia coli}

MVEDILAPGLRVVFCGINPGLSSAGTGFPFAHPANRFWKVIYQAGFTDRQLKPQEAQHLLDYRCGVTKLVDRPTVQANEVSKQELHAGGRKLIEKIEDYQPQALAILGKQAYEQGFSQRGAQWGKQTLTIGSTQIWVLPNPSGLSRVSLEKLVEAYRELDQALVV

>d1mla\_1 c.19.1.1 (3-127,198-307) Catalytic domain of malonyl-CoA ACP transacylase {Escherichia coli}

QFAFVFPGQGSQTVGMLADMAASYPIVEETFAEASAALGYDLWALTQQGPAEELNKTWQTQPALLTASVALYRVWQQQGGKAPAMMAGHSLGEYSALVCAGVIDFADAVRLVEMRGKFMQEAVPEXVPSHCALMKPAADKLAVELAKITFNAPTVPVVNNVDVKCETNGDAIRDALVRQLYNPVQWTKSVEYMAAQGVEHLYEVGPGKVLTGLTKRIVDTLTASALNEPSAMAAAL

>d1g7sa3 c.20.1.1 (A:329-459) Initiation factor IF2/eIF5b, domain 3 {Archaeon Methanobacterium thermoautotrophicum}

DPEKVREEILSEIEDIKIDTDEAGVVVKADTLGSLEAVVKILRDMYVPIKVADIGDVSRRDVVNAGIALQEDRVYGAIIAFNVKVIPSAAQELKNSDIKLFQGNVIYRLMEEYEEWVRGIEEEKKKKWMEA

>d1jj2i\_ c.21.1.1 (I:) Ribosomal protein L13 {Archaeon Haloarcula marismortui}

AEFDADVIVDARDCIMGRVASQVAEQALDGETVAVVNAERAVITGREEQIVEKYEKRVDIGNDNGYFYPKRPDGIFKRTIRGMLPHKKQRGREAFESVRVYLGNPYDEDGEVLDGTSLDRLSNIKFVTLGEISETLGANKTW

>d1dmga\_ c.22.1.1 (A:) Ribosomal protein L4 {Thermotoga maritima}

AQVDLLNVKGEKVGTLEISDFVFNIDPNYDVMWRYVDMQLSNRRAGTASTKTRGEVSGGGRKPWPQKHTGRARHGSIRSPIWRHGGVVHGPKPRDWSKKLNKKMKKLALRSALSVKYRENKLLVLDDLKLERPKTKSLKEILQNLQLSDKKTLIVLPWKEEGYMNVKLSGRNLPDVKVIIADNPNNSKNGEKAVRIDGLNVFDMLKYDYLVLTRDMVSKIEEVLG

>d1jj2c\_ c.22.1.1 (C:) Ribosomal protein L4 {Archaeon Haloarcula marismortui}

MQATIYDLDGNTDGEVDLPDVFETPVRSDLIGKAVRAAQANRKQDYGSDEYAGLRTPAESFGSGRGQAHVPKLDGRARRVPQAVKGRSAHPPKTEKDRSLDLNDKERQLAVRSALAATADADLVADRGHEFDRDEVPVVVSDDFEDLVKTQEVVSLLEALDVHADIDRADETKIKAGQGSARGRKYRRPASILFVTSDEPSTAARNLAGADVATASEVNTEDLAPGGAPGRLTVFTESALAEVAER

>d1hey\_\_ c.23.1.1 (-) CheY protein {Escherichia coli}

DKELKFLVVGNGGTGKSTVRNLLKELGFNNVEDAEDGVDALNKLQAGGYGFVISDWNMPNMDGLELLKTIRADGAMSALPVLMVTAEAKKENIIAAAQAGASGYVVKPFTAATLEEKLNKIFEKLGM

>d1jbea\_ c.23.1.1 (A:) CheY protein {Escherichia coli}

ADKELKFLVVDDFSTMRRIVRNLLKELGFNNVEEAEDGVDALNKLQAGGYGFVISDWNMPNMDGLELLKTIRADGAMSALPVLMVTAEAKKENIIAAAQAGASGYVVKPFTAATLEEKLNKIFEKLGM

>d1tmy\_\_ c.23.1.1 (-) CheY protein {Thermotoga maritima}

GKRVLIVDDAAFMRMMLKDIITKAGYEVAGEATNGREAVEKYKELKPDIVTMDITMPEMNGIDAIKEIMKIDPNAKIIVCSAMGQQAMVIEAIKAGAKDFIVKPFQPSRVVEALNKVS

>d1a04a2 c.23.1.1 (A:5-142) Nitrate/nitrite response regulator (NARL), receiver domain {Escherichia coli}

EPATILLIDDHPMLRTGVKQLISMAPDITVVGEASNGEQGIELAESLDPDLILLDLNMPGMNGLETLDKLREKSLSGRIVVFSVSNHEEDVVTALKRGADGYLLKDMEPEDLLKALHQAAAGEMVLSEALTPVLAASL

>d1ntr\_\_ c.23.1.1 (-) NTRC receiver domain {Salmonella typhimurium}

MQRGIVWVVDDDSSIRWVLERALAGAGLTCTTFENGNEVLAALASKTPDVLLSDIRMPGMDGLALLKQIKQRHPMLPVIIMTAHSDLDAAVSAYQQGAFDYLPKPFDIDEAVALVERAISHYQE

>d1dbwa\_ c.23.1.1 (A:) Transcriptional regulatory protein FixJ, receiver domain {Rhizobium meliloti}

MQDYTVHIVDDEEPVRKSLAFMLTMNGFAVKMHQSAEAFLAFAPDVRNGVLVTDLRMPDMSGVELLRNLGDLKINIPSIVITGHGDVPMAVEAMKAGAVDFIEKPFEDTVIIEAIERASEHLV

>d1qkka\_ c.23.1.1 (A:) Transcriptional regulatory protein DctD, receiver domain {Sinorhizobium meliloti}

PSVFLIDDDRDLRKAMQQTLELAGFTVSSFASATEALAGLSADFAGIVISDIRMPGMDGLALFRKILALDPDLPMILVTGHGDIPMAVQAIQDGAYDFIAKPFAADRLVQSARRAEEKRRLVMENRSLRRAAEAASEGL

>d1dz3a\_ c.23.1.1 (A:) Sporulation response regulator Spo0A {Bacillus stearothermophilus}

SIKVCIADDNRELVSLLDEYISSQPDMEVIGTAYNGQDCLQMLEEKRPDILLLDIIMPHLDGLAVLERIRAGFEHQPNVIMLTAFGQEDVTKKAVELGASYFILKPFDMENLAHHIRQVYGKT

>d1nat\_\_ c.23.1.1 (-) Sporulation response regulator Spo0F {Bacillus subtilis}

NEKILIVDDQYGIRILLNEVFNKEGYQTFQAANGLQALDIVTKERPDLVLLDMKIPGMDGIEILKRMKVIDENIRVIIMTAYGELDMIQESKELGALTHFAKPFDIDEIRDAVKKYLPL

>d1a2oa1 c.23.1.1 (A:1-140) Methylesterase CheB, N-terminal domain {Salmonella typhimurium}

MSKIRVLSVDDSALMRQIMTEIINSHSDMEMVATAPDPLVARDLIKKFNPDVLTLDVEMPRMDGLDFLEKLMRLRPMPVVMVSSLTGKGSEVTLRALELGAIDFVTKPQLGIREGMLAYSEMIAEKVRTAARARIAAHKP

>d1kgsa2 c.23.1.1 (A:2-123) PhoB receiver domain {Thermotoga maritima}

NVRVLVVEDERDLADLITEALKKEMFTVDVCYDGEEGMYMALNEPFDVVILDIMLPVHDGWEILKSMRESGVNTPVLMLTALSDVEYRVKGLNMGADDYLPKPFDLRELIARVRALIRRKSE

>d1b00a\_ c.23.1.1 (A:) PhoB receiver domain {Escherichia coli}

ARRILVVEDEAPIREMVCFVLEQNGFQPVEAEDYDSAVNQLNEPWPDLILLDWMLPGGSGIQFIKHLKRESMTRDIPVVMLTARGEEEDRVRGLETGADDYITKPFSPKELVARIKAVMRRI

>d1dcfa\_ c.23.1.2 (A:) Receiver domain of the ethylene receptor {Thale cress (Arabidopsis thaliana)}

HMSNFTGLKVLVMDENGVSRMVTKGLLVHLGCEVTTVSSNEECLRVVSHEHKVVFMDVCMPGVENYQIALRIHEKFTKQRHQRPLLVALSGNTDKSTKEKCMSFGLDGVLLKPVSLDNIRDVLSDLLEPRVLYE

>d1qo0d\_ c.23.1.3 (D:) Negative regulator of the amidase operon AmiR {Pseudomonas aeruginosa}

SANSLLGSLRELQVLVLNPPGEVSDALVLQLIRIGCSVRQCWPPPEAFDVPVDVVFTSIFQNRHHDEIAALLAAGTPRTTLVALVEYESPAVLSQIIELECHGVITQPLDAHRVLPVLVSARRISEEMAKLKQKTEQLQDRIAGQARINQAKVLLMQRHGWDEREAHQHLSREAMKRREPILKIAQELL

>d1fyva\_ c.23.2.1 (A:) Toll-like receptor 1, TLR1 {Human (Homo sapiens)}

NIPLEELQRNLQFHAFISYSGHDSFWVKNELLPNLEKEGMQICLHERNFVPGKSIVENIITCIEKSYKSIFVLSPNFVQSEWCHYELYFAHHNLFHEGSNSLILILLEPIPQYSIPSSYHKLKSLMARRTYLEWPKEKSKRGLFWANLRAAINIKLTEQAK

>d1fywa\_ c.23.2.1 (A:) Toll-like receptor 2, TLR2 {Human (Homo sapiens)}

SRNICYDAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNIIDSIEKSHKTVFVLSENFVKSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKTYLEWPMDEAQREGFWVNLRAAIKS

>d1eiwa\_ c.23.3.1 (A:) Hypothetical protein MTH538 {Archaeon Methanobacterium thermoautotrophicum}

VTAEIRLYITEGEVEDYRVFLERLEQSGLEWRPATPEDADAVIVLAGLWGTRRDEILGAVDLARKSSKPIITVRPYGLENVPPELEAVSSEVVGWNPHCIRDALEDALDVI

>d1jkja2 c.23.4.1 (A:122-287) Succinyl-CoA synthetase, alpha-chain, C-terminal domain {Escherichia coli}

NCPGVITPGECKIGIQPGHIHKPGKVGIVSRSGTLTYEAVKQTTDYGFGQSTCVGIGGDPIPGSNFIDILEMFEKDPQTEAIVMIGEIGGSAEEEAAAYIKEHVTKPVVGYIAGVTAPKGKRMGHAGAIIAGGKGTADEKFAALEAAGVKTVRSLADIGEALKTVL

>d1euca2 c.23.4.1 (A:131-306) Succinyl-CoA synthetase, alpha-chain, C-terminal domain {Pig (Sus scrofa)}

NCPGVINPGECKIGIMPGHIHKKGRIGIVSRSGTLTYEAVHQTTQVGLGQSLCVGIGGDPFNGTDFTDCLEIFLNDPATEGIILIGEIGGNAEENAAEFLKQHNSGPKSKPVVSFIAGLTAPPGRRMGHAGAIIAGGKGGAKEKITALQSAGVVVSMSPAQLGTTIYKEFEKRKML

>d1jkjb1 c.23.4.1 (B:239-388) Succinyl-CoA synthetase, beta-chain, C-terminal domain {Escherichia coli}

DPREAQAAQWELNYVALDGNIGCMVNGAGLAMGTMDIVKLHGGEPANFLDVGGGATKERVTEAFKIILSDDKVKAVLVNIFGGIVRCDLIADGIIGAVAEVGVNVPVVVRLEGNNAELGAKKLADSGLNIIAAKGLTDAAQQVVAAVEGK

>d1eucb1 c.23.4.1 (B:246-393) Succinyl-CoA synthetase, beta-chain, C-terminal domain {Pig (Sus scrofa)}

EPIENEAAKYDLKYIGLDGNIACFVNGAGLAMATCDIIFLNGGKPANFLDLGGGVKESQVYQAFKLLTADPKVEAILVNIFGGIVNCAIIANGITKACRELELKVPLVVRLEGTNVHEAQNILTNSGLPITSAVDLEDAAKKAVASVT

>d2fcr\_\_ c.23.5.1 (-) Flavodoxin {Chondrus crispus}

KIGIFFSTSTGNTTEVADFIGKTLGAKADAPIDVDDVTDPQALKDYDLLFLGAPTWNTGADTERSGTSWDEFLYDKLPEVDMKDLPVAIFGLGDAEGYPDNFCDAIEEIHDCFAKQGAKPVGFSNPDDYDYEESKSVRDGKFLGLPLDMVNDQIPMEKRVAGWVEAVVSETGV

>d1f4pa\_ c.23.5.1 (A:) Flavodoxin {Desulfovibrio vulgaris}

PKALIVYGSTTGNTEYTAETIARELADAGYEVDSRDAASVEAGGLFEGFDLVLLGCSTWGDDSIELQDDFIPLFDSLEETGAQGRKVACFGCGDSSWEYFCGAVDAIEEKLKNLGAEIVQDGLRIDGDPRAARDDIVGWAHDVRGAI

>d1rcf\_\_ c.23.5.1 (-) Flavodoxin {Anabaena, pcc 7119 and 7120}

SKKIGLFYGTQTGKTESVAEIIRDEFGNDVVTLHDVSQAEVTDLNDYQYLIIGCPTWNIGELQSDWEGLYSELDDVDFNGKLVAYFGTGDQIGYADNFQDAIGILEEKISQRGGKTVGYWSTDGYDFNDSKALRNGKFVGLALDEDNQSDLTDDRIKSWVAQLKSEFGL

>d1ag9a\_ c.23.5.1 (A:) Flavodoxin {Escherichia coli}

AITGIFFGSDTGNTENIAKMIQKQLGKDVADVHDIAKSSKEDLEAYDILLLGIPTWYYGEAQCDWDDFFPTLEEIDFNGKLVALFGCGDQEDYAEYFCDALGTIRDIIEPRGATIVGHWPTAGYHFEASKGLADDDHFVGLAIDEDRQPELTAERVEKWVKQISEELHLDEILNA

>d1czna\_ c.23.5.1 (A:) Flavodoxin {Anacystis nidulans and Synechococcus, pcc 7942}

AKIGLFYGTQTGVTQTIAESIQQEFGGESIVDLNDIANADASDLNAYDYLIIGCPTWNVGELQSDWEGIYDDLDSVNFQGKKVAYFGAGDQVGYSDNFQDAMGILEEKISSLGSQTVGYWPIEGYDFNESKAVRNNQFVGLAIDEDNQPDLTKNRIKTWVSQLKSEFGL

>d5nul\_\_ c.23.5.1 (-) Flavodoxin {Clostridium beijerinckii}

MKIVYWSGTGNTEKMAELIAKGIIESGKDVNTINVSDVNIDELLNEDILILGCSAMTDEVLEESEFEPFIEEISTKISGKKVALFGSYGWGDGKWMRDFEERMNGYGCVVVETPLIVQNEPDEAEQDCIEFGKKIANI

>d1fuea\_ c.23.5.1 (A:) Flavodoxin {Helicobacter pylori}

GKIGIFFGTDSGNAEAIAEKISKAIGNAEVVDVAKASKEQFNGFTKVILVAPTAGAGDLQTDWEDFLGTLEASDFANKTIGLVGLGDQDTYSETFAEGIFHIYEKAKAGKVVGQTSTDGYHFAASKAVEGGKFVGLVIDEDNQDDLTDERIAKWVEQVRGSFA

>d1bvyf\_ c.23.5.1 (F:) FMN-binding domain of the cytochrome P450bm-3 {Bacillus megaterium}

NTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNGHPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNL

>d1e5da1 c.23.5.1 (A:251-402) Rubredoxin oxygen:oxidoreductase (ROO), C-terminal domain {Desulfovibrio gigas}

PTNKVVIFYDSMWHSTEKMARVLAESFRDEGCTVKLMWCKACHHSQIMSEISDAGAVIVGSPTHNNGILPYVAGTLQYIKGLRPQNKIGGAFGSFGWSGESTKVLAEWLTGMGFDMPATPVKVKNVPTHADYEQLKTMAQTIARALKAKLAA

>d1ja1a2 c.23.5.2 (A:63-239) NADPH-cytochrome p450 reductase, N-terminal domain {Rat (Rattus norvegicus)}

PVKESSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDKSLVVFCMATYGEGDPTDNAQDFYDWLQETDVDLTGVKFAVFGLGNKTYEHFNAMGKYVDQRLEQLGAQRIFELGLGDDDGNLEEDFITWREQFWPAVCEFFGVEATGEE

>d1b1ca\_ c.23.5.2 (A:) NADPH-cytochrome p450 reductase, N-terminal domain {Human (Homo sapiens)}

SSFVEKMKKTGRNIIVFYGSQTGTAEEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDNALVVFCMATYGEGDPTDNAQDFYDWLQETDVDLSGVKFAVFGLGNKTYEHFNAMGKYVDKRLEQLGAQRIFELGLGDDDGNLEEDFITWREQFWPAVCEHFGV

>d1dxqa\_ c.23.5.3 (A:) NAD(P)H:quinone reductase {Mouse (Mus musculus)}

AARRALIVLAHSEKTSFNYAMKEAAVEALKKRGWEVLESDLYAMNFNPIISRNDITGELKDSKNFQYPSESSLAYKEGRLSPDIVAEHKKLEAADLVIFQFPLQWFGVPAILKGWFERVLVAGFAYTYAAMYDNGPFQNKKTLLSITTGGSGSMYSLQGVHGDMNVILWPIQSGILRFCGFQVLEPQLVYSIGHTPPDARMQILEGWKKRLETVWEETPLYFAPSSLFDLNFQAGFLLMKEVQEEQKKNKFGLSVGHHLGKSIPADNQIKARK

>d1qrda\_ c.23.5.3 (A:) NAD(P)H:quinone reductase {Rat (Rattus rattus)}

AVRRALIVLAHAERTSFNYAMKEAAVEALKKKGWEVVESDLYAMNFNPLISRNDITGEPKDSENFQYPVESSLAYKEGRLSPDIVAEQKKLEAADLVIFQFPLYWFGVPAILKGWFERVLVAGFAYTYATMYDKGPFQNKKTLLSITTGGSGSMYSLQGVHGDMNVILWPIQSGILRFCGFQVLEPQLVYSIGHTPPDARVQVLEGWKKRLETVWEESPLYFAPSSLFDLNFQAGFLLKKEVQEEQKKNKFGLSVGHHLGKSIPADNQIKARK

>d1d4aa\_ c.23.5.3 (A:) NAD(P)H:quinone reductase {Human (Homo sapiens)}

VGRRALIVLAHSERTSFNYAMKEAAAAALKKKGWEVVESDLYAMNFNPIISRKDITGKLKDPANFQYPAESVLAYKEGHLSPDIVAEQKKLEAADLVIFQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRSKKAVLSITTGGSGSMYSLQGIHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPADARIQILEGWKKRLENIWDETPLYFAPSSLFDLNFQAGFLMKKEVQDEEKNKKFGLSVGHHLGKSIPTDNQIKARK

>d1qr2a\_ c.23.5.3 (A:) Quinone reductase type 2 (menadione reductase) {Human (Homo sapiens)}

AGKKVLIVYAHQEPKSFNGSLKNVAVDELSRQGCTVTVSDLYAMNFEPRATDKDITGTLSNPEVFNYGVETHEAYKQRSLASDITDEQKKVREADLVIFQFPLYWFSVPAILKGWMDRVLCQGFAFDIPGFYDSGLLQGKLALLSVTTGGTAEMYTKTGVNGDSRYFLWPLQHGTLHFCGFKVLAPQISFAPEIASEEERKGMVAAWSQRLQTIWKEEPIPCTAHWHFGQ

>d1bmta2 c.23.6.1 (A:741-896) Methionine synthase, C-terminal domain {Escherichia coli}

EQGKTNGKMVIATVKGDVHDIGKNIVGVVLQCNNYEIVDLGVMVPAEKILRTAKEVNADLIGLSGLITPSLDEMVNVAKEMERQGFTIPLLIGGATTSKAHTAVKIEQNYSGPTVYVQNASRTVGVVAALLSDTQRDDFVARTRKEYETVRIQHGR

>d1fmfa\_ c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium tetanomorphum}

MEKKTIVLGVIGSDCHAVGNKILDHSFTNAGFNVVNIGVLSSQEDFINAAIETKADLICVSSLYGQGEIDCKGLREKCDEAGLKGIKLFVGGNIVVGKQNWPDVEQRFKAMGFDRVYPPGTSPETTIADMKEVLGVE

>d1ccwa\_ c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium cochlearium}

MEKKTIVLGVIGSDCHAVGNKILDHAFTNAGFNVVNIGVLSPQELFIKAAIETKADAILVSSLYGQGEIDCKGLRQKCDEAGLEGILLYVGGNIVVGKQHWPDVEKRFKDMGYDRVYAPGTPPEVGIADLKKDLNIE

>d7reqa2 c.23.6.1 (A:561-728) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

AQIRTISGVYSKEVKNTPEVEEARELVEEFEQAEGRRPRILLAKMGQDGHDRGQKVIATAYADLGFDVDVGPLFQTPEETARQAVEADVHVVGVSSLAGGHLTLVPALRKELDKLGRPDILITVGGVIPEQDFDELRKDGAVEIYTPGTVIPESAISLVKKLRASLDA

>d7reqb2 c.23.6.1 (B:476-638) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

TKPFPAAPARKGLAWHRDSEVFEQLMDRSTSVSERPKVFLACLGTRRDFGGREGFSSPVWHIAGIDTPQVEGGTTAEIVEAFKKSGAQVADLCSSAKVYAQQGLEVAKALKAAGAKALYLSGAFKEFGDDAAEAEKLIDGRLFMGMDVVDTLSSTLDILGVAK

>d1c4ka1 c.23.7.1 (A:1-107) Ornithine decarboxylase N-terminal "wing" domain {Lactobacillus sp., strain 30a}

SSSLKIASTQEARQYFDTDRVVVDAVGSDFTDVGAVIAMDYETDVIDAADATKFGIPVFAVTKDAQAISADELKKIFHIIDLENKFDATVNAREIETAVNNYEDSIL

>d1qcza\_ c.23.8.1 (A:) N5-carboxyaminoimidazole ribonucleotide (N5-CAIR) mutase PurE {Escherichia coli}

PARVAIVMGSKSDWATMQFAAEIFEILNVPHHVEVVSAHRTPDKLFSFAESAEENGYQVIIAGAGGAAHLPGMIAAKTLVPVLGVPVQSAALSGVDSLYSIVQMPRGIPVGTLAIGKAGAANAALLAAQILATHDKELHQRLNDWRKAQTDEVLENPDPRGAA

>d1cex\_\_ c.23.9.1 (-) Cutinase {Fungus (Fusarium solani), subsp. pisi}

RTTRDDLINGNSASCADVIFIYARGSTETGNLGTLGPSIASNLESAFGKDGVWIQGVGGAYRATLGDNALPRGTSSAAIREMLGLFQQANTKCPDATLIAGGYSQGAALAAASIEDLDSAIRDKIAGTVLFGYTKNLQNRGRIPNYPADRTKVFCNTGDLVCTGSLIVAAPHLAYGPDARGPAPEFLIEKVRAVRGS

>d1g66a\_ c.23.9.1 (A:) Acetylxylan esterase {Penicillium purpurogenum}

SCPAIHVFGARETTASPGYGSSSTVVNGVLSAYPGSTAEAINYPACGGQSSCGGASYSSSVAQGIAAVASAVNSFNSQCPSTKIVLVGYSQGGEIMDVALCGGGDPNQGYTNTAVQLSSSAVNMVKAAIFMGDPMFRAGLSYEVGTCAAGGFDQRPAGFSCPSAAKIKSYCDASDPYCCNGSNAATHQGYGSEYGSQALAFVKSKLG

>d1qoza\_ c.23.9.1 (A:) Acetylxylan esterase {Trichoderma reesei}

ECPAIHVFGARETTVSQGYGSSATVVNLVIQAHPGTTSEAIVYPACGGQASCGGISYANSVVNGTNAAAAAINNFHNSCPDTQLVLVGYSQGAQIFDNALCGGGDPGEGITNTAVPLTAGAVSAVKAAIFMGDPRNIHGLPYNVGTCTTQGFDARPAGFVCPSASKIKSYCDAADPYCCTGNDPNVHQGYGQEYGQQALAFINSQLS

>d1esc\_\_ c.23.10.1 (-) Esterase {Streptomyces scabies}

DPVPTVFFGDSYTANFGIAPVTNQDSERGWCFQAKENYPAVATRSLADKGITLDVQADVSCGGALIHHFWEKQELPFGAGELPPQQDALKQDTQLTVGSLGGNTLGFNRILKQCSDELRKPSLLPGDPVDGDEPAAKCGEFFGTGDGKQWLDDQFERVGAELEELLDRIGYFAPDAKRVLVGYPRLVPEDTTKCLTAAPGQTQLPFADIPQDALPVLDQIQKRLNDAMKKAAADGGADFVDLYAGTGANTACDGADRGIGGLLEDSQLELLGTKIPWYAHPNDKGRDIQAKQVADKIEEILN

>d1flca2 c.23.10.2 (A:1-150,A:307-427) Esterase domain of haemagglutinin-esterase-fusion glycoprotein HEF1 {Influenza C virus}

EKIKICLQKQVNSSFSLHNGFGGNLYATEEKRMFELVKPKAGASVLNQSTWIGFGDSRTDKSNSAFPRSADVSAKTADKFRFLSGGSLMLSMFGPPGKVDYLYQGCGKHKVFYEGVNWSPHAAINCYRKNWTDIKLNFQKNIYELASQSHXEKGPVTAVQSIWGKGRESDYAVDQACLSTPGCMLIQKQKPYIGEADDHHGDQEMRELLSGLDYEARCISQSGWVNETSPFTEKYLLPPKFGRCPLAAKEESIPKIPDGLLIPTSGTDTTVT

>d1es9a\_ c.23.10.3 (A:) Platelet-activating factor acetylhydrolase {Cow (Bos taurus)}

ENPASKPTPVQDVQGDGKWMSLHHRFVADSKDKEPEVVFIGDSLVQLMHQCEIWRELFSPLHALNFGIGGDSTQHVLWRLENGELEHIRPKIVVVWVGTNNHGHTAEQVTGGIKAIVQLVNERQPQARVVVLGLLPRGQHPNPLREKNRRVNELVRAALAGHPRAHFLDADPGFVHSDGTISHHDMYDYLHLSRLGYTPVCRALHSLLLRLL

>d1fxwf\_ c.23.10.3 (F:) Platelet-activating factor acetylhydrolase {Cow (Bos taurus)}

SNPAAIPHAAEDIQGDDRWMSQHNRFVLDCKDKEPDVLFVGDSMVQLMQQYEIWRELFSPLHALNFGIGGDTTRHVLWRLKNGELENIKPKVIVVWVGTNNHENTAEEVAGGIEAIVQLINTRQPQAKIIVLGLLPRGEKPNPLRQKNAKVNQLLKVSLPKLANVQLLDTDGGFVHSDGAISCHDMFDFLHLTGGGYAKICKPLHELIMQLL

>d1k7ca\_ c.23.10.4 (A:) Rhamnogalacturonan acetylesterase {Fungus (Aspergillus aculeatus)}

TTVYLAGDSTMAKNGGGSGTNGWGEYLASYLSATVVNDAVAGRSARSYTREGRFENIADVVTAGDYVIVEFGHNDGGSLSTDNGRTDCSGTGAEVCYSVYDGVNETILTFPAYLENAAKLFTAKGAKVILSSQTPNNPWETGTFVNSPTRFVEYAELAAEVAGVEYVDHWSYVDSIYETLGNATVNSYFPIDHTHTSPAGAEVVAEAFLKAVVCTGTSLKSVLTTTSFEGTCL

>d1iexa2 c.23.11.1 (A:389-603) Beta-D-glucan exohydrolase, C-terminal domain {Barley (Hordeum vulgare)}

LVLLKNGKTSTDAPLLPLPKKAPKILVAGSHADNLGYQCGGWTIEWQGDTGRTTVGTTILEAVKAAVDPSTVVVFAENPDAEFVKSGGFSYAIVAVGEHPYTETKGDNLNLTIPEPGLSTVQAVCGGVRCATVLISGRPVVVQPLLAASDALVAAWLPGSEGQGVTDALFGDFGFTGRLPRTWFKSVDQLPMNVGDAHYDPLFRLGYGLTTNATK

>d2naca2 c.23.12.1 (A:1-147,A:336-374) Formate dehydrogenase {Pseudomonas sp., strain 101}

AKVLCVLYDDPVDGYPKTYARDDLPKIDHYPGGQTLPTPKAIDFTPGQLLGSVSGELGLRKYLESNGHTLVVTSDKDGPDSVFERELVDADVVISQPFWPAYLTPERIAKAKNLKLALTAGIGSDHVDLQSAIDRNVTVAEVTYCNSXTTLTAQARYAAGTREILECFFEGRPIRDEYLIVQGGALA

>d1qp8a2 c.23.12.1 (A:1-82,A:264-302) Putative formate dehydrogenase {Archaeon Pyrobaculum aerophilum}

MELYVNFELPPEAEEELRKYFKIVRGGDLGNVEAALVSRITAEELAKMPRLKFIQVVTAGLDHLPWESIPPHVTVAGNAGSNXGYGNERVWRQMVMEAVRNLITYATGGRPRNIAKREDYIG

>d1dxy\_2 c.23.12.1 (1-100,300-330) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}

MKIIAYGARVDEIQYFKQWAKDTGNTLEYHTEFLDENTVEWAKGFDGINSLQTTPYAAGVFEKMHAYGIKFLTIRNVGTDNIDMTAMKQYGIRLSNVPAYXTETAVHNMVYFSLQHLVDFLTKGETSTEVTG

>d1gdha2 c.23.12.1 (A:2-100,A:292-321) D-glycerate dehydrogenase {Hyphomicrobium methylovorum}

KKKILITWPLPEAAMARARESYDVIAHGDDPKITIDEMIETAKSVDALLITLNEKCRKEVIDRIPENIKCISTYSIGFDHIDLDACKARGIKVGNAPHGXATQAREDMAHQANDLIDALFGGADMSYALA

>d1psda2 c.23.12.1 (A:7-107,A:296-326) Phosphoglycerate dehydrogenase {Escherichia coli}

EKDKIKFLLVEGVHQKALESLRAAGYTNIEFHKGALDDEQLKESIRDAHFIGLRSRTHLTEDVINAAEKLVAIGCFCIGTNQVDLDAAAKRGIPVFNAPFSXSTQEAQENIGLEVAGKLIKYSDNGSTLSAVN

>d2dlda2 c.23.12.1 (A:1-103,A:301-337) D-lactate dehydrogenase {Lactobacillus helveticus}

MTKVFAYAIRKDEEPFLNEWKEAHKDIDVDYTDKLLTPETAKLAKGADGVVVYQQLDYTADTLQALADAGVTKMSLRNVGVDNIDMDKAKELGFQITNVPVYSXYTTHAVRNMVVKAFNNNLKLINGEKPDSPVALNKNKF

>d1pjca2 c.23.12.2 (A:1-135,A:304-361) L-alanine dehydrogenase {Phormidium lapideum}

MEIGVPKEIKNQEFRVGLSPSSVRTLVEAGHTVFIETQAGIGAGFADQDYVQAGAQVVPSAKDAWSREMVVKVKEPLPAEYDLMQKDQLLFTYLHLAAARELTEQLMRVGLTAIAYETVELPNRSLPLLTPMSIIXVPWTATQALNNSTLPYVVKLANQGLKALETDDALAKGLNVQAHRLVHPAVQQVFPDLA

>d1f8ga2 c.23.12.2 (A:1-143,A:327-384) Nicotinamide nucleotide transhydrogenase dI component {Rhodospirillum rubrum}

MKIAIPKERRPGEDRVAISPEVVKKLVGLGFEVIVEQGAGVGASITDDALTAAGATIASTAAQALSQADVVWKVQRPMTAEEGTDEVALIKEGAVLMCHLGALTNRPVVEALTKRKITAYAMELMPRISRAQSMDILSSQSNLXVAADASPLFAKNLLNFLTPHVDKDTKTLVMKLEDETVSGTCVTRDGAIVHPALTGQGA

>d1a7aa2 c.23.12.3 (A:2-189,A:353-432) S-adenosylhomocystein hydrolase {Human (Homo sapiens)}

SDKLPYKVADIGLAAWGRKALDIAENEMPGLMRMRERYSASKPLKGARIAGCLHMTVETAVLIETLVTLGAEVQWSSCNIFSTQNHAAAAIAKAGIPVYAWKGETDEEYLWCIEQTLYFKDGPLNMILDDGGDLTNLIHTKYPQLLPGIRGISEETTTGVHNLYKMMANGILKVPAINVNDSVTKSKFXHPSFVMSNSFTNQVMAQIELWTHPDKYPVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGMSCDGPFKPDHYRY

>d1b3ra2 c.23.12.3 (A:4-189,A:353-431) S-adenosylhomocystein hydrolase {Rat (Rattus norvegicus)}

LPYKVADIGLAAWGRKALDIAENEMPGLMRMREMYSASKPLKGARIAGCLHMTVETAVLIETLVALGAEVRWSSCNIFSTQDHAAAAIAKAGIPVFAWKGETDEEYLWCIEQTLHFKDGPLNMILDDGGDLTNLIHTKHPQLLSGIRGISEETTTGVHNLYKMMANGILKVPAINVNDSVTKSKFDXPSFVMSNSFTNQVMAQIELWTHPDKYPVGVHFLPKKLDEAVAEAHLGKLNVKLTKLTEKQAQYLGMPINGPFKPDHYRY

>d2dhqa\_ c.23.13.1 (A:) Type II 3-dehydroquinate dehydratase {Mycobacterium tuberculosis}

LIVNVINGPNLGRLGRREPAVYGGTTHDELVALIEREAAELGLKAVVRQSDSEAQLLDWIHQAADAAEPVILNAGGLTHTSVALRDACAELSAPLIEVHISNVHAREEFRRHSYLSPIATGVIVGLGIQGYLLALRYLAEH

>d1d0ia\_ c.23.13.1 (A:) Type II 3-dehydroquinate dehydratase {Streptomyces coelicolor}

PRSLANAPIMILNGPNLNLLGQRQPEIYGSDTLADVEALCVKAAAAHGGTVDFRQSNHEGELVDWIHEARLNHCGIVINPAAYSHTSVAILDALNTCDGLPVVEVHISNIHQREPFRHHSYVSQRADGVVAGCGVQGYVFGVERIAALAG

>d1f8ya\_ c.23.14.1 (A:) Nucleoside 2-deoxyribosyltransferase {Lactobacillus leichmannii}

PKKTIYFGAGWFTDRQNKAYKEAMEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPINLMSWGVSDNVIKMSQLKDFNFNKPRFDFYEGAVY

>d1fjgb\_ c.23.15.1 (B:) Ribosomal protein S2 {Thermus thermophilus}

VKELLEAGVHFGHERKRWNPKFARYIYAERNGIHIIDLQKTMEELERTFRFIEDLAMRGGTILFVGTKKQAQDIVRMEAERAGMPYVNQRWLGGMLTNFKTISQRVHRLEELEALFASPEIEERPKKEQVRLKHELERLQKYLSGFRLLKRLPDAIFVVDPTKEAIAVREARKLFIPVIALADTDSDPDLVDYIIPGNDDAIRSIQLILSRAVDLIIQARGGVVEPSPSYALVQEAE

>d1f2va\_ c.23.17.1 (A:) Precorrin-8x methylmutase {Pseudomonas denitrificans}

PEYDYIRDGNAIYERSFAIIRAEADLSRFSEEEADLAVRMVHACGSVEATRQFVFSPDFVSSARAALKAGAPILCDAEMVAHGVTRARLPAGNEVICTLRDPRTPALAAEIGNTRSAAALKLWSERLAGSVVAIGNAPTALFFLLEMLRDGAPKPAAILGMPVGFVGAAESKDALAENSYGVPFAIVRGRLGGSAMTAAALNSLARPGL

>d1gpma2 c.23.16.1 (A:3-207) GMP synthetase {Escherichia coli}

ENIHKHRILILDFGSQYTQLVARRVRELGVYCELWAWDVTEAQIRDFNPSGIILSGGPESTTEENSPRAPQYVFEAGVPVFGVCYGMQTMAMQLGGHVEASNEREFGYAQVEVVNDSALVRGIEDALTADGKPLLDVWMSHGDKVTAIPSDFITVASTESCPFAIMANEEKRFYGVQFHPEVTHTRQGMRMLERFVRDICQCEAL

>d1a9xb2 c.23.16.1 (B:1653-1880) Carbamoyl phosphate synthetase, small subunit C-terminal domain {Escherichia coli}

LNGMDLAKEVTTAEAYSWTQGSWTLTGGLPQAKKEDELPFHVVAYDFGAKRNILRMLVDRGCRLTIVPAQTSAEDVLKMNPDGIFLSNGPGDPAPCDYAITAIQKFLETDIPVFGICLGHQLLALASGAKTVKMKFGHHGGNHPVKDVEKNVVMITAQNHGFAVDEATLPANLRVTHKSLFDGTLQGIHRTDKPAFSFQGNPEASPGPHDAAPLFDHFIELIEQYRKT

>d1qdlb\_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Archaeon Sulfolobus solfataricus}

MDLTLIIDNYDSFVYNIAQIVGELGSYPIVIRNDEISIKGIERIDPDRLIISPGPGTPEKREDIGVSLDVIKYLGKRTPILGVCLGHQAIGYAFGAKIRRARKVFHGKISNIILVNNSPLSLYYGIAKEFKATRYHSLVVDEVHRPLIVDAISAEDNEIMAIHHEEYPIYGVQFHPESVGTSLGYKILYNFLNRV

>d1i1qb\_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Salmonella typhimurium}

ADILLLDNIDSFTWNLADQLRTNGHNVVIYRNHIPAQTLIDRLATMKNPVLMLSPGPGVPSEAGCMPELLTRLRGKLPIIGICLGHQAIVEAYGGYVGQAGEILHGKATSIEHDGQAMFAGLANPLPVARYHSLVGSNVPAGLTINAHFNGMVMAVRHDADRVCGFQFHPESILTTQGARLLEQTLAWAQQK

>d1i7qb\_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Serratia marcescens}

ADILLLDNVDSFTYNLVDQLRASGHQVVIYRNQIGAEVIIERLQHMEQPVLMLSPGPGTPSEAGCMPELLQRLRGQLPIIGICLGHQAIVEAYGGQVGQAGEILHGKASAIAHDGEGMFAGMANPLPVARYHSLVGSNIPADLTVNARFGEMVMAVRDDRRRVCGFQFHPESILTTHGARLLEQTLAWALAK

>d1k9vf\_ c.23.16.1 (F:) GAT subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}

MRIGIISVGPGNIMNLYRGVKRASENFEDVSIELVESPRNDLYDLLFIPGVGHFGEGMRRLRENDLIDFVRKHVEDERYVVGVCLGMQLLFEESEEAPGVKGLSLIEGNVVKLRSRRLPHMGWNEVIFKDTFPNGYYYFVHTYRAVCEEEHVLGTTEYDGEIFPSAVRKGRILGFQFHPEKSSKIGRKLLEKVIECSLSR

>d1jvna2 c.23.16.1 (A:-3-229) GAT subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}

GSHMPVVHVIDVESGNLQSLTNAIEHLGYEVQLVKSPKDFNISGTSRLILPGVGNYGHFVDNLFNRGFEKPIREYIESGKPIMGICVGLQALFAGSVESPKSTGLNYIDFKLSRFDDSEKPVPEIGWNSCIPSENLFFGLDPYKRYYFVHSFAAILNSEKKKNLENDGWKIAKAKYGSEEFIAAVNKNNIFATQFHPEKSGKAGLNVIENFLKQQSPPIPNYSAEEKELLMN

>d1g2ia\_ c.23.16.2 (A:) Intracellular protease {Archaeon Pyrococcus horikoshii}

MKVLFLTANEFEDVELIYPYHRLKEEGHEVYIASFERGTITGKHGYSVKVDLTFDKVNPEEFDALVLPGGRAPERVRLNEKAVSIARKMFSEGKPVASICHGPQILISAGVLRGRKGTSYPGIKDDMINAGVEWVDAEVVVDGNWVSSRVPADLYAWMREFVKLLK

>d1cf9a1 c.23.16.3 (A:598-753) Catalase, C-terminal domain {Escherichia coli, HPII}

VKGRVVAILLNDEVRSADLLAILKALKAKGVHAKLLYSRMGEVTADDGTVLPIAATFAGAPSLTVDAVIVPCGNIADIADNGDANYYLMEAYKHLKPIALAGDARKFKATIKIADQGEEGIVEADSADGSFMDELLTLMAAHRVWSRIPKIDKIPA

>d1fyea\_ c.23.16.4 (A:) Aspartyl dipeptidase PepE {Salmonella typhimurium}

MELLLLSNSTLPGKAWLEHALPLIANQLNGRRSAVFIPFAGVTQTWDEYTDKTAEVLAPLGVNVTGIHRVADPLAAIEKAEIIIVGGGNTFQLLKESRERGLLAPMADRVKRGALYIGWSAGANLACPTIRTTNDMPIVDPNGFDALDLFPLQINPHFTNALPEGHKGETREQRIRELLVVAPELTVIGLPEGNWIQVSNGQAVLGGPNTTWVFKAGEEAVALEAGHRF

>d1a9xa2 c.24.1.1 (A:936-1073) Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain {Escherichia coli}

NSTMKKHGRALLSVREGDKERVVDLAAKLLKQGFELDATHGTAIVLGEAGINPRLVNKVHEGRPHIQDRIKNGEYTYIINTTSGRRAIEDSRVIRRSALQYKVHYDTTLNGGFATAMALNADATEKVISVQEMHAQIK

>d1b93a\_ c.24.1.2 (A:) Methylglyoxal synthase, MgsA {Escherichia coli}

MELTTRTLPARKHIALVAHDHCKQMLMSWVERHQPLLEQHVLYATGTTGNLISRATGMNVNAMLSGPMGGDQQVGALISEGKIDVLIFFWDPLNAVPHDPDVKALLRLATVWNIPVATNVATADFIIQSPHFNDAVDILIPDYQRYLA

>d1g8ma1 c.24.1.3 (A:4-200) IMP cyclohydrolase domain of bifunctional purine biosynthesis enzyme ATIC {Chicken (Gallus gallus)}

RQQLALLSVSEKAGLVEFARSLNALGLGLIASGGTATALRDAGLPVRDVSDLTGFPEMLGGRVKTLHPAVHAGILARNIPEDNADMNKQDFSLVRVVVCNLYPFVKTVSSPGVTVPEAVEKIDIGGVALLRAAAKNHARVTVVCDPADYSSVAKEMAASKDKDTSVETRRHLALKAFTHTAQYDAAISDYFRKEYSK

>d1fnc\_2 c.25.1.1 (155-314) Ferredoxin reductase (flavodoxin reductase) {Spinach (Spinacia oleracea)}

MLMPKDPNATIIMLGTGTGIAPFRSFLWKMFFEKHDDYKFNGLAWLFLGVPTSSSLLYKEEFEKMKEKAPDNFRLDFAVSREQTNEKGEKMYIQTRMAQYAVELWEMLKKDNTYVYMCGLKGMEKGIDDIMVSLAAAEGIDWIEYKRQLKKAEQWNVEVY

>d1qfza2 c.25.1.1 (A:154-308) Ferredoxin reductase (flavodoxin reductase) {Garden pea (Pisum sativum)}

DPNATVIMLGTGTGIAPFRSFLWKMFFEKHEDYQFNGLAWLFLGVPTSSSLLYKEEFEKMKEKAPENFRLDFAVSREQVNDKGEKMYIQTRMAQYAEELWELLKKDNTFVYMCGLKGMEKGIDDIMVSLAAKDGIDWIEYKRTLKKAEQWNVEVS

>d1fb3a2 c.25.1.1 (A:208-362) Ferredoxin reductase (flavodoxin reductase) {Paprika (Capsicum annuum)}

DPNATVIMLGTGTGIAPFRSFLWKMFFEKHDDYKFNGLAWLFLGVPTSSSLLYKEEFEKMKEKAPENFRLDFAVSREQTNEKGEKMYIQTRMAQYAEELWTLLKKDNTFVYMCGLKGMEQGIDDIMSSLAAKEGIDWADYKKQLKKAEQWNVEVY

>d1gawa2 c.25.1.1 (A:157-314) Ferredoxin reductase (flavodoxin reductase) {Maize (Zea mays), leaf isoform}

MPKDPNATIIMLATGTGIAPFRSFLWKMFFEKHDDYKFNGLGWLFLGVPTSSSLLYKEEFGKMKERAPENFRVDYAVSREQTNAAGERMYIQTRMAEYKEELWELLKKDNTYVYMCGLKGMEKGIDDIMVSLAEKDGIDWFDYKKQLKRGDQWNVEVY

>d1jb9a2 c.25.1.1 (A:163-316) Ferredoxin reductase (flavodoxin reductase) {Maize (Zea mays), root isoform}

DPNATHIMIATGTGVAPFRGYLRRMFMEDVPNYRFGGLAWLFLGVANSDSLLYDEEFTSYLKQYPDNFRYDKALSREQKNRSGGKMYVQDKIEEYSDEIFKLLDGGAHIYFCGLKGMMPGIQDTLKKVAERRGESWDQKLAQLKKNKQWHVEVY

>d1que\_2 c.25.1.1 (142-303) Ferredoxin reductase (flavodoxin reductase) {Cyanobacterium (Anabaena sp.), pcc 7119}

LPDDPEANVIMLATGTGIAPMRTYLWRMFKDAERAANPEYQFKGFSWLVFGVPTTPNILYKEELEEIQQKYPDNFRLTYAISREQKNPQGGRMYIQDRVAEHADQLWQLIKNQKTHTYICGLRGMEEGIDAALSAAAAKEGVTWSDYQKDLKKAGRWHVETY

>d1fdr\_2 c.25.1.1 (101-248) Ferredoxin reductase (flavodoxin reductase) {Escherichia coli}

DEVPHCETLWMLATGTAIGPYLSILRLGKDLDRFKNLVLVHAARYAADLSYLPLMQELEKRYEGKLRIQTVVSRETAAGSLTGRIPALIESGELESTIGLPMNKETSHVMLCGNPQMVRDTQQLLKETRQMTKHLRRRPGHMTAEHYW

>d1a8p\_2 c.25.1.1 (101-258) Ferredoxin reductase (flavodoxin reductase) {Azotobacter vinelandii}

TSDLLPGKHLYMLSTGTGLAPFMSLIQDPEVYERFEKVVLIHGVRQVNELAYQQFITEHLPQSEYFGEAVKEKLIYYPTVTRESFHNQGRLTDLMRSGKLFEDIGLPPINPQDDRAMICGSPSMLDESCEVLDGFGLKISPRMGEPGDYLIERAFVEK

>d1qfja2 c.25.1.1 (A:98-232) NAD(P)H:flavin oxidoreductase {Escherichia coli}

RDDEERPMILIAGGTGFSYARSILLTALARNPNRDITIYWGGREEQHLYDLCELEALSLKHPGLQVVPVVEQPEAGWRGRTGTVLTAVLQDHGTLAEHDIYIAGRFEMAKIARDLFCSERNAREDRLFGDAFAFI

>d2cnd\_2 c.25.1.1 (125-270) Nitrate reductase {Corn (Zea mays)}

GSFVINGKQRNARRLAMICGGSGITPMYQIIQAVLRDQPEDHTEMHLVYANRTEDDILLRDELDRWAAEYPDRLKVWYVIDQVKRPEEGWKYSVGFVTEAVLREHVPEGGDDTLALACGPPPMIQFAISPNLEKMKYDMANSFVVF

>d1ndh\_2 c.25.1.1 (126-272) cytochrome b5 reductase {Pig (Sus scrofa), liver}

GKFAIRPDKKSSPVIKTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKDILLRPELEELRNEHSARFKLWYTVDRAPEAWDYSQGFVNEEMIRDHLPPPEEEPLVLMCGPPPMIQYACLPNLERVGHPKERCFAF

>d1i7pa2 c.25.1.1 (A:154-300) cytochrome b5 reductase {Rat (Rattus norvegicus)}

GKFAIRADKKSNPVVRTVKSVGMIAGGTGITPMLQVIRAVLKDPNDHTVCYLLFANQSEKDILLRPELEELRNEHSSRFKLWYTVDKAPDAWDYSQGFVNEEMIRDHLPPPGEETLILMCGPPPMIQFACLPNLERVGHPKERCFTF

>d2pia\_2 c.25.1.2 (104-223) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}

EFPLDKRAKSFILVAGGIGITPMLSMARQLRAEGLRSFRLYYLTRDPEGTAFFDELTSDEWRSDVKIHHDHGDPTKAFDFWSVFEKSKPAQHVYCCGPQALMDTVRDMTGHWPSGTVHFE

>d1ep3b2 c.25.1.3 (B:103-262) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}

PVAEVTSTDKILIIGGGIGVPPLYELAKQLEKTGCQMTILLGFASENVKILENEFSNLKNVTLKIATDDGSYGTKGHVGMLMNEIDFEVDALYTCGAPAMLKAVAKKYDQLERLYISMESRMACGIGACYACVEHDKEDESHALKVCEDGPVFLGKQLSL

>d1ja1a3 c.25.1.4 (A:519-678) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}

RLPFKSTTPVIMVGPGTGIAPFMGFIQERAWLREQGKEVGETLLYYGCRRSDEDYLYREELARFHKDGALTQLNVAFSREQAHKVYVQHLLKRDREHLWKLIHEGGAHIYVAGDARNMAKDVQNTFYDIVAEFGPMEHTQAVDYVKKLMTKGRYSLNVWS

>d1ddga2 c.25.1.4 (A:447-599) Sulfite reductase flavoprotein {Escherichia coli}

LPANPETPVIMIGPGTGIAPFRAFMQQRAADEAPGKNWLFFGNPHFTEDFLYQVEWQRYVKEGVLTRIDLAWSRDQKEKVYVQDKLREQGAELWRWINDGAHIYVCGDANRMAKDVEQALLEVIAEFGGMDTEAADEFLSELRVERRYQRDVY

>d1f20a2 c.25.1.4 (A:1233-1397) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat (Rattus norvegicus)}

SFHLPRNPQVPCILVGPGTGIAPFRSFWQQRQFDIQHKGMNPCPMVLVFGCRQSKIDHIYREETLQAKNKGVFRELYTAYSREPDRPKKYVQDVLQEQLAESVYRALKEQGGHIYVCGDVTMAADVLKAIQRIMTQQGKLSEEDAGVFISRLRDDNRYHEDIFGV

>d1cqxa3 c.25.1.5 (A:262-403) Flavohemoglobin, C-terminal domain {Alcaligenes eutrophus}

DVDAKTPIVLISGGVGLTPMVSMLKVALQAPPRQVVFVHGARNSAVHAMRDRLREAAKTYENLDLFVFYDQPLPEDVQGRDYDYPGLVDVKQIEKSILLPDADYYICGPIPFMRMQHDALKNLGIHEARIHYEVFGPDLFAE

>d4ts1a\_ c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Bacillus stearothermophilus, nca 1503}

MDLLAELQWRGLVNQTTDEDGLRKLLNEERVTLYCGFDPTADSLHIGHLATILTMRRFQQAGHRPIALVGGATGLIGDPSGKKSERTLNAKETVEAWSARIKEQLGRFLDFEADGNPAKIKNNYDWIGPLDVITFLRDVGKHFSVNYMMAKESVQSRIETGISFTEFSYMMLQAYDFLRLYETEGCRLQIGGSDQWGNITAGLELIRKTKGEARAFGLTIPLVTKADGTKFGKTESGTIWLDKEKTSPYEFYQFWINTDDRDVIRYLKYFTFLSKEEIEALEQELREAPEKRAAQKTLAEEVTKLVHGEEALRQAIRYA

>d1jila\_ c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Staphylococcus aureus}

TNVLIEDLKWRGLIYQQTDEQGIEDLLNKEQVTLYCGADPTADSLHIGHLLPFLTLRRFQEHGHRPIVLIGGGTGMIGDPSGKSEERVLQTEEQVDKNIEGISKQMHNIFEFGTDHGAVLVNNRDWLGQISLISFLRDYGKHVGVNYMLGKDSIQSRLEHGISYTEFTYTILQAIDFGHLNRELNCKIQVGGSDQWGNITSGIELMRRMYGQTDAYGLTIPLVTKSDGKKFGKSESGAVWLDAEKTSPYEFYQFWINQSDEDVIKFLKYFTFLGKEEIDRLEQSKNEAPHLREAQKTLAEEVTKFIHGEDALNDAIRISQALF

>d1i6la\_ c.26.1.1 (A:) Tryptophanyl-tRNA synthetase (TrpRS) {Bacillus stearothermophilus}

MKTIFSGIQPSGVITIGNYIGALRQFVELQHEYNCYFCIVDQHAITVWQDPHELRQNIRRLAALYLAVGIDPTQATLFIQSEVPAHAQAAWMLQCIVYIGELERMTQFKEKSAGKEAVSAGLLTYPPLMAADILLYNTDIVPVGEDQKQHIELTRDLAERFNKRYGELFTIPEARIPKVGARIMSLVDPTKKMSKSDPNPKAYITLLDDAKTIEKKIKSAVTDSEGTIRYDKEAKPGISNLLNIYSTLSGQSIEELERQYEGKGYGVFKADLAQVVIETLRPIQERYHHWMESEELDRVLDEGAEKANRVASEMVRKMEQAMGLGR

>d1gtra2 c.26.1.1 (A:8-338) Glutaminyl-tRNA synthetase (GlnRS) {Escherichia coli}

TNFIRQIIDEDLASGKHTTVHTRFPPEPNGYLHIGHAKSICLNFGIAQDYKGQCNLRFDDTNPVKEDIEYVESIKNDVEWLGFHWSGNVRYSSDYFDQLHAYAIELINKGLAYVDELTPEQIREYRGTLTQPGKNSPYRDRSVEENLALFEKMRAGGFEEGKACLRAKIDMASPFIVMRDPVLYRIKFAEHHQTGNKWCIYPMYDFTHCISDALEGITHSLCTLEFQDNRRLYDWVLDNITIPVHPRQYEFSRLNLEYTVMSKRKLNLLVTDKHVEGWDDPRMPTISGLRRRGYTAASIREFCKRIGVTKQDNTIEMASLESCIREDLNEN

>d1gln\_2 c.26.1.1 (1-305) Glutamyl-tRNA synthetase (GluRS) {Thermus thermophilus}

MVVTRIAPSPTGDPHVGTAYIALFNYAWARRNGGRFIVRIEDTDRARYVPGAEERILAALKWLGLSYDEGPDVAAPTGPYRQSERLPLYQKYAEELLKRGWAYRAFETPEELEQIRKEKGGYDGRARNIPPEEAEERARRGEPHVIRLKVPRPGTTEVKDELRGVVVYDNQEIPDVVLLKSDGYPTYHLANVVDDHLMGVTDVIRAEEWLVSTPIHVLLYRAFGWEAPRFYHMPLLRNPDKTKISKRKSHTSLDWYKAEGFLPEALRNYLCLMGFSMPDGREIFTLEEFIQAFTWERVSLGGPVF

>d1a8h\_2 c.26.1.1 (1-348) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}

MEKVFYVTTPIYYVNAEPHLGHAYTTVVADFLARWHRLDGYRTFFLTGTDEHGETVYRAAQAAGEDPKAFVDRVSGRFKRAWDLLGIAYDDFIRTTEERHKKVVQLVLKKVYEAGDIYYGEYEGLYCVSCERFYTEKELVEGLCPIHGRPVERRKEGNYFFRMEKYRPWLQEYIQENPDLIRPEGYRNEVLAMLAEPIGDLSISRPKSRVPWGIPLPWDENHVTYVWFDALLNYVSALDYPEGEAYRTFWPHAWHLIGKDILKPHAVFWPTMLKAAGIPMYRHLNVGGFLLGPDGRKMSKTLGNVVDPFALLEKYGRDALRYYLLREIPYGQDTPVSEEALRTRYEAD

>d1f4la2 c.26.1.1 (A:4-140,A:176-388) Methionyl-tRNA synthetase (MetRS) {Escherichia coli}

AKKILVTCALPYANGSIHLGHMLEHIQADVWVRYQRMRGHEVNFICADDAHGTPIMLKAQQLGITPEQMIGEMSQEHQTDFAGFNISYDNYHSTHSEENRQLSELIYSRLKENGFIKNRTISQLYDPEKGMFLPDRFXVVSGATPVMRDSEHFFFDLPSFSEMLQAWTRSGALQEQVANKMQEWFESGLQQWDISRDAPYFGFEIPNAPGKYFYVWLDAPIGYMGSFKNLCDKRGDSVSFDEYWKKDSTAELYHFIGKDIVYFHSLFWPAMLEGSNFRKPSNLFVHGYVTVNGAKMSKSRGTFIKASTWLNHFDADSLRYYYTAKLSSRIDDIDLNLEDFVQRVNADIVNK

>d1ile\_3 c.26.1.1 (1-197,387-641) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}

MFKEVGEPNFPKLEEEVLAFWKREKIFQKSVENRKGGPRYTVYEGPPTANGLPHVGHAQARSYKDLFPRYKTMRGYYAPRRAGWDTHGLPVELEVEKKLGLKSKREIEAYGIERFNQACRESVFTYEKEWEAFTERIAYWVDLEDAYATLEPTYIESIWWSLKNLFDRGLLYRDHKVVPYCPRCGTPLSSHEVALGYXPHCWRCSTPLMYYATESWFIKNTLFKDELIRNNQEIHWVPPHIKEGRYGEWLKNLVDWALSRNRYWGTPLPIWVCQACGKEEAIGSFQELKARATKPLPEPFDPHRPYVDQVELACACGGTMRRVPYVIDVWYDSGAMPFASLHYPFEHEEVFRESFPADFIAEGIDQTRGWFNSLHQLGVMLFGSIAFKNVICHGLILDEKGQKMSKSKGNVVDPWDIIRKFGADALRWYIYVSAPPEADRRFGPNLVRETVRD

>d1ffya3 c.26.1.1 (A:1-200,A:395-644) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

MDYEKTLLMPKTDFPMRGGLPNKEPQIQEKWDAEDQYHKALEKNKGNETFILHDGPPYANGNLHMGHALNKILKDFIVRYKTMQGFYAPYVPGWDTHGLPIEQALTKKGVDRKKMSTAEFREKCKEFALEQIELQKKDFRRLGVRGDFNDPYITLKPEYEAAQIRIFGEMADKGLIYKGKKPVYWSPSSESSLAEAEIEYXPHDWRTKKPVIFRATPQWFASISKVRQDILDAIENTNFKVNWGKTRIYNMVRDRGEWVISRQRVWGVPLPVFYAENGEIIMTKETVNHVADLFAEHGSNIWFEREAKDLLPEGFTHPGSPNGTFTKETDIMDVWFDSGSSHRGVLETRPELSFPADMYLEGSDQYRGWFNSSITTSVATRGVSPYKFLLSHGFVMDGEGKKMSKSLGNVIVPDQVVKQKGADIARLWVSSTDYLADVRISDEILKQTSDD

>d1gaxa3 c.26.1.1 (A:1-189,A:343-578) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}

MDLPKAYDPKSVEPKWAEKWAKNPFVANPKSGKPPFVIFMPPPNVTGSLHMGHALDNSLQDALIRYKRMRGFEAVWLPGTDHAGIATQVVVERLLLKEGKTRHDLGREKFLERVWQWKEESGGTILKQLKRLGASADWSREAFTMDEKRSRAVRYAFSRYYHEGLAYRAPRLVNWCPRCETTLSDLEVEXTCSRCGTPIEYAIFPQWWLRMRPLAEEVLKGLRRGDIAFVPERWKKVNMDWLENVKDWNISRQLWWGHQIPAWYCEDCQAVNVPRPERYLEDPTSCEACGSPRLKRDEDVFDTWFSSALWPLSTLGWPEETEDLKAFYPGDVLVTGYDILFLWVSRMEVSGYHFMGERPFKTVLLHGLVLDEKGQKMSKSKGNVIDPLEMVERYGADALRFALIYLATGGQDIRLDLRWLEMARNF

>d1f7ua2 c.26.1.1 (A:136-483) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast (Saccharomyces cerevisiae)}

SCKLVENKKVIIEFSSPNIAKPFHAGHLRSTIIGGFLANLYEKLGWEVIRMNYLGDWGKQFGLLAVGFERYGNEEALVKDPIHHLFDVYVRINKDIEEEGDSIPLEQSTNGKAREYFKRMEDGDEEALKIWKRFREFSIEKYIDTYARLNIKYDVYSGESQVSKESMLKAIDLFKEKGLTHEDKGAVLIDLTKFNKKLGKAIVQKSDGTTLYLTRDVGAAMDRYEKYHFDKMIYVIASQQDLHAAQFFEILKQMGFEWAKDLQHVNFGMVQGMSTRKGTVVFLDNILEETKEKMHEVMKKNENKYAQIEHPEEVADLVGISAVMIQDMQGKRINNYEFKWERMLSFEG

>d1iq0a2 c.26.1.1 (A:97-466) Arginyl-tRNA synthetase (ArgRS) {Thermus thermophilus}

PFPRRPGVVLVEHTSVNPNKELHVGHLRNIALGDAIARILAYAGREVLVLNYIDDTGRQAAETLFALRHYGLTWDGKEKYDHFAGRAYVRLHQDPEYERLQPAIEEVLHALERGELREEVNRILLAQMATMHALNARYDLLVWESDIVRAGLLQKALALLEQSPHVFRPREGKYAGALVMDASPVIPGLEDPFFVLLRSNGTATYYAKDIAFQFWKMGILEGLRFRPYENPYYPGLRTSAPEGEAYTPKAEETINVVDVRQSHPQALVRAALALAGYPALAEKAHHLAYETVLLEGRQMSGRKGLAVSVDEVLEEATRRARAIVEEKNPDHPDKEEAARMVALGAIRFSMVKTEPKKQIDFRYQEALSFE

>d1coza\_ c.26.1.2 (A:) CTP:glycerol-3-phosphate cytidylyltransferase {Bacillus subtilis}

MKKVITYGTFDLLHWGHIKLLERAKQLGDYLVVAISTDEFNLQKQKKAYHSYEHRKLILETIRYVDEVIPEKNWEQKKQDIIDHNIDVFVMGDDWEGKFDFLKDQCEVVYLPRTEGISTTKIKEEI

>d1qjca\_ c.26.1.3 (A:) Phosphopantetheine adenylyltransferase {Escherichia coli}

KRAIYPGTFDPITNGHIDIVTRATQMFDHVILAIAASPSKKPMFTLEERVALAQQATAHLGNVEVVGFSDLMANFARNQHATVLIRGLRAVADFEYEMQLAHMNRHLMPELESVFLMPSKEWSFISSSLVKEVARHQGDVTHFLPENVHQALMAKLA

>d1f9aa\_ c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase {Archaeon Methanococcus jannaschii}

LRGFIIGRFQPFHKGHLEVIKKIAEEVDEIIIGIGSAQKSHTLENPFTAGERILMITQSLKDYDLTYYPIPIKDIEFNSIWVSYVESLTPPFDIVYSGNPLVRVLFEERGYEVKRPEMFNRKEYSGTEIRRRMLNGEKWEHLVPKAVVDVIKEIKGVERLRKLA

>d1ej2a\_ c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase {Archaeon Methanobacterium thermoautotrophicum}

MRGLLVGRMQPFHRGHLQVIKSILEEVDELIICIGSAQLSHSIRDPFTAGERVMMLTKALSENGIPASRYYIIPVQDIECNALWVGHIKMLTPPFDRVYSGNPLVQRLFSEDGYEVTAPPLFYRDRYSGTEVRRRMLDDGDWRSLLPESVVEVIDEINGVERIKHLA

>d1ihoa\_ c.26.1.4 (A:) Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC) {Escherichia coli}

MLIIETLPLLRQQIRRLRMEGKRVALVPTMGNLHDGHMKLVDEAKARADVVVVSIFVNPMQFDRPEDLARYPRTLQEDCEKLNKRKVDLVFAPSVKEIYPNGTETHTYVDVPGLSTMLEGASRPGHFRGVSTIVSKLFNLVQPDIACFGEKDFQQLALIRKMVADMGFDIEIVGVPIMRAKDGLALSSRNGYLTAEQRKIAPGLYKVLSSIADKLQAGERDLDEIITIAGQELNEKGFRADDIQIRDADTLLEVSETSKRAVILVAAWLGDARLIDNKMVEL

>d1g8fa2 c.26.1.5 (A:169-389) ATP sulfurylase central domain {Baker's yeast (Saccharomyces cerevisiae)}

YPGLRKTPAQLRLEFQSRQWDRVVAFQTRNPMHRAHRELTVRAAREANAKVLIHPVVGLTKPGDIDHHTRVRVYQEIIKRYPNGIAFLSLLPLAMRMSGDREAVWHAIIRKNYGASHFIVGRDHAGPGKNSKGVDFYGPYDAQELVESYKHELDIEVVPFRMVTYLPDEDRYAPIDQIDTTKTRTLNISGTELRRRLRVGGEIPEWFSYPEVVKILRESNP

>d1i2da2 c.26.1.5 (A:171-390) ATP sulfurylase central domain {Fungus (Penicillium chrysogenum)}

YVALRYTPAELRVHFDKLGWSRVVAFQTRNPMHRAHRELTVRAARSRQANVLIHPVVGLTKPGDIDHFTRVRAYQALLPRYPNGMAVLGLLGLAMRMGGPREAIWHAIIRKNHGATHFIVGRDHAGPGSNSKGEDFYGPYDAQHAVEKYKDELGIEVVEFQMVTYLPDTDEYRPVDQVPAGVKTLNISGTELRRRLRSGAHIPEWFSYPEVVKILRESNP

>d1jhda2 c.26.1.5 (A:174-396) ATP sulfurylase central domain {unnamed symbiont of Riftia pachyptila}

PDTFRTAVEIRNEIKEHGWSKVVAFQTRNPMHRAHEELCRMAMESLDADGVVVHMLLGKLKKGDIPAPVRDAAIRTMAEVYFPPNTVMVTGYGFDMLYAGPREAVLHAYFRQNMGATHFIIGRDHAGVGDYYGAFDAQTIFDDEVPEGAMEIEIFRADHTAYSKKLNKIVMMRDVPDHTKEDFVLLSGTKVREMLGQGIAPPPEFSRPEVAKILMDYYQSINS

>d1gpma1 c.26.2.1 (A:208-404) GMP synthetase, central domain {Escherichia coli}

WTPAKIIDDAVARIREQVGDDKVILGLSGGVDSSVTAMLLHRAIGKNLTCVFVDNGLLRLNEAEQVLDMFGDHFGLNIVHVPAEDRFLSALAGENDPEAKRKIIGRVFVEVFDEEALKLEDVKWLAQGTIYPDVIESAASATGKAHVIKSHHNVGGLPKEMKMGLVEPLKELFKDEVRKIGLELGLPYDMLYRHPFP

>d1ih8a\_ c.26.2.1 (A:) NH3-dependent NAD+-synthetase {Bacillus subtilis}

SMQEKIMRELHVKPSIDPKQEIEDRVNFLKQYVKKTGAKGFVLGISGGQDSTLAGRLAQLAVESIREEGGDAQFIAVRLPHGTQQDEDDAQLALKFIKPDKSWKFDIKSTVSAFSDQYQQETGDQLTDFNKGNVKARTRMIAQYAIGGQEGLLVLGTDHAAEAVTGFFTKYGDGGADLLPLTGLTKRQGRTLLKELGAPERLYLKEPTADLLDEKPQQSDETELGISYDEIDDYLEGKEVSAKVSEALEKRYSMTEHKRQVPASMFDDWWK

>d1ct9a1 c.26.2.1 (A:193-516) Asparagine synthetase B, C-terminal domain {Escherichia coli}

RDWFDYDAVKDNVTDKNELRQALEDSVKSHLMSDVPYGVLLSGGLDSSIISAITKKYAARRVEDQERSEAWWPQLHSFAVGLPGSPDLKAAQEVANHLGTVHHEIHFTVQEGLDAIRDVIYHIETYDVTTIRASTPMYLMSRKIKAMGIKMVLSGEGSDEVFGGYLYFHKAPNAKELHEETVRKLLALHMYDCARANKAMSAWGVEARVPFLDKKFLDVAMRINPQDKMCGNGKMEKHILRECFEAYLPASVAWRQKEQFSDGVGYSWIDTLKEVAAQQVSDQQLETARFRFPYNTPTSKEAYLYREIFEELFPLPSAAECVPG

>d1jgta1 c.26.2.1 (A:210-508) beta-Lactam synthetase {Streptomyces clavuligerus}

PGLSRRILPEGEAVAAVRAALEKAVAQRVTPGDTPLVVLSGGIDSSGVAACAHRAAGELDTVSMGTDTSNEFREARAVVDHLRTRHREITIPTTELLAQLPYAVWASESVDPDIIEYLLPLTALYRALDGPERRILTGYGADIPLGGMHREDRLPALDTVLAHDMATFDGLNEMSPVLSTLAGHWTTHPYWDREVLDLLVSLEAGLKRRHGRDKWVLRAAMADALPAETVNRPKLGVHEGSGTTSSFSRLLLDHGVAEDRVHEAKRQVVRELFDLTVGGGRHPSEVDTDDVVRSVADRT

>d1k92a1 c.26.2.1 (A:1-188) Argininosuccinate synthetase, N-terminal domain {Escherichia coli}

TTILKHLPVGQRIGIAFSGGLDTSAALLWMRQKGAVPYAYTANLGQPDEEDYDAIPRRAMEYGAENARLIDCRKQLVAEGIAAIQCGAFHNTTGGLTYFNTTPLGRAVTGTMLVAAMKEDGVNIWGDGSTYKGNDIERFYRYGLLTNAELQIYKPWLDTDFIDELGGRHEMSEFMIACGFDYKMSVEK

>d1sur\_\_ c.26.2.2 (-) Phosphoadenylyl sulphate (PAPS) reductase {Escherichia coli}

SKLDLNALNELPKVDRILALAETNAELEKLDAEGRVAWALDNLPGEYVLSSSFGIQAAVSLHLVNQIRPDIPVILTDTGYLFPETYRFIDELTDKLKLNLKVYRATESAAWQEARYGKLWEQGVEGIEKYNDINKVEPMNRALKELNAQTWFAGLRREQSGSRANLPVLAIQRGVFKVLPIIDWDNRTIYQYLQKHGLKYHPLWDEGYLSVGDTH

>d1dlja3 c.26.3.1 (A:295-402) UDP-glucose dehydrogenase (UDPGDH), C-terminal (UDP-binding) domain {Streptococcus pyogenes}

AKQIINVLKEQESPVKVVGVYRLIMKSNSDNFRESAIKDVIDILKSKDIKIIIYEPMLNKLESEDQSVLVNDLENFKKQANIIVTNRYDNELQDVKNKVYSRDIFGRD

>d2tpt\_2 c.27.1.1 (71-335) Thymidine phosphorylase {Escherichia coli}

DWKSLHLNGPIVDKHSTGGVGDVTSLMLGPMVAACGGYIPMISGRGLGHTGGTLDKLESIPGFDIFPDDNRFREIIKDVGVAIIGQTSSLAPADKRFYATRDITATVDSIPLITASILAKKLAEGLDALVMDVKVGSGAFMPTYELSEALAEAIVGVANGAGVRTTALLTDMNQVLASSAGNAVEVREAVQFLTGEYRNPRLFDVTMALCVEMLISGKLAKDDAEARAKLQAVLDNGKAAEVFGRMVAAQKGPTDFVENYAKYLP

>d1brwa2 c.27.1.1 (A:71-330) Pyrimidine nucleoside phosphorylase {Bacillus stearothermophilus}

LSSIRGVKVDKHSTGGVGDTTTLVLGPLVASVGVPVAKMSGRGLGHTGGTIDKLESVPGFHVEISKDEFIRLVNENGIAIIGQTGDLTPADKKLYALRDVTATVNSIPLIASSIMSKKIAAGADAIVLDVKTGAGAFMKKLDEARRLARVMVDIGKRVGRRTMAVISDMSQPLGYAVGNALEVKEAIETLKGNGPHDLTELCLTLGSHMVYLAEKAPSLDEARRLLEEAIRSGAAIAAFKTFLAAQGGDASVVDDLDKLP

>d1dnpa2 c.28.1.1 (A:1-200) N-terminal domain of DNA photolyase {Escherichia coli}

TTHLVWFRQDLRLHDNLALAAACRNSSARVLALYIATPRQWATHNMSPRQAELINAQLNGLQIALAEKGIPLLFREVDDFVASVEIVKQVCAENSVTHLFYNYQYEVNERARDVEVERALRNVVCEGFDDSVILPPGAVMTGNHEMYKVFTPFKNAWLKRLREGMPECVAAPKVRSSGSIEPSPSITLNYPRQSFDTAHF

>d1iqra2 c.28.1.1 (A:2-171) N-terminal domain of DNA photolyase {Thermus thermophilus}

GPLLVWHRGDLRLHDHPALLEALARGPVVGLVVLDPNNLKTTPRRRAWFLENVRALREAYRARGGALWVLEGLPWEKVPEAARRLKAKAVYALTSHTPYGRYRDGRVREALPVPLHLLPAPHLLPPDLPRAYRVYTPFSRLYRGAAPPLPPPEALPKGPEEGEIPREDPG

>d1qnf\_2 c.28.1.1 (1-204) N-terminal domain of DNA photolyase {Anacystis nidulans}

MAAPILFWHRRDLRLSDNIGLAAARAQSAQLIGLFCLDPQILQSADMAPARVAYLQGCLQELQQRYQQAGSRLLLLQGDPQHLIPQLAQQLQAEAVYWNQDIEPYGRDRDGQVAAALKTAGIRAVQLWDQLLHSPDQILSGSGNPYSVYGPFWKNWQAQPKPTPVATPTELVDLSPEQLTAIAPLLLSELPTLKQLGFDWDGGF

>d1efva1 c.29.1.1 (A:20-207) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}

QSTLVIAEHANDSLAPITLNTITAATRLGGEVSCLVAGTKCDKVAQDLCKVAGIAKVLVAQHDVYKGLLPEELTPLILATQKQFNYTHICAGASAFGKNLLPRVAAKLEVAPISDIIAIKSPDTFVRTIYAGNALCTVKCDEKVKVFSVRGTSFDAAATSGGSASSEKASSTSPVEISEWLDQKLTKS

>d1efvb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}

LRVLVAVKRVIDYAVKIRVKPDRTGVVTDGVKHSMNPFCEIAVEEAVRLKEKKLVKEVIAVSCGPAQCQETIRTALAMGADRGIHVEVPPAEAERLGPLQVARVLAKLAEKEKVDLVLLGKQAIDDDCNQTGQMTAGFLDWPQGTFASQVTLEGDKLKVEREIDGGLETLRLKLPAVVTADLRLNEPRYATLPNIMKAKKKKIEVIKPGDLGVDLTSKLSVISVEDPPQRTAGVKVETTEDLVAKLKEIGRI

>d1efpa1 c.29.1.1 (A:2-184) Electron transfer flavoprotein, ETFP {Paracoccus denitrificans}

AVLLLGEVTNGALNRDATAKAVAAVKALGDVTVLCAGASAKAAAEEAAKIAGVAKVLVAEDALYGHRLAEPTAALIVGLAGDYSHIAAPATTDAKNVMPRVAALLDVMVLSDVSAILDADTFERPIYAGNAIQVVKSKDAKKVFTIRTASFDAAGEGGTAPVTETAAAADPGLSSWVADEVAE

>d1efpb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETFP {Paracoccus denitrificans}

MKVLVPVKRLIDYNVKARVKSDGSGVDLANVKMSMNPFDEIAVEEAIRLKEKGQAEEIIAVSIGVKQAAETLRTALAMGADRAILVVAADDVQQDIEPLAVAKILAAVARAEGTELIIAGKQAIDNDMNATGQMLAAILGWAQATFASKVEIEGAKAKVTREVDGGLQTIAVSLPAVVTADLRLNEPRYASLPNIMKAKKKPLDEKTAADYGVDVAPRLEVVSVREPEGRKAGIKVGSVDELVGKL

>d1mjha\_ c.29.1.2 (A:) "Hypothetical" protein MJ0577 {Archaeon Methanococcus jannaschii}

VMYKKILYPTDFSETAEIALKHVKAFKTLKAEEVILLHVIDEREIKKRDIFSLLLGVAGLNKSVEEFENELKNKLTEEAKNKMENIKKELEDVGFKVKDIIVVGIPHEEIVKIAEDEGVDIIIMGSHGKTNLKEILLGSVTENVIKKSNKPVLVVKRKNS

>d1jmva\_ c.29.1.2 (A:) Universal stress protein A, UspA {Haemophilus influenzae}

MYKHILVAVDLSEESPILLKKAVGIAKRHDAKLSIIHVDVNFSDLYTGLIDVNMSSMQDRISTETQKALLDLAESVDYPISEKLSGSGDLGQVLSDAIEQYDVDLLVTGHHQDFWSKLMSSTRQVMNTIKIDMLVVPLRD

>d1dv1a2 c.30.1.1 (A:1-114) Biotin carboxylase (BC) subunit of acetyl-CoA carboxylase {Escherichia coli}

MLDKIVIANRGEIALRILRACKELGIKTVAVHSSADRDLKHVLLADETVCIGPAPSVKSYLNIPAIISAAEITGAVAIHPGYGFLSENANFAEQVERSGFIFIGPKAETIRLMG

>d1gsoa2 c.30.1.1 (A:-2-103) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}

EFMKVLVIGNGGREHALAWKAAQSPLVETVFVAPGNAGTALEPALQNVAIGVTDIPALLDFAQNEKIDLTIVGPEAPLVKGVVDTFRAAGLKIFGPTAGAAQLEG

>d1b6ra2 c.30.1.1 (A:1-78) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

MKQVCVLGNGQLGRMLRQAGEPLGIAVWPVGLDAEPAAVPFQQSVITAEIERWPETALTRQLARHPAFVNRDVFPIIA

>d1eyza2 c.30.1.1 (A:2-112) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

TLLGTALRPAATRVMLLGSGELGKEVAIECQRLGVEVIAVDRYADAPAMHVAHRSHVINMLDGDALRRVVELEKPHYIVPEIEAIATDMLIQLEEEGLNVVPCARATKLTM

>d1a9xa3 c.30.1.1 (A:1-127) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

MPKRTDIKSILILGAGPIVIGQACEFDYSGAQACKALREEGYRVINVNSNPATIMTDPEMADATYIEPIHWEVVRKIIEKERPDAVLPTMGGQTALNCALELERQGVLEEFGVTMIGATADAIDKAE

>d1a9xa4 c.30.1.1 (A:556-676) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

STDREKIMVLGGGPNRIGQGIEFDYCCVHASLALREDGYETIMVNCNPETVSTDYDTSDRLYFEPVTLEDVLEIVRIEKPKGVIVQYGGQTPLKLARALEAAGVPVIGTSPDAIDRAEDRE

>d1iow\_1 c.30.1.2 (1-96) D-Ala-D-Ala ligase {Escherichia coli, gene ddlB}

MTDKIAVLLGGTSAEREVSLNSGAAVLAGLREGGIDAYPVDPKEVDVTQLKSMGFQKVFIALHGRGGEDGTLQGMLELMGLPYTGSGVMASALSMD

>d1ehia1 c.30.1.2 (A:3-134) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}

KKRVALIFGGNSSEHDVSKRSAQNFYNAIEATGKYEIIVFAIAQNGFFLDTESSKKILALEDEQPIVDAFMKTVDASDPLARIHALKSAGDFDIFFPVVHGNLGEDGTLQGLFKLLDKPYVGAPLRGHAVSF

>d1e4ea1 c.30.1.2 (A:2-131) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}

NRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGITKSGVWKMCEKPCAEWENENCYSAVLSPDKKMHGLLVKKNHEYEINHVDVAFSALHGKSGEDGSIQGLFELSGIPFVGCDIQSSAICM

>d1gsa\_1 c.30.1.3 (1-122) Prokaryotic glutathione synthetase, N-terminal domain {Escherichia coli}

MIKLGIVMDPIANINIKKDSSFAMLLEAQRRGYELHYMEMGDLYLINGEARAHTRTLNVKQNYEEWFSFVGEQDLPLADLDVILMRKDPPFDTEFIYATYILERAEEKGTLIVNKPQSLRDC

>d2hgsa1 c.30.1.4 (A:202-303) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

PNALVLLIAQEKERNIFDQRAIENELLARNIHVIRRTFEDISEKGSLDQDRRLFVDGQEIAVVYFRDGYMPRQYSLQNWEARLLLERSHAAKCPDIATQLAG

>d1auva1 c.30.1.5 (A:112-213) Synapsin Ia domain {Cow (Bos taurus)}

AARVLLVIDEPHTDWAKYFKGKKIHGEIDIKVEQAEFSDLNLVAHANGGFSVDMEVLRNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPSI

>d1dhs\_\_ c.31.1.1 (-) Deoxyhypusine synthase, DHS {Human (Homo sapiens)}

APAGALAAVLKHSSTLPPESTQVRGYDFNRGVNYRALLEAFGTTGFQATNFGRAVQQVNAMIEKKLEPLTSCTIFLGYTSNLISSGIRETIRYLVQHNMVDVLVTTAGGVEEDLIKCLAPTYLGEFSLRGKELRENGINRIGNLLVPNENYCKFEDWLMPILDQMVMEQNTEGVKWTPSKMIARLGKEINNPESVYYWAQKNHIPVFSPALTDGSLGDMIFFHSYKNPGLVLDIVEDLRLINTQAIFAKCTGMIILGGGVVKHHIANANLMRNGADYAVYINTAQEFDGSDSGARPDEAVSWGKIRVDAQPVKVYADASLVFPLLVAETFAQKMDAFMHEKNED

>d1efva2 c.31.1.2 (A:208-331) C-terminal domain of the electron transfer flavoprotein alpha subunit {Human (Homo sapiens)}

DRPELTGAKVVVSGGRGLKSGENFKLLYDLADQLHAAVGASRAAVDAGFVPNDMQVGQTGKIVAPELYIAVGISGAIQHLAGMKDSKTIVAINKDPEAPIFQVADYGIVADLFKVVPEMTEILK

>d1efpa2 c.31.1.2 (A:185-308) C-terminal domain of the electron transfer flavoprotein alpha subunit {Paracoccus denitrificans}

SDRPELTSARRVVSGGRGLGSKESFAIIEELADKLGAAVGASRAAVDSGYAPNDWQVGQTGKVVAPELYVAVGISGAIQHLAGMKDSKVIVAINKDEEAPIFQIADYGLVGDLFSVVPELTGKL

>d1poxa1 c.31.1.3 (A:183-365) Pyruvate oxidase {Lactobacillus plantarum}

YASANNYQTPLLPEPDVQAVTRLTQTLLAAERPLIYYGIGARKAGKELEQLSKTLKIPLMSTYPAKGIVADRYPAYLGSANRVAQKPANEALAQADVVLFVGNNYPFAEVSKAFKNTRYFLQIDIDPAKLGKRHKTDIAVLADAQKTLAAILAQVSERESTPWWQANLANVKNWRAYLASLED

>d1pvda1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

QTPIDMSLKPNDAESEKEVIDTILALVKDAKNPVILADACCSRHDVKAETKKLIDLTQFPAFVTPMGKGSISEQHPRYGGVYVGTLSKPEVKEAVESADLILSVGALLSDKTKNIVEFHSDHMKIRNATFPGVQMKFVLQKLLTNIADAAKGYKPVAVPARTPANAAVP

>d1qpba1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

QTPIDMSLKPNDAESEKEVIDTILVLIKDAKNPVILADACCSRHDVKAETKKLIDLTQFPAFVTPMGKGSIDEQHPRYGGVYVGTLSKPEVKEAVESADLILSVGALLSDFNTGSFSYSYKTKNIVEFHSDHMKIRNATFPGVQMKFVLQKLLTAIADAAKGYKPVAVPARTPANAAVP

>d1zpda1 c.31.1.3 (A:188-362) Pyruvate decarboxylase {Zymomonas mobilis}

EASDEASLNAAVDETLKFIANRDKVAVLVGSKLRAAGAEEAAVKFTDALGGAVATMAAAKSFFPEENALYIGTSWGEVSYPGVEKTMKEADAVIALAPVFNDYSTTGWTDIPDPKKLVLAEPRSVVVNGIRFPSVHLKDYLTRLAQKVSKKTGSLDFFKSLNAGELKKAAPADPS

>d1bfd\_1 c.31.1.3 (182-341) Benzoylformate decarboxylase {Pseudomonas putida}

SVRLNDQDLDILVKALNSASNPAIVLGPDVDAANANADCVMLAERLKAPVWVAPSAPRCPFPTRHPCFRGLMPAGIAAISQLLEGHDVVLVIGAPVFRYHQYDPGQYLKPGTRLISVTCDPLEAARAPMGDAIVADIGAMASALANLVEESSRQLPTAAP

>d1jsca1 c.31.1.3 (A:280-460) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

AQDEFVMQSINKAADLINLAKKPVLYVGAGILNHADGPRLLKELSDRAQIPVTTTLQGLGSFDQEDPKSLDMLGMHGCATANLAVQNADLIIAVGARFDDRVTGNISKFAPEARRAAAEGRGGIIHFEVSPKNINKVVQTQIAVEGDATTNLGKMMSKIFPVKERSEWFAQINKWKKEYPY

>d1d4oa\_ c.31.1.4 (A:) Transhydrogenase domain III (dIII) {Cow (Bos taurus)}

GTHTEINLDNAIDMIREANSIIITPGYGLCAAKAQYPIADLVKMLSEQGKKVRFGIHPVAGRMPGQLNVLLAEAGVPYDIVLEMDEINHDFPDTDLVLVIGANDTVNSAAQEDPNSIIAGMPVLEVWKSKQVIVMKRSLGVGYAAVDNPIFYKPNTAMLLGDAKKTCDALQAKVRES

>d1hzzc\_ c.31.1.4 (C:) Transhydrogenase domain III (dIII) {Rhodospirillum rubrum}

SVKAGSAEDAAFIMKNASKVIIVPGYGMAVAQAQHALREMADVLKKEGVEVSYAIHPVAGRMPGHMNVLLAEANVPYDEVFELEEINSSFQTADVAFVIGANDVTNPAAKTDPSSPIYGMPILDVEKAGTVLFIKRSMASGYAGVENELFFRNNTMMLFGDAKKMTEQIVQAMN

>d1icia\_ c.31.1.5 (A:) AF1676 sir2 homolog {Archaeon Archaeoglobus fulgidus}

GSHHHHHHGSHMDEKLLKTIAESKYLVALTGAGVSAESGIPTFRGKDGLWNRYRPEELANPQAFAKDPEKVWKWYAWRMEKVFNAQPNKAHQAFAELERLGVLKCLITQNVDDLHERAGSRNVIHLHGSLRVVRCTSCNNSFEVESAPKIPPLPKCDKCGSLLRPGVVWFGEMLPPDVLDRAMREVERADVIIVAGTSAVVQPAASLPLIVKQRGGAIIEINPDETPLTPIADYSLRGKAGEVMDELVRHVRKALS

>d1j8fa\_ c.31.1.5 (A:) Sirt2 histone deacetylase {Human (Homo sapiens)}

GEADMDFLRNLFSQTLSLGSQKERLLDELTLEGVARYMQSERCRRVICLVGAGISTSAGIPDFRSPSTGLYDNLEKYHLPYPEAIFEISYFKKHPEPFFALAKELYPGQFKPTICHYFMRLLKDKGLLLRCYTQNIDTLERIAGLEQEDLVEAHGTFYTSHCVSASCRHEYPLSWMKEKIFSEVTPKCEDCQSLVKPDIVFFGESLPARFFSCMQSDFLKVDLLLVMGTSLQVQPFASLISKAPLSTPRLLINKEKAGQSDPFLGMIMGLGGGMDFDSKKAYRDVAWLGECDQGCLALAELLGWKKELEDLVRREHASIDAQS

>d1fsz\_1 c.32.1.1 (23-231) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}

SPEDKELLEYLQQTKAKITVVGCGGAGNNTITRLKMEGIEGAKTVAINTDAQQLIRTKADKKILIGKKLTRGLGAGGNPKIGEEAAKESAEEIKAAIQDSDMVFITCGLGGGTGTGSAPVVAEISKKIGALTVAVVTLPFVMEGKVRMKNAMEGLERLKQHTDTLVVIPNEKLFEIVPNMPLKLAFKVADEVLINAVKGLVELITKDGL

>d1tuba1 c.32.1.1 (A:1-245) Tubulin alpha-subunit {Pig (Sus scrofa)}

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRAVFVDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRIRKLADQCTGLQGFSVFHSFGGGTGSGFTSLLMERLSVDYGKKSKLEFSIYPAPQVSTAVVEPYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNRLIGQIVSSITASLRFD

>d1tubb1 c.32.1.1 (B:1-245) Tubulin beta-subunit {Pig (Sus scrofa)}

MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGSYHGDSDLQLERINVYYNEAAGNKYVPRAILVDLEPGTMDSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSVLDVVRKESESCDCLQGFQLTHSLGGGTGSGMGTLLISKIREEYPDRIMNTFSVVPSPKVSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTYGDLNHLVSATMSGVTTCLRFP

>d1nbaa\_ c.33.1.1 (A:) N-carbamoylsarcosine amidohydrolase {Arthrobacter sp.}

TFNDIEARLAAVLEEAFEAGTSIYNERGFKRRIGYGNRPAVIHIDLANAWTQPGHPFSCPGMETIIPNVQRINEAARAKGVPVFYTTNVYRNRDASSGTNDMGLWYSKIPTETLPADSYWAQIDDRIAPADGEVVIEKNRASAFPGTNLELFLTSNRIDTLIVTGATAAGCVRHTVEDAIAKGFRPIIPRETIGDRVPGVVQWNLYDIDNKFGDVESTDSVVQYLDALPQFEDTVPKTLSDPQPEVEAPADPV

>d1im5a\_ c.33.1.2 (A:) Pyrazinamidase/nicotinamidase {Archaeon Pyrococcus horikoshii}

PEEALIVVDMQRDFMPGGALPVPEGDKIIPKVNEYIRKFKEKGALIVATRDWHPENHISFRERGGPWPRHCVQNTPGAEFVVDLPEDAVIISKATEPDKEAYSGFEGTDLAKILRGNGVKRVYICGVATEYCVRATALDALKHGFEVYLLRDAVKGIKPEDEERALEEMKSRGIKIVQF

>d1yaca\_ c.33.1.2 (A:) YcaC {Escherichia coli}

TKPYVRLDKNDAAVLLVDHQAGLLSLVRDIEPDKFKNNVLALGDLAKYFNLPTILTTSAETGPNGPLVPELKAQFPDAPYIARPGNINAWDNEDFVKAVKATGKKQLIIAGVVTEVCVAFPALSAIEEGFDVFVVTDASGTFNEITRHSAWDRMSQAGAQLMTWFGVACELHRDWRNDIAGLATLFSNHIPDYRNLMTSYDTLT

>d1hi9a\_ c.99.1.1 (A:) Zn-dependent D-aminopeptidase DppA {Bacillus subtilis}

MKLYMSVDMEGISGLPDDTFVDSGKRNYERGRLIMTEEANYCIAEAFNSGCTEVLVNDSHSKMNNLMVEKLHPEADLISGDVKPFSMVEGLDDTFRGALFLGYHARASTPGVMSHSMIFGVRHFYINDRPVGELGLNAYVAGYYDVPVLMVAGDDRAAKEAEELIPNVTTAAVKQTISRSAVKCLSPAKRGRLLTEKTAFALQNKDKVKPLTPPDRPVLSIEFANYGQAEWANLMPGTEIKTGTTTVQFQAKDMLEAYQAMLVMTELAMRTSFC

>d1e20a\_ c.34.1.1 (A:) Halotolerance protein Hal3 {Mouse-ear cress (Arabidopsis thaliana)}

RKPRVLLAASGSVAAIKFGNLCHCFTEWAEVRAVVTKSSLHFLDKLSLPQEVTLYTDEDEWSSWNKIGDPVLHIELRRWADVLVIAPLSANTLGKIAGGLCDNLLTCIIRAWDYTKPLFVAPAMNTLMWNNPFTERHLLSLDELGITLIPPIKKRLACGDYGNGAMAEPSLIYSTVRLFWESQAH

>d1g5qa\_ c.34.1.1 (A:) Epidermin modifying enzyme (peptidyl-cysteine decarboxylase) EpiD {Staphylococcus epidermidis}

MYGKLLICATASINVININHYIVELKQHFDEVNILFSPSSKNFINTDVLKLFCDNLYDEIKDPLLNNINIVENHEYILVLPASANTINKIANGICDNLLTTVCLTGYQKLFIFPNMNIRMWGNPFLQKNIDLLKNNDVKVYSPDMNKSFEISSGRYKNNITMPNIENVLNFVLN

>d1k1ea\_ c.108.1.5 (A:) Probable phosphatase YrbI {Haemophilus influenzae, HI1679}

KLENIKFVITDVDGVLTDGQLHYDANGEAIKSFHVRDGLGIKMLMDADIQVAVLSGRDSPILRRRIADLGIKLFFLGKLEKETACFDLMKQAGVTAEQTAYIGDDSVDLPAFAACGTSFAVADAPIYVKNAVDHVLSTHGGKGAFREMSDMILQAQGKSSVFDTAQGFLKSVKSMGQ

>d1zrn\_\_ c.108.1.1 (-) L-2-Haloacid dehalogenase, HAD {Pseudomonas sp., strain YL}

YIKGIAFDLYGTLFDVHSVVGRCDEAFPGRGREISALWRQKQLEYTWLRSLMNRYVNFQQATEDALRFTCRHLGLDLDARTRSTLCDAYLRLAPFSEVPDSLRELKRRGLKLAILSNGSPQSIDAVVSHAGLRDGFDHLLSVDPVQVYKPDNRVYELAEQALGLDRSAILFVASNAWDATGARYFGFPTCWINRTGNVFEEMGQTPDWEVTSLRAVVELF

>d1qq5a\_ c.108.1.1 (A:) L-2-Haloacid dehalogenase, HAD {Xanthobacter autotrophicus}

MIKAVVFDAYGTLFDVQSVADATERAYPGRGEYITQVWRQKQLEYSWLRALMGRYADFWSVTREALAYTLGTLGLEPDESFLADMAQAYNRLTPYPDAAQCLAELAPLKRAILSNGAPDMLQALVANAGLTDSFDAVISVDAKRVFKPHPDSYALVEEVLGVTPAEVLFVSSNGFDVGGAKNFGFSVARVARLSQEALARELVSGTIAPLTMFKALRMREETYAEAPDFVVPALGDLPRLVRGMA

>d1ek1a1 c.108.1.2 (A:4-225) Epoxide hydrolase, N-terminal domain {Mouse (Mus musculus)}

RVAAFDLDGVLALPSIAGAFRRSEEALALPRDFLLGAYQTEFPEGPTEQLMKGKITFSQWVPLMDESYRKSSKACGANLPENFSISQIFSQAMAARSINRPMLQAAIALKKKGFTTCIVTNNWLDDGDKRDSLAQMMCELSQHFDFLIESCQVGMIKPEPQIYNFLLDTLKAKPNEVVFLDDFGSNLKPARDMGMVTILVHNTASALRELEKVTGTQFPEAP

>d1feza\_ c.108.1.3 (A:) Phosphonoacetaldehyde hydrolase {Bacillus cereus}

KIEAVIFDWAGTTVDYGCFAPLEVFMEIFHKRGVAITAEEARKPMGLLKIDHVRALTEMPRIASEWNRVFRQLPTEADIQEMYEEFEEILFAILPRYASPINAVKEVIASLRERGIKIGSTTGYTREMMDIVAKEAALQGYKPDFLVTPDDVPAGRPYPWMCYKNAMELGVYPMNHMIKVGDTVSDMKEGRNAGMWTVGVILGSSELGLTEEEVENMDSVELREKIEVVRNRFVENGAHFTIETMQELESVMEHIE

>d1j97a\_ c.108.1.4 (A:) Phosphoserine phosphatase {Archaeon Methanococcus jannaschii}

EKKKKLILFDFDSTLVNNETIDEIAREAGVEEEVKKITKEAMEGKLNFEQSLRKRVSLLKDLPIEKVEKAIKRITPTEGAEETIKELKNRGYVVAVVSGGFDIAVNKIKEKLGLDYAFANRLIVKDGKLTGDVEGEVLKENAKGEILEKIAKIEGINLEDTVAVGDGANDISMFKKAGLKIAFCAKPILKEKADICIEKRDLREILKYIK

>d1fs5a\_ c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Escherichia coli}

MRLIPLTTAEQVGKWAARHIVNRINAFKPTADRPFVLGLPTGGTPMTTYKALVEMHKAGQVSFKHVVTFNMDEYVGLPKEHPESYYSFMHRNFFDHVDIPAENINLLNGNAPDIDAECRQYEEKIRSYGKIHLFMGGVGNDGHIAFNEPASSLASRTRIKTLTHDTRVANSRFFDNDVNQVPKYALTVGVGTLLDAEEVMILVLGSQKALALQAAVEGCVNHMWTISCLQLHPKAIMVCDEPSTMELKVKTLRYFNELEAENIKGL

>d1d9ta\_ c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Human (Homo sapiens)}

MKLIILEHYSQASEWAAKYIRNRIIQFNPGPEKYFTLGLPTGSTPLGCYKKLIEYYKNGDLSFKYVKTFNMDEYVGLPRDHPESYHSFMWNNFFKHIDIHPENTHILDGNAVDLQAECDAFEEKIKAAGGIELFVGGIGPDGHIAFNEPGSSLVSRTRVKTLAMDTILANARFFDGELTKVPTMALTVGVGTVMDAREVMILITGAHKAFALYKAIEEGVNHMWTVSAFQQHPRTVFVCDEDATLELKVKTVKYFKGLMLVHNKLVDPLYSIKEKETEKSQ

>d1ig3a2 c.100.1.1 (A:10-178) Thiamin pyrophosphokinase, catalytic domain {Mouse (Mus musculus)}

HSSGLVPRGSHMEHAFTPLEPLLPTGNLKYCLVVLNQPLDARFRHLWKKALLRACADGGANHLYDLTEGERESFLPEFVSGDFDSIRPEVKEYYTKKGCDLISTPDQDHTDFTKCLQVLQRKIEEKELQVDVIVTLGGLGGRFDQIMASVNTLFQATHITPVPIIIIQK

>d1ig0a2 c.100.1.1 (A:3-223) Thiamin pyrophosphokinase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

EECIENPERIKIGTDLINIRNKMNLKELIHPNEDENSTLLILNQKIDIPRPLFYKIWKLHDLKVCADGAANRLYDYLDDDETLRIKYLPNYIIGDLDSLSEKVYKYYRKNKVTIIKQTTQYSTDFTKCVNLISLHFNSPEFRSLISNKDNLQSNHGIELEKGIHTLYNTMTESLVFSKVTPISLLALGGIGGRFDQTVHSITQLYTLSENASYFKLCYMTP

>d1f75a\_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Micrococcus luteus}

NINAAQIPKHIAIIMDGNGRWAKQKKMPRIKGHYEGMQTVRKITRYASDLGVKYLTLYAFSTENWSRPKDEVNYLMKLPGDFLNTFLPELIEKNVKVETIGFIDDLPDHTKKAVLEAKEKTKHNTGLTLVFALNYGGRKEIISAVQLIAERYKSGEISLDEISETHFNEYLFTANMPDPELLIRTSGEERLSNFLIWQCSYSEFVFIDEFWPDFNEESLAQCISIYQNR

>d1jp3a\_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Escherichia coli}

LPAHGCRHVAIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRAVSFAANNGIEALTLYAFSSENWNRPAQEVSALMELFVWALDSEVKSLHRHNVRLRIIGDTSRFNSRLQERIRKSEALTAGNTGLTLNIAANYGGRWDIVQGVRQLAEKVQQGNLQPDQIDEEMLNQHVCMHELAPVDLVIRTGGEHRISNFLLWQIAYAELYFTDVLWPDFDEQDFEGALNAFANRE

>d1pvda2 c.36.1.1 (A:2-181) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

SEITLGKYLFERLKQVNVNTVFGLPGDFNLSLLDKIYEVEGMRWAGNANELNAAYAADGYARIKGMSCIITTFGVGELSALNGIAGSYAEHVGVLHVVGVPSISHHTLGNGDFTVFHRMSANISETTAMITDIATAPAEIDRCIRTTYVTQRPVYLGLPANLVDLNVPAKLL

>d1pvda3 c.36.1.1 (A:361-556) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

ASTPLKQEWMWNQLGNFLQEGDVVIAETGTSAFGINQTTFPNNTYGISQVLWGSIGFTTGATLGAAFAAEEIDPKKRVILFIGDGSLQLTVQEISTMIRWGLKPYLFVLNNDGYTIEKLIHGPKAQYNEIQGWDHLSLLPTFGAKDYETHRVATTGEWDKLTQDKSFNDNSKIRMIEIMLPVFDAPQNLVKQAKLT

>d1zpda2 c.36.1.1 (A:2-187) Pyruvate decarboxylase {Zymomonas mobilis}

SYTVGTYLAERLVQIGLKHHFAVAGDYNLVLLDNLLLNKNMEQVYCCNELNCGFSAEGYARAKGAAAAVVTYSVGALSAFDAIGGAYAENLPVILISGAPNNNDHAAGHVLHHALGKTDYHYQLEMAKNITAAAEAIYTPEEAPAKIDHVIKTALREKKPVYLEIACNIASMPCAAPGPASALFND

>d1zpda3 c.36.1.1 (A:363-566) Pyruvate decarboxylase {Zymomonas mobilis}

APLVNAEIARQVEALLTPNTTVIAETGDSWFNAQRMKLPNGARVEYEMQWGHIGWSVPAAFGYAVGAPERRNILMVGDGSFQLTAQEVAQMVRLKLPVIIFLINNYGYTIEVMIHDGPYNNIKNWDYAGLMEVFNGNGGYDSGAAKGLKAKTGGELAEAIKVALANTDGPTLIECFIGREDCTEELVKWGKRVAAANSRKPVNK

>d1poxa2 c.36.1.1 (A:9-182) Pyruvate oxidase {Lactobacillus plantarum}

TNILAGAAVIKVLEAWGVDHLYGIPGGSINSIMDALSAERDRIHYIQVRHEEVGAMAAAADAKLTGKIGVCFGSAGPGGTHLMNGLYDAREDHVPVLALIGQFGTTGMNMDTFQEMNENPIYADVADYNVTAVNAATLPHVIDEAIRRAYAHQGVAVVQIPVDLPWQQISAEDW

>d1poxa3 c.36.1.1 (A:366-593) Pyruvate oxidase {Lactobacillus plantarum}

KQEGPLQAYQVLRAVNKIAEPDAIYSIDVGDINLNANRHLKLTPSNRHITSNLFATMGVGIPGAIAAKLNYPERQVFNLAGDGGASMTMQDLVTQVQYHLPVINVVFTNCQYGFIKDEQEDTNQNDFIGVEFNDIDFSKIADGVHMQAFRVNKIEQLPDVFEQAKAIAQHEPVLIDAVITGDRPLPAEKLRLDSAMSSAADIEAFKQRYEAQDLQPLSTYLKQFGLDD

>d1bfd\_2 c.36.1.1 (2-181) Benzoylformate decarboxylase {Pseudomonas putida}

ASVHGTTYELLRRQGIDTVFGNPGSNELPFLKDFPEDFRYILALQEACVVGIADGYAQASRKPAFINLHSAAGTGNAMGALSNAWNSHSPLIVTAGQQTRAMIGVEALLTNVDAANLPRPLVKWSYEPASAAEVPHAMSRAIHMASMAPQGPVYLSVPYDDWDKDADPQSHHLFDRHVSS

>d1bfd\_3 c.36.1.1 (342-524) Benzoylformate decarboxylase {Pseudomonas putida}

EPAKVDQDAGRLHPETVFDTLNDMAPENAIYLNESTSTTAQMWQRLNMRNPGSYYFCAAGGLGFALPAAIGVQLAEPERQVIAVIGDGSANYSISALWTAAQYNIPTIFVIMNNGTYGALRWFAGVLEAENVPGLDVPGIDFRALAKGYGVQALKADNLEQLKGSLQEALSAKGPVLIEVSTV

>d1jsca2 c.36.1.1 (A:83-270) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

PDMDTSFVGLTGGQIFNEMMSRQNVDTVFGYPGGAILPVYDAIHNSDKFNFVLPKHEQGAGHMAEGYARASGKPGVVLVTSGPGATNVVTPMADAFADGIPMVVFTGQVPTSAIGTDAFQEADVVGISRSCTKWNVMVKSVEELPLRINEAFEIATSGRPGPVLVDLPKDVTAAILRNPIPTKTTLPS

>d1jsca3 c.36.1.1 (A:461-648) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

AYMEETPGSKIKPQTVIKKLSKVANDTGRHVIVTTGVGQHQMWAAQHWTWRNPHTFITSGGLGTMGYGLPAAIGAQVAKPESLVIDIDGDASFNMTLTELSSAVQAGTPVKILILNNEEQGMVTQWQSLFYEHRYSHTHQLNPDFIKLAEAMGLKGLRVKKQEELDAKLKEFVSTKGPVLLEVEVDKK

>d1gpua1 c.36.1.2 (A:3-337) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}

QFTDIDKLAVSTIRILAVDTVSKANSGHPGAPLGMAPAAHVLWSQMRMNPTNPDWINRDRFVLSNGHAVALLYSMLHLTGYDLSIEDLKQFRQLGSRTPGHPEFELPGVEVTTGPLGQGISNAVGMAMAQANLAATYNKPGFTLSDNYTYVFLGDGCLQEGISSEASSLAGHLKLGNLIAIYDDNKITIDGATSISFDEDVAKRYEAYGWEVLYVENGNEDLAGIAKAIAQAKLSKDKPTLIKMTTTIGYGSLHAGSHSVHGAPLKADDVKQLKSKFGFNPDKSFVVPQEVYDHYQKTILKPGVEANNKWNKLFSEYQKKFPELGAELARRLSGQ

>d1gpua2 c.36.1.2 (A:338-534) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}

LPANWESKLPTYTAKDSAVATRKLSETVLEDVYNQLPELIGGSADLTPSNLTRWKEALDFQPPSSGSGNYSGRYIRYGIREHAMGAIMNGISAFGANYKPYGGTFLNFVSYAAGAVRLSALSGHPVIWVATHDSIGVGEDGPTHQPIETLAHFRSLPNIQVWRPADGNEVSAAYKNSLESKHTPSIIALSRQNLPQL

>d1dtwa1 c.36.1.3 (A:) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}

PQFPGASAEFIDKLEFIQPNVISGIPIYRVMDRQGQIINPSEDPHLPKEKVLKLYKSMTLLNTMDRILYESQRQGRISFYMTNYGEEGTHVGSAAALDNTDLVFGQYREAGVLMYRDYPLELFMAQCYGNISDLGKGRQMPVHYGCKERHFVTISSPLATQIPQAVGAAYAAKRANANRVVICYFGEGAASEGDAHAGFNFAATLECPIIFFCRNNGYAISTPTSEQYRGDGIAARGPGYGIMSIRVDGNDVFAVYNATKEARRRAVAENQPFLIEAMTYRIGHHSTSDDSSAYRSVDEVNYWDKQDHPISRLRHYLLSQGWWDEEQEKAWRKQSRRKVMEAFEQAERKPKPNPNLLFSDVYQEMPAQLRKQQESLARHLQTYGEHYPLDHFDK

>d1dtwb1 c.36.1.3 (B:17-204) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}

QTQKMNLFQSVTSALDNSLAKDPTAVIFGEDVAFGGVFRCTVGLRDKYGKDRVFNTPLCEQGIVGFGIGIAVTGATAIAEIQFADYIFPAFDQIVNEAAKYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSPEAFFAHCPGIKVVIPRSPFQAKGLLLSCIEDKNPCIFFEPKILYRAAAEEVPIE

>d1qs0a1 c.36.1.3 (A:) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

NEYAPLRLHVPEPTGRPGCQTDFSYLRLNDAGQARKPPVDVDAADTADLSYSLVRVLDEQGDAQGPWAEDIDPQILRQGMRAMLKTRIFDSRMVVAQRQKKMSFYMQSLGEEAIGSGQALALNRTDMCFPTYRQQSILMARDVSLVEMICQLLSNERDPLKGRQLPIMYSVREAGFFTISGNLATQFVQAVGWAMASAIKGDTKIASAWIGDGATAESDFHTALTFAHVYRAPVILNVVNNQWAISTFQAIAGGESTTFAGRGVGCGIASLRVDGNDFVAVYAASRWAAERARRGLGPSLIEWVTYRAGPHSTSDDPSKYRPADDWSHFPLGDPIARLKQHLIKIGHWSEEEHQATTAEFEAAVIAAQKEAEQYGTLANGHIPSAASMFEDVYKEMPDHLRRQRQEL

>d1qs0b1 c.36.1.3 (B:2-205) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

ATTTMTMIQALRSAMDVMLERDDNVVVYGQDVGYFGGVFRCTEGLQTKYGKSRVFDAPISESGIVGTAVGMGAYGLRPVVEIQFADYFYPASDQIVSEMARLRYRSAGEFIAPLTLRMPCGGGIYGGQTHSQSPEAMFTQVCGLRTVMPSNPYDAKGLLIASIECDDPVIFLEPKRLYNGPFDGHHDRPVTPWSKHPHSAVPDG

>d1ik6a1 c.36.1.3 (A:1-191) E1-beta subunit of pyruvate dehydrogenase {Archaeon Pyrobaculum aerophilum}

VAGVVMMANMAKAINMALHEEMERDERVVVLGEDVGKKGGVFLVTEGLYERFGPERVIDTPLNEGGILGFAMGMAMAGLKPVAEIQFVDFIWLGADELLNHIAKLRYRSGGNYKAPLVVRTPVGSGTRGGLYHSNSPEAIFVHTPGLVVVMPSTPYNAKGLLKAAIRGDDPVVFLEPKILYRAPREEVPEG

>d1keka1 c.36.1.4 (A:2-258) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

GKKMMTTDGNTATAHVAYAMSEVAAIYPITPSSTMGEEADDWAAQGRKNIFGQTLTIREMQSEAGAAGAVHGALAAGALTTTFTASQGLLLMIPNMYKISGELLPGVFHVTARAIAAHALSIFGDHQDIYAARQTGFAMLASSSVQEAHDMALVAHLAAIESNVPFMHFFDGFRTSHEIQKIEVLDYADMASLVNQKALAEFRAKSMNPEHPHVRGTAQNPDIYFQGREAANPYYLKVPGIVAEYMQKVASLTGRSY

>d1keka2 c.36.1.4 (A:786-1232) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

VKSEVLPRDSLKGSQFQEPLMEFSGACSGCGETPYVRVITQLFGERMFIANATGCSSIWGASAPSMPYKTNRLGQGPAWGNSLFEDAAEYGFGMNMSMFARRTHLADLAAKALESDASGDVKEALQGWLAGKNDPIKSKEYGDKLKKLLAGQKDGLLGQIAAMSDLYTKKSVWIFGGDGWAYDIGYGGLDHVLASGEDVNVFVMDTEVYSNTGGQSSKATPTGAVAKFAAAGKRTGKKDLARMVMTYGYVYVATVSMGYSKQQFLKVLKEAESFPGPSLVIAYATCINQGLRKGMGKSQDVMNTAVKSGYWPLFRYDPRLAAQGKNPFQLDSKAPDGSVEEFLMAQNRFAVLDRSFPEDAKRLRAQVAHELDVRFKELEHMAATNIFESFAPAGGKADGSVDFGEGAEFCTRDDTPMMARPDSGEACDQNRAGTSEQQGDLSKRTKK

>d1gky\_\_ c.37.1.1 (-) Guanylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SRPIVISGPSGTGKSTLLKKLFAEYPDSFGFSVSSTTRTPRAGEVNGKDYNFVSVDEFKSMIKNNEFIEWAQFSGNYYGSTVASVKQVSKSGKTCILDIDMQGVKSVKAIPELNARFLFIAPPSVEDLKKRLEGRGTETEESINKRLSAAQAELAYAETGAHDKVIVNDDLDKAYKELKDFIFAEK

>d1kgda\_ c.37.1.1 (A:) Guanylate kinase-like domain of Cask {Human (Homo sapiens)}

HMRKTLVLLGAHGVGRRHIKNTLITKHPDRFAYPIPHTTRPPKKDEENGKNYYFVSHDQMMQDISNNEYLEYGSHEDAMYGTKLETIRKIHEQGLIAILDVEPQALKVLRTAEFAPFVVFIAAPTITPGLNEDESLQRLQKESDILQRTYAHYFDLTIINNEIDETIRHLEEAVELVC

>d1kjwa2 c.37.1.1 (A:526-724) Guanylate kinase-like domain of Psd-95 {Rat (Rattus norvegicus)}

VTQMEVHYARPIIILGPTKDRANDDLLSEFPDKFGSCVPHTTRPKREYEIDGRDYHFVSSREKMEKDIQAHKFIEAGQYNSHLYGTSVQSVREVAEQGKHCILDVSANAVRRLQAAHLHPIAIFIRPRSLENVLEINKRITEEQARKAFDRATKLEQEFTECFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWVPARERL

>d1ukz\_\_ c.37.1.1 (-) Uridylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

PAFSPDQVSVIFVLGGPGAGKGTQCEKLVKDYSFVHLSAGDLLRAEQGRAGSQYGELIKNCIKEGQIVPQEITLALLRNAISDNVKANKHKFLIDGFPRKMDQAISFERDIVESKFILFFDCPEDIMLERLLERGKTSGRSDDNIESIKKRFNTFKETSMPVIEYFETKSKVVRVRCDRSVEDVYKDVQDAIRDSL

>d1deka\_ c.37.1.1 (A:) Deoxynucleoside monophosphate kinase {Bacteriophage T4}

MKLIFLSGVKRSGKDTTADFIMSNYSAVKYQLAGPIKDALAYAWGVFAANTDYPCLTRKEFEGIDYDRETNLNLTKLEVITIMEQAFCYLNGKSPIKGVFVFDDEGKESVNFVAFNKITDVINNIEDQWSVRRLMQALGTDLIVNNFDRMYWVKLFALDYLDKFNSGYDYYIVPDTRQDHEMDAARAMGATVIHVVRPGQKSNDTHITEAGLPIRDGDLVITNDGSLEELFSKIKNTLKVL

>d1j90a\_ c.37.1.1 (A:) Deoxyribonucleoside kinase {Fruit fly (Drosophila melanogaster)}

TQPFTVLIEGNIGSGKTTYLNHFEKYKNDICLLTEPVEKWRNVNGVNLLELMYKDPKKWAMPFQSYVTLTMLQSHTAPTNKKLKIMERSIFSARYCFVENMRRNGSLEQGMYNTLEEWYKFIEESIHVQADLIIYLRTSPEVAYERIRQRARSEESCVPLKYLQELHELHEDWLIHQRRPQSCKVLVLDADLNLE

>d1jaga\_ c.37.1.1 (A:) Deoxyguanosine kinase {Human (Homo sapiens)}

GPRRLSIEGNIAVGKSTFVKLLTKTYPEWHVATEPVATWQNIQAAGNQKACTAQSLGNLLDMMYREPARWSYTFQTFSFLSRLKVQLEPFPEKLLQARKPVQIFERSVYSDRYIFAKNLFENGSLSDIEWHIYQDWHSFLLWEFASRITLHGFIYLQASPQVCLKRLYQRAREEEKGIELAYLEQLHGQHEAWLIHKTTKLHFEALMNIPVLVLDVNDDFSEEVTKQEDLMREVNTFVKNL

>d1ckea\_ c.37.1.1 (A:) CMP kinase {Escherichia coli}

AIAPVITIDGPSGAGKGTLCKAMAEALQWHLLDSGAIYRVLALAALHHHVDVASEDALVPLASHLDVRFVSTNGNLEVILEGEDVSGEIRTQEVANAASQVAAFPRVREALLRRQRAFRELPGLIADGRDMGTVVFPDAPVKIFLDASSEERAHRRMLQLQVKGFSVNFERLLAEIKERDDRDRNRAVAPLVPAADALVLDSTTLSIEQVIEKALQYARQKLALA

>d1qf9a\_ c.37.1.1 (A:) UMP/CMP kinase {Dictyostelium discoideum}

MEKSKPNVVFVLGGPGSGKGTQCANIVRDFGWVHLSAGDLLRQEQQSGSKDGEMIATMIKNGEIVPSIVTVKLLKNAIDANQGKNFLVDGFPRNEENNNSWEENMKDFVDTKFVLFFDCPEEVMTQRLLKRGESSGRSDDNIESIKKRFNTFNVQTKLVIDHYNKFDKVKIIPANRDVNEVYNDVENLFKSMGF

>d1e2ka\_ c.37.1.1 (A:) Thymidine kinase {Herpes simplex virus type 1, different strains}

MPTLLRVYIDGPHGMGKTTTTQLLVALGSRDDIVYVPEPMTYWRVLGASETIANIYTTQHRLDQGEISAGDAAVVMTSAQITMGMPYAVTDAVLAPHIGGEAGSSHAPPPALTLIFDRHPIAALLCYPAARYLMGSMTPQAVLAFVALIPPTLPGTNIVLGALPEDRHIDRLAKRQRPGERLDLAMLAAIRRVYGLLANTVRYLQCGGSWREDWGQLSGTAVPPQGAEPQSNAGPRPHIGDTLFTLFRAPELLAPNGDLYNVFAWALDVLAKRLRSMHVFILDYDQSPAGCRDALLQLTSGMVQTHVTTPGSIPTICDLARTFAREMGE

>d3adk\_\_ c.37.1.1 (-) Adenylate kinase {Pig (Sus scrofa)}

MEEKLKKSKIIFVVGGPGSGKGTQCEKIVQKYGYTHLSTGDLLRAEVSSGSARGKMLSEIMEKGQLVPLETVLDMLRDAMVAKVDTSKGFLIDGYPREVKQGEEFERKIGQPTLLLYVDAGPETMTKRLLKRGETSGRVDDNEETIKKRLETYYKATEPVIAFYEKRGIVRKVNAEGSVDDVFSQVCTHLDTLK

>d1nksa\_ c.37.1.1 (A:) Adenylate kinase {Archaeon Sulfolobus acidocaldarius}

MKIGIVTGIPGVGKSTVLAKVKEILDNQGINNKIINYGDFMLATALKLGYAKDRDEMRKLSVEKQKKLQIDAAKGIAEEARAGGEGYLFIDTHAVIRTPSGYLPGLPSYVITEINPSVIFLLEADPKIILSRQKRDTTRNRNDYSDESVILETINFARYAATASAVLAGSTVKVIVNVEGDPSIAANEIIRSMK

>d2ak3a1 c.37.1.1 (A:0-124,A:162-225) Adenylate kinase {Cow (Bos taurus), mitochondrial izozyme-3}

GASARLLRAAIMGAPGSGKGTVSSRITKHFELKHLSSGDLLRDNMLRGTEIGVLAKTFIDQGKLIPDDVMTRLVLHELKNLTQYNWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRLTXDRPETVVKRLKAYEAQTEPVLEYYRKKGVLETFSGTETNKIWPHVYAFLQTKLPQRSQETSVTP

>d1ak2\_1 c.37.1.1 (14-146,177-233) Adenylate kinase {Cow (Bos taurus), mitochondrial izozyme-2}

PKGVRAVLLGPPGAGKGTQAPKLAKNFCVCHLATGDMLRAMVASGSELGKKLKATMDAGKLVSDEMVLELIEKNLETPPCKNGFLLDGFPRTVRQAEMLDDLMEKRKEKLDSVIEFSIPDSLLIRRITGRLIHXSDDNKKALKIRLEAYHTQTTPLVEYYSKRGIHSAIDASQTPDVVFASILAAFSKATS

>d1aky\_1 c.37.1.1 (3-130,169-220) Adenylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

ESIRMVLIGPPGAGKGTQAPNLQERFHAAHLATGDMLRSQIAKGTQLGLEAKKIMDQGGLVSDDIMVNMIKDELTNNPACKNGFILDGFPRTIPQAEKLDQMLKEQGTPLEKAIELKVDDELLVARITXNADALKKRLAAYHAQTEPIVDFYKKTGIWAGVDASQPPATVWADILNKLGKN

>d1e4ya1 c.37.1.1 (A:1-121,A:157-214) Adenylate kinase {Escherichia coli}

MRIILLGALVAGKGTQAQFIMEKYGIPQISTGDMLRAAVKSGSELGKQAKDIMDAGKLVTDELVIALVKERIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDYVLEFDVPDELIVDRIVXKDDQEETVRKRLVEYHQMTAPLIGYYSKEAEAGNTKYAKVDGTKPVAEVRADLEKILG

>d1zaka1 c.37.1.1 (A:3-127,A:159-222) Adenylate kinase {Maize (Zea mays)}

ADPLKVMISGAPASGKGTQCELIKTKYQLAHISAGDLLRAEIAAGSENGKRAKEFMEKGQLVPDEIVVNMVKERLRQPDAQENGWLLDGYPRSYSQAMALETLEIRPDTFILLDVPDELLVERVVXFDDTEEKVKLRLETYYQNIESLLSTYENIIVKVQGDATVDAVFAKIDELLGSILEKKNEMVSST

>d1zin\_1 c.37.1.1 (1-125,161-217) Adenylate kinase {Bacillus stearothermophilus}

MNLVLMGLPGAGKGTQAEKIVAAYGIPHISTGDMFRAAMKEGTPLGLQAKQYMDRGDLVPDEVTIGIVRERLSKDDCQNGFLLDGFPRTVAQAEALETMLADIGRKLDYVIHIDVRQDVLMERLTXADDNEATVANRLEVNMKQMKPLVDFYEQKGYLRNINGEQDMEKVFADIRELLGGLAR

>d1tmka\_ c.37.1.1 (A:) Thymidylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

GRGKLILIEGLDRTGKTTQCNILYKKLQPNCKLLKFPERSTRIGGLINEYLTDDSFQLSDQAIHLLFSANRWEIVDKIKKDLLEGKNIVMDRYVYSGVAYSAAKGTNGMDLDWCLQPDVGLLKPDLTLFLSTQDVDNNAEKSGFGDERYETVKFQEKVKQTFMKLLDKEIRKGDESITIVDVTNKGIQEVEALIWQIVEPVLSTHIDHDKFSFF

>d1e9ea\_ c.37.1.1 (A:) Thymidylate kinase {Human (Homo sapiens)}

ARRGALIVLEGVDRAGKSTQSRKLVEALCAAGHRAELLRFPERSTEIGKLLSSYLQKKSDVEDHSVHLLFSANRWEQVPLIKEKLSQGVTLVVDRYAFSGVAYTGAKENFSLDWCKQPDVGLPKPDLVLFLQLQLADAAKRGAFGHERYENGAFQERALRCFHQLMKDTTLNWKMVDASKSIEAVHEDIRVLSEDAIATATEKPLKELWK

>d4tmka\_ c.37.1.1 (A:) Thymidylate kinase {Escherichia coli}

RSKYIVIEGLEGAGKTTARNVVVETLEQLGIRDMVFTREPGGTQLAEKLRSLLLDIKSVGDEVITDKAEVLMFYAARVQLVETVIKPALANGTWVIGDRHDLSTQAYQGGGRGIDQHMLATLRDAVLGDFRPDLTLYLDVTPEVGLKRARARGELDRIEQESFDFFNRTRARYLELAAQDKSIHTIDATQPLEAVMDAIRTTVTHWVKEL

>d1g3ua\_ c.37.1.1 (A:) Thymidylate kinase {Mycobacterium tuberculosis}

MLIAIEGVDGAGKRTLVEKLSGAFRAAGRSVATLAFPRYGQSVAADIAAEALHGEHGDLASSVYAMATLFALDRAGAVHTIQGLCRGYDVVILDRYVASNAAYSAARLHENAAGKAAAWVQRIEFARLGLPKPDWQVLLAVSAELAGERSRGRAQRDPGRARDNYERDAELQQRTGAVYAELAAQGWGGRWLVVGADVDPGRLAATLA

>d1e6ca\_ c.37.1.2 (A:) Shikimate kinase {Erwinia chrysanthemi}

MTEPIFMVGARGCGMTTVGRELARALGYEFVDTDIFMQHTSGMTVADVVAAEGWPGFRRRESEALQAVATPNRVVATGGGMVLLEQNRQFMRAHGTVVYLFAPAEELALRLQASLQAHQRPTLTGRPIAEEMEAVLREREALYQDVAHYVVDATQPPAAIVCELMQTMRL

>d1qhxa\_ c.37.1.3 (A:) Chloramphenicol phosphotransferase {Streptomyces venezuelae}

MTTRMIILNGGSSAGKSGIVRCLQSVLPEPWLAFGVDSLIEAMPLKMQSAEGGIEFDADGGVSIGPEFRALEGAWAEGVVAMARAGARIIIDDVFLGGAAAQERWRSFVGDLDVLWVGVRCDGAVAEGRETARGDRVAGMAAKQAYVVHEGVEYDVEVDTTHKESIECAWAIAAHVVP

>d1d6ja\_ c.37.1.4 (A:) Adenosine-5'phosphosulfate kinase (APS kinase) {Penicillium chrysogenum}

HASALTRSERTELRNQRGLTIWLTGLSASGKSTLAVELEHQLVRDRRVHAYRLDGDNIRFGLNKDLGFSEADRNENIRRIAEVAKLFADSNSIAITSFISPYRKDRDTARQLHEVATPGEETGLPFVEVYVDVPVEVAEQRDPKGLYKKAREGVIKEFTGISAPYEAPANPEVHVKNYELPVQDAVKQIIDYLDTKGYLPAKK

>d1g8fa3 c.37.1.15 (A:390-511) ATP sulfurylase C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

PRPKQGFSIVLGNSLTVSREQLSIALLSTFLQFGGGRYYKIFEHNNKTELLSLIQDFIGSGSGLIIPDQWEDDKDSVVGKQNVYLLDTSSSADIQLESADEPISHIVQKVVLFLEDNGFFVF

>d1i2da3 c.37.1.15 (A:391-573) ATP sulfurylase C-terminal domain {Fungus (Penicillium chrysogenum)}

PRATQGFTIFLTGYMNSGKDAIARALQVTLNQQGGRSVSLLLGDTVRHELSSELGFTREDRHTNIQRIAFVATELTRAGAAVIAAPIAPYEESRKFARDAVSQAGSFFLVHVATPLEHCEQSDKRGIYAAARRGEIKGFTGVDDPYETPEKADLVVDFSKQSVRSIVHEIILVLESQGFLERQ

>d1aqua\_ c.37.1.5 (A:) Estrogen sulfotransferase {Mouse (Mus musculus)}

EYYEVFGEFRGVLMDKRFTKYWEDVEMFLARPDDLVIATYPKSGTTWISEVVYMIYKEGDVEKCKEDAIFNRIPYLECRNEDLINGIKQLKEKESPRIVKTHLPPKLLPASFWEKNCKMIYLCRNAKDVAVSYYYFLLMITSYPNPKSFSEFVEKFMQGQVPYGSWYDHVKAWWEKSKNSRVLFMFYEDMKEDIRREVVKLIEFLERKPSAELVDRIIQHTSFQEMKNNPSTNYTMMPEEMMNQKVSPFMRKGIIGDWKNHFPEALRERFDEHYKQQMKDCTVKFRME

>d1efha\_ c.37.1.5 (A:) Hydroxysteroid sulfotransferase {Human (Homo sapiens)}

DFLWFEGIAFPTMGFRSETLRKVRDEFVIRDEDVIILTYPKSGTNWLAEILCLMHSKGDAKWIQSVPIWERSPWVESEIGYTALSETESPRLFSSHLPIQLFPKSFFSSKAKVIYLMRNPRDVLVSGYFFWKNMKFIKKPKSWEEYFEWFCQGTVLYGSWFDHIHGWMPMREEKNFLLLSYEELKQDTGRTIEKICQFLGKTLEPEELNLILKNSSFQSMKENKMSNYSLLSVDYVVDKAQLLRKGVSGDWKNHFTVAQAEDFDKLFQEKMADLPRKLAAALE

>d1cjma\_ c.37.1.5 (A:) Aryl sulfotransferase sult1a3 {Human (Homo sapiens)}

SRPPLEYVKGVPLIKYFAEALGPLQSFQARPDDLLINTYPKSGTTWVSQILDMIYQGGDLEKCNRAPIYVRVPFLEVNDPGEPSGLETLKDTPPPRLIKSHLPLALLPQTLLDQKVKVVYVARNPKDVAVSYYHFHRMEKAHPEPGTWDSFLEKFMAGEVSYGSWYQHVQEWWELSRTHPVLYLFYEDMKENPKREIQKILEFVGRSLPEETMDFMVQHTSFKEMKKNPMTNYTTVPQELMDHSISPFMRKGMAGDWKTTFTVAQNERFDADYAEKMAGCSLSFRS

>d1nsta\_ c.37.1.5 (A:) Heparan sulfate N-deacetylase/N-sulfotransferase domain {Human (Homo sapiens)}

DPLWQDPCEDKRHKDIWSKEKTCDRFPKLLIIGPQKTGTTALYLFLGMHPDLSSNYPSSETFEEIQFFNGHNYHKGIDWYMEFFPIPSNTTSDFYFEKSANYFDSEVAPRRAAALLPKAKVLTILINPADRAYSWYQHQRAHDDPVALKYTFHEVITAGSDASSKLRALQNRCLVPGWYATHIERWLSAYHANQILVLDGKLLRTEPAKVMDMVQKFLGVTNTIDYHKTLAFDPKKGFWCQLLEGGKTKCLGKSKGRKYPEMDLDSRAFLKDYYRDHNIELSKLLYKMGQTLPTWLREDLQ

>d1fmja\_ c.37.1.5 (A:) Retinol dehydratase {Fall armyworm (Spodoptera frugiperda)}

PFPYEFRELNPEEDKLVKANLGAFPTTYVKLGPKGYMVYRPYLKDAANIYNMPLRPTDVFVASYQRSGTTMTQELVWLIENDLNFEAAKTYMSLRYIYLDGFMIYDPEKQEEYNDILPNPENLDMERYLGLLEYSSRPGSSLLAAVPPTEKRFVKTHLPLSLMPPNMLDTVKMVYLARDPRDVAVSSFHHARLLYLLNKQSNFKDFWEMFHRGLYTLTPYFEHVKEAWAKRHDPNMLFLFYEDYLKDLPGCIARIADFLGKKLSEEQIQRLCEHLNFEKFKNNGAVNMEDYREIGILADGEHFIRKGKAGCWRDYFDEEMTKQAEKWIKDNLKDTDLRYPNM

>d1a7j\_\_ c.37.1.6 (-) Phosphoribulokinase {Rhodobacter sphaeroides}

SKKHPIISVTGSSGAGTSTVKHTFDQIFRREGVKAVSIEGDAFHRFNRADMKAELDRRYAAGDATFSHFSYEANELKELERVFREYGETGQGRTRTYVHDDAEAARTGVAPGNFTDWRDFDSDSHLLFYEGLHGAVVNSEVNIAGLADLKIGVVPVINLEWIQKIHRDRATRGYTTEAVTDVILRRMHAYVHCIVPQFSQTDINFQRVPVVDTSNPFIARWIPTADESVVVIRFRNPRGIDFPYLTSMIHGSWMSRANSIVVPGNKLDLAMQLILTPLIDRVVRESKV

>d1esma\_ c.37.1.6 (A:) Pantothenate kinase PanK {Escherichia coli}

QTLMTPYLQFDRNQWAALRDSVPMTLSEDEIARLKGINEDLSLEEVAEIYLPLSRLLNFYISSNLRRQAVLEQFLGTNGQRIPYIISIAGSVAVGKSTTARVLQALLSRWPEHRRVELITTDGFLHPNQVLKERGLMKKKGFPESYDMHRLVKFVSDLKSGVPNVTAPVYSHLIYDVIPDGDKTVVQPDILILEGLNVLQSGMDYPHDPHHVFVSDFVDFSIYVDAPEDLLQTWYINRFLKFREGAFTDPDSYFHNYAKLTKEEAIKTAMTLWKEINWLNLKQNILPTRERASLILTKSANHAVEEVRLRK

>d1bif\_1 c.37.1.7 (37-249) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain {Rat (Rattus norvegicus)}

CPTLIVMVGLPARGKTYISKKLTRYLNFIGVPTREFNVGQYRRDMVKTYKSFEFFLPDNEEGLKIRKQCALAALNDVRKFLSEEGGHVAVFDATNTTRERRAMIFNFGEQNGYKTFFVESICVDPEVIAANIVQVKLGSPDYVNRDSDEATEDFMRRIECYENSYESLDEEQDRDLSYIKIMDVGQSYVVNRVADHIQSRIVYYLMNIHVTPR

>d1ctqa\_ c.37.1.8 (A:) cH-p21 Ras protein {Human (Homo sapiens)}

MTEYKLVVVGAGGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHQYREQIKRVKDSDDVPMVLVGNKCDLAARTVESRQAQDLARSYGIPYIETSAKTRQGVEDAFYTLVREIRQH

>d1ds6a\_ c.37.1.8 (A:) Rac {Human (Homo sapiens)}

MQAIKCVVVGDGAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDSKPVNLGLWDTAGQEDYDRLRPLSYPQTDVFLICFSLVSPASYENVRAKWFPEVRHHCPSTPIILVGTKLDLRDDKDTIEKLKEKKLAPITYPQGLALAKEIDSVKYLECSALTQRGLKTVFDEAIRAVLCPQP

>d1mh1\_\_ c.37.1.8 (-) Rac {Human (Homo sapiens)}

GSPQAIKCVVVGDGAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDGKPVNLGLWDTAGQEDYDRLRPLSYPQTDVSLICFSLVSPASFENVRAKWYPEVRHHCPNTPIILVGTKLDLRDDKDTIEKLKEKKLTPITYPQGLAMAKEIGAVKYLECSALTQRGLKTVFDEAIRAVLCPPP

>d1c1ya\_ c.37.1.8 (A:) Rap1A {Human (Homo sapiens)}

MREYKLVVLGSGGVGKSALTVQFVQGIFVEKYDPTIEDSYRKQVEVDCQQCMLEILDTAGTEQFTAMRDLYMKNGQGFALVYSITAQSTFNDLQDLREQILRVKDTEDVPMILVGNKCDLEDERVVGKEQGQNLARQWCNCAFLESSAKSKINVNEIFYDLVRQINR

>d1kao\_\_ c.37.1.8 (-) Rap2a {Human (Homo sapiens)}

MREYKVVVLGSGGVGKSALTVQFVTGTFIEKYDPTIEDFYRKEIEVDSSPSVLEILDTAGTEQFASMRDLYIKNGQGFILVYSLVNQQSFQDIKPMRDQIIRVKRYEKVPVILVGNKVDLESEREVSSSEGRALAEEWGCPFMETSAKSKTMVDELFAEIVRQMNYA

>d3raba\_ c.37.1.8 (A:) Rab3a {Rat (Rattus norvegicus)}

NFDYMFKILIIGNSSVGKTSFLFRYADDSFTPAFVSTVGIDFKVKTIYRNDKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITNEESFNAVQDWSTQIKTYSWDNAQVLLVGNKCDMEDERVVSSERGRQLADHLGFEFFEASAKDNINVKQTFERLVDVICEK

>d1huqa\_ c.37.1.8 (A:) Rab5c {Mouse (Mus musculus)}

ICQFKLVLLGESAVGKSSLVLRFVKGQFHEYQESTIGAAFLTQTVCLDDTTVKFEIWDTAGQERYHSLAPMYYRGAQAAIVVYDITNTDTFARAKNWVKELQRQASPNIVIALAGNKADLASKRAVEFQEAQAYADDNSLLFMETSAKTAMNVNEIFMAIAKKL

>d1d5ca\_ c.37.1.8 (A:) Rab6 {Malaria parasite (Plasmodium falciparum)}

KYKLVFLGEQAVGKTSIITRFMYDTFDNNYQSTIGIDFLSKTLYLDEGPVRLQLWDTAGQERFRSLIPSYIRDSAAAIVVYDITNRQSFENTTKWIQDILNERGKDVIIALVGNKTDLGDLRKVTYEEGMQKAQEYNTMFHETSAKAGHNIKVLFKKTASKL

>d1g16a\_ c.37.1.8 (A:) Rab-related protein Sec4 {Baker's yeast (Saccharomyces cerevisiae)}

SIMKILLIGDSGVGKSCLLVRFVEDKFNPSFITTIGIDFKIKTVDINGKKVKLQIWDTAGQERFRTITTAYYRGAMGIILVYDITDERTFTNIKQWFKTVNEHANDEAQLLLVGNKSDMETRVVTADQGEALAKELGIPFIESSAKNDDNVNEIFFTLAKLIQEKI

>d1byua\_ c.37.1.8 (A:) Ran {Dog (Canis familiaris)}

EPQVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYVPTLGVEVHPLVFHTNRGPIKFNVWDTAGQEKFGGLRDGYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFVAMPALAPPEVVMDPALAAQYEHDLEVAQTT

>d1i2ma\_ c.37.1.8 (A:) Ran {Human (Homo sapiens)}

QVQFKLVLVGDGGTGKTTFVKRHLTGEFEKKYVATLGVEVHPLVFHTNRGPIKFNVWDTAGQEKFGGLRDGYYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFV

>d1tx4b\_ c.37.1.8 (B:) RhoA {Human (Homo sapiens)}

AIRKKLVIVGDGACGKTCLLIVNSKDQFPEVYVPTVFENYVADIEVDGAQVELALWDTAGQEDYDRLRPLSYPDTDVILMCFSIDSPDSLENIPEKWTPEVKHFCPNVPIILVGNKKDLRNDEHTRRELAKMKQEPVKPEEGRDMANRIGAFGYMECSAKTKDGVREVFEMATRAAL

>d1hura\_ c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF1}

GNIFANLFKGLFGKKEMRILMVGLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRERVNEAREELMRMLAEDELRDAVLLVFANKQDLPNAMNAAEITDKLGLHSLRHRNWYIQATCATSGDGLYEGLDWLSNQLRNQK

>d1e0sa\_ c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF6}

GKVLSKIFGNKEMRILMLGLDAAGKTTILYKLKLGQSVTTIPTVGFNVETVTYKNVKFNVWDVGGQDKIRPLWRHYYTGTQGLIFVVDCADRDRIDEARQELHRIINDREMRDAIILIFANKQDLPDAMKPHEIQEKLGLTRIRDRNWYVQPSCATSGDGLYEGLTWLTSNYK

>d1fzqa\_ c.37.1.8 (A:) ADP-ribosylation factor {Mouse (Mus musculus), ARL3}

GLLSILRKLKSAPDQEVRILLLGLDNAGKTTLLKQLASEDISHITPTQGFNIKSVQSQGFKLNVWDIGGQRKIRPYWRSYFENTDILIYVIDSADRKRFEETGQELTELLEEEKLSCVPVLIFANKQDLLTAAPASEIAEGLNLHTIRDRVWQIQSCSALTGEGVQDGMNWVCKNV

>d1f6ba\_ c.37.1.8 (A:) SAR1 {Chinese hamster (Cricetulus griseus)}

SSVLQFLGLYKKTGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPTLHPTSEELTIAGMTFTTFDLGGHIQARRVWKNYLPAINGIVFLVDCADHERLLESKEELDSLMTDETIANVPILILGNKIDRPEAISEERLREMFGLYGQTTGKGSVSLKELNARPLEVFMCSVLKRQGYGEGFRWMAQYID

>d2ngra\_ c.37.1.8 (A:) CDC42 {Human (Homo sapiens)}

MQTIKCVVVGDGAVGKTCLLISYTTNKFPSEYVPTVFDNYAVTVMIGGEPYTLGLFDTAGQEDYDRLRPLSYPQTDVFLVCFSVVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRDDPSTIEKLAKNKQKPITPETAEKLARDLKAVKYVECSALTQKGLKNVFDEAILAALEPPEPKKSRRCVLL

>d1ek0a\_ c.37.1.8 (A:) Ypt51 {Baker's yeast (Saccharomyces cerevisiae)}

VTSIKLVLLGEAAVGKSSIVLRFVSNDFAENKEPTIGAAFLTQRVTINEHTVKFEIWDTAGQERFASLAPMYYRNAQAALVVYDVTKPQSFIKARHWVKELHEQASKDIIIALVGNKIDMLQEGGERKVAREEGEKLAEEKGLLFFETSAKTGENVNDVFLGIGEKIPLK

>d1h65a\_ c.37.1.8 (A:) Chloroplast protein translocon GTPase Toc34 {Garden pea (Pisum sativum)}

VREWSGINTFAPATQTKLLELLGNLKQEDVNSLTILVMGKGGVGKSSTVNSIIGERVVSISPFQSEGPRPVMVSRSRAGFTLNIIDTPGLIEGGYINDMALNIIKSFLLDKTIDVLLYVDRLDAYRVDNLDKLVAKAITDSFGKGIWNKAIVALTHAQFSPPDGLPYDEFFSKRSEALLQVVRSGASLKKDAQASDIPVVLIENSGRCNKNDSDEKVLPNGIAWIPHLVQTITEVALNKSESIFVDKNLIDKLAAAD

>d1azsc2 c.37.1.8 (C:36-66,C:202-393) Transducin (alpha subunit) {Cow (Bos taurus)}

VYRATHRLLLLGAGESGKSTIVKQMRILHVNXVLTSGIFETKFQVDKVNFHMFDVGGQRDERRKWIQCFNDVTAIIFVVASSSYNMVIREDNQTNRLQEALNLFKSIWNNRWLRTISVILFLNKQDLLAEKVLAGKSKIEDYFPEFARYTTPEDATPEPGEDPRVTRAKYFIRDEFLRISTASGDGRHYCYPHFTCAVDTENIRRVFNDCRDIIQRMHLRQYEL

>d1tada2 c.37.1.8 (A:27-56,A:178-342) Transducin (alpha subunit) {Cow (Bos taurus)}

ARTVKLLLLGAGESGKSTIVKQMKIIHQDGXTGIIETQFSFKDLNFRMFDVGGQRSERKKWIHCFEGVTCIIFIAALSAYDMVLVEDDEVNRMHESLHLFNSICNHRYFATTSIVLFLNKKDVFSEKIKKAHLSICFPDYNGPNTYEDAGNYIKVQFLELNMRRDVKEIYSHMTCATDTQNVKFVFDAVTDIIIKE

>d1bof\_2 c.37.1.8 (10-60,182-354) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

KAAVERSKMIDRNLREDGEKAAREVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHFTFKDLHFKMFDVGGQRSERKKWIHCFEGVTAIIFCVALSDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAAAYIQCQFEDLNKRKDTKEIYTHFTCATDTKNVQFVFDAVTDVIIKNNLKDCGLF

>d1cipa2 c.37.1.8 (A:32-60,A:182-347) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

REVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHFTFKDLHFKMFDVGGQRSERKKWIHCFEGVTAIIFCVALSDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAAAYIQCQFEDLNKRKDTKEIYTHFTCATDTKNVQFVFDAVTDVIIKNN

>d1fqja2 c.37.1.8 (A:28-60,A:182-344) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

RTVKLLLLGAGESGKSTIVKQMKIIHQDGYSLEXETQFSFKDLNFRMFDVGGQRSERKKWIHCFEGVTAIIFCVALSDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAGNYIKVQFLELNMRRDVKEIYSHMTCATDTQNVKFVFDAVTDIIIKENL

>d1gota2 c.37.1.8 (A:6-60,A:182-343) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

SAEEKHSRELEKKLKEDAEKDARTVKLLLLGAGESGKSTIVKQMKIIHQDGYSLEXETQFSFKDLNFRMFDVGGQRSERKKWIHCFEGVTAIIFCVALSDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAGNYIKVQFLELNMRRDVKEIYSHMTCATDTQNVKFVFDAVTDIIIKEN

>d1efca3 c.37.1.8 (A:8-204) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}

TKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARAFDQIDNAPEEKARGITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALEGDAEWEAKILELAGFLDSYIPEPER

>d1efm\_1 c.37.1.8 (12-190) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}

VNVGTIGHVDHGKTTLTAAITTVLAKTYGGAARXXXXXXXXXXXXXXGITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALEGDAEWEAKILE

>d1etu\_1 c.37.1.8 (5-200) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}

FERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGAAXXXXXXXXXXXXXXXGITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALEGDAEWEAKILELAGFLDSYIP

>d1exma3 c.37.1.8 (A:3-212) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Thermus thermophilus}

GEFIRTKPHVNVGTIGHVDHGKTTLTAALTFVTAAENPNVEVKDYGDIDKAPEERARGITINTAHVEYETAKRHYSHVDCPGHADYIKNMITGAAQMDGAILVVSAADGPMPQTREHILLARQVGVPYIVVFMNKVDMVDDPELLDLVEMEVRDLLNQYEFPGDEVPVIRGSALLALEQMHRNPKTRRGENEWVDKIWELLDAIDEYIPT

>d1d2ea3 c.37.1.8 (A:55-250) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Cow (Bos taurus), mitochondrial}

KPHVNVGTIGHVDHGKTTLTAAITKILAEGGGAKFKKYEEIDNAPEERARGITINAAHVEYSTAARHYAHTDCPGHADYVKNMITGTAPLDGCILVVAANDGPMPQTREHLLLARQIGVEHVVVYVNKADAVQDSEMVELVELEIRELLTEFGYKGEETPIIVGSALCALEQRDPELGLKSVQKLLDAVDTYIPVP

>d1f60a3 c.37.1.8 (A:2-240) Elongation factor eEF-1alpha, N-terminal (G) domain {Baker's yeast (Saccharomyces cerevisiae)}

GKEKSHINVVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVLDKLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGVGEFEAGISKDGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETSNFIKKVGYNPKTVPFVPISGWNGDNMIEATTNAPWYKGWEKETKAGVVKGKTLLEAIDAIEQPSRPT

>d1jnya3 c.37.1.8 (A:4-227) Elongation factor eEF-1alpha, N-terminal (G) domain {Archaeon Sulfolobus solfataricus}

KPHLNLIVIGHVDHGKSTLVGRLLMDRGFIDEKTVKEAEEAAKKLGKESEKFAFLLDRLKEERERGVTINLTFMRFETKKYFFTIIDAPGHRDFVKNMITGASQADAAILVVSAKKGEYEAGMSVEGQTREHIILAKTMGLDQLIVAVNKMDLTEPPYDEKRYKEIVDQVSKFMRSYGFNTNKVRFVPVVAPSGDNITHKSENMKWYNGPTLEEYLDQLELPPK

>d1dar\_2 c.37.1.8 (1-282) Elongation factor G (EF-G), N-terminal (G) domain {Thermus thermophilus}

MAVKVEYDLKRLRNIGIAAHIDAGKTTTTERILYYTGRIHKIGEVHEGAATMDFMEQERERGITITAAVTTCFWKDHRINIIDTPGHVDFTIEVERSMRVLDGAIVVFDSSQGVEPQSETVWRQAEKYKVPRIAFANKMDKTGADLWLVIRTMQERLGARPVVMQLPIGREDTFSGIIDVLRMKAYTYGNDLGTDIREIPIPEEYLDQAREYHEKLVEVAADFDENIMLKYLEGEEPTEEELVAAIRKGTIDLKITPVFLGSALKNKGVQLLLDAVVDYLPS

>d1g7sa4 c.37.1.8 (A:1-227) Initiation factor IF2/eIF5b, N-terminal (G) domain {Archaeon Methanobacterium thermoautotrophicum}

MKIRSPIVSVLGHVDHGKTTLLDHIRGSAVASREAGGITQHIGATEIPMDVIEGICGDFLKKFSIRETLPGLFFIDTPGHEAFTTLRKRGGALADLAILIVDINEGFKPQTQEALNILRMYRTPFVVAANKIDRIHGWRVHEGRPFMETFSKQDIQVQQKLDTKVYELVGKLHEEGFESERFDRVTDFASQVSIIPISAITGEGIPELLTMLMGLAQQYLREQLKIE

>d1egaa1 c.37.1.8 (A:4-182) GTPase Era, N-terminal domain {Escherichia coli}

DKSYCGFIAIVGRPNVGKSTLLNKLLGQKISITSRKAQTTRHRIVGIHTEGAYQAIYVDTPGLHMEEKRAINRLMNKAASSSIGDVELVIFVVEGTRWTPDDEMVLNKLREGKAPVILAVNKVDNVQEKADLLPHLQFLASQMNFLDIVPISAETGLNVDTIAAIVRKHLPEATHHFPE

>d1f5na2 c.37.1.8 (A:7-283) Interferon-induced guanylate-binding protein 1 (GBP1), N-terminal domain {Human (Homo sapiens)}

MTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLAGKKKGFSLGSTVQSHTKGIWMWCVPHPKKPGHILVLLDTEGLGDVEKGDNQNDSWIFALAVLLSSTFVYNSIGTINQQAMDQLYYVTELTHRIRSKSSPDENENEVEDSADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLTYSLKLKKGTSQKDETFNLPRLCIRKFFPKKKCFVFDRPVHRRKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLS

>d1jwyb\_ c.37.1.8 (B:) Dynamin G domain {Slime mold (Dictyostelium discoideum)}

DQLIPVINKLQDVFNTLGSDPLDLPQIVVVGSQSSGKSSVLENIVGRDFLPRGSGIVTRRPLILQLTHLPIADDGSQTQEWGEFLHKPNDMFYDFSEIREEIIRDTDRMTGKNKGISAQPINLKIYSPHVVNLTLVDLPGITKVPVGDQPTDIEQQIRRMVMAYIKKQNAIIVAVTPANTDLANSDALQLAKEVDPEGKRTIGVITKLDLMDKGTDAMEVLTGRVIPLTLGFIGVINRSQEDIIAKKSIRESLKSEILYFKNHPIYKSIANRSGTAYLSKTLNKLLMFHIRDTLPDLKVKVSKMLS

>d1br2a2 c.37.1.9 (A:80-789) Myosin S1, motor domain {Chicken (Gallus gallus), pectoral muscle}

PPKFSKVEDMAELTCLNEASVLHNLRERYFSGLIYTYSGLFCVVINPYKQLPIYSEKIIDMYKGKKRHEMPPHIYAIADTAYRSMLQDREDQSILCTGESGAGKTENTKKVIQYLAVVASSHKGKKDTSITQGPSFSYGELEKQLLQANPILEAFGNAKTVKNDNSSRFGKFIRINFDVTGYIVGANIETYLLEKSRAIRQAKDERTFHIFYYLIAGASEQMRNDLLLEGFNNYTFLSNGHVPIPAQQDDEMFQETLEAMTIMGFTEEEQTSILRVVSSVLQLGNIVFKKERNTDQASMPDNTAAQKVCHLMGINVTDFTRSILTPRIKVGRDVVQKAQTKEQADFAIEALAKAKFERLFRWILTRVNKALDKTKRQGASFLGILDIAGFEIFEINSFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGLDLQPCIELIERPTNPPGVLALLDEECWFPKATDTSFVEKLIQEQGNHAKFQKSKQLKDKTEFCILHYAGKVTYNASAWLTKNMDPLNDNVTSLLNQSSDKFVADLWKDVDRIVGLDQMAKMTESSLPSASKTKKGMFRTVGQLYKEQLTKLMTTLRNTNPNFVRCIIPNHEKRAGKLDAHLVLEQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILAANAIPKGFMDGKQACILMIKALELDPNLYRIGQSKIFFRTGVLAHLEEERD

>d2mysa2 c.37.1.9 (A:4-33,A:80-843) Myosin S1, motor domain {Chicken (Gallus gallus), pectoral muscle}

DAEMAAFGEAAPYLRKSEKERIEAQNKPFDXMNPPKYDKIEDMAMMTHLHEPAVLYNLKERYAAWMIYTYSGLFCVTVNPYKWLPVYNPKVVLAYRGKKRQEAPPHIFSISDNAYQFMLTDRENQSILITGESGAGKTVNTKRVIQYFATIAASGEKKKEEQSGKMQGTLEDQIISANPLLEAFGNAKTVRNDNSSRFGKFIRIHFGATGKLASADIETYLLEKSRVTFQLPAERSYHIFYQIMSNKKPELIDMLLITTNPYDYHYVSEGEITVPSIDDQEELMATDSAIDILGFSADEKTAIYKLTGAVMHYGNLKFKQKQREEQAEPDGTEVADKAAYLMGLNSAELLKALCYPRVGVGNEAVTKGETVSEVHNSVGALAKAVYEKMFLWMVIRINQQLDTKQPRQYFIGVLDIAGFEIFDFNSFEQLCINFTNEKLQQFFNHHMFVLEQEEYKKEGIEWEFIDFGMDLAACIELIEKPMGIFSILEEECMFPKATDTSFKNKLYDEHLGKSNNFQKPKPAKGKAEAHFSLVHYAGTVDYNISGWLEKNKDPLNETVIGLYQKSSVKTLALLFATYGGEAEGGGGKKGGKKKGSSFQTVSALFRENLNKLMANLRSTHPHFVRCIIPNETKTPGAMEHELVLHQLRCNGVLEGIRICRKGFPSRVLYADFKQRYRVLNASAIPEGQFMDSKKASEKLLGGGDVDHTQYAFGHTKVFFKAGLLGLLEEMRDDKLAEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNVKHWPWMKLFFKIKPLLK

>d1b7ta4 c.37.1.9 (A:5-28,A:77-835) Myosin S1, motor domain {Bay scallop (Aequipecten irradians)}

FSDPDFQYLAVDRKKLMKEQTAAFXMNPPKFEKLEDMANMTYLNEASVLYNLRSRYTSGLIYTYSGLFCIAVNPYRRLPIYTDSVIAKYRGKRKTEIPPHLFSVADNAYQNMVTDRENQSCLITGESGAGKTENTKKVIMYLAKVACAVKKKDEEASDKKEGSLEDQIIQANPVLEAYGNAKTTRNNNSSRFGKFIRIHFGPTGKIAGADIETYLLEKSRVTYQQSAERNYHIFYQICSNAIPELNDVMLVTPDSGLYSFINQGCLTVDNIDDVEEFKLCDEAFDILGFTKEEKQSMFKCTASILHMGEMKFKQRPREEQAESDGTAEAEKVAFLCGINAGDLLKALLKPKVKVGTEMVTKGQNMNQVVNSVGALAKSLYDRMFNWLVRRVNKTLDTKAKRNYYIGVLDIAGFEIFDFNSFEQLCINYTNERLQQFFNHHMFILEQEEYKKEGIAWEFIDFGMDLQMCIDLIEKPMGILSILEEECMFPKADDKSFQDKLYQNHMGKNRMFTKPGKPTRPNQGPAHFELHHYAGNVPYSITGWLEKNKDPINENVVALLGASKEPLVAELFKAPEEPAGGGKKKKGKSSAFQTISAVHRESLNKLMKNLYSTHPHFVRCIIPNELKQPGLVDAELVLHQLQCNGVLEGIRICRKGFPSRLIYSEFKQRYSILAPNAIPQGFVDGKTVSEKILAGLQMDPAEYRLGTTKVFFKAGVLGNLEEMRDERLSKIISMFQAHIRGYLIRKAYKKLQDQRIGLSVIQRNIRKWLVLRNWQWWKLYSKVKP

>d1lvk\_2 c.37.1.9 (2-33,80-759) Myosin S1, motor domain {Slime mold (Dictyostelium discoideum)}

NPIHDRTSDYHKYLKVKQGDSDLFKLTVSDKRXRNPIKFDGVEDMSELSYLNEPAVFHNLRVRYNQDLIYTYSGLFLVAVNPFKRIPIYTQEMVDIFKGRRRNEVAPHIFAISDVAYRSMLDDRQNQSLLITGESGAGKTENTKKVIQYLASVAGRNQANGSGVLEQQILQANPILEAFGNAKTTRNNNSSRFGKFIEIQFNNAGFISGASIQSYLLEKSRVVFQSTSERNYHIFYQLLAGATAEEKKALHLAGPESFNYLNQSGCVDIKGVSDEDEFKITRQAMDIVGFSQEEQMSIFKIIAGILHLGNIKFEKGAGEGAVLKDKTALNAASTVFGVNPSVLEKALMEPRILAGRDLVAQHLNVEKSSSSRDALVKALYGRLFLWLVKKINNVLCSERKAYFIGVLDISGFEIFKVNSFEQLCINYTNEKLQQFFNHHMFKVEQEKYLKEKINWTFIDFGLDSQATIDLIDGRQPPGILALLDEQSVFPNATDNTLITKLHSHFSKKNAKYEEPRFSKTEFGVTHYAGQVMYEIQDWLEKNKDPLQQDLELCFKDSSDNVVTKLFNDPNIASRAKKGANFLTVAAQYKEQLASLMATLETTNPHFVRCIIPNNKQLPAKLEDKVVLDQLRCNGVLEGIRITRKGFPNRIIYADFVKRYYDLAPNVPRDAEDSQKATDAVLKHLNIDPEQFRFGITKIFFRAGQLARIEEARE

>d1mnd\_2 c.37.1.9 (2-33,80-690) Myosin S1, motor domain {Slime mold (Dictyostelium discoideum)}

NPIHDRTSDYHKYLKVKQGDSDLFKLTVSDKRXRNPIKFDGVEDMSELSYLNEPAVFHNLRVRYNQDLIYTYSGLFLVAVNPFKRIPIYTQEMVDIFKGRRRNEVAPHIFAISDVAYRSMLDDRQNQSLLITGESGAGKTENTKKVIQYLASVAGRNQANGSGVLEQQILQANPILEAFGNAKTTRNNNSSRFGKFIEIQFNNAGFISGASIQSYLLEKSRVVFQSETERNYHIFYQLLAGATAEEKKALHLAGPESFNYLNQSGCVDIKGVSDEDEFKITRQAMDIVGFSQEEQMSIFKIIAGILHLGNIKFEKGAGEGAVLKDKTALNAASTVFGVNPSVLEKALMEPRILAGRDLVAQHLNVEKSSSSRDALVKALYGRLFLWLVKKINNVLCSERAAYFIGVLDISGFEIFKVNSFEQLCINYTNEKLQQFFNHHMFKVEQEEYLKEKINWTFIDFGLDSQATIDLIDGRQPPGILALLDEQSVFPNATDNTLITKLHSHFSKKNAKYEEPRFSKTEFGVTHYAGQVMYEIQDWLEKNKDPLQQDLELCFKDSSDNVVTKLFNDPNIASRAKKGANFITVAAQYKEQLASLMATLETTNPHFVRCIIPNNKQLPAKLEDKVVLDQLRCNGVLEGIRITRK

>d1bg2\_\_ c.37.1.9 (-) Kinesin {Human (Homo sapiens)}

DLAECNIKVMCRFRPLNESEVNRGDKYIAKFQGEDTVVIASKPYAFDRVFQSSTSQEQVYNDCAKKIVKDVLEGYNGTIFAYGQTSSGKTHTMEGKLHDPEGMGIIPRIVQDIFNYIYSMDENLEFHIKVSYFEIYLDKIRDLLDVSKTNLSVHEDKNRVPYVKGCTERFVCSPDEVMDTIDEGKSNRHVAVTNMNEHSSRSHSIFLINVKQENTQTEQKLSGKLYLVDLAGSEKVSKTGAEGAVLDEAKNINKSLSALGNVISALAEGSTYVPYRDSKMTRILQDSLGGNCRTTIVICCSPSSYNESETKSTLLFGQRAKTI

>g2kin.1 c.37.1.9 (A:,B:) Kinesin {Rat (Rattus norvegicus)}

ADPAECSIKVMCRFRPLNEAEILRGDKFIPKFKGEETVVIGQGKPYVFDRVLPPNTTQEQVYNACAKQIVKDVLEGYNGTIFAYGQTSSGKTHTMEGKLHDPQLMGIIPRIAHDIFDHIYSMDENLEFHIKVSYFEIYLDKIRDLLDVSKTNLAVHEDKNRVPYVKGCTERFVSSPEEVMDVIDEGKANRHVAVTNMNEHSSRSHSIFLINIKQENVETEKKLSGKLYLVDLAGSEKVXAKNINKSLSALGNVISALAEGTKTHVPYRDSKMTRILQDSLDGNCRTTIVICCSPSVFNEAETKSTLMFGQRAKTIKNTVSVNLELTAEEWKKKYEKEKE

>d1i6ia\_ c.37.1.9 (A:) Kinesin {Mouse (Mus musculus), kif1a}

GASVKVAVRVRPFNSREMSRDSKCIIQMSGSTTTIVNPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDLFSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLRVREHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKKKTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADRAKQIRNTVSVNHHHHH

>d1ii6a\_ c.37.1.9 (A:) Kinesin {Human (Homo sapiens), mitotic kinesin eg5}

GKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRKTYTFDMVFGASTKQIDVYRSVVCPILDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEEDPLAGIIPRTLHQIFEKLTDNGTEFSVKVSLLEIYNEELFDLLNPSSDVSERLQMFDDPRNKRGVIIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFSVTIHMKETTIDGEELVKIGKLNLVDLAGSENIGRSGAVDKRAREAGNINQSLLTLGRVITALVERTPHVPYRESKLTRILQDSLGGRTRTSIIATISPASLNLEETLSTLEYAHRAKNILNKPEV

>d1goja\_ c.37.1.9 (A:) Kinesin {Neurospora crassa}

SSSANSIKVVARFRPQNRVEIESGGQPIVTFQGPDTCTVDSKEAQGSFTFDRVFDMSCKQSDIFDFSIKPTVDDILNGYNGTVFAYGQTGAGKSYTMMGTSIDDPDGRGVIPRIVEQIFTSILSSAANIEYTVRVSYMEIYMERIRDLLAPQNDNLPVHEEKNRGVYVKGLLEIYVSSVQEVYEVMRRGGNARAVAATNMNQESSRSHSIFVITITQKNVETGSAKSGQLFLVDLAGSEKVGKTGASGQTLEEAKKINKSLSALGMVINALTDGKSSHVPYRDSKLTRILQESLGGNSRTTLIINCSPSSYNDAETLSTLRFGMRAKSIKNKAKVNAELSPAELKQMLAKAKTQ

>d2ncda\_ c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional) {Fruit fly (Drosophila melanogaster)}

LRQRTEELLRCNEQQAAELETCKEQLFQSNMERKELHNTVMDLRGNIRVFCRIRPPLESEENRMCCTWTYHDESTVELQSIDAQAKSKMGQQIFSFDQVFHPLSSQSDIFEMVSPLIQSALDGYNICIFAYGQTGSGKTYTMDGVPESVGVIPRTVDLLFDSIRGYRNLGWEYEIKATFLEIYNEVLYDLLSNEQKDMEIRMAKNNKNDIYVSNITEETVLDPNHLRHLMHTAKMNRATASTAGNERSSRSHAVTKLELIGRHAEKQEISVGSINLVDLAGSESPKTSTRMTETKNINRSLSELTNVILALLQKQDHIPYRNSKLTHLLMPSLGGNSKTLMFINVSPFQDCFQESVKSLRFAASVNSC

>d1f9va\_ c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional) {Baker's yeast (Saccharomyces cerevisiae), Kar}

GNIRVYCRIRPALKNLENSDTSLINVNEFDDNSGVQSMEVTKIQNTAQVHEFKFDKIFDQQDTNVDVFKEVGQLVQSSLDGYNVCIFAYGQTGSGKTFTMLNPGDGIIPSTISHIFNWINKLKTKGWDYKVNCEFIEIYNENIVDLLRSDNNNKEDTSIGLKHEIRHDQETKTTTITNVTSCKLESEEMVEIILKKANKLRSTASTASNEHSSASHSIFIIHLSGSNAKTGAHSYGTLNLVDLAGSERINVSQVVGDRLRETQNINKSLSCLGDVIHALGQPDSTKRHIPFRNSKLTYLLQYSLTGDSKTLMFVNISPSSSHINETLNSLRFASKVNSTRLV

>d1byi\_\_ c.37.1.10 (-) Dethiobiotin synthetase {Escherichia coli}

SKRYFVTGTDTEVGKTVASCALLQAAKAAGYRTAGYKPVASGSEKTPEGLRNSDALALQRNSSLQLDYATVNPYTFAEPTSPHIISAQEGRPIESLVMSAGLRALEQQADWVLVEGAGGWFTPLSDTFTFADWVTQEQLPVILVVGVKLGCINHAMLTAQVIQHAGLTLAGWVANDVTPPGKRHAEYMTTLTRMIPAPLLGEIPWLAENPENAATGKYINLALL

>d1qf5a\_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Escherichia coli}

GNNVVVLGTQWGDEGKGKIVDLLTERAKYVVRYQGGHNAGHTLVINGEKTVLHLIPSGILRENVTSIIGNGVVLSPAALMKEMKELEDRGIPVRERLLLSEACPLILDYHVALDNAREKARGAKAIGTTGRGIGPAYEDKVARRGLRVGDLFDKETFAEKLKEVMEYHNFQLVNYYKAEAVDYQKVLDDTMAVADILTSMVVDVSDLLDQARQRGDFVMFEGAQGTLLDIDHGTYPYVTSSNTTAGGVATGSGLGPRYVDYVLGILKAYSTRVGAGPFPTELFDETGEFLCKQGNEFGATTGRRRRTGWLDTVAVRRAVQLNSLSGFCLTKLDVLDGLKEVKLCVAYRMPDGREVTTTPLAADDWKGVEPIYETMPGWSESTFGVKDRSGLPQAALNYIKRIEELTGVPIDIISTGPDRTETMILRDPFDA

>d1dj2a\_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Mouse-ear cress (Arabidopsis thaliana)}

IGSLSQVSGVLGCQWGDEGKGKLVDILAQHFDIVARCQGGANAGHTIYNSEGKKFALHLVPSGILNEDTTCVIGNGVVVHLPGLFKEIDGLESNGVSCKGRILVSDRAHLLFDFHQEVDGLRESELAKSFIGTTKRGIGPAYSSKVIRNGIRVGDLRHMDTLPQKLDLLLSDAAARFQGFKYTPEMLREEVEAYKRYADRLEPYITDTVHFINDSISQKKKVLVEGGQATMLDIDFGTYPFVTSSSPSAGGICTGLGIAPSVVGDLIGVVKAYTTRVGSGPFPTENLGTGGDLLRLAGQEFGTTTGRPRRCGWLDIVALKFSCQINGFASLNLTKLDVLSDLNEIQLGVAYKRSDGTPVKSFPGDLRLLEELHVEYEVLPGWKSDISSVRNYSDLPKAAQQYVERIEELVGVPIHYIGIGPGRDALIYK

>d1dj3a\_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Bread wheat (Triticum aestivum)}

ADRVSSLSNVSGVLGSQWGDEGKGKLVDVLAPRFDIVARCQGGANAGHTIYNSEGKKFALHLVPSGILHEGTLCVVGNGAVIHVPGFFGEIDGLQSNGVSCDGRILVSDRAHLLFDLHQTVDGLREAELANSFIGTTKRGIGPCYSSKVTRNGLRVCDLRHMDTFGDKLDVLFEDAAARFEGFKYSKGMLKEEVERYKKFAERLEPFIADTVHVLNESIRQKKKILVEGGQATMLDIDFGTYPFVTSSSPSAGGICTGLGIAPRVIGDLIGVVKAYTTRVGSGPFPTELLGEEGDVLRKAGMEFGTTTGRPRRCGWLDIVALKYCCDINGFSSLNLTKLDVLSGLPEIKLGVSYNQMDGEKLQSFPGDLDTLEQVQVNYEVLPGWDSDISSVRSYSELPQAARRYVERIEELAGVPVHYIGVGPGRDALIYK

>d1j4ba\_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Mouse (Mus musculus)}

AAATGSRVTVVLGAQWGDEGKGKVVDLLATDADIVSRCQGGNNAGHTVVVDGKEYDFHLLPSGIINTKAVSFIGNGVVIHLPGLFEEAEKNEKKGLKDWEKRLIISDRAHLVFDFHQAVDGLQEVQRQAQEGKNIGTTKKGIGPTYSSKAARTGLRICDLLSDFDEFSARFKNLAHQHQSMFPTLEIDVEGQLKRLKGFAERIRPMVRDGVYFMYEALHGPPKKVLVEGANAALLDIDFGTYPFVTSSNCTVGGVCTGLGIPPQNIGDVYGVVKAYTTRVGIGAFPTEQINEIGDLLQNRGHEWGVTTGRKRRCGWLDLMILRYAHMVNGFTALALTKLDILDVLSEIKVGISYKLNGKRIPYFPANQEILQKVEVEYETLPGWKADTTGARKWEDLPPQAQSYVRFVENHMGVAVKWVGVGKSRESMIQLF

>d1eg7a\_ c.37.1.10 (A:) Formyltetrahydrofolate synthetase {Moorella thermoacetica}

DIEIAQAAKMKPVMELARGLGIQEDEVELYGKYKAKISLDVYRRLKDKPDGKLILVTAITPTPAGEGKTTTSVGLTDALARLGKRVMVCLREPSLGPSFGIKGGAAGGGYAQVVPMEDINLHFTGDIHAVTYAHNLLAAMVDNHLQQGNVLNIDPRTITWRRVIDLNERALRNIVIGLGGKANGVPRETGFDISVASEVMACLCLASDLMDLKERFSRKVVGYTYDGKPVTAGDLEAQGSMALLMKDAIKPNLVQTLENTPAFIHGGPFANIAHGCNSIIATKTALKLADYVVTEAGFGADLGAEKFYDVKCRYAGFKPDATVIVATVRALKMHGGVPKSDLATENLEALREGFANLEKHIENIGKFGVPAVVAINAFPTDTEAELNLLYELCAKAGAEVALSWAKGGEGGLELARKVLQTLESRPSNFHVLYNLDLSIKDKIAKIATEIYGADGVNYTAEADKAIQRYESLGYGNLPVVMAKTQYSFSDDMTKLGRPRNFTITVREVRLSAGGRLIVPITGAIMTMPGLPKRPAACNIDIDADGVITG

>d1fp6a\_ c.37.1.10 (A:) Nitrogenase iron protein {Azotobacter vinelandii}

AMRQCAIYGKGGIGKSTTTQNLVAALAEMGKKVMIVGCDPKADSTRLILHSKAQNTIMEMAAEAGTVEDLELEDVLKAGYGGVKCVESGGPEPGVGCAGRGVITAINFLEEEGAYEDDLDFVFYDVLGDVVCGGFAMPIRENKAQEIYIVCSGEMMAMYAANNISKGIVKYANSGSVRLGGLICNSRNTDREDELIIALANKLGTQMIHFVPRDNVVQRAEIRRMTVIEYDPKAKQADEYRALARKVVDNKLLVIPNPITMDELEELLMEFGIMEVEDESIVGKTAEEV

>d1cp2a\_ c.37.1.10 (A:) Nitrogenase iron protein {Clostridium pasteurianum}

MRQVAIYGKGGIGKSTTTQNLTSGLHAMGKTIMVVGCDPKADSTRLLLGGLAQKSVLDTLREEGEDVELDSILKEGYGGIRCVESGGPEPGVGCAGRGIITSINMLEQLGAYTDDLDYVFYDVLGDVVCGGFAMPIREGKAQEIYIVASGEMMALYAANNISKGIQKYAKSGGVRLGGIICNSRKVANEYELLDAFAKELGSQLIHFVPRSPMVTKAEINKQTVIEYDPTCEQAEEYRELARKVDANELFVIPKPMTQERLEEILMQYG

>d1hyqa\_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon Archaeoglobus fulgidus}

VRTITVASGKGGTGKTTITANLGVALAQLGHDVTIVDADITMANLELILGMEGLPVTLQNVLAGEARIDEAIYVGPGGVKVVPAGVSLEGLRKANPEKLEDVLTQIMESTDILLLDAPAGLERSAVIAIAAAQELLLVVNPEISSITDGLKTKIVAERLGTKVLGVVVNRITTLGIEMAKNEIEAILEAKVIGLIPEDPEVRRAAAYGKPVVLRSPNSPAARAIVELANYIA

>d1g3qa\_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon Pyrococcus furiosus}

MGRIISIVSGKGGTGKTTVTANLSVALGDRGRKVLAVDGDLTMANLSLVLGVDDPDVTLHDVLAGEANVEDAIYMTQFDNVYVLPGAVDWEHVLKADPRKLPEVIKSLKDKFDFILIDCPAGLQLDAMSAMLSGEEALLVTNPEISCLTDTMKVGIVLKKAGLAILGFVLNRYGRSDRDIPPEAAEDVMEVPLLAVIPEDPAIREGTLEGIPAVKYKPESKGAKAFVKLAEEIEKLA

>d1iona\_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon Pyrococcus horikoshii}

MTRIISIVSGKGGTGKTTVTANLSVALGEMGRKVLAVDGDLTMANLSLVLGVDDVNITLHDVLAGDAKLEDAIYMTQFENVYILPGAVDWEHVIKADPRKLPEVIKSLKGKYDFILIDCPAGLQLRAMSAMLSGEEAILVTNPEISCLTDTMKVGMVLKKAGLAILGFILNRYGRSERDIPPEAAQDVMDVPLLAVIPEDPVIREGTLEGIPAVKYKPESKGAQAFIKLAEEVDKLAGIKAKI

>d1jpna2 c.37.1.10 (A:89-296) GTPase domain of the signal sequence recognition protein Ffh {Thermus aquaticus}

EARLPVLKDRNLWFLVGLQGSGKTTTAAKLALYYKGKGRRPLLVAADTQRPAAREQLRLLGEKVGVPVLEVMDGESPESIRRRVEEKARLEARDLILVDTAGRLQIDEPLMGELARLKEVLGPDEVLLVLDAMTGQEALSVARAFDEKVGVTGLVLTKLDGDARGGAALSARHVTGKPIYFAGVSEKPEGLEPFYPERLAGRILGMGD

>d1j8mf2 c.37.1.10 (F:87-297) GTPase domain of the signal sequence recognition protein Ffh {Archaeon Acidianus ambivalens}

DKEPKVIPDKIPYVIMLVGVQGTGKTTTAGKLAYFYKKKGFKVGLVGADVYRPAALEQLQQLGQQIGVPVYGEPGEKDVVGIAKRGVEKFLSEKMEIIIVDTAGRHGYGEEAALLEEMKNIYEAIKPDEVTLVIDASIGQKAYDLASKFNQASKIGTIIITKMDGTAKGGGALSAVAATGATIKFIGTGEKIDELEVFNPRRFVARLHHHH

>d1fts\_2 c.37.1.10 (285-495) GTPase domain of the signal recognition particle receptor FtsY {Escherichia coli}

PLNVEGKAPFVILMVGVNGVGKTTTIGKLARQFEQQGKSVMLAAGDTFRAAAVEQLQVWGQRNNIPVIAQHTGADSASVIFDAIQAAKARNIDVLIADTAGRLQNKSHLMEELKKIVRVMKKLDVEAPHEVMLTIDASTGQNAVSQAKLFHEAVGLTGITLTKLDGTAKGGVIFSVADQFGIPIRYIGVGERIEDLRPFKADDFIEALFAR

>d1ihua1 c.37.1.10 (A:1-296) Arsenite-translocating ATPase ArsA {Escherichia coli}

MQFLQNIPPYLFFTGKGGVGKTSISCATAIRLAEQGKRVLLVSTDPASNVGQVFSQTIGNTIQAIASVPGLSALEIDPQAAAQQYRARIVDPIKGVLPDDVVSSINEQLSGACTTEIAAFDEFTGLLTDASLLTRFDHIIFDTAPTGHTIRLLQLPGAWSSFIDSNPEGASCLGPMAGLEKQREQYAYAVEALSDPKRTRLVLVARLQKSTLQEVARTHLELAAIGLKNQYLVINGVLPKTEAANDTLAAAIWEREQEALANLPADLAGLPTDTLFLQPVNMVGVSALSRLLSTQP

>d1ihua2 c.37.1.10 (A:308-586) Arsenite-translocating ATPase ArsA {Escherichia coli}

QRPDIPSLSALVDDIARNEHGLIMLMGKGGVGKTTMAAAIAVRLADMGFDVHLTTSDPAAHLSMTLNGSLNNLQVSRIDPHEETERYRQHVLETKGKELDEAGKRLLEEDLRSPCTEEIAVFQAFSRVIREAGKRFVVMDTAPTGHTLLLLDATGAYHREIAKKMGEKGHFTTPMMLLQDPERTKVLLVTLPETTPVLEAANLQADLERAGIHPWGWIINNSLSIADTRSPLLRMRAQQELPQIESVKRQHASRVALVPVLASEPTGIDKLKQLAGHHH

>d2reb\_1 c.37.1.11 (3-268) RecA protein, ATPase-domain {Escherichia coli}

DENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDIRRIGAVKEGENVVGSETRVKVVKNKIAAPFKQAEFQILYGEGI

>d1g19a1 c.37.1.11 (A:1-269) RecA protein, ATPase-domain {Mycobacterium tuberculosis}

MTQTPDREKALELAVAQIEKSYGKGSVMRLGDEARQPISVIPTGSIALDVALGIGGLPRGRVIEIYGPESSGKTTVALHAVANAQAAGGVAAFIDAEHALDPDYAKKLGVDTDSLLVSQPDTGEQALEIADMLIRSGALDIVVIDSVAALVPRAELEGEMGDSHVGLQARLMSQALRKMTGALNNSGTTAIFINQLRDKIGVMFGSPETTTGGKALKFYASVRMDVRRVETLKDGTNAVGNRTRVKVVKNKCLAPFKQAEFDILYGKGI

>d1cr1a\_ c.37.1.11 (A:) Gene 4 protein (g4p, DNA primase), helicase domain {Bacteriophage T7}

MRERIREHLSSEESVGLLFSGCTGINDKTLGARGGEVIMVTSGSGMGKSTFVRQQALQWGTAMGKKVGLAMLEESVEETAEDLIGLHNRVRLRQSDSLKREIIENGKFDQWFDELFGNDTFHLYDSFAEAETDRLLAKLAYMRSGLGCDVIILDHISIVVSASGESDERKMIDNLMTKLKGFAKSTGVVLVVICHLKNPDKGKAHEEGRPVSITDLRGSGALRQLSDTIIALERNQQGDMPNLVLVRILKCRFTGDTGIAGYMEYNKETGWLEPSSY

>d1g8ya\_ c.37.1.11 (A:) Hexameric replicative helicase repA {Escherichia coli, plasmid rsf1010}

ATHKPINILEAFAAAPPPLDYVLPNMVAGTVGALVSPGGAGKSMLALQLAAQIAGGPDLLEVGELPTGPVIYLPAEDPPTAIHHRLHALGAHLSAEERQAVADGLLIQPLIGSLPNIMAPEWFDGLKRAAEGRRLMVLDTLRRFHIEEENASGPMAQVIGRMEAIAADTGCSIVFLHHASKGAAMMGAGDQQQASRGSSVLVDNIRWQSYLSSMTSAEAEEWGVDDDQRRFFVRFGVSKANYGAPFADRWFRRHDGGVLKPA

>d1e9ra\_ c.37.1.11 (A:) Bacterial conjugative coupling protein TrwB {Escherichia coli}

VGQGEFGGAPFKRFLRGTRIVSGGKLKRMTREKAKQVTVAGVPMPRDAEPRHLLVNGATGTGKSVLLRELAYTGLLRGDRMVIVDPNGDMLSKFGRDKDIILNPYDQRTKGWSFFNEIRNDYDWQRYALSVVPRGKTDEAEEWASYGRLLLRETAKKLALIGTPSMRELFHWTTIATFDDLRGFLEGTLAESLFAGSNEASKALTSARFVLSDKLPEHVTMPDGDFSIRSWLEDPNGGNLFITWREDMGPALRPLISAWVDVVCTSILSLPEEPKRRLWLFIDELASLEKLASLADALTKGRKAGLRVVAGLQSTSQLDDVYGVKEAQTLRASFRSLVVLGGSRTDPKTNEDMSLSLGEHEVERDRYSKNTGKHHSTGRALERVRERVVMPAEIANLPDLTAYVGFAGNRPIAKVPLEIKQFANRQPAFVEGT

>d1e79a3 c.37.1.11 (A:95-379) Central domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

VDVPVGEELLGRVVDALGNAIDGKGPIGSKARRRVGLKAPGIIPRISVREPMQTGIKAVDSLVPIGRGQRELIIGDRQTGKTSIAIDTIINQKRFNDGTDEKKKLYCIYVAIGQKRSTVAQLVKRLTDADAMKYTIVVSATASDAAPLQYLAPYSGCSMGEYFRDNGKHALIIYDDLSKQAVAYRQMSLLLRRPPGREAYPGDVFYLHSRLLERAAKMNDAFGGGSLTALPVIETQAGDVSAYIPTNVISITDGQIFLETELFYKGIRPAINVGLSVSRVGSAAQ

>d1e79d3 c.37.1.11 (D:82-357) Central domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

IRIPVGPETLGRIMNVIGEPIDERGPIKTKQFAAIHAEAPEFVEMSVEQEILVTGIKVVDLLAPYAKGGKIGLFGGAGVGKTVLIMELINNVAKAHGGYSVFAGVGERTREGNDLYHEMIESGVINLKDATSKVALVYGQMNEPPGARARVALTGLTVAEYFRDQEGQDVLLFIDNIFRFTQAGSEVSALLGRIPSAVGYQPTLATDMGTMQERITTTKKGSITSVQAIYVPADDLTDPAPATTFAHLDATTVLSRAIAELGIYPAVDPLDSTSRI

>d1skyb3 c.37.1.11 (B:96-371) Central domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

EVPVGETLIGRVVNPLGQPVDGLGPVETTETRPIESRAPGVMDRRSVHEPLQTGIKAIDALVPIGRGQRELIIGDRQTGKTSVAIDTIINQKDQNMICIYVAIGQKESTVATVVETLAKHGAPDYTIVVTASASQPAPLLFLAPYAGVAMGEYFMIMGKHVLVVIDDLSKQAAAYRQLSLLLRRPPGREAYPGDIFYLHSRLLERAAKLSDAKGGGSLTALPFVETQAGDISAYIPTNVISITDGQIFLQSDLFFSGVRPAINAGLSVSRVGGAAQ

>d1skye3 c.37.1.11 (E:83-356) Central domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

ISVPVGQVTLGRVFNVLGEPIDLEGDIPADARRDPIHRPAPKFEELATEVEILETGIKVVDLLAPYIKGGKIGLFGGAGVGKTVLIQELIHNIAQEHGGISVFAGVGERTREGNDLYHEMKDSGVISKTAMVFGQMNEPPGARMRVALTGLTMAEYFRDEQGQDGLLFIDNIFRFTQAGSEVSALLGRMPSAIGYQPTLATEMGQLQERITSTAKGSITSIQAIYVPADDYTDPAPATTFSHLDATTNLERKLAEMGIYPAVDPLVSTSRALAP

>d1fx0a3 c.37.1.11 (A:97-372) Central domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

QIPVSEAYLGRVINALAKPIDGRGEITASESRLIESPAPGIMSRRSVYEPLQTGLIAIDAMIPVGRGQRELIIGDRQTGKTAVATDTILNQQGQNVICVYVAIGQKASSVAQVVTNFQERGAMEYTIVVAETADSPATLQYLAPYTGAALAEYFMYRERHTLIIYDDLSKQAQAYRQMSLLLRRPPGREAYPGDVFYLHSRLLERAAKLSSLLGEGSMTALPIVETQAGDVSAYIPTNVISITDGQIFLSADLFNAGIRPAINVGISVSRVGSAAQ

>d1fx0b3 c.37.1.11 (B:98-377) Central domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

LSVPVGGPTLGRIFNVLGEPVDNLRPVDTRTTSPIHRSAPAFTQLDTKLSIFETGIKVVNLLAPYRRGGKIGLFGGAGVGKTVLIMELINNIAKAHGGVSVFGGVGERTREGNDLYMEMKESGVINEQNIAESKVALVYGQMNEPPGARMRVGLTALTMAEYFRDVNEQDVLLFIDNIFRFVQAGSEVSALLGRMPSAVGYQPTLSTEMGSLQERITSTKEGSITSIQAVYVPADDLTDPAPATTFAHLDATTVLSRGLAAKGIYPAVDPLDSTSTMLQP

>d1cbua\_ c.37.1.11 (A:) Adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase CobU {Salmonella typhimurium}

MILVTGGARSGKSRHAEALIGDAPQVLYIATSQILDDEMAARIQHHKDGRPAHWRTAECWRHLDTLITADLAPDDAILLECITTMVTNLLFALGGENDPEQWDYAAMERAIDDEIQILIAACQRCPAKVVLVTNEVGMGIVPENRLARHFRDIAGRVNQRLAAAADEVWLVVSGIGVKIK

>d1g5ta\_ c.37.1.11 (A:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}

ERGIIIVFTGNGKGKTTAAFGTAARAVGHGKNVGVVQFIKGTWPNGERNLLEPHGVEFQVMATGFTWETQNREADTAACMAVWQHGKRMLADPLLDMVVLDELTYMVAYDYLPLEEVISALNARPGHQTVIITGRGCHRDILDLADTVSELRPVKHA

>d1g64b\_ c.37.1.11 (B:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}

QQRQQKVKDRVDARVAQAQEERGIIIVFTGNGKGKTTAAFGTAARAVGHGKNVGVVQFIKGTWPNGERNLLEPHGVEFQVMATGFTWETQNREADTAACMAVWQHGKRMLADPLLDMVVLDELTYMVAYDYLPLEEVISALNARPGHQTVIITGRGCHRDILDLADTVSELRPVKHAFDAGVKAQMGIDY

>d1b0ua\_ c.37.1.12 (A:) ATP-binding subunit of the histidine permease {Salmonella typhimurium}

NKLHVIDLHKRYGGHEVLKGVSLQARAGDVISIIGSSGSGKSTFLRCINFLEKPSEGAIIVNGQNINLVRDKDGQLKVADKNQLRLLRTRLTMVFQHFNLWSHMTVLENVMEAPIQVLGLSKHDARERALKYLAKVGIDERAQGKYPVHLSGGQQQRVSIARALAMEPDVLLFDEPTSALDPELVGEVLRIMQQLAEEGKTMVVVTHEMGFARHVSSHVIFLHQGKIEEEGDPEQVFGNPQSPRLQQFLKGSLKKLEH

>d1g6ha\_ c.37.1.12 (A:) MJ1267 {Archaeon Methanococcus jannaschii}

TMEILRTENIVKYFGEFKALDGVSISVNKGDVTLIIGPNGSGKSTLINVITGFLKADEGRVYFENKDITNKEPAELYHYGIVRTFQTPQPLKEMTVLENLLIGEICPGESPLNSLFYKKWIPKEEEMVEKAFKILEFLKLSHLYDRKAGELSGGQMKLVEIGRALMTNPKMIVMDEPIAGVAPGLAHDIFNHVLELKAKGITFLIIEHRLDIVLNYIDHLYVMFNGQIIAEGRGEEEIKNVLSDPKVVEIYIGE

>d1f3oa\_ c.37.1.12 (A:) MJ0796 {Archaeon Methanococcus jannaschii}

MIKLKNVTKTYKMGEEIIYALKNVNLNIKEGEFVSIMGPSGSGKSTMLNIIGCLDKPTEGEVYIDNIKTNDLDDDELTKIRRDKIGFVFQQFNLIPLLTALENVELPLIFKYRGAMSGEERRKRALECLKMAELEERFANHKPNQLSGGQQQRVAIARALANNPPIILADEPTGALDSKTGEKIMQLLKKLNEEDGKTVVVVTHDINVARFGERIIYLKDGEVEREEKLRGF

>d1jj7a\_ c.37.1.12 (A:) Peptide transporter Tap1, C-terminal ABC domain {Human (Homo sapiens)}

GLLTPLHLEGLVQFQDVSFAYPNRPDVLVLQGLTFTLRPGEVTALVGPNGSGKSTVAALLQNLYQPTGGQLLLDGKPLPQYEHRYLHRQVAAVGQEPQVFGRSLQENIAYGLTQKPTMEEITAAAVKSGAHSFISGLPQGYDTEVDEAGSQLSGGQRQAVALARALIRKPCVLILDDATSALDANSQLQVEQLLYESPERYSRSVLLITQHLSLVEQADHILFLEGGAIREGGTHQQLMEKKGCYWAMVQA

>d1g2912 c.37.1.12 (1:1-240) Maltose transport protein MalK, N-terminal domain {Archaeon Thermococcus litoralis}

MAGVRLVDVWKVFGEVTAVREMSLEVKDGEFMILLGPSGCGKTTTLRMIAGLEEPSRGQIYIGDKLVADPEKGIFVPPKDRDIAMVFQSYALYPHMTVYDNIAFPLKLRKVPRQEIDQRVREVAELLGLTELLNRKPRELSGGQRQRVALGRAIVRKPQVFLMDEPLSNLDAKLRVRMRAELKKLQRQLGVTTIYVTHDQVEAMTMGDRIAVMNRGVLQQVGSPDEVYDKPANTFVAGFI

>g1f2t.1 c.37.1.12 (A:,B:) Rad50 {Archaeon Pyrococcus furiosus}

MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFTKVGARDTYIDLIFEKDGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTEPSSKAISAFMEKLIPYNIFLNAIYIRQGQIDAILESXAREAALSKIGELASEIFAEFTEGKYSEVVVRAEENKVRLFVVWEGKERPLTFLSGGERIALGLAFRLAMSLYLAGEISLLILDEPTPYLDEERRRKLITIMERYLKKIPQVILVSHDEELKDAADHVIRISLENGSSKVEVVS

>g1ii8.1 c.37.1.12 (A:,B:) Rad50 {Archaeon Pyrococcus furiosus}

MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFTKVGARDTYIDLIFEKDGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTEPSSKAISAFMEKLIPYNIFLNAIYIRQGQIDAILESDEAREKVVREVLNLDKFETAYKKLSELKKTINNRIKEYRDILARTEXRERVKKEIKDLEKAKDFTEELIEKVKKYKALAREAALSKIGELASEIFAEFTEGKYSEVVVRAEENKVRLFVVWEGKERPLTFLSGGERIALGLAFRLAMSLYLAGEISLLILDEPTPYLDEERRRKLITIMERYLKKIPQVILVSHDEELKDAADHVIRISLENGSSKVEVVS

>d1e69a\_ c.37.1.12 (A:) Smc head domain {Thermotoga maritima}

MRLKKLYLKGFKSFGRPSLIGFSDRVTAIVGPNGSGKSNIIDAIKWVFGEQSKKELRASEKFDMIFAGSENLPPAGSAYVELVFEENGEEITVARELKRTGENTYYLNGSPVRLKDIRDRFAGTGLGVDFYSIVGQGQIDRIVNASPEELRLESSKHPTSLVPRGSYQRVNESFNRFISLLFFGGEGRLNIVSEAKSILDAGFEISIRKPGRRDQKLSLLSGGEKALVGLALLFALMEIKPSPFYVLDEVDSPLDDYNAERFKRLLKENSKHTQFIVITHNKIVMEAADLLHGVTMVNGVSAIVPVEV

>d1qhla\_ c.37.1.12 (A:) Cell division protein MukB {Escherichia coli}

RGKFRSLTLINWNGFFARTFDLDELVTTLSGGNGAGKSTTMAAFVTALIPDLTLLHFRNTTEAGATSGSRDKGLHGKLKAGVCYSMLDTINSRHQRVVVGVRLQQVAGRDRKVDIKPFAIQGLPMSVQPTQLVTETLNERQARVLPLNELKDKLEAMEGVQFKQFNSITDYHSLMFDLGIIARRLRSASDRSKFYRLIEASLYGGISSAITRSLRDYLLPEN

>d1ewqa2 c.37.1.12 (A:542-765) DNA repair protein MutS, the C-terminal domain {Thermus aquaticus}

YVRPRFGDRLQIRAGRHPVVERRTEFVPNDLEMAHELVLITGPNMAGKSTFLRQTALIALLAQVGSFVPAEEAHLPLFDGIYTRIGASDDLAGGKSTFMVEMEEVALILKEATENSLVLLDEVGRGTSSLDGVAIATAVAEALHERRAYTLFATHYFELTALGLPRLKNLHVAAREEAGGLVFYHQVLPGPASKSYGVEVAAMAGLPKEVVARARALLQAMAAR

>d1e3ma2 c.37.1.12 (A:567-800) DNA repair protein MutS, the C-terminal domain {Escherichia coli}

YTCPTFIDKPGIRITEGRHPVVEQVLNEPFIANPLNLSPQRRMLIITGPNMGGKSTYMRQTALIALMAYIGSYVPAQKVEIGPIDRIFTRVGAADDLASGRSTFMVEMTETANILHNATEYSLVLMDEIGRGTSTYDGLSLAWACAENLANKIKALTLFATHYFELTQLPEKMEGVANVHLDALEHGDTIAFMHSVQDGAASKSYGLAVAALAGVPKEVIKRARQKLRELESIS

>d1pjr\_1 c.37.1.13 (1-318) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}

MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFTNKAAREMRERVQSLLGGAAEDVWISTFHSMCVRILRRDIDRIGINRNFSILDPTDQLSVMKTILKEKNIDPKKFEPRTILGTISAAKNELLPPEQFAKRASTYYEKVVSDVYQEYQQRLLRNHSLDFDDLIMTTIQLFDRVPDVLHYYQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNICAVGDADQSIYRWRGADIQNILSFERDYPNAKVILLEQNYRSTKRILQAANEVIEHNVNRKPKRIWTENPEG

>d1pjr\_2 c.37.1.13 (319-651) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}

KPILYYEAMNEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANIPYQIVGGLKFYDRKEIKDILAYLRVIANPDDDLSLLRIINVPKRGIGASTIDKLVRYAADHELSLFEALGELEMIGLGAKAAGALAAFRSQLEQWTQLQEYVSVTELVEEVLDKSGYREMLKAERTIEAQSRLENLDEFLSVTKHFENVSDDKSLIAFLTDLALISDLDELDGTEQAAEGDAVMLMTLHAAKGLEFPVVFLIGMEEGIFPHNRSLEDDDEMEEERRLAYVGITRAEEELVLTSAQMRTLFGNIQMDPPSRFLNEIPAHLLETASR

>g1qhh.1 c.37.1.13 (A:,B:,C:,D:) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}

MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFTNKAAREMRERVQSLLGGAAEDVWISTFHSMCVRILRRDIDRIGINRNFSILDPTDQLSVMKTILKEKNIDPKKFEPRTILGTISAAKNELLPPEQFAKRXYYEKVVSDVYQEYQQRLLRNHSLDFDDLIMTTIQLFDRVPDVLHYYQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNICAVGDADQSIYRWRGADIQNILSFERDYPNAKVILLEQNYRSTKRILQAANEVIEHNVNRKPKRIWTENPEGKPILYYEAMNEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANIPYQIVGGLKFYDRKEIKDILAYLRVIANPDDDLSLLRIINVPKRGIGASTIDXLFEALGELEMIGLGAKAAGALAAFRSQLEQWTQLQEYVSVTELVEEVLDKSGYREMLKAERTIEAQSRLENLDEFLSVTKHFENVSDDKSLIAFLTDLALISXGDAVMLMTLHAAKGLEFPVVFLIGMEEGIFPHNRSLEDDDEMEEERRLAYVGITRAEEELVLTSAQMRTLFGNIQMDPPSRFLNEIPAHLLETASR

>d1uaaa1 c.37.1.13 (A:2-307) DEXX box DNA helicase {Escherichia coli, RepD}

RLNPGQQQAVEFVTGPCLVLAGAGSGKTRVITNKIAHLIRGCGYQARHIAAVTFTNKAAREMKERVGQTLGRKEARGLMISTFHTLGLDIIKREYAALGMKANFSLFDDTDQLALLKELTEGLIEDDKVLLQQLISTISNWKNDLKTPSQAAASAIGERDRIFAHCYGLYDAHLKACNVLDFDDLILLPTLLLQANEEVRKRWQNKIRYLLVDEYQDTNTSQYELVKLLVGSRARFTVVGDDDQSIYSWRGARPQNLVLLSQDFPALKVIKLEQNYRSSGRILKAANILIANNPHVFEKRLFSELG

>d1uaaa2 c.37.1.13 (A:308-640) DEXX box DNA helicase {Escherichia coli, RepD}

YGAELKVLSANNEEHEAERVTGELIAHHFVNKTQYKDYAILYRGNHQSRVFEKFLMQNRIPYKISGGTSFFSRPEIKDLLAYLRVLTNPDDDSAFLRIVNTPKREIGPATLKKLGEWAMTRNKSMFTASFDMGLSQTLSGRGYEALTRFTHWLAEIQRLAEREPIAAVRDLIHGMDYESWLYETSPSPKAAEMRMKNVNQLFSWMTEMLEGSELDEPMTLTQVVTRFTLRDMMERGESEEELDQVQLMTLHASKGLEFPYVYMVGMEEGFLPHQSSIDEDNIDEERRLAYVGITRAQKELTFTLCKERRQYGELVRPEPSRFLLELPQDDLIW

>d1hv8a1 c.37.1.13 (A:3-210) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}

VEYMNFNELNLSDNILNAIRNKGFEKPTDIQMKVIPLFLNDEYNIVAQARTGSGKTASFAIPLIELVNENNGIEAIILTPTRELAIQVADEIESLKGNKNLKIAKIYGGKAIYPQIKALKNANIVVGTPGRILDHINRGTLNLKNVKYFILDEADEMLNMGFIKDVEKILNACNKDKRILLFSATMPREILNLAKKYMGDYSFIKAKI

>d1hv8a2 c.37.1.13 (A:211-365) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}

NANIEQSYVEVNENERFEALCRLLKNKEFYGLVFCKTKRDTKELASMLRDIGFKAGAIHGDLSQSQREKVIRLFKQKKIRILIATDVMSRGIDVNDLNCVINYHLPQNPESYMHRIGRTGRAGKKGKAISIINRREYKKLRYIERAMKLKIKKLK

>d1gm5a3 c.37.1.13 (A:286-549) RecG helicase domain {Thermotoga maritima}

ETLPERILEKRKLLGVKDAYYGMHFPKTFYHLEKARERLAYEELFVLQLAFQKIRKEREKHGGIPKKIEGKLAEEFIKSLPFKLTNAQKRAHQEIRNDMISEKPMNRLLQGDVGSGKTVVAQLAILDNYEAGFQTAFMVPTSILAIQHYRRTVESFSKFNIHVALLIGATTPSEKEKIKSGLRNGQIDVVIGTHALIQEDVHFKNLGLVIIDEQHRFGVKQREALMNKGKMVDTLVMSATPIPRSMALAFYGDLDVTVIDEMPP

>d1gm5a4 c.37.1.13 (A:550-755) RecG helicase domain {Thermotoga maritima}

GRKEVQTMLVPMDRVNEVYEFVRQEVMRGGQAFIVYPLIEESDKLNVKSAVEMYEYLSKEVFPEFKLGLMHGRLSQEEKDRVMLEFAEGRYDILVSTTVIEVGIDVPRANVMVIENPERFGLAQLHQLRGRVGRGGQEAYCFLVVGDVGEEAMERLRFFTLNTDGFKIAEYDLKTRGPGEFFGVKQHGLSGFKVADLYRDLKLLEW

>d1fuka\_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IKQFYVNVEEEEYKYECLTDLYDSISVTQAVIFCNTRRKVEELTTKLRNDKFTVSAIYSDLPQQERDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYDLPANKENYIHRIGRGGRFGRKGVAINFVTNEDVGAMRELEKFYSTQIEELPSDIATLLN

>d1qdea\_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IQTNYDKVVYKFDDMELDENLLRGVFGYGFEEPSAIQQRAIMPIIEGHDVLAQAQSGTGKTGTFSIAALQRIDTSVKAPQALMLAPTRELALQIQKVVMALAFHMDIKVHACIGGTSFVEDAEGLRDAQIVVGTPGRVFDNIQRRRFRTDKIKMFILDEADEMLSSGFKEQIYQIFTLLPPTTQVVLLSATMPNDVLEVTTKFMRNPVRILV

>d1c4oa1 c.37.1.13 (A:2-409) Nucleotide excision repair enzyme UvrB {Thermus thermophilus}

TFRYRGPSPKGDQPKAIAGLVEALRDGERFVTLLGATGTGKTVTMAKVIEALGRPALVLAPNKILAAQLAAEFRELFPENAVEYFISYYDYYQPEAYVPGKDLYIEKDASINPEIERLRHSTTRSLLTRRDVIVVASVSAIYGLGDPREYRARNLVVERGKPYPREVLLERLLELGYQRNDIDLSPGRFRAKGEVLEIFPAYETEPIRVELFGDEVERISQVHPVTGERLRELPGFVLFPATHYLSPEGLEEILKEIEKELWERVRYFEERGEVLYAQRLKERTLYDLEMLRVMGTCPGVENYARYFTGKAPGEPPYTLLDYFPEDFLVFLDESHVTVPQLQGMYRGDYARKKTLVDYGFRLPSALDNRPLRFEEFLERVSQVVFVSATPGPFELAHSGRVVEQIIRP

>d1c4oa2 c.37.1.13 (A:410-583) Nucleotide excision repair enzyme UvrB {Thermus thermophilus}

TGLLDPLVRVKPTENQILDLMEGIRERAARGERTLVTVLTVRMAEELTSFLVEHGIRARYLHHELDAFKRQALIRDLRLGHYDCLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRAARNARGEVWLYADRVSEAMQRAIEETNRRRALQEAYNLEHGITPETV

>d1d9xa1 c.37.1.13 (A:2-414) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}

EGRFQLVAPYEPQGDQPQAIAKLVDGLRRGVKHQTLLGATGTGKTFTISNVIAQVNKPTLVIAHNKTLAGQLYSELKEFFPHNAVEYFVSYYDYYQPEAYVPQTDTYIEKDAKINDEIDKLRHSATSALFERRDVIIVASVSCIYGLGSPEEYRELVVSLRVGMEIERNALLRRLVDIQYDRNDIDFRGTFRVRGDVVEIFPASRDEHCIRVEFFGDEIERIRAEVDALTGKVLGEREHVAIFPASHFVTREEKMRLAIQNIEQELEERLAELRAQGKLLEAQRLEQRTRYDLEMMREMGFCSGIENYSRHLALRPPGSTPYTLLDYFPDDFLIIVDESHVTLPQLRGMYNGDRARKQVLVDHGFRLPSALDNRPLTFEEFEQKINQIIYVSATPGPYELEHSPGVVEQIIRP

>d1d9xa2 c.37.1.13 (A:415-595) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}

TGLLDPTIDVRPTKGQIDDLIGEIRERVERNERTLVTTLTKKMAEDLTDYLKEAGIKVAYLHSEIKTLERIEIIRDLRLGKYDVLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRAARNANGHVIMYADTITKSMEIAIQETKRRRAIQEEYNRKHGIVPRTVKKEIRDV

>d1jr3a2 c.37.1.13 (A:3-242) gamma subunit of DNA polymerase III, N-domain {Escherichia coli}

YQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAKGLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRFKVYLIDEVHMLSRHSFNALLKTLEEPPEHVKFLLATTDPQKLPVTILSRCLQFHLKALDVEQIRHQLEHILNEEHIAHEPRALQLLARAAEGSLRDALSLTDQAIASGDGQVSTQAVSAMLG

>d1a5t\_2 c.37.1.13 (1-207) delta prime subunit of DNA polymerase III, N-domain {Escherichia coli}

MRWYPWLRPDFEKLVASYQAGRGHHALLIQALPGMGDDALIYALSRYLLCQQPQGHKSCGHCRGCQLMQAGTHPDYYTLAPEKGKNTLGVDAVREVTEKLNEHARLGGAKVVWVTDAALLTDAAANALLKTLEEPPAETWFFLATREPERLLATLRSRCRLHYLAPPPEQYAVTWLSREVTMSQDALLAALRLSAGSPGAALALFQG

>d1jqlb\_ c.37.1.13 (B:) delta subunit of DNA polymerase III, N-domain {Escherichia coli}

MIRLYPEQLRAQLNEGLRAAYLLLGNDPLLLQESQDAVRQVAAAQGFEEHHTFSIDPNTDWNAIFSLCQAMSLFASRQTLLLLLPENGPNAAINEQLLTLTGLLHDDLLLIVRGNKLSKAQENAAWFTALANRSVQVTCQ

>d1jr3d2 c.37.1.13 (D:1-211) delta subunit of DNA polymerase III, N-domain {Escherichia coli}

MIRLYPEQLRAQLNEGLRAAYLLLGNDPLLLQESQDAVRQVAAAQGFEEHHTFSIDPNTDWNAIFSLCQAMSLFASRQTLLLLLPENGPNAAINEQLLTLTGLLHDDLLLIVRGNKLSKAQENAAWFTALANRSVQVTCQTPEQAQLPRWVAARAKQLNLELDDAANQVLCYCYEGNLLALAQALERLSLLWPDGKLTLPRVEQAVNDAAH

>d1iqpa2 c.37.1.13 (A:2-232) Replication factor C {Archaeon Pyrococcus furiosus}

SEEIREVKVLEKPWVEKYRPQRLDDIVGQEHIVKRLKHYVKTGSMPHLLFAGPPGVGKTTAALALARELFGENWRHNFLELNASDERGINVIREKVKEFARTKPIGGASFKIIFLDEADALTQDAQQALRRTMEMFSSNVRFILSCNYSSKIIEPIQSRCAIFRFRPLRDEDIAKRLRYIAENEGLELTEEGLQAILYIAEGDMRRAINILQAAAALDKKITDENVFMVAS

>d1hqca2 c.37.1.13 (A:5-242) Holliday junction helicase RuvB {Thermus thermophilus}

ALRPKTLDEYIGQERLKQKLRVYLEAAKARKEPLEHLLLFGPPGLGKTTLAHVIAHELGVNLRVTSGPAIEKPGDLAAILANSLEEGDILFIDEIHRLSRQAEEHLYPAMEDFVMDIVIGQGPAARTIRLELPRFTLIGATTRPGLITAPLLSRFGIVEHLEYYTPEELAQGVMRDARLLGVRITEEAALEIGRRSRGTMRVAKRLFRRVRDFAQVAGEEVITRERALEALAALGLDE

>d1in4a2 c.37.1.13 (A:17-254) Holliday junction helicase RuvB {Thermotoga maritima}

QFLRPKSLDEFIGQENVKKKLSLALEAAKMRGEVLDHVLLAGPPGLGKTTLAHIIASELQTNIHVTSGPVLVKQGDMAAILTSLERGDVLFIDEIHRLNKAVEELLYSAIEDFQIDIMIGKGPSAKSIRIDIQPFTLVGATTRSGLLSSPLRSRFGIILELDFYTVKELKEIIKRAASLMDVEIEDAAAEMIAKRSRGTPRIAIRLTKRVRDMLTVVKADRINTDIVLKTMEVLNIDD

>d1fnna2 c.37.1.13 (A:1-276) CDC6, N-domain {Archaeon Pyrobaculum aerophilum}

AIVVDDSVFSPSYVPKRLPHREQQLQQLDILLGNWLRNPGHHYPRATLLGRPGTGKTVTLRKLWELYKDKTTARFVYINGFIYRNFTAIIGEIARSLNIPFPRRGLSRDEFLALLVEHLRERDLYMFLVLDDAFNLAPDILSTFIRLGQEADKLGAFRIALVIVGHNDAVLNNLDPSTRGIMGKYVIRFSPYTKDQIFDILLDRAKAGLAEGSYSEDILQMIADITGAQTPLDTNRGDARLAIDILYRSAYAAQQNGRKHIAPEDVRKSSKEVLFG

>d1d2na\_ c.37.1.13 (A:) Hexamerization domain of N-ethylmalemide-sensitive fusion (NSF) protein {Chinese hamster (Cricetulus griseus)}

EDYASYIMNGIIKWGDPVTRVLDDGELLVQQTKNSDRTPLVSVLLEGPPHSGKTALAAKIAEESNFPFIKICSPDKMIGFSETAKCQAMKKIFDDAYKSQLSCVVVDDIERLLDYVPIGPRFSNLVLQALLVLLKKAPPQGRKLLIIGTTSRKDVLQEMEMLNAFSTTIHVPNIATGEQLLEALELLGNFKDKERTTIAQQVKGKKVWIGIKKLLMLIEMSLQMDPEYRVRKFLALLREEGASPLD

>d1e32a2 c.37.1.13 (A:201-458) Membrane fusion atpase p97, D1 domain {Mouse (Mus musculus)}

VGYDDVGGCRKQLAQIKEMVELPLRHPALFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFFLINGPEIMSKLAGESESNLRKAFEEAEKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGLKQRAHVIVMAATNRPNSIDPALRRFGRFDREVDIGIPDATGRLEILQIHTKNMKLADDVDLEQVANETHGHVGADLAALCSEAALQAIRKKMDLIDLEDETIDAEVMNSLAVTMDDFRWALSQ

>d1g6oa\_ c.37.1.13 (A:) Hexameric traffic ATPase, HP0525 {Helicobacter pylori}

LSAEDKKFLEVERALKEAALNPLRHATEELFGDFLKMENITEICYNGNKVVWVLKNNGEWQPFDVRDRKAFSLSRLMHFARCCASFKKKTIDNYENPILSSNLANGERVQIVLSPVTVNDETISISIRIPSKTTYPHSFFEEQGFYNLLDNKEQAISAIKDGIAIGKNVIVCGGTGSGKTTYIKSIMEFIPKEERIISIEDTEEIVFKHHKNYTQLFFGGNITSADCLKSCLRMRPDRIILGELRSSEAYDFYNVLCSGHKGTLTTLHAGSSEEAFIRLANMSSSNSAARNIKFESLIEGFKDLIDMIVHINHHKQCDEFYIK

>d1ht1e\_ c.37.1.13 (E:) HslU {Escherichia coli}

HSEMTPREIVSELDKHIIGQDNAKRSVAIALRNRWRRMQLNEELRHEVTPKNILMIGPTGVGKTEIARRLAKLANAPFIKVEATKFTEVGYVGKEVDSIIRDLTDAAVKMVRVQAIEKNRYRAEELAEERILDVLIPPAKNNWGQTEQQQEPSAARQAFRKKLREGQLDDKEIEIDLAAAPMGVEIMAPPGMEEMTSQLQSMFQNLGGQKQKARKLKIKDAMKLLIEEEAAKLVNPEELKQDAIDAVEQHGIVFIDEIDKICKRGESSGPDVSREGVQRDLLPLVEGCTVSTKHGMVKTDHILFIASGAFQIAKPSDLIPELQGRLPIRVELQALTTSDFERILTEPNASITVQYKALMATEGVNIEFTDSGIKRIAEAAWQVNESTENIGARRLHTVLERLMEEISYDASDLSGQNITIDADYVSKHLDALVADEDLSRFIL

>d1g41a\_ c.37.1.13 (A:) HslU {Haemophilus influenzae}

SEMTPREIVSELDQHIIGQADAKRAVAIALRNRWRRMQLQEPLRHEVTPKNILMIGPTGVGKTEIARRLAKLANAPFIKVEATKFTEVGYVGKEVDSIIRDLTDSAMKLVRQQEIAKNRARAEDVAEERILDALLPPAKNQWGEVENHDSHSSTRQAFRKKLREGQLDDKEIEIDVSAGVSMGVEIMAPPGMEEMTNQLQSLFQNLGSDKTKKRKMKIKDALKALIDDEAAKLINPEELKQKAIDAVEQNGIVFIDEIDKICKKGEYSGADVSREGVQRDLLPLVEGSTVSTKHGMVKTDHILFIASGAFQVARPSDLIPELQGRLPIRVELTALSAADFERILTEPHASLTEQYKALMATEGVNIAFTTDAVKKIAEAAFRVNEKTENIGARRLHTVMERLMDKISFSASDMNGQTVNIDAAYVADALGEVVENEDLSRFIL

>d1g8pa\_ c.37.1.13 (A:) ATPase subunit of magnesium chelatase, BchI {Rhodobacter capsulatus}

RPVFPFSAIVGQEDMKLALLLTAVDPGIGGVLVFGDRGTGKSTAVRALAALLPEIEAVEGCPVSSPNVEMIPDWATVLSTNVIRKPTPVVDLPLGVSEDRVVGALDIERAISKGEKAFEPGLLARANRGYLYIDECNLLEDHIVDLLLDVAQSGENVVERDGLSIRHPARFVLVGSGNPEEGDLRPQLLDRFGLSVEVLSPRDVETRVEVIRRRDTYDADPKAFLEEWRPKDMDIRNQILEARERLPKVEAPNTALYDCAALCIALGSDGLRGELTLLRSARALAALEGATAVGRDHLKRVATMALSHRLRRDPLDEAGSTARVARTVEETLP

>d1a1va1 c.37.1.14 (A:190-325) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}

PPAVPQSFQVAHLHAPTGSGKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGVDPNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETAGARLVVLATATP

>d1a1va2 c.37.1.14 (A:326-624) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}

PGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHLIFCHSKKKCDELAAKLVALGINAVAYYRGLDVSVIPTSGDVVVVATDALMTGFTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCECYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLTHIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEVTLTHPITKYIMTCMS

>d1cu1a3 c.37.1.14 (A:326-631) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}

PGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIRGGRHLIFCHSKKKCDELAAKLSGLGINAVAYYRGLDVSVIPTIGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVDFSLDPTFTIETTTVPQDAVSRSQRRGRTGRGRRGIYRFVTPGERPSGMFDSSVLCECYDAGCAWYELTPAETSVRLRAYLNTPGLPVCQDHLEFWESVFTGLTHIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEVTLTHPITKYIMACMSADLEVVT

>d1gkub1 c.37.1.16 (B:1-250) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAASLCLFPEDFLLKEFVEFFRKCVGEPRAIQKMWAKRILRKESFAATAPTGVGKTSFGLAMSLFLALKGKRCYVIFPTSLLVIQAAETIRKYAEKAGVGTENLIGYYHGRIPKREKENFMQNLRNFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVDKLLHLLGFHYDLKTKSWVGEARGCLMVSTATAKKGKKAELFRQLLNFDIGSSRIT

>d1gkub2 c.37.1.16 (B:251-498) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

VRNVEDVAVNDESISTLSSILEKLGTGGIIYARTGEEAEEIYESLKNKFRIGIVTATKKGDYEKFVEGEIDHLIGTAHYYGTLVRGLDLPERIRFAVFVGCPSFRVTIEDIDSLSPQMVKLLAYLYRNVDEIERLLPAVERHIDEVREILKKVMGKERPQAKDVVVREGEVIFPDLRTYIQGSGRTSRLFAGGLTKGASFLLEDDSELLSAFIERAKLYDIEFKSIDEVDFEKLSRELDESRDRYRRR

>d1gl9b1 c.37.1.16 (B:2-250) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

IPVVYSNLCPVCGGDLESKEIEKHVCFRKKRSLCLFPEDFLLKEFVEFFRKCVGEPRAIQKMWAKRILRKESFAATAPTGVGKTSFGLAMSLFLALKGKRCYVIFPTSLLVIQAAETIRKYAEKAGVGTENLIGYYHGRIPKREKENFMQNLRNFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVDKLLHLLGFHYDLKTKSWVGEARGCLMVSTATAKKGKKAELFRQLLNFDIGSSRIT

>d1ble\_\_ c.38.1.1 (-) Fructose permease, subunit IIb {Bacillus subtilis}

MNIVLARIDDRFIHGQILTRWIKVHAADRIIVVSDDIAQDEMRKTLILSVAPSNVKASAVSVSKMAKAFHSPRYEGVTAMLLFENPSDIVSLIEAGVPIKTVNVGGMRFENHRRQITKSVSVTEQDIKAFETLSDKGVKLELRQLPSDASEDFVQILRNVT

>d1d0va\_ c.39.1.1 (A:) Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) {Salmonella typhimurium}

LHALLRDIPAPDAEAMARTQQHIDGLLKPPGSLGRLETLAVQLAGMPGLNGTPQVGEKAVLVMCADHGVWDEGVAVSPKIVTAIQAANMTRGTTGVCVLAAQAGAKVHVIDVGIDAEPIPGVVNMRVARGCGNIAVGPAMSRLQAEALLLEVSRYACDLAQRGVTLFGVGELGMANTTPAAAMVSVFTGSDAKEVVGIGANLPPSRIDNKVDVVRRAIAINQPNPRDGIDVLSKVGGFDLVGMTGVMLGAARCGLPVLLDGFLSYSAALAACQIAPAVRPYLIPSHFSAEKGARIALAHLSMEPYLHMAMRLGEGSGAALAMPIVEAACAMFHNMGELAASNIVLP

>d1chd\_\_ c.40.1.1 (-) Methylesterase CheB, C-terminal domain {Salmonella typhimurium}

LLSSEKLIAIGASTGGTEAIRHVLQPLPLSSPAVIITQHMPPGFTRSFAERLNKLCQISVKEAEDGERVLPGHAYIAPGDKHMELARSGANYQIKIHDGPPVNRHRPSVDVLFHSVAKHAGRNAVGVILTGMGNDGAAGMLAMYQAGAWTIAQNEASCVVFGMPREAINMGGVSEVVDLSQVSQQMLAKISAGQAIRI

>d1csee\_ c.41.1.1 (E:) Subtilisin {Bacillus subtilis, carlsberg}

AQTVPYGIPLIKADKVQAQGFKGANVKVAVLDTGIQASHPDLNVVGGASFVAGEAYNTDGNGHGTHVAGTVAALDNTTGVLGVAPSVSLYAVKVLNSSGSGSYSGIVSGIEWATTNGMDVINMSLGGASGSTAMKQAVDNAYARGVVVVAAAGNSGNSGSTNTIGYPAKYDSVIAVGAVDSNSNRASFSSVGAELEVMAPGAGVYSTYPTNTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNRLSSTATYLGSSFYYGKGLINVEAAAQ

>d1bh6a\_ c.41.1.1 (A:) Subtilisin {Bacillus licheniformis}

AQTVPYGIPLIKADKVQAQGYKGANVKVGIIDTGIASSHTDLKVVGGASFVSGESYNTDGNGHGTHVAGTVAALDNTTGVLGVAPNVSLYAIKVLNSSGSGSYSAIVSGIEWATQNGLDVINMSLGGPSGSTALKQAVDKAYASGIVVVAAAGNSGNSGSQNTIGYPAKYDSVIAVGAVDSNKNRASFSSVGSELEVMAPGVSVYSTYPSNTYTSLNGTSMASPHVAGAAALILSKYPTLSASQVRNRLSSTATNLGDSFYYGKGLINVEAAAQ

>d1gci\_\_ c.41.1.1 (-) Subtilisin {Bacillus lentus}

AQSVPWGISRVQAPAAHNRGLTGSGVKVAVLDTGISTHPDLNIRGGASFVPGEPSTQDGNGHGTHVAGTIAALNNSIGVLGVAPSAELYAVKVLGASGSGSVSSIAQGLEWAGNNGMHVANLSLGSPSPSATLEQAVNSATSRGVLVVAASGNSGAGSISYPARYANAMAVGATDQNNNRASFSQYGAGLDIVAPGVNVQSTYPGSTYASLNGTSMATPHVAGAAALVKQKNPSWSNVQIRNHLKNTATSLGSTNLYGSGLVNAEAATR

>d1s01\_\_ c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}

AQSVPYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLKVAGGASFVPSETPNFQDDNSHGTHVAGTVAALDNSIGVLGVAPSSALYAVKVLGDAGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVASGVVVVAAAGNEGSTGSSSTVGYPGKYPSVIAVGAVDASNQRASFSSVGPELDVMAPGVSICSTLPGNKYGAKSGTSMASPHVAGAAALILSKHPNWTNTQVRSSLQNTTTKLGDSFYYGKGLINVQAAAQ

>d1sue\_\_ c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}

AKCVSYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLNVAGGASFVPSETNPFQDNNSHGTHVAGTVLAVAPSASLYAVKVLGADGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVASGVVVVAAAGNEGTSGSSSTVGYPGKYPSVIAVGAVDSSNQRASFSSVGPELDVMAPGVSICSTLPGNKYGAKSGTSMASPHVAGAAALILSKHPNWTNTQVRSSLENTTTKLGDSFYYGKGLINVEAAAQ

>d1sup\_\_ c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}

AQSVPYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLKVAGGASMVPSETNPFQDNNSHGTHVAGTVAALNNSIGVLGVAPSASLYAVKVLGADGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVASGVVVVAAAGNEGTSGSSSTVGYPGKYPSVIAVGAVDSSNQRASFSSVGPELDVMAPGVSIQSTLPGNKYGAYNGTSMASPHVAGAAALILSKHPNWTNTQVRSSLENTTTKLGDSFYYGKGLINVQAAAQ

>d1meea\_ c.41.1.1 (A:) Messentericopeptidase {Bacillus mesentericus}

AQSVPYGISQIKAPALHSQGYTGSNVKVAVIDSGIDSSHPDLNVRGGASFVPSETNPYQDGSSHGTHVAGTIAALNNSIGVLGVAPSASLYAVKVLDSTGSGQYSWIINGIEWAISNNMDVINMSLGGPTGSTALKTVVDKAVSSGIVVAAAAGNEGSSGSTSTVGYPAKYPSTIAVGAVNSANQRASFSSAGSELDVMAPGVSIQSTLPGGTYGAYNGTSMATPHVAGAAALILSKHPTWTNAQVRDRLESTATYLGSSFYYGKGLINVQAAAQ

>d1dbia\_ c.41.1.1 (A:) Thermostable serine protease {Bacillus sp., AK.1}

WTPNDTYYQGYQYGPQNTYTDYAWDVTKGSSGQEIAVIDTGVDYTHPDLDGKVIKGYDFVDNDYDPMDLNNHGTHVAGIAAAETNNATGIAGMAPNTRILAVRALDRNGSGTLSDIADAIIYAADSGAEVINLSLGCDCHTTTLENAVNYAWNKGSVVVAAAGNNGSSTTFEPASYENVIAVGAVDQYDRLASFSNYGTWVDVVAPGVDIVSTITGNRYAYMSGTSMASPHVAGLAALLASQGRNNIEIRQAIEQTADKISGTGTYFKYGRINSYNAVTY

>d1thm\_\_ c.41.1.1 (-) Thermitase {Thermoactinomyces vulgaris}

YTPNDPYFSSRQYGPQKIQAPQAWDIAEGSGAKIAIVDTGVQSNHPDLAGKVVGGWDFVDNDSTPQNGNGHGTHCAGIAAAVTNNSTGIAGTAPKASILAVRVLDNSGSGTWTAVANGITYAADQGAKVISLSLGGTVGNSGLQQAVNYAWNKGSVVVAAAGNAGNTAPNYPAYYSNAIAVASTDQNDNKSSFSTYGSWVDVAAPGSSIYSTYPTSTYASLSGTSMATPHVAGVAGLLASQGRSASNIRAAIENTADKISGTGTYWAKGRVNAYKAVQY

>d1ic6a\_ c.41.1.1 (A:) Proteinase K {Fungus (Tritirachium album), strain limber}

AAQTNAPWGLARISSTSPGTSTYYYDESAGQGSCVYVIDTGIEASHPEFEGRAQMVKTYYYSSRDGNGHGTHCAGTVGSRTYGVAKKTQLFGVKVLDDNGSGQYSTIIAGMDFVASDKNNRNCPKGVVASLSLGGGYSSSVNSAAARLQSSGVMVAVAAGNNNADARNYSPASEPSVCTVGASDRYDRRSSFSNYGSVLDIFGPGTDILSTWIGGSTRSISGTSMATPHVAGLAAYLMTLGKTTAASACRYIADTANKGDLSNIPFGTVNLLAYNNYQA

>d1ga6a\_ c.41.1.2 (A:) Serine-carboxyl proteinase PSCP {Pseudomonas sp.}

AGTAKGHNPTEFPTIYDASSAPTAANTTVGIITIGGVSQTLQDLQQFTSANGLASVNTQTIQTGSSNGDYSDDQQGQGEWDLDSQSIVGSAGGAVQQLLFYMADQSASGNTGLTQAFNQAVSDNVAKVINVSLGWCEADANADGTLQAEDRIFATAAAQGQTFSVSSGDEGVYECNNRGYPDGSTYSVSWPASSPNVIAVGGTTLYTTSAGAYSNETVWNEGLDSNGKLWATGGGYSVYESKPSWQSVVSGTPGRRLLPDISFDAAQGTGALIYNYGQLQQIGGTSLASPIFVGLWARLQSANSNSLGFPAASFYSAISSTPSLVHDVKSGNNGYGGYGYNAGTGWDYPTGWGSLDIAKLSAYIRSNGF

>d1d3va\_ c.42.1.1 (A:) Arginase {Rat (Rattus norvegicus)}

KPIEIIGAPFSKGQPRGGVEKGPAALRKAGLVEKLKETEYNVRDHGDLAFVDVPNDSPFQIVKNPRSVGKANEQLAAVVAETQKNGTISVVLGGDHSMAIGSISGHARVHPDLCVIWVDAHTDINTPLTTSSGNLHGQPVAFLLKELKGKFPDVPGFSWVTPCISAKDIVYIGLRDVDPGEHYIIKTLGIKYFSMTEVDKLGIGKVMEETFSYLLGRKKRPIHLSFDVDGLDPVFTPATGTPVVGGLSYREGLYITEEIYKTGLLSGLDIMEVNPTLGKTPEEVTRTVNTAVALTLSCFGTKREGNHK

>d2ceva\_ c.42.1.1 (A:) Arginase {Bacillus caldovelox}

KPISIIGVPMDLGQTRRGVDMGPSAMRYAGVIERLERLHYDIEDLGDIPIGKAERLHEQGDSRLRNLKAVAEANEKLAAAVDQVVQRGRFPLVLGGDHSIAIGTLAGVAKHYERLGVIWYDAHGDVNTAETSPSGNIHGMPLAASLGFGHPALTQIGGYSPKIKPEHVVLIGVRSLDEGEKKFIREKGIKIYTMHEVDRLGMTRVMEETIAYLKERTDGVHLSLDLDGLDPSDAPGVGTPVIGGLTYRESHLAMEMLAEAQIITSAEFVEVNPILDERNKTASVAVALMGSLFGEKLM

>d1c3pa\_ c.42.1.2 (A:) HDAC homologue {Aquifex aeolicus}

KKVKLIGTLDYGKYRYPKNHPLKIPRVSLLLRFKDAMNLIDEKELIKSRPATKEELLLFHTEDYINTLMEAERCQCVPKGAREKYNIGGYENPVSYAMFTGSSLATGSTVQAIEEFLKGNVAFNPAGGMHHAFKSRANGFCYINNPAVGIEYLRKKGFKRILYIDLDAHHCDGVQEAFYDTDQVFVLSLHQSPEYAFPFEKGFLEEIGEGKGKGYNLNIPLPKGLNDNEFLFALEKSLEIVKEVFEPEVYLLQLGTDPLLEDYLSKFNLSNVAFLKAFNIVREVFGEGVYLGGGGYHPYALARAWTLIWCELSGREVPEKLNNKAKELLKSIDFEEFDDEVDRSYMLETLKDPWRGGEVRKEVKDTLEKAKA

>d1hf2a2 c.102.1.1 (A:1-99) Cell-division inhibitor MinC, N-terminal domain {Thermotoga maritima}

MVDFKMTKEGLVLLIKDYQNLEEVLNAISARITQMGGFFAKGDRISLMIENHNKHSQDIPRIVSHLRNLGLEVSQILVGSTVEGKENDLKVQSRTTVES

>d1jkea\_ c.110.1.1 (A:) D-Tyr tRNAtyr deacylase {Escherichia coli}

MIALIQRVTRASVTVEGEVTGEIGAGLLVLLGVEKDDDEQKANRLCERVLGYRIFSDAEGKMNLNVQQAGGSVLVVSQFTLAADTERGMRPSFSKGASPDRAEALYDYFVERCRQQEMNTQTGRFAADMQVSLVNDGPVTFWLQV

>d1nocb\_ c.43.1.1 (B:) Chloramphenicol acetyltransferase {Escherichia coli}

ITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAFLKTVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQG

>d3cla\_\_ c.43.1.1 (-) Chloramphenicol acetyltransferase {Escherichia coli}

MNYTKFDVKNWVRREHFEFYRHRLPCGFSLTSKIDITTLKKSLDDSAYKFYPVMIYLIAQAVNQFDELRMAIKDDELIVWDSVDPQFTVFHQETETFSALSCPYSSDIDQFMVNYLSVMERYKSDTKLFPQGVTPENHLNISALPWVNFDSFNLNVANFTDYFAPIITMAKYQQEGDRLLLPLSVQVHHAVCDGFHVARFINRLQELCNSKLK

>d1eaf\_\_ c.43.1.1 (-) Dihydrolipoamide acetyltransferase {Azotobacter vinelandii}

IPPIPPVDFAKYGEIEEVPMTRLMQIGATNLHRSWLNVPHVTQFESADITELEAFRVAQKAVAKKAGVKLTVLPLLLKACAYLLKELPDFNSSLAPSGQALIRKKYVHIGFAVDTPDGLLVPVIRNVDQKSLLQLAAEAAELAEKARSKKLGADAMQGACFTISSLGHIGGTAFTPIVNAPEVAILGVSKASMQPVWDGKAFQPRLMLPLSLSYDHRVINGAAAARFTKRLGDLLADIRAILL

>d1b5sa\_ c.43.1.1 (A:) Dihydrolipoamide acetyltransferase {Bacillus stearothermophilus}

AAAKPATTEGEFPETREKMSGIRRAIAKAMVHSKHTAPHVTLMDEADVTKLVAHRKKFKAIAAEKGIKLTFLPYVVKALVSALREYPVLNTSIDDETEEIIQKHYYNIGIAADTDRGLLVPVIKHADRKPIFALAQEINELAEKARDGKLTPGEMKGASCTITNIGSAGGQWFTPVINHPEVAILGIGRIAEKPIVRDGEIVAAPMLALSLSFDHRMIDGATAQKALNHIKRLLSDPELLLM

>d1e2o\_\_ c.43.1.1 (-) Dihydrolipoamide succinyltransferase {Escherichia coli}

ARSEKRVPMTRLRKRVAERLLEAKNSTAMLTTFNEVNMKPIMDLRKQYGEAFEKRHGIRLGFMSFYVKAVVEALKRYPEVNASIDGDDVVYHNYFDVSMAVSTPRGLVTPVLRDVDTLGMADIEKKIKELAVKGRDGKLTVEDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAVNGQVEILPMMYLALSYDHRLIDGRESVGFLVTIKELLEDPTRLLLDV

>d1phr\_\_ c.44.1.1 (-) Tyrosine phosphatase {Cow (Bos taurus)}

VTKSVLFVCLGNICRSPIAEAVFRKLVTDQNISDNWVIDSGAVSDWNVGRSPDPRAVSCLRNHGINTAHKARQVTKEDFVTFDYILCMDESNLRDLNRKSNQVKNCRAKIELLGSYDPQKQLIIEDPYYGNDADFETVYQQCVRCCRAFLEKVR

>d5pnt\_\_ c.44.1.1 (-) Tyrosine phosphatase {Human (Homo sapiens)}

AEQATKSVLFVCLGNICRSPIAEAVFRKLVTDQNISENWRVDSAATSGYEIGNPPDYRGQSCMKRHGIPMSHVARQITKEDFATFDYILCMDESNLRDLNRKSNQVKTCKAKIELLGSYDPQKQLIIEDPYYGNDSDFETVYQQCVRCCRAFLEKAH

>d1d1qa\_ c.44.1.1 (A:) Tyrosine phosphatase {Baker's yeast (Saccharomyces cerevisiae)}

IEKPKISVAFIALGNFCRSPMAEAIFKHEVEKANLENRFNKIDSFGTSNYHVGESPDHRTVSICKQHGVKINHKGKQIKTKHFDEYDYIIGMDESNINNLKKIQPEGSKAKVCLFGDWNTNDGTVQTIIEDPWYGDIQDFEYNFKQITYFSKQFLKKEL

>d1jf8a\_ c.44.1.1 (A:) Arsenate reductase ArsC {Staphylococcus aureus}

DKKTIYFISTGNSARSQMAEGWGKEILGEGWNVYSAGIETHGVNPKAIEAMKEVDIDISNHTSDLIDNDILKQSDLVVTLCSDADNNCPILPPNVKKEHWGFDDPAGKEWSEFQRVRDEIKLAIEKFKLR

>d1jl3a\_ c.44.1.1 (A:) Arsenate reductase ArsC {Bacillus subtilis}

NKIIYFLCTGNSCRSQMAEGWAKQYLGDEWKVYSAGIEAHGLNPNAVKAMKEVGIDISNQTSDIIDSDILNNADLVVTLCGDAADKCPMTPPHVKREHWGFDDPARAQGTEEEKWAFFQRVRDEIGNRLKEFAETGK

>d1iiba\_ c.44.2.1 (A:) Enzyme IIB-cellobiose {Escherichia coli}

KKHIYLFSSAGMSTSLLVSKMRAQAEKYEVPVIIEAFPETLAGEKGQNADVVLLGPQIAYMLPEIQRLLPNKPVEVIDSLLYGKVDGLGVLKAAVAAIKKAAA

>d1vhra\_ c.45.1.1 (A:) VH1-related dual-specificity phosphatase, VHR {Human (Homo sapiens)}

SVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSFMHVNTNANFYKDSGITYLGIKANDTQEFNLSAYFERAADFIDQALAQKNGRVLVHCREGYSRSPTLVIAYLMMRQKMDVKSALSIVRQNREIGPNDGFLAQLCQLNDRLAKEGKLKP

>d1mkp\_\_ c.45.1.1 (-) Mapk phosphatase Pyst1 (mkp3) {Human (Homo sapiens)}

ASFPVEILPFLYLGCAKDSTNLDVLEEFGIKYILNVTPNLPNLFENAGEFKYKQIPISDHWSQNLSQFFPEAISFIDEARGKNCGVLVHSLAGISRSVTVTVAYLMQKLNLSMNDAYDIVKMKKSNISPNFNFMGQLLDFERTL

>d1d5ra2 c.45.1.1 (A:14-187) Phoshphoinositide phosphatase Pten (Pten tumor suppressor), N-terminal domain {Human (Homo sapiens)}

RRYQEDGFDLDLTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNLCAERHYDTAKFNCRVAQYPFEDHNPPQLELIKPFCEDLDQWLSEDDNHVAAIHCKAGKGRTGVMICAYLLHRGKFLKAQEALDFYGEVRTRDKKGVTIPSQRRYVYYYSYLLKNHLD

>d1i9sa\_ c.45.1.1 (A:) mRNA capping enzyme, triphosphatase domain {Mouse (Mus musculus)}

KIPPRWLNCPRRGQPVAGRFLPLKTMLGPRYDSQVAEENRFHPSMLSNYLKSLKVKMSLLVDLTNTSRFYDRNDIEKEGIKYIKLQCKGHGECPTTENTETFIRLCERFNERSPPELIGVHCTHGFNRTGFLICAFLVEKMDWSIEAAVATFAQARPPGIYKGDYLKELFRRYGDIEEAPPPPVLPDWCFEDED

>d1fpza\_ c.45.1.1 (A:) Kinase associated phosphatase (kap) {Human (Homo sapiens)}

TPIHISWLSLSRVNCSQFLGLCALPGCKFKDVRRNVQKDTEELKSCGIQDIFVFCTRGELSKYRVPNLLDLYQQCGIITHHHPIADGGTPDIASCCEIMEELTTCLKNYRKTLIHSYGGLGRSCLVAACLLLYLSDTISPEQAIDSLRDLRGSGAIQTIKQYNYLHEFRDKLAAHL

>d1eeoa\_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), 1B}

EMEKEFEQIDKSGSWAAIYQDIRHEASDFPCRVAKLPKNKNRNRYRDVSPFDHSRIKLHQEDNDYINASLIKMEEAQRSYILTQGPLPNTCGHFWEMVWEQKSRGVVMLNRVMEKGSLKCAQYWPQKEEKEMIFEDTNLKLTLISEDIKSYYTVRQLELENLTTQETREILHFHYTTWPDFGVPESPASFLNFLFKVRESGSLSPEHGPVVVHSSAGIGRSGTFCLADTCLLLMDKRKDPSSVDIKKVLLEMRKFRMGLIQTADQLRFSYLAVIEGAKFIMGDSSVQDQWKELSHED

>d1rpma\_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), mu}

AIRVADLLQHITQMKCAEGYGFKEEYESFFEGQSAPWDSAKKDENRMKNRYGNIIAYDHSRVRLQTIEGDTNSDYINGNYIDGYHRPNHYIATQGPMQETIYDFWRMVWHENTASIIMVTNLVEVGRVKCCKYWPDDTEIYKDIKVTLIETELLAEYVIRTFAVEKRGVHEIREIRQFHFTGWPDHGVPYHATGLLGFVRQVKSKSPPSAGPLVVHCSAGAGRTGCFIVIDIMLDMAEREGVVDIYNCVRELRSRRVNMVQTEEQYVFIHDAILEACL

>d1yfoa\_ c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus)}

KYPPLPVDKLEEEINRRMADDNKLFREEFNALPACPIQATCEAASKEENKEKNRYVNILPYDHSRVHLTPVEGVPDSDYINASFINGYQEKNKFIAAQGPKEETVNDFWRMIWEQNTATIVMVTNLKERKECKCAQYWPDQGCWTYGNVRVSVEDVTVLVDYTVRKFCIQQVGDVTNRKPQRLITQFHFTSWPDFGVPFTPIGMLKFLKKVKACNPQYAGAIVVHCSAGVGRTGTFVVIDAMLDMMHSERKVDVYGFVSRIRAQRCQMVQTDMQYVFIYQALLEHYLY

>d2shpa1 c.45.1.2 (A:219-525) Tyrosine phosphatase {Human (Homo sapiens), shp-2}

TRINAAEIESRVRELSKLAETTDKVKQGFWEEFETLQQQECKLLYSRKEGQRQENKNKNRYKNILPFDHTRVVLHDGDPNEPVSDYINANIIMPEFETKCNNSKPKKSYIATQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSKCVKYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKVGQGNTERTVWQYHFRTWPDHGVPSDPGGVLDFLEEVHHKQESIMDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRSQRSGMVQTEAQYRSIYMAVQHYIETL

>d1fpra\_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), shp-1}

GFWEEFESLQKQEVKNLHQRLEGQRPENKGKNRYKNILPFDHSRVILQGRDSNIPGSDYINANYIKNQLLGPDENAKTYIASQGCLEATVNDFWQMAWQENSRVIVMTTREVEKGRNKCVPYWPEVGMQRAYGPYSVTNCGEHDTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGVPSEPGGVLSFLDQINQRQESLPHAGPIIVHSSAGIGRTGTIIVIDMLMENISTKGLDCDIDIQKTIQMVRAQRSGMVQTEAQYKFIYVAIAQFIETTKKKLEVL

>d1jlna\_ c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus), ptp-sl/br7}

GSPREKVAMEYLQSASRVLTRSQLRDVVASSHLLQSEFMEIPMNFVDPKEIDIPRHGTKNRYKTILPNPLSRVCLRPKNITDSLSTYINANYIRGYSGKEKAFIATQGPMINTVNDFWQMVWQEDSPVIVMITKLKEKNEKCVLYWPEKRGIYGKVEVLVTGVTECDNYTIRNLVLKQGSHTQHVKHYWYTSWPDHKTPDSAQPLLQLMLDVEEDRLASEGRGPVVVHCSAGIGRTGCFIATSIGCQQLKEEGVVDALSIVCQLRVDRGGMVQTSEQYEFVHHALCLFESRLSPETV

>d1ypta\_ c.45.1.2 (A:) Tyrosine phosphatase {Yersinia enterocolitica}

PEARAELSSRLTTLRNTLAPATNDPRYLQACGGEKLNRFRDIQCRRQTAVRADLNANYIQVGNTRTIACQYPLQSQLESHFRMLAENRTPVLAVLASSSEIANQRFGMPDYFRQSGTYGSITVESKMTQQVGLGDGIMADMYTLTIREAGQKTISVPVVHVGNWPDQTAVSSEVTKALASLVDQTAETKRNMYESKGSSAVADDSKLRPVIHCRAGVGRTAQLIGAMCMNDSRNSQLSVEDMVSQMRVQRNGIMVQKDEQLDVLIKLAEGQGRPLLNS

>d1g4us2 c.45.1.2 (S:297-539) SptP tyrosine phosphatase, catalytic domain {Salmonella typhimurium}

PQTMSGPTLGLARFAVSSIPINQQTQVKLSDGMPVPVNTLTFDGKPVALAGSYPKNTPDALEAHMKMLLEKECSCLVVLTSEDQMQAKQLPPYFRGSYTFGEVHTNSQKVSSASQGEAIDQYNMQLSCGEKRYTIPVLHVKNWPDHQPLPSTDQLEYLADRVKNSNQNGAPGRSSSDKHLPMIHCLGGVGRTGTMAAALVLKDNPHSNLEQVRADFRDSRNNRMLEDASQFVQLKAMQAQLLM

>d1lara1 c.45.1.2 (A:1307-1623) RPTP Lar {Human (Homo sapiens)}

MITDLADNIERLKANDGLKFSQEYESIDPGQQFTWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQNAYIATQGPLPETMGDFWRMVWEQRTATVVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLLDTVELATYTVRTFALHKSGSSEKRELRQFQFMAWPDHGVPEYPTPILAFLRRVKACNPLDAGPMVVHCSAGVGRTGCFIVIDAMLERMKHEKTVDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASS

>d1lara2 c.45.1.2 (A:1628-1876) RPTP Lar {Human (Homo sapiens)}

SRFISANLPCNKFKNRLVNIMPYELTRVCLQPIRGVEGSDYINASFLDGYRQQKAYIATQGPLAESTEDFWRMLWEHNSTIIVMLTKLREMGREKCHQYWPAERSARYQYFVVDPMAEYNMPQYILREFKVTDARDGQSRTIRQFQFTDWPEQGVPKTGEGFIDFIGQVHKTKEQFGQDGPITVHCSAGVGRTGVFITLSIVLERMRYEGVVDMFQTVKTLRTQRPAMVQTEDQYQLCYRAALEYLGSF

>d1larb1 c.45.1.2 (B:1340-1623) RPTP Lar {Human (Homo sapiens)}

TWENSNLEVNKPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQNAYIATQGPLPETMGDFWRMVWEQRTATVVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLLDTVELATYTVRTFALHKSGSSEKRELRQFQFMAWPDHGVPEYPTPILAFLRRVKACNPLDAGPMVVHCSAGVGRTGCFIVIDAMLERMKHEKTVDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLLASS

>d1c25\_\_ c.46.1.1 (-) CDC25a {Human (Homo sapiens)}

MLIGDFSKGYLFHTVAGKHQDLKYISPEIMASVLNGKFANLIKEFVIIDCRYPYEYEGGHIKGAVNLHMEEEVEDFLLKKPIVPTDGKRVIVVFHCEFSSERGPRMCRYVRERDRLGNEYPKLHYPELYVLKGGYKEFFMKCQSYCEPPSYRPMHHEDFKE

>d1qb0a\_ c.46.1.1 (A:) CDC25b {Human (Homo sapiens)}

DHRELIGDYSKAFLLQTVDGKHQDLKYISPETMVALLTGKFSNIVDKFVIVDCRYPYEYEGGHIKTAVNLPLERDAESFLLKSPIAPCSLDKRVILIFHCEFSSERGPRMCRFIRERDRAVNDYPSLYYPEMYILKGGYKEFFPQHPNFCEPQDYRPMNHEAFKDELKTFRLKTRSWA

>d1hzma\_ c.46.1.1 (A:) Erk2 binding domain of Mapk phosphatase mkp-3 {Human (Homo sapiens)}

MIDTLRPVPFASEMAISKTVAWLNEQLELGNERLLLMDCRPQELYESSHIESAINVAIPGIMLRRLQKGNLPVRALFTRGEDRDRFTRRCGTDTVVLYDESSSDWNENTGGESLLGLLLKKLKDEGCRAFYLEGGFSKFQAEFSLHCETNLDGS

>d1gmxa\_ c.46.1.3 (A:) Sulfurtransferase GlpE {Escherichia coli}

MDQFECINVADAHQKLQEKEAVLVDIRDPQSFAMGHAVQAFHLTNDTLGAFMRDNDFDTPVMVMCYHGNSSKGAAQYLLQQGYDVVYSIDGGFEAWQRQFPAEVAYGA

>d1rhs\_1 c.46.1.2 (1-149) Rhodanese {Cow (Bos taurus)}

VHQVLYRALVSTKWLAESVRAGKVGPGLRVLDASWYSPGTREARKEYLERHVPGASFFDIEECRDKASPYEVMLPSEAGFADYVGSLGISNDTHVVVYDGDDLGSFYAPRVWWMFRVFGHRTVSVLNGGFRNWLKEGHPVTSEPSRPEP

>d1rhs\_2 c.46.1.2 (150-293) Rhodanese {Cow (Bos taurus)}

AIFKATLNRSLLKTYEQVLENLESKRFQLVDSRAQGRYLGTQPEPDAVGLDSGHIRGSVNMPFMNFLTEDGFEKSPEELRAMFEAKKVDLTKPLIATCRKGVTACHIALAAYLCGKPDVAIYDGSWFEWFHRAPPETWVSQGKG

>d1e0ca1 c.46.1.2 (A:1-135) Sulfurtransferase {Azotobacter vinelandii}

MDDFASLPLVIEPADLQARLSAPELILVDLTSAARYAEGHIPGARFVDPKRTQLGQPPAPGLQPPREQLESLFGELGHRPEAVYVVYDDEGGGWAGRFIWLLDVIGQQRYHYLNGGLTAWLAEDRPLSRELPAPA

>d1e0ca2 c.46.1.2 (A:136-271) Sulfurtransferase {Azotobacter vinelandii}

GGPVALSLHDEPTASRDYLLGRLGAADLAIWDARSPQEYRGEKVLAAKGGHIPGAVNFEWTAAMDPSRALRIRTDIAGRLEELGITPDKEIVTHCQTHHRSGLTYLIAKALGYPRVKGYAGSWGEWGNHPDTPVEL

>d2trxa\_ c.47.1.1 (A:) Thioredoxin {Escherichia coli}

SDKIIHLTDDSFDTDVLKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKLNIDQNPGTAPKYGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

>d1thx\_\_ c.47.1.1 (-) Thioredoxin {Anabaena sp., pcc 7120}

SKGVITITDAEFESEVLKAEQPVLVYFWASWCGPCQLMSPLINLAANTYSDRLKVVKLEIDPNPTTVKKYKVEGVPALRLVKGEQILDSTEGVISKDKLLSFLDTHLN

>d1dbya\_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}

MEAGAVNDDTFKNVVLESSVPVLVDFWAPWCGPCRIIAPVVDEIAGEYKDKLKCVKLNTDESPNVASEYGIRSIPTIMVFKGGKKCETIIGAVPKATIVQTVEKYLN

>d1ep7a\_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}

GGSVIVIDSKAAWDAQLAKGKEEHKPIVVDFTATWCGPCKMIAPLFETLSNDYAGKVIFLKVDVDAVAAVAEAAGITAMPTFHVYKDGVKADDLVGASQDKLKALVAKHAAA

>d1quwa\_ c.47.1.1 (A:) Thioredoxin {Bacillus acidocaldarius}

ATMTLTDANFQQAIQGDKPVLVDFWAAWCGPCRMMAPVLEEFAEAHADKVTVAKLNVDENPETTSQFGIMSIPTLILFKGGRPVKQLIGYQPKEQLEAQLADVLQ

>d1f9ma\_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin F}

MEAIVGKVTEVNKDTFWPIVKAAGDKPVVLDMFTQWCGPCKAMAPKYEKLAEEYLDVIFLKLDCNQENKTLAKELGIRVVPTFKILKENSVVGEVTGAKYDKLLEAIQAARS

>d1fb6a\_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin M}

VQDVNDSSWKEFVLESEVPVMVDFWAPWCGPCKLIAPVIDELAKEYSGKIAVYKLNTDEAPGIATQYNIRSIPTVLFFKNGERKESIIGAVPKSTLTDSIEKYL

>d1erv\_\_ c.47.1.1 (-) Thioredoxin {Human (Homo sapiens)}

MVKQIESKTAFQEALDAAGDKLVVVDFSATWCGPCKMIKPFFHSLSEKYSNVIFLEVDVDDCQDVASECEVKSMPTFQFFKKGQKVGEFSGANKEKLEATINELV

>d1aba\_\_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Bacteriophage T4}

MFKVYGYDSNIHKCGPCDNAKRLLTVKKQPFEFINIMPEKGVFDDEKIAELLTKLGRDTQIGLTMPQVFAPDGSHIGGFDQLREYFK

>d1qfna\_ c.47.1.1 (A:) Glutaredoxin (Thioltransferase) {Escherichia coli}

MQTVIFGRSGCPYSVRAKDLAEKLSNERDDFQYQYVDIRAEGITKEDLQQKAGKPVETVPQIFVDQQHIGGYTDFAAWVKENLDA

>d3grx\_\_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Escherichia coli, GRX3}

ANVEIYTKETCPYSHRAKALLSSKGVSFQELPIDGNAAKREEMIKRSGRTTVPQIFIDAQHIGGYDDLYALDARGGLDPLLK

>d1kte\_\_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Pig (Sus scrofa)}

AQAFVNSKIQPGKVVVFIKPTCPFCRKTQELLSQLPFKEGLLEFVDITATSDTNEIQDYLQQLTGARTVPRVFIGKECIGGCTDLESMHKRGELLTRLQQVGAVK

>d1jhb\_\_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Human (Homo sapiens)}

AQEFVNCKIQPGKVVVFIKPTCPYCRRAQEILSQLPIKQGLLEFVDITATNHTNEIQDYLQQLTGARTVPRVFIGKDCIGGCSDLVSLQQSGELLTRLKQIGALQ

>d1h75a\_ c.47.1.1 (A:) Glutaredoxin-like NRDH-redoxin {Escherichia coli}

MRITIYTRNDCVQCHATKRAMENRGFDFEMINVDRVPEAAEALRAQGFRQLPVVIAGDLSWSGFRPDMINRLHPAP

>d1fo5a\_ c.47.1.1 (A:) MJ0307, thioredoxin/glutaredoxin-like protein {Archaeon Methanococcus jannaschii}

MSKVKIELFTSPMCPHCPAAKRVVEEVANEMPDAVEVEYINVMENPQKAMEYGIMAVPTIVINGDVEFIGAPTKEALVEAIKKRL

>d1iloa\_ c.47.1.1 (A:) MTH985, a thioredoxin {Archaeon Methanobacterium thermoautotrophicum}

MMKIQIYGTGCANCQMLEKNAREAVKELGIDAEFEKIKEMDQILEAGLTALPGLAVDGELKIMGRVASKEEIKKILS

>d1gh2a\_ c.47.1.1 (A:) Thioredoxin-like protein, N-terminal domain {Human (Homo sapiens)}

VGVKPVGSDPDFQPELSGAGSRLAVVKFTMRGCGPCLRIAPAFSSMSNKYPQAVFLEVDVHQCQGTAATNNISATPTFQFFRNKVRIDQYQGADAVGLEEKIKQHLE

>d1bjx\_\_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}

AATTLPDGAAAESLVESSEVAVIGFFKDVESDSAKQFLQAAEAIDDIPFGITSNSDVFSKYQLDKDGVVLFKKFDEGRNNFEGEVTKENLLDFIKHNQLPLVIEFTEQTA

>d1mek\_\_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}

DAPEEEDHVLVLRKSNFAEALAAHKYLLVEFYAPWCGHCKALAPEYAKAAGKLKAEGSEIRLAKVDATEESDLAQQYGVRGYPTIKFFRNGDTASPKEYTAGREADDIVNWLKKRTGPAA

>d1a8l\_1 c.47.1.2 (1-119) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}

MGLISDADKKVIKEEFFSKMVNPVKLIVFVRKDHCQYCDQLKQLVQELSELTDKLSYEIVDFDTPEGKELAKRYRIDRAPATTITQDGKDFGVRYFGLPAGHEFAAFLEDIVDVSREET

>d1a8l\_2 c.47.1.2 (120-226) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}

NLMDETKQAIRNIDQDVRILVFVTPTCPYCPLAVRMAHKFAIENTKAGKGKILGDMVEAIEYPEWADQYNVMAVPKIVIQVNGEDRVEFEGAYPEKMFLEKLLSALS

>d1hyua3 c.47.1.2 (A:1-102) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}

MLDTNMKTQLRAYLEKLTKPVELIATLDDSAKSAEIKELLAEIAELSDKVTFKEDNTLPVRKPSFLITNPGSQQGPRFAGSPLGHEFTSLVLALLWTGGHPS

>d1hyua4 c.47.1.2 (A:103-198) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}

KEAQSLLEQIRDIDGDFEFETYYSLSCHNCPDVVQALNLMAVLNPRIKHTAIDGGTFQNEITERNVMGVPAVFVNGKEFGQGRMTLTEIVAKVDTG

>d1a8y\_1 c.47.1.3 (3-126) Calsequestrin {Rabbit (Oryctolagus cuniculus)}

GLDFPEYDGVDRVINVNAKNYKNVFKKYEVLALLYHEPPEDDKASQRQFEMEELILELAAQVLEDKGVGFGLVDSEKDAAVAKKLGLTEEDSIYVFKEDEVIEYDGEFSADTLVEFLLDVLEDP

>d1a8y\_2 c.47.1.3 (127-228) Calsequestrin {Rabbit (Oryctolagus cuniculus)}

VELIEGERELQAFENIEDEIKLIGYFKNKDSEHYKAFKEAAEEFHPYIPFFATFDSKVAKKLTLKLNEIDFYEAFMEEPVTIPDKPNSEEEIVNFVEEHRRS

>d1a8y\_3 c.47.1.3 (229-347) Calsequestrin {Rabbit (Oryctolagus cuniculus)}

TLRKLKPESMYETWEDDMDGIHIVAFAEEADPDGYEFLEILKSVAQDNTDNPDLSIIWIDPDDFPLLVPYWEKTFDIDLSAPQIGVVNVTDADSVWMEMDDEEDLPSAEELEDWLEDVL

>d1fvka2 c.47.1.4 (A:1-64,A:129-188) Disulphide-bond formation facilitator (DSBA) {Escherichia coli}

AQYEDGKQYTTLEKPVAGAPQVLEFFSFFCPHCYQFEEVLHISDNVKKKLPEGVKMTKYHVNFMXFVVKSLVAQQEKAAADVQLRGVPAMFVNGKYQLNPQGMDTSNMDVFVQQYADTVKYLSEK

>d1bed\_2 c.47.1.4 (1-62,127-181) Disulphide-bond formation facilitator (DSBA) {Vibrio cholerae}

AQFKEGEHYQVLKTPASSSPVVSEFFSFYCPHCNTFEPIIAQLKQQLPEGAKFQKNHVSFMGXFAVDSMVRRFDKQFQDSGLTGVPAVVVNNRYLVQGQSVKSLDEYFDLVNYLLTLK

>d1aqwa2 c.47.1.5 (A:1-76) Glutathione S-transferase {Human (Homo sapiens), class pi}

PPYTVVYFPVRGRCAALRMLLADQGQSWKEEVVTVETWQEGSLKASCLYGQLPKFQDGDLTLYQSNTILRHLGRTL

>d2gsra2 c.47.1.5 (A:1-76) Glutathione S-transferase {Pig (Sus scrofa), class pi}

PPYTITYFPVRGRCEAMRMLLADQDQSWKEEVVTMETWPPLKPSCLFRQLPKFQDGDLTLYQSNAILRHLGRSFGL

>d1glqa2 c.47.1.5 (A:1-78) Glutathione S-transferase {Mouse (Mus musculus), class pi}

PPYTIVYFPVRGRCEAMRMLLADQGQSWKEEVVTIDTWMQGLLKPTCLYGQLPKFEDGDLTLYQSNAILRHLGRSLGL

>d1gtua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}

PMILGYWDIRGLAHAIRLLLEYTDSSYEEKKYTMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDGAHKITQSNAILCYIARKHN

>d1hna\_2 c.47.1.5 (1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}

PMTLGYWNIRGLAHSIRLLLEYTDSSYEEKKYTMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDGTHKITQSNAILRYIARKHN

>d3gtub2 c.47.1.5 (B:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}

SCESSMVLGYWDIRGLAHAIRLLLEFTDTSYEEKRYTCGEAPDYDRSQWLDVKFKLDLDFPNLPYLLDGKNKITQSNAILRYIA

>d2gsta2 c.47.1.5 (A:1-84) Glutathione S-transferase {Rat (Rattus norvegicus), class mu}

PMILGYWNVRGLTHPIRLLLEYTDSSYEEKRYAMGDAPDYDRSQWLNEKFKLGLDFPNLPYLIDGSRKITQSNAIMRYLARKHH

>d1gsua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Chicken (Gallus gallus), class mu}

VVTLGYWDIRGLAHAIRLLLEYTETPYQERRYKAGPAPDFDPSDWTNEKEKLGLDFPNLPYLIDGDVKLTQSNAILRYIARKHN

>d1gsea2 c.47.1.5 (A:2-80) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}

AEKPKLHYFNARGKMESTRWLLAAAGVEFEEKFIKSAEDLDKLRNDGYLMFQQVPMVEIDGMKLVQTRAILNYIASKYN

>d1gula2 c.47.1.5 (A:4-80) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}

RPKLHYPNGRGRMESVRWVLAAAGVEFDEEFLETKEQLYKLQDGNHLLFQQVPMVEIDGMKLVQTRSILHYIADKHN

>d1f3aa2 c.47.1.5 (A:1-79) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-1)}

AGKPVLHYFNARGRMECIRWLLAAAGVEFEEKFIQSPEDLEKLKKDGNLMFDQVPMVEIDGMKLAQTRAILNYIATKYD

>d1b48a2 c.47.1.5 (A:2-79) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-4)}

AAKPKLYYFNGRGRMESIRWLLAAAGVEFEEEFLETREQYEKMQKDGHLLFGQVPLVEIDGMMLTQTRAILSYLAAKY

>d1ljra2 c.47.1.5 (A:1-79) Glutathione S-transferase {Human (Homo sapiens), class theta}

MGLELFLDLVSQPSRAVYIFAKKNGIPLELRTVDLVKGQHKSKEFLQINSLGKLPTLKDGDFILTESSAILIYLSCKYQ

>d1pd212 c.47.1.5 (1:1-75) Glutathione S-transferase {Rat (Rattus norvegicus), class sigma}

MPNYKLLYFNMRGRAEIIRYIFAYLDIKYEDHRIEQADWPKIKPTLPFGKIPVLEVEGLTLHQSLAIARYLTKNT

>d2gsq\_2 c.47.1.5 (1-75) Glutathione S-transferase {Squid (Ommastrephes sloani pacificus), class sigma}

PKYTLHYFPLMGRAELCRFVLAAHGEEFTDRVVEMADWPNLKATMYSNAMPVLDIDGTKMSQSMCIARHLAREFG

>d1eema2 c.47.1.5 (A:5-102) Glutathione S-transferase {Human (Homo sapiens), class omega}

SARSLGKGSAPPGPVPEGSIRIYSMRFCPFAERTRLVLKAKGIRHEVININLKNKPEWFFKKNPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKKL

>d1fw1a2 c.47.1.5 (A:5-87) Glutathione S-transferase {Human (Homo sapiens), class zeta}

KPILYSYFRSSCSWRVRIALALKGIDYKTVPINLIKDGGQQFSKDFQALNPMKQVPTLKIDGITIHQSLAIIEYLEETRPTPR

>d1duga2 c.47.1.5 (A:1-80) Glutathione S-transferase {Schistosoma japonicum}

SPILGYWKIKGLVQPTRLLLEYLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPYYIDGDVKLTQSMAIIRYIADKHNM

>d1fhe\_2 c.47.1.5 (1-80) Glutathione S-transferase {Fasciola hepatica}

PAKLGYWKLRGLAQPVRLFLEYLGEEYEEHLYGRDDREKWMSEKFNMGLDLPNLPYYIDDKCKLTQSVAIMRYIADKHGM

>d2fhea2 c.47.1.5 (A:1-80) Glutathione S-transferase {Fasciola hepatica}

PAKLGYWKIRGLQQPVRLLLEYLGEKYEEQIYERDDGEKWFSKKFELGLDLPNLPYYIDDKCKLTQSLAILRYIADKHGM

>d1gnwa2 c.47.1.5 (A:2-85) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}

GIKVFGHPASIATRRVLIALHEKNLDFELVHVELKDGEHKKEPFLSRNPFGQVPAFEDGDLKLFESRAITQYIAHRYENQGTNL

>d1axda2 c.47.1.5 (A:1-80) Glutathione S-transferase {Maize (Zea mays), type I}

APMKLYGAVMSWNLTRCATALEEAGSDYEIVPINFATAEHKSPEHLVRNPFGQVPALQDGDLYLFESRAICKYAARKNKP

>d1aw9\_2 c.47.1.5 (2-82) Glutathione S-transferase {Maize (Zea mays), type III}

APLKLYGMPLSPNVVRVATVLNEKGLDFEIVPVDLTTGAHKQPDFLALNPFGQIPALVDGDEVLFESRAINRYIASKYASE

>d1e6ba2 c.47.1.5 (A:8-87) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana), class zeta}

KLKLYSYWRSSCAHRVRIALALKGLDYEYIPVNLLKGDQFDSDFKKINPMGTVPALVDGDVVINDSFAIIMYLDEKYPEP

>d1a0fa2 c.47.1.5 (A:1-80) Glutathione S-transferase {Escherichia coli}

MKLFYKPGACSLASHITLRESGKDFTLVSVDLMKKRLENGDDYFAVNPKGQVPALLLDDGTLLTEGVAIMQYLADSVPDR

>d1pmt\_2 c.47.1.5 (1-80) Glutathione S-transferase {Proteus mirabilis}

MKLYYTPGSCSLSPHIVLRETGLDFSIERIDLRTKKTESGKDFLAINPKGQVPVLQLDNGDILTEGVAIVQYLADLKPDR

>d1f2ea2 c.47.1.5 (A:1-80) Glutathione S-transferase {Sphingomonas paucimobilis}

MKLFISPGACSLAPHIALRETGADFEAVKVDLAVRKTEAGEDFLTVNPSGKVPALTLDSGETLTENPAILLYIADQNPAS

>d1g7oa2 c.47.1.5 (A:1-75) Glutaredoxin 2 {Escherichia coli}

MKLYIYDHCPYCLKARMIFGLKNIPVELHVLLNDDAETPTRMVGQKQVPILQKDDSRYMPESMDIVHYVDKLDGK

>d1k0da2 c.47.1.5 (A:109-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}

QPLEGYTLFSHRSAPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVNPNARVPALIDHGMDNLSIWESGAILLHLVNKYYKETGNPL

>d1k0dd2 c.47.1.5 (D:99-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}

YSRITKFFQEQPLEGYTLFSHRSAPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVNPNARVPALIDHGMDNLSIWESGAILLHLVNKYYKETGNPL

>d1k0ma2 c.47.1.5 (A:6-91) Chloride intracellular channel 1 (clic1) {Human (Homo sapiens)}

PQVELFVKAGSDGAKIGNCPFSQRLFMVLWLKGVTFNVTTVDTKRRTETVQKLCPGGELPFLLYGTEVHTDTNKIEEFLEAVLCPP

>d2trcp\_ c.47.1.6 (P:) Phosducin {Rat (Rattus norvegicus)}

EGQATHTGPKGVINDWRKFKLESEDGDSIPPSKKEILRQMSSPQSRDDKDSKERMSRKMSIQEYELIHQDKEDEGCLRKYRRQCMQDMHQKLSFGPRYGFVYELETGEQFLETIEKEQKVTTIVVNIYEDGVRGCDALNSSLECLAAEYPMVKFCKIRASNTGAGDRFSSDVLPTLLVYKGGELISNFISVAEQFAEDFFAADVESFLNEYGLLPER

>d1a0rp\_ c.47.1.6 (P:) Phosducin {Cow (Bos taurus)}

FEGQASHTGPKGVINDWRKFKLESEDSDSVAHSKKEILRQMSSPQSRDDKDSKERFSRKMSVQEYELIHKDKEDENCLRKYRRQCMQDMHQKLSFGPRYGFVYELESGEQFLETIEKEQKITTIVVHIYEDGIKGCDALNSSLICLAAEYPMVKFCKIKASNTGAGDRFSSDVLPTLLVYKGGELLSNFISVTEQLAEEFFTGDVESFLNEYGLLPEK

>d1g7ea\_ c.47.1.7 (A:) Endoplasmic reticulum protein ERP29, N-domain {Rat (Rattus norvegicus)}

LHTKGALPLDTVTFYKVIPKSKFVLVKFDTQYPYGEKQDEFKRLAENSASSDDLLVAEVGISDYGDKLNMELSEKYKLDKESYPVFYLFRDGDFENPVPYSGAVKVGAIQRWLKGQGVYLGM

>d1qgva\_ c.47.1.8 (A:) spliceosomal protein U5-15Kd {Human (Homo sapiens)}

SYMLPHLHNGWQVDQAILSEEDRVVVIRFGHDWDPTCMKMDEVLYSIAEKVKNFAVIYLVDITEVPDFNKMYELYDPCTVMFFFRNKHIMIDLGTGNNNKINWAMEDKQEMVDIIETVYRGARKGRGLVVSPKDYST

>d1eeja1 c.47.1.9 (A:61-216) Disulfide bond isomerase, DsbC, C-terminal domain {Escherichia coli}

NVTNKMLLKQLNALEKEMIVYKAPQEKHVITVFTDITCGYCHKLHEQMADYNALGITVRYLAFPRQGLDSDAEKEMKAIWCAKDKNKAFDDVMAGKSVAPASCDVDIADHYALGVQLGVSGTPAVVLSNGTLVPGYQPPKEMKEFLDEHQKMTSGK

>d1gp1a\_ c.47.1.10 (A:) Glutathione peroxidase {Cow (Bos taurus)}

RTVYAFSARPLAGGEPFNLSSLRGKVLLIENVASLXGTTVRDYTQMNDLQRRLGPRGLVVLGFPCNQFGHQENAKNEEILNCLKYVRPGGGFEPNFMLFEKCEVNGEKAHPLFAFLREVLPTPSDDATALMTDPKFITWSPVCRNDVSWNFEKFLVGPDGVPVRRYSRRFLTIDIEPDIETLLSQ

>d1qk8a\_ c.47.1.10 (A:) Tryparedoxin I {Crithidia fasciculata}

GLDKYLPGIEKLRRGDGEVEVKSLAGKLVFFYFSASWCPPCRGFTPQLIEFYDKFHESKNFEVVFCTWDEEEDGFAGYFAKMPWLAVPFAQSEAVQKLSKHFNVESIPTLIGVDADSGDVVTTRARATLVKDPEGEQFPWKDA

>d1i5ga\_ c.47.1.10 (A:) Tryparedoxin II {Crithidia fasciculata}

SGLKKFFPYSTNVLKGAAADIALPSLAGKTVFFYFSASWCPPSRAFTPQLIDFYKAHAEKKNFEVMLISWDESAEDFKDYYAKMPWLALPFEDRKGMEFLTTGFDVKSIPTLVGVEADSGNIITTQARTMVVKDPEAKDFPWPN

>d1e2ya\_ c.47.1.10 (A:) Tryparedoxin peroxidase (thioredoxin peroxidase homologue) {Crithidia fasciculata}

GAAKLNHPAPEFDDMALMPNGTFKKVSLSSYKGKYVVLFFYPMDFTFVCPTEIIQFSDDAKRFAEINTEVISCSCDSEYSHLQWTSVDRKKGGLGPMAIPMLADKTKAIARAYGVLDEDSGVAYRGVFIIDPNGKLRQIIINDMPIGRNVEEVIRLVEALQFVEEHG

>d1qq2a\_ c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys peroxiredoxin) {Norway rat (Rattus norvegicus)}

SGNAKIGHPAPSFKATAVMPDGQFKDISLSDYKGKYVVFFFYPLDFTFVCPTEIIAFSDRAEEFKKLNCQVIGASVDSHFSHLAWINTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLKADEGISFRGLFIIDDKGILRQITINDLPVGRSVDEILRLVQAFQFTDKHGEVCPA

>d1qmva\_ c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys peroxiredoxin) {Human (Homo sapiens)}

SGNARIGKPAPDFKATAVVDGAFKEVKLSDYKGKYVVLFFYPLDFTFVAPTEIIAFSNRAEDFRKLGCEVLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLLADVTRRLSEDYGVLKTDEGIAYRGLFIIDGKGVLRQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKEYFSKHN

>d1hd2a\_ c.47.1.10 (A:) Peroxiredoxin 5 {Human (Homo sapiens)}

APIKVGDAIPAVEVFEGEPGNKVNLAELFKGKKGVLFGVPGAFTPGCSKTHLPGFVEQAEALKAKGVQVVACLSVNDAFVTGEWGRAHKAEGKVRLLADPTGAFGKETDLLLDDSLVSIFGNRRLKRFSMVVQDGIVKALNVEPDGTGLTCSLAPNIISQL

>d1prxa\_ c.47.1.10 (A:) HorF6 peroxidase {Human (Homo sapiens)}

LLLGDVAPNFEANTTVGRIRFHDFLGDSWGILFSHPRDFTPVCTTELGRAAKLAPEFAKRNVKLIALSIDSVEDHLAWSKDINAYNSEEPTEKLPFPIIDDRNRELAILLGMLDPAEKDEKGMPVTARVVFVFGPDKKLKLSILYPATTGRNFDEILRVVISLQLTAEKRVATPVDWKDGDSVMVLPTIPEEEAKKLFPKGVFTKELPSGKKYLRYTPQP

>d1kyga\_ c.47.1.10 (A:) Alkyl hydroperoxide reductase AhpC {Salmonella typhimurium}

SLINTKIKPFKNQAFKNGEFIEVTEKDTEGRWSVFFFYPADFTFVCPTELGDVADHYEELQKLGVDVYSVSTDTHFTHKAWHSSSETIAKIKYAMIGDPTGALTRNFDNMREDEGLADRATFVVDPQGIIQAIEVTAEGIGRDASDLLRKIKAAQYVAAHPGEVCP

>d1jfua\_ c.47.1.10 (A:) Membrane-anchored thioredoxin-like protein TlpA, soluble domain {Bradyrhizobium japonicum}

TGDPACRAAVATAQKIAPLAHGEVAALTMASAPLKLPDLAFEDADGKPKKLSDFRGKTLLVNLWATWCVPCRKEMPALDELQGKLSGPNFEVVAINIDTRDPEKPKTFLKEANLTRLGYFNDQKAKVFQDLKAIGRALGMPTSVLVDPQGCEIATIAGPAEWASEDALKLIRAATG

>d1foha3 c.47.1.10 (A:462-662) Phenol hydroxylase, C-terminal domain {Soil-living yeast (Trichosporon cutaneum)}

NLVTDKKSSKQELAKNCVVGTRFKSQPVVRHSEGLWMHFGDRLVTDGRFRIIVFAGKATDATQMSRIKKFSAYLDSENSVISLYTPKVSDRNSRIDVITIHSCHRDDIEMHDFPAPALHPKWQYDFIYADCDSWHHPHPKSYQAWGVDETKGAVVVVRPDGYTSLVTDLEGTAEIDRYFSGILVEPKEKSGAQTEADWTKS

>d1f37a\_ c.47.1.11 (A:) Thioredoxin-like 2Fe-2S ferredoxin {Aquifex aeolicus}

AEFKHVFVCVQDRPPGHPQGSCAQRGSREVFQAFMEKIQTDPQLFMTTVITPTGCMNACMMGPVVVVYPDGVWYGQVKPEDVDEIVEKHLKGGEPVERLVISKGKPPGM

>d1j9ba\_ c.47.1.12 (A:) Arsenate reductase ArsC {Escherichia coli}

NITIYHNPACGTSRNTLEMIRNSGTEPTIILYLENPPSRDELVKLIADMGISVRALLRKNVEPYEQLGLAEDKFTDDQLIDFMLQHPILINRPIVVTPLGTRLCRPSEVVLDILQDAQKGAFTKEDGEKVVDEAGKRL

>d1qmha1 c.47.2.1 (A:185-279) RNA 3'-terminal phosphate cyclase, RPTC, insert domain {Escherichia coli}

ERGNIVQMRGEVLLAGVPRHVAEREIATLAGSFSLHEQNIHNLPRDQGPGNTVSLEVESENITERFFVVGEKRVSAEVVAAQLVKEVKRYLASTA

>d1gpua3 c.48.1.1 (A:535-680) Transketolase {Baker's yeast (Saccharomyces cerevisiae)}

EGSSIESASKGGYVLQDVANPDIILVATGSEVSLSVEAAKTLAAKNIKARVVSLPDFFTFDKQPLEYRLSVLPDNVPIMSVEVLATTCWGKYAHQSFGIDRFGASGKAPEVFKFFGFTPEGVAERAQKTIAFYKGDKLISPLKKAF

>d1dtwb2 c.48.1.2 (B:205-342) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}

PYNIPLSQAEVIQEGSDVTLVAWGTQVHVIREVASMAKEKLGVSCEVIDLRTIIPWDVDTICKSVIKTGRLLISHEAPLTGGFASEISSTVQEECFLNLEAPISRVCGYDTPFPHIFEPFYIPDKWKCYDALRKMINY

>d1qs0b2 c.48.1.2 (B:206-339) 2-oxoisovalerate dehydrogenase E1b {Pseudomonas putida}

YYTVPLDKAAITRPGNDVSVLTYGTTVYVAQVAAEESGVDAEVIDLRSLWPLDLDTIVESVKKTGRCVVVHEATRTCGFGAELVSLVQEHCFHHLEAPIERVTGWDTPYPHAQEWAYFPGPSRVGAALKKVMEV

>d1ik6a2 c.48.1.2 (A:192-326) E1-beta subunit of pyruvate dehydrogenase {Archaeon Pyrobaculum aerophilum}

DYVVEIGKARVAREGDDVTLVTYGAVVHKALEAAERVKASVEVVDLQTLNPLDFDTVLKSVSKTGRLIIAHDSPKTGGLGAEVRALVAEKALDRLTAPVIRLAGPDVPQSPIAADAAYAPTVERIIKAIEYVMRY

>d1keka3 c.48.1.3 (A:259-415) Pyruvate-ferredoxin oxidoreductase, PFOR, domain II {Desulfovibrio africanus}

KLFDYVGAPDAERVIVSMGSSCETIEEVINHLAAKGEKIGLIKVRLYRPFVSEAFFAALPASAKVITVLDRTKEPGAPGDPLYLDVCSAFVERGEAMPKILAGRYGLGSKEFSPAMVKSVYDNMSGAKKNHFTVGIEDDVTGTSLPVDNAFADTTPK

>d1a49a3 c.49.1.1 (A:396-530) Pyruvate kinase, C-terminal domain {Rabbit (Oryctolagus cuniculus)}

ELARSSSHSTDLMEAMAMGSVEASYKCLAAALIVLTESGRSAHQVARYRPRAPIIAVTRNHQTARQAHLYRGIFPVVCKDPVQEAWAEDVDLRVNLAMNVGKARGFFKKGDVVIVLTGWRPGSGFTNTMRVVPVP

>d1pkla3 c.49.1.1 (A:358-498) Pyruvate kinase, C-terminal domain {Leishmania mexicana}

NEYVFFNSIKKLQHIPMSADEAVCSSAVNSVYETKAKAMVVLSNTGRSARLVAKYRPNCPIVCVTTRLQTCRQLNITQGVESVFFDADKLGHDEGKEHRVAAGVEFAKSKGYVQTGDYCVVIHADHKVKGYANQTRILLVE

>d1a3wa3 c.49.1.1 (A:367-500) Pyruvate kinase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

DMRNCTPKPTSTTETVAASAVAAVFEQKAKAIIVLSTSGTTPRLVSKYRPNCPIILVTRCPRAARFSHLYRGVFPFVFEKEPVSDWTDDVEARINFGIEKAKEFGILKKGDTYVSIQGFKAGAGHSNTLQVSTV

>d1e0ta3 c.49.1.1 (A:354-470) Pyruvate kinase, C-terminal domain {Escherichia coli}

ITEAVCRGAVETAEKLDAPLIVVATQGGKSARAVRKYFPDATILALTTNEKTAHQLVLSKGVVPQLVKEITSTDDFYRLGKELALQSGLAHKGDVVVMVSGALVPSGTTNTASVHVL

>d1e79g\_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Cow (Bos taurus)}

ATLKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGVGSLALYEKADIKTPEDKKKHLIIGVSSDRGLCGAIHSSVAKQMKSEAANLAAAGKEVKIIGVGDKIRSILHRTHSDQFLVTFKEVGRRPPTFGDASVIALELLNSGYEFDEGSIIFNRFRSVISYKTEEKPIFSLDTISSAESMSIYDDIDADVLRNYQEYSLANIIYYSLKESTTSEQSARMTAMDNASKNASEMIDKLTLTFNRTRQAVITKELIEIISGAAAL

>d1mabg\_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Rat (Rattus norvegicus)}

RDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGTGSLALYEKAEIKGPEDKKKHLIIGVSSDRGLCGAIHSSVAKQMKNDMAALTAAGKEVMIVGIGEKIKSILYRTHSDQFLVSFKDVGRKPPTFGDASVIALELLNSGYEFDEGSIIFNQFKSVISYKTEEKPIFSFSTVVAAENMSIYDDIDADVLQNYQEYNLANIIYYSLKESTTSEQSARMTAMDNASKNASDMIDKLTLTFNRTRQAVITKELIEIISGAAALD

>d1fs0g\_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Escherichia coli}

KITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGNLEYKHPYLEDRDVKRVGYLVVSTDRGLCGGLNINLFKKLLAEMKTWTDKGVQCDLAMIGSKGVSFFNSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRLDKLYIVSNKFINTMSQVPTISQLLPLPASDDDDLKHKSWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLASEQAARMVAMK

>d1lam\_1 c.50.1.1 (1-159) Leucine aminopeptidase, N-terminal domain {Cow (Bos taurus)}

TKGLVLGIYSKEKEEDEPQFTSAGENFNKLVSGKLREILNISGPPLKAGKTRTFYGLHEDFPSVVVVGLGKKTAGIDEQENWHEGKENIRAAVAAGCRQIQDLEIPSVEVDPCGDAQAAAEGAVLGLYEYDDLKQKRKVVVSAKLHGSEDQEAWQRGVL

>d1kmma1 c.51.1.1 (A:326-424) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Escherichia coli}

DPVVDIYLVASGADTQSAAMALAERLRDELPGVKLMTNHGGGNFKKQFARADKWGARVAVVLGESEVANGTAVVKDLRSGEQTAVAQDSVAAHLRTLLG

>d1qe0a1 c.51.1.1 (A:326-420) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Staphylococcus aureus}

IEENLDLFIVTMGDQADRYAVKLLNHLRHNGIKADKDYLQRKIKGQMKQADRLGAKFTIVIGDQELENNKIDVKNMTTGESETIELDALVEYFKK

>d1h4vb1 c.51.1.1 (B:326-421) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Thermus thermophilus}

EKGPDLYLIPLTEEAVAEAFYLAEALRPRLRAEYALAPRKPAKGLEEALKRGAAFAGFLGEDELRAGEVTLKRLATGEQVRLSREEVPGYLLQALG

>d1atia1 c.51.1.1 (A:395-505) Glycyl-tRNA synthetase (GlyRS), C-terminal domain {Thermus thermophilus}

QLAPIKVAVIPLVKNRPEITEYAKRLKARLLALGLGRVLYEDTGNIGKAYRRHDEVGTPFAVTVDYDTIGQSKDGTTRLKDTVTVRDRDTMEQIRLHVDELEGFLRERLRW

>d1qf6a1 c.51.1.1 (A:533-642) Threonyl-tRNA synthetase (ThrRS), C-terminal domain {Escherichia coli}

FPTWLAPVQVVIMNITDSQSEYVNELTQKLSNAGIRVKADLRNEKIGFKIREHTLRRVPYMLVCGDKEVESGKVAVRTRRGKDLGSMDVNEVIEKLQQEIRSRSLKQLEE

>d1hc7a1 c.51.1.1 (A:277-403) C-terminal domain of ProRS {Thermus thermophilus}

RGLVLPPRLAPIQVVIVPIYKDESRERVLEAAQGLRQALLAQGLRVHLDDRDQHTPGYKFHEWELKGVPFRVELGPKDLEGGQAVLASRLGGKETLPLAALPEALPGKLDAFHEELYRRALAFREDH

>d1g5ha1 c.51.1.1 (A:343-469) The aaRS-like accessory subunit of mitochondrial polymerase gamma, C-terminal domain {Mouse (Mus musculus)}

RKVLKLHPCLAPIKVALDVGKGPTVELRQVCQGLLNELLENGISVWPGYSETVHSSLEQLHSKYDEMSVLFSVLVTETTLENGLIQLRSRDTTMKEMMHISKLRDFLVKYLASASNVAAALDHHHHH

>d1crza2 c.51.2.1 (A:7-140) TolB, N-terminal domain {Escherichia coli}

DSGVDSGRPIGVVPFQWAGPGAAPEDIGGIVAADLRNSGKFNPLDRARLPQQPGSAQEVQPAAWSALGIDAVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQWLRYAGHTASDEVFEKLTGIKG

>d1eexb\_ c.51.3.1 (B:) Diol dehydratase, beta subunit {Klebsiella oxytoca}

GFLTEVGEARQGTQQDEVIIAVGPAFGLAQTVNIVGIPHKSILREVIAGIEEEGIKARVIRCFKSSDVAFVAVEGNRLSGSGISIGIQSKGTTVIHQQGLPPLSNLELFPQAPLLTLETYRQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVA

>d1b78a\_ c.51.4.1 (A:) XTP pyrophosphatase {Archaeon Methanococcus jannaschii}

KIYFATGNPNKIKEANIILKDLKDVEIEQIKISYPEIQGTLEEVAEFGAKWVYNILKKPVIVEDSGFFVEALNGFPGTYSKFVQETIGNEGILKLLEGKDNRNAYFKTVIGYCDENGVRLFKGIVKGRVSEEIRSKGYGFAYDSIFIPEEEERTFAEMTTEEKSQISHRKKAFEEFKKFLLDRI

>d1ex2a\_ c.51.4.2 (A:) Maf protein {Bacillus subtilis}

MTKPLILASQSPRRKELLDLLQLPYSIIVSEVEEKLNRNFSPEENVQWLAKQKAKAVADLHPHAIVIGADTMVCLDGECLGKPQDQEEAASMLRRLSGRSHSVITAVSIQAENHSETFYDKTEVAFWSLSEEEIWTYIETKEPMDKAGAYGIQGRGALFVKKIDGDYYSVMGLPISKTMRALRHF

>d1ihna\_ c.103.1.1 (A:) Hypothetical protein MT938 (MTH938) {Archaeon Methanobacterium thermoautotrophicum}

SHMFSDCRFGSVTYRGREYRSDIVVHVDGSVTPRRKEISRRKYGTSHVMAEEELEELLEEKPESIIIGSGVHGALETGFRSDATVLPTCEAIKRYNEERSAGRRVAAIIHVTC

>d1ckqa\_ c.52.1.1 (A:) Restriction endonuclease EcoRI {Escherichia coli}

SQGVIGIFGDYAKAHDLAVGEVSKLVKKALSNEYPQLSFRYRDSIKKTEINEALKKIDPDLGGTLFVSNSSIKPDGGIVEVKDDYGEWRVVLVAEAKHQGKDIINIRNGLLVGKRGDQDLMAAGNAIERSHKNISEIANFMLSESHFPYVLFLEGSNFLTENISITRPDGRVVNLEYNSGILNRLDRLTAANYGMPINSNLCINKFVNHKDKSIMLQAASIYTQGDGREWDSKIMFEIMFDISTTSLRVLGRDLFEQLTSK

>d1az3a\_ c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia coli}

SLRSDLINALYDENQKYDVCGIISAEGKIYPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEPKQQNHYPDFTLYKPSEPNKKIAIDIKTTYTNKENEKIKFTLGGYTSFIRNNTKNIVYPFDQYIAHWIIGYVYTRVATRKSSLKTYNINELNEIPKPYKGVKVFLQDKWVIAGDLAGSGNTTNIGSIHAHYKDFVEGKGIFDSEDEFLDYWR

>d1eona\_ c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia coli}

SLRSDLINALYDENQKYDVCGIISAEGKIYPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEPKQQNHYPDFTLYKPSEPNKKIAIDIKTTYTNKENEKIKFTLGGYTSFIRNNTKNIVYPFDQYIAHWIIGYVYTRVATRKSSLKTYNINELNEIPKPYKGVKVFLQDKWVIAGDLAGSGNTTNIGSIHAHYKDFVEGKGIFDSEDEFLDYWRNYERTSQLRNDKYNNISEYRNWIYRGRK

>d1bam\_\_ c.52.1.3 (-) Restriction endonuclease BamHI {Bacillus amyloliquefaciens}

MEVEKEFITDEAKELLSKDKLIQQAYNEVKTSICSPIWPATSKTFTINNTEKNCNGVVPIKELCYTLLEDTYNWYREKPLDILKLEKKKGGPIDVYKEFIENSELKRVGMEFETGNISSAHRSMNKLLLGLKHGEIDLAIILMPIKQLAYYLTDRVTNFEELEPYFELTEGQPFIFIGFNAEAYNSNVPLIPKGSDGMSKRSIKKWKDKVENK

>d1dmua\_ c.52.1.4 (A:) Restriction endonuclease BglI {Bacillus subtilis}

MYNLHREKIFMSYNQNKQYLEDNPEIQEKIELYGLNLLNEVISDNEEEIRADYNEANFLHPFWMNYPPLDRGKMPKGDQIPWIEVGEKAVGSKLTRLVSQREDITVREIGLPTGPDERYLLTSPTIYSLTNGFTDSIMMFVDIKSVGPRDSDYDLVLSPNQVSGNGDWAQLEGGIQNNQQTIQGPRSSQIFLPTIPPLYILSDGTIAPVVHLFIKPIYAMRSLTKGDTGQSLYKIKLASVPNGLGLFCNPGYAFDSAYKFLFRPGKDDRTKSLLQKRVRVDLRVLDKIGPRVMTIDMDK

>d1dfma\_ c.52.1.5 (A:) Restriction endonuclease BglII {Bacillus subtilis}

MKIDITDYNHADEILNPQLWKEIEETLLKMPLHVKASDQASKVGSLIFDPVGTNQYIKDELVPKHWKNNIPIPKRFDFLGTDIDFGKRDTLVEVQFSNYPFLLNNTVRSELFHKSNMDIDEEGMKVAIIITKGHMFPASNSSLYYEQAQNQLNSLAEYNVFDVPIRLVGLIEDFETDIDIVSTTYADKRYSRTITKRDTVKGKVIDTNTPNTRRRKRGTIVTY

>d3pvia\_ c.52.1.6 (A:) Restriction endonuclease PvuII {Proteus vulgaris}

SHPDLNKLLELWPHIQEYQDLALKHGINDIFQGNGGKLLQVLLITGLTVLPGREGNDAVDNAGQEYELKSINIDLTKGFSTHHHMNPVIIAKYRQVPWIFAIYRGIAIEAIYRLEPKDLEFYYDKWERKWYSDGHKDINNPKIPVKYVMEHGTKIY

>d1cfr\_\_ c.52.1.7 (-) Restriction endonuclease Cfr10I {Citrobacter freundii}

MDIISKSGEGNKYTINSAIAFVAYASHIDINTTEFSKVLSGLRDFINDEAIRLGGKISDGSFNKCNGDWYEWLIGIRAIEFFLESETNFIVVKMPNATSFDVMSIYKSCLSEFIYDLRSKLSLNNVNLITSNPDFSIIDIRGRREELKSMLKDISFSNISLSTISEIDNLYKNFIDYAELEHIKSFLSVKTTFRPDRRLQLAHEGSLMKALYTHLQTRTWTINPTGIRYYAAATSIGNADVIGLKTVATHSITDVKSLPQSAVDEIFKINSVLDVDSCLSHIL

>d1knva\_ c.52.1.7 (A:) Restriction endonuclease Bse634I {Bacillus stearothermophilus}

NLTNSNCVEEYKENGKTKIRIKPFNALIELYHHQTPTGSIKENLDKLENYVKDVVKAKGLAIPTSGAFSNTRGTWFEVMIAIQSWNYRVKRELNDYLIIKMPNVKTFDFRKIFDNETREKLHQLEKSLLTHKQQVRLITSNPDLLIIRQKDLIKSEYNLPINKLTHENIDVALTLFKDIEGKCKWDSLVAGVGLKTSLRPDRRLQLVHEGNILKSLFAHLKMRYWNPKAEFKYYGASSEPVSKADDDALQTAATHTIVNVNSTPERAVDDIFSLTSFEDIDKMLDQIIKK

>d1d02a\_ c.52.1.8 (A:) Restriction endonuclease MunI {Eubacteria (Mycoplasma unidentified)}

LSGRLNWQALAGLKASGAEQNLYNVFNAVFEGTKYVLYEKPKHLKNLYAQVVLPDDVIKEIFNPLIDLSTTQWGVSPAFAIENTETHKILFGEIKRQDGWVEGKDPSAGRGNAHERSCKLFTPGLLKAYRTIGGINDEEILPFWVVFEGDITRDPKRVREITFWYDHYQDNYFMWRPNESGEKLVQHFNEKLKKYLD

>d1ev7a\_ c.52.1.9 (A:) Restriction endonuclease NaeI {Nocardia aerocolonigenes}

EPDDDLERVRATLYSLDPDGDRTAGVLRDTLDQLYDGQRTGRWNFDQLHKTEKTHMGTLVEINLHREFQFGDGFETDYEIAGVQVDCKFSMSQGAWMLPPESIGHICLVIWASDQQCAWTAGLVKVIPQFLGTANRDLKRRLTPEGRAQVVKLWPDHGKLQENLLLHIPGDVRDQIFSAKSSRGNQHGQARVNELFRRVHGRLIGRAVIATVAQQDDFMKRVRGSGGARSILRPEGIIILGHQDNDPKVANDLGLPVPRKGQVVAARVVPADEGDQRQTAEIQGRRWAVAVPGDPIVEAPVV

>d1fiua\_ c.52.1.10 (A:) Restriction endonuclease NgoIV {Neisseria gonorrhoeae}

MQPLFTQERRIFHKKLLDGNILATNNRGVVSNADGSNTRSFNIAKGIADLLHSETVSERLPGQTSGNAFEAICSEFVQSAFEKLQHIRPGDWNVKQVGSRNRLEIARYQQYAHLTALAKAAEENPELAAALGSDYTITPDIIVTRNLIADAEINRNEFLVDENIATYASLRAGNGNMPLLHASISCKWTIRSDRAQNARSEGLNLVRNRKGRLPHIVVVTAEPTPSRISSIALGTGEIDCVYHFALYELEQILQSLNYEDALDLFYIMVNGKRLKDISDLPLDLAV

>d1dc1a\_ c.52.1.11 (A:) Restriction endonuclease BsobI {Bacillus stearothermophilus}

KPFENHLKSVDDLKTTYEEYRAGFIAFALEKNKRSTPYIERARALKVAASVAKTPKDLLYLEDIQDALLYASGISDKAKKFLTEDDKKESINNLIENFLEPAGEEFIDELIFRYLLFQGDSLGGTMRNIAGALAQQKLTRAIISALDIANIPYKWLDSRDKKYTNWMDKPEDDYELETFAKGISWTINGKHRTLMYNITVSLVKKNVDICLFNCEPEIYTPQKVHQQPEKYLLLGELKGGIDPAGADEHWKTANTALTRIRNKFSEKGLSPKTIFIGAAIEHSMAEEIWDQLQSGSLTNSANLTKTEQVGSLCRWIINI

>d1kc6a\_ c.52.1.19 (A:) Restriction endonuclease HincII {Haemophilus influenzae}

SFIKPIYQDINSILIGQKVKRPKSGTLSGHAAGEPFEKLVYKFLKENLSDLTFKQYEYLNDLFMKNPAIIGHEARYKLFNSPTLLFLLSRGKAATENWSIENLFEEKQNDTADILLVKDQFYELLDVKTRNISKSAQAPNIISAYKLAQTCAKMIDNKEFDLFDINYLEVDWELNGEDLVCVSTSFAELFKSEPSELYINWAAAMQIQFHVRDLDQGFNGTREEWAKSYLKHFVTQAEQRAISMIDKFVKPFKKYIL

>d2foka4 c.52.1.12 (A:387-579) Restriction endonuclease FokI, C-terminal (catalytic) domain {Flavobacterium okeanokoites}

KSELEEKKSELRHKLKYVPHEYIELIEIARNSTQDRILEMKVMEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDYGVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRNKHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKAQLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLTLEEVRRKFNNGEINF

>d1avqa\_ c.52.1.13 (A:) lambda exonuclease {Bacteriophage lambda}

SHMTPDIILQRTGIDVRAVEQGDDAWHKLRLGVITASEVHNVIAKPRSGKKWPDMKMSYFHTLLAEVCTGVAPEVNAKALAWGKQYENDARTLFEFTSGVNVTESPIIYRDESMRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLGGFEAIKSAYMAQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVIERDEKYMASFDEIVPEFIEKMDEALAEIGFVFGEQWR

>d1azo\_\_ c.52.1.14 (-) DNA mismatch repair protein MutH from {Escherichia coli}

PRPLLSPPETEEQLLAQAQQLSGYTLGELAALVGLVTPENLKRDKGWIGVLLEIWLGASAGSKPEQDFAALGVELKTIPVDSLGRPLETTFVCVAPLTGNSGVTWETSHVRHKLKRVLWIPVEGEASIPLAQRRVGSPLLWSPNEEEDRQLREDWEELMDMIVLGQVERITARHGEYLQIRPKAANAKALTEAIGARGERILTLPRGFYLKKNFTSALLARHFLIQ

>d1cw0a\_ c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {Escherichia coli}

ADVHDKATRSKNMRAIATRDTAIEKRLASLLTGQGLAFRVQDASLPGRPDFVVDEYRCVIFTHGCFWHHHHCYLFKVPATRTEFWLEKIGKNVERDRRDISRLQELGWRVLIVWECALRGREKLTDEALTERLEEWICGEGASAQIDTQGIHLLA

>d1vsra\_ c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {Escherichia coli}

AIEKRLASLLTGQGLAFRVQDASLPGRPDFVVDEYRCVIFTHGCFWHHHHCYLFKVPATRTEFWLEKIGKNVERDRRDISRLQELGWRVLIVWECALRGREKLTDEALTERLEEWICGEGASAQIDTQGIHLLA

>d1f1za2 c.52.1.16 (A:8-168) TnsA endonuclease, N-terminal domain {Escherichia coli}

FSEVQIARRIKEGRGQGHGKDYIPWLTVQEVPSSGRSHRIYSHKTGRVHHLLSDLELAVFLSLEWESSVLDIREQFPLLPSDTRQIAIDSGIKHPVIRGVDQVMSTDFLVDCKDGPFEQFAIQVKPAAALQDERTLEKLELERRYWQQKQIPWFIFTDKEI

>d1fzra\_ c.52.1.17 (A:) Endonuclease I (Holliday junction resolvase) {Bacteriophage T7}

SGLEDKVSKQLESKGIKFEYEEWKVPYVIPASNHTYTPDFLLPNGIFVKTKGLWESDDRKKHLLIREQHPELDIRIVFSSSRTKLYKGSPTSYGEFCEKHGIKFADKLIPAEWIKEPKKEVPFDRLKRK

>d1gefa\_ c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Pyrococcus furiosus}

MYRKGAQAERELIKLLEKHGFAVVRSAGSKKVDLVAGNGKKYLCIEVKVTKKDHLYVGKRDMGRLIEFSRRFGGIPVLAVKFLNVGWRFIEVSPKIEKFVFTPSSGVSLEVLLGIQKTLE

>d1hh1a\_ c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Sulfolobus solfataricus}

SAVERNIVSRLRDKGFAVVRAPASGSKRKDPIPDIIALKNGVIILIEMKSRKDIEGKIYVRREQAEGIIEFARKSGGSLFLGVKKPGVLKFIPFEKLRRTETGNYVADSEIEGLDLEDLVRLVEAKISRTLD

>d1a79a1 c.52.2.1 (A:83-179) tRNA splicing endonuclease, C-terminal domain {Archaeon Methanococcus jannaschii}

ERLCLKYLVYKDLRTRGYIVKTGLKYGADFRLYERGANIDKEHSVYLVKVFPEDSSFLLSELTGFVRVAHSVRKKLLIAIVDADGDIVYYNMTYVKP

>d1dzfa1 c.52.3.1 (A:5-143) Eukaryotic RPB5 N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

NERNISRLWRAFRTVKEMVKDRGYFITQEEVELPLEDFKAKYCDSMGRPQRKMMSFQANPTEESISKFPDMGSLWVEFCDEPSVGVKTMKTFVIHIQEKNFQTGIFVYQNNITPSAMKLVPSIPPATIETFNEAALVVN

>d1gdta2 c.53.1.1 (A:1-140) gamma,delta resolvase, catalytic domain {Escherichia coli}

MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDVILVKKLDRLGRDTADMIQLIKEFDAQGVSIRFIDDGISTDGEMGKMVVTILSAVAQAERQRILERTNEGRQEAMAKGVVF

>d1hx7a\_ c.53.1.1 (A:) gamma,delta resolvase, catalytic domain {Escherichia coli}

MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDVILVKKLDRLGRDTADMIQLIKEFDAQGVSIRFIDDGISTDGEMGK

>d2rsla\_ c.53.1.1 (A:) gamma,delta resolvase, catalytic domain {Escherichia coli}

MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDVILVKKLDRLGRDTADMIQLIKEFDAQGVSIRFIDDGISTDGEMGKMVVTILSAVAQAERQRI

>d1tfr\_2 c.53.1.2 (12-180) T4 RNase H {Bacteriophage T4}

KEGICLIDFSQIALSTALVNFPDKEKINLSMVRHLILNSIKFNVKKAKTLGYTKIVLCIDNAKSGYWRRDFAYYYKKNRGKAREESTWDWEGYFESSHKVIDELKAYMPYIVMDIDKYEADDHIAVLVKKFSLEGHKILIISSDGDFTQLHKYPNVKQWSPMHKKWVKI

>d1bgxt2 c.53.1.2 (T:1-173) 5' to 3' exonuclease domain of DNA polymerase {Thermus aquaticus}

MRGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGEPVQAVYGFAKSLLKALKEDGDAVIVVFDAKAPSFRHEAYGGYKAGRAPTPEDFPRQLALIKELVDLLGLARLEVPGYEADDVLASLAKKAEKEGYEVRILTADKDLYQLLSDRIHVLHPEGYLITPAWLWEKYG

>d1xo1a2 c.53.1.2 (A:19-185) T5 5'-exonuclease {Bacteriophage T5}

RRNLMIVDGTNLGFRFKHNNSKKPFASSYVSTIQSLAKSYSARTTIVLGDKGKSVFRLEHLPEYAGNRDEKYAQRTEEEKALDEQFFEYLKDAFELCKTTFPTFTIRGVEADDMAAYIVKLIGHLYDHVWLISTDGDWDTLLTDKVSRFSFTTRREYHLRDMYEHHN

>d1a77\_2 c.53.1.2 (2-208) Flap endonuclease-1 {Archaeon Methanococcus jannaschii}

GVQFGDFIPKNIISFEDLKGKKVAIDGMNALYQFLTSIRLRDGSPLRNRKGEITSAYNGVFYKTIHLLENDITPIWVFDGEPPKLKEKTRKVRREMKEKAELKMKEAIKKEDFEEAAKYAKRVSYLTPKMVENCKYLLSLMGIPYVEAPSEGEAQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLTTTKEMPELIELNEVLEDLR

>d1b43a2 c.53.1.2 (A:1-219) Fen-1 nuclease {Archaeon Pyrococcus furiosus}

GVPIGEIIPRKEIELENLYGKKIAIDALNAIYQFLSTIRQKDGTPLMDSKGRITSHLSGLFYRTINLMEAGIKPVYVFDGEPPEFKKKELEKRREAREEAEEKWREALEKGEIEEARKYAQRATRVNEMLIEDAKKLLELMGIPIVQAPSEGEAQAAYMAAKGSVYASASQDYDSLLFGAPRLVRNLTITGKRKLPGKNVYVEIKPELIILEEVLKELK

>d1ekja\_ c.53.2.1 (A:) beta-carbonic anhydrase {Pea (Pisum sativum)}

EASERIKTGFLHFKKEKYDKNPALYGELAKGQSPPFMVFACSDSRVCPSHVLDFQPGEAFVVRNVANLVPPYDQAKYAGTGAAIEYAVLHLKVSNIVVIGHSACGGIKGLLSFPFDGTYSTDFIEEWVKIGLPAKAKVKAQHGDAPFAELCTHCEKEAVNASLGNLLTYPFVREGLVNKTLALKGGYYDFVKGSFELWGLEFGLSSTFSV

>d1g5ca\_ c.53.2.1 (A:) beta-carbonic anhydrase {Archaeon Methanobacterium thermoautotrophicum}

IIKDILRENQDFRFRDLSDLKHSPKLCIITCMDSRLIDLLERALGIGRGDAKVIKNAGNIVDDGVIRSAAVAIYALGDNEIIIVGHTDCGMARLDEDLIVSRMRELGVEEEVIENFSIDVLNPVGDEEENVIEGVKRLKSSPLIPESIGVHGLIIDINTGRLKPLYLDE

>d1i6pa\_ c.53.2.1 (A:) beta-carbonic anhydrase {Escherichia coli}

KDIDTLISNNALWSKMLVEEDPGFFEKLAQAQKPRFLWIGCSDSRVPAERLTGLEPGELFVHRNVANLVIHTDLNCLSVVQYAVDVLEVEHIIICGHYGCGGVQAAVENPELGLINNWLLHIRDIWFKHSSLLGEMPQERRLDTLCELNVMEQVYNLGHSTIMQSAWKRGQKVTIHGWAYGIHDGLLRDLDVTATNRETLEQRYRHGISNLKLK

>d1ddza1 c.53.2.1 (A:84-325) beta-carbonic anhydrase {Red alga (Porphyridium purpureum)}

VMSDLEKKFIELEAKLVAQPAGQAMPGKSNIFANNEAWRQEMLKQDPEFFNRLANGQSPEYLWIGCADSRVPANQLLDLPAGEVFVHRNIANQCIHSDISFLSVLQYAVQYLKVKHILVCGHYGCGGAKAALGDSRLGLIDNWLRHIRDVRRMNAKYLDKCKDGDEELNRLIELNVLEQVHNVCATSIVQDAWDAGQELTVQGVVYGVGDGKLRDLGVVVNSSDDISKFYRTKSDSGALKAG

>d1ddza2 c.53.2.1 (A:326-564) beta-carbonic anhydrase {Red alga (Porphyridium purpureum)}

NPNAPLVQVTKGGESELDSTMEKLTAELVQQTPGKLKEGANRVFVNNENWRQKMLKQDPQFFSNLAHTQTPEILWIGCADSRVPANQIINLPAGEVFVHRNIANQCIHSDMSFLSVLQYAVQYLKVKRVVVCGHYACGGCAAALGDSRLGLIDNWLRHIRDVRRHNQAELSRITDPKDSLNRLIEINVLEQMHNVCATSIVQDAWDAGQELEVQGVVYGVGDGKLRDMGVVAKANDDIG

>d1pdo\_\_ c.54.1.1 (-) IIA domain of mannose transporter, IIA-Man {Escherichia coli}

TIAIVIGTHGWAAEQLLKTAEMLLGEQENVGWIDFVPGENAETLIEKYNAQLAKLDTTKGVLFLVDTWGGSPFNAASRIVVDKEHYEVIAGVNIPMLVETLMARDDDPSFDELVALAVETGREGVKALK

>d1bupa1 c.55.1.1 (A:4-188) Heat shock protein 70kDa, ATPase fragment {Cow (Bos taurus)}

GPAVGIDLGSTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMNPTNTVFDAKRLIGRRFDDAVVQSDMKHWPFMVVNDAGRPKVQVEYKGETKSFYPEEVSSMVLTKMKEIAEAYLGKTVTNAVVTVPAYFNDSQRQATKDAGTIAGLNVLRIINEPTAAAIAYGLDKK

>d1bupa2 c.55.1.1 (A:189-381) Heat shock protein 70kDa, ATPase fragment {Cow (Bos taurus)}

VGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEDFDNRMVNHFIAEFKRKHKKDISENKRAVRRLRTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALRDAKLDKSQIHDIVLVGGSTRIPKIQKLLQDFFNGKELNKSINPDEAVAYGAAVQAAILS

>d1hjoa1 c.55.1.1 (A:3-188) Heat shock protein 70kDa, ATPase fragment {Human (Homo sapiens)}

KAAAIGIDLGTTYSCVGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDAKRLIGRKFGDPVVQSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRT

>d1hjoa2 c.55.1.1 (A:189-382) Heat shock protein 70kDa, ATPase fragment {Human (Homo sapiens)}

GKGERNVLIFDLGGGTFDVSILTIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFFNGRDLNKSINPDEAVAYGAAVQAAILMG

>d1dkgd1 c.55.1.1 (D:3-185) Heat shock protein 70kDa, ATPase fragment {Escherichia coli, gene dnaK}

KIIGIDLGTTNSCVAIMDGTTPRVLENAEGDRTTPSIIAYTQDGETLVGQPAKRQAVTNPQNTLFAIKRLIGRRFQDEEVQRDVSIMPFKIIAADNGDAWVEVKGQKMAPPQISAEVLKKMKKTAEDYLGEPVTEAVITVPAYFNDAQRQATKDAGRIAGLEVKRIINEPTAAALAYGLDKGT

>d1dkgd2 c.55.1.1 (D:186-383) Heat shock protein 70kDa, ATPase fragment {Escherichia coli, gene dnaK}

GNRTIAVYDLGGGTFDISIIEIDEVDGEKTFEVLATNGDTHLGGEDFDSRLINYLVEEFKKDQGIDLRNDPLAMQRLKEAAEKAKIELSSAQQTDVNLPYITADATGPKHMNIKVTRAKLESLVEDLVNRSIELLKVALQDAGLSVSDIDDVILVGGQTRMPMVQKKVAEFFGKEPRKDVNPDEAVAIGAAVQGGVLT

>d1j6za1 c.55.1.1 (A:4-146) Actin {Rabbit (Oryctolagus cuniculus)}

ETTALVCDNGSGLVKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQKDSYVGDEAQSKRGILTLKYPIEHGIITNWDDMEKIWHHTFYNELRVAPEEHPTLLTEAPLNPKANREKMTQIMFETFNVPAMYVAIQAVLSLYASG

>d1j6za2 c.55.1.1 (A:147-372) Actin {Rabbit (Oryctolagus cuniculus)}

RTTGIVLDSGDGVTHNVPIYEGYALPHAIMRLDLAGRDLTDYLMKILTERGYSFVTTAEREIVRDIKEKLCYVALDFENEMATAASSSSLEKSYELPDGQVITIGNERFRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIRKDLYANNVMSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWITKQEYDEAGPSIVHR

>d1d4xa1 c.55.1.1 (A:4-146) Actin {Nematode (Caenorhabditis elegans)}

EVAALVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGVMVGMGQKDSYVGDEAQSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASG

>d1d4xa2 c.55.1.1 (A:147-375) Actin {Nematode (Caenorhabditis elegans)}

RTTGVVLDSGDGVTHTVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITVGNERFRCPEAMFQPSFLGMESAGIHETSYNSIMKCDIDIRKDLYANTVLSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHRKCF

>d1c0fa1 c.55.1.1 (A:1-146) Actin {Slime mold (Dictyostelium discoideum)}

DGEDVQALVIDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHTGKDSYVGDEAQSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASG

>d1dgaa2 c.55.1.1 (A:147-375) Actin {Slime mold (Dictyostelium discoideum)}

RTTGIVMDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYMMKILTERGYSFTTTAEREIVRDIKEKLAYVALDFEQEMATAASSSALEKSYELPDGQVITIGNERFRCPEALFQPSFLGMESAGIHETTYNSIMKCDVDIRKDLYGNVVLSGGTTMFPGIADRMNKELTALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQQMWISKEEYDESGPSIVHRKCF

>d1yaga1 c.55.1.1 (A:4-146) Actin {Baker's yeast (Saccharomyces cerevisiae)}

EVAALVIDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGIMVGMGQKDSYVGDEAQSKRGILTLRYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPMNPKSNREKMTQIMFETFNVPAFYVSIQAVLSLYSSG

>d1yaga2 c.55.1.1 (A:147-375) Actin {Baker's yeast (Saccharomyces cerevisiae)}

RTTGIVLDSGDGVTHVVPIYAGFSLPHAILRIDLAGRDLTDYLMKILSERGYSFSTTAEREIVRDIKEKLCYVALDFEQEMQTAAQSSSIEKSYELPDGQVITIGNERFRAPEALFHPSVLGLESAGIDQTTYNSIMKCDVDVRKELYGNIVMSGGTTMFPGIAERMQKEITALAPSSMKVKIIAPPERKYSVWIGGSILASLTTFQQMWISKQEYDESGPSIVHHKCF

>d1jcfa1 c.55.1.1 (A:1-140) Prokaryotic actin homolog MreB {Thermotoga maritima}

MLRKDIGIDLGTANTLVFLRGKGIVVNEPSVIAIDSTTGEILKVGLEAKNMIGKTPATIKAIRPMRDGVIADYTVALVMLRYFINKAKGGMNLFKPRVVIGVPIGITDVERRAILDAGLEAGASKVFLIEEPMAAAIGSN

>d1jcfa2 c.55.1.1 (A:141-336) Prokaryotic actin homolog MreB {Thermotoga maritima}

LNVEEPSGNMVVDIGGGTTEVAVISLGSIVTWESIRIAGDEMDEAIVQYVRETYRVAIGERTAERVKIEIGNVFPSKENDELETTVSGIDLSTGLPRKLTLKGGEVREALRSVVVAIVESVRTTLEKTPPELVSDIIERGIFLTGGGSLLRGLDTLLQKETGISVIRSEEPLTAVAKGAGMVLDKVNILKKLQGAG

>d1k8ka1 c.55.1.1 (A:3-160) Actin-related protein 3, Arp3 {Cow (Bos taurus)}

GRLPACVVDCGTGYTKLGYAGNTEPQFIIPSCIAIKESAKVGDQAQRRVMKGVDDLDFFIGDEAIEKPTYATKWPIRHGIVEDWDLMERFMEQVIFKYLRAEPEDHYFLLTEPPLNTPENREYTAEIMFESFNVPGLYIAVQAVLALAASWTSRQVGE

>d1k8ka2 c.55.1.1 (A:161-418) Actin-related protein 3, Arp3 {Cow (Bos taurus)}

RTLTGTVIDSGDGVTHVIPVAEGYVIGSCIKHIPIAGRDITYFIQQLLRDREVGIPPEQSLETAKAVKERYSYVCPDLVKEFNKYDTDGSKWIKQYTGINAISKKEFSIDVGYERFLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVRRPLYKNIVLSGGSTMFRDFGRRLQRDLKRTVDARLKLSEELSGGRLKPKPIDVQVITHHMQRYAVWFGGSMLASTPEFYQVCHTKKDYEEIGPSICRHNPVFGVMS

>d1k8kb1 c.55.1.1 (B:154-343) Actin-related protein 2, Arp2 {Cow (Bos taurus)}

GVVVDSGDGVTHICPVYEGFSLPHLTRRLDIAGRDITRYLIKLLLLRGYAFNHSADFETVRMIKEKLCYVGYNIEQEQKLALETTVLVESYTLPDGRIIKVGGERFEAPEALFQPHLINVEGVGVAELLFNTIQAADIDTRSEFYKHIVLSGGSTMYPGLPSRLERELKQLYLERVLKGDVEKLSKFKIR

>d1e4ft1 c.55.1.1 (T:7-199) Cell division protein FtsA {Thermotoga maritima}

TVFYTSIDIGSRYIKGLVLGKRDQEWEALAFSSVKSRGLDEGEIKDAIAFKESVNTLLKELEEQLQKSLRSDFVISFSSVSFEREDTVIERDFGEEKRSITLDILSEMQSEALEKLKENGKTPLHIFSKRYLLDDERIVFNPLDMKASKIAIEYTSIVVPLKVYEMFYNFLQDTVKSPFQLKSSLVSTAEGVL

>d1e4ft2 c.55.1.1 (T:200-390) Cell division protein FtsA {Thermotoga maritima}

TTPEKDRGVVVVNLGYNFTGLIAYKNGVPIKISYVPVGMKHVIKDVSAVLDTSFEESERLIITHGNAVYNDLKEEEIQYRGLDGNTIKTTTAKKLSVIIHARLREIMSKSKKFFREVEAKIVEEGEIGIPGGVVLTGGGAKIPRINELATEVFKSPVRTGCYANSDRPSIINADEVANDPSFAAAFGNVFA

>d1huxa\_ c.55.1.5 (A:) Hydroxyglutaryl-CoA dehydratase component A {Acidaminococcus fermentans}

SIYTLGIDVGSTASKCIILKDGKEIVAKSLVAVGTGTSGPARSISEVLENAHMKKEDMAFTLATGYGRNSLEGIADKQMSELSCHAMGASFIWPNVHTVIDIGGQDVKVIHVENGTMTNFQMNDKCAAGTGRFLDVMANILEVKVSDLAELGAKSTKRVAISSTCTVFAESEVISQLSKGTDKIDIIAGIHRSVASRVIGLANRVGIVKDVVMTGGVAQNYGVRGALEEGLGVEIKTSPLAQYNGALGAALYAYKKAAK

>d1g99a1 c.55.1.2 (A:1-156) Acetate kinase {Archaeon Methanosarcina thermophila}

MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIITQKKFDGKKLEKLTDLPTHKDALEEVVKALTDDEFGVIKDMGEINAVGHRVVHGGEKFTTSALYDEGVEKAIKDCFELAPLHNPPNMMGISACAEIMPGTPMVIVFDTAFHQTMP

>d1g99a2 c.55.1.2 (A:157-398) Acetate kinase {Archaeon Methanosarcina thermophila}

PYAYMYALPYDLYEKHGVRKYGFHGTSHKYVAERAALMLGKPAEETKIITCHLGNGSSITAVEGGKSVETSMGFTPLEGLAMGTRCGSIDPAIVPFLMEKEGLTTREIDTLMNKKSGVLGVSGLSNDFRDLDEAASKGNRKAELALEIFAYKVKKFIGEYSAVLNGADAVVFTAGIGENSASIRKRILTGLDGIGIKIDDEKNKIRGQEIDISTPDAKVRVFVIPTNEELAIARETKEIVET

>d1ig8a1 c.55.1.3 (A:18-224) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}

DVPKELMQQIENFEKIFTVPTETLQAVTKHFISELEKGLSKKGGNIPMIPGWVMDFPTGKESGDFLAIDLGGTNLRVVLVKLGGDRTFDTTQSKYRLPDAMRTTQNPDELWEFIADSLKAFIDEQFPQGISEPIPLGFTFSFPASQNKINEGILQRWTKGFDIPNIENHDVVPMLQKQITKRNIPIEVVALINDTTGTLVASYYTDP

>d1ig8a2 c.55.1.3 (A:225-486) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}

ETKMGVIFGTGVNGAYYDVCSDIEKLQGKLSDDIPPSAPMAINCEYGSFDNEHVVLPRTKYDITIDEESPRPGQQTFEKMSSGYYLGEILRLALMDMYKQGFIFKNQDLSKFDKPFVMDTSYPARIEEDPFENLEDTDDLFQNEFGINTTVQERKLIRRLSELIGARAARLSVCGIAAICQKRGYKTGHIAADGSVYNRYPGFKEKAANALKDIYGWTQTSLDDYPIKIVPAEDGSGAGAAVIAALAQKRIAEGKSVGIIGA

>d1bdg\_1 c.55.1.3 (13-222) Hexokinase {Blood fluke (Schistosoma mansoni)}

FSDQQLFEKVVEILKPFDLSVVDYEEICDRMGESMRLGLQKSTNEKSSIKMFPSYVTKTPNGTETGNFLALDLGGTNYRVLSVTLEGKGKSPRIQERTYCIPAEKMSGSGTELFKYIAETLADFLENNGMKDKKFDLGFTFSFPCVQKGLTHATLVRWTKGFSADGVEGHNVAELLQTELDKRELNVKCVAVVNDTVGTLASCALEDP

>d1bdg\_2 c.55.1.3 (223-460) Hexokinase {Blood fluke (Schistosoma mansoni)}

KCAVGLIVGTGTNVAYIEDSSKVELMDGVKEPEVVINTEWGAFGEKGELDCWRTQFDKSMDIDSLHPGKQLYEKMVSGMYLGELVRHIIVYLVEQKILFRGDLPERLKVRNSLLTRYLTDVERDPAHLLYNTHYMLTDDLHVPVVEPIDNRIVRYACEMVVKRAAYLAGAGIACILRRINRSEVTVGVDGSLYKFHPKFCERMTDMVDKLKPKNTRFCLRLSEDGSGKGAAAIAASC

>d1czan1 c.55.1.3 (N:16-222) Mammalian type I hexokinase {Human (Homo sapiens)}

DDQVKKIDKYLYAMRLSDETLIDIMTRFRKEMKNGLSRDFNPTATVKMLPTFVRSIPDGSEKGDFIALDLGGSSFRILRVQVNHEKNQNVHMESEVYDTPENIVHGSGSQLFDHVAECLGDFMEKRKIKDKKLPVGFTFSFPCQQSKIDEAILITWTKRFKASGVEGADVVKLLNKAIKKRGDYDANIVAVVNDTVGTMMTCGYDDQ

>d1czan2 c.55.1.3 (N:223-465) Mammalian type I hexokinase {Human (Homo sapiens)}

HCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRAIDAYSLNPGKQLFEKMVSGMYLGELVRLILVKMAKEGLLFEGRITPELLTRGKFNTSDVSAIEKNKEGLHNAKEILTRLGVEPSDDDCVSVQHVCTIVSFRSANLVAATLGAILNRLRDNKGTPRLRTTVGVDGSLYKTHPQYSRRFHKTLRRLVPDSDVRFLLSESGSGKGAAMVTAVAYRLAE

>d1czan3 c.55.1.3 (N:466-670) Mammalian type I hexokinase {Human (Homo sapiens)}

QHRQIEETLAHFHLTKDMLLEVKKRMRAEMELGLRKQTHNNAVVKMLPSFVRRTPDGTENGDFLALDLGGTNFRVLLVKIRSGKKRTVEMHNKIYAIPIEIMQGTGEELFDHIVSCISDFLDYMGIKGPRMPLGFTFSFPCQQTSLDAGILITWTKGFKATDCVGHDVVTLLRDAIKRREEFDLDVVAVVNDTVGTMMTCAYEEP

>d1czan4 c.55.1.3 (N:671-913) Mammalian type I hexokinase {Human (Homo sapiens)}

TCEVGLIVGTGSNACYMEEMKNVEMVEGDQGQMCINMEWGAFGDNGCLDDIRTHYDRLVDEYSLNAGKQRYEKMISGMYLGEIVRNILIDFTKKGFLFRGQISETLKTRGIFETKFLSQIESDRLALLQVRAILQQLGLNSTCDDSILVKTVCGVVSRRAAQLCGAGMAAVVDKIRENRGLDRLNVTVGVDGTLYKLHPHFSRIMHQTVKELSPKCNVSFLLSEDGSGKGAALITAVGVRLRT

>d1bg3a1 c.55.1.3 (A:1-222) Mammalian type I hexokinase {Rat (Rattus norvegicus)}

MIAAQLLAYYFTELKDDQVKKIDKYLYAMRLSDEILIDILTRFKKEMKNGLSRDYNPTASVKMLPTFVRSIPDGSEKGDFIALDLGGSSFRILRVQVNHEKNQNVSMESEIYDTPENIVHGSGTQLFDHVADCLGDFMEKKKIKDKKLPVGFTFSFPCRQSKIDEAVLITWTKRFKASGVEGADVVKLLNKAIKKRGDYDANIVAVVNDTVGTMMTCGYDDQ

>d1bg3a2 c.55.1.3 (A:223-465) Mammalian type I hexokinase {Rat (Rattus norvegicus)}

QCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRELDRGSLNPGKQLFEKMVSGMYMGELVRLILVKMAKEGLLFEGRITPELLTRGKFNTSDVSAIEKDKEGIQNAKEILTRLGVEPSDVDCVSVQHICTIVSFRSANLVAATLGAILNRLRDNKGTPRLRTTVGVDGSLYKMHPQYSRRFHKTLRRLVPDSDVRFLLSESGTGKGAAMVTAVAYRLAE

>d1bg3a3 c.55.1.3 (A:466-670) Mammalian type I hexokinase {Rat (Rattus norvegicus)}

QHIRQIEETLAHFRLSKQTLMEVKKRLRTEMEMGLRKETNSKATVKMLPSFVRSIPDGTEHGDFLALDLGGTNFRVLLVKIRSGKKRTVEMHNKIYSIPLEIMQGTGDELFDHIVSCISDFLDYMGIKGPRMPLGFTFSFPCHQTNLDCGILISWTKGFKATDCEGHDVASLLRDAVKRREEFDLDVVAVVNDTVGTMMTCAYEEP

>d1bg3a4 c.55.1.3 (A:671-911) Mammalian type I hexokinase {Rat (Rattus norvegicus)}

TCEIGLIVGTGTNACYMEEMKNVEMVEGNQGQMCINMEWGAFGDNGCLDDIRTDFDKVVDEYSLNSGKQRFEKMISGMYLGEIVRNILIDFTKKGFLFRGQISEPLKTRGIFETKFLSQIESDRLALLQVRAILQQLGLNSTCDDSILVKTVCGVVSKRAAQLCGAGMAAVVEKIRENRGLDHLNVTVGVDGTLYKLHPHFSRIMHQTVKELSPKCTVSFLLSEDGSGKGAALITAVGVRL

>d1bu6o1 c.55.1.4 (O:3-253) Glycerol kinase {Escherichia coli}

KKYIVALDQGTTSSRAVVMDHDANIISVSQREFEQIYPKPGWVEHDPMEIWATQSSTLVEVLTKADISSDQIAAIGITNQRETTIVWEKETGKPIYNAIVWQCRRTAEICEHLKRDGLEDYIRSNTGLVIDPYFSGTKVKWILDHVEGSRERARRGELLFGTVDTWLIWKMTQGRVHVTDYTNASRTMLFNIHTLDWDDKMLEVLDIPREMLPEVRRSSEVYGQTNIGGKGGTRIPISGIAGDQQAALFGQ

>d1bu6o2 c.55.1.4 (O:254-499) Glycerol kinase {Escherichia coli}

LCVKEGMAKNTYGTGCFMLMNTGEKAVKSENGLLTTIACGPTGEVNYALEGAVFMAGASIQWLRDEMKLINDAYDSEYFATKVQNTNGVYVVPAFTGLGAPYWDPYARGAIFGLTRGVNANHIIRATLESIAYQTRDVLEAMQADSGIRLHALRVDGGAVANNFLMQFQSDILGTRVERPEVREVTALGAAYLAGLAVGFWQNLDELQEKAVIEREFRPGIETTERNYRYAGWKKAVKRAMAWEEH

>d1chma1 c.55.2.1 (A:2-156) Creatinase {Pseudomonas putida}

QMPKTLRIRNGDKVRSTFSAQEYANRQARLRAHLAAENIDAAIFTSYHNINYYSDFLYCSFGRPYALVVTEDDVISISANIDGGQPWRRTVGTDNIVYTDWQRDNYFAAIQQALPKARRIGIEHDHLNLQNRDKLAARYPDAELVDVAAACMRMR

>d1az9\_1 c.55.2.1 (1-176) Aminopeptidase P {Escherichia coli}

SEISRQEFQRRRQALVEQMQPGSAALIFAAPEVTRSADSEYPYRQNSDFWYFTGFNEPEAVLVLIKSDDTHNHSVLFNRVRDLTAEIWFGRRLGQDAAPEKLGVDRALAFSEINQQLYQLLNGLDVVYHAQGEYAYADVIVNSALEKLRKGSRQNLTAPATMIDWRPVVHEMRLFK

>d1jl1a\_ c.55.3.1 (A:) RNase H (RNase HI) {Escherichia coli}

KQVEIFTAGSALGNPGPGGYGAILRYRGREKTFSAGYTRTTNNRMELMAAIVALEALKEHAEVILSTDSQYVRQGITQWIHNWKKRGWKTADKKPVKNVDLWQRLDAALGQHQIKWEWVKGHAGHPENERADELARAAAMNPTLEDTGYQVE

>d1ril\_\_ c.55.3.1 (-) RNase H (RNase HI) {Thermus thermophilus}

RKRVALFTDGACLGNPGPGGWAALLRFHAHEKLLSGGEACTTNNRMELKAAIEGLKALKEPCEVDLYTDSHYLKKAFTEGWLEGWRKRGWRTAEGKPVKNRDLWEALLLAMAPHRVRFHFVKGHTGHPENERVDREARRQAQSQAKT

>d1jl2a\_ c.55.3.1 (A:) RNase H (RNase HI) {Chimeric (Escherichia coli/Thermus thermophilus)}

KQVEIFTDGSALGNPGPGGYGAILRYRGREKTFSAGYTRTTNNRMELKAAIEGLKALKEPAEVDLYTDSHYLKKAFTEGWLEGWRKRGWRTAEGKPVKNRDLWEALLLAMAPHRVRFHFVKGHAGHPENERADELARAAAMNPTLEDTGY

>d1ekea\_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Methanococcus jannaschii}

MIIIGIDEAGRGPVLGPMVVCAFAIEKEREEELKKLGVKDSKELTKNKRAYLKKLLENLGYVEKRILEAEEINQLMNSINLNDIEINAFSKVAKNLIEKLNIRDDEIEIYIDACSTNTKKFEDSFKDKIEDIIKERNLNIKIIAEHKADAKYPVVSAASIIAKAERDEIIDYYKKIYGDIGSGYPSDPKTIKFLEDYFKKHKKLPDIARTHWKTCKRILDKSKQT

>d1i39a\_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Archaeoglobus fulgidus}

MKAGIDEAGKGCVIGPLVVAGVACSDEDRLRKLGVKDSKKLSQGRREELAEEIRKICRTEVLKVSPENLDERMAAKTINEILKECYAEIILRLKPEIAYVDSPDVIPERLSRELEEITGLRVVAEHKADEKYPLVAAASIIAKVEREREIERLKEKFGDFGSGYASDPRTREVLKEWIASGRIPSCVRMRWKTVSNLRQK

>d1io2a\_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Thermococcus kodakaraensis}

MKIAGIDEAGRGPVIGPMVIAAVVVDENSLPKLEELKVRDSKKLTPKRREKLFNEILGVLDDYVILELPPDVIGSREGTLNEFEVENFAKALNSLKVKPDVIYADAADVDEERFARELGERLNFEAEVVAKHKADDIFPVVSAASILAKVTRDRAVEKLKEEYGEIGSGYPSDPRTRAFLENYYREHGEFPPIVRKGWKTLKKIAEKVESEKK

>d1c9ra1 c.55.3.1 (A:430-558) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANAATKLGKAGYVTNKGRQKVVPLTNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAQPDKSESELVNQIIEALIKKEAVYLAWVPAHAGIGGNAAVDALVSAGIAA

>d1hrha1 c.55.3.1 (A:432-556) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}

EPIVGAETFYVDGAANRETKLGKAGYVTNKGRQKVVPLTNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAQPDKSESELVNQIIEQLIKKEKVYLAWVPAHKGIGGNEQVDKLVSAGI

>d1jlaa1 c.55.3.1 (A:430-553) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANRETKLGKAGYVTNRGRQKVVTLTDTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAQPDQSESELVNQIIEQLIKKEKVYLAWVPAHKGIGGNEQVDKLVS

>d1vrta1 c.55.3.1 (A:430-539) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANRETKLGKAGYVTNRGRQKVVTLTDTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAQPDQSESELVNQIIEQLIKKEKVYLAWVPAH

>d1asu\_\_ c.55.3.2 (-) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}

PLREPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAAQHHWATAIAVLGRPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMVERANRLLKDKIRVLAEGDGFMKRIPTSKQGELLAKAMYALNHFERGENTKTNL

>d1c0ma2 c.55.3.2 (A:49-216) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}

GVNPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAVQHHWATAIAVLGRPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMVERANRLLKDRIRVLAEGDGFMKRIPTSKQGELLAKAMYALNHKERGENTKTPIQKHWRPT

>d1cxqa\_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}

GRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAAQHHWATAIAVLGRPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMVERANRLLKDKIRVLAEGDGFMKRIPTSKQGELLAKAMYALNH

>d1exqa\_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}

SSPGIWQLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKTIHTDNGSNFTGATVRAACDWAGIKQEDGIPYNPQSQGVVESMNKELKKIIGQVRDQAEHLKTAVQMAVFIHNKKRKGGIGGYSAGERIVDIIATDIQ

>d1hyva\_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}

SPGIWQLDCTHLEGKVILVAVHVASGYIEAEVIPAETGQETAYFLLKLAGRWPVKTVHTDNGSNFTSTTVKAACWWAGIKQEFGIPYNPQSQGVIESMNKELKKIIGQVRDQAEHLKTAVQMAVFIHNKKRKGGIGGYSAGERIVDIIATDIQT

>d1c6va\_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Simian immunodeficiency virus}

NSDLGTWQMDCTHLEGKIVIVAVHVASGFIEAEVIPQETGRQTALFLLKLAGRWPITHLHTDNGANFASQEVKMVAWWAGIEHTFGVPYNPQSQGVVEAMNHHLKNQIDRIREQANSVETIVLMAVHCMNHKRRGGIGDMTPAERLINMITTEQEIQFQ

>d1bco\_2 c.55.3.3 (258-480) mu transposase, core domain {Bacteriophage mu}

EHLDAMQWINGDGYLHNVFVRWFNGDVIRPKTWFWQDVKTRKILGWRCDVSENIDSIRLSFMDVVTRYGIPEDFHITIDNTRGAANKWLTGGAPNRYRFKVKEDDPKGLFLLMGAKMHWTSVVAGKGWGQAKPVERAFGVGGLEEYVDKHPALAGAYTGPNPQAKPDNYGDRAVDAELFLKTLAEGVAMFNARTGRETEMCGGKLSFDDVFEREYARTIVRKP

>d1b7ea\_ c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}

SAEAIRKAGAMQTVKLAQEFPELLAIEDTTSLSYRHQVAEELGKLGSIQDKSRGWWVHSVLLLEATTFRTVGLLHQEWWMRPDDPADADEKESGKWLAAAATSRLRMGSMMSNVIAVCDREADIHAYLQDKLAHNERFVVRSKHPRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPARKASLSLRSGRITLKQGNITLNAVLAEEINPPKGETPLKWLLLTSEPVESLAQALRVIDIYTHRWRIEEFHKAWKTGAGAERQRMEEPDNLERMVSILSFVAVRLLQLRESFTLPQALRAQGLLKEAEHVESQSAETVLTPDECQLLGYLDKGKRKRKEKGSLQWAYMAIARLGGFMDSKRTGIASWGALWEGWEALQSKLDGFLAAKDLMAQ

>d1f3ia\_ c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}

ALHRAADWAKSVFSSAALGDPRRTARLVNVAAQLAKYSGKSITISSEGSKAAQEGAYRFIRNPNVSAEAIRKAGAMQTVKLAQEFPELLAIEDTTSLSYRHQVAEELGKLGSIQDKSRGWWVHSVLLLEATTFRTVGLLHQEWWMRPDDPADADEKESGKWLAAAATSRLRMGSMMSNVIAVCDREADIHAYLQDKLAHNERFVVRSKHPRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPARKASLSLRSGRITLKQGNITLNAVLAEEINPPKGETPLKWLLLTSEPVESLAQALRVIDIYTHRWRIEEFHKAWKTGAGAERQRMEEPDNLERMVSILSFVAVRLLQLRESFTLPQALRAQGLLKEAEHVESQSAETVLTPDECQLLGYLDKGKRKRKEKAGSLQWAYMAIARLGGFMDSKRTGIASWGALWEGWEALQSKLDGFLAAKDLMAQGIKIG

>d1kfsa1 c.55.3.5 (A:324-518) Exonuclease domain of prokaryotic DNA polymerase {Escherichia coli}

MISYDNYVTILDEETLKAWIAKLEKAPVFAFDTETDSLDNISANLVGLSFAIEPGVAAYIPVAHDYLDAPDQISRERALELLKPLLEDEKALKVGQNLKYDRGILANYGIELRGIAFDTMLESYILNSVAGRHDMDSLAERWLKHKTITFEEIAGKGKNQLTFNQIALEEAGRYAAEDADVTLQLHLKMWPDLQK

>d1qtma1 c.55.3.5 (A:293-422) Exonuclease domain of prokaryotic DNA polymerase {Thermus aquaticus}

ALEEAPWPPPEGAFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSERLFANLWGRLEG

>d1xwl\_1 c.55.3.5 (297-468) Exonuclease domain of prokaryotic DNA polymerase {Bacillus stearothermophilus, newly identified strain as yet unnamed}

AKMAFTLADRVTEEMLADKAALVVEVVEENYHDAPIVGIAVVNEHGRFFLRPETALADPQFVAWLGDETKKKSMFDSKRAAVALKWKGIELCGVSFDLLLAAYLLDPAQGVDDVAAAAKMKQYEAVRPDEAVYGKGAKRAVPDEPVLAEHLVRKAAAIWELERPFLDELRRN

>d1t7pa1 c.55.3.5 (A:1-210) Exonuclease domain of T7 DNA polymerase {Bacteriophage T7}

MIVSDIEANALLESVTKFHCGVIYDYSTAEYVSYRPSDFGAYLDALEAEVARGGLIVFHNGHKYDVPALTKLAKLQLNREFHLPRENCIDTLVLSRLIHSNLKDTDMGLLRSGKLPGALEAWGYRLGEMKGEYKDDFKRMLEEQGEEYVDGMEWWNFNEEMMDYNVQDVVVTKALLEKLLSDKHYFPPEIDFTDVGYTTFWSES

>d1noya\_ c.55.3.5 (A:) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Bacteriophage T4}

DEFYISIETVGNNIVERYIDENGKERTREVEYLPTMFRHCKEESKYKDIYGKNCAPQKFPSMKDARDWMKRMEDIGLEALGMNDFKLAYISDTYGSEIVYDRKFVRVANCDIEVTGDKFPDPMKAEYEIDAITHYDSIDDRFYVFDLLNSMYGSVSKWDAKLAAKLDCEGGDEVPQEILDRVIYMPFDNERDMLMEYINLWEQKRPAIFTGWNIEGFDVPYIMNRVKMILGERSMKRFSPIGRVKSKLLQNMYGSKEIYSIDGVSILDYLDLYKKFAFTNLPSFSLESVAQHETKKGKLPYDGPINKLRETNHQRYISYNIIDVESVQAIDKIRGFIDLVLSMSYYAKMPFSGVMSPIKTWDAIIFNSLKGE

>d1ih7a1 c.55.3.5 (A:1-375) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Bacteriophage RB69}

MKEFYLTVEQIGDSIFERYIDSNGRERTREVEYKPSLFAHCPESQATKYFDIYGKPCTRKLFANMRDASQWIKRMEDIGLEALGMDDFKLAYLSDTYNYEIKYDHTKIRVANFDIEVTSPDGFPEPSQAKHPIDAITHYDSIDDRFYVFDLLNSPYGNVEEWSIEIAAKLQEQGGDEVPSEIIDKIIYMPFDNEKELLMEYLNFWQQKTPVILTGWNVESFDIPYVYNRIKNIFGESTAKRLSPHRKTRVKVIENMYGSREIITLFGISVLDYIDLYKKFSFTNQPSYSLDYISEFELNVGKLKYDGPISKLRESNHQRYISYNIIDVYRVLQIDAKRQFINLSLDMGYYAKIQIQSVFSPIKTWDAIIFNSLKE

>d1tgoa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Thermococcus gorgonarius}

MILDTDYITEDGKPVIRIFKKENGEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGTTVRVVRAEKVKKKFLGRPIEVWKLYFTHPQDVPAIRDKIKEHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNIDLPYVDVVSTEKEMIKRFLKVVKEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFILGREGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEEIAQAWETGEGLERVARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRS

>d1qhta1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Thermococcus sp., 9on-7}

MILDTDYITENGKPVIRVFKKENGEFKIEYDRTFEPYFYALLKDDSAIEDVKKVTAKRHGTVVKVKRAEKVQKKFLGRPIEVWKLYFNHPQDVPAIRDRIRAHPAVVDIYEYDIPFAKRYLIDKGLIPMEGDEELTMLAFAIATLYHEGEEFGTGPILMISYADGSEARVITWKKIDLPYVDVVSTEKEMIKRFLRVVREKDPDVLITYNGDNFDFAYLKKRCEELGIKFTLGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGKPKEKVYAEEIAQAWESGEGLERVARYSMEDAKVTYELGREFFPMEAQLSRLIGQSLWDVSRS

>d1d5aa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Desulfurococcus tok}

MILDADYITEDGKPVIRVFKKEKGEFKIDYDRDFEPYIYALLKDDSAIEDIKKITAERHGTTVRVTRAERVKKKFLGRPVEVWKLYFTHPQDVPAIRDKIREHPAVVDIYEYDIPFAKRYLIDRGLIPMEGDEELRMLAFDIETLAHAGAAAGAGPILMISYADEEGARVITWKNIDLPYVESVSTEKEMIKRFLKVIQEKDPDVLITYNGDNFDFAYLKKRSEMLGVKFILGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLETVYEPVFGQPAEKVYAEEIAEAWASGEGLERVARYSMEDAKATYELGKEFFPMEAQLSRLVGQSLWDVSRS

>d1gcxa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Pyrococcus kodakaraensis}

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLGRPVEVWKLYFTHPQDVPAIRDKIREHPAVIDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNVDLPYVDVVSTEREMIKRFLRVVKEKDPDVLITYNGDNFDFAYLKKRCEKLGINFALGRDGSEPKIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAVFGQPKEKVYAEEITTAWETGENLERVARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRS

>d1fxxa\_ c.55.3.5 (A:) Exonuclease I {Escherichia coli}

QSTFLFHDYETFGTHPALDRPAQFAAIRTDSEFNVIGEPEVFYCKPADDYLPQPGAVLITGITPQEARAKGENEAAFAARIHSLFTVPKTCILGYNNVRFDDEVTRNIFYRNFYDPYAWSWQHDNSRWDLLDVMRACYALRPEGINWPENDDGLPSFRLEHLTKANGIEHSNAHDAMADVYATIAMAKLVKTRQPRLFDYLFTHRNKHKLMALIDVPQMKPLVHVSGMFGAWRGNTSWVAPLAWHPENRNAVIMVDLAGDISPLLELDSDTLRERLYTAKTDLGDNAAVPVKLVHINKCPVLAQANTLRPEDADRLGINRQHCLDNLKILRENPQVREKVVAIFAEAEPFTPSDNVDAQLYNGFFSDADRAAMKIVLETEPRNLPALDITFVDKRIEKLLFNYRARNFPGTLDYAEQQRWLEHRRQVFTPEFLQGYADELQMLVQQYADDKEKVALLKALWQYADEIVEH

>d1hjra\_ c.55.3.6 (A:) RuvC resolvase {Escherichia coli}

AIILGIDPGSRVTGYGVIRQVGRQLSYLGSGCIRTKVDDLPSRLKLIYAGVTEIITQFQPDYFAIEQVFMAKNADSALKLGQARGVAIVAAVNQELPVFEYAARQVKQTVVGIGSAEKSQVQHMVRTLLKLPANPQADAADALAIAITHCHVSQNAMQ

>d1kcfa2 c.55.3.7 (A:39-256) Mitochondrial resolvase ydc2 catalytic domain {Fission yeast (Schizosaccharomyces pombe)}

TSRVLGIDLGIKNFSYCFASQNEDSKVIIHNWSVENLTEKNGLDIQWTEDFQPSSMADLSIQLFNTLHEKFNPHVILMERQRYRSGIATIPEWTLRVNMLESMLYALHYAEKRNSIEQKIQYPFLLSLSPKSTYSYWASVLNTKASFSKKKSRVQMVKELIDGQKILFENEEALYKWNNGSRVEFKKDDMADSALIASGWMRWQAQLKHYRNFCKQFL

>d1jj2m\_ c.55.4.1 (M:) Ribosomal protein L18 (L18p) {Archaeon Haloarcula marismortui}

ATGPRYKVPMRRRREARTDYHQRLRLLKSGKPRLVARKSNKHVRAQLVTLGPNGDDTLASAHSSDLAEYGWEAPTGNMPSAYLTGLLAGLRAQEAGVEEAVLDIGLNSPTPGSKVFAIQEGAIDAGLDIPHNDDVLADWQRTRGAHIAEYDEQLEEPLYSGDFDAADLPEHFDELRETLLDGDIEL

>d1fjgk\_ c.55.4.1 (K:) Ribosomal protein S11 {Thermus thermophilus}

KRQVASGRAYIHASYNNTIVTITDPDGNPITWSSGGVIGYKGSRKGTPYAAQLAALDAAKKAMAYGMQSVDVIVRGTGAGREQAIRALQASGLQVKSIVDDTPVPHNGCRPKKKFRKAS

>d1dt9a1 c.55.4.2 (A:143-276) Middle domain of eukaryotic peptide chain release factor subunit 1, ERF1 {Human (Homo sapiens)}

DSKFGFIVIDGSGALFGTLQGNTREVLHKFTVDLPKKHGRGGQSALRFARLRMEKRHNYVRKVAETAVQLFISGDKVNVAGLVLAGSADFKTELSQSDMFDQRLQSKVLKLVDISYGGENGFNQAIELSTEVLS

>d1eo1a\_ c.55.5.1 (A:) Hypothetical protein MTH1175 {Archaeon Methanobacterium thermoautotrophicum}

MKIAIASSGTDLGSEVSRFFGRAPYFMIVEMKKGNIESSEVIENPSASASGGAGIRTAQIIANNGVKAVIASSPGPNAFEVLNELGIKIYRATGTSVEENLKLFTEGNLEEIRSPGSGRGRRRR

>d1ewqa3 c.55.6.1 (A:121-266) DNA repair protein MutS, domain II {Thermus aquaticus}

LLQESLLPREANYLAAIATGDGWGLAFLDVSTGEFKGTVLKSKSALYDELFRHRPAEVLLAPELLENGAFLDEFRKRFPVMLSEAPFEPEGEGPLALRRARGALLAYAQRTQGGALSLQPFRFYDPGAFMRLPEATLRALEVFEPL

>d1e3ma3 c.55.6.1 (A:117-269) DNA repair protein MutS, domain II {Escherichia coli}

GTISDEALLQERQDNLLAAIWQDSKGFGYATLDISSGRFRLSEPADRETMAAELQRTNPAELLYAEDFAEMSLIEGRRGLRRRPLWEFEIDTARQQLNLQFGTRDLVGFGVENAPRGLCAAGCLLQYAKDTQRTTLPHIRSITMEREQDSIIM

>d1sfe\_2 c.55.7.1 (12-92) Ada DNA repair protein {Escherichia coli}

LAVRYALADCELGRCLVAESERGICAILLGDDDATLISELQQMFPAADNAPADLMFQQHVREVIASLNQRDTPLTLPLDIR

>d1qnta2 c.55.7.1 (A:6-91) O6-alkylguanine-DNA alkyltransferase {Human (Homo sapiens)}

EMKRTTLDSPLGKLELSGCEQGLHEIKLLGKGTSAADAVEVPAPAAVLGGPEPLMQCTAWLNAYFHQPEAIEEFPVPALHHPVFQQ

>d1mgta2 c.55.7.1 (A:1-88) O6-alkylguanine-DNA alkyltransferase {Archaeon Pyrococcus kodakaraensis}

MLSVEKFRVGERVVWIGVIFSGRVQGIAFAFDRGTLMKRIHDLAEHLGKRGVSISLDVQPSDYPEKVFKVLIGELDNASFLRELSFEG

>d1cfza\_ c.56.1.1 (A:) Hydrogenase maturating endopeptidase HybD {Escherichia coli}

MRILVLGVGNILLTDEAIGVRIVEALEQRYILPDYVEILDGGTAGMELLGDMANRDHLIIADAIVSKKNAPGTMMILRDEEVPALFTNKISPHQLGLADVLSALRFTGEFPKKLTLVGVIPESLEPHIGLTPTVEAMIEPALEQVLAALRESGVEAIPRSDS

>d1c8ba\_ c.56.1.2 (A:) Germination protease {Bacillus megaterium}

MEKELDLSQYSVRTDLAVEAKDIALENQPKPNNQSEIKGVIVKEKEEQGVKISMVEITEEGAEAIGKKKGRYVTLESVGIREQDTEKQEEAMEEVFAKELNFFIKSLNIPDDASCLVVGLGNLSVTPDALGPKAVDNLLITRHLFELQPESVQDGFRPVSAIVPGVMGMTGIETSDIIFGVVKKVNPDFIIAIDALAARSIERVNATIQISDSGIHPGSGVGNKRKEISYETLGIPVIAIGIPTVVDAVSITSDTIDFILKHFGREMKEQGKPSKSLLPSGMTFGEKKKLTEDDLPNEEQRQTYLGMIGTLPDEEKRRLIHEVLAPLGHNLMVTPKEVDMFIEDMANVVAGGLNAALHHEVDQENFGAYTH

>d1ulb\_\_ c.56.2.1 (-) Purine nucleoside phosphorylase, PNP {Human (Homo sapiens)}

MENGYTYEDYKNTAEWLLSHTKHRPQVAIICGSGLGGLTDKLTQAQIFDYSEIPNFPRSTVPGHAGRLVFGFLNGRACVMMQGRFHMYEGYPLWKVTFPVRVFHLLGVDTLVVTNAAGGLNPKFEVGDIMLIRDHINLPGFSGQNPLRGPNDERFGDRFPAMSDAYDRTMRQRALSTWKQMGEQRELQEGTYVMVAGPSFETVAECRVLQKLGADAVGMSTVPEVIVARHCGLRVFGFSLITNKVIMDYESLEKANHEEVLAAGKQAAQKLEQFVSILMASIPLPDKAS

>d1b8oa\_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cow (Bos taurus)}

NGYTYEDYQDTAKWLLSHTEQRPQVAVICGSGLGGLVNKLTQAQTFDYSEIPNFPESTVPGHAGRLVFGILNGRACVMMQGRFHMYEGYPFWKVTFPVRVFRLLGVETLVVTNAAGGLNPNFEVGDIMLIRDHINLPGFSGENPLRGPNEERFGVRFPAMSDAYDRDMRQKAHSTWKQMGEQRELQEGTYVMLGGPNFETVAECRLLRNLGADAVGMSTVPEVIVARHCGLRVFGFSLITNKVIMDYESQGKANHEEVLEAGKQAAQKLEQFVSLLMASI

>d1k9sa\_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Escherichia coli}

ATPHINAEMGDFADVVLMPGDPLRAKYIAETFLEDAREVNNVRGMLGFTGTYKGRKISVMGHGMGIPSCSIYTKELITDFGVKKIIRVGSCGAVLPHVKLRDVVIGMGACTDSKVNRIRFKDHDFAAIADFDMVRNAVDAAKALGIDARVGNLFSADLFYSPDGEMFDVMEKYGILGVEMEAAGIYGVAAEFGAKALTICTVSDHIRTHEQTTAAERQTTFNDMIKIALESVLLGDK

>d1qe5a\_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cellulomonas sp.}

PPLDDPATDPFLVARAAADHIAQATGVEGHDMALVLGSGWGGAAELLGEVVAEVPTHEIPGFSSVTRSIRVERADGSVRHALVLGSRTHLYEGKGVRAVVHGVRTAAATGAETLILTNGCGGLNQEWGAGTPVLLSDHINLTARSPLEGPTFVDLTDVYSPRLRELAHRVDPTLPEGVYAQFPGPHYETPAEVRMAGILGADLVGMSTTLEAIAARHCGLEVLGVSLVTNLAAGISPTPLSHAEVIEAGQAAGPRISALLADIAKR

>d1g2oa\_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Mycobacterium tuberculosis}

DPDELARRAAQVIADRTGIGEHDVAVVLGSGWLPAVAALGSPTTVLPQAELPGFVPPTAAGHAGELLSVPIGAHRVLVLAGRIHAYEGHDLRYVVHPVRAARAAGAQIMVLTNAAGGLRADLQVGQPVLISDHLNLTARSPLVGGEFVDLTDAYSPRLRELARQSDPQLAEGVYAGLPGPHYETPAEIRMLQTLGADLVGMSTVHETIAARAAGAEVLGVSLVTNLAAGITGEPLSHAEVLAAGAASATRMGALLADVIARF

>d1k3fa\_ c.56.2.1 (A:) Uridine phosphorylase {Escherichia coli}

MSKSDVFHLGLTKNDLQGATLAIVPGDPDRVEKIAALMDKPVKLASHREFTTWRAELDGKPVIVCSTGIGGPSTSIAVEELAQLGIRTFLRIGTTGAIQPHINVGDVLVTTASVRLDGASLHFAPLEFPAVADFECTTALVEAAKSIGATTHVGVTASSDTFYPGQERYDTYSGRVVRHFKGSMEEWQAMGVMNYEMESATLLTMCASQGLRAGMVAGVIVNRTQQEIPNAETMKQTESHAVKIVVEAARRLL

>d1cb0a\_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Human (Homo sapiens)}

AVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDALILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEEGCTHVIVTTACGSLREEIQPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIETAKKLGLRCHSKGTMVTIEGPRFSSRAESFMFRTWGADVINMTTVPEVVLAKEAGICYASIAMATDYDCWKEHEEAVSVDRVLKTLKENANKAKSLLLTTIPQIGSTEWSETLHNLKNMAQFSVLLP

>d1je0a\_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Archaeon Sulfolobus solfataricus}

PVHILAKKGEVAERVLVVGDPGRARLLSTLLQNPKLTNENRGFLVYTGKYNGETVSIATHGIGGPSIAIVLEELAMLGANVFIRYGTTGALVPYINLGEYIIVTGASYNQGGLFYQYLRDNACVASTPDFELTNKLVTSFSKRNLKYYVGNVFSSDAFYAEDEEFVKKWSSRGNIAVEMECATLFTLSKVKGWKSATVLVVSDNLAKGGIWITKEELEKSVMDGAKAVLDTLTS

>d2pth\_\_ c.56.3.1 (-) Peptidyl-tRNA hydrolase {Escherichia coli}

TIKLIVGLANPGAEYAATRHNAGAWFVDLLAERLRAPLREEAKFFGYTSRVTLGGEDVRLLVPTTFMNLSGKAVAAMASFFRINPDEILVAHDELDLPPGVAKFKLGGGHGGHNGLKDIISKLGNNPNFHRLRIGIGHPGDKNKVVGFVLGKPPVSEQKLIDEAIDEAARCTEMWFTDGLTKATNRLHAFKAQ

>d1a2za\_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Archaeon Thermococcus litoralis}

MKKVLITGFEPFGGDSKNPTEQIAKYFDRKQIGNAMVYGRVLPVSVKRATIELKRYLEEIKPEIVINLGLAPTYSNITVERIAVNIIDARIPDNDGYQPIDEKIEEDAPLAYMATLPVRAITKTLRDNGIPATISYSAGTYLCNYVMFKTLHFSKIEGYPLKAGFIHVPYTPDQVVNKFFLLGKNTPSMCLEAEIKAIELAVKVSLDYLEKDRDDIKIPL

>d1auga\_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Bacillus amyloliquefaciens}

MEKKVLLTGFDPFGGETVNPSWEAVKRLNGAAEGPASIVSEQVPTVFYKSLAVLREAIKKHQPDIIICVGQAGGRMQITPERVAINLNEARIPDNEGNQPVGEDISQGGPAAYWTGLPIKRIVEEIKKEGIPAAVSYTAGTFVCNHLFYGLMDEISRHHPHIRGGFIHIPYIPEQTLQKSAPSLSLDHITKALKIAAVTAAVHEDDIETG

>d1iofa\_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Archaeon Pyrococcus furiosus}

MKVLVTGFEPFGGEKINPTERIAKDLDGIKIGDAQVFGRVLPVVFGKAKEVLEKTLEEIKPDIAIHVGLAPGRSAISIERIAVNAIDARIPDNEGKKIEDEPIVPGAPTAYFSTLPIKKIMKKLHERGIPAYISNSAGLYLCNYVMYLSLHHSATKGYPKMSGFIHVPYIPEQIIDKIGKGQVPPSMCYEMELEAVKVAIEVALEELL

>d2ctc\_\_ c.56.5.1 (-) Carboxypeptidase A {Cow (Bos taurus)}

ARSTNTFNYATYHTLDEIYDFMDLLVAEHPQLVSKLQIGRSYEGRPIYVLKFSTGGSNRPAIWIDLGIHSREWITQATGVWFAKKFTEDYGQDPSFTAILDSMDIFLEIVTNPDGFAFTHSQNRLWRKTRSVTSSSLCVGVDANRNWDAGFGKAGASSSPCSETYHGKYANSEVEVKSIVDFVKDHGNFKAFLSIHSYSQLLLYPYGYTTQSIPDKTELNQVAKSAVEALKSLYGTSYKYGSIITTIYQASGGSIDWSYNQGIKYSFTFELRDTGRYGFLLPASQIIPTAQETWLGVLTIMEHTLNN

>d1pca\_1 c.56.5.1 (1-308) Carboxypeptidase A {Pig (Sus scrofa)}

ARTTSTFNYATYHTLEEIYDFMDILVAEHPALVSKLQIGRSYEGRPIYVLKFSTGGSNRPAIWIDSGIHSREWITQASGVWFAKKITENYGQNSSFTAILDSMDIFLEIVTNPNGFAFTHSDNRLWRKTRSKASGSLCVGSDSNRNWDAGFGGAGASSSPCAETYHGKYPNSEVEVKSITDFVKNNGNIKAFISIHSYSQLLLYPYGYKTQSPADKSELNQIAKSAVAALKSLYGTSYKYGSIITVIYQASGGVIDWTYNQGIKYSFSFELRDTGRRGFLLPASQIIPTAQETWLALLTIMEHTLNNS

>d1dtda\_ c.56.5.1 (A:) Carboxypeptidase A {Human (Homo sapiens)}

FNFGAYHTLEEISQEMDNLVAEHPGLVSKVNIGSSFENRPMNVLKFSTGGDKPAIWLDAGIHAREWVTQATALWTANKIVSDYGKDPSITSILDALDIFLLPVTNPDGYVFSQTKNRMWRKTRSKVSAGSLCVGVDPNRNWDAGFGGPGASSNPCSDSYHGPSANSEVEVKSIVDFIKSHGKVKAFIILHSYSQLLMFPYGYKCTKLDDFDELSEVAQKAAQSLSRLHGTKYKVGPICSVIYQASGGSIDWSYDYGIKYSFAFELRDTGRYGFLLPARQILPTAEETWLGLKAIMEHVRDHPY

>d1nsa\_1 c.56.5.1 (4-308) Carboxypeptidase B {Pig (Sus scrofa)}

TTGHSYEKYNNWETIEAWTEQVTSKNPDLISRSAIGTTFDGDNIYLLKVGKPGSNKPAIFMDCGFHAREWISQAFCQWFVRDAVRTYGYEAHMTEFLDNLDFYVLPVLNIDGYIYTWTKNRMWRKTRSTNAGSSCTGTDPNRNFNAGWCTVGASVNPCNETYCGSAAESEKETKALADFIRNNLSSIKAYLTIHSYSQMILYPYSYDYKLPENDAELNSLAKGAVKELASLYGTSYSYGPGSTTIYPAAGGSDDWAYNQGIKYSFTFELRDKGRFGFVLPESQIQATCQETMLAVKYVTNYTLEHL

>d1cpb\_\_ c.56.5.1 (-) Carboxypeptidase B {Cow (Bos taurus)}

TTGHSYEKYNNWETIEAWTEQVASENPDLISRSAIGTTFLGNTIYLLKVGKPGSNKPAVFMDCGFHAREWISPAFCQWFVREXXXXXXXEIHMTEFLDKLDFYVLPVVNIDGYIYTWTTNRMWRKTRSTRAGSSCTGTDLNRNFDAGWCSIGASNNPCSETYCGSAAESEKESKAVADFIRNHLSSIKAYLTIHSYSQMMLYPYSYDYKLPKNNVELNTLAKGAVKKLASLHGTTYSYGPGATTIYPASGGSDDWAYDQGIKYSFTFELRDKGRYGFVLPESQIQPTCEETMLAIKYVTSYVLEHL

>d1h8la2 c.56.5.1 (A:4-304) Carboxypeptidase D, catalytic domain {Crested duck (Lophonetta specularioides)}

QAVQPVDFRHHHFSDMEIFLRRYANEYPSITRLYSVGKSVELRELYVMEISDNPGIHEAGEPEFKYIGNMHGNEVVGRELLLNLIEYLCKNFGTDPEVTDLVQSTRIHIMPSMNPDGYEKSQEGDRGGTVGRNNSNNYDLNRNFPDQFFQVTDPPQPETLAVMSWLKTYPFVLSANLHGGSLVVNYPFDDDEQGIAIYSKSPDDAVFQQLALSYSKENKKMYQGSPCKDLYPTEYFPHGITNGAQWYNVPGGMQDWNYLNTNCFEVTIELGCVKYPKAEELPKYWEQNRRSLLQFIKQVHR

>d1obr\_\_ c.56.5.2 (-) Carboxypeptidase T {Thermoactinomyces vulgaris}

DFPSYDSGYHNYNEMVNKINTVASNYPNIVKKFSIGKSYEGRELWAVKISDNVGTDENEPEVLYTALHHAREHLTVEMALYTLDLFTQNYNLDSRITNLVNNREIYIVFNINPDGGEYDISSGSYKSWRKNRQPNSGSSYVGTDLNRNYGYKWGCCGGSSGSPSSETYRGRSAFSAPETAAMRDFINSRVVGGKQQIKTLITFHTYSELILYPYGYTYTDVPSDMTQDDFNVFKTMANTMAQTNGYTPQQASDLYITDGDMTDWAYGQHKIFAFTFEMYPTSYNPGFYPPDEVIGRETSRNKEAVLYVAEKADCPYSVIGKSC

>d1lam\_2 c.56.5.3 (160-484) Leucine aminopeptidase, C-terminal domain {Cow (Bos taurus)}

FASGQNLARRLMETPANEMTPTKFAEIVEENLKSASIKTDVFIRPKSWIEEQEMGSFLSVAKGSEEPPVFLEIHYKGSPNASEPPLVFVGKGITFDSGGISIKAAANMDLMRADMGGAATICSAIVSAAKLDLPINIVGLAPLCENMPSGKANKPGDVVRARNGKTIQVDNTDAEGRLILADALCYAHTFNPKVIINAATLTGAMDIALGSGATGVFTNSSWLWNKLFEASIETGDRVWRMPLFEHYTRQVIDCQLADVNNIGKYRSAGACTAAAFLKEFVTHPKWAHLDIAGVMTNKDEVPYLRKGMAGRPTRTLIEFLFRFSQ

>d1amp\_\_ c.56.5.4 (-) Aminopeptidase {Aeromonas proteolytica}

MPPITQQATVTAWLPQVDASQITGTISSLESFTNRFYTTTSGAQASDWIASEWQALSASLPNASVKQVSHSGYNQKSVVMTITGSEAPDEWIVIGGHLDSTIGSHTNEQSVAPGADDDASGIAAVTEVIRVLSENNFQPKRSIAFMAYAAEEVGLRGSQDLANQYKSEGKNVVSALQLDMTNYKGSAQDVVFITDYTDSNFTQYLTQLMDEYLPSLTYGFDTCGYACSDHASWHNAGYPAAMPFESKFNDYNPRIHTTQDTLANSDPTGSHAKKFTQLGLAYAIEMGSATG

>d1qq9a\_ c.56.5.4 (A:) Aminopeptidase {Streptomyces griseus}

APDIPLANVKAHLTQLSTIAANNGGNRAHGRPGYKASVDYVKAKLDAAGYTTTLQQFTSGGATGYNLIANWPGGDPNKVLMAGAHLDSVSSGAGINDNGSGSAAVLETALAVSRAGYQPDKHLRFAWWGAEELGLIGSKFYVNNLPSADRSKLAGYLNFDMIGSPNPGYFVYDDDPVIEKTFKNYFAGLNVPTEIETEGDGRSDHAPFKNVGVPVGGLFTGAGYTKSAAQAQKWGGTAGQAFDRCYHSSCDSLSNINDTALDRNSDAAAHAIWTLSS

>d1cg2a1 c.56.5.4 (A:26-213,A:327-414) Carboxypeptidase G2, catalytic domain {Pseudomonas sp., strain rs-16}

QKRDNVLFQAATDEQPAVIKTLEKLVNIETGTGDAEGIAAAGNFLEAELKNLGFTVTRSKSAGLVVGDNIVGKIKGRGGKNLLLMSHMDTVYLKGILAKAPFRVEGDKAYGPGIADDKGGNAVILHTLKLLKEYGVRDYGTITVLFNTDEEKGSFGSRDLIQEEAKLADYVLSFEPTSAGDEKLSLGTXFNAGEGGKKLVDKAVAYYKEAGGTLGVEERTGGGTDAAYAALSGKPVIESLGLPGFGYHSDKAEYVDISAIPRRLYMAARLIMDLGAG

>d1de4c3 c.56.5.5 (C:122-189,C:383-608) Transferrin receptor ectodomain, protease-like domain {Human (Homo sapiens)}

LYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQKDENLALYVENQFREFKLSKVWRDQHFVKXEIKILNIFGVIKGFVEPDHYVVVGAQRDAWGPGAAKSGVGTALLLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYTLIEKTMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAAFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAAEVAGQFVIKLTHDVELN

>d1boub\_ c.56.6.1 (B:) LigB subunit of an aromatic-ring-opening dioxygenase LigAB {Pseudomonas paucimobilis}

ARVTTGITSSHIPALGAAIQTGTSDNDYWGPVFKGYQPIRDWIKQPGNMPDVVILVYNDHASAFDMNIIPTFAIGCAETFKPADEGWGPRPVPDVKGHPDLAWHIAQSLILDEFDMTIMNQMDVDHGCTVPLSMIFGEPEEWPCKVIPFPVNVVTYPPPSGKRCFALGDSIRAAVESFPEDLNVHVWGTGGMSHQLQGPRAGLINKEFDLNFIDKLISDPEELSKMPHIQYLRESGSEGVELVMWLIMRGALPEKVRDLYTFYHIPASNTALGAMILQPEETAGTPLEPRKVMSGHSL

>d1di6a\_ c.57.1.1 (A:) MogA {Escherichia coli}

ATLRIGLVSISDRASSGVYQDKGIPALEEWLTSALTTPFELETRLIPDEQAIIEQTLCELVDEMSCHLVLTTGGTGPARRDVTPDATLAVADREMPGFGEQMRQISLHFVPTAILSRQVGVIRKQALILNLPGQPKSIKETLEGVKDAEGNVVVHGIFASVPYCIQLLEGPYVETAPEVVAAFRPKSARR

>d1jlja\_ c.57.1.1 (A:) Gephyrin N-terminal domain {Human (Homo sapiens)}

HQIRVGVLTVSDSCFRNLAEDRSGINLKDLVQDPSLLGGTISAYKIVPDEIEEIKETLIDWCDEKELNLILTTGGTGFAPRDVTPEATKEVIEREAPGMALAMLMGSLNVTPLGMLSRPVCGIRGKTLIINLPGSKKGSQECFQFILPALPHAIDLLRDAIVKVKEVHD

>d1eava\_ c.57.1.1 (A:) Plant CNX1 G domain {Mouse-ear cress (Arabidopsis thaliana)}

GPEYKVAILTVSDTVSAGAGPDRSGPRAVSVVDSSSEKLGGAKVVATAVVPDEVERIKDILQKWSDVDEMDLILTLGGTGFTPRDVTPEATKKVIERETPGLLFVMMQESLKITPFAMLSRSAAGIRGSTLIINMPGNPNAVAECMEALLPALKHALKQI

>d1g8la3 c.57.1.2 (A:178-326) MoeA, central domain {Escherichia coli}

VRVALFSTGDELQLPGQPLGDGQIYDTNRLAVHLMLEQLGCEVINLGIIRDDPHALRAAFIEADSQADVVISSGGVSVGEADYTKTILEELGEIAFWKLAIKPGKPFAFGKLSNSWFCGLPGNPVSATLTFYQLVQPLLAKLSGNTASG

>d1bgva2 c.58.1.1 (A:1-194) Glutamate dehydrogenase {Clostridium symbiosum}

SKYVDRVIAEVEKKYADEPEFVQTVEEVLSSLGPVVDAHPEYEEVALLERMVIPERVIEFRVPWEDDNGKVHVNTGYRVQFNGAIGPYKGGLRFAPSVNLSIMKFLGFEQAFKDSLTTLPMGGAKGGSDFDPNGKSDREVMRFCQAFMTELYRHIGPDIDVPAGDLGVGAREIGYMYGQYRKIVGGFYNGVLTG

>d1gtma2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}

ADPYEIVIKQLERAAQYMEISEEALEFLKRPQRIVEVTIPVEMDDGSVKVFTGFRVQHNWARGPTKGGIRWHPEETLSTVKALAAWMTWKTAVMDLPYGGGKGGIIVDPKKLSDREKERLARGYIRAIYDVISPYEDIPAPDVYTNPQIMAWMMDEYETISRRKTPAFGIITGKPLSI

>d1euza2 c.58.1.1 (A:4-180) Glutamate dehydrogenase {Archaeon Thermococcus profundus}

IDPFEMAVKQLERAAQYMDISEEALEWLKKPMRIVEVSVPIEMDDGSVKVFTGFRVQHNWARGPTKGGIRWHPAETLSTVKALATWMTWKVAVVDLPYGGGKGGIIVNPKELSEREQERLARAYIRAVYDVIGPWTDIPAPDVYTNPKIMGWMMDEYETIMRRKGPAFGVITGKPLS

>d1bvua2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Thermococcus litoralis}

QDPFEIAVKQLERAAQYMDISEEALEFLKRPQRIVEVSIPVEMDDGSVKVFTGFRVQYNWARGPTKGGIRWHPEETLSTVKALAAWMTWKTAVMDLPYGGGKGGVICNPKEMSDREKERLARGYVRAIYDVISPYTDIPAPDVYTNPQIMAWMMDEYETISRRKDPSFGVITGKPPSV

>d1b26a2 c.58.1.1 (A:4-178) Glutamate dehydrogenase {Thermotoga maritima}

SLYEMAVEQFNRAASLMDLESDLAEVLRRPKRVLIVEFPVRMDDGHVEVFTGYRVQHNVARGPAKGGIRYHPDVTLDEVKALAFWMTWKTAVMNLPFGGGKGGVRVDPKKLSRNELERLSRRFFSEIQVIIGPYNDIPAPDVNTNADVIAWYMDTYSMNVGHTVLGIVTGKPVEL

>d1hwxa2 c.58.1.1 (A:1-208) Glutamate dehydrogenase {Cow (Bos taurus)}

ADREDDPNFFKMVEGFFDRGASIVEDKLVEDLKTRQTQEQKRNRVRGILRIIKPCNHVLSLSFPIRRDDGSWEVIEGYRAQHSHQRTPCKGGIRYSTDVSVDEVKALASLMTYKCAVVDVPFGGAKAGVKINPKNYTDEDLEKITRRFTMELAKKGFIGPGVDVPAPNMSTGEREMSWIADTYASTIGHYDINAHACVTGKPISQGGI

>d1leha2 c.58.1.1 (A:1-134) Leucine dehydrogenase {Bacillus sphaericus}

MEIFKYMEKYDYEQLVFCQDEASGLKAVIAIHDTTLGPALGGARMWTYNAEEEAIEDALRLARGMTYKNAAAGLNLGGGKTVIIGDPFADKNEDMFRALGRFIQGLNGRYITAEDVGTTVDDMDLIHQETDYVT

>d1c1da2 c.58.1.1 (A:1-148) Phenylalanine dehydrogenase {Rhodococcus sp., M4}

SIDSALNWDGEMTVTRFDAMTGAHFVIRLDSTQLGPAAGGTRAAQYSNLADALTDAGKLAGAMTLKMAVSNLPMGGGKSVIALPAPRHSIDPSTWARILRIHAENIDKLSGNYWTGPDVNTNSADMDTLNDTTEFVFGRSLERGGAGS

>d1a4ia2 c.58.1.2 (A:2-126) Tetrahydrofolate dehydrogenase/cyclohydrolase {Human (Homo sapiens)}

APAEILNGKEISAQIRARLKNQVTQLKEQVPGFTPRLAILQVGNRDDSNLYINVKLKAAEEIGIKATHIKLPRTTTESEVMKYITSLNEDSTVHGFLVQLPLDSENSINTEEVINAIAPEKDVDG

>d1b0aa2 c.58.1.2 (A:2-122) Tetrahydrofolate dehydrogenase/cyclohydrolase {Escherichia coli}

AAKIIDGKTIAQQVRSEVAQKVQARIAAGLRAPGLAVVLVGSNPASQIYVASKRKACEEVGFVSRSYDLPETTSEAELLELIDTLNADNTIDGILVQLPLPAGIDNVKVLERIHPDKDVDG

>d1edza2 c.58.1.2 (A:3-148) Tetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}

KPGRTILASKVAETFNTEIINNVEEYKKTHNGQGPLLVGFLANNDPAAKMYATWTQKTSESMGFRYDLRVIEDKDFLEEAIIQANGDDSVNGIMVYFPVFGNAQDQYLQQVVCKEKDVEGLNHVYYQNLYHNVRYLDKENRLKSIL

>d1do8a2 c.58.1.3 (A:21-279) Mitochondrial NAD(P)-dependenent malic enzyme {Human (Homo sapiens)}

IKEKGKPLMLNPRTNKGMAFTLQERQMLGLQGLLPPKIETQDIQALRFHRNLKKMTSPLEKYIYIMGIQERNEKLFYRILQDDIESLMPIVYTPTVGLACSQYGHIFRRPKGLFISISDRGHVRSIVDNWPENHVKAVVVTDGERILGLGDLGVYGMGIPVGKLCLYTACAGIRPDRCLPVCIDVGTDNIALLKDPFYMGLYQKRDRTQQYDDLIDEFMKAITDRYGRNTLIQFEDFGNHNAFRFLRKYREKYCTFNDD

>d2uaga2 c.59.1.1 (A:298-437) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}

GLPHRFEVVLEHNGVRWINDSKATNVGSTEAALNGLHVDGTLHLLLGGDGKSADFSPLARYLNGDNVRLYCFGRDGAQLAALRPEVAEQTETMEQAMRLLAPRVQPGDMVLLSPACASLDQFKNFEQRGNEFARLAKELG

>d1e8ca2 c.59.1.1 (A:338-497) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}

VCGRMEVFTAPGKPTVVVDYAHTPDALEKALQAARLHCAGKLWCVFGCGGDRDKGKRPLMGAIAEEFADVAVVTDDNPRTEEPRAIINDILAGMLDAGHAKVMEGRAEAVTCAVMQAKENDVVLVAGKGHEDYQIVGNQRLDYSDRVTVARLLGVIARSH

>d1gg4a1 c.59.1.1 (A:313-447) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

VPGRLFPIQLAENQLLLDDSYNANVGSMTAAVQVLAEMPGYRVLVVGDMAELGAESEACHVQVGEAAKAAGIDRVLSVGKQSHAISTASGVGEHFADKTALITRLKLLIAEQQVITILVKGSRSAAMEEVVRALQ

>d1jbwa1 c.59.1.2 (A:297-425) Folylpolyglutamate synthetase, C-terminal domain {Lactobacillus casei}

WPARLEKISDTPLIVIDGAHNPDGINGLITALKQLFSQPITVIAGILADKDYAAMADRLTAAFSTVYLVPVPGTPRALPEAGYEALHEGRLKDSWQEALAASLNDVPDQPIVITGSLYLASAVRQTLLG

>d1qhfa\_ c.60.1.1 (A:) Phosphoglycerate mutase {Baker's yeast (Saccharomyces cerevisiae)}

PKLVLVRHGQSEWNEKNLFTGWVDVKLSAKGQQEAARAGELLKEKKVYPDVLYTSKLSRAIQTANIALEKADRLWIPVNRSWRLNERHYGDLQGKDKAETLKKFGEEKFNTYRRSFDVPPPPIDASSPFSQKGDERYKYVDPNVLPETESLALVIDRLLPYWQDVIAKDLLSGKTVMIAAHGNSLRGLVKHLEGISDADIAKLNIPTGIPLVFELDENLKPSKPSYYLDPEAAAAGAAAV

>d3pgm\_\_ c.60.1.1 (-) Phosphoglycerate mutase {Baker's yeast (Saccharomyces cerevisiae)}

PKLVLVRHGQSEWNEKNLFTGWVDVKLSAKGQQEAARAGELLKEKGVNVLVDYTSKLSRAIQTANIALEKADRLWIPVNRSWRLNERHYGDLQGKDKAQTLKKFGEEKFNTYRRSFDVPPPPIDASSPFSQKGDERYKYVDPNVLPETESLALVIDRLLPYWQDVIAKLVGKTSMIAAHGNSLRGLVKHLEGISDADIAKLNIPPGTILVFELDENLKPSKPSYYLDPEA

>d1fzta\_ c.60.1.1 (A:) Phosphoglycerate mutase {Yeast (Schizosaccharomyces pombe)}

MTTEAAPNLLVLTRHGESEWNKLNLFTGWKDPALSETGIKEAKLGGERLKSRGYKFDIAFTSALQRAQKTCQIILEEVGEPNLETIKSEKLNERYYGDLQGLNKDDARKKWGAEQVQIWRRSYDIAPPNGESLKDTAERVLPYYKSTIVPHILKGEKVLIAAHGNSLRALIMDLEGLTGDQIVKRELATGVPIVYHLDKDGKYVSKELIDN

>d1e58a\_ c.60.1.1 (A:) Phosphoglycerate mutase {Escherichia coli}

AVTKLVLVRHGESQWNKENRFTGWYDVDLSEKGVSEAKAAGKLLKEEGYSFDFAYTSVLKRAIHTLWNVLDELDQAWLPVEKSWKLNERHYGALQGLNKAETAEKYGDEQVKQWRRGFAVTPPELTKDDERYPGHDPRYAKLSEKELPLTESLALTIDRVIPYWNETILPRMKSGERVIIAAHGNSLRALVKYLDNMSEEEILELNIPTGVPLVYEFDENFKPLKRYYLGNADEIAAKAAAVANQGK

>d1ebba\_ c.60.1.1 (A:) Broad specificity phosphatase YhfR {Bacillus stearothermophilus}

ATTLYLTRHGETKWNVERRMQGWQDSPLTEKGRQDAMRLGKRLEAVELAAIYTSTSGRALETAEIVRGGRLIPIYQDERLREIHLGDWEGKTHDEIRQMDPIAFDHFWQAPHLYAPQRGERFCDVQQRALEAVQSIVDRHEGETVLIVTHGVVLKTLMAAFKDTPLDHLWSPPYMYGTSVTIIEVDGGTFHVAVEGDVSHIE

>d1rpa\_\_ c.60.1.2 (-) Acid phosphatase {Rat (Rattus norvegicus)}

KELKFVTLVFRHGDRGPIETFPNDPIKESSWPQGFGQLTKWGMGQHYELGSYIRRRYGRFLNNSYKHDQVYIRSTDVDRTLMSAMTNLAALFPPEGNSIWNPRLLWQPIPVHTVSLSEDRLLYLPFRDCPRFQELKSETLKSEEFLKRLQPYKSFIDTLPSLSGFEDQDLFEIWSRLYDPLYCESVHNFTLPTWATEDAMTKLKELSELSLLSLYGIHKQKEKSRLQGGVLVNEILKNMKLATQPQKARKLIMYSAHDTTVSGLQMALDVYNGLLPPYASCHIMELYQDNGGHFVEMYYRNETQNEPYPLTLPGCTHSCPLEKFAELLDPVIPQDWATECMG

>d2hpaa\_ c.60.1.2 (A:) Acid phosphatase {Human (Homo sapiens)}

KELKFVTLVFRHGDRSPIDTFPTDPIKESSWPQGFGQLTQLGMEQHYELGEYIRKRYRKFLNESYKHEQVYIRSTDVDRTLMSAMTNLAALFPPEGVSIWNPILLWQPIPVHTVPLSEDQLLYLPFRNCPRFQELESETLKSEEFQKRLHPYKDFIATLGKLSGLHGQDLFGIWSKVYDPLYCESVHNFTLPSWATEDTMTKLRELSELSLLSLYGIHKQKEKSRLQGGVLVNEILNHMKRATQIPSYKKLIMYSAHDTTVSGLQMALDVYNGLLPPYASCHLTELYFEKGEYFVEMYYRNETQHEPYPLMLPGCSPSCPLERFAELVGPVIPQDWSTECMT

>d1ihp\_\_ c.60.1.3 (-) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus ficuum}

SCDTVDQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDSKGKKYSALIEEIQQNATTFDGKYAFLKTYNYSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSSNNTLDPGTCTVFEDSELADTVEANFTATFVPSIRQRLENDLSGVTLTDTEVTYLMDMCSFDTISTSTVDTKLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWTVPFASRLYVEMMQCQAEQEPLVRVLVNDRVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA

>d1qfxa\_ c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus niger}

KQFSQEFRDGYSILKHYGGNGPYSERVSYGIARDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALAKVYSINTTEYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVVPFFSSGYGRVIETARKFGEGFFGYNYSTNAALNIISESEVMGADSLTPTCDTDNDQTTCDNLTYQLPQFKVAAARLNSQNPGMNLTASDVYNLMVMASFELNARPFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANASLTLLNQGPKEAGSLFFNFAHDTNITPILAALGVLIPNEDLPLDRVAFGNPYSIGNIVPMGGHLTIERLSCQATALSDEGTYVRLVLNEAVLPFNDCTSGPGYSCPLANYTSILNKNLPDYTTTCNVSASYPQYLSFWWNYNTTTELNYRSSPIACQEGDAMD

>d1dkla\_ c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Escherichia coli}

SEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGWLTPRGGELIAYLGHYQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQADTSSPDPLFNPLKTGVCQLDNANVTDAILSRAGGSIADFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTALTPHPPQKQAYGVTLPTSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL

>d1bif\_2 c.60.1.4 (250-468) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain {Rat (Rattus norvegicus)}

SIYLCRHGESELNLKGRIGGDPGLSPRGREFSKHLAQFISDQNIKDLKVFTSQMKRTIQTAEALSVPYEQFKVLNEIDAGVCEEMTYEEIQDHYPLEFALRDQDKYRYRYPKGESYEDLVQRLEPVIMELERQENVLVICHQAVMRCLLAYFLDKAAEELPYLKCPLHTVLKLTPVAYGCKVESIFLNVAAVNTHRDRPQNVDISRPSEEALVTVPAHQ

>d1fbta\_ c.60.1.4 (A:) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain {Rat (Rattus norvegicus)}

RSIYLCRHGESELNLRGRIGGDSGLSARGKQYAYALANFIRSQGISSLKVWTSHMKRTIQTAEALGVPYEQWKALNEIDAGVCEEMTYEEIQEHYPEEFALRDQDKYRYRYPKGESYEDLVQRLEPVIMELERQENVLVICHQAVMRCLLAYFLDKSSDELPYLKCPLHTVLKLTPVAYGCRVESIYLNV

>d1nula\_ c.61.1.1 (A:) Xantine-guanine PRTase (XPRTase) {Escherichia coli}

EKYIVTWDMLQIHARKLASRLMPSEQWKGIIAVSRGGLVPGALLARELGIRHVDTVCISSYDHDNQRELKVLKRAEGDGEGFIVIDDLVDTGGTAVAIREMYPKAHFVTIFAKPAGRPLVDDYVVDIPQDTWIEQPWDMGVVFVPPISGR

>d1hgxa\_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Tritrichomonas foetus}

MDDLERVLYNQDDIQKRIRELAAELTEFYEDKNPVMICVLTGAVFFYTDLLKHLDFQLEPDYIICSSYSGTKSTGNLTISKDLKTNIEGRHVLVVEDIIDTGLTMYQLLNNLQMRKPASLKVCTLCDKDIGKKAYDVPIDYCGFVVENRYIIGYGFDFHNKYRNLPVIGILKE

>d1fsga\_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Toxoplasma gondii}

GSHMASKPIEDYGKGKGRIEPMYIPDNTFYNADDFLVPPHCKPYIDKILLPGGLVKDRVEKLAYDIHRTYFGEELHIICILKGSRGFFNLLIDYLATIQKYSGRESSVPPFFEHYVRLKSYQNDNSTGQLTVLSDDLSIFRDKHVLIVEDIVDTGFTLTEFGERLKAVGPKSMRIATLVEKRTDRSNSLKGDFVGFSIEDVWIVGCCYDFNEMFRDFDHVAVLSDAARKKFEK

>d1gph11 c.61.1.1 (1:235-465) Glutamine PRPP amidotransferase, C-terminal domain {Bacillus subtilis}

ICSMEYIYFSRPDSNIDGINVHSARKNLGKMLAQESAVEADVVTGVPDSSISAAIGYAEATGIPYELGLIKNRYVGRTFIQPSQALREQGVRMKLSAVRGVVEGKRVVMVDDSIVRGTTSRRIVTMLREAGATEVHVKISSPPIAHPCFYGIDTSTHEELIASSHSVDEIRQEIGADTLSFLSVEGLLKGIGRKYDDSNCGQCLACFTGKYPTEIYQDTVLPHVKEAVLTK

>d1ecfa1 c.61.1.1 (A:250-492) Glutamine PRPP amidotransferase, C-terminal domain {Escherichia coli}

NPCLFEYVYFARPDSFIDKISVYSARVNMGTKLGEKIAREWEDLDIDVVIPIPETSCDIALEIARILGKPYRQGFVKNRYVGRTFIMPGQQLRRKSVRRKLNANRAEFRDKNVLLVDDSIVRGTTSEQIIEMAREAGAKKVYLASAAPEIRFPNVYGIDMPSATELIAHGREVDEIRQIIGADGLIFQDLNDLIDAVRAENPDIQQFECSVFNGVYVTKDVDQGYLDFLDTLRNDDAKAVQRQ

>d1dqna\_ c.61.1.1 (A:) Guanine PRTase {Giardia lamblia}

MICSVTGKPVKDVLSTFFKDRNDVLESEVKKFHLLATFEECKALAADTARRMNEYYKDVAEPVTLVALLTGAYLYASLLTVHLTFPYTLHFVKVSSYKGTRQESVVFDEEDLKQLKEKREVVLIDEYVDSGHTIFSIQEQIKHAKICSCFVKDVDAIKKHSALADTKMFYGYTPMPKGSWLIGFGLDDNGLRRGWAHLFDINLSESEVTEFRRRLTEHIKGLNINGVNRY

>d1bzya\_ c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGPRTase) {Human (Homo sapiens)}

SPGVVISDDEPGYDLDLFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKEMGGHHIVALCVLKGGYKFFADLLDYIKALNRNSDRSIPMTVDFIRLKSYCNDQSTGDIKVIGGDDLSTLTGKNVLIVEDIIDTGKTMQTLLSLVRQYNPKMVKVASLLVKRTPRSVGYKPDFVGFEIPDKFVVGYALDYNEYFRDLNHVCVISETGKAKYKA

>d1cjba\_ c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGPRTase) {Plasmodium falciparum}

PIPNNPGAGENAFDPVFVNDDDGYDLDSFMIPAHYKKYLTKVLVPNGVIKNRIEKLAYDIKKVYNNEEFHILCLLKGSRGFFTALLKHLSRIHNYSAVETSKPLFGEHYVRVKSYCNDQSTGTLEIVSEDLSCLKGKHVLIVEDIIDTGKTLVKFCEYLKKFEIKTVAIACLFIKRTPLWNGFKADFVGFSIPDHFVVGYSLDYNEIFRDLDHCCLVNDEGKKKYKAT

>d1tc1a\_ c.61.1.1 (A:) Hypoxanthine PRTase {Trypanosoma cruzi}

YEFAEKILFTEEEIRTRIKEVAKRIADDYKGKGLRPYVNPLVLISVLKGSFMFTADLCRALCDFNVPVRMEFICVSSYGEGLTSSGQVRMLLDTRHSIEGHHVLIVEDIVDTALTLNYLYHMYFTRRPASLKTVVLLDKREGRRVPFSADYVVANIPNAFVIGYGLDYDDTYRELRDIVVLRPE

>d1qb7a\_ c.61.1.1 (A:) Adenine PRTase {Leishmania donovani}

PFKEVSPNSFLLDDSHALSQLLKKSYRWYSPVFSPRNVPRFADVSSITESPETLKAIRDFLVQRYRAMSPAPTHILGFDARGFLFGPMIAVELEIPFVLMRKADKNAGLLIRSEPYEKEYKEAAPEVMTIRYGSIGKGSRVVLIDDVLATGGTALSGLQLVEASDAVVVEMVSILSIPFLKAAEKIHSTANSRYKDIKFISLLSDDALTEENCGDSKNYTGPRVLSCGDVLAEHPH

>d1g2qa\_ c.61.1.1 (A:) Adenine PRTase {Baker's yeast (Saccharomyces cerevisiae)}

MPIASYAQELKLALHQYPNFPSEGILFEDFLPIFRNPGLFQKLIDAFKLHLEEAFPEVKIDYIVGLESRGFLFGPTLALALGVGFVPVRKAGKLPGECFKATYEKEYGSDLFEIQKNAIPAGSNVIIVDDIIATGGSAAAAGELVEQLEANLLEYNFVMELDFLKGRSKLNAPVFTLL

>d1oroa\_ c.61.1.1 (A:) Orotate PRTase {Escherichia coli}

MKPYQRQFIEFALSKQVLKFGEFTLKSGRKSPYFFNAGLFNTGRDLALLGRFYAEALVDSGIEFDLLFGPAYKGIPIATTTAVALAEHHDLDLPYCFNRKEAKDHGEGGNLVGSALQGRVMLVDDVITAGTAIRESMEIIQANGATLAGVLISLDRQERGRGEISAIQEVERDYNCKVISIITLKDLIAYLEEKPEMAEHLAAVKAYREEFGV

>d1a3c\_\_ c.61.1.1 (-) Uracil PRTase {Bacillus subtilis}

QKAVILDEQAIRRALTRIAHEMIERNKGMNNCILVGIKTRGIYLAKRLAERIEQIEGNPVTVGEIDITLYRDDLSKKTSNDEPLVKGADIPVDITDQKVILVDDVLYTGRTVRAGMDALVDVGRPSSIQLAVLVDRGHRELPIRADYIGKNIPTSKSEKVMVQLDEVDQNDLVAIYEN

>d1bd3a\_ c.61.1.1 (A:) Uracil PRTase {Toxoplasma gondii}

QEESILQDIITRFPNVVLMKQTAQLRAMMTIIRDKETPKEEFVFYADRLIRLLIEEALNELPFQKKEVTTPLDVSYHGVSFYSKICGVSIVRAGESMESGLRAVCRGVRIGKILIQRDETTAEPKLIYEKLPADIRERWVMLLDPMCATAGSVCKAIEVLLRLGVKEERIIFVNILAAPQGIERVFKEYPKVRMVTAAVDICLNSRYYIVPGIGDFGDRYFGTM

>d1dkra1 c.61.1.2 (A:8-166) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}

NLKIFSLNSNPELAKEIADIVGVQLGKCSVTRFSDGEVQINIEESIRGCDCYIIQSTSDPVNEHIMELLIMVDALKRASAKTINIVIPYYGYARQDRKARSREPITAKLFANLLETAGATRVIALDLHAPQIQGFFDIPIDHLMGVPILGEYFEGKNLE

>d1dkra2 c.61.1.2 (A:167-316) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}

DIVIVSPDHGGVTRARKLADRLKAPIAIIDKRRPRPNVAEVMNIVGNIEGKTAILIDDIIDTAGTITLAANALVENGAKEVYACCTHPVLSGPAVERINNSTIKELVVTNSIKLPEEKKIERFKQLSVGPLLAEAIIRVHEQQSVSYLFS

>d1lfaa\_ c.62.1.1 (A:) Integrin CD11a/CD18 (Leukocyte function associated antigen-1, LFA-1) {Human (Homo sapiens)}

GNVDLVFLFDGSMSLQPDEFQKILDFMKDVMKKLSNTSYQFAAVQFSTSYKTEFDFSDYVKRKDPDALLKHVKHMLLLTNTFGAINYVATEVFREELGARPDATKVLIIITDGEATDSGNIDAAKDIIRYIIGIGKHFQTKESQETLHKFASKPASEFVKILDTFEKLKDLFTELQKKIYVIE

>d1atza\_ c.62.1.1 (A:) von Willebrand factor A3 domain {Human (Homo sapiens)}

QPLDVILLLDGSSSFPASYFDEMKSFAKAFISKANIGPRLTQVSVLQYGSITTIDVPWNVVPEKAHLLSLVDVMQREGGPSQIGDALGFAVRYLTSEMHGARPGASKAVVILVTDVSVDSVDAAADAARSNRVTVFPIGIGDRYDAAQLRILAGPAGDSNVVKLQRIEDLPTMVTLGNSFLHKL

>d1fnsa\_ c.62.1.1 (A:) von Willebrand factor A1 domain {Human (Homo sapiens)}

MYCSRLLDLVFLLDGSSRLSEAEFEVLKAFVVDMMERLRVSQKWVRVAVVEYHDGSHAYIGLKDRKRPSELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKIDRPEASRIALLLMASQEPQRMSRNFVRYVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVLSSVDELEQQRDEIVSYLCDLAPEAP

>d1ido\_\_ c.62.1.1 (-) Integrin CR3 (CD11b/CD18, Mac-1), alpha subunit {Human (Homo sapiens)}

DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREK

>d1qc5a\_ c.62.1.1 (A:) Integrin alpha1-beta1 {Human (Homo sapiens)}

STQLDIVIVLDGSNSIYPWDSVTAFLNDLLERMDIGPKQTQVGIVQYGENVTHEFNLNKYSSTEEVLVAAKKIVQRGGRQTMTALGTDTARKEAFTEARGARRGVKKVMVIVTDGESHDNHRLKKVIQDCEDENIQRFSIAILGSYNRGNLSTEKFVEEIKSIASEPTEKHFFNVSDEIALVTIVKTLGERI

>d1ck4a\_ c.62.1.1 (A:) Integrin alpha1-beta1 {Rat (Rattus norvegicus)}

TQLDIVIVLDGSNSIYPWESVIAFLNDLLKRMDIGPKQTQVGIVQYGENVTHEFNLNKYSSTEEVLVAANKIGRQGGLQTMTALGIDTARKEAFTEARGARRGVKKVMVIVTDGESHDNYRLKQVIQDCEDENIQRFSIAILGHYNRGNLSTEKFVEEIKSIASEPTEKHFFNVSDELALVTIVKALGERIFA

>d1aoxa\_ c.62.1.1 (A:) Integrin alpha2-beta1 {Human (Homo sapiens)}

SCPSLIDVVVVCDESNSIYPWDAVKNFLEKFVQGLDIGPTKTQVGLIQYANNPRVVFNLNTYKTKEEMIVATSQTSQYGGDLTNTFGAIQYARKYAYSAASGGRRSATKVMVVVTDGESHDGSMLKAVIDQCNHDNILRFGIAVLGYLNRNALDTKNLIKEIKAIASIPTERYFFNVSDEAALLEKAGTLGEQIFSIEGGT

>d1jv2b2 c.62.1.1 (B:107-354) Integrin beta A domain {Human (Homo sapiens)}

VEDYPVDIYYLMDLSYSMKDDLWSIQNLGTKLATQMRKLTSNLRIGFGAFVDKPVSPYMYISPPEALENPCYDMKTTCLPMFGYKHVLTLTDQVTRFNEEVKKQSVSRNRDAPEGGFDAIMQATVCDEKIGWRNDASHLLVFTTDAKTHIALDGRLAGIVQPNDGQCHVGSDNHYSASTTMDYPSLGLMTEKLSQKNINLIFAVTENVVNLYQNYSELIPGTTVGVLSMDSSNVLQLIVDAYGKIRSK

>d1poia\_ c.63.1.1 (A:) Glutaconate-CoA transferase alpha {Acidaminococcus fermentans}

SKVMTLKDAIAKYVHSGDHIALGGFTTDRKPYAAVFEILRQGITDLTGLGGAAGGDWDMLIGNGRVKAYINCYTANSGVTNVSRRFRKWFEAGKLTMEDYSQDVIYMMWHAAALGLPFLPVTLMQGSGLTDEWGISKEVRKTLDKVPDDKFKYIDNPFKPGEKVVAVPVPQVDVAIIHAQQASPDGTVRIWGGKFQDVDIAEAAKYTIVTCEEIISDEEIRRDPTKNDIPGMCVDAVVLAPYGAHPSQCYGLYDYDNPFLKVYDKVSKTQEDFDAFCKEWVFDLKDHDEYLNKLGATRLINLKVVPGLGYHIDMTKE

>d1poib\_ c.63.1.1 (B:) Glutaconate-CoA transferase beta {Acidaminococcus fermentans}

DYTNYTNKEMQAVTIAKQIKNGQVVTVGTGLPLIGASVAKRVYAPDCHIIVESGLMDCSPVEVPRSVGDLRFMAHCGCIWPNVRFVGFEINEYLHKANRLIAFIGGAQIDPYGNVNSTSIGDYHHPKTRFTGSGGANGIATYSNTIIMMQHEKRRFMNKIDYVTSPGWIDGPGGRERLGLPGDVGPQLVVTDKGILKFDEKTKRMYLAAYYPTSSPEDVLENTGFDLDVSKAVELEAPDPAVIKLIREEIDPGQAFIQVP

>d1keka4 c.64.1.1 (A:416-668) Pyruvate-ferredoxin oxidoreductase, PFOR, domain III {Desulfovibrio africanus}

GTIQCQFWGLGADGTVGANKQAIKIIGDNTDLFAQGYFSYDSKKSGGITISHLRFGEKPIQSTYLVNRADYVACHNPAYVGIYDILEGIKDGGTFVLNSPWSSLEDMDKHLPSGIKRTIANKKLKFYNIDAVKIATDVGLGGRINMIMQTAFFKLAGVLPFEKAVDLLKKSIHKAYGKKGEKIVKMNTDAVDQAVTSLQEFKYPDSWKDAPAETKAEPMTNEFFKNVVKPILTQQGDKLPVSAFEADGRFPLG

>d1jkxa\_ c.65.1.1 (A:) Glycinamide ribonucleotide transformylase, GART {Escherichia coli}

MNIVVLISGNGSNLQAIIDACKTNKIKGTVRAVFSNKADAFGLERARQAGIATHTLIASAFDSREAYDRELIHEIDMYAPDVVVLAGFMRILSPAFVSHYAGRLLNIHPSLLPKYPGLHTHRQALENGDEEHGTSVHFVTDELDGGPVILQAKVPVFAGDSEDDITARVQTQEHAIYPLVISWFADGRLKMHENAAWLDGQRLPPQGYA

>d1fmta2 c.65.1.1 (A:1-206) Methionyl-tRNAfmet formyltransferase {Escherichia coli}

SESLRIIFAGTPDFAARHLDALLSSGHNVVGVFTQPDRPAGRGKKLMPSPVKVLAEEKGLPVFQPVSLRPQENQQLVAELQADVMVVVAYGLILPKAVLEMPRLGCINVHGSLLPRWRGAAPIQRSLWAGDAETGVTIMQMDVGLDTGDMLYKLSCPITAEDTSGTLYDKLAELGPQGLITTLKQLADGTAKPEVQDETLVTYAEK

>d1vid\_\_ c.66.1.1 (-) Catechol O-methyltransferase, COMT {Rat (Rattus norvegicus)}

TKEQRILRYVQQNAKPGDPQSVLEAIDTYCTQKEWAMNVGDAKGQIMDAVIREYSPSLVLELGAYCGYSAVRMARLLQPGARLLTMEMNPDYAAITQQMLNFAGLQDKVTILNGASQDLIPQLKKKYDVDTLDMVFLDHWKDRYLPDTLLLEKCGLLRKGTVLLADNVIVPGTPDFLAYVRGSSSFECTHYSSYLEYMKVVDGLEKAIYQGPS

>d1fp1d2 c.66.1.12 (D:129-372) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}

RGYLASFTTFLCYPALLQVWMNFKEAVVDEDIDLFKNVHGVTKYEFMGKDKKMNQIFNKSMVDVCATEMKRMLEIYTGFEGISTLVDVGGGSGRNLELIISKYPLIKGINFDLPQVIENAPPLSGIEHVGGDMFASVPQGDAMILKAVCHNWSDEKCIEFLSNCHKALSPNGKVIIVEFILPEEPNTSEESKLVSTLDNLMFITVGGRERTEKQYEKLSKLSGFSKFQVACRAFNSLGVMEFYK

>d1fp2a2 c.66.1.12 (A:109-352) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}

LCLAPMVECVLDPTLSGSYHELKKWIYEEDLTLFGVTLGSGFWDFLDKNPEYNTSFNDAMASDSKLINLALRDCDFVFDGLESIVDVGGGTGTTAKIICETFPKLKCIVFDRPQVVENLSGSNNLTYVGGDMFTSIPNADAVLLKYILHNWTDKDCLRILKKCKEAVTNDGKRGKVTIIDMVIDKKKDENQVTQIKLLMDVNMACLNGKERNEEEWKKLFIEAGFQHYKISPLTGFLSLIEIYP

>d1ej0a\_ c.66.1.2 (A:) RNA methyltransferase FtsJ {Escherichia coli}

GLRSRAWFKLDEIQQSDKLFKPGMTVVDLGAAPGGWSQYVVTQIGGKGRIIACDLLPMDPIVGVDFLQGDFRDELVMKALLERVGDSKVQVVMSDMAPNMSGTPAVDIPRAMYLVELALEMCRDVLAPGGSFVVKVFQGEGFDEYLREIRSLFTKVKVRKPDSSRARSREVYIVATGRKP

>d1fbna\_ c.66.1.3 (A:) Fibrillarin homologue {Archaeon Methanococcus jannaschii}

MEDIKIKEIFENIYEVDLGDGLKRIATKSIVKGKKVYDEKIIKIGDEEYRIWNPNKSKLAAAIIKGLKVMPIKRDSKILYLGASAGTTPSHVADIADKGIVYAIEYAPRIMRELLDACAERENIIPILGDANKPQEYANIVEKVDVIYEDVAQPNQAEILIKNAKWFLKKGGYGMIAIKARSIDVTKDPKEIFKEQKEILEAGGFKIVDEVDIEPFEKDHVMFVGIWEGK

>d1dusa\_ c.66.1.4 (A:) Hypothetical protein MJ0882 {Archaeon Methanococcus jannaschii}

FSEKPTTKSDVKIVEDILRGKKLKFKTDSGVFSYGKVDKGTKILVENVVVDKDDDILDLGCGYGVIGIALADEVKSTTMADINRRAIKLAKENIKLNNLDNYDIRVVHSDLYENVKDRKYNKIITNPPIRAGKEVLHRIIEEGKELLKDNGEIWVVIQTKQGAKSLAKYMKDVFGNVETVTIKGGYRVLKSKKL

>d1im8a\_ c.66.1.14 (A:) Hypothetical protein HI0319 (YecO) {Haemophilus influenzae}

FIFDENVAEVFPDMIQRSVPGYSNIITAIGMLAERFVTADSNVYDLGCSRGAATLSARRNINQPNVKIIGIDNSQPMVERCRQHIAAYHSEIPVEILCNDIRHVEIKNASMVILNFTLQFLPPEDRIALLTKIYEGLNPNGVLVLSEKFRFEDTKINHLLIDLHHQFKRANGYSELEVSQKRTALENVMRTDSIETHKVRLKNVGFSQVELWFQCFNFGSMIAVK

>d1d2ha\_ c.66.1.5 (A:) Glycine -methyltransferase {Rat (Rattus norvegicus)}

TAEYKAWLLGLLRQHGCHRVLDVACGTGVDSIMLVEEGFSVTSVDASDKMLKYALKERWNRRKEPAFDKWVIEEANWLTLDKDVPAGDGFDAVICLGNSFAHLPDSKGDQSEHRLALKNIASMVRPGGLLVIDHKNYDYILSTGCAPPGKNIYYKSDLTKDITTSVLTVNNKAHMVTLDYTVQVPGAGRDGAPGFSKFRLSYYPHCLASFTELVQEAFGGRCQHSVLGDFKPYRPGQAYVPCYFIHVLKKTG

>d1xvaa\_ c.66.1.5 (A:) Glycine -methyltransferase {Rat (Rattus norvegicus)}

VDSVYRTRSLGVAAEGIPDQYADGEAARVWQLYIGDTRSRTAEYKAWLLGLLRQHGCHRVLDVACGTGVDSIMLVEEGFSVTSVDASDKMLKYALKERWNRRKEPAFDKWVIEEANWLTLDKDVPAGDGFDAVICLGNSFAHLPDSKGDQSEHRLALKNIASMVRPGGLLVIDHRNYDYILSTGCAPPGKNIYYKSDLTKDITTSVLTVNNKAHMVTLDYTVQVPGAGRDGAPGFSKFRLSYYPHCLASFTELVQEAFGGRCQHSVLGDFKPYRPGQAYVPCYFIHVLKKTG

>d1hnna\_ c.66.1.15 (A:) Phenylethanolamine N-methyltransferase, PNMTase {Human (Homo sapiens)}

AVASAYQRFEPRAYLRNNYAPPRGDLCNPNGVGPWKLRCLAQTFATGEVSGRTLIDIGSGPTVYQLLSACSHFEDITMTDFLEVNRQELGRWLQEEPGAFNWSMYSQHACLIEGKGECWQDKERQLRARVKRVLPIDVHQPQPLGAGSPAPLPADALVSAFCLEAVSPDLASFQRALDHITTLLRPGGHLLLIGALEESWYLAGEARLTVVPVSEEEVREALVRSGYKVRDLRTYIMPAHLQTGVDDVKGVFFAWAQKVGL

>d1khha\_ c.66.1.16 (A:) Guanidinoacetate methyltransferase {Rat (Rattus norvegicus)}

RWETPYMHSLAAAAASRGGRVLEVGFGMAIAASRVQQAPIKEHWIIECNDGVFQRLQNWALKQPHKVVPLKGLWEEVAPTLPDGHFDGILYDTYPLSEETWHTHQFNFIKTHAFRLLKPGGILTYCNLTSWGELMKSKYTDITAMFEETQVPALLEAGFQRENICTEVMALVPPADCRYYAFPQMITPLVTKH

>d1g6q1\_ c.66.1.6 (1:) Arginine methyltransferase, HMT1 {Baker's yeast (Saccharomyces cerevisiae)}

DYYFDSYDHYGIHEEMLQDTVRTLSYRNAIIQNKDLFKDKIVLDVGCGTGILSMFAAKHGAKHVIGVDMSSIIEMAKELVELNGFSDKITLLRGKLEDVHLPFPKVDIIISEWMGYFLLYESMMDTVLYARDHYLVEGGLIFPDKCSIHLAGLEDSQYKDEKLNYWQDVYGFDYSPFVPLVLHEPIVDTVERNNVNTTSDKLIEFDLNTVKISDLAFKSNFKLTAKRQDMINGIVTWFDIVFPAPKGKRPVEFSTGPHAPYTHWKQTIFYFPDDLDAETGDTIEGELVCSPNEKNNRDLNIKISYKFESNGIDGNSRSRKNEGSYLMH

>d1f3la\_ c.66.1.6 (A:) Arginine methyltransferase, HMT1 {Rat (Rattus norvegicus)}

DLQEDEDGVYFSSYGHYGIHEEMLKDKVRTESYRDFIYQNPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVIAVDQSEILYQAMDIIRLNKLEDTIVLIKGKIEEVSLPVEKVDVIISEWMGYFLLFESMLDSVLYAKSKYLAKGGSVYPDICTISLVAVSDVSKHADRIAFWDDVYGFNMSCMKKAVIPEAVVEVVDHKTLISDPCDIKHIDCHTTSISDLEFSSDFTLRTTKTAMCTAVAGYFDIYFEKNCHNRVVFSTGPQSTKTHWKQTIFLLEKPFPVKAGEALKGKITVHKNKKDPRSLIVTLTLNSSTQTYSLQ

>d1dl5a1 c.66.1.7 (A:1-213) Protein-L-isoaspartyl O-methyltransferase {Thermotoga maritima}

MREKLFWILKKYGVSDHIAKAFLEIPREEFLTKSYPLSYVYEDIVLVSYDDGEEYSTSSQPSLMALFMEWVGLDKGMRVLEIGGGTGYNAAVMSRVVGEKGLVVSVEYSRKICEIAKRNVERLGIENVIFVCGDGYYGVPEFSPYDVIFVTVGVDEVPETWFTQLKEGGRVIVPINLKLSRRQPAFLFKKKDPYLVGNYKLETRFITAGGNLG

>d1jg1a\_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Archaeon Pyrococcus furiosus}

EKELYEKWMRTVEMLKAEGIIRSKEVERAFLKYPRYLSVEDKYKKYAHIDEPLPIPAGQTVSAPHMVAIMLEIANLKPGMNILEVGTGSGWNAALISEIVKTDVYTIERIPELVEFAKRNLERAGVKNVHVILGDGSKGFPPKAPYDVIIVTAGAPKIPEPLIEQLKIGGKLIIPVGSYHLWQELLEVRKTKDGIKIKNHGGVAFVPLIGEYGWK

>d1kr5a\_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Human (Homo sapiens)}

ASHSELIHNLRKNGIIKTDKVFEVMLATDRSHYAKCNPYMDSPQSIGFQATISAPHMHAYALELLFDQLHEGAKALDVGSGSGILTACFARMVGCTGKVIGIDHIKELVDDSVNNVRKDDPTLLSSGRVQLVVGDGRMGYAEEAPYDAIHVGAAAPVVPQALIDQLKPGGRLILPVGPAGGNQMLEQYDKLQDGSIKMKPLMGVIYVPLTDKEKQWSR

>d1i9ga\_ c.66.1.13 (A:) Probable methyltransferase Rv2118c {Mycobacterium tuberculosis}

TGPFSIGERVQLTDAKGRRYTMSLTPGAEFHTHRGSIAHDAVIGLEQGSVVKSSNGALFLVLRPLLVDYVMSMPRGPQVIYPKDAAQIVHEGDIFPGARVLEAGAGSGALTLSLLRAVGPAGQVISYEQRADHAEHARRNVSGCYGQPPDNWRLVVSDLADSELPDGSVDRAVLDMLAPWEVLDAVSRLLVAGGVLMVYVATVTQLSRIVEALRAKQCWTEPRAWETLQRGWNVVGLAVRPQHSMRGHTAFLVATRRLAPGAVA

>d1af7\_2 c.66.1.8 (92-284) Chemotaxis receptor methyltransferase CheR, C-terminal domain {Salmonella typhimurium}

NLTAFFREAHHFPILAEHARRRHGEYRVWSAAASTGEEPYSIAITLADALGMAPGRWKVFASDIDTEVLEKARSGIYRLSELKTLSPQQLQRYFMRGTGPHEGLVRVRQELANYVEFSSVNLLEKQYNVPGPFDAIFCRNVMIYFDKTTQEDILRRFVPLLKPDGLLFAGHSENFSNLVREFSLRGQTVYALS

>d3mag\_\_ c.66.1.9 (-) Polymerase regulatory subunit VP39 {Vaccinia virus}

MDVVSLDKPFMYFEEIDNELDYEPESANEVAKKLPYQGQLKLLLGELFFLSKLQRHGILDGATVVYIGSAPGTHIRYLRDHFYNLGVIIKWMLIDGRHHDPILNGLRDVTLVTRFVDEEYLRSIKKQLHPSKIILISDVRSPKRGGNESTADLLSNYALQNVMISILNPVASSLKWRCPFPDQWIKDFYIPHGNKMLQPFAPSYSAEMRLLSIYTGENMRLTRVTKSDAVNYEKKMYYLNKIVRNKVVVNFDYPNQEYDYFHMYFMLRTVYCNKTFPTTKAKVLFLQQSIFRFLNIP

>d1yub\_\_ c.66.1.9 (-) rRNA methyltransferase {Streptococcus pneumoniae, Ermam}

MNKNIKYSQNFLTSEKVLNQIIKQLNLKETDTVYEIGTGKGHLTTKLAKISKQVTSIELDSHLFNLSSEKLKLNTRVTLIHQDILQFQFPNKQRYKIVGNIPYHLSTQIIKKVVFESRASDIYLIVEEGFYKRTLDIHRTLGLLLHTQVSIQQLLKLPAECFHPKPKVNSVLIKLTRHTTDVPDKYWKLYTYFVSKWVNREYRQLFTKNQFHQAMKHAKVNNLSTITYEQVLSIFNSYLLFNGRK

>d1qama\_ c.66.1.9 (A:) rRNA methyltransferase {Bacillus subtilis, Ermc'}

QNFITSKHNIDKIMTNIRLNEHDNIFEIGSGKGHFTLELVQRCNFVTAIEIDHKLCKTTENKLVDHDNFQVLNKDILQFKFPKNQSYKIFGNIPYNISTDIIRKIVFDSIADEIYLIVEYGFAKRLLNTKRSLALFLMAEVDISILSMVPREYFHPKPKVNSSLIRLNRKKSRISHKDKQKYNYFVMKWVNKEYKKIFTKNQFNNSLKHAGIDDLNNISFEQFLSLFNSYKLFNK

>d1i4wa\_ c.66.1.9 (A:) Transcription factor sc-mtTFB {Baker's yeast (Saccharomyces cerevisiae)}

PIPGIKDISKLKFFYGFKYLWNPTVYNKIFDKLDLTKTYKHPEELKVLDLYPGVGIQSAIFYNKYCPRQYSLLEKRSSLYKFLNAKFEGSPLQILKRDPYDWSTYSNLIDEERIFVPEVQSSDHINDKFLTVANVTGEGSEGLIMQWLSCIGNKNWLYRFGKVKMLLWMPSTTARKLLARPGMHSRSKCSVVREAFTDTKLIAISDANELKGFDSQCIEEWDPILFSAAEIWPTKGKPIALVEMDPIDFDFDVDNWDYVTRHLMILKRTPLNTVMDSLGHGGQQYFNSRITDKDLLKKCPIDLTNDEFIYLTKLFMEWPFKP

>d6mhta\_ c.66.1.10 (A:) DNA methylase HhaI, coenzyme-binding domain {Haemophilus haemolyticus}

MIEIKDKQLTGLRFIDLFAGLGGFRLALESCGAECVYSNEWDKYAQEVYEMNFGEKPEGDITQVNEKTIPDHDILCAGFPCQAFSISGKQKGFEDSRGTLFFDIARIVREKKPKVVFMENVKNFASHDNGNTLEVVKNTMNELDYSFHAKVLNALDYGIPQKRERIYMICFRNDLNIQNFQFPKPFELNTFVKDLLLPDSEVEHLVIDRKDLVMTNQEIEQTTPKTVRLGIVGKGGQGERIYSTRGIAITLSAYGGGIFAKTGGYLVNGKTRKLHPRECARVMGYPDSYKVHPSTSQAYKQFGNSVVINVLQYIAYNIGSSLNFKPY

>d1g38a\_ c.66.1.10 (A:) DNA methylase TaqI, coenzyme-binding domain {Thermus aquaticus}

VETPPEVVDFMVSLAEAPRGGRVLEPACAHGPFLRAFREAHGTGYRFVGVEIDPKALDLPPWAEGILADFLLWEPGEAFDLILGNPPYGIVGEASKYPIHVFKAVKDLYKKAFSTWKGKYNLYGAFLEKAVRLLKPGGVLVFVVPATWLVLEDFALLREFLAREGKTSVYYLGEVFPQKKVSAVVIRFQKSGKGLSLWDTQESESGFTPILWAEYPHWEGEIIRFETEETRKLEISGMPLGDLFHIRFAARSPEFKKHPAVRKEPGPGLVPVLTGRNLKPGWVDYEKNHSGLWMPKERAKELRDFYATPHLVVAHTKGTRVVAAWDERAYPWREEFHLLPKEGVRLDPSSLVQWLNSEAMQKHVRTLYRDFVPHLTLRMLERLPVRREYGFHT

>d1dcta\_ c.66.1.10 (A:) DNA methylase HaeIII, coenzyme-binding domain {Haemophilus aegyptius}

MNLISLFSGAGGLDLGFQKAGFRIICANEYDKSIWKTYESNHSAKLIKGDISKISSDEFPKCDGIIGGPPCQSWSEGGSLRGIDDPRGKLFYEYIRILKQKKPIFFLAENVKGMMAQRHNKAVQEFIQEFDNAGYDVHIILLNANDYGVAQDRKRVFYIGFRKELNINYLPPIPHLIKPTFKDVIWDLKDNPIPALDKNKTNGNKCIYPNHEYFIGSYSTIFMSRNRVRQWNEPAFTVQASGRQCQLHPQAPVMLKVSKNLNKFVEGKEHLYRRLTVRECARVQGFPDDFIFHYESLNDGYKMIGNAVPVNLAYEIAKTIKSAL

>d2dpma\_ c.66.1.10 (A:) DpnM DNA adenine methyltransferase {Streptococcus pneumoniae}

TLQPFTKWTGGKRQLLPVIRELIPKTYNRYFEPFVGGGALFFDLAPKDAVINDFNAELINCYQQIKDNPQELIEILKVHQEYNSKEYYLDLRSADRDERIDMMSEVQRAARILYMLRVNFNGLYRVNSKNQFNVPYGRYKNPKIVDEELISAISVYINNNQLEIKVGDFEKAIVDVRTGDFVYFDPPYIPLSETSAFTSYTHEGFSFADQVRLRDAFKRLSDTGAYVMLSNSSSALVEELYKDFNIHYVEATRTNGAKSSSRGKISEIIVTNYEK

>d1g55a\_ c.66.1.10 (A:) DNMT2 {Human (Homo sapiens)}

EPLRVLELYSGVGGMHHALRESCIPAQVVAAIDVNTVANEVYKYNFPHTQLLAKTIEGITLEEFDRLSFDMILMSPPCQPFTRIGRQGDMTDSRTNSFLHILDILPRLQKLPKYILLENVKGFEVSSTRDLLIQTIENCGFQYQEFLLSPTSLGIPNSRLRYFLIAKLQSEPLPFQAPGQVLMEFPKIEIHRKNQQDSDLSVKMLKDFLEDDTDVNQYLLPPKSLLRYALLLDIVQPTCRRSVCFTKGYGSYIEGTGSVLQTAEDVQVENIYKSLTNLSQEEQITKLLILKLRYFTPKEIANLLGFPPEFGFPEKITVKQRYRLLGNSLNVHVVAKLIKILYE

>d1booa\_ c.66.1.11 (A:) m.PvuII N4 cytosine-specific DNA methyltransferase {Proteus vulgaris}

NFGKKPAYTTSNGSMYIGDSLELLESFPEESISLVMTSPPFALQRKKEYGNLEQHEYVDWFLSFAKVVNKKLKPDGSFVVDFGGAYMKGVPARSIYNFRVLIRMIDEVGFFLAEDFYWFNPSKLPSPIEWVNKRKIRVKDAVNTVWWFSKTEWPKSDITKVLAPYSDRMKKLIEDPDKFYTPKTRPSGHDIGKSFSKDNGGSIPPNLLQISNSESNGQYLANCKLMGIKAHPARFPAKLPEFFIRMLTEPDDLVVDIFGGSNTTGLVAERESRKWISFEMKPEYVAASAFRFLDNNISEEKITDIYNRILNGESLDLNSI

>d1eg2a\_ c.66.1.11 (A:) m.RsrI N6 adenosine-specific DNA methyltransferase {Rhodobacter sphaeroides}

GTTRHVYDVCDCLDTLAKLPDDSVQLIICDPPYNIMLADWDDHMDYIGWAKRWLAEAERVLSPTGSIAIFGGLQYQGEAGSGDLISIISHMRQNSKMLLANLIIWNYPNGMSAQRFFANRHEEIAWFAKTKKYFFDLDAVREPYDEETKAAYMKDKRLNPESVEKGRNPTNVWRMSRLNGNSLERVGHPTQKPAAVIERLVRALSHPGSTVLDFFAGSGVTARVAIQEGRNSICTDAAPVFKEYYQKQLTFLQDDGLIDKARSYEIVEGAANFGAALQR

>d1inla\_ c.66.1.17 (A:) Spermidine synthase {Thermotoga maritima}

RTLKELERELQPRQHLWYFEYYTGNNVGLFMKMNRVIYSGQSDIQRIDIFENPDLGVVFALDGITMTTEKDEFMYHEMLAHVPMFLHPNPKKVLIIGGGDGGTLREVLKHDSVEKAILCEVDGLVIEAARKYLKQTSCGFDDPRAEIVIANGAEYVRKFKNEFDVIIIDSTDPTAGQGGHLFTEEFYQACYDALKEDGVFSAETEDPFYDIGWFKLAYRRISKVFPITRVYLGFMTTYPSGMWSYTFASKGIDPIKDFDPEKVRKFNKELKYYNEEVHVASFALPNFVKKELGLM

>d1kpga\_ c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1 {Mycobacterium tuberculosis}

DELKPHFANVQAHYDLSDDFFRLFLDPTQTYSCAYFERDDMTLQEAQIAKIDLALGKLGLQPGMTLLDVGCGWGATMMRAVEKYDVNVVGLTLSKNQANHVQQLVANSENLRSKRVLLAGWEQFDEPVDRIVSIGAFEHFGHERYDAFFSLAHRLLPADGVMLLHTITGLHPKEIHERGLPMSFTFARFLKFIVTEIFPGGRLPSIPMVQECASANGFTVTRVQSLQPHYAKTLDLWSAALQANKGQAIALQSEEVYERYMKYLTGCAEMFRIGYIDVNQFTCQK

>d1kpia\_ c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1 {Mycobacterium tuberculosis}

QLKPPVEAVRSHYDKSNEFFKLWLDPSMTYSCAYFERPDMTLEEAQYAKRKLALDKLNLEPGMTLLDIGCGWGSTMRHAVAEYDVNVIGLTLSENQYAHDKAMFDEVDSPRRKEVRIQGWEEFDEPVDRIVSLGAFEHFADGAGDAGFERYDTFFKKFYNLTPDDGRMLLHTITIPDKEEAQELGLTSPMSLLRFIKFILTEIFPGGRLPRISQVDYYSSNAGWKVERYHRIGANYVPTLNAWADALQAHKDEAIALKGQETCDIYMHYLRGCSDLFRDKYTDVCQFTLVK

>d7aata\_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken (Gallus gallus), mitochondria}

SSWWSHVEMGPPDPILGVTEAFKRDTNSKKMNLGVGAYRDDNGKPYVLNCVRKAEAMIAAKKMDKEYLPIAGLADFTRASAELALGENSEAFKSGRYVTVQGISGTGSLRVGANFLQRFFKFSRDVYLPKPSWGNHTPIFRDAGLQLQAYRYYDPKTCSLDFTGAMEDISKIPEKSIILLHACAHNPTGVDPRQEQWKELASVVKKRNLLAYFDMAYQGFASGDINRDAWALRHFIEQGIDVVLSQSYAKNMGLYGERAGAFTVICRDAEEAKRVESQLKILIRPMYSNPPMNGARIASLILNTPELRKEWLVEVKGMADRIISMRTQLVSNLKKEGSSHNWQHITDQIGMFCFTGLKPEQVERLTKEFSIYMTKDGRISVAGVASSNVGYLAHAIHQVTK

>d2csta\_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken (Gallus gallus), cytosolic form}

AASIFAAVPRAPPVAVFKLTADFREDGDSRKVNLGVGAYRTDEGQPWVLPVVRKVEQLIAGDGSLNHEYLPILGLPEFRANASRIALGDDSPAIAQKRVGSVQGLGGTGALRIGAEFLRRWYNGNNNTATPVYVSSPTWENHNSVFMDAGFKDIRTYRYWDAAKRGLDLQGLLDDMEKAPEFSIFILHACAHNPTGTDPTPDEWKQIAAVMKRRCLFPFFDSAYQGFASGSLDKDAWAVRYFVSEGFELFCAQSFSKNFGLYNERVGNLSVVGKDEDNVQRVLSQMEKIVRTTWSNPPSQGARIVATTLTSPQLFAEWKDNVKTMADRVLLMRSELRSRLESLGTPGTWNHITDQIGMFSFTGLNPKQVEYMIKEKHIYLMASGRINMCGLTTKNLDYVAKSIHEAVTKIQ

>d1ajsa\_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Pig (Sus scrofa), cytosolic form}

APPSVFAEVPQAQPVLVFKLIADFREDPDPRKVNLGVGAYRTDDCQPWVLPVVRKVEQRIANNSSLNHEYLPILGLAEFRTCASRLALGDDSPALQEKRVGGVQSLGGTGALRIGAEFLARWYNGTNNKDTPVYVSSPTWENHNGVFTTAGFKDIRSYRYWDTEKRGLDLQGFLSDLENAPEFSIFVLHACAHNPTGTDPTPEQWKQIASVMKRRFLFPFFDSAYQGFASGNLEKDAWAIRYFVSEGFELFCAQSFSKNFGLYNERVGNLTVVAKEPDSILRVLSQMQKIVRVTWSNPPAQGARIVARTLSDPELFHEWTGNVKTMADRILSMRSELRARLEALKTPGTWNHITDQIGMFSFTGLNPKQVEYLINQKHIYLLPSGRINMCGLTTKNLDYVATSIHEAVTKIQ

>d1yaaa\_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Baker's yeast (Saccharomyces cerevisiae), cytosolic form}

SATLFNNIELLPPDALFGIKQRYGQDQRATKVDLGIGAYRDDNGKPWVLPSVKAAEKLIHNDSSYNHEYLGITGLPSLTSNAAKIIFGTQSDALQEDRVISVQSLSGTGALHISAKFFSKFFPDKLVYLSKPTWANHMAIFENQGLKTATYPYWANETKSLDLNGFLNAIQKAPEGSIFVLHSCAHNPTGLDPTSEQWVQIVDAIASKNHIALFDTAYQGFATGDLDKDAYAVRLGVEKLSTVSPVFVCQSFAKNAGMYGERVGCFHLALTKQAQNKTIKPAVTSQLAKIIRSEVSNPPAYGAKIVAKLLETPELTEQWHKDMVTMSSRITKMRHALRDHLVKLGTPGNWDHIVNQCGMFSFTGLTPQMVKRLEETHAVYLVASGRASIAGLNQGNVEYVAKAIDEVVRFYA

>d1qisa\_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Escherichia coli}

MFENITAAPADPILGLADLFRADERPGKINLGIGVYKDETGKTPVLTSVKKAEQYLLENETTKNYLGIDGIPEFGRCTQELLFGKGSALINDKRARTAQTPGGTGALRVAADFLAKNTSVKRVWVSNPSWPNHKSVFNSAGLEVREYAYYDAENHTLDFDALINSLNEAQAGDVVLFHGFCHNPTGIDPTLEQWQTLAQLSVEKGWLPLFDFAYQGFARGLEEDAEGLRAFAAMHKELIVASSYSKNFGLYNERVGACTLVAADSETVDRAFSQMKAAIRANYSNPPAHGASVVATILSNDALRAIWEQELTDMRQRIQRMRQLFVNTLQEKGANRDFSFIIKQNGMFSFSGLTKEQVLRLREEFGVYAVASGRVNVAGMTPDNMAPLCEAIVAVL

>d1bjwa\_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Thermus thermophilus}

MRGLSRRVQAMKPSATVAVNAKALELRRQGVDLVALTAGEPDFDTPEHVKEAARRALAQGKTKYAPPAGIPELREALAEKFRRENGLSVTPEETIVTVGGKQALFNLFQAILDPGDEVIVLSPYWVSYPEMVRFAGGVVVEVETLPEEGFVPDPERVRRAITPRTKALVVNSPNNPTGAVYPKEVLEALARLAVEHDFYLVSDEIYEHLLYEGEHFSPGRVAPEHTLTVNGAAKAFAMTGWRIGYACGPKEVIKAMASVSSQSTTSPDTIAQWATLEALTNQEASRAFVEMAREAYRRRRDLLLEGLTALGLKAVRPSGAFYVLMDTSPIAPDEVRAAERLLEAGVAVVPGTDFAAFGHVRLSYATSEENLRKALERFARVL

>d2ay1a\_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Paracoccus denitrificans}

MLGNLKPQAPDKILALMGEFRADPRQGKIDLGVGVYKDATGHTPIMRAVHAAEQRMLETETTKTYAGLSGEPEFQKAMGELILGDGLKSETTATLATVGGTGALRQALELARMANPDLRVFVSDPTWPNHVSIMNFMGLPVQTYRYFDAETRGVDFEGMKADLAAAKKGDMVLLHGCCHNPTGANLTLDQWAEIASILEKTGALPLIDLAYQGFGDGLEEDAAGTRLIASRIPEVLIAASCSKNFGIYRERTGCLLALCADAATRELAQGAMAFLNRQTYSFPPFHGAKIVSTVLTTPELRADWMAELEAVRSGMLRLREQLAGELRDLSGSDRFGFVAEHRGMFSRLGATPEQVKRIKEEFGIYMVGDSRINIAGLNDNTIPILARAIIEVGV

>d3tata\_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Escherichia coli}

MFQKVDAYAGDPILTLMERFKEDPRSDKVNLSIGLYYNEDGIIPQLQAVAEAEARLNAQPHGASLYLPMEGLNCYRHAIAPLLFGADHPVLKQQRVATIQTLGGSGALKVGADFLKRYFPESGVWVSDPTWENHVAIFAGAGFEVSTYPWYDEATNGVRFNDLLATLKTLPARSIVLLHPCCHNPTGADLTNDQWDAVIEILKARELIPFLDIAYQGFGAGMEEDAYAIRAIASAGLPALVSNSFSKIFSLYGERVGGLSVMCEDAEAAGRVLGQLKATVRRNYSSPPNFGAQVVAAVLNDEALKASWLAEVEEMRTRILAMRQELVKVLSTEMPERNFDYLLNQRGMFSYTGLSAAQVDRLREEFGVYLIASGRMCVAGLNTANVQRVAKAFAAVM

>d1gdea\_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Archaeon Pyrococcus horikoshii}

ALSDRLELVSASEIRKLFDIAAGMKDVISLGIGEPDFDTPQHIKEYAKEALDKGLTHYGPNIGLLELREAIAEKLKKQNGIEADPKTEIMVLLGANQAFLMGLSAFLKDGEEVLIPTPAFVSYAPAVILAGGKPVEVPTYEEDEFRLNVDELKKYVTDKTRALIINSPCNPTGAVLTKKDLEEIADFVVEHDLIVISDEVYEHFIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGWRLGFVAAPSWIIERMVKFQMYNATCPVTFIQYAAAKALKDERSWKAVEEMRKEYDRRRKLVWKRLNEMGLPTVKPKGAFYIFPRIRDTGLTSKKFSELMLKEARVAVVPGSAFGKAGEGYVRISYATAYEKLEEAMDRMERVLKERKLV

>d1bw0a\_ c.67.1.1 (A:) Tyrosine aminotransferase (TAT) {Trypanosoma cruzi}

WDVSMSNHAGLVFNPIRTVSDNAKPSPSPKPIIKLSVGDPTLDKNLLTSAAQIKKLKEAIDSQECNGYFPTVGSPEAREAVATWWRNSFVHKEELKSTIVKDNVVLCSGGSHGILMAITAICDAGDYALVPQPGFPHYETVCKAYGIGMHFYNCRPENDWEADLDEIRRLKDDKTKLLIVTNPSNPCGSNFSRKHVEDIVRLAEELRLPLFSDEIYAGMVFKGKDPNATFTSVADFETTVPRVILGGTAKNLVVPGWRLGWLLYVDPHGNGPSFLEGLKRVGMLVCGPCTVVQAALGEALLNTPQEHLDQIVAKIEESAMYLYNHIGECIGLAPTMPRGAMYLMSRIDLEKYRDIKTDVEFFEKLLEEENVQVLPGTIFHAPGFTRLTTTRPVEVYREAVERIKAFCQRHAA

>d1fg7a\_ c.67.1.1 (A:) Histidinol-phosphate aminotransferase {Escherichia coli}

TVTITDLARENVRNLTPYQSARRLGGNGDVWLNANEYPTAVEFQLTQQTLNRYPECQPKAVIENYAQYAGVKPEQVLVSRGADEGIELLIRAFCEPGKDAILYCPPTYGMYSVSAETIGVECRTVPTLDNWQLDLQGISDKLDGVKVVYVCSPNNPTGQLINPQDFRTLLELTRGKAIVVADEAYIEFCPQASLAGWLAEYPHLAILRTLSKAFALAGLRCGFTLANEEVINLLMKVIAPYPLSTPVADIAAQALSPQGIVAMRERVAQIIAEREYLIAALKEIPCVEQVFDSETNYILARFKASSAVFKSLWDQGIILRDQNKQPSLSGCLRITVGTREESQRVIDALRAEQV

>d1kusa\_ c.67.1.1 (A:) L-threonine-O-3-phosphate decarboxylase CobD {Salmonella enterica}

HGGNIREPATVLGISPDQLLDFSANINPLGMPVSVKRALIDNLDCIERYPDADYFHLHQALARHHQVPASWILAGNGETESIFTVASGLKPRRAMIVTPGFAEYGRALAQSGCEIRRWSLREADGWQLTDAILEALTPDLDCLFLCTPNNPTGLLPERPLLQAIADRCKSLNINLILDEAFIDFIPHETGFIPALKDNPHIWVLRSLTKFYAIPGLRLGYLVNSDDAAMARMRRQQMPWSVNALAALAGEVALQDSAWQQATWHWLREEGARFYQALCQLPLLTVYPGRANYLLLRCEREDIDLQRRLLTQRILIRSCANYPGLDSRYYRVAIRSAAQNERLLAALRNVLTGIAP

>d1jg8a\_ c.67.1.1 (A:) Low-specificity threonine aldolase {Thermatoga maritima}

MIDLRSDTVTKPTEEMRKAMAQAEVGDDVYGEDPTINELERLAAETFGKEAALFVPSGTMGNQVSIMAHTQRGDEVILEADSHIFWYEVGAMAVLSGVMPHPVPGKNGAMDPDDVRKAIRPRNIHFPRTSLIAIENTHNRSGGRVVPLENIKEICTIAKEHGINVHIDGARIFNASIASGVPVKEYAGYADSVMFCLSKGLCAPVGSVVVGDRDFIERARKARKMLGGGMRQAGVLAAAGIIALTKMVDRLKEDHENARFLALKLKEIGYSVNPEDVKTNMVILRTDNLKVNAHGFIEALRNSGVLANAVSDTEIRLVTHKDVSRNDIEEALNIFEKLFRKFS

>d1tpla\_ c.67.1.2 (A:) Tyrosine phenol-lyase {Citrobacter intermedius}

MNYPAEPFRIKSVETVSMIPRDERLKKMQEAGYNTFLLNSKDIYIDLLTDSGTNAMSDKQWAGMMMGDEAYAGSENFYHLERTVQELFGFKHIVPTHQGRGAENLLSQLAIKPGQYVAGNMYKNGAVFVDIVRDEAHDAGLNIAFKGDIDLKKLQKLIDEKGAENIAYICLAVTVNLAGGQPVSMANMRAVRELTAAHGIKVFYDATRCVENAYFIKEQEQGFENKSIAEIVHEMFSYADGCTMSGKKDCLVNIGGFLCMNDDEMFSSAKELVVVYEGMPSYGGLAGRDMEAMAIGLREAMQYEYIEHRVKQVRYLGDKLKAAGVPIVEPVGGHAVFLDARRFCEHLTQDEFPAQSLAASIYVETGVRSMERGIKLETVRLTIPRRVYTYAHMDVVADGIIKLYQHKEDIRGLKFIYFFTARFDYI

>d1ax4a\_ c.67.1.2 (A:) Tryptophan indol-lyase (tryptophanase) {Proteus vulgaris}

AKRIVEPFRIKMVEKIRVPSREEREAALKEAGYNPFLLPSSAVYIDLLTDSGTNAMSDHQWAAMITGDEAYAGSRNYYDLKDKAKELFNYDYIIPAHQGRGAENILFPVLLKYKQKEGKAKNPVFISNFHFDTTAAHVELNGCKAINIVTEKAFDSETYDDWKGDFDIKKLKENIAQHGADNIVAIVSTVTCNSAGGQPVSMSNLKEVYEIAKQHGIFVVMDSARFCENAYFIKARDPKYKNATIKEVIFDMYKYADALTMSAKKDPLLNIGGLVAIRDNEEIFTLARQRCVPMEGFVTYGGLAGRDMAAMVQGLEEGTEEEYLHYRIGQVKYLGDRLREAGIPIQYPTGGHAVFVDCKKLVPQIPGDQFPAQAVINALYLESGVRAVEIGSFLLGRDPATGEQKHADMEFMRLTIARRVYTNDHMDYIADALIGLKEKFATLKGLEFEYEPPVLRHFTARLKPI

>d1js3a\_ c.67.1.6 (A:) DOPA decarboxylase {Pig (Sus scrofa)}

MNASDFRRRGKEMVDYMADYLEGIEGRQVYPDVQPGYLRPLIPATAPQEPDTFEDILQDVEKIIMPGVTHWHSPYFFAYFPTASSYPAMLADMLCGAIGCIGFSWAASPACTELETVMMDWLGKMLQLPEAFLAGEAGEGGGVIQGSASEATLVALLAARTKVVRRLQAASPGLTQGAVLEKLVAYASDQAHSSVERAGLIGGVKLKAIPSDGKFAMRASALQEALERDKAAGLIPFFVVATLGTTSCCSFDNLLEVGPICHEEDIWLHVDAAYAGSAFICPEFRHLLNGVEFADSFNFNPHKWLLVNFDCSAMWVKRRTDLTGAFKLDPVYLKHSHQGSGLITDYRHWQLPLGRRFRSLKMWFVFRMYGVKGLQAYIRKHVQLSHEFEAFVLQDPRFEVCAEVTLGLVCFRLKGSDGLNEALLERINSARKIHLVPCRLRGQFVLRFAICSRKVESGHVRLAWEHIRGLAAELLA

>d1cl1a\_ c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Escherichia coli}

KLDTQLVNAGRSKKYTLGAVNSVIQRASSLVFDSVEAKKHATRNRANGELFYGRRGTLTHFSLQQAMCELEGGAGCVLFPCGAAAVANSILAFIEQGDHVLMTNTAYEPSQDFCSKILSKLGVTTSWFDPLIGADIVKHLQPNTKIVFLESPGSITMEVHDVPAIVAAVRSVVPDAIIMIDNTWAAGVLFKALDFGIDVSIQAATKYLVGHSDAMIGTAVCNARCWEQLRENAYLMGQMVDADTAYITSRGLRTLGVRLRQHHESSLKVAEWLAEHPQVARVNHPALPGSKGHEFWKRDFTGSSGLFSFVLKKKLNNEELANYLDNFSLFSMAYSWGGYESLILANQPEHIAAIRPQGEIDFSGTLIRLHIGLEDVDDLIADLDAGFARIV

>d1ibja\_ c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Thale cress (Arabidopsis thaliana)}

ASVSTLLVNLDNKFDPFDAMSTPLYQTATFKQPSAIENGPYDYTRSGNPTRDALESLLAKLDKADRAFCFTSGMAALSAVTHLIKNGEEIVAGDDVYGGSDRLLSQVVPRSGVVVKRVNTTKLDEVAAAIGPQTKLVWLESPTNPRQQISDIRKISEMAHAQGALVLVDNSIMSPVLSRPLELGADIVMHSATKFIAGHSDVMAGVLAVKGEKLAKEVYFLQNSEGSGLAPFDCWLCLRGIKTMALRIEKQQENARKIAMYLSSHPRVKKVYYAGLPDHPGHHLHFSQAKGAGSVFSFITGSVALSKHLVETTKYFSIAVSFGSVKSLISMPCFMSHASIPAEVREARGLTEDLVRISAGIEDVDDLISDLDIAFKTFPL

>d1cs1a\_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Escherichia coli}

RKQATIAVRSGLNDDEQYGCVVPPIHLSSTYNFTGFNEPRAHDYSRRGNPTRDVVQRALAELEGGAGAVLTNTGMSAIHLVTTVFLKPGDLLVAPHDCYGGSYRLFDSLAKRGCYRVLFVDQGDEQALRAALAEKPKLVLVESPSNPLLRVVDIAKICHLAREVGAVSVVDNTFLSPALQNPLALGADLVLHSCTKYLNGHSDVVAGVVIAKDPDVVTELAWWANNIGVTGGAFDSYLLLRGLRTLVPRMELAQRNAQAIVKYLQTQPLVKKLYHPSLPENQGHEIAARQQKGFGAMLSFELDGDEQTLRRFLGGLSLFTLAESLGGVESLISHAATMTHAGMAPEARAAAGISETLLRISTGIEDGEDLIADLENGFRAANKG

>d1qgna\_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Common tobacco (Nicotiana tabacum)}

MKYASFLNSDGSVAIHAGERLGRGIVTDAITTPVVNTSAYFFNKTSELIDFKEKRRASFEYGRYGNPTTVVLEEKISALEGAESTLLMASGMCASTVMLLALVPAGGHIVTTTDCYRKTRIFIETILPKMGITATVIDPADVGALELALNQKKVNLFFTESPTNPFLRCVDIELVSKLCHEKGALVCIDGTFATPLNQKALALGADLVLHSATKFLGGHNDVLAGCISGPLKLVSEIRNLHHILGGALNPNAAYLIIRGMKTLHLRVQQQNSTALRMAEILEAHPKVRHVYYPGLQSHPEHHIAKKQMTGFGGAVSFEVDGDLLTTAKFVDALKIPYIAPSFGGCESIVDQPAIMSYWDLSQSDRAKYGIMDNLVRFSFGVEDFDDLKADILQALDSI

>d1e5ea\_ c.67.1.3 (A:) Methionine gamma-lyase, MGL {Trichomonas vaginalis}

ERMTPATACIHANPQKDQFGAAIPPIYQTSTFVFDNCQQGGNRFAGQESGYIYTRLGNPTVSNLEGKIAFLEKTEACVATSSGMGAIAATVLTILKAGDHLISDECLYGCTHALFEHALTKFGIQVDFINTAIPGEVKKHMKPNTKIVYFETPANPTLKIIDMERVCKDAHSQEGVLVIADNTFCSPMITNPVDFGVDVVVHSATKYINGHTDVVAGLICGKADLLQQIRMVGIKDITGSVISPHDAWLITRGLSTLNIRMKAESENAMKVAEYLKSHPAVEKVYYPGFEDHEGHDIAKKQMRMYGSMITFILKSGFEGAKKLLDNLKLITLAVSLGGCESLIQHPASMTHAVVPKEEREAAGITDGMIRLSVGIEDADELIADFKQGLDALLR

>d1d2fa\_ c.67.1.3 (A:) Modulator in mal gene expression, MalY {Escherichia coli}

LLPFTISDMDFATAPCIIEALNQRLMHGVFGYSRWKNDEFLAAIAHWFSTQHYTAIDSQTVVYGPSVIYMVSELIRQWSETGEGVVIHTPAYDAFYKAIEGNQRTVMPVALEKQADGWFCDMGKLEAVLAKPECKIMLLCSPQNPTGKVWTCDELEIMADLCERHGVRVISDEIHMDMVWGEQPHIPWSNVARGDWALLTSGSKSFNIPALTGAYGIIENSSSRDAYLSALKGRDGLSSPSVLALTAHIAAYQQGAPWLDALRIYLKDNLTYIADKMNAAFPELNWQIPQSTYLAWLDLRPLNIDDNALQKALIEQEKVAIMPGYTYGEEGRGFVRLNAGCPRSKLEKGVAGLINAIRAVR

>d1c7na\_ c.67.1.3 (A:) Cystalysin {Treponema denticola}

MIYDFTTKISRKNLGSLKWDLMYSQNPEVGNEVVPLSVADMEFKNPPELIEGLKKYLDETVLGYTGPTEEYKKTVKKWMKDRHQWDIQTDWIINTAGVVPAVFNAVREFTKPGDGVIIITPVYYPFFMAIKNQERKIIECELLEKDGYYTIDFQKLEKLSKDKNNKALLFCSPHNPVGRVWKKDELQKIKDIVLKSDLMLWSDEIHFDLIMPGYEHTVFQSIDEQLADKTITFTAPSKTFNIAGMGMSNIIIKNPDIRERFTKSRDATSGMPFTTLGYKACEICYKECGKWLDGCIKVIDKNQRIVKDFFEVNHPEIKAPLIEGTYLQWIDFRALKMDHKAMEEFMIHKAQIFFDEGYIFGDGGIGFERINLAAPSSVIQESLERLNKALKDLK

>d1eg5a\_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Thermotoga maritima}

MRVYFDNNATTRVDDRVLEEMIVFYREKYGNPNSAHGMGIEANLHMEKAREKVAKVLGVSPSEIFFTSCATESINWILKTVAETFEKRKRTIITTPIEHKAVLETMKYLSMKGFKVKYVPVDSRGVVKLEELEKLVDEDTFLVSIMAANNEVGTIQPVEDVTRIVKKKNKETLVHVDAVQTIGKIPFSLEKLEVDYASFSAHKFHGPKGVGITYIRKGVPIRPLIHGGGQERGLRSGTQNVPGIVGAARAMEIAVEELSEAAKHMEKLRSKLVSGLMNLGAHIITPLEISLPNTLSVSFPNIRGSTLQNLLSGYGIYVSTSSACTSKDERLRHVLDAMGVDRRIAQGAIRISLCKYNTEEEVDYFLKKIEEILSFL

>d1jf9a\_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Escherichia coli}

IFSVDKVRADFPVLSREVNGLPLAYLDSAASAQKPSQVIDAEAEFYRHGYAAVHRGIHTLSAQATEKMENVRKRASLFINARSAEELVFVRGTTEGINLVANSWGNSNVRAGDNIIISQMEHHANIVPWQMLCARVGAELRVIPLNPDGTLQLETLPTLFDEKTRLLAITHVSNVLGTENPLAEMITLAHQHGAKVLVDGAQAVMHHPVDVQALDCDFYVFSGHKLYGPTGIGILYVKEALLQEMPPWEGGGSMIATVSLSEGTTWTKAPWRFEAGTPNTGGIIGLGAALEYVSALGLNNIAEYEQNLMHYALSQLESVPDLTLYGPQNRLGVIAFNLGKHHAYDVGSFLDNYGIAVRTGHHCAMPLMAYYNVPAMCRASLAMYNTHEEVDRLVTGLQRIHRLLG

>d1elua\_ c.67.1.3 (A:) Cystine C-S lyase {Synechocystis sp.}

QFPGLANKTYFNFGGQGILPTVALEAITAMYGYLQENGPFSIAANQHIQQLIAQLRQALAETFNVDPNTITITDNVTTGCDIVLWGLDWHQGDEILLTDCEHPGIIAIVQAIAARFGITYRFFPVAATLNQGDAAAVLANHLGPKTRLVILSHLLWNTGQVLPLAEIMAVCRRHQGNYPVRVLVDGAQSAGSLPLDFSRLEVDYYAFTGHKWFAGPAGVGGLYIHGDCLGEINPTYVGWRSITYGAKGEPTGWAEGGKRFEVATSAYPQYAGLLAALQLHQRQGTAEERYQAICQRSEFLWRGLNQLPHVHCLATSAPQAGLVSFTVDSPLGHRAIVQKLEEQRIYLRTIADPDCIRACCHYITDEEEINHLLARLADFGP

>d2dkb\_\_ c.67.1.4 (-) Dialkylglycine decarboxylase {Pseudomonas cepacia}

LNDDATFWRNARHHLVRYGGTFEPMIIERAKGSFVYDADGRAILDFTSGQMSAVLGHCHPEIVSVIGEYAGKLDHLFSEMLSRPVVDLATRLANITPPGLDRALLLSTGAESNEAAIRMAKLVTGKYEIVGFAQSWHGMTGAAASATYSAGRKGVGPAAVGSFAIPAPFTYRPRFERNGAYDYLAELDYAFDLIDRQSSGNLAAFIAEPILSSGGIIELPDGYMAALKRKCEARGMLLILDEAQTGVGRTGTMFACQRDGVTPDILTLSKTLGAGLPLAAIVTSAAIEERAHELGYLFYTTHVSDPLPAAVGLRVLDVVQRDGLVARANVMGDRLRRGLLDLMERFDCIGDVRGRGLLLGVEIVKDRRTKEPADGLGAKITRECMNLGLSMNIVQLPGMGGVFRIAPPLTVSEDEIDLGLSLLGQAIERAL

>d2gsaa\_ c.67.1.4 (A:) Glutamate-1-semialdehyde aminomutase (aminotransferase) {Synechococcus sp., strain GR6}

FKTIKSDEIFAAAQKLMPGGVSSPVRAFKSVGGQPIVFDRVKDAYAWDVDGNRYIDYVGTWGPAICGHAHPEVIEALKVAMEKGTSFGAPCALENVLAEMVNDAVPSIEMVRFVNSGTEACMAVLRLMRAYTGRDKIIKFEGCYHGHADMFLVKAGSGVATLGLPSSPGVPKKTTANTLTTPYNDLEAVKALFAENPGEIAGVILEPIVGNSGFIVPDAGFLEGLREITLEHDALLVFDEVMTGFRIAYGGVQEKFGVTPDLTTLGKIIGGGLPVGAYGGKREIMQLVAPAGPMYQAGTLSGNPLAMTAGIKTLELLRQPGTYEYLDQITKRLSDGLLAIAQETGHAACGGQVSGMFGFFFTEGPVHNYEDAKKSDLQKFSRFHRGMLEQGIYLAPSQFEAGFTSLAHTEEDIDATLAAARTVMSAL

>d2oata\_ c.67.1.4 (A:) Ornithine aminotransferase {Human (Homo sapiens)}

GPPTSDDIFEREYKYGAHNYHPLPVALERGKGIYLWDVEGRKYFDFLSSYSAVNQGHCHPKIVNALKSQVDKLTLTSRAFYNNVLGEYEEYITKLFNYHKVLPMNTGVEAGETACKLARKWGYTVKGIQKYKAKIVFAAGNFWGRTLSAISSSTDPTSYDGFGPFMPGFDIIPYNDLPALERALQDPNVAAFMVEPIQGEAGVVVPDPGYLMGVRELCTRHQVLFIADEIQTGLARTGRWLAVDYENVRPDIVLLGKALSGGLYPVSAVLCDDDIMLTIKPGEHGSTYGGNPLGCRVAIAALEVLEEENLAENADKLGIILRNELMKLPSDVVTAVRGKGLLNAIVIKETKDWDAWKVCLRLRDNGLLAKPTHGDIIRFAPPLVIKEDELRESIEIINKTILSF

>d1gtxa\_ c.67.1.4 (A:) 4-aminobutyrate aminotransferase, GABA-aminotransferase {Pig (Sus scrofa)}

FDYDGPLMKTEVPGPRSRELMKQLNIIQNAEAVHFFCNYEESRGNYLVDVDGNRMLDLYSQISSIPIGYSHPALVKLVQQPQNVSTFINRPALGILPPENFVEKLRESLLSVAPKGMSQLITMACGSCSNENAFKTIFMWYRSKERGQSAFSKEELETCMINQAPGCPDYSILSFMGAFHGRTMGCLATTHSKAIHKIDIPSFDWPIAPFPRLKYPLEEFVKENQQEEARCLEEVEDLIVKYRKKKKTVAGIIVEPIQSEGGDNHASDDFFRKLRDISRKHGCAFLVDEVQTGGGSTGKFWAHEHWGLDDAADVMTFSKKMMTGGFFHKEEFRPNAPYRIFNTWLGDPSKNLLLAEVINIIKREDLLSNAAHAGKVLLTGLLDLQARYPQFISRVRGRGTFCSFDTPDESIRNKLISIARNKGVMLGGCGDKSIRFRPTLVFRDHHAHLFLNIFSDILADFK

>d1bt4a\_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Bacillus circulans, subsp. alkalophilus}

SERAYNFNAGPAALPLEVLERAQAEFVDYQHTGMSIMEMSHRGAVYEAVHNEAQARLLALLGNPTGYKVLFIQGGASTQFAMIPMNFLKEGQTANYVMTGSWASKALKEAKLIGDTHVAASSEASNYMTLPKLQEIQLQDNAAYLHLTSNETIEGAQFKAFPDTGSVPLIGDMSSDILSRPFDLNQFGLVYAGAQKNLGPSGVTVVIVREDLVAESPKHLPTMLRYDTYVKNNSLYNTPPSFGIYMVNEVLKWIEERGGLEGVQQANRKKASLIYDAIDQSGGFYRGCVDVDSRSDMNITFRLASEELEKEFVKASEQEGFVGLKGHRSVGGLRASIYNAVPYESCEALVQFMEHFKRSRG

>d1bjna\_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Escherichia coli}

QIFNFSSGPAMLPAEVLKQAQQELRDWNGLGTSVMEVSHRGKEFIQVAEEAEKDFRDLLNVPSNYKVLFCHGGGRGQFAAVPLNILGDKTTADYVDAGYWAASAIKEAKKYCTPNVFDAKVTVDGLRAVKPMREWQLSDNAAYMHYCPNETIDGIAIDETPDFGADVVVAADFSSTILSRPIDVSRYGVIYAGAQKNIGPAGLTIVIVREDLLGKANIACPSILDYSILNDNGSMFNTPPTFAWYLSGLVFKWLKANGGVAEMDKINQQKAELLYGVIDNSDFYRNDVAKRNRSRMNVPFQLADSALDKLFLEESFAAGLHALKGHRVVGGMRASIYNAMPLEGVKALTDFMVEFERRHG

>d1cj0a\_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Rabbit (Oryctolagus cuniculus)}

WSSHEQMLAQPLKDSDAEVYDIIKKESNRQRVGLELIASENFASRAVLEALGSCLNNKYSEGYPGQRYYGGTEHIDELETLCQKRALQAYGLDPQCWGVNVQPYSGSPANFAVYTALVEPHGRIMGLDLPDGGHLTHGFMTDKKKISATSIFFESMAYKVNPDTGYIDYDRLEENARLFHPKLIIAGTSCYSRNLDYGRLRKIADENGAYLMADMAHISGLVVAGVVPSPFEHCHVVTTTTHKTLRGCRAGMIFYRRGVRSVDPKTGKEILYNLESLINSAVFPGLQGGPHNHAIAGVAVALKQAMTPEFKEYQRQVVANCRALSAALVELGYKIVTGGSDNHLILVDLRSKGTDGGRAEKVLEACSIACNKNTCPGDKSALRPSGLRLGTPALTSRGLLEKDFQKVAHFIHRGIELTVQIQDDTGPRATLKEFKEKLAGDEKHQRAVRALRQEVESFAALFPLPGLPGF

>d1ejia\_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Mouse (Mus musculus)}

MADRDATLWASHEKMLSQPLKDSDAEVYSIIKKESNRQRVGLELIASENFASRAVLEALGSSLNNKYSEGYPGQRYYGGTEFIDELEMLCQKRALQAYHLDPQCWGVNVQPYSGSPANFAVYTALVEPHGRIMGLDLPDGGHLTHGFMTDKKKISATSIFFESMPYKVYPETGYINYDQLEENASLFHPKLIIAGTSCYSRNLDYARLRKIADDNGAYLMADMAHISGLVAAGVVPSPFEHCHVVTTTTHKTLRGCRAGMIFYRKGVRSVDPKTGKETYYELESLINSAVFPGLQGGPHNHAIAGVAVALKQAMTTEFKIYQLQVLANCRALSDALTELGYKIVTGGSDNHLILMDLRSKGTDGGRAEKVLEACSIACNKNTCPGDKSALRPSGLRLGTPALTSRGLLEEDFQKVAHFIHRGIELTLQIQSHMATKATLKEFKEKLAGDEKIQSAVATLREEVENFASNFSLPGLPDF

>d1bj4a\_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Human (Homo sapiens)}

DADLWSSHDAMLAQPLKDSDVEVYNIIKKESNRQRVGLELIASENFASRAVLEALGSCLNNKYSEGYPGQRYYGGTEFIDELETLCQKRALQAYKLDPQCWGVNVQPYSGSPANFAVYTALVEPHGRIMGLDLPDGGHLTHGFMTDKKKISATSIFFESMPYKVNPDTGYINYDQLEENARLFHPKLIIAGTSCYSRNLEYARLRKIADENGAYLMADMAHISGLVAAGVVPSPFEHCHVVTTTTHKTLRGCRAGMIFYRKGVKSVDPATGKEILYNLESLINSAVFPGLQGGPHNHAIAGVAVALKQAMTLEFKVYQHQVVANCRALSEALTELGYKIVTGGSDNHLILVDLRSKGTDGGRAEKVLEACSIACNKNTCPGDRSALRPSGLRLGTPALTSRGLLEKDFQKVAHFIHRGIELTLQIQSDTGVAATLKEFKERLAGDKYQAAVQALREEVESFASLFPLPGL

>d1dfoa\_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Escherichia coli}

LKREMNIADYDAELWQAMEQEKVRQEEHIELIASENYTSPRVMQAQGSQLTNKYAEGYPGKRYYGGCEYVDIVEQLAIDRAKELFGADYANVQPHSGSQANFAVYTALLEPGDTVLGMNLAHGGHLTHGSPVNFSGKLYNIVPYGIDATGHIDYADLEKQAKEHKPKMIIGGFSAYSGVVDWAKMREIADSIGAYLFVDMAHVAGLVAAGVYPNPVPHAHVVTTTTHKTLAGPRGGLILAKGGSEELYKKLNSAVFPGGQGGPLMHVIAGKAVALKEAMEPEFKTYQQQVAKNAKAMVEVFLERGYKVVSGGTDNHLFLVDLVDKNLTGKEADAALGRANITVNKNSVPNDPKSPFVTSGIRVGTPAITRRGFKEAEAKELAGWMCDVLDSINDEAVIERIKGKVLDICARYPVYA

>d1b9ha\_ c.67.1.4 (A:) 3-amino-5-hydroxybenzoic acid synthase (AHBA synthase) {Amycolatopsis mediterranei}

KAPEFPAWPQYDDAERNGLVRALEQGQWWRMGGDEVNSFEREFAAHHGAAHALAVTNGTHALELALQVMGVGPGTEVIVPAFTFISSSQAAQRLGAVTVPVDVDAATYNLDPEAVAAAVTPRTKVIMPVHMAGLMADMDALAKISADTGVPLLQDAAHAHGARWQGKRVGELDSIATFSFQNGKLMTAGEGGAVVFPDGETEKYETAFLRHSCGRPRDDRRYFHKIAGSNMRLNEFSASVLRAQLARLDEQIAVRDERWTLLSRLLGAIDGVVPQGGDVRADRNSHYMAMFRIPGLTEERRNALVDRLVEAGLPAFAAFRAIYRTDAFWELGAPDESVDAIARRCPNTDAISSDCVWLHHRVLLAGEPELHATAEIIADAVARA

>d1fc4a\_ c.67.1.4 (A:) 2-amino-3-ketobutyrate CoA ligase {Escherichia coli}

GSHMRGEFYQQLTNDLETARAEGLFKEERIITSAQQADITVADGSHVINFCANNYLGLANHPDLIAAAKAGMDSHGFGMASVRFICGTQDSHKELEQKLAAFLGMEDAILYSSCFDANGGLFETLLGAEDAIISDALNHASIIDGVRLCKAKRYRYANNDMQELEARLKEAREAGARHVLIATDGVFSMDGVIANLKGVCDLADKYDALVMVDDSHAVGFVGENGRGSHEYCDVMGRVDIITGTLGKALGGASGGYTAARKEVVEWLRQRSRPYLFSNSLAPAIVAASIKVLEMVEAGSELRDRLWANARQFREQMSAAGFTLAGADHAIIPVMLGDAVVAQKFARELQKEGIYVTGFFYPVVPKGQARIRTQMSAAHTPEQITRAVEAFTRIGKQLGVIA

>d1bs0a\_ c.67.1.4 (A:) PLP-dependent acyl-CoA synthase (8-amino-7-oxonanoate synthase, AONS) {Escherichia coli}

SWQEKINAALDARRAADALRRRYPVAQGAGRWLVADDRQYLNFSSNDYLGLSHHPQIIRAWQQGAEQFGIGSGGSGHVSGYSVVHQALEEELAEWLGYSRALLFISGFAANQAVIAAMMAKEDRIAADRLSHASLLEAASLSPSQLRRFAHNDVTHLARLLASPCPGQQMVVTEGVFSMDGDSAPLAEIQQVTQQHNGWLMVDDAHGTGVIGEQGRGSCWLQKVKPELLVVTFGKGFGVSGAAVLCSSTVADYLLQFARHLIYSTSMPPAQAQALRASLAVIRSDEGDARREKLAALITRFRAGVQDLPFTLADSCSAIQPLIVGDNSRALQLAEKLRQQGCWVTAIRPPTVPAGTARLRLTLTAAHEMQDIDRLLEVLHGNG

>d1qj5a\_ c.67.1.4 (A:) Adenosylmethionine-8-amino-7-oxononanoate aminotransferase, BioA {Escherichia coli}

MTTDDLAFDQRHILHPYTSMTSPLPVYPVVSAEGCELILSDGRRLVDGMSSWWAAIHGYNHPQLNAAMKSQIDAMSHVMFGGITHAPAIELCRKLVAMTPQPLECVFLADSGSVAVEVAMKMALQYWQAKGEARQRFLTFRNGYHGDTFGAMSVCDPDNSMHSLWKGYLPENLFAPAPQSRMDGEWDERDMVGFARLMAAHRHEIAAVIIEPIVQGAGGMRMYHPEWLKRIRKICDREGILLIADEIATGFGRTGKLFACEHAEIAPDILCLGKALTGGTMTLSATLTTREVAETISNGEAGCFMHGPTFMGNPLACAAANASLAILESGDWQQQVADIEVQLREQLAPARDAEMVADVRVLGAIGVVETTHPVNMAALQKFFVEQGVWIRPFGKLIYLMPPYIILPQQLQRLTAAVNRAVQDETFFCQ

>d1b8ga\_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {Apple (Malus domestica)}

MLSRNATFNSHGQDSSYFLGWQEYEKNPYHEVHNTNGIIQMGLAENQLCFDLLESWLAKNPEAAAFKKNGESIFAELALFQDYHGLPAFKKAMVDFMAEIRGNKVTFDPNHLVLTAGATSANETFIFCLADPGEAVLIPTPYYPGFDRDLKWRTGVEIVPIHCTSSNGFQITETALEEAYQEAEKRNLRVKGVLVTNPSNPLGTTMTRNELYLLLSFVEDKGIHLISDEIYSGTAFSSPSFISVMEVLKDRNCDENSEVWQRVHVVYSLSKDLGLPGFRVGAIYSNDDMVVAAATKMSSFGLVSSQTQHLLSAMLSDKKLTKNYIAENHKRLKQRQKKLVSGLQKSGISCLNGNAGLFCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNISPGSSCHCTEPGWFRVCFANLPERTLDLAMQRLKAFVG

>d1iaya\_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {Tomato (Lycopersicon esculentum)}

ILSKLATNEEHGENSPYFDGWKAYDSDPFHPLKNPNGVIQMGLAENQLCLDLIEDWIKRNPKGSICSEGIKSFKAIANFQDYHGLPEFRKAIAKFMEKTRGGRVRFDPERVVMAGGATGANETIIFCLADPGDAFLVPSPYYPAFNRDLRWRTGVQLIPIHCESSNNFKITSKAVKEAYENAQKSNIKVKGLILTNPSNPLGTTLDKDTLKSVLSFTNQHNIHLVCDEIYAATVFDTPQFVSIAEILDEQEMTYCNKDLVHIVYSLSKDMGLPGFRVGIIYSFNDDVVNCARKMSSFGLVSTQTQYFLAAMLSDEKFVDNFLRESAMRLGKRHKHFTNGLEVVGIKCLKNNAGLFCWMDLRPLLRESTFDSEMSLWRVIINDVKLNVSPGSSFECQEPGWFRVCFANMDDGTVDIALARIRRFVGVEK

>d1c4ka2 c.67.1.5 (A:108-569) Ornithine decarboxylase major domain {Lactobacillus sp., strain 30a}

PPFFKSLKEYVSRYLIQFDCPGHQGGQYYRKHPAGREFYDFFGETVFRADLCNADVALGDLLIHEGPAVAAEKHAARVYNADKTYFVLGGSSNANNTVTSALVSNGDLVLFDRNNHKSVYNSALAMAGGRPVYLQTNRNPYGFIGGIYDSDFDEKKIRELAAKVDPERAKWKRPFRLAVIQLGTYDGTIYNAHEVVKRIGHLCDYIEFDSAWVGYEQFIPMMRNSSPLLIDDLGPEDPGIIVVQSVHKQQAGFSQTSQIHKKDSHIKGQLRYCDHKHFNNSFNLFMSTSPFYPMYAALDVNAAMQEGEAGRKLWHDLLITTIEARKKLIKAGSMFRPFVPPVVNGKKWEDGDTEDMANNIDYWRFEKGAKWHAYEGYGDNQYYVDPNKFMLTTPGINPETGDYEDFGVPATIVANYLRDHGIIPEKSDLNSILFLMTPAETPAKMNNLITQLLQLQRLIEED

>d1qg8a\_ c.68.1.1 (A:) Spore coat polysaccharide biosynthesis protein SpsA {Bacillus subtilis}

PKVSVIMTSYNKSDYVAKSISSILSQTFSDFELFIMDDNSNEETLNVIRPFLNDNRVRFYQSDISGVKERTEKTRYAALINQAIEMAEGEYITYATDDNIYMPDRLLKMVRELDTHPEKAVIYSASKTYHLNENRDIVKETVRPAAQVTWNAPCAIDHCSVMHRYSVLEKVKEKFGSYWDESPAFYRIGDARFFWRVNHFYPFYPLDEELDLNYITDQSIHFQLFELEKNEFVRNLPPQRNCRELRESLKKLGMG

>d1j8wb\_ c.68.1.2 (B:) beta 1,4 galactosyltransferase (b4GalT1) {Cow (Bos taurus)}

TACPEESPLLVGPMLIEFNIPVDLKLVEQQNPKVKLGGRYTPMDCISPHKVAIIIPFRNRQEHLKYWLYYLHPILQRQQLDYGIYVINQAGESMFNRAKLLNVGFKEALKDYDYNCFVFSDVDLIPMNDHNTYRCFSQPRHISVAMDKFGFSLPYVQYFGGVSALSKQQFLSINGFPNNYWGWGGEDDDIYNRLAFRGMSVSRPNAVIGKCRMIRHSRDKKNEPNPQRFDRIAHTKETMLSDGLNSLTYMVLEVQRYPLYTKITVDIGTPS

>d1ezia\_ c.68.1.3 (A:) CMP acylneuraminate synthetase {Neisseria meningitidis}

MEKQNIAVILARQNSKGLPLKNLRKMNGISLLGHTINAAISSKCFDRIIVSTDGGLIAEEAKNFGVEVVLRPAELASDTASSISGVIHALETIGSNSGTVTLLQPTSPLRTGAHIREAFSLFDEKIKGSVVSACPMEHHPLKTLLQINNGEYAPMRHLSDLEQPRQQLPQAFRPNGAIYINDTASLIANNCFFIAPTKLYIMSHQDSIDIDTELDLQQAENILN

>d1ga8a\_ c.68.1.4 (A:) Galactosyltransferase LgtC {Neisseria meningitidis}

MDIVFAADDNYAAYLCVAAKSVEAAHPDTEIRFHVLDAGISEANRAAVAANLRGGGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKLGEYIADCDKVLYLDIDVLVRDSLTPLWDTDLGDNWLGASIDLFVERQEGYKQKIGMADGEYYFNAGVLLINLKKWRRHDIFKMSSEWVEQYKDVMQYQDQDILNGLFKGGVCYANSRFNFMPTNYAFMANWFASRHTDPLYRDRTNTVMPVAVSHYCGPAKPWHRDCTAWGAERFTELAGSLTTVPEEWRGKL

>d1g93a\_ c.68.1.9 (A:) alpha-1,3-galactosyltransferase catalytic domain {Cow (Bos taurus)}

KLKLSDWFNPFKRPEVVTMTKWKAPVVWEGTYNRAVLDNYYAKQKITVGLTVFAVGRYIEHYLEEFLTSANKHFMVGHPVIFYIMVDDVSRMPLIELGPLRSFKVFKIKPEKRWQDISMMRMKTIGEHIVAHIQHEVDFLFCMDVDQVFQDKFGVETLGESVAQLQAWWYKADPNDFTYERRKESAAYIPFGEGDFYYHAAIFGGTPTQVLNITQECFKGILKDKKNDIEAQWHDESHLNKYFLLNKPTKILSPEYCWDYHIGLPADIKLVKMSWQT

>d1hv9a2 c.68.1.5 (A:4-251) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, N-terminal domain {Escherichia coli}

NAMSVVILAAGKGTRMYSDLPKVLHTLAGKAMVQHVIDAANELGAAHVHLVYGHGGDLLKQALKDDNLNWVLQAEQLGTGHAMQQAAPFFADDEDILMLYGDVPLISVETLQRLRDAKPQGGIGLLTVKLDDPTGYGRITRENGKVTGIVEHKDATDEQRQIQEINTGILIANGADMKRWLAKLTNNNAQGEYYITDIIALAYQEGREIVAVHPQRLSEVEGVNNRLQLSRLERVYQSEQAEKLLLAG

>d1hm9a2 c.68.1.5 (A:2-251) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, N-terminal domain {Streptococcus pneumoniae}

SNFAIILAAGKGTRMKSDLPKVLHKVAGISMLEHVFRSVGAIQPEKTVTVVGHKAELVEEVLAGQTEFVTQSEQLGTGHAVMMTEPILEGLSGHTLVIAGDTPLITGESLKNLIDFHINHKNVATILTAETDNPFGYGRIVRNDNAEVLRIVEQKDATDFEKQIKEINTGTYVFDNERLFEALKNINTNNAQGEYYITDVIGIFRETGEKVGAYTLKDFDESLGVNDRVALATAESVMRRRINHKHMVNG

>d1fxoa\_ c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Pseudomonas aeruginosa}

KRKGIILAGGSGTRLHPATLAISKQLLPVYDKPMIYYPLSTLMLAGIREILIISTPQDTPRFQQLLGDGSNWGLDLQYAVQPSPDGLAQAFLIGESFIGNDLSALVLGDNLYYGHDFHELLGSASQRQTGASVFAYHVLDPERYGVVEFDQGGKAISLEEKPLEPKSNYAVTGLYFYDQQVVDIARDLKPSPRGELEITDVNRAYLERGQLSVEIMGRGYAWLDTGTHDSLLEAGQFIATLENRQGLKVACPEEIAYRQKWIDAAQLEKLAAPLAKNGYGQYLKRLLTETVY

>d1iina\_ c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Salmonella enterica}

MKTRKGIILAGGSGTRLYPVTMAVSQQLLPIYDKPMIYYPLSTLMLAGIRDILIISTPQDTPRFQQLLGDGSQWGLNLQYKVQPSPDGLAQAFIIGEEFIGHDDCALVLGDNIFYGHDLPKLMEAAVNKESGATVFAYHVNDPERYGVVEFDQKGTAVSLEEKPLQPKSNYAVTGLYFYDNSVVEMAKNLKPSARGELEITDINRIYMEQGRLSVAMMGRGYAWLDTGTHQSLIEASNFIATIEERQGLKVSCPEEIAFRKNFINAQQVIELAGPLSKNDYGKYLLKMV

>d1h5ra\_ c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Escherichia coli}

KMRKGIILAGGSGTRLYPVTMAVSKQLLPIYDKPMIYYPLSTLMLAGIRDILIISTPQDTPRFQQLLGDGSQWGLNLQYKVQPSPDGLAQAFIIGEEFIGGDDCALVLGDNIFYGHDLPKLMEAAVNKESGATVFAYHVNDPERYGVVEFDKNGTAISLEEKPLEPKSNYAVTGLYFYDNDVVQMAKNLKPSARGELEITDINRIYLEQGRLSVAMMGRGYAWLDTGTHQSLIEASNFIATIEERQGLKVSCPEEIAFRKGFIDVEQVRKLAVPLIKNNYGQYLYKMTKD

>d1fgga\_ c.68.1.7 (A:) 1,3-Glucuronyltransferase I (glcAT-I) {Human (Homo sapiens)}

MTIYVVTPTYARLVQKAELVRLSQTLSLVPRLHWLLVEDAEGPTPLVSGLLAASGLLFTHLVVLTPKAQRLREGEPGWVHPRGVEQRNKALDWLRGRGGAVGGEKDPPPPGTQGVVYFADDDNTYSRELFEEMRWTRGVSVWPVGLVGGLRFEGPQVQDGRVVGFHTAWEPSRPFPVDMAGFAVALPLLLDKPNAQFDSTAPRGHLESSLLSHLVDPKDLEPRAANCTRVLVWHTRTEKPKMKQEEQLQRQGRGSDPAIEV

>d1fo8a\_ c.68.1.10 (A:) N-acetylglucosaminyltransferase I {Rabbit (Oryctolagus cuniculus)}

LAVIPILVIACDRSTVRRCLDKLLHYRPSAELFPIIVSQDCGHEETAQVIASYGSAVTHIRQPDLSNIAVQPDHRKFQGYYKIARHYRWALGQIFHNFNYPAAVVVEDDLEVAPDFFEYFQATYPLLKADPSLWCVSAWNDNGKEQMVDSSKPELLYRTDFFPGLGWLLLAELWAELEPKWPKAFWDDWMRRPEQRKGRACVRPEISRTMTFGRKGVSHGQFFDQHLKFIKLNQQFVPFTQLDLSYLQQEAYDRDFLARVYGAPQLQVEKVRTNDRKELGEVRVQYTGRDSFKAFAKALGVMDDLKSGVPRAGYRGIVTFLFRGRRVHLAPPQTWDGYDPSWT

>d1e5ka\_ c.68.1.8 (A:) Molybdenum cofactor biosynthesis protein MobA {Escherichia coli}

MTTITGVVLAGGKARRMGGVDKGLLELNGKPLWQHVADALMTQLSHVVVNANRHQEIYQASGLKVIEDSLADYPGPLAGMLSVMQQEAGEWFLFCPCDTPYIPPDLAARLNHQRKDAPVVWVHDGERDHPTIALVNRAIEPLLLEYLQAGERRVMVFMRLAGGHAVDFSDHKDAFVNVNTPEELARWQ

>d1i52a\_ c.68.1.13 (A:) 4-diphosphocytidyl-2-c-methylerythritol (CDP-me) synthase (YgbP) {Escherichia coli}

HLDVCAVVPAAGFGRRMQTECPKQYLSIGNQTILEHSVHALLAHPRVKRVVIAISPGDSRFAQLPLANHPQITVVDGGDERADSVLAGLKAAGDAQWVLVHDAARPCLHQDDLARLLALSETSRTGGILAAPVRDTMKRAEPGKNAIAHTVDRNGLWHALTPQFFPRELLHDCLTRALNEGATITDEASALEYCGFHPQLVEGRADNIKVTRPEDLALAEFYLTR

>d1h7ea\_ c.68.1.13 (A:) CMP:2-keto-3-deoxy-manno-octonic acid (CMP-KDO)synthetase, KdsB {Escherichia coli}

SKAVIVIPARYGSSRLPGKPLLDIVGKPMIQHVYERALQVAGVAEVWVATDDPRVEQAVQAFGGKAIMTRNDHESGTDRLVEVMHKVEADIYINLQGDEPMIRPRDVETLLQGMRDDPALPVATLCHAISAAEAAEPSTVKVVVNTRQDALYFSRSPIPYPRNAEKARYLKHVGIYAYRRDVLQNYSQLPESMPEQAESLEQLRLMNAGINIRTFEVAATGPGVDTPACLEKVRALMAQELAENA

>d1jyka\_ c.68.1.13 (A:) CTP:phosphocholine cytidylytransferase LicC {Streptococcus pneumoniae}

EIRVKAIILAAGLGTRLRPLTENTPKALVQVNQKPLIEYQIEFLKEKGINDIIIIVGYLKEQFDYLKEKYGVRLVFNDKYADYNNFYSLYLVKEELANSYVIDADNYLFKNMFRNDLTRSTYFSVYREDCTNEWFLVYGDDYKVQDIIVDSKAGRILSGVSFWDAPTAEKIVSFIDKAYVSGEFVDLYWDNMVKDNIKELDVYVEELEGNSIYEIDSVQDYRKLEEILK

>d1jw9b\_ c.111.1.1 (B:) Molybdenum cofactor biosynthesis protein MoeB {Escherichia coli}

AELSDQEMLRYNRQIILRGFDFDGQEALKDSRVLIVGLGGLGCAASQYLASAGVGNLTLLDFDTVSLSNLQRQTLHSDATVGQPKVESARDALTRINPHIAITPVNALLDDAELAALIAEHDLVLDCTDNVAVRNQLNAGCFAAKVPLVSGAAIRMEGQITVFTYQDGEPCYRCLSRLFGENALTCVEAGVMAPLIGVIGSLQAMEAIKMLAGYGKPASGKIVMYDAMTCQFREMKLMRNPGCEVCG

>d1ea5a\_ c.69.1.1 (A:) Acetylcholinesterase {Electric ray (Torpedo californica)}

SELLVNTKSGKVMGTRVPVLSSHISAFLGIPFAEPPVGNMRFRRPEPKKPWSGVWNASTYPNNCQQYVDEQFPGFSGSEMWNPNREMSEDCLYLNIWVPSPRPKSTTVMVWIYGGGFYSGSSTLDVYNGKYLAYTEEVVLVSLSYRVGAFGFLALHGSQEAPGNVGLLDQRMALQWVHDNIQFFGGDPKTVTIFGESAGGASVGMHILSPGSRDLFRRAILQSGSPNCPWASVSVAEGRRRAVELGRNLNCNLNSDEELIHCLREKKPQELIDVEWNVLPFDSIFRFSFVPVIDGEFFPTSLESMLNSGNFKKTQILLGVNKDEGSFFLLYGAPGFSKDSESKISREDFMSGVKLSVPHANDLGLDAVTLQYTDWMDDNNGIKNRDGLDDIVGDHNVICPLMHFVNKYTKFGNGTYLYFFNHRASNLVWPEWMGVIHGYEIEFVFGLPLVKELNYTAEEEALSRRIMHYWATFAKTGNPNEPHSQESKWPLFTTKEQKFIDLNTEPMKVHQRLRVQMCVFWNQFLPKLLNAT

>d1maaa\_ c.69.1.1 (A:) Acetylcholinesterase {Mouse (Mus musculus)}

EDPQLLVRVRGGQLRGIRLKAPGGPVSAFLGIPFAEPPVGSRRFMPPEPKRPWSGVLDATTFQNVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRPASPTPVLIWIYGGGFYSGAASLDVYDGRFLAQVEGAVLVSMNYRVGTFGFLALPGSREAPGNVGLLDQRLALQWVQENIAAFGGDPMSVTLFGESAGAASVGMHILSLPSRSLFHRAVLQSGTPNGPWATVSAGEARRRATLLARLVGCPPGGAGGNDTELIACLRTRPAQDLVDHEWHVLPQESIFRFSFVPVVDGDFLSDTPEALINTGDFQDLQVLVGVVKDEGSYFLVYGVPGFSKDNESLISRAQFLAGVRIGVPQASDLAAEAVVLHYTDWLHPEDPTHLRDAMSAVVGDHNVVCPVAQLAGRLAAQGARVYAYIFEHRASTLTWPLWMGVPHGYEIEFIFGLPLDPSLNYTTEERIFAQRLMKYWTNFARTGDPNDPRDRKSPQWPPYTTAAQQYVSLNLKPLEVRRGLRAQTCAFWNRFLPKLLSAT

>d1f8ua\_ c.69.1.1 (A:) Acetylcholinesterase {Human (Homo sapiens)}

DAELLVTVRGGRLRGIRLKTPGGPVSAFLGIPFAEPPMGPRRFLPPEPKQPWSGVVDATTFQSVCYQYVDTLYPGFEGTEMWNPNRELSEDCLYLNVWTPYPRPTSPTPVLVWIYGGGFYSGASSLDVYDGRFLVQAERTVLVSMNYRVGAFGFLALPGSREAPGNVGLLDQRLALQWVQENVAAFGGDPTSVTLFGQSAGAASVGMHLLSPPSRGLFHRAVLQSGAPNGPWATVGMGEARRRATQLAHLVGCPPGGTGGNDTELVACLRTRPAQVLVNHEWHVLPQESVFRFSFVPVVDGDFLSDTPEALINAGDFHGLQVLVGVVKDEGSYFLVYGAPGFSKDNESLISRAEFLAGVRVGVPQVSDLAAEAVVLHYTDWLHPEDPARLREALSDVVGDHNVVCPVAQLAGRLAAQGARVYAYVFEHRASTLSWPLWMGVPHGYEIEFIFGIPLDPSRNYTAEEKIFAQRLMRYWANFARTGDPNEPRDPKAPQWPPYTAGAQQYVSLDLRPLEVRRGLRAQACAFWNRFLPKLLSAT

>d1dx4a\_ c.69.1.1 (A:) Acetylcholinesterase {Fruit fly (Drosophila melanogaster)}

DRLVVQTSSGPVRGRSVTVQGREVHVYTGIPYAKPPVEDLRFRKPVPAEPWHGVLDATGLSATCVQERYEYFPGFSGEEIWNPNTNVSEDCLYINVWAPAKARLRHGRGANGGEHPNGKQADTDHLIHNGNPQNTTNGLPILIWIYGGGFMTGSATLDIYNADIMAAVGNVIVASFQYRVGAFGFLHLAPEMPSEFAEEAPGNVGLWDQALAIRWLKDNAHAFGGNPEWMTLFGESAGSSSVNAQLMSPVTRGLVKRGMMQSGTMNAPWSHMTSEKAVEIGKALINDCNCNASMLKTNPAHVMSCMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAFLPADPMTLMKTADLKDYDILMGNVRDEGTYFLLYDFIDYFDKDDATALPRDKYLEIMNNIFGKATQAEREAIIFQYTSWEGNPGYQNQQQIGRAVGDHFFTCPTNEYAQALAERGASVHYYYFTHRTSTSLWGEWMGVLHGDEIEYFFGQPLNNSLQYRPVERELGKRMLSAVIEFAKTGNPAQDGEEWPNFSKEDPVYYIFSTDDKIEKLARGPLAARCSFWNDYLPKVRSW

>d2bce\_\_ c.69.1.1 (-) Bile-salt activated lipase (cholesterol esterase) {Cow (Bos taurus)}

AKLGSVYTEGGFVEGVNKKLSLFGDSVDIFKGIPFAAAPKALEKPERHPGWQGTLKAKSFKKRCLQATLTQDSTYGNEDCLYLNIWVPQGRKEVSHDLPVMIWIYGGAFLMGASQGANFLSNYLYDGEEIATRGNVIVVTFNYRVGPLGFLSTGDSNLPGNYGLWDQHMAIAWVKRNIEAFGGDPDNITLFGESAGGASVSLQTLSPYNKGLIKRAISQSGVGLCPWAIQQDPLFWAKRIAEKVGCPVDDTSKMAGCLKITDPRALTLAYKLPLGSTEYPKLHYLSFVPVIDGDFIPDDPVNLYANAADVDYIAGTNDMDGHLFVGMDVPAINSNKQDVTEEDFYKLVSGLTVTKGLRGANATYEVYTEPWAQDSSQETRKKTMVDLETDILFLIPTKIAVAQHKSHAKSANTYTYLFSQPSRMPIYPKWMGADHADDLQYVFGKPFATPLGYRAQDRTVSKAMIAYWTNFARTGDPNTGHSTVPANWDPYTLEDDNYLEINKQMDSNSMKLHLRTNYLQFWTQTYQALPTVTSAGASLLPPEDNSQASPVPPADNSGAPTEPSAGDSEVAQMPVVIGF

>d1f6wa\_ c.69.1.1 (A:) Bile-salt activated lipase (cholesterol esterase) {Human (Homo sapiens)}

AKLGAVYTEGGFVEGVNKKLGLLGDSVDIFKGIPFAAPTKALENPQPHPGWQGTLKAKNFKKRCLQATITQDSTYGDEDCLYLNIWVPQGRKQVSRDLPVMIWIYGGAFLMGSGHGANFLNNYLYDGEEIATRGNVIVVTFNYRVGPLGFLSTGDANLPGNYGLRDQHMAIAWVKRNIAAFGGDPDNITLFGESAGGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQKNPLFWAKKVAEKVGCPVGDAARMAQCLKVTDPRALTLAYKVPLAGLEYPMLHYVGFVPVIDGDFIPDDPINLYANAADIDYIAGTNNMDGHIFASIDMPAINKGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENKKKTVVDFETDVLFLVPTEIALAQHRANAKSAKTYAYLFSHPSRMPVYPKWVGADHADDIQYVFGKPFATPTGYRPQDRTVSKAMIAYWTNFAKTGDPNMGDSAVPTHWEPYTTENSGYLEITKKMGSSSMKRSLRTNFLRYWTLTYLALPTVT

>d1qe3a\_ c.69.1.1 (A:) Thermophylic para-nitrobenzyl esterase (PNB esterase) {Bacillus subtilis}

THQIVTTQYGKVKGTTENGVHKWKGIPYAKPPVGQWRFKAPEPPEVWEDVLDATAYGPICPQPSDLLSLSYTELPRQSEDCLYVNVFAPDTPSQNLPVMVWIHGGAFYLGAGSEPLYDGSKLAAQGEVIVVTLNYRLGPFGFLHLSSFDEAYSDNLGLLDQAAALKWVRENISAFGGDPDNVTVFGESAGGMSIAALLAMPAAKGLFQKAIMESGASRTMTKEQAASTAAAFLQVLGINESQLDRLHTVAAEDLLKAADQLRIAEKENIFQLFFQPALDPKTLPEEPEKSIAEGAASGIPLLIGTTRDEGYLFFTPDSDVHSQETLDAALEYLLGKPLAEKAADLYPRSLESQIHMMTDLLFWRPAVAYASAQSHYAPVWMYRFDWHPEKPPYNKAFHALELPFVFGNLDGLERMAKAEITDEVKQLSHTIQSAWITFAKTGNPSTEAVNWPAYHEETRETVILDSEITIENDPESEKRQKLF

>d1jkma\_ c.69.1.2 (A:) Carboxylesterase {Bacillus subtilis, brefeldin A esterase}

PGRLGDESSGPRTDPRFSPAMVEALATFGLDAVAAAPPVSASDDLPTVLAAVGASHDGFQAVYDSIALDLPTDRDDVETSTETILGVDGNEITLHVFRPAGVEGVLPGLVYTHGGGMTILTTDNRVHRRWCTDLAAAGSVVVMVDFRNAWTAEGHHPFPSGVEDCLAAVLWVDEHRESLGLSGVVVQGESGGGNLAIATTLLAKRRGRLDAIDGVYASIPYISGGYAWDHERRLTELPSLVENDGYFIENGGMALLVRAYDPTGEHAEDPIAWPYFASEDELRGLPPFVVAVNELDPLRDEGIAFARRLARAGVDVAARVNIGLVHGADVIFRHWLPAALESTVRDVAGFAADRARLR

>d1evqa\_ c.69.1.2 (A:) Carboxylesterase {Alicyclobacillus acidocaldarius}

LDPVIQQVLDQLNRMPAPDYKHLSAQQFRSQQSLFPPVKKEPVAEVREFDMDLPGRTLKVRMYRPEGVEPPYPALVYYHGGGWVVGDLETHDPVCRVLAKDGRAVVFSVDYRLAPEHKFPAAVEDAYDALQWIAERAADFHLDPARIAVGGDSAGGNLAAVTSILAKERGGPALAFQLLIYPSTGYDPAHPPASIEENAEGYLLTGGMMLWFRDQYLNSLEELTHPWFSPVLYPDLSGLPPAYIATAQYDPLRDVGKLYAEALNKAGVKVEIENFEDLIHGFAQFYSLSPGATKALVRIAEKLRDALA

>d1jjia\_ c.69.1.2 (A:) Carboxylesterase {Archaeon Archaeoglobus fulgidus}

MLDMPIDPVYYQLAEYFDSLPKFDQFSSAREYREAINRIYEERNRQLSQHERVERVEDRTIKGRNGDIRVRVYQQKPDSPVLVYYHGGGFVICSIESHDALCRRIARLSNSTVVSVDYRLAPEHKFPAAVYDCYDATKWVAENAEELRIDPSKIFVGGDSAGGNLAAAVSIMARDSGEDFIKHQILIYPVVNFVAPTPSLLEFGEGLWILDQKIMSWFSEQYFSREEDKFNPLASVIFADLENLPPALIITAEYDPLRDEGEVFGQMLRRAGVEASIVRYRGVLHGFINYYPVLKAARDAINQIAALLVFD

>d1jjfa\_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase z {Clostridium thermocellum}

SLPTMPPSGYDQVRNGVPRGQVVNISYFSTATNSTRPARVYLPPGYSKDKKYSVLYLLHGIGGSENDWFEGGGRANVIADNLIAEGKIKPLIIVTPNTNAAGPGIADGYENFTKDLLNSLIPYIESNYSVYTDREHRAIAGLSMGGGQSFNIGLTNLDKFAYIGPISAAPNTYPNERLFPDGGKAAREKLKLLFIACGTNDSLIGFGQRVHEYCVANNINHVYWLIQGGGHDFNVWKPGLWNFLQMADEAGLTRD

>d1gkla\_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase y {Clostridium thermocellum}

SFKYESAVQYRPAPDSYLNPCPQAGRIVKETYTGINGTKSLNVYLPYGYDPNKKYNIFYLMHGGGENENTIFSNDVKLQNILDHAIMNGELEPLIVVTPTFNGGNCTAQNFYQEFRQNVIPFVESKYSTYAESTTPQGIAASRMHRGFGGFAMGGLTTWYVMVNCLDYVAYFMPLSGDYWYGNSPQDKANSIAEAINRSGLSKREYFVFAATGSEDIAYANMNPQIEAMKALPHFDYTSDFSKGNFYFLVAPGATHWWGYVRHYIYDALPYFFHELEHHHHHH

>d1f0na\_ c.69.1.3 (A:) Antigen 85b {Mycobacterium tuberculosis}

SRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYYQSGLSIVMPVGGQSSFYSDWYSPACGKAGCQTYKWETFLTSELPQWLSANRAVKPTGSAAIGLSMAGSSAMILAAYHPQQFIYAGSLSALLDPSQGMGPSLIGLAMGDAGGYKAADMWGPSSDPAWERNDPTQQIPKLVANNTRLWVYCGNGTPNELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNFPPNGTHSWEYWGAQLNAMKGDLQSSLGAG

>d1dqza\_ c.69.1.3 (A:) Antigen 85c {Mycobacterium tuberculosis}

RPGLPVEYLQVPSASMGRDIKVQFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQSSFYTDWYQPSQSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYYPQQFPYAASLSGFLNPSESWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTRIWVYCGNGTPSDLGGDNIPAKFLEGLTLRTNQTFRDTYAADGGRNGVFNFPPNGTHSWPYWNEQLVAMKADIQHVLNG

>d1ju3a2 c.69.1.21 (A:5-351) Bacterial cocaine esterase N-terminal domain {Rhodococcus sp. mb1}

NYSVASNVMVPMRDGVRLAVDLYRPDADGPVPVLLVRNPYDKFDVFAWSTQSTNWLEFVRDGYAVVIQDTRGLFASEGEFVPHVDDEADAEDTLSWILEQAWCDGNVGMFGVSYLGVTQWQAAVSGVGGLKAIAPSMASADLYRAPWYGPGGALSVEALLGWSALIGTGLITSRSDARPEDAADFVQLAAILNDVAGAASVTPLAEQPLLGRLIPWVIDQVVDHPDNDESWQSISLFERLGGLATPALITAGWYDGFVGESLRTFVAVKDNADARLVVGPWSHSNLTGRNADRKFGIAATYPIQEATTMHKAFFDRHLRGETDALAGVPKVRLFVMGIDEWRDETDW

>d1qfma2 c.69.1.4 (A:431-710) Prolyl oligopeptidase, C-terminal domain {Pig (Sus scrofa)}

DASDYQTVQIFYPSKDGTKIPMFIVHKKGIKLDGSHPAFLYGYGGFNISITPNYSVSRLIFVRHMGGVLAVANIRGGGEYGETWHKGGILANKQNCFDDFQCAAEYLIKEGYTSPKRLTINGGSNGGLLVATCANQRPDLFGCVIAQVGVMDMLKFHKYTIGHAWTTDYGCSDSKQHFEWLIKYSPLHNVKLPEADDIQYPSMLLLTADHDDRVVPLHSLKFIATLQYIVGRSRKQNNPLLIHVDTKAGHGAGKPTAKVIEEVSDMFAFIARCLNIDWIP

>g1wht.1 c.69.1.5 (A:,B:) Serine carboxypeptidase II {Wheat (Triticum vulgaris)}

GHAADRIARLPGQPAVDFDMYSGYITVDEGAGRSLFYLLQEAPEDAQPAPLVLWLNGGPGCSSVAYGASEELGAFRVKPRGAGLVLNEYRWNKVANVLFLDSPAGVGFSYTNTSSDIYTSGDNRTAHDSYAFLAKWFERFPHYKYRDFYIAGESYAGHYVPELSQLVHRSKNPVINLKGFMVGNGLIDDYHDYVGTFEFWWNHGIVSDDTYRRLKEACLHDSFIHPSPACDAATDVATAEQGNIDMYSLYTPVCNIXSYDPCTERYSTAYYNRRDVQMALHANVTGAMNYTWATCSDTINTHWHDAPRSMLPIYRELIAAGLRIWVFSGDTDAVVPLTATRYSIGALGLPTTTSWYPWYDDQEVGGWSQVYKGLTLVSVRGAGHEVPLHRPRQALVLFQYFLQGKPMPGQ

>d1cpy\_\_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (Saccharomyces cerevisiae)}

KIKDPKILGIDPNVTQYTGYLDVEDEDKHFFFWTFESRNDPAKDPVILWLNGGPGCSSLTGLFFALGPSSIGPDLKPIGNPYSWNSNATVIFLDQPVNVGFSYSGSSGVSNTVAAGKDVYNFLELFFDQFPEYVNKGQDFHIAGASYAGHYIPVFASEILSHKDRNFNLTSVLIGNGLTDPLTQYNYYEPMACGEGGEPSVLPSEECSAMEDSLERCLGLIESCYDSQSVWSCVPATIYCNNAQLAPYQRTGRNVYDIRKDCEGGNLCYPTLQDIDDYLNQDYVKEAVGAEVDHYESCNFDINRNFLFAGDWMKPYHTAVTDLLNQDLPILVYAGDKDFICNWLGNKAWTDVLPWKYDEEFASQKVRNWTASITDEVAGEVKSYKHFTYLRVFNGGHMVPFDVPENALSMVNEWIHGGFSL

>d1ac5\_\_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (Saccharomyces cerevisiae), kex1(delta)p}

LPSSEEYKVAYELLPGLSEVPDPSNIPQMHAGHIPLRSEDADEQDSSDLEYFFWKFTNNDSNGNVDRPLIIWLNGGPGCSSMDGALVESGPFRVNSDGKLYLNEGSWISKGDLLFIDQPTGTGFSVEQNKDEGKIDKNKFDEDLEDVTKHFMDFLENYFKIFPEDLTRKIILSGESYAGQYIPFFANAILNHNKFSKIDGDTYDLKALLIGNGWIDPNTQSLSYLPFAMEKKLIDESNPNFKHLTNAHENCQNLINSASTDEAAHFSYQECENILNLLLSYTRESSQKGTADCLNMYNFNLKDSYPSCGMNWPKDISFVSKFFSTPGVIDSLHLDSDKIDHWKECTNSVGTKLSNPISKPSIHLLPGLLESGIEIVLFNGDKDLICNNKGVLDTIDNLKWGGIKGFSDDAVSFDWIHKSKSTDDSEEFSGYVKYDRNLTFVSVYNASHMVPFDKSLVSRGIVDIYSNDVMIIDNNGKNVMITT

>d1ivya\_ c.69.1.5 (A:) Human 'protective protein', HPP {Human (Homo sapiens)}

APDQDEIQRLPGLAKQPSFRQYSGYLKSSGSKHLHYWFVESQKDPENSPVVLWLNGGPGCSSLDGLLTEHGPFLVQPDGVTLEYNPYSWNLIANVLYLESPAGVGFSYSDDKFYATNDTEVAQSNFEALQDFFRLFPEYKNNKLFLTGESYAGIYIPTLAVLVMQDPSMNLQGLAVGNGLSSYEQNDNSLVYFAYYHGLLGNRLWSSLQTHCCSQNKCNFYDNKDLECVTNLQEVARIVGNSGLNIYNLYAPCAGGVPSHFRYEKDTVVVQDLGNIFTRLPLKRMWHQALLRSGDKVRMDPPCTNTTAASTYLNNPYVRKALNIPEQLPQWDMCNFLVNLQYRRLYRSMNSQYLKLLSSQKYQILLYNGDVDMACNFMGDEWFVDSLNQKMEVQRRPWLVKYGDSGEQIAGFVKEFSHIAFLTIKGAGHMVPTDKPLAAFTMFSRFLNKQPY

>d1hlga\_ c.69.1.6 (A:) Gastric lipase {Human (Homo sapiens)}

SPEVTMNISQMITYWGYPNEEYEVVTEDGYILEVNRIPYGKKNSGNTGQRPVVFLQHGLLASATNWISNLPNNSLAFILADAGYDVWLGNSRGNTWARRNLYYSPDSVEFWAFSFDEMAKYDLPATIDFIVKKTGQKQLHYVGHSQGTTIGFIAFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKIFYPHNFFDQFLATEVCSREMLNLLCSNALFIICGFDSKNFNTSRLDVYLSHNPAGTSVQNMFHWTQAVKSGKFQAYDWGSPVQNRMHYDQSQPPYYNVTAMNVPIAVWNGGKDLLADPQDVGLLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEVYNDIVSMISEDKK

>d1azwa\_ c.69.1.7 (A:) Proline iminopeptidase {Xanthomonas campestris, pv. citri}

MRTLYPEITPYQQGSLKVDDRHTLYFEQCGNPHGKPVVMLHGGPGGGCNDKMRRFHDPAKYRIVLFDQRGSGRSTPHADLVDNTTWDLVADIERLRTHLGVDRWQVFGGSWGSTLALAYAQTHPQQVTELVLRGIFLLRRFELEWFYQEGASRLFPDAWEHYLNAIPPVERADLMSAFHRRLTSDDEATRLAAAKAWSVWEGATSFLHVDEDFVTGHEDAHFALAFARIENHYFVNGGFFEVEDQLLRDAHRIADIPGVIVHGRYDVVCPLQSAWDLHKAWPKAQLQISPASGHSAFEPENVDALVRATDGFA

>d1qtra\_ c.69.1.7 (A:) Proline iminopeptidase {Serratia marcescens}

LRGLYPPLAAYDSGWLDTGDGHRIYWELSGNPNGKPAVFIHGGPGGGISPHHRQLFDPERYKVLLFDQRGCGRSRPHASLDNNTTWHLVADIERLREMAGVEQWLVFGGSWGSTLALAYAQTHPERVSEMVLRGIFTLRKQRLHWYYQDGASRFFPEKWERVLSILSDDERKDVIAAYRQRLTSADPQVQLEAAKLWSVWEGETVTLLPSRESASFGEDDFALAFARIENHYFTHLGFLESDDQLLRNVPLIRHIPAVIVHGRYDMACQVQNAWDLAKAWPEAELHIVEGAGHSYDEPGILHQLMIATDRFAGK

>d1b6g\_\_ c.69.1.8 (-) Haloalkane dehalogenase {Xanthobacter autotrophicus}

MVNAIRTPDQRFSNLDQYPFSPNYLDDLPGYPGLRAHYLDEGNSDAEDVFLCLHGEPTWSYLYRKMIPVFAESGARVIAPDFFGFGKSDKPVDEEDYTFEFHRNFLLALIERLDLRNITLVVQDWGGFLGLTLPMADPSRFKRLIIMNACLMTDPVTQPAFSAFVTQPADGFTAWKYDLVTPSDLRLDQFMKRWAPTLTEAEASAYAAPFPDTSYQAGVRKFPKMVAQRDQACIDISTEAISFWQNDWNGQTFMAIGMKDKLLGPDVMYPMKALINGCPEPLEIADAGHFVQEFGEQVAREALKHFAETE

>d1bn7a\_ c.69.1.8 (A:) Haloalkane dehalogenase {Rhodococcus sp.}

IGTGFPFDPHYVEVLGERMHYVDVGPRDGTPVLFLHGNPTSSYLWRNIIPHVAPSHRCIAPDLIGMGKSDKPDLDYFFDDHVRYLDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIACMEFIRPIPTWDEWPEFARETFQAFRTADVGRELIIDQNAFIEGVLPKCVVRPLTEVEMDHYREPFLKPVDREPLWRFPNEIPIAGEPANIVALVEAYMNWLHQSPVPKLLFWGTPGVLIPPAEAARLAESLPNCKTVDIGPGLHYLQEDNPDLIGSEIARWLPGLA

>d1cv2a\_ c.69.1.8 (A:) Haloalkane dehalogenase {Sphingomonas paucimobilis, UT26, LinB}

GAKPFGEKKFIEIKGRRMAYIDEGTGDPILFQHGNPTSSYLWRNIMPHCAGLGRLIACDLIGMGDSDKLDPSGPERYAYAEHRDYLDALWEALDLGDRVVLVVHDWGSALGFDWARRHRERVQGIAYMEAIAMPIEWADFPEQDRDLFQAFRSQAGEELVLQDNVFVEQVLPGLILRPLSEAEMAAYREPFLAAGEARRPTLSWPRQIPIAGTPADVVAIARDYAGWLSESPIPKLFINAEPGALTTGRMRDFCRTWPNQTEITVAGAHFIQEDSPDEIGAAIAAFVRRLRPA

>d1din\_\_ c.69.1.9 (-) Dienelactone hydrolase {Pseudomonas sp., B13}

MLTEGISIQSYDGHTFGALVGSPAKAPAPVIVIAQEIFGVNAFMRETVSWLVDQGYAAVCPDLYARQAPGTALDPQDERQREQAYKLWQAFDMEAGVGDLEAAIRYARHQPYSNGKVGLVGYALGGALAFLVAAKGYVDRAVGYYGVGLEKQLNKVPEVKHPALFHMGGQDHFVPAPSRQLITEGFGANPLLQVHWYEEAGHSFARTSSSGYVASAAALANERTLDFLAPLQS

>d1c4xa\_ c.69.1.10 (A:) 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (BPHD) {Rhodococcus sp., strain rha1}

TVEIIEKRFPSGTLASHALVAGDPQSPAVVLLHGAGPGAHAASNWRPIIPDLAENFFVVAPDLIGFGQSEYPETYPGHIMSWVGMRVEQILGLMNHFGIEKSHIVGNSMGGAVTLQLVVEAPERFDKVALMGSVGAPMNARPPELARLLAFYADPRLTPYRELIHSFVYDPENFPGMEEIVKSRFEVANDPEVRRIQEVMFESMKAGMESLVIPPATLGRLPHDVLVFHGRQDRIVPLDTSLYLTKHLKHAELVVLDRCGHWAQLERWDAMGPMLMEHFRA

>d1ek1a2 c.69.1.11 (A:226-544) Mammalian epoxide hydrolase, C-terminal domain {Mouse (Mus musculus)}

LPVPCNPNDVSHGYVTVKPGIRLHFVEMGSGPALCLCHGFPESWFSWRYQIPALAQAGFRVLAIDMKGYGDSSSPPEIEEYAMELLCKEMVTFLDKLGIPQAVFIGHDWAGVMVWNMALFYPERVRAVASLNTPFMPPDPDVSPMKVIRSIPVFNYQLYFQEPGVAEAELEKNMSRTFKSFFRASDETGFIAVHKATEIGGILVNTPEDPNLSKITTEEEIEFYIQQFKKTGFRGPLNWYRNTERNWKWSCKGLGRKILVPALMVTAEKDIVLRPEMSKNMEKWIPFLKRGHIEDCGHWTQIEKPTEVNQILIKWLQTE

>d1ehya\_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Agrobacterium radiobacter}

AIRRPEDFKHYEVQLPDVKIHYVREGAGPTLLLLHGWPGFWWEWSKVIGPLAEHYDVIVPDLRGFGDSEKPDLNDLSKYSLDKAADDQAALLDALGIEKAYVVGHDFAAIVLHKFIRKYSDRVIKAAIFDPIQPDFGPVYFGLGHVHESWYSQFHQLDMAVEVVGSSREVCKKYFKHFFDHWSYRDELLTEEELEVHVDNCMKPDNIHGGFNYYRANIRPDAALWTDLDHTMSDLPVTMIWGLGDTCVPYAPLIEFVPKYYSNYTMETIEDCGHFLMVEKPEIAIDRIKTAFR

>d1qo7a\_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Aspergillus niger}

KAFAKFPSSASISPNPFTVSIPDEQLDDLKTLVRLSKIAPPTYESLQADGRFGITSEWLTTMREKWLSEFDWRPFEARLNSFPQFTTEIEGLTIHFAALFSEREDAVPIALLHGWPGSFVEFYPILQLFREEYTPETLPFHLVVPSLPGYTFSSGPPLDKDFGLMDNARVVDQLMKDLGFGSGYIIQGGDIGSFVGRLLGVGFDACKAVHLNLCAMRAPPEGPSIESLSAAEKEGIARMEKFMTDGLAYAMEHSTRPSTIGHVLSSSPIALLAWIGEKYLQWVDKPLPSETILEMVSLYWLTESFPRAIHTYRETTPTASAPNGATMLQKELYIHKPFGFSFFPKDLCPVPRSWIATTGNLVFFRDHAEGGHFAALERPRELKTDLTAFVEQVW

>d1brt\_\_ c.69.1.12 (-) Bromoperoxidase A2 {Streptomyces aureofaciens}

PFITVGQENSTSIDLYYEDHGTGQPVVLIHGFPLSGHSWERQSAALLDAGYRVITYDRRGFGQSSQPTTGYDYDTFAADLNTVLETLDLQDAVLVGFSTGTGEVARYVSSYGTARIAKVAFLASLEPFLLKTDDNPDGAAPQEFFDGIVAAVKADRYAFYTGFFNDFYNLDENLGTRISEEAVRNSWNTAASGGFFAAAAAPTTWYTDFRADIPRIDVPALILHGTGDRTLPIENTARVFHKALPSAEYVEVEGAPHGLLWTHAEEVNTALLAFLAK

>d1a8q\_\_ c.69.1.12 (-) Bromoperoxidase A1 {Streptomyces aureofaciens}

PICTTRDGVEIFYKDWGQGRPVVFIHGWPLNGDAWQDQLKAVVDAGYRGIAHDRRGHGHSTPVWDGYDFDTFADDLNDLLTDLDLRDVTLVAHSMGGGELARYVGRHGTGRLRSAVLLSAIPPVMIKSDKNPDGVPDEVFDALKNGVLTERSQFWKDTAEGFFSANRPGNKVTQGNKDAFWYMAMAQTIEGGVRCVDAFGYTDFTEDLKKFDIPTLVVHGDDDQVVPIDATGRKSAQIIPNAELKVYEGSSHGIAMVPGDKEKFNRDLLEFLNK

>d1a88a\_ c.69.1.12 (A:) Chloroperoxidase L {Streptomyces lividans}

GTVTTSDGTNIFYKDWGPRDGLPVVFHHGWPLSADDWDNQMLFFLSHGYRVIAHDRRGHGRSDQPSTGHDMDTYAADVAALTEALDLRGAVHIGHSTGGGEVARYVARAEPGRVAKAVLVSAVPPVMVKSDTNPDGLPLEVFDEFRAALAANRAQFYIDVPSGPFYGFNREGATVSQGLIDHWWLQGMMGAANAHYECIAAFSETDFTDDLKRIDVPVLVAHGTDDQVVPYADAAPKSAELLANATLKSYEGLPHGMLSTHPEVLNPDLLAFVKS

>d1a8s\_\_ c.69.1.12 (-) Chloroperoxidase F {Pseudomonas fluorescens}

TTFTTRDGTQIYYKDWGSGQPIVFSHGWPLNADSWESQMIFLAAQGYRVIAHDRRGHGRSSQPWSGNDMDTYADDLAQLIEHLDLRDAVLFGFSTGGGEVARYIGRHGTARVAKAGLISAVPPLMLKTEANPGGLPMEVFDGIRQASLADRSQLYKDLASGPFFGFNQPGAKSSAGMVDWFWLQGMAAGHKNAYDCIKAFSETDFTEDLKKIDVPTLVVHGDADQVVPIEASGIASAALVKGSTLKIYSGAPHGLTDTHKDQLNADLLAFIKG

>d1thta\_ c.69.1.13 (A:) Myristoyl-ACP-specific thioesterase {Vibrio harveyi}

QCKTIAHVLRVNNGQELHVWETPPKENVPFKNNTILIASGFARRMDHFAGLAEYLSTNGFHVFRYDSLHHVGLSSGSIDEFTMTTGKNSLCTVYHWLQTKGTQNIGLIAASLSARVAYEVISDLELSFLITAVGVVNLRDTLEKALGFDYLSLPIDELPNDLDFEGHKLGSEVFVRDCFEHHWDTLDSTLDKVANTSVPLIAFTANNDDWVKQEEVYDMLAHIRTGHCKLYSLLGSSHDLGENLVVLRNFYQSVTKAAIAMDGGSLEIDVDFIEPDFEQLTIATVNERRLKAEIENRTPEMA

>d1ei9a\_ c.69.1.13 (A:) Palmitoyl protein thioesterase 1 {Cow (Bos taurus)}

DPPAPLPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIHVLSLEIGKTLREDVENSFFLNVNSQVTTVCQILAKDPKLQQGYNAMGFSQGGQFLRAVAQRCPSPPMVNLISVGGQHQGVFGLPRCPGESSHICDFIRKTLNAGAYNKAIQERLVQAEYWHDPIREDIYRNHSIFLADINQERGVNESYKKNLMALKKFVMVKFLNDTIVDPVDSEWFGFYRSGQAKETIPLQESTLYTQDRLGLKAMDKAGQLVFLALEGDHLQLSEEWFYAHIIPFLE

>d1auoa\_ c.69.1.14 (A:) Carboxylesterase {Pseudomonas fluorescens}

MTEPLILQPAKPADACVIWLHGLGADRYDFMPVAEALQESLLTTRFVLPQAPTRPVTINGGYEMPSWYDIKAMSPARSISLEELEVSAKMVTDLIEAQKRTGIDASRIFLAGFSQGGAVVFHTAFINWQGPLGGVIALSTYAPTFGDELELSASQQRIPALCLHGQYDDVVQNAMGRSAFEHLKSRGVTVTWQEYPMGHEVLPQEIHDIGAWLAARLG

>d1fj2a\_ c.69.1.14 (A:) Acyl protein thioesterase 1 {Human (Homo sapiens)}

MDPEFMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAEAFAGIRSSHIKYICPHAPVRPVTLNMNVAMPSWFDIIGLSPDSQEDESGIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGALSLYTALTTQQKLAGVTALSCWLPLRASFPQGPIGGANRDISILQCHGDCDPLVPLMFGSLTVEKLKTLVNPANVTFKTYEGMMHSSCQQEMMDVKQFIDKLLPPI

>d1qlwa\_ c.69.1.15 (A:) A novel bacterial esterase {Alcaligenes sp.}

VPKTPAGPLTLSGQGSFFVGGRDVTSETLSLSPKYDAHGTVTVDQMYVRYQIPQRAKRYPITLIHGCCLTGMTWETTPDGRMGWDEYFLRKGYSTYVIDQSGRGRSATDISAINAVKLGKAPASSLPDLFAAGHEAAWAIFRFGPRYPDAFKDTQFPVQAQAELWQQMVPDWLGSMPTPNPTVANLSKLAIKLDGTVLLSHSQSGIYPFQTAAMNPKGITAIVSVEPGECPKPEDVKPLTSIPVLVVFGDHIEEFPRWAPRLKACHAFIDALNAAGGKGQLMSLPALGVHGNSHMMMQDRNNLQVADLILDWIGRNTA

>d1jfra\_ c.69.1.16 (A:) Lipase {Streptomyces exfoliatus}

NPYERGPAPTNASIEASRGPYATSQTSVSSLVASGFGGGTIYYPTSTADGTFGAVVISPGFTAYQSSIAWLGPRLASQGFVVFTIDTNTTLDQPDSRGRQLLSALDYLTQRSSVRTRVDATRLGVMGHSMGGGGSLEAAKSRTSLKAAIPLTGWNTDKTWPELRTPTLVVGADGDTVAPVATHSKPFYESLPGSLDKAYLELRGASHFTPNTSDTTIAKYSISWLKRFIDSDTRYEQFLCPIPRPSLTIAEYRGTCPHTS

>d1tca\_\_ c.69.1.17 (-) Triacylglycerol lipase {Yeast (Candida antarctica), form b}

LPSGSDPAFSQPKSVLDAGLTCQGASPSSVSKPILLVPGTGTTGPQSFDSNWIPLSTQLGYTPCWISPPPFMLNDTQVNTEYMVNAITALYAGSGNNKLPVLTWSQGGLVAQWGLTFFPSIRSKVDRLMAFAPDYKGTVLAGPLDALAVSAPSVWQQTTGSALTTALRNAGGLTQIVPTTNLYSATDEIVQPQVSNSPLDSSYLFNGKNVQAQAVCGPLFVIDHAGSLTSQFSYVVGRSALRSTTGQARSADYGITDCNPLPANDLTPEQKVAAAALLAPAAAAIVAGPKQNCEPDLMPYARPFAVGKRTCSGIVTP

>d3tgl\_\_ c.69.1.17 (-) Triacylglycerol lipase {Rhizomucor miehei}

GIRAATSQEINELTYYTTLSANSYCRTVIPGATWDCIHCDATEDLKIIKTWSTLIYDTNAMVARGDSEKTIYIVFRGSSSIRNWIADLTFVPVSYPPVSGTKVHKGFLDSYGEVQNELVATVLDQFKQYPSYKVAVTGHSLGGATVLLCALDLYQREEGLSSSNLFLYTQGQPRVGDPAFANYVVSTGIPYRRTVNERDIVPHLPPAAFGFLHAGEEYWITDNSPETVQVCTSDLETSDCSNSIVPFTSVLDHLSYFGINTGLCT

>d1tia\_\_ c.69.1.17 (-) Triacylglycerol lipase {Penicillium camembertii}

DVSTSELDQFEFWVQYAAASYYEADYTAQVGDKLSCSKGNCPEVEATGATVSYDFSDSTITDTAGYIAVDHTNSAVVLAFRGSYSVRNWVADATFVHTNPGLCDGCLAELGFWSSWKLVRDDIIKELKEVVAQNPNYELVVVGHSLGAAVATLAATDLRGKGYPSAKLYAYASPRVGNAALAKYITAQGNNFRFTHTNDPVPKLPLLSMGYVHVSPEYWITSPNNATVSTSDIKVIDGDVSFDGNTGTGLPLLTDFEAHIWYFVQVDAGKG

>d1tib\_\_ c.69.1.17 (-) Triacylglycerol lipase {Thermomyces (Humicola) lanuginosa}

EVSQDLFNQFNLFAQYSAAAYCGKNNDAPAGTNITCTGNACPEVEKADATFLYSFEDSGVGDVTGFLALDNTNKLIVLSFRGSRSIENWIGNLNFDLKEINDICSGCRGHDGFTSSWRSVADTLRQKVEDAVREHPDYRVVFTGHSLGGALATVAGADLRGNGYDIDVFSYGAPRVGNRAFAEFLTVQTGGTLYRITHTNDIVPRLPPREFGYSHSSPEYWIKSGTLVPVTRNDIVKIEGIDATGGNNQPNIPDIPAHLWYFGLIGTCL

>d1lgya\_ c.69.1.17 (A:) Triacylglycerol lipase {Rhizopus niveus}

KVVAATTAQIQEFTKYAGIAATAYCRSVVPGNKWDCVQCQKWVPDGKIITTFTSLLSDTNGYVLRSDKQKTIYLVFRGTNSFRSAITDIVFNFSDYKPVKGAKVHAGFLSSYEQVVNDYFPVVQEQLTAHPTYKVIVTGHSLGGAQALLAGMDLYQREPRLSPKNLSIFTVGGPRVGNPTFAYYVESTGIPFQRTVHKRDIVPHVPPQSFGFLHPGVESWIKSGTSNVQICTSEIETKDCSNSIVPFTSILDHLSYFDINEGSCL

>d1thg\_\_ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (Geotrichum candidum), ATCC 34614}

EAPTAVLNGNEVISGVLEGKVDTFKGIPFADPPLNDLRFKHPQPFTGSYQGLKANDFSPACMQLDPGNSLTLLDKALGLAKVIPEEFRGPLYDMAKGTVSMNEDCLYLNVFRPAGTKPDAKLPVMVWIYGGAFVYGSSAAYPGNSYVKESINMGQPVVFVSINYRTGPFGFLGGDAITAEGNTNAGLHDQRKGLEWVSDNIANFGGDPDKVMIFGESAGAMSVAHQLIAYGGDNTYNGKKLFHSAILQSGGPLPYHDSSSVGPDISYNRFAQYAGCDTSASANDTLECLRSKSSSVLHDAQNSYDLKDLFGLLPQFLGFGPRPDGNIIPDAAYELFRSGRYAKVPYISGNQEDEGTAFAPVALNATTTPHVKKWLQYIFYDASEASIDRVLSLYPQTLSVGSPFRTGILNALTPQFKRVAAILSDMLFQSPRRVMLSATKDVNRWTYLSTHLHNLVPFLGTFHGNELIFQFNVNIGPANSYLRYFISFANHHDPNVGTNLLQWDQYTDEGKEMLEIHMTDNVMRTDDYRIEGISNFETDVNLYG

>d1lpp\_\_ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (Candida rugosa), formerly Cylindracea}

APTATLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYSGSLDGQKFTSYGPSCMQQNPEGTYEENLPKAALDLVMQSKVFEAVSPSSEDCLTINVVRPPGTKAGANLPVMLWIFGGGFEVGGTSTFPPAQMITKSIAMGKPIIHVSVNYRVSSWGFLAGDEIKAEGSANAGLKDQRLGMQWVADNIAAFGGDPTKVTIFGESAGSMSVMCHILWNDGDNTYKGKPLFRAGIMQSGAMVPSDAVDGIYGNEIFDLLASNAGCGSASDKLACLRGVSSDTLEDATNNTPGFLAYSSLRLSYLPRPDGVNITDDMYALVREGKYANIPVIIGDQNDEGTFFGTSSLNVTTDAQAREYFKQSFVHASDAEIDTLMTAYPGDITQGSPFDTGILNALTPQFKRISAVLGDLGFTLARRYFLNHYTGGTKYSFLSKQLSGLPVLGTFHSNDIVFQDYLLGSGSLIYNNAFIAFATDLDPNTAGLLVKWPEYTSSSQSGNNLMMINALGLYTGKDNFRTAGYDALFSNPPSFFV

>d1clea\_ c.69.1.17 (A:) Type-B carboxylesterase/lipase {Candida cylindracea, cholesterol esterase}

APTAKLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYSGSLNGQKFTSYGPSCMQQNPEGTFEENLGKTALDLVMQSKVFQAVLPQSEDCLTINVVRPPGTKAGANLPVMLWIFGGGFEIGSPTIFPPAQMVTKSVLMGKPIIHVAVNYRVASWGFLAGDDIKAEGSGNAGLKDQRLGMQWVADNIAGFGGDPSKVTIFGESAGSMSVLCHLIWNDGDNTYKGKPLFRAGIMQSGAMVPSDPVDGTYGNEIYDLFVSSAGCGSASDKLACLRSASSDTLLDATNNTPGFLAYSSLRLSYLPRPDGKNITDDMYKLVRDGKYASVPVIIGDQNDEGTVFGLSSLNVTTNAQARAYFKQSFIHASDAEIDTLMAAYPQDITQGSPFDTGIFNAITPQFKRISAVLGDLAFIHARRYFLNHFQGGTKYSFLSKQLSGLPIMGTFHANDIVWQDYLLGSGSVIYNNAFIAFATDLDPNTAGLLVNWPKYTSSSQSGNNLMMINALGLYTGKDNFRTAGYDALMTNPSSFFV

>d1i6wa\_ c.69.1.18 (A:) Lipase A {Bacillus subtilis}

HNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFWDKTGTNYNNGPVLSRFVQKVLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKVANVVTLGGANRLTTGKALPGTDPNQKILYTSIYSSADMIVMNYLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN

>d4lipd\_ c.69.1.18 (D:) Lipase {Burkholderia cepacia (formerly Pseudomonas cepacia)}

DNYAATRYPIILVHGLTGTDKYAGVLEYWYGIQEDLQQRGATVYVANLSGFQSDDGPNGRGEQLLAYVKTVLAATGATKVNLVGHSQGGLTSRYVAAVAPDLVASVTTIGTPHRGSEFADFVQGVLAYDPTGLSSTVIAAFVNVFGILTSSSNNTNQDALAALKTLTTAQAATYNQNYPSAGLGAPGSCQTGAPTETVGGNTHLLYSWAGTAIQPTISVFGVTGATDTSTIPLVDPANALDPSTLALFGTGTVMVNRGSGQNDGVVSKCSALYGQVLSTSYKWNHLDEINQLLGVRGANAEDPVAVIRTHANRLKLAGV

>d1ex9a\_ c.69.1.18 (A:) Lipase {Pseudomonas aeruginosa}

STYTQTKYPIVLAHGMLGFDNILGVDYWFGIPSALRRDGAQVYVTEVSQLDTSEVRGEQLLQQVEEIVALSGQPKVNLIGHSHGGPTIRYVAAVRPDLIASATSVGAPHKGSDTADFLRQIPPGSAGEAVLSGLVNSLGALISFLSSGSTGTQNSLGSLESLNSEGAARFNAKYPQGIPTSACGEGAYKVNGVSYYSWSGSSPLTNFLDPSDAFLGASSLTFKNGTANDGLVGTCSSHLGMVIRDNYRMNHLDEVNQVFGLTSLFETSPVSVYRQHANRLKNASL

>d1cvl\_\_ c.69.1.18 (-) Lipase {Chromobacterium viscosum}

ADTYAATRYPVILVHGLAGTDKFANVVDYWYGIQSDLQSHGAKVYVANLSGFQSDDGPNGRGEQLLAYVKQVLAATGATKVNLIGHSQGGLTSRYVAAVAPQLVASVTTIGTPHRGSEFADFVQDVLKTDPTGLSSTVIAAFVNVFGTLVSSSHNTDQDALAALRTLTTAQTATYNRNFPSAGLGAPGSCQTGAATETVGGSQHLLYSWGGTAIQPTSTVLGVTGATDTSTGTLDVANVTDPSTLALLATGAVMINRASGQNDGLVSRCSSLFGQVISTSYHWNHLDEINQLLGVRGANAEDPVAVIRTHVNRLKLQGV

>d1hpla2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Horse (Equus caballus)}

NEVCYERLGCFSDDSPWAGIVERPLKILPWSPEKVNTRFLLYTNENPDNFQEIVADPSTIQSSNFNTGRKTRFIIHGFIDKGEESWLSTMCQNMFKVESVNCICVDWKSGSRTAYSQASQNVRIVGAEVAYLVGVLQSSFDYSPSNVHIIGHSLGSHAAGEAGRRTNGAVGRITGLDPAEPCFQGTPELVRLDPSDAQFVDVIHTDIAPFIPNLGFGMSQTAGHLDFFPNGGKEMPGCQKNVLSQIVDIDGIWQGTRDFAACNHLRSYKYYTDSILNPDGFAGFSCASYSDFTANKCFPCSSEGCPQMGHYADRFPGRTKGVGQLFYLNTGDASNFA

>d1etha2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Pig (Sus scrofa)}

SEVCFPRLGCFSDDAPWAGIVQRPLKILPWSPKDVDTRFLLYTNQNQNNYQELVADPSTITNSNFRMDRKTRFIIHGFIDKGEEDWLSNICKNLFKVESVNCICVDWKGGSRTGYTQASQNIRIVGAEVAYFVEVLKSSLGYSPSNVHVIGHSLGSHAAGEAGRRTNGTIERITGLDPAEPCFQGTPELVRLDPSDAKFVDVIHTDAAPIIPNLGFGMSQTVGHLDFFPNGGKQMPGCQKNILSQIVDIDGIWEGTRDFVACNHLRSYKYYADSILNPDGFAGFPCDSYNVFTANKCFPCPSEGCPQMGHYADRFPGKTNGVSQVFYLNTGDASNF

>d1lpbb2 c.69.1.19 (B:1-336) Pancreatic lipase, N-terminal domain {Human (Homo sapiens)}

KEVCYERLGCFSDDSPWSGITERPLHILPWSPKDVNTRFLLYTNENPNNFQEVAADSSSISGSNFKTNRKTRFIIHGFIDKGEENWLANVCKNLFKVESVNCICVDWKGGSRTGYTQASQNIRIVGAEVAYFVEFLQSAFGYSPSNVHVIGHSLGAHAAGEAGRRTNGTIGRITGLDPAEPCFQGTPELVRLDPSDAKFVDVIHTDGAPIVPNLGFGMSQVVGHLDFFPNGGVEMPGCKKNILSQIVDIDGIWEGTRDFAACNHLRSYKYYTDSIVNPDGFAGFPCASYNVFTANKCFPCPSGGCPQMGHYADRYPGKTNDVGQKFYLDTGDASNFA

>d1gpl\_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain {Guinea pig (Cavia porcellus)}

AEVCYSHLGCFSDEKPWAGTSQRPIKSLPSDPKKINTRFLLYTNENQNSYQLITATDIATIKASNFNLNRKTRFIIHGFTDSGENSWLSDMCKNMFQVEKVNCICVDWKGGSKAQYSQASQNIRVVGAEVAYLVQVLSTSLNYAPENVHIIGHSLGAHTAGEAGKRLNGLVGRITGLDPAEPYFQDTPEEVRLDPSDAKFVDVIHTDISPILPSLGFGMSQKVGHMDFFPNGGKDMPGCKTGISCNHHRSIEYYHSSILNPEGFLGYPCASYDEFQESGCFPCPAKGCPKMGHFADQYPGKTNAVEQTFFLNTGASDNFT

>d1rp1\_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain {Dog (Canis familiaris)}

KEVCYEQIGCFSDAEPWAGTAIRPLKVLPWSPERIGTRFLLYTNKNPNNFQTLLPSDPSTIGASNFQTDKKTRFIIHGFIDKGEENWLLDMCKNMFKVEEVNCICVDWKKGSQTSYTQAANNVRVVGAQVAQMLSMLSANYSYSPSQVQLIGHSLGAHVAGEAGSRTPGLGRITGLDPVEASFQGTPEEVRLDPTDADFVDVIHTDAAPLIPFLGFGTSQQMGHLDFFPNGGEEMPGCKKNALSQIVDLDGIWEGTRDFVACNHLRSYKYYSESILNPDGFASYPCASYRAFESNKCFPCPDQGCPQMGHYADKFAQKYFLNTGDSSNFA

>d1bu8a2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Rat (Rattus norvegicus)}

KEVCYGHLGCFSNDKPWAGMLQRPLKIFPWSPEDIDTRFLLYTNENPNNYQKISATEPDTIKFSNFQLDRKTRFIVHGFIDKGEDGWLLDMCKKMFQVEKVNCICVDWRRGSRTEYTQASYNTRVVGAEIAFLVQVLSTEMGYSPENVHLIGHSLGAHVVGEAGRRLEGHVGRITGLDPAEPCFQGLPEEVRLDPSDAMFVDVIHTDSAPIIPYLGFGMSQKVGHLDFFPNGGKEMPGCQKNILSTIVDINGIWEGTQNFVACNHLRSYKYYASSILNPDGFLGYPCSSYEKFQQNDCFPCPEEGCPKMGHYADQFEGKTATVEQTVYLNTGDSGNFT

>d1qj4a\_ c.69.1.20 (A:) Hydroxynitrile lyase {Rubber tree (Hevea brasiliensis)}

AFAHFVLIHTICHGAWIWHKLKPLLEALGHKVTALDLAASGVDPRQIEEIGSFDEYSEPLLTFLEALPPGEKVILVGESCGGLNIAIAADKYCEKIAAAVFHNSVLPDTEHCPSYVVDKLMEVFPDWKDTTYFTYTKDGKEITGLKLGFTLLRENLYTLCGPEEYELAKMLTRKGSLFQNILAKRPFFTKEGYGSIKKIYVWTDQDEIFLPEFQLWQIENYKPDKVYKVEGGDHKLQLTKTKEIAEILQEVADTYN

>d1e89a\_ c.69.1.20 (A:) Hydroxynitrile lyase {Cassava (Manihot esculenta)}

PISKMVTAHFVLIHTICHGAWIWHKLKPALERAGHKVTALDMAASGIDPRQIEQINSFDEYSEPLLTFLEKLPQGEKVIIVGEACAGLNIAIAADRYVDKIAAGVFHNSLLPDTVHSPSYTVEKLLESFPDWRDTEYFTFTNITGETITTMKLGFVLLRENLFTKCTDGEYELAKMVMRKGSLFQNVLAQRPKFTEKGYGSIKKVYIWTDQDKIFLPDFQRWQIANYKPDKVYQVQGGDHKLQLTKTEEVAHILQEVADAYA

>d1keza\_ c.69.1.22 (A:) Erythromycin polyketide synthase {Saccharopolyspora erythraea}

SSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICCAGTAAISGPHEFTRLAGALRGIAPVRAVPQPGYEEGEPLPSSMAAVAAVQADAVIRTQGDKPFVVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETVRMDDTRLTALGAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDTVAVPGDHFTMVQEHADAIARHIDAWLGGG

>d2masa\_ c.70.1.1 (A:) Inosine-uridine nucleoside N-ribohydrolase, IU-NH {Crithidia fasciculata}

AKKIILDCDPGLDDAVAILLAHGNPEIELLAITTVVGNQTLAKVTRNAQLVADIAGITGVPIAAGCDKPLVRKIMTAGHIHGESGMGTVAYPAEFKNKVDERHAVNLIIDLVMSHEPKTITLVPTGGLTNIAMAARLEPRIVDRVKEVVLMGGGYHEGNATSVAEFNIIIDPEAAHIVFNESWQVTMVGLDLTHQALATPPILQRVKEVDTNPARFMLEIMDYYTKIYQSNRYMAAAAVHDPCAVAYVIDPSVMTTERVPVDIELTGKLTLGMTVADFRNPRPEHCHTQVAVKLDFEKFWGLVLDALERIGDP

>d1ezra\_ c.70.1.1 (A:) Nucleoside hydrolase {Leishmania major}

PRKIILDCDPGIDDAVAIFLAHGNPEIELLAITTVVGNQSLEKVTQNARLVADVAGIVGVPVAAGCTKPLVRGVRNASHIHGETGMGNVSYPPEFKTKLDGRHAVQLIIDLIMSHEPKTITLVPTGGLTNIAMAVRLEPRIVDRVKEVVLMGGGYHTGNASPVAEFNVFIDPEAAHIVFNESWNVTMVGLDLTHLALATPAVQKRVREVGTKPAAFMLQILDFYTKVYEKEHDTYGKVHDPCAVAYVIDPTVMTTERVPVDIELNGALTTGMTVADFRYPRPKNCRTQVAVKLDFDKFWCLVIDALERIGDP

>d1hoza\_ c.70.1.1 (A:) Inosine-adenosine-guanosine preferring nucleoside hydrolase {Trypanosoma vivax}

GSAKNVVLDHDGNLDDFVAMVLLASNTEKVRLIGALCTDADCFVENGFNVTGKIMCLMHNNMNLPLFPIGKSAATAVNPFPKEWRCLAKNMDDMPILNIPENVELWDKIKAENEKYEGQQLLADLVMNSEEKVTICVTGPLSNVAWCIDKYGEKFTSKVEECVIMGGAVDVRGNVFLPSTDGTAEWNIYWDPASAKTVFGCPGLRRIMFSLDSTNTVPVRSPYVQRFGEQTNFLLSILVGTMWAMCTHCELLRDGDGYYAWDALTAAYVVDQKVANVDPVPIDVVVDKQPNEGATVRTDAENYPLTFVARNPEAEFFLDMLLRSARAC

>d1ra9\_\_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Escherichia coli}

MISLIAALAVDRVIGMENAMPWNLPADLAWFKRNTLDKPVIMGRHTWESIGRPLPGRKNIILSSQPGTDDRVTWVKSVDEAIAACGDVPEIMVIGGGRVYEQFLPKAQKLYLTHIDAEVEGDTHFPDYEPDDWESVFSEFHDADAQNSHSYCFEILERR

>d3dfr\_\_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Lactobacillus casei}

TAFLWAQNRNGLIGKDGHLPWHLPDDLHYFRAQTVGKIMVVGRRTYESFPKRPLPERTNVVLTHQEDYQAQGAVVVHDVAAVFAYAKQHLDQELVIAGGAQIFTAFKDDVDTLLVTRLAGSFEGDTKMIPLNWDDFTKVSSRTVEDTNPALTHTYEVWQKKA

>d1df7a\_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Mycobacterium tuberculosis}

MVGLIWAQATSGVIGRGGDIPWRLPEDQAHFREITMGHTIVMGRRTWDSLPAKVRPLPGRRNVVLSRQADFMASGAEVVGSLEEALTSPETWVIGGGQVYALALPYATRCEVTEVDIGLPREAGDALAPVLDETWRGETGEWRFSRSGLRYRLYSYHRS

>d1d1ga\_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Thermotoga maritima}

AKVIFVLAMDVSGKIASSVESWSSFEDRKNFRKITTEIGNVVMGRITFEEIGRPLPERLNVVLTRRPKTSNNPSLVFFNGSPADVVKFLEGKGYERVAVIGGKTVFTEFLREKLVDELFVTVEPYVFGKGIPFFDEFEGYFPLKLLEMRRLNERGTLFLKYSVE

>d1vdra\_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Haloferax volcanii}

ELVSVAALAENRVIGRDGELPWPSIPADKKQYRSRIADDPVVLGRTTFESMRDDLPGSAQIVMSRSERSFSVDTAHRAASVEEAVDIAASLDAETAYVIGGAAIYALFQPHLDRMVLSRVPGEYEGDTYYPEWDAAEWELDAETDHEGFTLQEWVRS

>d8dfr\_\_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Chicken (Gallus gallus)}

VRSLNSIVAVCQNMGIGKDGNLPWPPLRNEYKYFQRMTSTSHVEGKQNAVIMGKKTWFSIPEKNRPLKDRINIVLSRELKEAPKGAHYLSKSLDDALALLDSPELKSKVDMVWIVGGTAVYKAAMEKPINHRLFVTRILHEFESDTFFPEIDYKDFKLLTEYPGVPADIQEEDGIQYKFEVYQKSV

>d1hfq\_\_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Human (Homo sapiens)}

VGSLNCIVAVSQNMGIGKNGDLPWPPLRNESRYFQRMTTTSSVEGKQNLVIMGKKTWFSIPEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDALKLTEQPELANKVDMVWIVGGSSVYKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKFEVYEKND

>d1dyr\_\_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Fungus (Pneumocystis carinii)}

NQQKSLTLIVALTTSYGIGRSNSLPWKLKKEISYFKRVTSFVPTFDSFESMNVVLMGRKTWESIPLQFRPLKGRINVVITRNESLDLGNGIHSAKSLDHALELLYRTYGSESSVQINRIFVIGGAQLYKAAMDHPKLDRIMATIIYKDIHCDVFFPLKFRDKEWSSVWKKEKHSDLESWVGTKVPHGKINEDGFDYEFEMWTRDL

>d1aoea\_ c.71.1.1 (A:) Dihydrofolate reductases, eukaryotic type {Yeast (Candida albicans)}

MLKPNVAIIVAALKPALGIGYKGKMPWRLRKEIRYFKDVTTRTTKPNTRNAVIMGRKTWESIPQKFRPLPDRLNIILSRSYENEIIDDNIIHASSIESSLNLVSDVERVFIIGGAEIYNELINNSLVSHLLITEIEHPSPESIEMDTFLKFPLESWTKQPKSELQKFVGDTVLEDDIKEGDFTYNYTLWTRK

>d1ekqa\_ c.72.1.2 (A:) Hydroxyethylthiazole kinase (THZ kinase, ThiK) {Bacillus subtilis}

MDAQSAAKCLTAVRRHSPLVHSITNNVVTNFTANGLLALGASPVMAYAKEEVADMAKIAGALVLNIGTLSKESVEAMIIAGKSANEHGVPVILDPVGAGATPFRTESARDIIREVRLAAIRGNAAEIAHTVGVTDWLIKGVDAGEGGGDIIRLAQQAAQKLNTVIAITGEVDVIADTSHVYTLHNGHKLLTKVTGAGCLLTSVVGAFCAVEENPLFAAIAAISSYGVAAQLAAQQTADKGPGSFQIELLNKLSTVTEQDVQEWATIERV

>d1jxha\_ c.72.1.2 (A:) 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate kinase (HMP-phosphate kinase, ThiD) {Salmonella typhimurium}

MQRINALTIAGTDPSGGAGIQADLKTFSALGAYGCSVITALVAENTCGVQSVYRIEPDFVAAQLDSVFSDVRIDTTKIGMLAETDIVEAVAERLQRHHVRNVVLDTVMLAKSGDPLLSPSAIETLRVRLLPQVSLITPNLPEAAALLDAPHARTEQEMLAQGRALLAMGCEAVLMKGGHLEDAQSPDWLFTREGEQRFSAPRVNTKNTHGTGCTLSAALAALRPRHRSWGETVNEAKAWLSAALAQADTLEVGKGIGPVHHFHAWW

>d1rkd\_\_ c.72.1.1 (-) Ribokinase {Escherichia coli}

AGSLVVLGSINADHILNLQSFPTPGETVTGNHYQVAFGGKGANQAVAAGRSGANIAFIACTGDDSIGESVRQQLATDNIDITPVSVIKGESTGVALIFVNGEGENVIGIHAGANAALSPALVEAQRERIANASALLMQLESPLESVMAAAKIAHQNKTIVALNPAPARELPDELLALVDIITPNETEAEKLTGIRVENDEDAAKAAQVLHEKGIRTVLITLGSRGVWASVNGEGQRVPGFRVQAVDTIAAGDTFNGALITALLEEKPLPEAIRFAHAAAAIAVTRKGAQPSVPWREEIDAFLDRQR

>d1bx4a\_ c.72.1.1 (A:) Adenosine kinase {Human (Homo sapiens)}

VRENILFGMGNPLLDISAVVDKDFLDKYSLKPNDQILAEDKHKELFDELVKKFKVEYHAGGSTQNSIKVAQWMIQQPHKAATFFGCIGIDKFGEILKRKAAEAHVDAHYYEQNEQPTGTCAACITGDNRSLIANLAAANCYKKEKHLDLEKNWMLVEKARVCYIAGFFLTVSPESVLKVAHHASENNRIFTLNLSAPFISQFYKESLMKVMPYVDILFGNETEAATFAREQGFETKDIKEIAKKTQALPKMNSKRQRIVIFTQGRDDTIMATESEVTAFAVLDQDQKEIIDTNGAGDAFVGGFLSQLVSDKPLTECIRAGHYAASIIIRRTGCTFPEKPDFH

>d1dgya\_ c.72.1.1 (A:) Adenosine kinase {Toxoplasma gondii}

GPMRVFAIGNPILDLVAEVPSSFLDEFFLKRGDATLATPEQMRIYSTLDQFNPTSLPGGSALNSVRVVQKLLRKPGSAGYMGAIGDDPRGQVLKELCDKEGLATRFMVAPGQSTGTCAVLINEKERTLCTHLGACGSFRIPENWTTFASGALIFYATAYTLTATPKNALEVAGYAHGIPNAIFTLNLSAPFCVELYKDAMQSLLLHTNILFGNEEEFAHLAKVHNLVAAEKVALSVANKEHAVEVCTGALRLLTAGQNTGATKLVVMTRGHNPVIAAEQTADGTVVVHEVGVPVVAAEKIVDTNGAGDAFVGGFLYGLSQGKTVKQCIMCGNACAQDVIQHVGFSLSF

>d1gc5a\_ c.72.1.3 (A:) ADP-dependent glucokinase {Archaeon Thermococcus litoralis}

MKESLKDRIRLWKRLYVNAFENALNAIPNVKGVLLAYNTNIDAIKYLDADDLEKRVTEKGKEKVFEIIENPPEKISSIEELLGGILRSIKLGKAMEWFVESEEVRRYLREWGWDELRIGGQAGIMANLLGGVYRIPTIVHVPQNPKLQAELFVDGPIYVPVFEGNKLKLVHPKDAIAEEEELIHYIYEFPRGFQVFDVQAPRENRFIANADDYNARVYMRREFREGFEEITRNVELAIISGLQVLKEYYPDGTTYKDVLDRVESHLNILNRYNVKSHFEFAYTANRRVREALVELLPKFTSVGLNEVELASIMEIIGDEELAKEVLEGHIFSVIDAMNVLMDETGIERIHFHTYGYYLALTQYRGEEVRDALLFASLAAAAKAMKGNLERIEQIRDALSVPTNERAIVLEEELEKEFTEFENGLIDMVDRQLAFVPTKIVASPKSTVGIGDTISSSAFVSEFGMRKR

>d2uaga3 c.72.2.1 (A:94-297) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}

DIELFCREAQAPIVAITGSNGKSTVTTLVGEMAKAAGVNVGVGGNIGLPALMLLDDECELYVLELSSFQLETTSSLQAVAATILNVTEDHMDRYPFGLQQYRAAKLRIYENAKVCVVNADDALTMPIRGADERCVSFGVNMGDYHLNHQQGETWLRVKGEKVLNVKEMKLSGQHNYTNALAALALADAAGLPRASSLKALTTFT

>d1e8ca3 c.72.2.1 (A:88-337) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}

QLNERLSALAGRFYHEPSDNLRLVGVTGTNGKTTTTQLLAQWSQLLGEISAVMGTVGNGLLGKVIPTENTTGSAVDVQHELAGLVDQGATFCAMEVSSHGLVQHRVAALKFAASVFTNLSRDHLDYHGDMEHYEAAKWLLYSEHHCGQAIINADDEVGRRWLAKLPDAVAVSMEDHINPNCHGRWLKATEVNYHDSGATIRFSSSWGDGEIESHLMGAFNVSNLLLALATLLALGYPLADLLKTAARLQP

>d1gg4a4 c.72.2.1 (A:82-312) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

DTRLAFGELAAWVRQQVPARVVALTGSSGKTSVKEMTAAILSQCGNTLYTAGNLNNDIGVPMTLLRLTPEYDYAVIELGANHQGEIAWTVSLTRPEAALVNNLAAAHLEGFGSLAGVAKAKGEIFSGLPENGIAIMNADNNDWLNWQSVIGSRKVWRFSPNAANSDFTATNIHVTSHGTEFTLQTPTGSVDVLLPLPGRHNIANALAAAALSMSVGATLDAIKAGLANLKA

>d1jbwa2 c.72.2.2 (A:1-296) Folylpolyglutamate synthetase {Lactobacillus casei}

MNYTETVAYIHSFPRLAKTGDHRRILTLLHALGNPQQQGRYIHVTGTNGKGSAANAIAHVLEASGLTVGLYTSPFIMRFNERIMIDHEPIPDAALVNAVAFVRAALERLQQQQADFNVTEFEFITALAYWYFRQRQVDVAVIEVGIGGDTDSTNVITPVVSVLTEVALDHQKLLGHTITAIAKHKAGIIKRGIPVVTGNLVPDAAAVVAAKVATTGSQWLRFDRDFSVPKAKLHGWGQRFTYEDQDGRISDLEVPLVGDYQQRNMAIAIQTAKVYAKQTEWPLTPQNIRQGLAASH

>d1jzta\_ c.104.1.1 (A:) Hypothetical protein YNL200c (YNU0\_YEAST) {Baker's yeast (Saccharomyces cerevisiae)}

LKVVSSKLAAEIDKELMGPQIGFTLQQLMELAGFSVAQAVCRQFPLRGKTETEKGKHVFVIAGPGNNGGDGLVCARHLKLFGYNPVVFYPKRSERTEFYKQLVHQLNFFKVPVLSQDEGNWLEYLKPEKTLCIVDAIFGFSFKPPMREPFKGIVEELCKVQNIIPIVSVDVPTGWDVDKGPISQPSINPAVLVSLTVPKPCSSHIRENQTTHYVGGRFIPRDFANKFGFEPFGYESTDQILKL

>d1b7ba\_ c.73.1.1 (A:) Carbamate kinase {Enterococcus faecium}

GKKMVVALGGNAILSNDASAHAQQQALVQTSAYLVHLIKQGHRLIVSHGNGPQVGNLLLQQQAADSEKNPAMPLDTCVAMTQGSIGYWLSNALNQELNKAGIKKQVATVLTQVVVDPADEAFKNPTKPIGPFLTEAEAKEAMQAGAIFKEDAGRGWRKVVPSPKPIDIHEAETINTLIKNDIITISCGGGGIPVVGQELKGVEAVIDKDFASEKLAELVDADALVILTGVDYVCINYGKPDEKQLTNVTVAELEEYKQAGHFAPGSMLPKIEAAIQFVESQPNKQAIITSLENLGSMSGDEIVGTVV

>d1e19a\_ c.73.1.1 (A:) Carbamate kinase {Archaeon Pyrococcus furiosus}

GKRVVIALGGNALQQRGQKGSYEEMMDNVRKTARQIAEIIARGYEVVITHGNGPQVGSLLLHMDAGQATYGIPAQPMDVAGAMSQGWIGYMIQQALKNELRKRGMEKKVVTIITQTIVDKNDPAFQNPTKPVGPFYDEETAKRLAREKGWIVKEDSGRGWRRVVPSPDPKGHVEAETIKKLVERGVIVIASGGGGVPVILEDGEIKGVEAVIDKDLAGEKLAEEVNADIFMILTDVNGAALYYGTEKEQWLREVKVEELRKYYEEGHFKAGSMGPKVLAAIRFIEWGGERAIIAHLEKAVEALEGKTGTQVLP

>d1eqja1 c.105.1.1 (A:77-310) 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain {Bacillus stearothermophilus}

QSLTRINIAIREGEFDRNETFLAAMNHVKQHGTSLHLFGLLSDGGVHSHIHHLYALLRLAAKEGVKRVYIHGFLDGRDVGPQTAPQYIKELQEKIKEYGVGEIATLSGRYYSMDRDKRWDRVEKAYRAMVYGEGPTYRDPLECIEDSYKHGIYDEFVLPSVIVREDGRPVATIQDNDAIIFYNFRPDRAIQISNTFTNEDFREFDRGPKHPKHLFFVCLTHFSETVAGYVAFKP

>d1eqja2 c.76.1.3 (A:3-76,A:311-510) 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain {Bacillus stearothermophilus}

KKPVALIILDGFALRDETYGNAVAQANKPNFDRYWNEYPHTTLKACGEAVGLPEGQMGNSEVGHLNIGAGRIVYXTNLDNTIGEVLSQHGLRQLRIAETEKYPHVTFFMSGGREEEFPGEDRILINSPKVPTYDLKPEMSAYEVTDALLKEIEADKYDAIILNYANPDMVGHSGKLEPTIKAVEAVDECLGKVVDAILAKGGIAIITADHGNADEVLTPDGKPQTAHTTNPVPVIVTKKGIKLRDGGILGDLAPTMLDLLGLPQPKEMTGKSLIV

>d1ed8a\_ c.76.1.1 (A:) Alkaline phosphatase {Escherichia coli}

TPEMPVLENRAAQGDITAPGGARRLTGDQTAALRDSLSDKPAKNIILLIGDGMGDSEITAARNYAEGAGGFFKGIDALPLTGQYTHYALNKKTGKPDYVTDSAASATAWSTGVKTYNGALGVDIHEKDHPTILEMAKAAGLATGNVSTAELQDATPAALVAHVTSRKCYGPSATSEKCPGNALEKGGKGSITEQLLNARADVTLGGGAKTFAETATAGEWQGKTLREQAQARGYQLVSDAASLNSVTEANQQKPLLGLFADGNMPVRWLGPKATYHGNIDKPAVTCTPNPQRNDSVPTLAQMTDKAIELLSKNEKGFFLQVEGASIDKQDHAANPCGQIGETVDLDEAVQRALEFAKKEGNTLVIVTADHAHASQIVAPDTKAPGLTQALNTKDGAVMVMSYGNSEEDSQEHTGSQLRIAAYGPHAANVVGLTDQTDLFYTMKAALGLK

>d1ew2a\_ c.76.1.1 (A:) Alkaline phosphatase {Human (Homo sapiens)}

IIPVEEENPDFWNREAAEALGAAKKLQPAQTAAKNLIIFLGDGMGVSTVTAARILKGQKKDKLGPEIPLAMDRFPYVALSKTYNVDKHVPDSGATATAYLCGVKGNFQTIGLSAAARFNQCNTTRGNEVISVMNRAKKAGKSVGVVTTTRVQHASPAGTYAHTVNRNWYSDADVPASARQEGCQDIATQLISNMDIDVILGGGRKYMFRMGTPDPEYPDDYSQGGTRLDGKNLVQEWLAKRQGARYVWNRTELMQASLDPSVTHLMGLFEPGDMKYEIHRDSTLDPSLMEMTEAALRLLSRNPRGFFLFVEGGRIDHGHHESRAYRALTETIMFDDAIERAGQLTSEEDTLSLVTADHSHVFSFGGYPLRGSSIFGLAPGKARDRKAYTVLLYGNGPGYVLKDGARPDVTESESGSPEYRQQSAVPLDEETHAGEDVAVFARGPQAHLVHGVQEQTFIAHVMAFAACLEPYTACDLAPP

>d1auk\_\_ c.76.1.2 (-) Arylsulfatase A {Human (Homo sapiens)}

RPPNIVLIFADDLGYGDLGCYGHPSSTTPNLDQLAAGGLRFTDFYVPVSLCTPSRAALLTGRLPVRMGMYPGVLVPSSRGGLPLEEVTVAEVLAARGYLTGMAGKWHLGVGPEGAFLPPHQGFHRFLGIPYSHDQGPCQNLTCFPPATPCDGGCDQGLVPIPLLANLSVEAQPPWLPGLEARYMAFAHDLMADAQRQDRPFFLYYASHHTHYPQFSGQSFAERSGRGPFGDSLMELDAAVGTLMTAIGDLGLLEETLVIFTADNGPETMRMSRGGCSGLLRCGKGTTYEGGVREPALAFWPGHIAPGVTHELASSLDLLPTLAALAGAPLPNVTLDGFDLSPLLLGTGKSPRQSLFFYPSYPDEVRGVFAVRTGKYKAHFFTQGSAHSDTTADPACHASSSLTAHEPPLLYDLSKDPGENYNLLGGVAGATPEVLQALKQLQLLKAQLDAAVTFGPSQVARGEDPALQICCHPGCTPRPACCHCP

>d1fsu\_\_ c.76.1.2 (-) Arylsulfatase B (4-sulfatase) {Human (Homo sapiens)}

SRPPHLVFLLADDLGWNDVGFHGSRIRTPHLDALAAGGVLLDNYYTQPLXTPSRSQLLTGRYQIRTGLQHQIIWPCQPSCVPLDEKLLPQLLKEAGYTTHMVGKWHLGMYRKECLPTRRGFDTYFGYLLGSEDYYSHERCTLIDALNVTRCALDFRDGEEVATGYKNMYSTNIFTKRAIALITNHPPEKPLFLYLALQSVHEPLQVPEEYLKPYDFIQDKNRHHYAGMVSLMDEAVGNVTAALKSSGLWNNTVFIFSTDNGGQTLAGGNNWPLRGRKWSLWEGGVRGVGFVASPLLKQKGVKNRELIHISDWLPTLVKLARGHTNGTKPLDGFDVWKTISEGSPSPRIELLHNIDPNFVDSSPCPRNSMAPAKDDSSLPEYSAFNTSVHAAIRHGNWKLLTGYPGCGYWFPPPSQYNVSEIPSSDPPTKTLWLFDIDRDPEERHDLSREYPHIVTKLLSRLQFYHKHSVPVYFPAQDPRCDPKATGVWGPWM

>d1hdha\_ c.76.1.2 (A:) Arylsulfatase B (4-sulfatase) {Pseudomonas aeruginosa}

KRPNFLVIVADDLGFSDIGAFGGEIATPNLDALAIAGLRLTDFHTASTCSPTRSMLLTGTDHHIAGIGTMAEALTPELEGKPGYEGHLNERVVALPELLREAGYQTLMAGKWHLGLKPEQTPHARGFERSFSLLPGAANHYGFEPPYDESTPRILKGTPALYVEDERYLDTLPEGFYSSDAFGDKLLQYLKERDQSRPFFAYLPFSAPHWPLQAPREIVEKYRGRYDAGPEALRQERLARLKELGLVEADVEAHPVLALTREWEALEDEERAKSARAMEVYAAMVERMDWNIGRVVDYLRRQGELDNTFVLFMSDNGAEGALLEAFPKFGPDLLGFLDRHYDNSLENIGRANSYVWYGPRWAQAATAPSRLYKAFTTQGGIRVPALVRYPRLSRQGAISHAFATVMDVTPTLLDLAGVRHPGKRWRGREIAEPRGRSWLGWLSGETEAAHDENTVTGWELFGMRAIRQGDWKAVYLPAPVGPATWQLYDLARDPGEIHDLADSQPGKLAELIEHWKRYVSETGVV

>d1k30a\_ c.112.1.1 (A:) Glycerol-3-phosphate (1)-acyltransferase {Cushaw squash (Cucurbita moschata)}

SHSRKFLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQNYRNAVIESGNPKADEIVLSNMTVALDRILLDVEDPFVFSSHHKAIREPFDYYIFGQNYIRPLIDFGNSFVGNLSLFKDIEEKLQQGHNVVLISNHQTEADPAIISLLLEKTNPYIAENTIFVAGDRVLADPLCKPFSIGRNLICVYSKKHMFDIPELTETKRKANTRSLKEMALLLRGGSQLIWIAPSGGRDRPDPSTGEWYPAPFDASSVDNMRRLIQHSDVPGHLFPLALLCHDIMPPPSQVEIEIGEKRVIAFNGAGLSVAPEISFEEIAATHKNPEEVREAYSKALFDSVAMQYNVLKTAISGKQGLGASTADVSLSQPW

>d1e4bp\_ c.74.1.1 (P:) L-fuculose-1-phosphate aldolase {Escherichia coli}

MERNKLARQIIDTCLEMTRLGLNQGTAGQVSVRYQDGMLITPTGIPYEKLTESHIVFIDGNGKHEEGKLPSSEWRFHMAAYQSRPDANAVVHNHAVHCTAVSILNRSIPAIHYMIAAAGGNSIPCAPYATFGTRELSEHVALALKNRKATLLQHHGLIACEVNLEKALWLAHEVEVLAQLYLTTLAITDPVPVLSDEEIAVVLEKF

>d1jdia\_ c.74.1.1 (A:) L-ribulose-5-phosphate 4-epimerase {Escherichia coli}

MLEDLKRQVLEANLALPKHNLVTLTWGNVSAVDRERGVFVIKPSGVDYSIMTADDMVVVSIETGEVVEGAKKPSSDTPTHRLLYQAFPSIGGIVHTHSRHATIWAQAGQSIPATGTTHADYFYGTIPCTRKMTDAEINGEYEWETGNVIVETFEKQGIDAAQMPGVLVHSHGPFAWGKNAEDAVHNAIVLEEVAYMGIFCRQLAPQLPDMQQTLLNKHYLRKH

>d1j9la\_ c.106.1.1 (A:) SurE homolog TM1662 (TM107 ?) {Thermotoga maritima}

MRILVTNDDGIQSKGIIVLAELLSEEHEVFVVAPDKERSATGHSITIHVPLWMKKVFISERVVAYSTTGTPADCVKLAYNVVMDKRVDLIVSGVNRGPNMGMDILHSGTVSGAMEGAMMNIPSIAISSANYESPDFEGAARFLIDFLKEFDFSLLDPFTMLNINVPAGEIKGWRFTRQSRRRWNDYFEERVSPFGEKYYWMMGEVIEDDDRDDVDYKAVREGYVSITPIHPFLTNEQCLKKLREVYD

>d1cjya2 c.75.1.1 (A:142-721) Cytosolic phospholipase A2 catalytic domain {Human (Homo sapiens)}

PDLRFSMALCDQEKTFRQQRKEHIRESMKKLLGPKNSEGLHSARDVPVVAILGSGGGFRAMVGFSGVMKALYESGILDCATYVAGLSGSTWYMSTLYSHPDFPEKGPEEINEELMKNVSHNPLLLLTPQKVKRYVESLWKKKSSGQPVTFTDIFGMLIGETLIHNRMNTTLSSLKEKVNTAQCPLPLFTCLHVKPDVSELMFADWVEFSPYEIGMAKYGTFMAPDLFGSKFFMGTVVKKYEENPLHFLMGVWGSAFSILFNRVLGVSGSQSRGSTMEEELENITTKHIVSNDSSDSDDESHEPKGTENEDAGSDYQSDNQASWIHRMIMALVSDSALFNTREGRAGKVHNFMLGLNLNTSYPLSPLSDFATQDSFDDDELDAAVADPDEFERIYEPLDVKSKKIHVVDSGLTFNLPYPLILRPQRGVDLIISFDFSARPSDSSPPFKELLLAEKWAKMNKLPFPKIDPYVFDREGLKECYVFKPKNPDMEKDCPTIIHFVLANINFRKYKAPGVPRETEEEKEIADFDIFDDPESPFSTFNFQYPNQAFKRLHDLMHFNTLNNIDVIKEAMVESIEYRRQ

>d1xaa\_\_ c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Thermus thermophilus}

MKVAVLPGDGIGPEVTEAALKVLRALDEAEGLGLAYEVFPFGGAAIDAFGEPFPEPTRKGVEEAEAVLLGSVGGPKWDGLPRKIRPETGLLSLRKSQDLFANLRPAKVFPGLERLSPLKEEIARGVDVLIVRELTGGIYFGEPRGMSEAEAWNTERYSKPEVERVARVAFEAARKRRKHVVSVDKANVLEVGEFWRKTVEEVGRGYPDVALEHQYVDAMAMHLVRSPARFDVVVTGNIFGDILSDLASVLPGSLGLLPSASLGRGTPVFEPVHGSAPDIAGKGIANPTAAILSAAMMLEHAFGLVELARKVEDAVAKALLETPPPDLGGSAGTEAFTATVLRHLA

>d1xad\_\_ c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Chimera (Thermus thermophilus) and (Bacillus subtilis)}

MKVAVLPGDGIGPEVTEAALKVLRALDEAEGLGLAYEVFPFGGAAIDAFGEPFPEPTRKGVEEAEAVLLGSVGGPKWDQNPRELRPEKGLLSIRKQLDLFANLRPVKVFESLSDASPLKKEYIDNVDFVIVRELTGGIYFGEPRGMSEAEAWNTERYSKPEVERVARVAFEAARKRRKHVVSVDKANVLEVGEFWRKTVEEVGRGYPDVALEHQYVDAMAMHLVRSPARFDVVVTGNIFGDILSDLASVLPGSLGLLPSASLGRGTPVFEPVHGSAPDIAGKGIANPTAAILSAAMMLEHAFGLVELARKVEDAVAKALLETPPPDLGGSAGTEAFTATVLRHLA

>d2ayqa\_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Bacillus coagulans}

MKMKLAVLPGDGIGPEVMDAAIRVLKTVLDNDGHEAVFENALIGGAAIDEAGTPLPEETLDICRRSDAILLGAVGGPKWDHNPASLRPEKGLLGLRKEMGLFANLRPVKAYATLLNASPLKRERVENVDLVIVRELTGGLYFGRPSERRGPGENEVVDTLAYTREEIERIIEKAFQLAQIRRKKLASVDKANVLESSRMWREIAEETAKKYPDVELSHMLVDSTSMQLIANPGQFDVIVTENMFGDILSDEASVITGSLGMLPSASLRSDRFGMYEPVHGSAPDIAGQGKANPLGTVLSAALMLRYSFGLEKEAAAIEKAVDDVLQDGYCTGDLQVANGKVVSTIELTDRLIEKLN

>d1a05a\_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Thiobacillus ferrooxidans}

MKKIAIFAGDGIGPEIVAAARQVLDAVDQAAHLGLRCTEGLVGGAALDASDDPLPAASLQLAMAADAVILGAVGGPRWDAYPPAKRPEQGLLRLRKGLDLYANLRPAQIFPQLLDASPLRPELVRDVDILVVRELTGDIYFGQPRGLEVIDGKRRGFNTMVYDEDEIRRIAHVAFRAAQGRRKQLCSVDKANVLETTRLWREVVTEVARDYPDVRLSHMYVDNAAMQLIRAPAQFDVLLTGNMFGDILSDEASQLTGSIGMLPSASLGEGRAMYEPIHGSAPDIAGQDKANPLATILSVAMMLRHSLNAEPWAQRVEAAVQRVLDQGLRTADIAAPGTPVIGTKAMGAAVVNALNLK

>d1cnza\_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Salmonella typhimurium}

MSKNYHIAVLPGDGIGPEVMAQALKVMDAVRSRFDMRITTSHYDVGGIAIDNHGHPLPKATVEGCEQADAILFGSVGGPKWENLPPESQPERGALLPLRKHFKLFSNLRPAKLYQGLEAFCPLRADIAANGFDILCVRELTGGIYFGQPKGREGSGQYEKAFDTEVYHRFEIERIARIAFESARKRRRKVTSIDKANVLQSSILWREIVNDVAKTYPDVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMITGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGKNIANPIAQILSLALLLRYSLDANDAATAIEQAINRALEEGVRTGDLARGAAAVSTDEMGDIIARYVAEGV

>d1cm7a\_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Escherichia coli}

MSKNYHIAVLPGDGIGPEVMTQALKVLDAVRNRFAMRITTSHYDVGGAAIDNHGQPLPPATVEGCEQADAVLFGSVGGPKWEHLPPDQQPERGALLPLRKHFKLFSNLRPAKLYQGLEAFCPLRADIAANGFDILCVRELTGGIYFGQPKGREGSGQYEKAFDTEVYHRFEIERIARIAFESARKRRHKVTSIDKANVLQSSILWREIVNEIATEYPDVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMITGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGKNIANPIAQILSLALLLRYSLDADDAACAIERAINRALEEGIRTGDLARGAAAVSTDEMGDIIARYVAEGV

>d1iso\_\_ c.77.1.1 (-) Isocitrate dehydrogenase, ICDH {Escherichia coli}

SKVVVPAQGKKITLQNGKLNVPENPIIPYIEGDGIGVDVTPAMLKVVDAAVEKAYKGERKISWMEIYTGEKSTQVYGQDVWLPAETLDLIREYRVAIKGPLTTPVGGGIRSLNVALRQELDLYICLRPVRYYQGTPSPVKHPELTDMVIFRENSEDIYAGIEWKADSADAEKVIKFLREEMGVKKIRFPEHCGIGIKPMSEEGTKRLVRAAIEYAIANDRDSVTLVHKGNIMKFTEGAFKDWGYQLAREEFGGELIDGGPWLKVKNPNTGKEIVIKDVIADAFLQQILLRPAEYDVIACMNLNGDYISDALAAQVGGIGIAPGANIGDEYALFEATHGTAPDIAGQDKANPGSIILSAEMMLRHMGWTEAADLIVKGMEGAINAKTVTKDFESLMDGAKLLKCSEFGDAIIENM

>d1hqsa\_ c.77.1.1 (A:) Isocitrate dehydrogenase, ICDH {Bacillus subtilis}

MAQGEKITVSNGVLNVPNNPIIPFIEGDGTGPDIWNAASKVLEAAVEKAYKGEKKITWKEVYAGEKAYNKTGEWLPAETLDVIREYFIAIKGPLTTPVGGGIRSLNVALRQELDLFVCLRPVRYFTGVPSPVKRPEDTDMVIFRENTEDIYAGIEYAKGSEEVQKLISFLQNELNVNKIRFPETSGIGIKPVSEEGTSRLVRAAIDYAIEHGRKSVTLVHKGNIMKFTEGAFKNWGYELAEKEYGDKVFTWAQYDRIAEEQGKDAANKAQSEAEAAGKIIIKDSIADIFLQQILTRPNEFDVVATMNLNGDYISDALAAQVGGIGIAPGANINYETGHAIFEATHGTAPKYAGLDKVNPSSVILSGVLLLEHLGWNEAADLVIKSMEKTIASKVVTYDFARLMDGATEVKCSEFGEELIKNMD

>d1ekxa1 c.78.1.1 (A:1-150) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}

ANPLYQKHIISINDLSRDDLNLVLATAAKLKANPQPELLKHKVIASCFFEASTRTRLSFETSMHRLGASVVGFSDSANTSLGKKGETLADTISVISTYVDAIVMRHPQEGAARLATEFSGNVPVLNAGDGSNQHPTQTLLDLFTIQETQG

>d1ekxa2 c.78.1.1 (A:151-310) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}

RLDNLHVAMVGDLKYGRTVHSLTQALAKFDGNRFYFIAPDALAMPQYILDMLDEKGIAWSLHSSIEEVMAEVDILYMTRVQKERLDPSEYANVKAQFVLRASDLHNAKANMKVLHPLPRVDEIATDVDKTPHAWYFQQAGNGIFARQALLALVLNRDLVL

>d2atca2 c.78.1.1 (A:151-305) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}

RLNNLHVAMVGDLKYGRTVHSLTQALAKFDGNRFYFIAPDALAMPEYILDMLDEKGIAWSLHSSIEEVMTRVQKERLDPSEYABVKAQFLVRANSLGGLHNAKMNAKVLHPLPRVDEIATDVDKTPHAWYFQQAGNGIFARQALLALVLNRDLVL

>d2at2a1 c.78.1.1 (A:1-144) Aspartate carbamoyltransferase catalytic subunit {Bacillus subtilis}

MKHLTTMSELSTEEIKDLLQTAQELKSGKTDNQLTGKFAANLFFEPSTRTRFSFEVAEKKLGMNVLNLDGTSTSVQKGETLYDTIRTLESIGVDVCVIRHSEDEYYEELVSQVNIPILNAGDGCGQHPTQSLLDLMTIYEEFNT

>d2at2a2 c.78.1.1 (A:145-295) Aspartate carbamoyltransferase catalytic subunit {Bacillus subtilis}

FKGLTVSIHGDIKHSRVARSNAEVLTRLGARVLFSGPSEWQDEENTFGTYVSMDEAVESSDVVMLLRIQNERHQSAVSQEGYLNKYGLTVERAERMKRHAIIMHPAPVNRGVEIDDSLVESEKSRIFKQMKNGVFIRMAVIQCALQTNVKR

>d1dxha1 c.78.1.1 (A:1-150) Ornithine transcarbamoylase {Pseudomonas aeruginosa}

AFNMHNRNLLSLMHHSTRELRYLLDLSRDLKRAKYTGTEQQHLKRKNIALIFEKTSTRTRCAFEVAAYDQGANVTYIDPNSSQIGHKESMKDTARVLGRMYDAIEYRGFKQEIVEELAKFAGVPVFNGLTDEYHPTQMLADVLTMREHSD

>d1dxha2 c.78.1.1 (A:151-335) Ornithine transcarbamoylase {Pseudomonas aeruginosa}

KPLHDISYAYLGDARNNMGNSLLLIGAKLGMDVRIAAPKALWPHDEFVAQCKKFAEESGAKLTLTEDPKEAVKGVDFVHTDVWVSMGEPVEAWGERIKELLPYQVNMEIMKATGNPRAKFMHCLPAFHNSETKVGKQIAEQYPNLANGIEVTEDVFESPYNIAFEQAENRMHTIKAILVSTLADI

>d1duvg1 c.78.1.1 (G:1-150) Ornithine transcarbamoylase {Escherichia coli}

SGFYHKHFLKLLDFTPAELNSLLQLAAKLKADKKSGKEEAKLTGKNIALIFEKDSTRTRCSFEVAAYDQGARVTYLGPSGSQIGHKESIKDTARVLGRMYDGIQYRGYGQEIVETLAEYASVPVWNGLTNEFHPTQLLADLLTMQEHLPG

>d1duvg2 c.78.1.1 (G:151-333) Ornithine transcarbamoylase {Escherichia coli}

KAFNEMTLVYAGDARNNMGNSMLEAAALTGLDLRLVAPQACWPEAALVTECRALAQQNGGNITLTEDVAKGVEGADFIYTDVWVSMGEAKEKWAERIALLREYQVNSKMMQLTGNPEVKFLHCLPAFHDDQTTLGKKMAEEFGLHGGMEVTDEVFESAASIVFDQAENRMHTIKAVMVATLSK

>d1a1s\_1 c.78.1.1 (1-150) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}

VVSLAGRDLLCLQDYTAEEIWTILETAKMFKIWQKIGKPHRLLEGKTLAMIFQKPSTRTRVSFEVAMAHLGGHALYLNAQDLQLRRGETIADTARVLSRYVDAIMARVYDHKDVEDLAKYATVPVINGLSDFSHPCQALADYMTIWEKKG

>d1a1s\_2 c.78.1.1 (151-313) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}

TIKGVKVVYVGDGNNVAHSLMIAGTKLGADVVVATPEGYEPDEKVIKWAEQNAAESGGSFELLHDPVKAVKDADVIYTDVWASMGQEAEAEERRKIFRPFQVNKDLVKHAKPDYMFMHCLPAHRGEEVTDDVIDSPNSVVWDQAENRLHAQKAVLALVMGGIK

>d1otha1 c.78.1.1 (A:34-184) Ornithine transcarbamoylase {Human (Homo sapiens)}

KVQLKGRDLLTLKNFTGEEIKYMLWLSADLKFRIKQKGEYLPLLQGKSLGMIFEKRSTRTRLSTETGFALLGGHPCFLTTQDIHLGVNESLTDTARVLSSMADAVLARVYKQSDLDTLAKEASIPIINGLSDLYHPIQILADYLTLQEHYS

>d1otha2 c.78.1.1 (A:185-354) Ornithine transcarbamoylase {Human (Homo sapiens)}

SLKGLTLSWIGDGNNILHSIMMSAAKFGMHLQAATPKGYEPDASVTKLAEQYAKENGTKLLLTNDPLEAAHGGNVLITDTWISMGREEEKKKRLQAFQGYQVTMKTAKVAASDWTFLHCLPRKPEEVDDEVFYSPRSLVFPEAENRKWTIMAVMVSLLTDYSPQLQKPKF

>d1b74a1 c.78.2.1 (A:1-105) Glutamate racemase {Aquifex pyrophilus}

MKIGIFDSGVGGLTVLKAIRNRYRKVDIVYLGDTARVPYGIRSKDTIIRYSLECAGFLKDKGVDIIVVACNTASAYALERLKKEINVPVFGVIEPGVKEALKKSR

>d1b74a2 c.78.2.1 (A:106-252) Glutamate racemase {Aquifex pyrophilus}

NKKIGVIGTPATVKSGAYQRKLEEGGADVFAKACPLFAPLAEEGLLEGEITRKVVEHYLKEFKGKIDTLILGCTHYPLLKKEIKKFLGDAEVVDSSEALSLSLHNFIKDDGSSSLELFFTDLSPNLQFLIKLILGRDYPVKLAEGVF

>d1qopb\_ c.79.1.1 (B:) Tryptophan synthase, beta-subunit {Salmonella typhimurium}

TTLLNPYFGEFGGMYVPQILMPALNQLEEAFVSAQKDPEFQAQFADLLKNYAGRPTALTKCQNITAGTRTTLYLKREDLLHGGAHKTNQVLGQALLAKRMGKSEIIAETGAGQHGVASALASALLGLKCRIYMGAKDVERQSPNVFRMRLMGAEVIPVHSGSATLKDACNEALRDWSGSYETAHYMLGTAAGPHPYPTIVREFQRMIGEETKAQILDKEGRLPDAVIACVGGGSNAIGMFADFINDTSVGLIGVEPGGHGIETGEHGAPLKHGRVGIYFGMKAPMMQTADGQIEESYSISAGLDFPSVGPQHAYLNSIGRADYVSITDDEALEAFKTLCRHEGIIPALESSHALAHALKMMREQPEKEQLLVVNLSGRGDKDIFTVHDIL

>d1fcja\_ c.79.1.1 (A:) O-acetylserine sulfhydrylase (Cystein synthase) {Salmonella typhimurium}

SKIYEDNSLTIGHTPLVRLNRIGNGRILAKVESRNPSFSVKCRIGANMIWDAEKRGVLKPGVELVEPTNGNTGIALAYVAAARGYKLTLTMPETMSIERRKLLKALGANLVLTEGAKGMKGAIQKAEEIVASDPQKYLLLQQFSNPANPEIHEKTTGPEIWEDTDGQVDVFISGVGTGGTLTGVTRYIKGTKGKTDLITVAVEPTDSPVIAQALAGEEIKPGPHKIQGIGAGFIPGNLDLKLIDKVVGITNEEAISTARRLMEEEGILAGISSGAAVAAALKLQEDESFTNKNIVVILPSSG

>d1tdj\_1 c.79.1.1 (5-335) Allosteric threonine deaminase N-terminal domain {Escherichia coli}

QPLSGAPEGAEYLRAVLRAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGLTEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLDRVFVPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEYLDDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIALHNIRGERLAHILSGANVNFHGLRYVSERCELGE

>d1e5xa\_ c.79.1.1 (A:) Threonine synthase {Mouse-ear cress (Arabidopsis thaliana)}

IETAVKPPHRTEDNIRDEARRNRSNAVNPFSAKYVPFNAAPGSTESYSLDEIVYRSRSGGLLDVEHDMEALKRFDGAYWRDLFDSRVGKSTWPYGSGVWSKKEWVLPEIDDDDIVSAFEGNSNLFWAERFGKQFLGMNDLWVKHCGISHTGSFKDLGMTVLVSQVNRLRKMKRPVVGVGCASTGDTSAALSAYCASAGIPSIVFLPANKISMAQLVQPIANGAFVLSIDTDFDGCMKLIREITAELPIYLANSLNSLRLEGQKTAAIEILQQFDWQVPDWVIVPGGNLGNIYAFYKGFKMCQELGLVDRIPRMVCAQAANANPLYLHYKSGWKDFKPMTASTTFASAIQIGDPVSIDRAVYALKKCNGIVEEATEEELMDAMAQADSTGMFICPHTGVALTALFKLRNQGVIAPTDRTVVVSTAHGLKFTQSKIDYHSNAIPDMACRFSNPPVDVKADFGAVMDVLKSYLGSNTLTS

>d1f2da\_ c.79.1.1 (A:) 1-aminocyclopropane-1-carboxylate deaminase {Yeast (Hansenula saturnus)}

AGVAKFAKYPLTFGPSPISNLNRLSQHLGSKVNVYAKREDCNSGLAFGGNKLRKLEYIVPDIVEGDYTHLVSIGGRQSNQTRMVAALAAKLGKKCVLIQEDWVPIPEAEKDVYNRVGNIELSRIMGADVRVIEDGFDIGMRKSFANALQELEDAGHKPYPIPAGCSEHKYGGLGFVGFADEVINQEVELGIKFDKIVVCCVTGSTTAGILAGMAQYGRQDDVIAIDASFTSEKTKEQTLRIANNTAKLIGVEHEFKDFTLDTRFAYPCYGVPNEGTIEAIRTCAEQEGVLTDPVYEGKSMQGLIALIKEDYFKPGANVLYVHLGGAPALSAYSSFFPTKTA

>d1jbqa\_ c.79.1.1 (A:) Cystathionine beta-synthase {Human (Homo sapiens)}

WIRPDAPSRCTWQLGRPASESPHHHTAPAKSPKILPDILKKIGDTPMVRINKIGKKFGLKCELLAKCEFFNAGGSVKDRISLRMIEDAERDGTLKPGDTIIEPTSGNTGIGLALAAAVRGYRCIIVMPEKMSSEKVDVLRALGAEIVRTPTNARFDSPESHVGVAWRLKNEIPNSHILDQYRNASNPLAHYDTTADEILQQCDGKLDMLVASVGTGGTITGIARKLKEKCPGCRIIGVDPEGSILAEPEELNQTEQTTYEVEGIGYDFIPTVLDRTVVDKWFKSNDEEAFTFARMLIAQEGLLCGGSAGSTVAVAVKAAQELQEGQRCVVILPDSVRNYMTKFLSDRWMLQKGFL

>d1jeoa\_ c.80.1.3 (A:) Probable 3-hexulose-6-phosphate isomerase MJ1247 {Archaeon Methanococcus jannaschii}

LEELDIVSNNILILKKFYTNDEWKNKLDSLIDRIIKAKKIFIFGVGRSGYIGRCFAMRLMHLGFKSYFVGETTTPSYEKDDLLILISGSGRTESVLTVAKKAKNINNNIIAIVCECGNVVEFADLTIPLEVKKSKYLPMGTTFEETALIFLDLVIAEIMKRLNLDESEIIKRHCNLL

>d1moq\_\_ c.80.1.1 (-) "Isomerase domain" of glucosamine 6-phosphate synthase (GLMS) {Escherichia coli}

GDKGIYRHYMQKEIYEQPNAIKNTLTGRISHGQVDLSELGPNADELLSKVEHIQILACGTSYNSGMVSRYWFESLAGIPCDVEIASEFRYRKSAVRRNSLMITLSQSGETADTLAGLRLSKELGYLGSLAICNVPGSSLVRESDLALMTNAGTEIGVASTKAFTTQLTVLLMLVAKLSRLKGLDASIEHDIVHGLQALPSRIEQMLSQDKRIEALAEDFSDKHHALFLGRGDQYPIALEGALKLKEISYIHAEAYAAGELKHGPLALIDADMPVIVVAPNNELLEKLKSNIEEVRARGGQLYVFADQDAGFVSSDNMHIIEMPHVEEVIAPIFYTVPLQLLAYHVALIKGTDVDQPRNLAKSVTVE

>d1g98a\_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Rabbit (Oryctolagus cuniculus)}

AALTRNPQFQKLQQWHREHGSELNLRHLFDTDKERFNHFSLTLNTNHGHILLDYSKNLVTEEVMHMLLDLAKSRGVEAARESMFNGEKINSTEDRAVLHVALRNRSNTPIVVDGKDVMPEVNKVLDKMKAFCQRVRSGDWKGYTGKTITDVINIGIGGSDLGPLMVTEALKPYSSGGPRVWFVSNIDGTHIAKTLACLNPESSLFIIASKTFTTQETITNAKTAKDWFLLSAKDPSTVAKHFVALSTNTAKVKEFGIDPQNMFEFWDWVGGRYSLWSAIGLSIALHVGFDNFEQLLSGAHWMDQHFRTTPLEKNAPVLLAMLGIWYINCFGCETQAVLPYDQYLHRFAAYFQQGDMESNGKYITKSGARVDHQTGPIVWGEPGTNGQHAFYQLIHQGTKMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMKGKSTEEARKELQAAGKSPEDLMKLLPHKVFEGNRPTNSIVFTKLTPFILGALIAMYEHKIFVQGVVWDINSFDQWGVELGKQLAKKIEPELDGSSPVTSHDSSTNGLINFIKQQREAK

>d1iata\_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Human (Homo sapiens)}

AALTRDPQFQKLQQWYREHRSELNLRRLFDANKDRFNHFSLTLNTNHGHILVDYSKNLVTEDVMRMLVDLAKSRGVEAARERMFNGEKINYTEGRAVLHVALRNRSNTPILVDGKDVMPEVNKVLDKMKSFCQRVRSGDWKGYTGKTITDVINIGIGGSDLGPLMVTEALKPYSSGGPRVWYVSNIDGTHIAKTLAQLNPESSLFIIASKTFTTQETITNAETAKEWFLQAAKDPSAVAKHFVALSTNTTKVKEFGIDPQNMFEFWDWVGGRYSLWSAIGLSIALHVGFDNFEQLLSGAHWMDQHFRTTPLEKNAPVLLALLGIWYINCFGCETHAMLPYDQYLHRFAAYFQQGDMESNGKYITKSGTRVDHQTGPIVWGEPGTNGQHAFYQLIHQGTKMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMRGKSTEEARKELQAAGKSPEDLERLLPHKVFEGNRPTNSIVFTKLTPFMLGALVAMYEHKIFVQGIIWDINSFDQWGVELGKQLAKKIEPELDGSAQVTSHDASTNGLINFIKQQREARV

>d1c7qa\_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Bacillus stearothermophilus}

AISFDYSNALPFMQENELDYLSEFVKAAHHMLHERKGPGSDFLGWVDWPIRYDKNEFSRIKQAAERIRNHSDALVVIGIGGSYLGARAAIEALSHTFHNQMNDTTQIYFAGQNISSTYISHLLDVLEGKDLSINVISKSGTTTEPAIAFRIFRDYMEKKYGKEEARKRIYVTTDRTKGALKKLADQEGYETFVIPDNIGGRYSVLTAVGLLPIAVAGLNIDRMMEGAASAYHKYNNPDLLTNESYQYAAVRNILYRKGKAIELLVNYEPSLHYVSEWWKQLFGESEGKDQKGLFPASVDFTTDLHSMGQYVQEGRRNLIETVLHVKKPQIELTIQEDPENIDGLNFLAGKTLDEVNKKAFQGTLLAHVDGGVPNLIVELDEMNEYTFGEMVYFFEKACGISGHLLGVNPFDQPGVEAYKKNMFALLGKPGFEDEKAALMKRL

>d1eu1a2 c.81.1.1 (A:4-625) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter sphaeroides}

ANGEVMSGCHWGVFKARVENGRAVAFEPWDKDPAPSHQLPGVLDSIYSPTRIKYPMVRREFLEKGVNADRSTRGNGDFVRVTWDEALDLVARELKRVQESYGPTGTFGGSYGWKSPGRLHNCQVLMRRALNLAGGFVNSSGDYSTAAAQIIMPHVMGTLEVYEQQTAWPVVVENTDLMVFWAADPMKTNEIGWVIPDHGAYAGMKALKEKGTRVIAINPVRTETADYFGADVVSPRPQTDVALMLGMAHTLYSEDLHDKDFLENCTTGFDLFAAYLTGESDGTPKTAEWAAEICGLPAEQIRELARSFVAGRTMLAAGWSIQRMHHGEQAHWMLVTLASMIGQIGLPGGGFGLSYHYSNGGSPTSDGPALGGISDGGKAVEGAAWLSESGATSIPCARVVDMLLNPGGEFQFNGATATYPDVKLAYWAGGNPFAHHQDRNRMLKAWEKLETFIVQDFQWTATARHADIVLPATTSYERNDIESVGDYSNRAILAMKKVVDPLYEARSDYDIFAALAERLGKGAEFTEGRDEMGWISSFYEAAVKQAEFKNVAMPSFEDFWSEGIVEFPITEGANFVRYADFREDPLFNPLGTPSGLIEIYSKNIEKMGYDDCPAHPTWMEPA

>d1dmr\_2 c.81.1.1 (3-625) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter capsulatus}

LANGTVMSGSHWGVFTATVENGRATAFTPWEKDPHPSPMLAGVLDSIYSPTRIKYPMVRREFLEKGVNADRSTRGNGDFVRVSWDQALDLVAAEVKRVEETYGPEGVFGGSYGWKSPGRLHNCTTLLRRMLTLAGGYVNGAGDYSTGAAQVIMPHVVGTLEVYEQQTAWPVLAENTEVMVFWAADPIKTSQIGWVIPEHGAYPGLEALKAKGTKVIVIDPVRTKTVEFFGAEHITPKPQTDVAIMLGMAHTLVAEDLYDKDFIANYTSGFDKFLPYLDGETDSTPKTAEWAEGISGVPAETIKELARLFESKRTMLAAGWSMQRMHHGEQAHWMLVTLASMLGQIGLPGGGFGLSYHYSGGGTPSTSGPALAGITDGGAATKGPEWLAASGASVIPVARVVDMLENPGAEFDFNGTRSKFPDVKMAYWVGGNPFVHHQDRNRMVKAWEKLETFVVHDFQWTPTARHADIVLPATTSYERNDIETIGDYSNTGILAMKKIVEPLYEARSDYDIFAAVAERLGKGAEFTEGKDEMGWIKSFYDDAAKQGKAAGVQMPAFDAFWAEGIVEFPVTDGADFVRYASFREDPLLNPLGTPTGLIEIYSKNIEKMGYDDCPAHPTWMEPL

>d1aa6\_2 c.81.1.1 (1-564) Formate dehydrogenase H {Escherichia coli}

MKKVVTVCPYCASGCKINLVVDNGKIVRAEAAQGKTNQGTLCLKGYYGWDFINDTQILTPRLKTPMIRRQRGGKLEPVSWDEALNYVAERLSAIKEKYGPDAIQTTGSSRGTGNETNYVMQKFARAVIGTNNVDCCARVCHGPSVAGLHQSVGNGAMSNAINEIDNTDLVFVFGYNPADSHPIVANHVINAKRNGAKIIVCDPRKIETARIADMHIALKNGSNIALLNAMGHVIIEENLYDKAFVASRTEGFEEYRKIVEGYTPESVEDITGVSASEIRQAARMYAQAKSAAILWGMGVTQFYQGVETVRSLTSLAMLTGNLGKPHAGVNPVRGQNNVQGACDMGALPDTYPGYQYVKDPANREKFAKAWGVESLPAHTGYRISELPHRAAHGEVRAAYIMGEDPLQTDAELSAVRKAFEDLELVIVQDIFMTKTASAADVILPSTSWGEHEGVFTAADRGFQRFFKAVEPKWDLKTDWQIISEIATRMGYPMHYNNTQEIWDELRHLCPDFYGATYEKMGELGFIQWPCRDTSDADQGTSYLFKEKFDTPNGLAQFFTCDWVA

>d1tmo\_2 c.81.1.1 (5-631) Trimethylamine N-oxide reductase {Shewanella massilia}

NEDEWLTTGSHFGAFKMKRKNGVIAEVKPFDLDKYPTDMINGIRGMVYNPSRVRYPMVRLDFLLKGHKSNTHQRGDFRFVRVTWDKALTLFKHSLDEVQTQYGPSGLHAGQTGWRATGQLHSSTSHMQRAVGMHGNYVKKIGDYSTGAGQTILPYVLGSTEVYAQGTSWPLILEHSDTIVLWSNDPYKNLQVGWNAETHESFAYLAQLKEKVKQGKIRVISIDPVVTKTQAYLGCEQLYVNPQTDVTLMLAIAHEMISKKLYDDKFIQGYSLGFEEFVPYVMGTKDGVAKTPEWAAPICGVEAHVIRDLAKTLVKGRTQFMMGWCIQRQQHGEQPYWMAAVLATMIGQIGLPGGGISYGHHYSSIGVPSSGAAAPGAFPRNLDENQKPLFDSSDFKGASSTIPVARWIDAILEPGKTIDANGSKVVYPDIKMMIFSGNNPWNHHQDRNRMKQAFHKLECVVTVDVNWTATCRFSDIVLPACTTYERNDIDVYGAYANRGILAMQKMVEPLFDSLSDFEIFTRFAAVLGKEKEYTRNMGEMEWLETLYNECKAANAGKFEMPDFATFWKQGYVHFGDGEVWTRHADFRNDPEINPLGTPSGLIEIFSRKIDQFGYDDCKGHPTWMEKT

>d1g8ka2 c.81.1.1 (A:4-682) Arsenite oxidase large subunit {Alcaligenes faecalis}

NDRITLPPANAQRTNMTCHFCIVGCGYHVYKWPELEEGGRAPEQNALGLDFRKQLPPLAVTLTPAMTNVVTEHDGARYDIMVVPDKACVVNSGLSSTRGGKMASYMYTPTGDGKERLSAPRLYAADEWVDTTWDHAMALYAGLIKKTLDKDGPQGVFFSCFDHGGAGGGFENTWGTGKLMFSAIQTPMVRIHNRPAYNSECHATREMGIGELNNAYEDAQLADVIWSIGNNPYESQTNYFLNHWLPNLQGATTSKKKERFPNENFPQARIIFVDPRETPSVAIARHVAGNDRVLHLAIEPGTDTALFNGLFTYVVEQGWIDKPFIEAHTKGFDDAVKTNRLSLDECSNITGVPVDMLKRAAEWSYKPKASGQAPRTMHAYEKGIIWGNDNYVIQSALLDLVIATHNVGRRGTGCVRMGGHQEGYTRPPYPGDKKIYIDQELIKGKGRIMTWWGCNNFQTSNNAQALREAILQRSAIVKQAMQKARGATTEEMVDVIYEATQNGGLFVTSINLYPTKLAEAAHLMLPAAHPGEMNLTSMNGERRIRLSEKFMDPPGTAMADCLIAARIANALRDMYQKDGKAEMAAQFEGFDWKTEEDAFNDGFRRAGQPGAPAIDSQGGSTGHLVTYDRLRKSGNNGVQLPVVSWDESKGLVGTEMLYTEGKFDTDDGKAHFKPAPWNG

>d2napa2 c.81.1.1 (A:4-600) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}

RPEKWVKGVCRYCGTGCGVLVGVKDGKAVAIQGNPNNHNAGLLCLKGSLLIPVLNSKERVTQPLVRRHKGGKLEPVSWDEALDLMASRFRSSIDMYGPNSVAWYGSGQCLTEESYVANKIFKGGFGTNNVDGNPRLCMASAVGGYVTSFGKDEPMGTYADIDQATCFFIIGSNTSEAHPVLFRRIARRKQVEPGVKIIVADPRRTNTSRIADMHVAFRPGTDLAFMHSMAWVIINEELDNPRFWQRYVNFMDAEGKPSDFEGYKAFLENYRPEKVAEICRVPVEQIYGAARAFAESAATMSLWCMGINQRVQGVFANNLIHNLHLITGQICRPGATSFSLTGQPNACGGVRDGGALSHLLPAGRAIPNAKHRAEMEKLWGLPEGRIAPEPGYHTVALFEALGRGDVKCMIICETNPAHTLPNLNKVHKAMSHPESFIVCIEAFPDAVTLEYADLVLPPAFWCERDGVYGCGERRYSLTEKAVDPPGQCRPTVNTLVEFARRAGVDPQLVNFRNAEDVWNEWRMVSKGTTYDFWGMTRERLRKESGLIWPCPSEDHPGTSLRYVRGQDPCVPADHPDRFFFYGKPDGRAVIWMRPAKG

>d1ad3a\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus norvegicus)}

SISDTVKRAREAFNSGKTRSLQFRIQQLEALQRMINENLKSISGALASDLGKNEWTSYYEEVAHVLEELDTTIKELPDWAEDEPVAKTRQTQQDDLYIHSEPLGVVLVIGAWNYPFNLTIQPMVGAVAAGNAVILKPSEVSGHMADLLATLIPQYMDQNLYLVVKGGVPETTELLKERFDHIMYTGSTAVGKIVMAAAAKHLTPVTLELGGKSPCYVDKDCDLDVACRRIAWGKFMNSGQTCVAPDYILCDPSIQNQIVEKLKKSLKDFYGEDAKQSRDYGRIINDRHFQRVKGLIDNQKVAHGGTWDQSSRYIAPTILVDVDPQSPVMQEEIFGPVMPIVCVRSLEEAIQFINQREKPLALYVFSNNEKVIKKMIAETSSGGVTANDVIVHITVPTLPFGGVGNSGMGAYHGKKSFETFSHRRSCLVKSLLNEEAHKARYPPSPA

>d1bi9a\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus norvegicus), retinal type II}

MASLQLLPSPTPNLEIKYTKIFINNEWQNSESGRVFPVCNPATGEQVCEVQEADKVDIDKAVQAARLAFSLGSVWRRMDASERGRLLDKLADLVERDRATLATMESLNGGKPFLQAFYIDLQGVIKTLRYYAGWADKIHGMTIPVDGDYFTFTRHEPIGVCGQIIPWNFPLLMFTWKIAPALCCGNTVVIKPAEQTPLSALYMGALIKEAGFPPGVVNILPGYGPTAGAAIASHIGIDKIAFTGSTEVGKLIQEAAGRSNLKRVTLELGGKSPNIIFADADLDYAVEQAHQGVFFNQGQCCTAGSRIFVEESIYEEFVKRSVERAKRRIVGSPFDPTTEQGPQIDKKQYNKILELIQSGVAEGAKLECGGKGLGRKGFFIEPTVFSNVTDDMRIAKEEIFGPVQEILRFKTMDEVIERANNSDFGLVAAVFTNDINKALMVSSAMQAGTVWINCYNALNAQSPFGGFKMSGNGREMGEFGLREYSEVKTVTVKIPQKNS

>d1ag8a\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Cow (Bos taurus), mitochondrial}

VPTPNQQPEVLYNQIFINNEWHDAVSKKTFPTVNPSTGDVICHVAEGDKADVDRAVKAARAAFQLGSPWRRMDASERGRLLNRLADLIERDRTYLAALETLDNGKPYIISYLVDLDMVLKCLRYYAGWADKYHGKTIPIDGDYFSYTRHEPVGVCGQIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNVIPGFGPTAGAAIASHEDVDKVAFTGSTEVGHLIQVAAGKSNLKRVTLEIGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCCCAGSRTFVQEDIYAEFVERSVARAKSRVVGNPFDSRTEQGPQVDETQFKKVLGYIKSGKEEGLKLLCGGGAAADRGYFIQPTVFGDLQDGMTIAKEEIFGPVMQILKFKSMEEVVGRANNSKYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKLSGSGRELGEYGLQAYTEVKTVTVRVPQKNS

>d1cw3a\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Human (Homo sapiens), mitochondrial}

AVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPSTGEVICQVAEGDKEDVDKAVKAARAAFQLGSPWRRMDASHRGRLLNRLADLIERDRTYLAALETLDNGKPYVISYLVDLDMVLKCLRYYAGWADKYHGKTIPIDGDFFSYTRHEPVGVCGQIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVVNIVPGFGPTAGAAIASHEDVDKVAFTGSTEIGRVIQVAAGSSNLKRVTLELGGKSPNIIMSDADMDWAVEQAHFALFFNQGQCCCAGSRTFVQEDIYDEFVERSVARAKSRVVGNPFDSKTEQGPQVDETQFKKILGYINTGKQEGAKLLCGGGIAADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEEVVGRANNSTYGLAAAVFTKDLDKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEYGLQAYTEVKTVTVKVPQKNS

>d1bxsa\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Sheep (Ovis aries)}

DVPAPLTNLQFKYTKIFINNEWHSSVSGKKFPVFNPATEEKLCEVEEGDKEDVDKAVKAARQAFQIGSPWRTMDASERGRLLNKLADLIERDRLLLATMEAMNGGKLFSNAYLMDLGGCIKTLRYCAGWADKIQGRTIPMDGNFFTYTRSEPVGVCGQIIPWNFPLLMFLWKIGPALSCGNTVVVKPAEQTPLTALHMGSLIKEAGFPPGVVNIVPGYGPTAGAAISSHMDVDKVAFTGSTEVGKLIKEAAGKSNLKRVSLELGGKSPCIVFADADLDNAVEFAHQGVFYHQGQCCIAASRLFVEESIYDEFVRRSVERAKKYVLGNPLTPGVSQGPQIDKEQYEKILDLIESGKKEGAKLECGGGPWGNKGYFIQPTVFSDVTDDMRIAKEEIFGPVQQIMKFKSLDDVIKRANNTFYGLSAGIFTNDIDKAITVSSALQSGTVWVNCYSVVSAQCPFGGFKMSGNGRELGEYGFHEYTEVKTVTIKISQKNS

>d1a4sa\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Baltic cod (Gadus callarias)}

AQLVDSMPSASTGSVVVTDDLNYWGGRRIKSKDGATTEPVFEPATGRVLCQMVPCGAEEVDQAVQSAQAAYLKWSKMAGIERSRVMLEAARIIRERRDNIAKLEVINNGKTITEAEYDIDAAWQCIEYYAGLAPTLSGQHIQLPGGAFAYTRREPLGVCAGILAWNYPFMIAAWKCAPALACGNAVVFKPSPMTPVTGVILAEIFHEAGVPVGLVNVVQGGAETGSLLCHHPNVAKVSFTGSVPTGKKVMEMSAKTVKHVTLELGGKSPLLIFKDCELENAVRGALMANFLTQGQVCTNGTRVFVQREIMPQFLEEVVKRTKAIVVGDPLLTETRMGGLISKPQLDKVLGFVAQAKKEGARVLCGGEPLTPSDPKLKNGYFMSPCVLDNCRDDMTCVKEEIFGPVMSVLPFDTEEEVLQRANNTTFGLASGVFTRDISRAHRVAANLEAGTCYINTYSISPVEVPFGGYKMSGFGRENGQATVDYYSQLKTVIVEMGDVDSLF

>d1euha\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Streptococcus mutans}

TKQYKNYVNGEWKLSENEIKIYEPASGAELGSVPAMSTEEVDYVYASAKKAQPAWRALSYIERAAYLHKVADILMRDKEKIGAILSKEVAKGYKSAVSEVVRTAEIINYAAEEGLRMEGEVLEGGSFEAASKKKIAVVRREPVGLVLAISPFNYPVNLAGSKIAPALIAGNVIAFKPPTQGSISGLLLAEAFAEAGLPAGVFNTITGRGSEIGDYIVEHQAVNFINFTGSTGIGERIGKMAGMRPIMLELGGKDSAIVLEDADLELTAKNIIAGAFGYSGQRCTAVKRVLVMESVADELVEKIREKVLALTIGNPEDDADITPLIDTKSADYVEGLINDANDKGATALTEIKREGNLICPILFDKVTTDMRLAWEEPFGPVLPIIRVTSVEEAIEISNKSEYGLQASIFTNDFPRAFGIAEQLEVGTVHINNKTQRGTDNFPFLGAKKSGAGIQGVKYSIEAMTTVKSVVFDIK

>d1ez0a\_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Vibrio harveyi}

TDNVFYATNAFTGEALPLAFPVHTEVEVNQAATAAAKVARDFRRLNNSKRASLLRTIASELEARSDDIIARAHLETALPEVRLTGEIARTANQLRLFADVVNSGSYHQAILDTPNPTRAPLPKPDIRRQQIALGPVAVFGASNFPLAFSAAGGDTASALAAGCPVIVKGHTAHPGTSQIVAECIEQALKQEQLPQAIFTLLQGNQRALGQALVSHPEIKAVGFTGSVGGGRALFNLAHERPEPIPFYGELGAINPTFIFPSAMRAKADLADQFVASMTMGCGQFCTKPGVVFALNTPETQAFIETAQSLIRQQSPSTLLTPGIRDSYQSQVVSRGSDDGIDVTFSQAESPCVASALFVTSSENWRKHPAWEEEIFGPQSLIVVCENVADMLSLSEMLAGSLTATIHATEEDYPQVSQLIPRLEEIAGRLVFNGWPTGVEVGYAMVHGGPYPASTHSASTSVGAEAIHRWLRPVAYQALPESLLPDSLKAENPLEIARAVDGKAA

>d1k75a\_ c.82.1.2 (A:) L-histidinol dehydrogenase HisD {Escherichia coli}

NTIIDWNSCTAEQQRQLLMRPAISASESITRTVNDILDNVKARGDEALREYSAKFDKTTVTALKVSAEEIAAASERLSDELKQAMAVAVKNIETFHTAQKLPPVDVETQPGVRCQQVTRPVASVGLYIPGGSAPLFSTVLMLATPASIAGCKKVVLCSPPPIADEILYAAQLCGVQDVFNVGGAQAIAALAFGTESVPKVDKIFGPGNAFVTEAKRQVSQRLDGAAIDMPAGPSEVLVIADSGATPDFVASDLLSQAEHGPDSQVILLTPAADMARRVAEAVERQLAELPRAETARQALNASRLIVTKDLAQCVEISNQYGPEHLIIQTRNARELVDSITSAGSVFLGDWSPESAGDYASGTNHVLPTYGYTATCSSLGLADFQKRMTVQELSKEGFSALASTIETLAAAERLTAHKNAVTLRVNALKEQA

>d1aco\_2 c.83.1.1 (2-528) Aconitase, first 3 domains {Cow (Bos taurus)}

RAKVAMSHFEPHEYIRYDLLEKNIDIVRKRLNRPLTLSEKIVYGHLDDPANQEIERGKTYLRLRPDRVAMQDATAQMAMLQFISSGLPKVAVPSTIHCDHLIEAQLGGEKDLRRAKDINQEVYNFLATAGAKYGVGFWRPGSGIIHQIILENYAYPGVLLIGTDSHTPNGGGLGGICIGVGGADAVDVMAGIPWELKCPKVIGVKLTGSLSGWTSPKDVILKVAGILTVKGGTGAIVEYHGPGVDSISCTGMATICNMGAEIGATTSVFPYNHRMKKYLSKTGRADIANLADEFKDHLVPDSGCHYDQLIEINLSELKPHINGPFTPDLAHPVAEVGSVAEKEGWPLDIRVGLIGSCTNSSYEDMGRSAAVAKQALAHGLKCKSQFTITPGSEQIRATIERDGYAQVLRDVGGIVLANACGPCIGQWDRKDIKKGEKNTIVTSYNRNFTGRNDANPETHAFVTSPEIVTALAIAGTLKFNPETDFLTGKDGKKFKLEAPDADELPRAEFDPGQDTYQHPPKDSSGQR

>d3pmga1 c.84.1.1 (A:1-190) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

VKIVTVKTKAYPDQKPGTSGLRKRVKVFQSSTNYAENFIQSIISTVEPAQRQEATLVVGGDGRFYMKEAIQLIVRIAAANGIGRLVIGQNGILSTPAVSCIIRKIKAIGGIILTASHNPGGPNGDFGIKFNISNGGPAPEAITDKIFQISKTIEEYAICPDLKVDLGVLGKQQFDLENKFKPFTVEIVDS

>d3pmga2 c.84.1.1 (A:191-303) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

VEAYATMLRNIFDFNALKELLSGPNRLKIRIDAMHGVVGPYVKKILCEELGAPANSAVNCVPLEDFGGHHPDPNLTYAADLVETMKSGEHDFGAAFDGDGDRNMILGKHGFFV

>d3pmga3 c.84.1.1 (A:304-420) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

NPSDSVAVIAANIFSIPYFQQTGVRGFARSMPTSGALDRVANATKIALYETPTGWKFFGNLMDASKLSLCGEESFGTGSDHIREKDGLWAVLAWLSILATRKQSVEDILKDHWHKFG

>d1kfia1 c.84.1.1 (A:3-205) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

QVIPAPRVQVTQPYAGQKPGTSGLRKKVSEATQPNYLENFVQSIFNTLRKDELKPKNVLFVGGDGRYFNRQAIFSIIRLAYANDISEVHVGQAGLMSTPASSHYIRKVNEEVGNCIGGIILTASHNPGGKEHGDFGIKFNVRTGAPAPEDFTDQIYTHTTKIKEYLTVDYEFEKHINLDQIGVYKFEGTRLEKSHFEVKVVDT

>d1kfia2 c.84.1.1 (A:206-323) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

VQDYTQLMQKLFDFDLLKGLFSNKDFSFRFDGMHGVAGPYAKHIFGTLLGCSKESLLNCDPSEDFGGGHPDPNLTYAHDLVELLDIHKKKDVGTVPQFGAACDGDADRNMILGRQFFV

>d1kfia3 c.84.1.1 (A:324-443) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

TPSDSLAVIAANANLIFKNGLLGAARSMPTSGALDKVAAKNGIKLFETPTGWKFFGNLMDAGLINLCGEESFGTGSNHIREKDGIWAVLAWLTILAHKNKNTDHFVTVEEIVTQYWQQFG

>d1k2yx1 c.84.1.1 (X:5-154) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

KAPTLPASIFRAYDIRGVVGDTLTAETAYWIGRAIGSESLARGEPCVAVGRDGRLSGPELVKQLIQGLVDCGCQVSDVGMVPTPVLYYAANVLEGKSGVMLTGAHNPPDYNGFKIVVAGETLANEQIQALRERIEKNDLASGVGSVEQVD

>d1k2yx2 c.84.1.1 (X:155-258) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

ILPRYFKQIRDDIAMAKPMKVVVDCGNGVAGVIAPQLIEALGCSVIPLYCEVDGNFPNHHPDPGKPENLKDLIAKVKAENADLGLAFDGDGDRVGVVTNTGTII

>d1k2yx3 c.84.1.1 (X:259-367) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

YPDRLLMLFAKDVVSRNPGADIIFDVKCTRRLIALISGYGGRPVMWKTGHSLIKKKMKETGALLAGEMSGHVFFKERWFGFDDGIYSAARLLEILSQDQRDSEHVFSAF

>d1k2yx4 c.84.1.1 (X:368-463) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

PSDISTPEINITVTEDSKFAIIEALQRDAQWGEGNITTLDGVRVDYPKGWGLVRASNTTPVLVLRFEADTEEELERIKTVFRNQLKAVDSSLPVPF

>d1fuia2 c.85.1.1 (A:1-355) L-fucose isomerase, N-terminal and second domains {Escherichia coli}

MKKISLPKIGIRPVIDGRRMGVRESLEEQTMNMAKATAALLTEKLRHACGAAVECVISDTCIAGMAEAAACEEKFSSQNVGLTITVTPCWCYGSETIDMDPTRPKAIWGFNGTERPGAVYLAAALAAHSQKGIPAFSIYGHDVQDADDTSIPADVEEKLLRFARAGLAVASMKGKSYLSLGGVSMGIAGSIVDHNFFESWLGMKVQAVDMTELRRRIDQKIYDEAELEMALAWADKNFRYGEDENNKQYQRNAEQSRAVLRESLLMAMCIRDMMQGNSKLADIGRVEESLGYNAIAAGFQGQRHWTDQYPNGDTAEAILNSSFDWNGVREPFVVATENDSLNGVAMLMGHQLTGT

>d1fw8a\_ c.86.1.1 (A:) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SKYSLAPVAKELQSLLGKDVTFLNDCVGPEVEAAVKASAPGSVILLENLRYHIEEEGSRKVDGQKVKASKEDVQKFRHELSSLADVYINDAFGTAHRAHSSMVGFDLPQRAAGFLLEKELKYFGKALENPTRPFLAILGGAKVADKIQLIDNLLDKVDSIIIGGGMAFTFKKVLENTEIGDSIFDKAGAEIVPKLMEKAKAKGVEVVLPVDFIIADAFSADANTKTVTDKEGIPAGWQGLDNGPESRKLFAATVAKAKTIVWNGPPGVFEFEKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATVAKKYGVTDKISHVSTGGGASLELLEGKELPGVAFLSEKKSLSSKLSVQDLDLKDKRVFIRVDFNVPLDGKKITSNQRIVAALPTIKYVLEHHPRYVVLASHLGRPNGERN

>d1qpg\_\_ c.86.1.1 (-) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SLSSKLSVQDLDLKDKRVFIRVDFNVPLDGKKITSNQRIVAALPTIKYVLEHHPRYVVLASHLGQPNGERNEKYSLAPVAKELQSLLGKDVTFLNDCVGPEVEAAVKASAPGSVILLENLRYHIEEEGSRKVDGQKVKASKEDVQKFRHELSSLADVYINDAFGTAHRAHSSMVGFDLPQRAAGFLLEKELKYFGKALENPTRPFLAILGGAKVADKIQLIDNLLDKVDSIIIGGGMAFTFKKVLENTEIGDSIFDKAGAEIVPKLMEKAKAKGVEVVLPVDFIIADAFSADANTKTVTDKEGIPAGWQGLDNGPESRKLFAATVAKAKTIVWNGPPGVFEFEKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATVAKKYGVTDKISHVSTGGGASLELLEGKELPGVAFLSEKK

>d1php\_\_ c.86.1.1 (-) Phosphoglycerate kinase {Bacillus stearothermophilus}

MNKKTIRDVDVRGKRVFCRVDFNVPMEQGAITDDTRIRAALPTIRYLIEHGAKVILASHLGRPKGKVVEELRLDAVAKRLGELLERPVAKTNEAVGDEVKAAVDRLNEGDVLLLENVRFYPGEEKNDPELAKAFAELADLYVNDAFGAAHRAHASTEGIAHYLPAVAGFLMEKELEVLGKALSNPDRPFTAIIGGAKVKDKIGVIDNLLEKVDNLIIGGGLAYTFVKALGHDVGKSLLEEDKIELAKSFMEKAKEKGVRFYMPVDVVVADRFANDANTKVVPIDAIPADWSALDIGPKTRELYRDVIRESKLVVWNGPMGVFEMDAFAHGTKAIAEALAEALDTYSVIGGGDSAAAVEKFGLADKMDHISTGGGASLEFMEGKQLPGVVALEDK

>d1vpe\_\_ c.86.1.1 (-) Phosphoglycerate kinase {Thermotoga maritima}

EKMTIRDVDLKGKRVIMRVDFNVPVKDGVVQDDTRIRAALPTIKYALEQGAKVILLSHLGRPKGEPSPEFSLAPVAKRLSELLGKEVKFVPAVVGDEVKKAVEELKEGEVLLLENTRFHPGETKNDPELAKFWASLADIHVNDAFGTAHRAHASNVGIAQFIPSVAGFLMEKEIKFLSKVTYNPEKPYVVVLGGAKVSDKIGVITNLMEKADRILIGGAMMFTFLKALGKEVGSSRVEEDKIDLAKELVEKAKEKGVEIVLPVDAVIAQKIEPGVEKKVVRIDDGIPEGWMGLDIGPETIELFKQKLSDAKTVVWNGPMGVFEIDDFAEGTKQVALAIAALTEKGAITVVGGGDSAAAVNKFGLEDKFSHVSTGGGASLEFLEGKELPGIASMRIKKA

>d16pk\_\_ c.86.1.1 (-) Phosphoglycerate kinase {Trypanosoma brucei}

EKKSINECDLKGKKVLIRVDFNVPVKNGKITNDYRIRSALPTLKKVLTEGGSCVLMSHLGRPKGIPMAQAGKIRSTGGVPGFQQKATLKPVAKRLSELLLRPVTFAPDCLNAADVVSKMSPGDVVLLENVRFYKEEGSKKAKDREAMAKILASYGDVYISDAFGTAHRDSATMTGIPKILGNGAAGYLMEKEISYFAKVLGNPPRPLVAIVGGAKVSDKIQLLDNMLQRIDYLLIGGAMAYTFLKAQGYSIGKSKCEESKLEFARSLLKKAEDRKVQVILPIDHVCHTEFKAVDSPLITEDQNIPEGHMALDIGPKTIEKYVQTIGKCKSAIWNGPMGVFEMVPYSKGTFAIAKAMGRGTHEHGLMSIIGGGDSASAAELSGEAKRMSHVSTGGGASLELLEGKTLPGVTVLDDK

>d1hdia\_ c.86.1.1 (A:) Phosphoglycerate kinase {Pig (Sus scrofa)}

NKLTLDKLNVKGKRVVMRVDFNVPMAAAQITNNARIKAAVPSIKFCLDDGAKSVVLMSHLGRPDGSPMPDKYSLQPVAAELKSALGKAVLFLKDCVGPAVEKACADPAAGSVILLENLRFHVEEEGKGKDASGNKAAGEPAKIKAFRASLSALGDVYVNDAFGTAHRAHSSMVGVNLPKKAGAFLMKKELNYFAAAAESPERPFLAILGGAKVADKIQLINNMLDKVNEMIIGGGMAFTFLKVLNNMEIGTSLFDEAGKKIVKNLMSKAAANGVKITLPVDFVTADKFDEQAKIGQATVASGIPAGWMGLDCGPKSSAKYSEAVARAKQIVWNGPVGVFEWEAFAQGTKALMDEVVKATSRGCITIIGGGDTATCCAKWNTEDNVSHVSTGGGASLELLEGKVLPGVDALSNV

>d1jixa\_ c.87.1.1 (A:) beta-Glucosyltransferase (DNA-modifying) {Bacteriophage T4}

MKIAIINMGNNVINFKTVPSSETIYLFKVISEMGLNVDIISLKNGVYTKSFDEVDVNDYDRLIVVNSSINFFGGKPNLAILSAQKFMAKYKSKIYYLFTDIRLPFSQSWPNVKNRPWAYLYTEEELLIKSPIKVISQGINLDIAKAAHKKVDNVIEFEYFPIEQYKIHMNDFQLSKPTKKTLDVIYGGSFRSGQRESKMVEFLFDTGLNIEFFGNAREKQFKNPKYPWTKAPVFTGKIPMNMVSEKNSQAIAALIIGDKNYNDNFITLRVWETMASDAVMLIDEEFDTKHRIINDARFYVNNRAELIDRVNELKHSDVLRKEMLSIQHDILNKTRAKKAEWQDAFKKAIDL

>d1f0ka\_ c.87.1.2 (A:) Peptidoglycan biosynthesys glycosyltransferase MurG {Escherichia coli}

KRLMVMAGGTGGHVFPGLAVAHHLMAQGWQVRWLGTADRMEADLVPKHGIEIDFIRISGLRGKGIKALIAAPLRIFNAWRQARAIMKAYKPDVVLGMGGYVSGPGGLAAWSLGIPVVLHEQNGIAGLTNKWLAKIATKVMQAFPGAFPNAEVVGNPVRTDVLALPLPQQRLAGREGPVRVLVVGGSQGARILNQTMPQVAAKLGDSVTIWHQSGKGSQQSVEQAYAEAGQPQHKVTEFIDDMAAAYAWADVVVCRSGALTVSEIAAAGLPALFVPFQHKDRQQYWNALPLEKAGAAKIIEQPQLSVDAVANTLAGWSRETLLTMAERARAASIPDATERVANEVSRVARAL

>d1f6da\_ c.87.1.3 (A:) UDP-N-acetylglucosamine 2-epimerase {Escherichia coli}

MKVLTVFGTRPEAIKMAPLVHALAKDPFFEAKVCVTAQHREMLDQVLKLFSIVPDYDLNIMQPGQGLTEITCRILEGLKPILAEFKPDVVLVHGDTTTTLATSLAAFYQRIPVGHVEAGLRTGDLYSPWPEEANRTLTGHLAMYHFSPTETSRQNLLRENVADSRIFITGNTVIDALLWVRDQVMSSDKLRSELAANYPFIDPDKKMILVTGHRRESFGRGFEEICHALADIATTHQDIQIVYPVHLNPNVREPVNRILGHVKNVILIDPQEYLPFVWLMNHAWLILTDSGGIQEEAPSLGKPVLVMRDTTERPEAVTAGTVRLVGTDKQRIVEEVTRLLKDENEYQAMSRAHNPYGDGQACSRILEALKNNRISL

>d1iira\_ c.87.1.5 (A:) UDP-glucosyltransferase GtfB {Amycolatopsis orientalis}

MRVLLATCGSRGDTEPLVALAVRVRDLGADVRMCAPPDCAERLAEVGVPHVPVGPSARAPIQRAKPLTAEDVRRFTTEAIATQFDEIPAAAEGCAAVVTTGLLAAAIGVRSVAEKLGIPYFYAFHCPSYVPSPYYPPPPLGEPSTQDTIDIPAQWERNNQSAYQRYGGLLNSHRDAIGLPPVEDIFTFGYTDHPWVAADPVLAPLQPTDLDAVQTGAWILPDERPLSPELAAFLDAGPPPVYLGFGSLGAPADAVRVAIDAIRAHGRRVILSRGWADLVLPDDGADCFAIGEVNHQVLFGRVAAVIHHGGAGTTHVAARAGAPQILLPQMADQPYYAGRVAELGVGVAHDGPIPTFDSLSAALATALTPETHARATAVAGTIRTDGAAVAARLLLDAVSRE

>d1em6a\_ c.87.1.4 (A:) Glycogen phosphorylase {Human (Homo sapiens)}

ENVAELKKSFNRHLHFTLVKDRNVATTRDYYFALAHTVRDHLVGRWIRTQQHYYDKCPKRVYYLSLEFYMGRTLQNTMINLGLQNACDEAIYQLGLDIEELEEIEEDAGLGNGGLGRLAACFLDSMATLGLAAYGYGIRYEYGIFNQKIRDGWQVEEADDWLRYGNPWEKSRPEFMLPVHFYGKVEHTNTGTKWIDTQVVLALPYDTPVPGYMNNTVNTMRLWSARAPNDFNLRDFNVGDYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQEYFVVAATLQDIIRRFKASKFGSTRGAGTVFDAFPDQVAIQLNDTHPALAIPELMRIFVDIEKLPWSKAWELTQKTFAYTNHTVLPEALERWPVDLVEKLLPRHLEIIYEINQKHLDRIVALFPKDVDRLRRMSLIEEEGSKRINMAHLCIVGSHAVNGVAKIHSDIVKTKVFKDFSELEPDKFQNKTNGITPRRWLLLCNPGLAELIAEKIGEDYVKDLSQLTKLHSFLGDDVFLRELAKVKQENKLKFSQFLETEYKVKINPSSMFDVQVKRIHEYKRQLLNCLHVITMYNRIKKDPKKLFVPRTVIIGGKAAPGYHMAKMIIKLITSVADVVNNDPMVGSKLKVIFLENYRVSLAEKVIPATDLSEQISTAGTEASGTGNMKFMLNGALTIGTMDGANVEMAEEAGEENLFIFGMRIDDVAALDKKGYEAKEYYEALPELKLVIDQIDNGFFSPKQPDLFKDIINMLFYHDRFKVFADYEAYVKCQDKVSQLYMNPKAWNTMVLKNIAASGKFSSDRTIKEYAQNIWNVEPS

>d1a8i\_\_ c.87.1.4 (-) Glycogen phosphorylase {Rabbit (Oryctolagus cuniculus)}

QEKRKQISVRGLAGVENVTELKKNFNRHLHFTLVKDRNVATPRDYYFALAHTVRDHLVGRWIRTQQHYYEKDPKRIYYLSLEFYMGRTLQNTMVNLALENACDEATYQLGLDMEELEEIEEDAGLGNGGLGRLAACFLDSMATLGLAAYGYGIRYEFGIFNQKICGGWQMEEADDWLRYGNPWEKARPEFTLPVHFYGRVEHTSQGAKWVDTQVVLAMPYDTPVPGYRNNVVNTMRLWSAKAPNDFNLKDFNVGGYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQEYFVVAATLQDIIRRFKSSKFGCRDPVRTNFDAFPDKVAIQLNDTHPSLAIPELMRVLVDLERLDWDKAWEVTVKTCAYTNHTVIPEALERWPVHLLETLLPRHLQIIYEINQRFLNRVAAAFPGDVDRLRRMSLVEEGAVKRINMAHLCIAGSHAVNGVARIHSEILKKTIFKDFYELEPHKFQNKTNGITPRRWLVLCNPGLAEIIAERIGEEYISDLDQLRKLLSYVDDEAFIRDVAKVKQENKLKFAAYLEREYKVHINPNSLFDVQVKRIHEYKRQLLNCLHVITLYNRIKKEPNKFVVPRTVMIGGKAAPGYHMAKMIIKLITAIGDVVNHDPVVGDRLRVIFLENYRVSLAEKVIPAADLSEQISTAGTEASGTGNMKFMLNGALTIGTMDGANVEMAEEAGEENFFIFGMRVEDVDRLDQRGYNAQEYYDRIPELRQIIEQLSSGFFSPKQPDLFKDIVNMLMHHDRFKVFADYEEYVKCQERVSALYKNPREWTRMVIRNIATSGKFSSDRTIAQYAREIWGVEPSRQRLP

>d1ygpa\_ c.87.1.4 (A:) Glycogen phosphorylase {Baker's yeast (Saccharomyces cerevisiae)}

TRRLTGFLPQEIKSIDTMIPLLSRALWNKHQVKKFNKAEDFQDRFIDHVETTLARSLYNCDDMVAYEAASMSIRDNLVIDWNKTQQKFTTRDPKRVYYLSLEFLMGRALDNALINMKIEDPEDPAASKGKPREMIKGALDELGFKLEDVLDQEPDAGLGNGGLGRLAACFVDSMATEGIPAWGYGLRYEYGIFAQKIIDGYQVETPDYWLNSGNPWEIERNEVQIPVTFYGYVDRPEGGKTTLSASQWIGGERVLAVAYDFPVPGFKTSNVNNLRLWQARPTTEFDLNKFNNGDYKNSVAQQQRAESITAVLYPNDNFAQGKELRLKQQYFWCAASLHDILRRFKKSKRPWTEFPDQVAIQLNDTHPTLAIVELQRVLVDLEKLDWHEAWDIVTKTFAYTNHTVMQEALEKWPRRLFGHLLPRHLEIIYDINWFFLEDVAKKFPKDVDLLSRISIIEENSPERQIRMAFLAIVGSHKVNGVVELHSELIKTTIFKDFIKFYGPSKFVNVTNGITPRRWLKQANPSLAKLISETLNDPTEEYLLDMAKLTQLEKYVEDKEFLKKWNQVKLNNKIRLVDLIKKENDGVDIINREYLDDTLFDMQVKRIHEYKRQQLNVFGIIYRYLAMKNMLKNGASIEEVARKYPRKVSIFGGKSAPGYYMAKLIIKLINCVADIVNNDESIEHLLKVVFVADYNVSKAEIIIPASDLSEHISTAGTEASGTSNMKFVMNGGLIIGTVDGANVEITREIGEDNVFLFGNLSENVEELRYNHQYHPQDLPSSLDSVLSYIESGQFSPENPNEFKPLVDSIKYHGDYYLVSDDFESYLATHELVDQEFHNQRSEWLKKSVLSLANVGFFSSDRCIEEYSDTIWNVEPVT

>d1qm5a\_ c.87.1.4 (A:) Maltodextrin phosphorylase (MALP) {Escherichia coli}

SQPIFNDKQFQEALSRQWQRYGLNSAAEMTPRQWWLAVSEALAEMLRAQPFAKPVANQRHVNYISMEFLIGRLTGNNLLNLGWYQDVQDSLKAYDINLTDLLEEEIDPALGNGGLGRLAACFLDSMATVGQSATGYGLNYQYGLFRQSFVDGKQVEAPDDWHRSNYPWFRHNEALDVQVGIGGKVTKDGRWEPEFTITGQAWDLPVVGYRNGVAQPLRLWQATHAHPFDLTKFNDGDFLRAEQQGINAEKLTKVLYPNDNHTAGKKLRLMQQYFQCACSVADILRRHHLAGRKLHELADYEVIQLNDTHPTIAIPELLRVLIDEHQMSWDDAWAITSKTFAYTNHTLMPEALERWDVKLVKGLLPRHMQIINEINTRFKTLVEKTWPGDEKVWAKLAVVHDKQVHMANLCVVGGFAVNGVAALHSDLVVKDLFPEYHQLWPNKFHNVTNGITPRRWIKQCNPALAALLDKSLQKEWANDLDQLINLEKFADDAKFRDQYREIKQANKVRLAEFVKVRTGIEINPQAIFDIQIKRLHEYKRQHLNLLHILALYKEIRENPQADRVPRVFLFGAKAAPGYYLAKNIIFAINKVADVINNDPLVGDKLKVVFLPDYCVSAAEKLIPAADISEQISTAGKEASGTGNMKLALNGALTVGTLDGANVEIAEKVGEENIFIFGHTVEQVKAILAKGYDPVKWRKKDKVLDAVLKELESGKYSDGDKHAFDQMLHSIGKQGGDPYLVMADFAAYVEAQKQVDVLYRDQEAWTRAAILNTARCGMFSSDRSIRDYQARIWQAKR

>d4ecaa\_ c.88.1.1 (A:) Asparaginase type II {Escherichia coli}

LPNITILATGGTIAGGGDSATKSNYTVGKVGVENLVNAVPQLKDIANVKGEQVVNIGSQDMNDNVWLTLAKKINTDCDKTDGFVITHGVDTMEETAYFLDLTVKCDKPVVMVGAMRPSTSMSADGPFNLYNAVVTAADKASANRGVLVVMNDTVLDGRDVTKTNTTDVATFKSVNYGPLGYIHNGKIDYQRTPARKHTSDTPFDVSKLNELPKVGIVYNYANASDLPAKALVDAGYDGIVSAGVGNGNLYKSVFDTLATAAKTGTAVVRSSRVPTGATTQDAEVDDAKYGFVASGTLNPQKARVLLQLALTQTKDPQQIQQIFNQY

>d1wsaa\_ c.88.1.1 (A:) Asparaginase type II {Wolinella succinogenes}

KPQVTILATGGTIAGSGESSVKSSYSAGAVTVDKLLAAVPAINDLATIKGEQISSIGSQEMTGKVWLKLAKRVNELLAQKETEAVIITHGTDTMEETAFFLNLTVKSQKPVVLVGAMRPGSSMSADGPMNLYNAVNVAINKASTNKGVVIVMNDEIHAAREATKLNTTAVNAFASPNTGKIGTVYYGKVEYFTQSVRPHTLASEFDISKIEELPRVDILYAHPDDTDVLVNAALQAGAKGIIHAGMGNGNPFPLTQNALEKAAKSGVVVARSSRVGSGSTTQEAEVDDKKLGFVATESLNPQKARVLLMLALTKTSDREAIQKIFSTY

>d1jsra\_ c.88.1.1 (A:) Asparaginase type II {Erwinia chrysanthemi}

LPNIVILATGGTIAGSAATGTQTTGYKAGALGVDTLINAVPEVKKLANVKGEQFSNMASENMTGDVVLKLSQRVNELLARDDVDGVVITHGTDTVEESAYFLHLTVKSDKPVVFVAAMRPATAISADGPMNLLEAVRVAGDKQSRGRGVMVVINDRIGSARYITKTNASTLDTFRANEEGYLGVIIGNRIYYQNRIDKLHTTRSVFDVRGLTSLPKVDILYGYQDDPEYLYDAAIQHGVKGIVYAGMGAGSVSVRGIAGMRKALEKGVVVMRSTRTGNGIVPPDEELPGLVSDSLNPAHARILLMLALTRTSDPKVIQEYFHTY

>d1agx\_\_ c.88.1.1 (-) Glutaminase-asparaginase {Acinetobacter glutaminasificans}

KNNVVIVATGGTIAGAGASSTNSATYSAAKVPVDALIKAVPQVNDLANITGIQALQVASESITDKELLSLARQVNDLVKKPSVNGVVITHGTDTMEETAFFLNLVVHTDKPIVLVGSMRPSTALSADGPLNLYSAVALASSNEAKNKGVMVLMNDSIFAARDVTKGINIHTHAFVSQWGALGTLVEGKPYWFRSSVKKHTNNSEFNIEKIQGDALPGVQIVYGSDNMMPDAYQAFAKAGVKAIIHAGTGNGSMANYLVPEVRKLHDEQGLQIVRSSRVAQGFVLRNAEQPDDKYGWIAAHDLNPQKARLLMALALTKTNDAKEIQNMFWNY

>d4pgaa\_ c.88.1.1 (A:) Glutaminase-asparaginase {Pseudomonas sp., 7A}

KLANVVILATGGTIAGAGASAANSATYQAAKVGVDKLIAGVPELADLANVRGEQVMQIASESITNDDLLKLGKRVAELADSNDVDGIVITHGTDTLEETAYFLNLVQKTDKPIVVVGSMRPGTAMSADGMLNLYNAVAVASNKDSRGKGVLVTMNDEIQSGRDVSKSINIKTEAFKSAWGPLGMVVEGKSYWFRLPAKRHTVNSEFDIKQISSLPQVDIAYSYGNVTDTAYKALAQNGAKALIHAGTGNGSVSSRVVPALQQLRKNGTQIIRSSHVNQGGFVLRNAEQPDDKNDWVVAHDLNPEKARILAMVAMTKTQDSKELQRIFWEY

>d1pfka\_ c.89.1.1 (A:) Phosphofructokinase {Escherichia coli}

MIKKIGVLTSGGDAPGMNAAIRGVVRSALTEGLEVMGIYDGYLGLYEDRMVQLDRYSVSDMINRGGTFLGSARFPEFRDENIRAVAIENLKKRGIDALVVIGGDGSYMGAMRLTEMGFPCIGLPGTIDNDIKGTDYTIGFFTALSTVVEAIDRLRDTSSSHQRISVVEVMGRYCGDLTLAAAIAGGCEFVVVPEVEFSREDLVNEIKAGIAKGKKHAIVAITEHMCDVDELAHFIEKETGRETRATVLGHIQRGGSPVPYDRILASRMGAYAIDLLLAGYGGRCVGIQNEQLVHHDIIDAIENMKRPFKGDWLDCAKKLY

>d3pfk\_\_ c.89.1.1 (-) Phosphofructokinase {Bacillus stearothermophilus}

MKRIGVLTSGGDSPGMNAAIRSVVRKAIYHGVEVYGVYHGYAGLIAGNIKKLEVGDVGDIIHRGGTILYTARCPEFKTEEGQKKGIEQLKKHGIQGLVVIGGDGSYQGAKKLTEHGFPCVGVPGTIDNDIPGTDFTIGFDTALNTVIDAIDKIRDTATSHERTYVIEVMGRHAGDIALWSGLAGGAETILIPEADYDMNDVIARLKRGHERGKKHSIIIVAEGVGSGVDFGRQIQEATGFETRVTVLGHVQRGGSPTAFDRVLASRLGARAVELLLEGKGGRCVGIQNNQLVDHDIAEALANKHTIDQRMYALSKELSI

>d1cbf\_\_ c.90.1.1 (-) Cobalt precorrin-4 methyltransferase CbiF {Bacillus megaterium}

GLVPRGSHMKLYIIGAGPGDPDLITVKGLKLLQQADVVLYADSLVSQDLIAKSKPGAEVLKTAGMHLEEMVGTMLDRMREGKMVVRVHTGDPAMYGAIMEQMVLLKREGVDIEIVPGVTSVFAAAAAAEAELTIPDLTQTVILTRAEGRTPVPEFEKLTDLAKHKCTIALFLSSTLTKKVMKEFINAGWSEDTPVVVVYKATWPDEKIVRTTVKDLDDAMRTNGIRKQAMILAGWALDP

>d1i74a\_ c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase (family II) {Streptococcus mutans}

SKILVFGHQNPDSDAIGSSMAYAYLKRQLGVDAQAVALGNPNEETAFVLDYFGIQAPPVVKSAQAEGAKQVILTDHNEFQQSIADIREVEVVEVVDHHRVANFETANPLYMRLEPVGSASSIVYRLYKENGVAIPKEIAGVMLSGLISDTLLLKSPTTHASDPAVAEDLAKIAGVDLQEYGLAMLKAGTNLASKTAAQLVDIDAKTFELNGSQVRVAQVNTVDINEVLERQNEIEEAIKASQAANGYSDFVLMITDILNSNSEILALGNNTDKVEAAFNFTLKNNHAFLAGAVSRKKQVVPQLTESFNG

>d1k20a\_ c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase (family II) {Streptococcus gordonii}

SKILVFGHQNPDSDAIGSSYAFAYLAREAYGLDTEAVALGEPNEETAFVLDYFGVAAPRVITSAKAEGAEQVILTDHNEFQQSVADIAEVEVYGVVDHHRVANFETANPLYMRLEPVGSASSIVYRMFKEHSVAVSKEIAGLMLSGLISDTLLLKSPTTHPTDKAIAPELAELAGVNLEEYGLAMLKAGTNLASKSAEELIDIDAKTFELNGNNVRVAQVNTVDIAEVLERQAEIEAAIEKAIADNGYSDFVLMITDIINSNSEILAIGSNMDKVEAAFNFVLENNHAFLAGAVSRKKQVVPQLTESFNA

>d1k23a\_ c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase (family II) {Bacillus subtilis}

MEKILIFGHQNPDTDTICSAIAYADLKNKLGFNAEPVRLGQVNGETQYALDYFKQESPRLVETAANEVNGVILVDHNERQQSIKDIEEVQVLEVIDHHRIANFETAEPLYYRAEPVGCTATILNKMYKENNVKIEKEIAGLMLSAIISDSLLFKSPTCTDQDVAAAKELAEIAGVDAEEYGLNMLKAGADLSKKTVEELISLDAKEFTLGSKKVEIAQVNTVDIEDVKKRQAELEAVISKVVAEKNLDLFLLVITDILENDSLALAIGNEAAKVEKAFNVTLENNTALLKGVVSRKKQVVPVLTDAM

>d1ayl\_1 c.91.1.1 (228-540) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Escherichia coli}

IASMHCSANVGEKGDVAVFFGLSGTGKTTLSTDPKRRLIGDDEHGWDDDGVFNFEGGCYAKTIKLSKEAEPEIYNAIRRDALLENVTVREDGTIDFDDGSKTENTRVSYPIYHIDNIVKPVSKAGHATKVIFLTADAFGVLPPVSRLTADQTQYHFLSGFTAKLAGTERGITEPTPTFSACFGAAFLSLHPTQYAEVLVKRMQAAGAQAYLVNTGWNGTGKRISIKDTRAIIDAILNGSLDNAETFTLPMFNLAIPTELPGVDTKILDPRNTYASPEQWQEKAETLAKLFIDNFDKYTDTPAGAALVAAGPKL

>d1ii2a1 c.91.1.1 (A:201-523) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Trypanosoma cruzi}

HLCMHASANVGKQGDVTVFFGLSGTGKTTLSADPHRNLIGDDEHVWTDRGVFNIEGGCYAKAIGLNPKTEKDIYDAVRFGAVAENCVLDKRTGEIDFYDESICKNTRVAYPLSHIEGALSKAIAGHPKNVIFLTNDAFGVMPPVARLTSAQAMFWFVMGYTANVPGVEAGGTRTARPIFSSCFGGPFLVRHATFYGEQLAEKMQKHNSRVWLLNTGYAGGRADRGAKRMPLRVTRAIIDAIHDGTLDRTEYEEYPGWGLHIPKYVAKVPEHLLNPRKAWKDVRQFNETSKELVAMFQESFSARFAAKASQEMKSAVPRYVEFA

>d1khba1 c.91.1.1 (A:260-622) Cytosolic phosphoenolpyruvate carboxykinase (GTP-hydrolysing) {Human (Homo sapiens)}

WLAEHMLVLGITNPEGEKKYLAAAFPSACGKTNLAMMNPSLPGWKVECVGDDIAWMKFDAQGHLRAINPENGFFGVAPGTSVKTNPNAIKTIQKNTIFTNVAETSDGGVYWEGIDEPLASGVTITSWKNKEWSSEDGEPCAHPNSRFCTPASQCPIIDAAWESPEGVPIEGIIFGGRRPAGVPLVYEALSWQHGVFVGAAMRSEATAAAEHKGKIIMHDPFAMRPFFGYNFGKYLAHWLSMAQHPAAKLPKIFHVNWFRKDKEGKFLWPGFGENSRVLEWMFNRIDGKASTKLTPIGYIPKEDALNLKGLGHINMMELFSISKEFWDKEVEDIEKYLVDQVNADLPCEIEREILALKQRISQM

>d1jb1a\_ c.91.1.2 (A:) HPr kinase HprK C-terminal domain {Lactobacillus casei}

ERRSMHGVLVDIYGLGVLITGDSGVGKSETALELVQRGHRLIADDRVDVYQQDEQTIVGAAPPILSHLLEIRGLGIIDVMNLFGAGAVREDTTISLIVHLENWTPDKTFDRLGSGEQTQLIFDVPVPKITVPVKVGRNLAIIIEVAAMNFRAKSMGYDATKTFEKNLNHLIEH

>d1ayl\_2 c.109.1.1 (1-227) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Escherichia coli}

MRVNNGLTPQELEAYGISDVHDIVYNPSYDLLYQEELDPSLTGYERGVLTNLGAVAVDTGIFTGRSPKDKYIVRDDTTRDTFWWADKGKGKNDNKPLSPETWQHLKGLVTRQLSGKRLFVVDAFCGANPDTRLSVRFITEVAWQAHFVKNMFIRPSDEELAGFKPDFIVMNGAKCTNPQWKEQGLNSENFVAFNLTERMQLIGGTWYGGEMKKGMFSMMNYLLPLKG

>d1ii2a2 c.109.1.1 (A:2-200) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Trypanosoma cruzi}

PPTIHRNLLSPELVQWALKIEKDSRLTARGALAVMSYAKTGRSPLDKRIVDTDDVRENVDWGKVNMKLSEESFARVRKIAKEFLDTREHLFVVDCFAGHDERYRLKVRVFTTRPYHALFMRDMLIVPTPEELATFGEPDYVIYNAGECKADPSIPGLTSTTCVALNFKTREQVILGTEYAGEMKKGILTVMFELMPQMN

>d1khba2 c.109.1.1 (A:10-259) Cytosolic phosphoenolpyruvate carboxykinase (GTP-hydrolysing) {Human (Homo sapiens)}

NLSAKVVQGSLDSLPQAVREFLENNAELCQPDHIHICDGSEEENGRLLGQMEEEGILRRLKKYDNCWLALTDPRDVARIESKTVIVTQEQRDTVPIPKTGLSQLGRWMSEEDFEKAFNARFPGCMKGRTMYVIPFSMGPLGSPLSKIGIELTDSPYVVASMRIMTRMGTPVLEALGDGEFVKCLHSVGCPLPLQKPLVNNWPCNPELTLIAHLPDRREIISFGSGYGGNSLLGKKCFALRMASRLAKEEG

>d1doza\_ c.92.1.1 (A:) Ferrochelatase {Bacillus subtilis}

SRKKMGLLVMAYGTPYKEEDIERYYTHIRRGRKPEPEMLQDLKDRYEAIGGISPLAQITEQQAHNLEQHLNEIQDEITFKAYIGLKHIEPFIEDAVAEMHKDGITEAVSIVLAPHFSTFSVQSYNKRAKEEAEKLGGLTITSVESWYDEPKFVTYWVDRVKETYASMPEDERENAMLIVSAHSLPEKIKEFGDPYPDQLHESAKLIAEGAGVSEYAVGWQSEGNTPDPWLGPDVQDLTRDLFEQKGYQAFVYVPVGFVADHLEVLYDNDYECKVVTDDIGASYYRPEMPNAKPEFIDALATVVLKKLGR

>d1hrka\_ c.92.1.1 (A:) Ferrochelatase {Human (Homo sapiens)}

RKPKTGILMLNMGGPETLGDVHDFLLRLFLDRDLMTLPIQNKLAPFIAKRLTPKIQEQYRRIGGGSPIKIWTSKQGEGMVKLLDELSPNTAPHKYYIGFRYVHPLTEEAIEEMERDGLERAIAFTQYPQYSCSTTGSSLNAIYRYYNQVGRKPTMKWSTIDRWPTHHLLIQCFADHILKELDHFPLEKRSEVVILFSAHSLPMSVVNRGDPYPQEVSATVQKVMERLEYCNPYRLVWQSKVGPMPWLGPQTDESIKGLCERGRKNILLVPIAFTSDHIETLYELDIEYSQVLAKECGVENIRRAESLNGNPLFSKALADLVHSHIQSNELCSKQLTLSCPLCVNPVCRETKSFFTSQQL

>d1qgoa\_ c.92.1.2 (A:) Cobalt chelatase CbiK {Salmonella typhimurium}

KKALLVVSFGTSYHDTCEKNIVACERDLAASCPDRDLFRAFTSGMIIRKLRQRDGIDIDTPLQALQKLAAQGYQDVAIQSLHIINGDEYEKIVREVQLLRPLFTRLTLGVPLLSSHNDYVQLMQALRQQMPSLRQTEKVVFMGHGASHHAFAAYACLDHMMTAQRFPARVGAVESYPEVDILIDSLRDEGVTGVHLMPLMLVAGDHAINDMASDDGDSWKMRFNAAGIPATPWLSGLGENPAIRAMFVAHLHQALNM

>d1efdn\_ c.92.2.1 (N:) Periplasmic ferric siderophore binding protein FhuD {Escherichia coli}

GIDPNRIVALEWLPVELLLALGIVPYGVADTINYRLWVSEPPLPDSVIDVGLRTEPNLELLTEMKPSFMVWSAGYGPSPEMLARIAPGRGFNFSDGKQPLAMARKSLTEMADLLNLQSAAETHLAQYEDFIRSMKPRFVKRGARPLLLTTLIDPRHMLVFGPNSLFQEILDEYGIPNAWQGETNFWGSTAVSIDRLAAYKDVDVLCFDHDNSKDMDALMATPLWQAMPFVRAGRFQRVPAVWFYGATLSAMHFVRVLDNAIG

>d1toaa\_ c.92.2.2 (A:) Periplasmic zinc binding protein TroA {Treponema pallidum}

GKPLVVTTIGMIADAVKNIAQGDVHLKGLMGPGVDPHLYTATAGDVEWLGNADLILYNGLHLETKMGEVFSKLRGSRLVVAVSETIPVSQRLSLEEAEFDPHVWFDVKLWSYSVKAVYESLCKLLPGKTREFTQRYQAYQQQLDKLDAYVRRKAQSLPAERRVLVTAHDAFGYFSRAYGFEVKGLQGVSTASEASAHDMQELAAFIAQRKLPAIFIESSIPHKNVEALRDAVQARGHVVQIGGELFSDAMGDAGTSEGTYVGMVTHNIDTIVAALAR

>d1psza\_ c.92.2.2 (A:) Pneumococcal surface antigen PssA {Pneumococcus (Streptococcus pneumoniae)}

KKDTTSGQKLKVVATNSIIADITKNIAGDKIDLHSIVPIGQDPHEYEPLPEDVKKTSEADLIFYNGINLETGGNAWFTKLVENAKKTENKDYFAVSDGVDVIYLEGQNEKGKEDPHAWLNLENGIIFAKNIAKQLSAKDPNNKEFYEKNLKEYTDKLDKLDKESKDKFNKIPAEKKLIVTSEGAFKYFSKAYGVPSAYIWEINTEEEGTPEQIKTLVEKLRQTKVPSLFVESSVDDRPMKTVSQDTNIPIYAQIFTDSIAEQGKEGDSYYSMMKYNLDKIAEGLAK

>d1mioa\_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}

SENLKDEILEKYIPKTKKTRSGHIVIKTEETPNPEIVANTRTVPGIITARGCAYAGCKGVVMGPIKDMVHITHGPIGCSFYTWGGRRFKSKPENGTGLNFNEYVFSTDMQESDIVFGGVNKLKDAIHEAYEMFHPAAIGVYATCPVGLIGDDILAVAATASKEIGIPVHAFSCEGYKGVSQSAGHHIANNTVMTDIIGKGNKEQKKYSINVLGEYNIGGDAWEMDRVLEKIGYHVNATLTGDATYEKVQNADKADLNLVQCHRSINYIAEMMETKYGIPWIKCNFIGVDGIVETLRDMAKCFDDPELTKRTEEVIAEEIAAIQDDLDYFKEKLQGKTACLYVGGSRSHTYMNMLKSFGVDSLVAGFEFAHRDDYEGREVIPTIKIDADSKNIPEITVTPDEQKYRVVIPEDKVEELKKAGVPLSSYGGMMKEMHDGTILIDDMNHHDMEVVLEKLKPDMFFAGIKEKFVIQKGGVLSKQLHSYDYNGPYAGFRGVVNFGHELVNGIYTPAWKMITPPWKKASSES

>d1miob\_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}

LDATPKEIVERKALRINPAKTCQPVGAMYAALGIHNCLPHSHGSQGCCSYHRTVLSRHFKEPAMASTSSFTEGASVFGGGSNIKTAVKNIFSLYNPDIIAVHTTCLSETLGDDLPTYISQMEDAGSIPEGKLVIHTNTPSYVGSHVTGFANMVQGIVNYLSENTGAKNGKINVIPGFVGPADMREIKRLFEAMDIPYIMFPDTSGVLDGPTTGEYKMYPEGGTKIEDLKDTGNSDLTLSLGSYASDLGAKTLEKKCKVPFKTLRTPIGVSATDEFIMALSEATGKEVPASIEEERGQLIDLMIDAQQYLQGKKVALLGDPDEIIALSKFIIELGAIPKYVVTGTPGMKFQKEIDAMLAEAGIEGSKVKVEGDFFDVHQWIKNEGVDLLISNTYGKFIAREENIPFVRFGFPIMDRYGHYYNPKVGYKGAIRLVEEITNVILDKIERECTEEDFEVVR

>d2mina\_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}

SREEVESLIQEVLEVYPEKARKDRNKHLAVNDPAVTQSKKCIISNKKSQPGLMTIRGCAYAGSKGVVWGPIKDMIHISHGPVGCGQYSRAGRRNYYIGTTGVNAFVTMNFTSDFQEKDIVFGGDKKLAKLIDEVETLFPLNKGISVQSECPIGLIGDDIESVSKVKGAELSKTIVPVRCEGFRGVSQSLGHHIANDAVRDWVLGKRDEDTTFASTPYDVAIIGDYNIGGDAWSSRILLEEMGLRCVAQWSGDGSISEIELTPKVKLNLVHCYRSMNYISRHMEEKYGIPWMEYNFFGPTKTIESLRAIAAKFDESIQKKCEEVIAKYKPEWEAVVAKYRPRLEGKRVMLYIGGLRPRHVIGAYEDLGMEVVGTGYEFAHNDDYDRTMKEMGDSTLLYDDVTGYEFEEFVKRIKPDLIGSGIKEKFIFQKMGIPFREMHSWDYSGPYHGFDGFAIFARDMDMTLNNPCWKKLQAPWE

>d2minb\_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}

SQQVDKIKASYPLFLDQDYKDMLAKKRDGFEEKYPQDKIDEVFQWTTTKEYQELNFQREALTVNPAKACQPLGAVLCALGFEKTMPYVHGSQGCVAYFRSYFNRHFREPVSCVSDSMTEDAAVFGGQQNMKDGLQNCKATYKPDMIAVSTTCMAEVIGDDLNAFINNSKKEGFIPDEFPVPFAHTPSFVGSHVTGWDNMFEGIARYFTLKSMDDKVVGSNKKINIVPGFETYLGNFRVIKRMLSEMGVGYSLLSDPEEVLDTPADGQFRMYAGGTTQEEMKDAPNALNTVLLQPWHLEKTKKFVEGTWKHEVPKLNIPMGLDWTDEFLMKVSEISGQPIPASLTKERGRLVDMMTDSHTWLHGKRFALWGDPDFVMGLVKFLLELGCEPVHILCHNGNKRWKKAVDAILAASPYGKNATVYIGKDLWHLRSLVFTDKPDFMIGNSYGKFIQRDTLHKGKEFEVPLIRIGFPIFDRHHLHRSTTLGYEGAMQILTTLVNSILERLDEETRGMQATDYNHDLVR

>d1qgua\_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Klebsiella pneumoniae}

TNATGERNLALIQEVLEVFPETARKERRKHMMVSDPKMKSVGKCIISNRKSQPGVMTVRGCAYAGSKGVVFGPIKDMAHISHGPVGCGQYSRAGRRNYYTGVSGVDSFGTLNFTSDFQERDIVFGGDKKLSKLIEEMELLFPLTKGITIQSECPVGLIGDDISAVANASSKALDKPVIPVRCEGFRGVSQSLGHHIANDVVRDWILNNREGQPFETTPYDVAIIGDYNIGGDAWASRILLEEMGLRVVAQWSGDGTLVEMENTPFVKLNLVHCYRSMNYIARHMEEKHQIPWMEYNFFGPTKIAESLRKIADQFDDTIRANAEAVIARYEGQMAAIIAKYRPRLEGRKVLLYMGGLRPRHVIGAYEDLGMEIIAAGYEFAHNDDYDRTLPDLKEGTLLFDDASSYELEAFVKALKPDLIGSGIKEKYIFQKMGVPFRQMHSWDYSGPYHGYDGFAIFARDMDMTLNNPAWNELTAPWL

>d1qgub\_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Klebsiella pneumoniae}

SQTIDKINSCYPLFEQDEYQELFRNKRQLEEAHDAQRVQEVFAWTTTAEYEALNFRREALTVDPAKACQPLGAVLCSLGFANTLPYVHGSQGCVAYFRTYFNRHFKEPIACVSDSMTEDAAVFGGNNNMNLGLQNASALYKPEIIAVSTTCMAEVIGDDLQAFIANAKKDGFVDSSIAVPHAHTPSFIGSHVTGWDNMFEGFAKTFTADYQGQPGKLPKLNLVTGFETYLGNFRVLKRMMEQMAVPCSLLSDPSEVLDTPADGHYRMYSGGTTQQEMKEAPDAIDTLLLQPWQLLKSKKVVQEMWNQPATEVAIPLGLAATDELLMTVSQLSGKPIADALTLERGRLVDMMLDSHTWLHGKKFGLYGDPDFVMGLTRFLLELGCEPTVILSHNANKRWQKAMNKMLDASPYGRDSEVFINCDLWHFRSLMFTRQPDFMIGNSYGKFIQRDTLAKGKAFEVPLIRLGFPLFDRHHLHRQTTWGYEGAMNIVTTLVNAVLEKLDSDTSQLGKTDYSFDLVR

>d1jr2a\_ c.113.1.1 (A:) Uroporphyrinogen III synthase (U3S, HemD) {Human (Homo sapiens)}

MKVLLLKDAKEDDCGQDPYIRELGLYGLEATLIPVLSFEFLSLPSFSEKLSHPEDYGGLIFTSPRAVEAAELCLEQNNKTEVWERSLKEKWNAKSVYVVGNATASLVSKIGLDTEGETCGNAEKLAEYICSRESSALPLLFPCGNLKREILPKALKDKGIAMESITVYQTVAHPGIQGNLNSYYSQQGVPASITFFSPSGLTYSLKHIQELSGDNIDQIKFAAIGPTTARALAAQGLPVSCTAESPTPQALATGIRKALQ

>d2dri\_\_ c.93.1.1 (-) D-ribose-binding protein {Escherichia coli, strain k-12}

KDTIALVVSTLNNPFFVSLKDGAQKEADKLGYNLVVLDSQNNPAKELANVQDLTVRGTKILLINPTDSDAVGNAVKMANQANIPVITLDRQATKGEVVSHIASDNVLGGKIAGDYIAKKAGEGAKVIELQGIAGTSAARERGEGFQQAVAAHKFNVLASQPADFDRIKGLNVMQNLLTAHPDVQAVFAQNDEMALGALRALQTAGKSDVMVVGFDGTPDGEKAVNDGKLAATIAQLPDQIGAKGVETADKVLKGEKVQAKYPVDLKLVVKQ

>d8abp\_\_ c.93.1.1 (-) L-arabinose-binding protein {Escherichia coli}

NLKLGFLVKQPEEPWFQTEWKFADKAGKDLGFEVIKIAVPDGEKTLNAIDSLAASGAKGFVICTPDPKLGSAIVAKARGYDMKVIAVDDQFVNAKGKPMDTVPLVMLAATKIGERQGQELYKEMQKRGWDVKESAVMAITANELDTARRRTTGSMDALKAAGFPEKQIYQVPTKSNDIPGAFDAANSMLVQHPEVKHWLIVGMNDSTVLGGVRATEGQGFKAADIIGIGINGVDAVSELSKAQATGFYGSLLPSPDVHGYKSSEMLYNWVAKDVEPPKFTEVTDVVLITRDNFKEELEKKGLGGK

>d1rpja\_ c.93.1.1 (A:) D-allose-binding protein {Escherichia coli}

AAEYAVVLKTLSNPFWVDMKKGIEDEAKTLGVSVDIFASPSEGDFQSQLQLFEDLSNKNYKGIAFAPLSSVNLVMPVARAWKKGIYLVNLDEKIDMDNLKKAGGNVEAFVTTDNVAVGAKGASFIIDKLGAEGGEVAIIEGKAGNASGEARRNGATEAFKKASQIKLVASQPADWDRIKALDVATNVLQRNPNIKAIYCANDTMAMGVAQAVANAGKTGKVLVVGTDGIPEARKMVEAGQMTATVAQNPADIGATGLKLMVDAEKSGKVIPLDKAPEFKLVDSILVTQ

>d2gbp\_\_ c.93.1.1 (-) Galactose/glucose-binding protein {Escherichia coli}

ADTRIGVTIYKYDDNFMSVVRKAIEQDAKAAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAINLVDPAAAGTVIEKARGQNVPVVFFNKEPSRKALDSYDKAYYVGTDSKESGIIQGDLIAKHWAANQGWDLNKDGQIQFVLLKGEPGHPDAEARTTYVIKELNDKGIKTEQLQLDTAMWDTAQAKDKMDAWLSGPNANKIEVVIANNDAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGALAGTVLNDANNQAKATFDLAKNLADGKGAADGTNWKIDNKVVRVPYVGVDKDNLAEFSKK

>d1gca\_\_ c.93.1.1 (-) Galactose/glucose-binding protein {Salmonella typhimurium, strain lt2}

ADTRIGVTIYKYDDNFMSVVRKAIEKDGKSAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAINLVDPAAAGTVIEKARGQNVPVVFFNKEPSRKALDSYDKAYYVGTDSKESGVIQGDLIAKHWQANQGWDLNKDGKIQYVLLKGEPGHPDAEARTTYVVKELNDKGIQTEQLALDTAMWDTAQAKDKMDAWLSGPNANKIEVVIANNDAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGAMAGTVLNDANNQAKATFDLAKNLAEGKGAADGTSWKIENKIVRVPYVGVDKDNLSEFTQK

>d1pea\_\_ c.93.1.1 (-) Amide receptor/negative regulator of the amidase operon (AmiC) {Pseudomonas aeruginosa}

PLIGLLFSETGVTADIERSQRYGALLAVEQLNREGGVGGRPIETLSQDPGGDPDRYRLCAEDFIRNRGVRFLVGCYMSHTRKAVMPVVERADALLCYPTPYEGFEYSPNIVYGGPAPNQNSAPLAAYLIRHYGERVVFIGSDYIYPRESNHVMRHLYRQHGGTVLEEIYIPLYPSDDDLQRAVERIYQARADVVFSTVVGTGTAELYRAIARRYGDGRRPPIASLTTSEAEVAKMESDVAEGQVVVAPYFSSIDTPASRAFVQACHGFFPENATITAWAEAAYWQTLLLGRAAQAAGNWRVEDVQRHLYDIDIDAPQGPVRVERQNNHSRLSSRIAEIDARGVFQVRWQSPEPIRPDPYVVVHNLDDW

>d1jx6a\_ c.93.1.1 (A:) Quorum-sensing signal (autoinducer-2) binding protein LuxP {Vibrio harveyi}

GYWGYQEFLDEFPEQRNLTNALSEAVRAQPVPLSKPTQRPIKISVVYPGQQVSDYWVRNIASFEKRLYKLNINYQLNQVFTRPNADIKQQSLSLMEALKSKSDYLIFTLDTTRHRKFVEHVLDSTNTKLILQNITTPVREWDKHQPFLYVGFDHAEGSRELATEFGKFFPKHTYYSVLYFSEGYISDVRGDTFIHQVNRDNNFELQSAYYTKATKQSGYDAAKASLAKHPDVDFIYACSTDVALGAVDALAELGREDIMINGWGGGSAELDAIQKGDLDITVMRMNDDTGIAMAEAIKWDLEDKPVPTVYSGDFEIVTKADSPERIEALKKRAFRYSD

>d1dbqa\_ c.93.1.1 (A:) Purine repressor (PurR), C-terminal domain {Escherichia coli}

KSIGLLATSSEAAYFAEIIEAVEKNCFQKGYTLILGNAWNNLEKQRAYLSMMAQKRVDGLLVMCSEYPEPLLAMLEEYRHIPMVVMDWGEAKADFTDAVIDNAFEGGYMAGRYLIERGHREIGVIPGPLERNTGAGRLAGFMKAMEEAMIKVPESWIVQGDFEPESGYRAMQQILSQPHRPTAVFCGGDIMAMGALCAADEMGLRVPQDVSLIGYDNVRNARYFTPALTTIHQPKDSLGETAFNMLLDRIVNKREEPQSIEVHPRLIERRSVADGPFRDYRR

>d1jyea\_ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}

LLIGVATSSLALHAPSQIVAAILSRADQLGASVVVSMVERSGVEACKTAVHNLLAQRVSGLIINYPLDDQDAIAVEAACTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLAGPLSSVSARLRLAGWHKYLTRNQIQPIAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMRAITESGLRVGADISVVGYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAP

>d1tlfa\_ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}

SLLIGVATSSLALHAPSQIVAAIKSRADQLGASVVVSMVERSGVEACKAAVHNLLAQRVSGLIINYPLDDQDAIAVEAACTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLAGPLSSVSARLRLAGWHKYLTRNQIQPIAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMRAITESGLRVGADISVVGYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRL

>d1byka\_ c.93.1.1 (A:) Trehalose repressor, C-terminal domain {Escherichia coli}

SDKVVAIIVTRLDSLSENLAVQTMLPAFYEQGYDPIMMESQFSPQLVAEHLGVLKRRNIDGVVLFGFTGITEEMLAHWQSSLVLLARDAKGFASVCYDDEGAIKILMQRLYDQGHRNISYLGVPHSDVTTGKRRHEAYLAFCKAHKLHPVAALPGLAMKQGYENVAKVITPETTALLCATDTLALGASKYLQEQRIDTLQLASVGNTPLMKFLHPEIVTVDPGYAEAGRQAACQLIAQVTGRSEPQQIIIPATLS

>d2liv\_\_ c.93.1.1 (-) Leucine-,isoleucine-,valine-binding (LIV) protein {Escherichia coli}

EDIKVAVVGAMSGPVAQYGDQEFTGAEQAVADINAKGGIKGNKLQIAKYDDACDPKQAVAVANKVVNDGIKYVIGHLCSSSTQPASDIYEDEGILMITPAATAPELTARGYQLILRTTGLDSDQGPTAAKYILEKVKPQRIAIVHDKQQYGEGLARAVQDGLKKGNANVVFFDGITAGEKDFSTLVARLKKENIDFVYYGGYHPEMGQILRQARAAGLKTQFMGPEGVANVSLSNIAGESAEGLLVTKPKNYDQVPANKPIVDAIKAKKQDPSGAFVWTTYAALQSLQAGLNQSDDPAEIAKYLKANSVDTVMGPLTWDEKGDLKGFEFGVFDWHANGTATDAK

>d2lbp\_\_ c.93.1.1 (-) Leucine-binding protein {Escherichia coli}

DDIKVAVVGAMSGPIAQWGIMEFNGAEQAIKDINAKGGIKGDKLVGVEYDDACDPKQAVAVANKIVNDGIKYVIGHLCSSSTQPASDIYEDEGILMISPGATAPELTQRGYQHIMRTAGLDSSQGPTAAKYILETVKPQRIAIIHDKQQYGEGLARSVQDGLKAANANVVFFDGITAGEKDFSALIARLKKENIDFVYYGGYYPEMGQMLRQARSVGLKTQFMGPEGVGNASLSNIAGDAAEGMLVTMPKRYDQDPANQGIVDALKADKKDPSGPYVWITYAAVQSLATALERTGSDEPLALVKDLKANGANTVIGPLNWDEKGDLKGFDFGVFQWHADGSSTKAK

>d1dp4a\_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Rat (Rattus norvegicus)}

SDLTVAVVLPLTNTSYPWSWARVGPAVELALARVKARPDLLPGWTVRMVLGSSENAAGVCSDTAAPLAAVDLKWEHSPAVFLGPGCVYSAAPVGRFTAHWRVPLLTAGAPALGIGVKDEYALTTRTGPSHVKLGDFVTALHRRLGWEHQALVLYADRLGDDRPCFFIVEGLYMRVRERLNITVNHQEFVEGDPDHYPKLLRAVRRKGRVIYICSSPDAFRNLMLLALNAGLTGEDYVFFHLDVFGQSLKSAQGLVPQKPWERGDGQDRSARQAFQAAKIITYKEPDNPEYLEFLKQLKLLADKKFNFTVEDGLKNIIPASFHDGLLLYVQAVTETLAQGGTVTDGENITQRMWNRSFQGVTGYLKIDRNGDRDTDFSLWDMDPETGAFRVVLNYNGTSQELMAVSEHKLYWPLGYPPPDVPKCGF

>d1jdpa\_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Human (Homo sapiens)}

EALPPQKIEVLVLLPQDDSYLFSLTRVRPAIEYALRSVEGNGTGRRLLPPGTRFQVAYEDSDCGNRALFSLVDRVAAARGAKPDLILGPVCEYAAAPVARLASHWDLPMLSAGALAAGFQHKDSEYSHLTRVAPAYAKMGEMMLALFRHHHWSRAALVYSDDKLERNCYFTLEGVHEVFQEEGLHTSIYSFDETKDLDLEDIVRNIQASERVVIMCASSDTIRSIMLVAHRHGMTSGDYAFFNIELFNSSSYGDGSWKRGDKHDFEAKQAYSSLQTVTLLRTVKPEFEKFSMEVKSSVEKQGLNMEDYVNMFVEGFHDAILLYVLALHEVLRAGYSKKDGGKIIQQTWNRTFEGIAGQVSIDANGDRYGDFSVIAMTDVEAGTQEVIGDYFGKEGRFEMRP

>d1ewka\_ c.93.1.1 (A:) Metabotropic glutamate receptor subtype 1 {Rat (Rattus norvegicus)}

RSVARMDGDVIIGALFSVHHQPPAEKVPERKCGEIREQYGIQRVEAMFHTLDKINADPVLLPNITLGSEIRDSCWHSSVALEQSIEFIRDSLISIRDEKDGLNRCLPDGQTLPPGRTKKPIAGVIGPGSSSVAIQVQNLLQLFDIPQIAYSATSIDLSDKTLYKYFLRVVPSDTLQARAMLDIVKRYNWTYVSAVHTEGNYGESGMDAFKELAAQEGLCIAHSDKIYSNAGEKSFDRLLRKLRERLPKARVVVCFCEGMTVRGLLSAMRRLGVVGEFSLIGSDGWADRDEVIEGYEVEANGGITIKLQSPEVRSFDDYFLKLRLDTNTRNPWFPEFWQHRFQCRLPGHLLENPNFKKVCTGNESLEENYVQDSKMGFVINAIYAMAHGLQNMHHALCPGHVGLCDAMKPIDGRKLLDFLIKSSFVGVSGEEVWFDEKGDAPGRYDIMNLQYTEANRYDYVHVGTWHEGVLNIDDYKI

>d1jeta\_ c.94.1.1 (A:) Oligo-peptide binding protein (OPPA) {Salmonella typhimurium}

ADVPAGVQLADKQTLVRNNGSEVQSLDPHKIEGVPESNVSRDLFEGLLISDVEGHPSPGVAEKWENKDFKVWTFHLRENAKWSDGTPVTAHDFVYSWQRLADPNTASPYASYLQYGHIANIDDIIAGKKPATDLGVKALDDHTFEVTLSEPVPYFYKLLVHPSVSPVPKSAVEKFGDKWTQPANIVTNGAYKLKNWVVNERIVLERNPQYWDNAKTVINQVTYLPISSEVTDVNRYRSGEIDMTYNNMPIELFQKLKKEIPNEVRVDPYLCTYYYEINNQKAPFNDVRVRTALKLALDRDIIVNKVKNQGDLPAYSYTPPYTDGAKLVEPEWFKWSQQKRNEEAKKLLAEAGFTADKPLTFDLLYNTSDLHKKLAIAVASIWKKNLGVNVNLENQEWKTFLDTRHQGTFDVARAGWCADYNEPTSFLNTMLSDSSNNTAHYKSPAFDKLIADTLKVADDTQRSELYAKAEQQLDKDSAIVPVYYYVNARLVKPWVGGYTGKDPLDNIYVKNLYIIKH

>d1pda\_1 c.94.1.1 (3-219) Porphobilinogen deaminase (hydroxymethylbilane synthase), N-terminal domain {Escherichia coli}

DNVLRIATRQSPLALWQAHYVKDKLMASHPGLVVELVPMVTRGDVILDTPLAKVGGKGLFVKELEVALLENRADIAVHSMKDVPVEFPQGLGLVTICEREDPRDAFVSNNYDSLDALPAGSIVGTSSLRRQCQLAERRPDLIIRSLRGNVGTRLSKLDNGEYDAIILAVAGLKRLGLESRIRAALPPEISLPAVGQGAVGIECRLDDSRTRELLAAL

>d1lst\_\_ c.94.1.1 (-) Lysine-,arginine-,ornithine-binding (LAO) protein {Salmonella typhimurium}

ALPQTVRIGTDTTYAPFSSKDAKGEFIGFDIDLGNEMCKRMQVKCTWVASDFDALIPSLKAKKIDAIISSLSITDKRQQEIAFSDKLYAADSRLIAAKGSPIQPTLESLKGKHVGVLQGSTQEAYANDNWRTKGVDVVAYANQDLIYSDLTAGRLDAALQDEVAASEGFLKQPAGKEYAFAGPSVKDKKYFGDGTGVGLRKDDTELKAAFDKALTELRQDGTYDKMAKKYFDFNVYGDK

>d1sbp\_\_ c.94.1.1 (-) Sulphate-binding protein {Salmonella typhimurium}

KDIQLLNVSYDPTRELYEQYNKAFSAHWKQETGDNVVIDQSHGGSGKQATSVINGIEADTVTLALAYDVNAIAERGRIDKNWIKRLPDDSAPYTSTIVFLVRKGNPKQIHDWNDLIKPGVSVITPNPKSSGGARWNYLAAWGYALHHNNNDQAKAEDFVKALFKNVEVLDSGARGSTNTFVERGIGDVLIAWENEALLATNELGKDKFEIVTPSESILAEPTVSVVDKVVEKKDTKAVAEAYLKYLYSPEGQEIAAKNFYRPRDADVAKKYDDAFPKLKLFTIDEVFGGWAKAQKDHFADGGTFDQISK

>d1ixh\_\_ c.94.1.1 (-) Phosphate-binding protein {Escherichia coli}

EASLTGAGATFPAPVYAKWADTYQKETGNKVNYQGIGSSGGVKQIIANTVDFGASDAPLSDEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLNPGLKLPSQNIAVVRRADGSGTSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGKGNDGIAAFVQRLPGAIGYVEYAYAKQNNLAYTKLISADGKPVSPTEENFANAAKGADWSKTFAQDLTNQKGEDAWPITSTTFILIHKDQKKPEQGTEVLKFFDWAYKTGAKQANDLDYASLPDSVVEQVRAAWKTNIKDSSGKPLY

>d3mbp\_\_ c.94.1.1 (-) D-maltodextrin-binding protein, MBP {Escherichia coli}

KIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEALKDAQTRITK

>d1elja\_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Pyrococcus furiosus}

MKIEEGKVVIWHAMQPNELEVFQSLAEEYMALCPEVEIVFEQKPNLEDALKAAIPTGQGPDLFIWAHDWIGKFAEAGLLEPIDEYVTEDLLNEFAPMAQDAMQYKGHYYALPFAAETVAIIYNKEMVSEPPKTFDEMKAIMEKYYDPANEKYGIAWPINAYFISAIAQAFGGYYFDDKTEQPGLDKPETIEGFKFFFTEIWPYMAPTGDYNTQQSIFLEGRAPMMVNGPWSINDVKKAGINFGVVPLPPIIKDGKEYWPRPYGGVKLIYFAAGIKNKDAAWKFAKWLTTSEESIKTLALELGYIPVLTKVLDDPEIKNDPVIYGFGQAVQHAYLMPKSPKMSAVWGGVDGAINEILQDPQNADIEGILKKYQQEILNNMQ

>d1eu8a\_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Thermococcus litoralis}

IEEGKIVFAVGGAPNEIEYWKGVIAEFEKKYPGVTVELKRQATDTEQRRLDLVNALRGKSSDPDVFLMDVAWLGQFIASGWLEPLDDYVQKDNYDLSVFFQSVINLADKQGGKLYALPVYIDAGLLYYRKDLLEKYGYSKPPETWQELVEMAQKIQSGERETNPNFWGFVWQGKQYEGLVCDFVEYVYSNGGSLGEFKDGKWVPTLNKPENVEALQFMVDLIHKYKISPPNTYTEMTEEPVRLMFQQGNAAFERNWPYAWGLHNADDSPVKGKVGVAPLPHFPGHKSAATLGGWHIGISKYSDNKALAWEFVKFVESYSVQKGFAMNLGWNPGRVDVYDDPAVVSKSPHLKELRAVFENAVPRPIVPYYPQLSEIIQKYVNSALAGKISPQEALDKAQKEAEELVKQ

>d3thia\_ c.94.1.1 (A:) Thiaminase I {Paenibacillus thiaminolyticus}

ITLKVAIYPYVPDPARFQAAVLDQWQRQEPGVKLEFTDWDSYSADPPDDLDVFVLDSIFLSHFVDAGYLLPFGSQDIDQAEDVLPFALQGAKRNGEVYGLPQILCTNLLFYRKGDLKIGQVDNIYELYKKIGTSHSEQIPPPQNKGLLINMAGGTTKASMYLEALIDVTGQYTEYDLLPPLDPLNDKVIRGLRLLINMAGEKPSQYVPEDGDAYVRASWFAQGSGRAFIGYSESMMRMGDYAEQVRFKPISSSAGQDIPLFYSDVVSVNSKTAHPELAKKLANVMASADTVEQALRPQADGQYPQYLLPARHQVYEALMQDYPIYSELAQIVNKPSNRVFRLGPEVRTWLKDAKQVLPEALG

>d1mrp\_\_ c.94.1.1 (-) Ferric-binding protein {Haemophilus influenzae}

DITVYNGQHKEAATAVAKAFEQETGIKVTLNSGKSEQLAGQLKEEGDKTPADVFYTEQTATFADLSEAGLLAPISEQTIQQTAQKGVPLAPKKDWIALSGRSRVVVYDHTKLSEKDMEKSVLDYATPKWKGKIGYVSTSGAFLEQVVALSKMKGDKVALNWLKGLKENGKLYAKNSVALQAVENGEVPAALINNYYWYNLAKEKGVENLKSRLYFVRHQDPGALVSYSGAAVLKASKNQAEAQKFVDFLASKKGQEALVAARAEYPLRADVVSPFNLEPYEKLEAPVVSATTAQDKEHAIKLIEEAGLK

>d1d9ya\_ c.94.1.1 (A:) Ferric-binding protein {Neisseria gonorrhoeae}

DITVYNGQHKEAAQAVADAFTRATGIKVKLNCAKGDQLAGQIKEEGSRSPADVFYSEQIPALATLSAANLLEPLPASTINETRGKGVPVAAKKDWVALSGRSRVVVYDTRKLSEKDLEKSVLNYATPKWKNRIGYVPTSGAFLEQIVAIVKLKGEAAALKWLKGLKEYGKPYAKNSVALQAVENGEIDAALINNYYWHAFAREKGVQNVHTRLNFVRHRDPGALVTYSGAAVLKSSQNKDEAKKFVAFLAGKEGQRALTAVRAEYPLNPHVVSTFNLEPIAKLEAPQVSATTVSEKEHATRLLEQAGMK

>d1dpe\_\_ c.94.1.1 (-) Dipeptide-binding protein {Escherichia coli}

KTLVYCSEGSPEGFNPQLFISGTTYDASSVPLYNRLVEFKIGTTEVIPGLAEKWEVSEDGKTYTFHLRKGVKWHDNKEFKPTRELNADDVVFSFDRQKNAQNPYHKVSGGSYEYFEGMGLPELISEVKKVDDNTVQFVLTRPEAPFLADLAMDFASILSKEYADAMMKAGTPEKLDLNPIGTGPFQLQQYQKDSRIRYKAFDGYWGTKPQIDTLVFSITPDASVRYAKLQKNECQVMPYPNPADIARMKQDKSINLMEMPGLNVGYLSYNVQKKPLDDVKVRQALTYAVNKDAIIKAVYQGAGVSAKNLIPPTMWGYNDDVQDYTYDPEKAKALLKEAGLEKGFSIDLWAMPVQRPYNPNARRMAEMIQADWAKVGVQAKIVTYEWGEYLKRAKDGEHQTVMMGWTGDNGDPDNFFATEFSCAASEQGSNYSKWCYKPFEDLIQPARATDDHNKRVELYKQAQVVMHDQAPALIIAHSTVFEPVRKEVKGYVVDPLGKHHFENVSIE

>d1hsla\_ c.94.1.1 (A:) Histidine-binding protein {Escherichia coli}

AIPQKIRIGTDPTYAPFESKNAQGELVGFDIDLAKELCKRINTQCTFVENPLDALIPSLKAKKIDAIMSSLSITEKRQQEIAFTDKLYAADSRLVVAKNSDIQPTVASLKGKRVGVLQGTTQETFGNEHWAPKGIEIVSYQGQDNIYSDLTAGRIDAAFQDEVAASEGFLKQPVGKDYKFGGPAVKDEKLFGVGTGMGLRKEDNELREALNKAFAEMRADGTYEKLAKKYFDFDVYGG

>d1pot\_\_ c.94.1.1 (-) Spermidine/putrescine-binding protein PotD {Escherichia coli}

NNTLYFYNWTEYVPPGLLEQFTKETGIKVIYSTYESNETMYAKLKTYKDGAYDLVVPSTYYVDKMRKEGMIQKIDKSKLTNFSNLDPDMLNKPFDPNNDYSIPYIWGATAIGVNGDAVDPKSVTSWADLWKPEYKGSLLLTDDAREVFQMALRKLGYSGNTTDPKEIEAAYNELKKLMPNVAAFNSDNPANPYMEGEVNLGMIWNGSAFVARQAGTPIDVVWPKEGGIFWMDSLAIPANAKNKEGALKLINFLLRPDVAKQVAETIGYPTPNLAARKLLSPEVANDKTLYPDAETIKNGEWQNDVGAASSIYEEYYQKLKAG

>d1a99a\_ c.94.1.1 (A:) Putrescine receptor (PotF) {Escherichia coli}

QKTLHIYNWSDYIAPDTVANFEKETGIKVVYDVFDSNEVLEGKLMAGSTGFDLVVPSASFLERQLTAGVFQPLDKSKLPEWKNLDPELLKLVAKHDPDNKFAMPYMWATTGIGYNVDKVKAVLGENAPVDSWDLILKPENLEKLKSCGVSFLDAPEEVFATVLNYLGKDPNSTKADDYTGPATDLLLKLRPNIRYFHSSQYINDLANGDICVAIGWAGDVWQASNRAKEAKNGVNVSFSIPKEGAMAFFDVFAMPADAKNKDEAYQFLNYLLRPDVVAHISDHVFYANANKAATPLVSAEVRENPGIYPPADVRAKLFTLKVQDPKIDRVRTRAWTKVKSG

>d1wdna\_ c.94.1.1 (A:) Glutamine-binding protein {Escherichia coli}

KLVVATDTAFVPFEFKQGDLYVGFDVDLWAAIAKELKLDYELKPMDFSGIIPALQTKNVDLALAGITITDERKKAIDFSDGYYKSGLLVMVKANNNDVKSVKDLDGKVVAVKSGTGSVDYAKANIKTKDLRQFPNIDNAYMELGTNRADAVLHDTPNILYFIKTAGNGQFKAVGDSLEAQQYGIAFPKGSDELRDKVNGALKTLRENGTYNEIYKKWFGTEPK

>d1ftka\_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Rat (Rattus norvegicus), GluR2}

KTVVVTTILESPYVMMKKNHEMLEGNERYEGYCVDLAAEIAKHCGFKYKLTIVGDGKYGARDADTKIWNGMVGELVYGKADIAIAPLTITLVREEVIDFSKPFMSLGISIMIKKPGTDGNPIESAEDLSKQTEIAYGTLDSGSTKEFFRRSKIAVFDKMWTYMRSAEPSVFVRTTAEGVARVRKSKGKYAYLLESTMNEYIEQRKPCDTMKVGGNLDSKGYGIATPKGSSLGNAVNLAVLKLNEQGLLDKLKNKWWYDKGEC

>d1ii5a\_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Synechocystis sp., GluR0}

GSAMALKVGVVGNPPFVFYGEGKNAAFTGISLDVWRAVAESQKWNSEYVRQNSISAGITAVAEGELDILIGPISVTPERAAIEGITFTQPYFSSGIGLLIPGTATPLFRSVGDLKNKEVAVVRDTTAVDWANFYQADVRETNNLTAAITLLQKKQVEAVMFDRPALIYYTRQNPNLNLEVTEIRVSLEPYGFVLKENSPLQKTINVEMLNLLYSRVIAEFTERWLG

>d1amf\_\_ c.94.1.1 (-) Molybdate-binding protein, ModA {Escherichia coli}

GKITVFAAASLTNAMQDIATQFKKEKGVDVVSSFASSSTLARQIEAGAPADLFISADQKWMDYAVDKKAIDTATRQTLLGNSLVVVAPKASVQKDFTIDSKTNWTSLLNGGRLAVGDPEHVPAGIYAKEALQKLGAWDTLSPKLAPAEDVRGALALVERNEAPLGIVYGSDAVASKGVKVVATFPEDSHKKVEYPVAVVEGHNNATVKAFYDYLKGPQAAEIFKRYGFTIK

>d1atg\_\_ c.94.1.1 (-) Molybdate-binding protein, ModA {Azotobacter vinelandii}

ELKVVTATNFLGTLEQLAGQFAKQTGHAVVISSGSSGPVYAQIVNGAPYNVFFSADEKSPEKLDNQGFALPGSRFTYAIGKLVLWSAKPGLVDNQGKVLAGNGWRHIAISNPQIAPYGLAGTQVLTHLGLLDKLTAQERIVEANSVGQAHSQTASGAADLGFVALAQIIQAAAKIPGSHWFPPANYYEPIVQQAVITKSTAEKANAEQFMSWMKGPKAVAIIKAAGYVLPQ

>d1al3\_\_ c.94.1.1 (-) Cofactor-binding fragment of CysB {Klebsiella aerogenes}

TWPDKGSLYVATTHTQARYALPGVIKGFIERYPRVSLHMHQGSPTQIAEAVSKGNADFAIATEALHLYDDLVMLPCYHWNRSIVVTPEHPLATKGSVSIEELAQYPLVTYTFGFTGRSELDTAFNRAGLTPRIVFTATDADVIKTYVRLGLGVGVIASMAVDPVSDPDLVKLDANGIFSHSTTKIGFRRSTFLRSYMYDFIQRFAPHLTRDVVDTAVALRSNEDIEAMFKDIKLPEK

>d1i6aa\_ c.94.1.1 (A:) Hydrogen peroxide-inducible genes activator OxyR, regulatory domain {Escherichia coli}

ETMSGPLHIGLIPTVGPYLLPHIIPMLHQTFPKLEMYLHEAQTHQLLAQLDSGKLDAVILALVKESEAFIEVPLFDEPMLLAIYEDHPWANREAVPMADLAGEKLLMLEDGHCLRDQAMGFCFEAGADEDTHFRATSLETLRNMVAAGSGITLLPALAVPPERKRDGVVYLPAIKPEPRRTIGLVYRPGSPLRSRYEQLAEAIRARMDGHFD

>d1kwha\_ c.94.1.1 (A:) Alginate-binding periplasmic protein AlgQ2 {Sphingomonas sp.}

KEATWVTDKPLTLKIHMHFRDKWVWDENWPVAKESFRLTNVKLQSVANKAATNSQEQFNLMMASGDLPDVVGGDNLKDKFIQYGQEGAFVPLNKLIDQYAPHIKAFFKSHPEVERAIKAPDGNIYFIPYVPDGVVARGYFIREDWLKKLNLKPPQNIDELYTVLKAFKEKDPNGNGKADEVPFIDRHPDEVFRLVNFWGARSSGSDNYMDFYIDNGRVKHPWAETAFRDGMKHVAQWYKEGLIDKEIFTRKAKAREQMFGGNLGGFTHDWFASTMTFNEGLAKTVPGFKLIPIAPPTNSKGQRWEEDSRQKVRPDGWAITVKNKNPVETIKFFDFYFSRPGRDISNFGVPGVTYDIKNGKAVFKDSVLKSPQPVNNQLYDMGAQIPIGFWQDYDYERQWTTPEAQAGIDMYVKGKYVMPGFEGVNMTREERAIYDKYWADVRTYMYEMGQAWVMGTKDVDKTWDEYQRQLKLRGLYQVLQMMQQAYDRQYKN

>d1cb6a2 c.94.1.2 (A:1335-1691) Lactoferrin {Human (Homo sapiens)}

EEEVAARRARVVWCAVGEQELRKCNQWSGLSEGSVTCSSASTTEDCIALVLKGEADAMSLDGGYVYTAGKCGLVPVLAENYKSQQSSDPDPNCVDRPVEGYLAVAVVRRSDTSLTWNSVKGKKSCHTAVDRTAGWNIPMGLLFNQTGSCKFDEYFSQSCAPGSDPRSNLCALCIGDEQGENKCVPNSNERYYGYTGAFRCLAENAGDVAFVKDVTVLQNTDGNNNEAWAKDLKLADFALLCLDGKRKPVTEARSCHLAMAPNHAVVSRMDKVERLKQVLLHQQAKFGRNGSDCPDKFCLFQSETKNLLFNDNTECLARLHGKTTYEKYLGPQYVAGITNLKKCSTSPLLEACEFLRK

>d1lct\_\_ c.94.1.2 (-) Lactoferrin {Human (Homo sapiens)}

RSVQWCAVSNPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIQAIAENRADAVTLDGGFIYEAGLAPYKLRPVAAEVYGTERQPRTHYYAVAVVKKGGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLRPFLNWTGPPEPIEAAVARFFSASCVPGADKGQFPNLCRLCAGTGENKCAFSSQEPYFSYSGAFKCLRDGAGDVAFIRESTVFEDLSDEAERDEYELLCPDNTRKPVDKFKDCHLARVPSHAVVARSVNGKEDAIWNLLRQAQEKFGKDKSPKFQLFGSPSGQKDLLFKDSAIGFSRVPPRIDSGLYLGSGYFTA

>d1lgbc\_ c.94.1.2 (C:) Lactoferrin {Human (Homo sapiens)}

HYYAVAVVKKGGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLRPFLNWTGPPEPIEAAVARFFSASCVPGADKGQFPNLCRLCAGTGENKCAFSSQEPYFSYSGAFKCLKDGAGDVAFIRESTVFEDLSDEAERDEYELLCPDNTRKPVDKFKDCHLAR

>d1ce2a1 c.94.1.2 (A:1-333) Lactoferrin {Domestic water buffalo (Bubalus arnee bubalis)}

APRKNVRWCTISQPEWLKCHRWQWRMKKLGAPSITCVRRASVLECIRAITEKKADAVTLDGGMVFEAGRDPYKLRPVAAEIYGTKESPQTHYYAVAVVKKGSNFQLDQLQGRNSCHTGLGRSAGWNIPMGILRPYLSWTESLEPLQGAVAKFFSASCVPCVDRQAYPNLCQLCKGEGENQCACSPREPYFGYSGAFKCLQDGAGDVAFVKETTVFENLPEKADRDQYELLCLNNTRAPVDAFKECHLAQVPSHAVVARSVDGKEDLIWKLLSKAQEKFGKNKSGSFQLFGSPPGQRDLLFKDSALGFLRIPSKVDSALYLGSRYLTALKNLRE

>d1ce2a2 c.94.1.2 (A:334-689) Lactoferrin {Domestic water buffalo (Bubalus arnee bubalis)}

TAEEVQARRARVVWCAVGPEEQKKCQQWSQQSGQIVTCATASTTDDCIALVLKGEADALSLDGGYIYTAGKCGLVPVLAENRKSSKHSSLDCVLRPTEGYLAVAVVKKANEGLTWNSLKGKKSCHTAVDRTAGWNIPMGLIANQTGSCAFDEFFSQSCAPGADPKSRLCALCAGDDQGLDKCVPNSKEKYYGYTGAFRCLAEDVGDVAFVKNDTVWENTNGESTADWAKNLNREDFRLLCLDGTRKPVTEAQSCHLAVAPNHAVVSLSERAAHVEQVLLHQQALFGENGKNCPDKFCLFKSETKNLLFNDNTECLAKLGGRPTYEEYLGTEYVTAIANLKKCSTSPLLEACAFLTR

>d1b1xa1 c.94.1.2 (A:1-333) Lactoferrin {Horse (Equus caballus)}

APRKSVRWCTISPAEAAKCAKFQRNMKKVRGPSVSCIRKTSSFECIQAIAANKADAVTLDGGLVYEAGLHPYKLRPVAAEVYQTRGKPQTRYYAVAVVKKGSGFQLNQLQGVKSCHTGLGRSAGWNIPIGTLRPYLNWTGPPEPLQKAVANFFSASCVPCADGKQYPNLCRLCAGTEADKCACSSQEPYFGYSGAFKCLENGAGDVAFVKDSTVFENLPDEAERDKYELLCPDNTRKPVDAFKECHLARVPSHAVVARSVDGREDLIWKLLHRAQEEFGRNKSSAFQLFGSTPGEQDLLFKDSALGFVRIPSQIDSGLYLGANYLTATQNLRE

>d1b1xa2 c.94.1.2 (A:334-689) Lactoferrin {Horse (Equus caballus)}

TAAEVAARRERVVWCAVGPEEERKCKQWSDVSNRKVACASASTTEECIALVLKGEADALNLDGGFIYVAGKCGLVPVLAENQKSQNSNAPDCVHRPPEGYLAVAVVRKSDADLTWNSLSGKKSCHTGVGRTAAWNIPMGLLFNQTGSCKFDKFFSQSCAPGADPQSSLCALCVGNNENENKCMPNSEERYYGYTGAFRCLAEKAGDVAFVKDVTVLQNTDGKNSEPWAKDLKQEDFELLCLDGTRKPVAEAESCHLARAPNHAVVSQSDRAQHLKKVLFLQQDQFGGNGPDCPGKFCLFKSETKNLLFNDNTECLAELQGKTTYEQYLGSEYVTSITNLRRCSSSPLLEACAFLRA

>d1dtza1 c.94.1.2 (A:1-333) Lactoferrin {Arabian camel (Camelus dromedarius)}

ASKKSVRWCTTSPAESKKCAQWQRRMKKVRGPSVTCVKKTSRFECIQAISTEKADAVTLDGGLVYDAGLDPYKLRPIAAEVYGTENQPQTHYYAVAIAKKGTNFQLNQLQGLKSCHTGLGRSAGWNIPMGLLRPFLDWTGPPEPLQKAVAKFFSASCVPCVDGKEYPNLCQLCAGTGENKCACSSQEPYFGYSGAFKCLQDGAGDVAFVKDSTVFESLPAKADRDQYELLCPNNTRKPVDAFQECHLARVPSHAVVARSVNGKEDLIWKLLVKAQEKFGRGKPSAFQLFGSPAGQKDLLFKDSALGLLRIPKKIDSGLYLGSNYITAIRGLRE

>d1dtza2 c.94.1.2 (A:334-689) Lactoferrin {Arabian camel (Camelus dromedarius)}

TAAEVELRRAQVVWCAVGSDEQLKCQEWSRQSNQSVVCATASTTEDCIALVLKGEADALSLDGGYIYIAGKCGLVPVLAESQQSPESSGLDCVHRPVKGYLAVAVVRKANDKITWNSLRGKKSCHTAVDRTAGWNIPMGPLFKDTDSCRFDEFFSQSCAPGSDPRSKLCALCAGNEEGQLKCVPNSSERLYGYTGAFRCLAENVGDVAFVKDVTVLDNTDGKGTEQWAKDLKLGDFELLCLNGTRKPVTEAESCHLPVAPNHAVVSRIDKVAHLRQVLLRQQAHFGRNGEDCPGKFCLFQSKTKNLLFNDNTECLAKLQGKTTYDEYLGPQYVTAIAKLRRCSTSPLLEACAFLMR

>d1dot\_1 c.94.1.2 (1-334) Ovotransferrin {Duck (Anas platyrhynchos)}

APPKTTVRWCTISSAEEKKCNSLKDHMQQERVTLSCVQKATYLDCIKAISNNEADAISLDGGQVFEAGLAPYKLKPIAAEVYERSGGSTTSYYAVAVVKKGTDFMIKDLRGKTSCHTGLGRSAGWNIPIGTLIHREDIEWEGIESGISEQAVAKFFSASCVPGATIEQKLCRQCKGDAKTKCLRNGPYSGYSGAFQCLKDGKGDVAFVKHTTVQENAPEEKDEYELLCLDGSRQPVDSYKTCNWARVAAHAVVARDDSKIDDIWSFLGMQAYSLGVDTTSDFHLFGPPGKKDPVLKDLLFKDSAIMLKRVPELMDSQLYLGFEYYSAIQSLRKD

>d1dot\_2 c.94.1.2 (335-686) Ovotransferrin {Duck (Anas platyrhynchos)}

QLTVGPRENKIQWCAVGKDEKSKCDRWSVVSNGEVECTILDDNKDCIVKITKGEADAISLDGGFVYTAGVCGLVPVVGESYEDETQCSKDEEQPAYYFAVAVVKKSSAITWNNLQGKKSCHTAVGRTAGWNIPMGLIHNKTGSCDFDDYFSEGCAPGSPPNSRLCKLCQGSGENLLEKCVASSHEKYYGYTGALRCLVEQGDVAFIKHSTVGENVSGSNKDDWAKGLTRDDFELLCTNGKRAKTMDYKTCHLAKVPTHAVVARPEKANKIRELLEGQEKLFGLHGTEKERFMMFQSQTKDLLFKALTKCLVKLRQGITYKEFLGDEYYASVASLNTCNPSDLLQVCTFLEDK

>d1gv8a\_ c.94.1.2 (A:) Ovotransferrin {Duck (Anas platyrhynchos)}

SYYAVAVVKKGTDFMIKDLRGKTSCHTGLGRSAGWNIPIGTLIHRGDIEWEGIESGSVEQAVAKFFSASCVPGATTEQKLCRQCKGDAKTKCLRNAPYSGYSGAFQCLKDGKGDVAFVKHTTVQENAPEEKDEYELLCLDGTRQPVDSYKTCNWARVAA

>d1ieja\_ c.94.1.2 (A:) Ovotransferrin {Chicken (Gallus gallus)}

KSVIRWCTISSPEEKKCNNLRDLTQQERISLTCVQKATYLDCIKAIANNEADAITLDGGQVFEAGLAPYKLKPIAAEVYEHTEGSTTSYYAVAVVKKGTEFTVNDLQGKTSCHTGLGRSAGWNIPIGTLLHRGAIEWEGIESGSVEQAVAKFFSASCVPGATIEQKLCRQCKGDPKTKCARNAPYSGYSGAFHCLKDGKGDVAFVKHTTVNENAPDQKDEYELLCLDGSRQPVDNYKTCNWARVAAHAVVARDDNKVEDIWSFLSKAQSDFGVDTKSDFHLFGPPGKKDPVLKDLLFKDSAIMLKRVPSLMDSQLYLGFEYYSAIQSMR

>d1iq7a\_ c.94.1.2 (A:) Ovotransferrin {Chicken (Gallus gallus)}

RIQWCAVGKDEKSKCDRWSVVSNGDVECTVVDETKDCIIKIMKGEADAVALDGGLVYTAGVCGLVPVMAERYDDESQCSKTDERPASYFAVAVARKDSNVNWNNLKGKKSCHTAVGRTAGWVIPMGLIHNRTGTCNFDEYFSEGCAPGSPPNSRLCQLCQGSGGIPPEKCVASSHEKYFGYTGALRCLVEKGDVAFIQHSTVEENTGGKNKADWAKNLQMDDFELLCTDGRRANVMDYRECNLAEVPTHAVVVRPEKANKIRDLLERQEKRFGVNGSEKSKFMMFESQNKDLLFKDLTKCLFKVREGTTYKEFLGDKFYTVISSLKTCNPSDILQMCSFLEGK

>d1jnfa1 c.94.1.2 (A:3-334) Transferrin {Rabbit (Oryctolagus cuniculus)}

EKTVRWCAVNDHEASKCANFRDSMKKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLDAGLVHEAGLTPNNLKPVVAEFYGSKENPKTFYYAVALVKKGSNFQLNELQGKKSCHTGLGRSAGWNIPIGLLLCDLPEPRKPLEKAVASFFSGSCVPCADGADFPQLCQLCPGCGCSSVQPYFGYSGAFKCLKDGLGDVAFVKQETIFENLPSKDERDQYELLCLDNTRKPVDEYEQCHLARVPSHAVVARSVDGKEDLIWELLNQAQEHFGKDKSGDFQLFSSPHGKNLLFKDSAYGFFKVPPRMDANLYLGYEYVTAVRNLREGICPDP

>d1jnfa2 c.94.1.2 (A:335-676) Transferrin {Rabbit (Oryctolagus cuniculus)}

LQDECKAVKWCALGHHERLKCDEWSVTSGGLIECESAETPEDCIAKIMNGEADAMSLDGGYVYIAGQCGLVPVLAENYESTDCKKAPEEGYLSVAVVKKSNPDINWNNLEGKKSCHTAVDRTAGWNIPMGLLYNRINHCRFDEFFRQGCAPGSQKNSSLCELCVGPSVCAPNNREGYYGYTGAFRCLVEKGDVAFVKSQTVLQNTGGRNSEPWAKDLKEEDFELLCLDGTRKPVSEAHNCHLAKAPNHAVVSRKDKAACVKQKLLDLQVEFGNTVADCSSKFCMFHSKTKDLLFRDDTKCLVDLRGKNTYEKYLGADYIKAVSNLRKCSTSRLLEACTFHKH

>d1tfd\_\_ c.94.1.2 (-) Transferrin {Rabbit (Oryctolagus cuniculus)}

VRWCAVNDHEASKCANFRDSMKKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLDAGLVHEAGLTPNNLKPVVAEFYGSKENPKTFYYAVALVKKGSNFQLNELQGKKSCHTGLGRSAGWNIPIGLLYCDLPEPRKPLEKAVASFFSGSCVPCADGADFPQLCQLCPGCGCSSSQPYFGYSGAFKCLKDGLGDVAFVKQETIFENLPSKDERDQYELLCLDNTRKPVDEYEQCHLARVPSHAVVARSVDGKEDLIWELLNQAQEHFGKDKSGDFQLFSSPHGKNLLFKDSAYGFFK

>d1a8e\_\_ c.94.1.2 (-) Transferrin {Human (Homo sapiens)}

DKTVRWCAVSEHEATKCQSFRDHMKSVIPSDGPSVACVKKASYLDCIRAIAANEADAVTLDAGLVYDAYLAPNNLKPVVAEFYGSKEDPQTFYYAVAVVKKDSGFQMNQLRGKKSCHTGLGRSAGWNIPIGLLYCDLPEPRKPLEKAVANFFSGSCAPCADGTDFPQLCQLCPGCGCSTLNQYFGYSGAFKCLKDGAGDVAFVKHSTIFENLANKADRDQYELLCLDNTRKPVDEYKDCHLAQVPSHTVVARSMGGKEDLIWELLNQAQEHFGKDKSKEFQLFSSPHGKDLLFKDSAHGFLKVPPRMDAKMYLGYEYVTAIRNLREGTC

>d1h76a1 c.94.1.2 (A:3-333) Transferrin {Pig (Sus scrofa)}

QKTVRWCTISNQEANKCSSFRENMSKAVKNGPLVSCVKKSSYLDCIKAIRDKEADAVTLDAGLVFEAGLAPYNLKPVVAEFYGQKDNPQTHYYAVAVVKKGSNFQWNQLQGKRSCHTGLGRSAGWIIPMGLLYDQLPEPRKPIEKAVASFFSSSCVPCADPVNFPKLCQQCAGKGAEKCACSNHEPYFGYAGAFNCLKEDAGDVAFVKHSTVLENLPDKADRDQYELLCRDNTRRPVDDYENCYLAQVPSHAVVARSVDGQEDSIWELLNQAQEHFGRDKSPDFQLFSSSHGKDLLFKDSANGFLKIPSKMDSSLYLGYQYVTALRNLREE

>d1h76a2 c.94.1.2 (A:342-687) Transferrin {Pig (Sus scrofa)}

ECKKVRWCAIGHEETQKCDAWSINSGGKIECVSAENTEDCIAKIVKGEADAMSLDGGYIYIAGKCGLVPVLAENYKTEGENCVNTPEKGYLAVAVVKKSSGPDLNWNNLKGKKSCHTAVDRTAGWNIPMGLLYNKINSCKFDQFFGEGCAPGSQRNSSLCALCIGSERAPGRECLANNHERYYGYTGAFRCLVEKGDVAFVKDQVVQQNTDGKNKDDWAKDLKQMDFELLCQNGAREPVDNAENCHLARAPNHAVVARDDKVTCVAEELLKQQAQFGRHVTDCSSSFCMFKSNTKDLLFRDDTQCLARVGKTTYESYLGADYITAVANLRKCSTSKLLEACTFHSA

>d1afwa1 c.95.1.1 (A:25-293) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

KNSLLEKRPEDVVIVAANRSAIGKGFKGAFKDVNTDYLLYNFLNEFIGRFPEPLRADLNLIEEVACGNVLNVGAGATEHRAACLASGIPYSTPFVALNRQCSSGLTAVNDIANKIKVGQIDIGLALGVESMTNNYKNVNPLGMISSEELQKNREAKKCLIPMGITNENVAANFKISRKDQDEFAANSYQKAYKAKNEGLFEDEILPIKLPDGSICQSDEGPRPNVTAESLSSIRPAFIKDRGTTTAGNASQVSDGVAGVLLARRSVANQ

>d1afwa2 c.95.1.1 (A:294-417) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

LNLPVLGRYIDFQTVGVPPEIMGVGPAYAIPKVLEATGLQVQDIDIFEINEAFAAQALYCIHKLGIDLNKVNPRGGAIALGHPLGCTGARQVATILRELKKDQIGVVSMCIGTGMGAAAIFIKE

>d1qfla1 c.95.1.1 (A:4-268) Biosynthetic thiolase {Zoogloea ramigera}

SIVIASAARTAVGSFNGAFANTPAHELGATVISAVLERAGVAAGEVNEVILGQVLPAGEGQNPARQAAMKAGVPQEATAWGMNQLCGSGLRAVALGMQQIATGDASIIVAGGMESMSMAPHCAHLRGGVKMGDFKMIDTMIKDGLTDAFYGYHMGTTAENVAKQWQLSRDEQDAFAVASQNKAEAAQKDGRFKDEIVPFIVKGRKGDITVDADEYIRHGATLDSMAKLRPAFDKEGTVTAGNASGLNDGAAAALLMSEAEASRRG

>d1qfla2 c.95.1.1 (A:269-392) Biosynthetic thiolase {Zoogloea ramigera}

IQPLGRIVSWATVGVDPKVMGTGPIPASRKALERAGWKIGDLDLVEANEAFAAQACAVNKDLGWDPSIVNVNGGAIAIGHPIGASGARILNTLLFEMKRRGARKGLATLCIGGGMGVAMCIESL

>d1ek4a1 c.95.1.1 (A:1-253) Beta-ketoacyl-ACP synthase I {Escherichia coli}

MKRVVITGLGIVSSIGNNQQEVLASLREGRSGITFSQELKDSGMRSHVWGNVKLDTTGLIDRKVVRFMSDASIYAFLSMEQAIADAGLSPEAYQNNPRVGLIAGSGGGSPRFQVFGADAMRGPRGLKAVGPYVVTKAMASGVSACLATPFKIHGVNYSISSASATSAHCIGNAVEQIQLGKQDIVFAGGGEELCWEMACEFDAMGALSTKYNDTPEKASRTYDAHRDGFVIAGGGGMVVVEELEHALARGAHI

>d1ek4a2 c.95.1.1 (A:254-406) Beta-ketoacyl-ACP synthase I {Escherichia coli}

YAEIVGYGATSDGADMVAPSGEGAVRCMKMAMHGVDTPIDYLNSHGTSTPVGDVKELAAIREVFGDKSPAISATKAMTGHSLGAAGVQEAIYSLLMLEHGFIAPSINIEELDEQAAGLNIVTETTDRELTTVMSNSFGFGGTNATLVMRKLKD

>d1kas\_1 c.95.1.1 (2-251) Beta-ketoacyl-ACP synthase II {Escherichia coli}

KRRVVVTGLGMLSPVGNTVESTWKALLAGQSGISLIDHFDTSAYATKFAGLVKDFNCEDIISRKEQRKMDAFIQYGIVAGVQAMQDSGLEITEENATRIGAAIGSGIGGLGLIEENHTSLMNGGPRKISPFFVPSTIVNMVAGHLTIMYGLRGPSISIATACTSGVHNIGHAARIIAYGDADVMVAGGAEKASTPLGVGGFGAARALSTRNDNPQAASRPWDKERDGFVLGDGAGMLVLEEYEHAKKRGA

>d1kas\_2 c.95.1.1 (252-412) Beta-ketoacyl-ACP synthase II {Escherichia coli}

KIYAELVGFGMSSDAYHMTSPPENGAGAALAMANALRDAGIEASQIGYVNAHGTSTPAGDKAEAQAVKTIFGEAASRVLVSSTKSMTGHLLGAAGAVESIYSILALRDQAVPPTINLDNPDEGCDLDFVPHEARQVSGMEYTLCNSFGFGGTNGSLIFKKI

>d1e5ma1 c.95.1.1 (A:6-255) Beta-ketoacyl-ACP synthase II {Synechocystis sp.}

KKRVVVTGLGAITPIGNTLQDYWQGLMEGRNGIGPITRFDASDQACRFGGEVKDFDATQFLDRKEAKRMDRFCHFAVCASQQAINDAKLVINELNADEIGVLIGTGIGGLKVLEDQQTILLDKGPSRCSPFMIPMMIANMASGLTAINLGAKGPNNCTVTACAAGSNAIGDAFRLVQNGYAKAMICGGTEAAITPLSYAGFASARALSFRNDDPLHASRPFDKDRDGFVMGEGSGILILEELESALARGA

>d1e5ma2 c.95.1.1 (A:256-416) Beta-ketoacyl-ACP synthase II {Synechocystis sp.}

KIYGEMVGYAMTCDAYHITAPVPDGRGATRAIAWALKDSGLKPEMVSYINAHGTSTPANDVTETRAIKQALGNHAYNIAVSSTKSMTGHLLGGSGGIEAVATVMAIAEDKVPPTINLENPDPECDLDYVPGQSRALIVDVALSNSFGFGGHNVTLAFKKYQ

>d1hnja1 c.95.1.1 (A:1-174) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}

MYTKIIGTGSYLPEQVRTNADLEKMVDTSDEWIVTRTGIRERHIAAPNETVSTMGFEAATRAIEMAGIEKDQIGLIVVATTSATHAFPSAACQIQSMLGIKGCPAFDVAAACAGFTYALSVADQYVKSGAVKYALVVGSDVLARTCDPTDRGTIIIFGDGAGAAVLAASEEPGI

>d1hnja2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}

ISTHLHADGSYGELLTLPNADRVNPENSIHLTMAGNEVFKVAVTELAHIVDETLAANNLDRSQLDWLVPHQANLRIISATAKKLGMSMDNVVVTLDRHGNTSAASVPCALDEAVRDGRIKPGQLVLLEAFGGGFTWGSALVRF

>d1hzpa1 c.95.1.1 (A:-10-174) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}

MTEIATTSGARSVGLLSVGAYRPERVVTNDEICQHIDSSDEWIYTRTGIKTRRFAADDESAASMATEACRRALSNAGLSAADIDGVIVTTNTHFLQTPPAAPMVAASLGAKGILGFDLSAGCAGFGYALGAAADMIRGGGAATMLVVGTEKLSPTIDMYDRGNCFIFADGAAAVVVGETPFQGI

>d1hzpa2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}

GPTVAGSDGEQADAIRQDIDWITFAQNPSGPRPFVRLEGPAVFRWAAFKMGDVGRRAMDAAGVRPDQIDVFVPHQANSRINELLVKNLQLRPDAVVANDIEHTGNTSAASIPLAMAELLTTGAAKPGDLALLIGYGAGLSYAAQVVRM

>d1bi5a1 c.95.1.2 (A:1-235) Chalcone synthase {Alfalfa (Medicago sativa)}

MVSVSEIRKAQRAEGPATILAIGTANPANCVEQSTYPDFYFKITNSEHKTELKEKFQRMCDKSMIKRRYMYLTEEILKENPNVCEYMAPSLDARQDMVVVEVPRLGKEAAVKAIKEWGQPKSKITHLIVCTTSGVDMPGADYQLTKLLGLRPYVKRYMMYQQGAFAGGTVLRLAKDLAENNKGARVLVVCSEVTAVTFRGPSDTHLDSLVGQALFGDGAAALIVGSDPVPEIEKP

>d1bi5a2 c.95.1.2 (A:236-389) Chalcone synthase {Alfalfa (Medicago sativa)}

IFEMVWTAQTIAPDSEGAIDGHLREAGLTFHLLKDVPGIVSKNITKALVEAFEPLGISDYNSIFWIAHPGGPAILDQVEQKLALKPEKMNATREVLSEYGNMSSACVLFILDEMRKKSTQNGLKTTGEGLEWGVLFGFGPGLTIETVVLRSVAI

>d1ee0a1 c.95.1.2 (A:20-235) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}

GLATILAIGTATPPNCVAQADYADYYFRVTKSEHMVDLKEKFKRICEKTAIKKRYLALTEDYLQENPTMCEFMAPSLNARQDLVVTGVPMLGKEAAVKAIDEWGLPKSKITHLIFCTTAGVDMPGADYQLVKLLGLSPSVKRYMLYQQGAAAGGTVLRLAKDLAENNKGSRVLIVCSEITAILFHGPNENHLDSLVAQALFGDGAAALIVGSGPHL

>d1ee0a2 c.95.1.2 (A:236-395) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}

AVERPIFEIVSTDQTILPDTEKAMKLHLREGGLTFQLHRDVPLMVAKNIENAAEKALSPLGITDWNSVFWMVHPGGRAILDQVERKLNLKEDKLRASRHVLSEYGNLISACVLFIIDEVRKRSMAEGKSTTGEGLDCGVLFGFGPGMTVETVVLRSVRVT

>d1feha1 c.96.1.1 (A:210-574) Fe-only hydrogenase, catalytic domain {Clostridium pasteurianum}

HMDRVKNALNAPEKHVIVAMAPSVRASIGELFNMGFGVDVTGKIYTALRQLGFDKIFDINFGADMTIMEEATELVQRIENNGPFPMFTSCCPGWVRQAENYYPELLNNLSSAKSPQQIFGTASKTYYPSISGLDPKNVFTVTVMPCTSKKFEADRPQMEKDGLRDIDAVITTRELAKMIKDAKIPFAKLEDSEADPAMGEYSGAGAIFGATGGVMEAALRSAKDFAENAELEDIEYKQVRGLNGIKEAEVEINNNKYNVAVINGASNLFKFMKSGMINEKQYHFIEVMACHGGCVNGGGQPHVNPKDLEKVDIKKVRASVLYNQDEHLSKRKSHENTALVKMYQNYFGKPGEGRAHEILHFKYKK

>d1hfel1 c.96.1.1 (L:87-398) Fe-only hydrogenase larger subunit, C-domain {Desulfovibrio desulfuricans}

WVPEVEKKLKDGKVKCIAMPAPAVRYALGDAFGMPVGSVTTGKMLAALQKLGFAHCWDTEFTADVTIWEEGSEFVERLTKKSDMPLPQFTSCCPGWQKYAETYYPELLPHFSTCKSPIGMNGALAKTYGAERMKYDPKQVYTVSIMPCIAKKYEGLRPELKSSGMRDIDATLTTRELAYMIKKAGIDFAKLPDGKRDSLMGESTGGATIFGVTGGVMEAALRFAYEAVTGKKPDSWDFKAVRGLDGIKEATVNVGGTDVKVAVVHGAKRFKQVCDDVKAGKSPYHFIEYMACPGGCVCGGGQPVMPGVLEAM

>d1aln\_1 c.97.1.1 (1-150) Cytidine deaminase {Escherichia coli}

MHPRFQTAFAQLADNLQSALEPILADKYFPALLTGEQVSSLKSATGLDEDALAFALLPLAAACARTPLSNFNVGAIARGVSGTWYFGANMEFIGATMQQTVHAEQSAISHAWLSGEKALAAITVNYTPCGHCRQFMNELNSGLDLRIHLP

>d1aln\_2 c.97.1.1 (151-294) Cytidine deaminase {Escherichia coli}

GREAHALRDYLPDAFGPKDLEIKTLLMDEQDHGYALTGDALSQAAIAAANRSHMPYSKSPSGVALECKDGRIFSGSYAENAAFNPTLPPLQGALILLNLKGYDYPDIQRAVLAEKADAPLIQWDATSATLKALGCHSIDRVLLA

>d1g8ma2 c.97.2.1 (A:201-593) AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC {Chicken (Gallus gallus)}

GVSQLPLRYGMNPHQSPAQLYTTRPKLPLTVVNGSPGFINLCDALNAWQLVKELKQALGIPAAASFKHVSPAGAAVGIPLSEEEAQVCMVHDLHKTLTPLASAYARSRGADRMSSFGDFIALSDICDVPTAKIISREVSDGVVAPGYEEEALKILSKKKNGGYCVLQMDPNYEPDDNEIRTLYGLQLMQKRNNAVIDRSLFKNIVTKNKTLPESAVRDLIVASIAVKYTQSNSVCYAKDGQVIGIGAGQQSRIHCTRLAGDKANSWWLRHHPRVLSMKFKAGVKRAEVSNAIDQYVTGTIGEDEDLVKWQAMFEEVPAQLTEAEKKQWIAKLTAVSLSSDAFFPFRDNVDRAKRIGVQFIVAPSGSAADEVVIEACNELGITLIHTNLRLFHH

>d1rgea\_ d.1.1.1 (A:) RNase Sa {Streptomyces aureofaciens}

DVSGTVCLSALPPEATDTLNLIASDGPFPYSQDGVVFQNRESVLPTQSYGYYHEYTVITPGARTRGTRRIITGEATQEDYYTGDHYATFSLIDQTC

>d1fus\_\_ d.1.1.1 (-) RNase F1 {Fusarium moniliforme}

ESATTCGSTNYSASQVRAAANAACQYYQNDDTAGSSTYPHTYNNYEGFDFPVDGPYQEFPIKSGGVYTGGSPGADRVVINTNCEYAGAITHTGASGNNFVGCSGTN

>d1i0va\_ d.1.1.1 (A:) RNase T1 {Aspergillus oryzae}

ACDYTCGSNCYSSSDVSTAQAAGYKLHEDGETVGSNSYPHKYNNYEGFDFSVSSPYYEWPILSSGDVYSGGSPGADRVVFNENNQLAGVITHTGASGNNFVECT

>d1rtu\_\_ d.1.1.1 (-) RNase U2 {Ustilago sphaerogena}

CDIPQSTNCGGNVYSNDDINTAIQGALDDVANGDRPDNYPHQYYXEASEDITLCCGSGPWSEFPLVYNGPYYSSRDNYVSPGPDRVIYQTNTGEFCATVTHTGAASYDGFTQCS

>d1a2pa\_ d.1.1.1 (A:) Barnase/Binase {Bacillus amyloliquefaciens}

VINTFDGVADYLQTYHKLPDNYITKSEAQALGWVASKGNLADVAPGKSIGGDIFSNREGKLPGKSGRTWREADINYTSGFRNSDRILYSSDWLIYKTTDHYQTFTKIR

>d1goua\_ d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}

AVINTFDGVADYLIRYKRLPNDYITKSQASALGWVASKGDLAEVAPGKSIGGDVFSNREGRLPSAGSRTWREADINYVSGFRNADRLVYSSDWLIYKTTDHYATFTRIR

>d2rbia\_ d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}

VINTFDGVADYLIRYKRLPDNYITKSQASALGWVASKGNLAEVAPGKSIGGDVFSNREGRLPSASGRTWREADINYVSGFRNADRLVYSSDWLIYKTTDNYATFTRIR

>d1rds\_\_ d.1.1.1 (-) RNase Ms {Molsin (Aspergillus saitoi)}

ESCEYTCGSTCYWSSDVSAAKAKGYSLYESGDTIDDYPHEYHDYEGFDFPVSGTYYEYPIMSDYDVYTGGSPGADRVIFNGDDELAGVITHTGASGDDFVACSSS

>d0rst\_\_ d.1.1.1 (-) RNase St {Streptomyces erythreus}

QAPCGDTSGFEEVRLADLPPEATDTYELIEKGGPYPYPEDGTVFENREGILPDCAEGYYHEYTVKTPSGDDRGARRFVVGDGGEYFYTEDHYESFRLTIVN

>d1aqza\_ d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus restrictus), restrictocin}

ATWTCINQQLNPKTNKWEDKRLLYSQAKAESNSHHAPLSDGKTGSSYPHWFTNGYDGNGKLIKGRTPIKFGKADCDRPPKHSQNGMGKDDHYLLEFPTFPDGHDYKFDSKKPKENPGPARVIYTYPNKVFCGIVAHQRGNQGDLRLCSH

>d1de3a\_ d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus giganteus), alpha-Sarcin}

AVTWTCLNDQKNPKTNKYETKRLLYNQNKAESNSHHAPLSDGKTGSSYPHWFTNGYDGDGKLPKGRTPIKFGKSDCDRPPKHSKDGNGKTDHYLLEFPTFPDGHDYKFDSKKPKENPGPARVIYTYPNKVFCGIIAHTKENQGELKLCSH

>d1cnsa\_ d.2.1.1 (A:) Plant class II chitinase {Barley (Hordeum vulgare)}

SVSSIVSRAQFDRMLLHRNDGACQAKGFYTYDAFVAAAAAFSGFGTTGSADVQKREVAAFLAQTSHETTGGWATAPDGAFAWGYCFKQERGASSDYCTPSAQWPCAPGKRYYGRGPIQLSHNYNYGPAGRAIGVDLLANPDLVATDATVSFKTAMWFWMTAQPPKPSSHAVIVGQWSPSGADRAAGRVPGFGVITNIINGGIECGHGQDSRVADRIGFYKRYCDILGVGYGNNLDCYSQRPFA

>d1dxja\_ d.2.1.1 (A:) Plant class II chitinase {Jack bean (Canavalia ensiformis)}

DVGSVIDASLFDQLLKHRNDPACEGKGFYSYNAFVTAARSFGGFGTTGDTNTRKREVAAFLAQTSHETTGGAAGSPDGPYAWGYCFVTERDKSNKYCDPGTPCPAGKSYYGRGPIQLTHNYNYAQAGRALGVDLINNPDLVARDAVISFKTAIWFWMTPQGNKPSCHDVITNRWTPSAADVAANRTPGFGVITNIINGGIECGRGPSPASGDRIGFYKRYCDVLHLSYGPNLNCRDQRPFGG

>d1lsg\_1 d.2.1.2 (1-144) Lysozyme {Chicken (Gallus gallus)}

MKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRLQQHHLGGAKQAGDV

>d3lzt\_\_ d.2.1.2 (-) Lysozyme {Chicken (Gallus gallus)}

KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL

>d1jse\_\_ d.2.1.2 (-) Lysozyme {Turkey (Meleagris gallopavo)}

KVYGRCELAAAMKRLGLDNYRGYSLGNWVCAAKFESNFNTHATNRNTDGSTDYGILQINSRWWCNDGRTPGSKNLCNIPCSALLSSDITASVNCAKKIASGGNGMNAWVAWRNRCKGTDVHAWIRGCRL

>d1hhl\_\_ d.2.1.2 (-) Lysozyme {Guinea fowl (Numida meleagris)}

KVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNSQATNRNTDGSTDYGVLQINSRWWCNDGRTPGSRNLCNIPCSALQSSDITATANCAKKIVSDGDGMNAWVAWRKHCKGTDVRVWIKGCRL

>d1ghla\_ d.2.1.2 (A:) Lysozyme {Pheasant (Phasianus colchicus)}

GKVYGRCELAAAMKRMGLDNYRGYSLGNWVCAAKFESNFNTGATNRNTDGSTDYGILQINSRWWCNDGRTPGSKNLCHIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRKHCKGTDVNVWIRGCRL

>d1jsf\_\_ d.2.1.2 (-) Lysozyme {Human (Homo sapiens)}

KVFERCELARTLKRLGMDGYRGISLANWMCLAKWESGYNTRATNYNAGDRSTDYGIFQINSRYWCNDGKTPGAVNACHLSCSALLQDNIADAVACAKRVVRDPQGIRAWVAWRNRCQNRDVRQYVQGCGV

>d2eql\_\_ d.2.1.2 (-) Lysozyme {Horse (Equus caballus), milk}

KVFSKCELAHKLKAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSEYLASCNL

>d1qqya\_ d.2.1.2 (A:) Lysozyme {Dog (Canis familiaris), milk}

MKIFSKCELARKLKSMGMDGFHGYSLANWVCMAEYESNFNTQAFNGRNSNGSSDYGIFQLNSKWWCKSNSHSSANACNIMCSKFLDDNIDDDIACAKRVVKDPNGMSAWVAWVKHCKGKDLSKYLASCNL

>d1jug\_\_ d.2.1.2 (-) Lysozyme {Australian echidna (Tachyglossus aculeatus)}

KILKKQELCKNLVAQGMNGYQHITLPNWVCTAFHESSYNTRATNHNTDGSTDYGILQINSRYWCHDGKTPGSKNACNISCSKLLDDDITDDLKCAKKIAGEAKGLTPWVAWKSKCRGHDLSKFKC

>d1lmq\_\_ d.2.1.2 (-) Lysozyme {Rainbow trout (Oncorhynchus mykiss)}

KVYDRCELARALKASGMDGYAGNSLPNWVCLSKWESSYNTQATNRNTDGSTDYGIFQINSRYWCDDGRTPGAKNVCGIRCSQLLTDDLTVAIRCAKRVVLDPNGIGAWVAWRLHCQNQDLRSYVAGCGV

>d1gd6a\_ d.2.1.2 (A:) Lysozyme {Silkworm (Bombyx mori)}

KTFTRCGLVHELRKHGFEENLMRNWVCLVEHESSRDTSKTNTNRNGSKDYGLFQINDRYWCSKGASPGKDCNVKCSDLLTDDITKAAKCAKKIYKRHRFDAWYGWKNHCQGSLPDISSC

>d1iiza\_ d.2.1.2 (A:) Lysozyme {Tasar silkworm (Antheraea mylitta)}

KRFTRCGLVNELRKQGFDENLMRDWVCLVENESARYTDKIANVNKNGSRDYGLFQINDKYWCSKGSTPGKDCNVTCSQLLTDDITVASTCAKKIYKRTKFDAWSGWDNHCNHSNPDISSC

>d1alc\_\_ d.2.1.2 (-) alpha-Lactalbumin {Baboon (Papio cynocephalus)}

KQFTKCELSQNLYDIDGYGRIALPELICTMFHTSGYDTQAIVENDESTEYGLFQISNALWCKSSQSPQSRNICDITCDKFLDDDITDDIMCAKKILDIKGIDYWIAHKALCTEKLEQWLCEK

>d1b9oa\_ d.2.1.2 (A:) alpha-Lactalbumin {Human (Homo sapiens)}

KQFTKCELSQLLKDIDGYGGIALPELICTMFHTSGYDTQAIVENDESTEYGLFQISNKLWCKSSQVPQSRNICDISCDKFLDDDITDDIMCAKKILDIKGIDYWLAHKALCTEKLEQWLCEKL

>d1hfx\_\_ d.2.1.2 (-) alpha-Lactalbumin {Guinea pig (Cavia porcellus)}

KQLTKCALSHELNDLAGYRDITLPEWLCIIFHISGYDTQAIVKNSDHKEYGLFQINDKDFCESSTTVQSRNICDISCDKLLDDDLTDDIMCVKKILDIKGIDYWLAHKPLCSDKLEQWYCEAQ

>d1fkqa\_ d.2.1.2 (A:) alpha-Lactalbumin {Goat (Capra hircus)}

MEQLTKCEVFQKLKDLKDYGGVSLPEWVCVAFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCKDDQNPHSRNICNISCDKFLDDDLTDDIVCAKKILDKVGINYWLAHKALCSEKLDQWLCEKL

>d1f6ra\_ d.2.1.2 (A:) alpha-Lactalbumin {Cow (Bos taurus)}

EQLTKCEVFRELKDLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNNDSTEYGLFQINNKIWCKDDQNPHSSNICNISCDKFLDDDLTDDIMCVKKILDKVGINYWLAHKALCSEKLDQWLCEKL

>d1j8wa\_ d.2.1.2 (A:) alpha-Lactalbumin {Mouse (Mus musculus)}

TELTKCKVSHAIKDMDGYQGISLLEWTCVLFHTSGYDSQAVVNDNGSTEYGLFQISERFWCKSSEFPESENICGISCDKLLDDELDDDIVCAKKIVAIKGIDYWKAYKPMCSEKLEQWRCEKP

>d169la\_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQKRWDAAAAALAAAAWAAATPNRAKRVITTFRTGTWDAYK

>d174la\_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLAAAADLAAAKAALAAAIGRNTNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRMLQQKRWDEAAVNLAKSRWYNQTPNRAKRVITTFRTGTWDAYKNL

>d176la\_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHTLKVDGNSNAAKSELDKAIGRNTNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRMLQQKRWDEAAVNLAKSRWYNQTPNRAKRVITTFRTGTWDAYKNL

>d189l\_\_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNLFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPDLNVAKSELDKAIGRNCNGVITKDEAEKLFNQDVDAAVRGILRNPKLKPVYDSLDAVRRCALINMVFQMGETGVAGFTDSLRMLQQKRWDEAAANLAKSRWYNQTPDRAKRVITTFRTGTWDAYKNL

>d191l\_\_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRACAGAITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSLDAVRRCALINMVFQMGETGVAGFTNSLRMLQQKRWDAAAAALAKSRWYNQTPNRAKRVITTFRTGTWDAYK

>d192l\_\_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLAAAKAALAAAIGRNTNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRMLQQKRWAAAAAALAKSRWYNQTPNRAKRVITTFRTGTWDAYK

>d217l\_\_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKEELDKAIGRNTNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRMLQQKRWDEAAVNLAKSRWYNQTPNRAKRVITTFRTGTWDAYK

>d1k28a3 d.2.1.3 (A:130-345) Tail-associated lysozyme gp5, catalytic domain {Bacteriophage T4}

NVLNQGGEVGYDSSSNVIQDSNLDTAINPDDRPLSEIPTDDNPNMSMAEMLRRDEGLRLKVYWDTEGYPTIGIGHLIMKQPVRDMAQINKVLSKQVGREITGNPGSITMEEATTLFERDLADMQRDIKSHSKVGPVWQAVNRSRQMALENMAFQMGVGGVAKFNTMLTAMLAGDWEKAYKAGRDSLWYQQTKGRASRVTMIILTGNLESYGVEVKT

>d1am7a\_ d.2.1.4 (A:) Lambda lysozyme {Bacteriophage lambda}

MVEINNQRKAFLDMLAWSEGTDNGRQKTRNHGYDVIVGGELFTDYSDHPRKLVTLNPKLKSTGAGRYQLLSRWWDAYRKQLGLKDFSPKSQDAVALQQIKERGALPMIDRGDIRQAIDRCSNIWASLPGAGYGQFEHKADSLIAKFKEAGGTVR

>d153l\_\_ d.2.1.5 (-) Lysozyme {Goose (Anser anser anser)}

RTDCYGNVNRIDTTGASCKTAKPEGLSYCGVSASKKIAERDLQAMDRYKTIIKKVGEKLCVEPAVIAGIISRESHAGKVLKNGWGDRGNGFGLMQVDKRSHKPQGTWNGEVHITQGTTILINFIKTIQKKFPSWTKDQQLKGGISAYNAGAGNVRSYARMDIGTTHDDYANDVVARAQYYKQHGY

>d1qsaa2 d.2.1.6 (A:451-618) 70 kDa soluble lytic transglycosylase, SLT70 {Escherichia coli}

LAYNDLFKRYTSGKEIPQSYAMAIARQESAWNPKVKSPVGASGLMQIMPGTATHTVKMFSIPGYSSPGQLLDPETNINIGTSYLQYVYQQFGNNRIFSSAAYNAGPGRVRTWLGNSAGRIDAVAFVESIPFSETRGYVKNVLAYDAYYRYFMGDKPTLMSATEWGRRY

>d1qusa\_ d.2.1.6 (A:) 36 kDa soluble lytic transglycosylase, SLT35 {Escherichia coli}

MVEPQHNVMQMGGDFANNPNAQQFIDKMVNKHGFDRQQLQEILSQAKRLDSVLRLMDNQAPTTSVKPPSGPNGAWLRYRKKFITPDNVQNGVVFWNQYEDALNRAWQVYGVPPEIIVGIIGVETRWGRVMGKTRILDALATLSFNYPRRAEYFSGELETFLLMARDEQDDPLNLKGSFAGAMGYGQFMPSSYKQYAVDFSGDGHINLWDPVDAIGSVANYFKAHGWVKGDQVAVMANGQAPGLPNGFKTKYSISQLAAAGLTPQQPLGNHQQASLLRLDVGTGYQYWYGLPNFYTITRYNHSTHYAMAVWQLGQAVALARVQ

>d1chka\_ d.2.1.7 (A:) Endochitosanase {Streptomyces sp., strain N174}

AGAGLDDPHKKEIAMELVSSAENSSLDWKAQYKYIEDIGDGRGYTGGIIGFCSGTGDMLELVQHYTDLEPGNILAKYLPALKKVNGSASHSGLGTPFTKDWATAAKDTVFQQAQNDERDRVYFDPAVSQAKADGLRALGQFAYYDAIVMHGPGNDPTSFGGIRKTAMKKARTPAQGGDETTYLNGFLDARKAAMLTEAAHDDTSRVDTEQRVFLKAGNLDLNPPLKWKTYGDPYVINS

>d1qgia\_ d.2.1.7 (A:) Endochitosanase {Bacillus circulans}

ASPDDNFSPETLQFLRNNTGLDGEQWNNIMKLINKPEQDDLNWIKYYGYCEDIEDERGYTIGLFGATTGGSRDTHPDGPDLFKAYDAAKGASNPSADGALKRLGINGKMKGSILEIKDSEKVFCGKIKKLQNDAAWRKAMWETFYNVYIRYSVEQARQRGFTSAVTIGSFVDTALNQGATGGSDTLQGLLARSGSSSNEKTFMKNFHAKRTLVVDTNKYNKPPNGKNRVKQWDTLVDMGKMNLKNVDSEIAQVTDWEMK

>d1aec\_\_ d.3.1.1 (-) Actinidin {Chinese gooseberry or kiwifruit (Actinidia chinensis)}

LPSYVDWRSAGAVVDIKSQGECGGCWAFSAIATVEGINKIVTGVLISLSEQELIDCGRTQNTRGCNGGYITDGFQFIINNGGINTEENYPYTAQDGECNVDLQNEKYVTIDTYENVPYNNEWALQTAVTYQPVSVALDAAGDAFKQYSSGIFTGPCGTAIDHAVTIVGYGTEGGIDYWIVKNSWDTTWGEEGYMRILRNVGGAGTCGIATMPSYPVKY

>d2act\_\_ d.3.1.1 (-) Actinidin {Chinese gooseberry or kiwifruit (Actinidia chinensis)}

LPSYVDWRSAGAVVDIKSQGECGGCWAFSAIATVEGINKITSGSLISLSEQELIDCGRTQNTRGCDGGYITDGFQFIINDGGINTEENYPYTAQDGDCDVALQDQKYVTIDTYENVPYNNEWALQTAVTYQPVSVALDAAGDAFKQYASGIFTGPCGTAVDHAIVIVGYGTEGGVDYWIVKNSWDTTWGEEGYMRILRNVGGAGTCGIATMPSYPVKY

>d1ppn\_\_ d.3.1.1 (-) Papain {Papaya (Carica papaya)}

IPEYVDWRQKGAVTPVKNQGSCGSCWAFSAVVTIEGIIKIRTGNLNEYSEQELLDCDRRSYGCNGGYPWSALQLVAQYGIHYRNTYPYEGVQRYCRSREKGPYAAKTDGVRQVQPYNEGALLYSIANQPVSVVLEAAGKDFQLYRGGIFVGPCGNKVDHAVAAVGYGPNYILIKNSWGTGWGENGYIRIKRGTGNSYGVCGLYTSSFYPVKN

>d1pcia\_ d.3.1.1 (A:) Caricain (protease omega) {Papaya (Carica papaya)}

LTSTERLIQLFNSWMLNHNKFYENVDEKLYRFEIFKDNLNYIDETNKKNNSYWLGLNEFADLSNDEFNEKYVGSLIDATIEQSYDEEFINEDIVNLPENVDWRKKGAVTPVRHQGSCGSCWAFSAVATVEGINKIRTGKLVELSEQELVDCERRSHGCKGGYPPYALEYVAKNGIHLRSKYPYKAKQGTCRAKQVGGPIVKTSGVGRVQPNNEGNLLNAIAKQPVSVVVESKGRPFQLYKGGIFEGPCGTKVDGAVTAVGYGKSGGKGYILIKNSWGTAWGEKGYIRIKRAPGNSPGVCGLYKSSYYPTKN

>d1ppo\_\_ d.3.1.1 (-) Caricain (protease omega) {Papaya (Carica papaya)}

LPENVDWRKKGAVTPVRHQGSCGSCWAFSAVATVEGINKIRTGKLVELSEQELVDCERRSHGCKGGYPPYALEYVAKNGIHLRSKYPYKAKQGTCRAKQVGGPIVKTSGVGRVQPNNEGNLLNAIAKQPVSVVVESKGRPFQLYKGGIFEGPCGTKVDHAVTAVGYGKSGGKGYILIKNSWGTAWGEKGYIRIKRAPGNSPGVCGLYKSSYYPTKN

>d1yal\_\_ d.3.1.1 (-) Chymopapain {Papaya (Carica papaya)}

YPQSIDWRAKGAVTPVKNQGACGSCWAFSTIATVEGINKIVTGNLLELSEQELVDCDKHSYGCKGGYQTTSLQYVANNGVHTSKVYPYQAKQYKCRATDKPGPKVKITGYKRVPSNCETSFLGALANQPLSVLVEAGGKPFQLYKSGVFDGPCGTKLDHAVTAVGYGTSDGKNYIIIKNSWGPNWGEKGYMRLKRQSGNSQGTCGVYKSSYYPFKGFA

>d1gece\_ d.3.1.1 (E:) Glycyl endopeptidase {Papaya (Carica papaya)}

LPESVDWRAKGAVTPVKHQGYCESCWAFSTVATVEGINKIKTGNLVELSEQELVDCDLQSYGCNRGYQSTSLQYVAQNGIHLRAKYPYIAKQQTCRANQVGGPKVKTNGVGRVQSNNEGSLLNAIAHQPVSVVVESAGRDFQNYKGGIFEGSCGTKVDHAVTAVGYGKSGGKGYILIKNSWGPGWGENGYIRIRRASGNSPGVCGVYRSSYYPIKN

>d1cqda\_ d.3.1.1 (A:) Proline-specific cysteine protease {Ginger rhizome (Zingiber officinale)}

LPDSIDWRENGAVVPVKNQGGCGSCWAFSTVAAVEGINQIVTGDLISLSEQQLVDCTTANHGCRGGWMNPAFQFIVNNGGINSEETYPYRGQDGICNSTVNAPVVSIDSYENVPSHNEQSLQKAVANQPVSVTMDAAGRDFQLYRSGIFTGSCNISANHALTVVGYGTENDKDFWIVKNSWGKNWGESGYIRAERNIENPDGKCGITRFASYPVKK

>d3gcb\_\_ d.3.1.1 (-) Bleomycin hydrolase {Baker's yeast (Saccharomyces cerevisiae), Gal6}

AFQGAMASSIDISKINSWNKEFQSDLTHQLATTVLKNYNADDALLNKTRLQKQDNRVFNTVVSTDSTPVTNQKSSGRAWLFAATNQLRLNVLSELNLKEFELSQAYLFFYDKLEKANYFLDQIVSSADQDIDSRLVQYLLAAPTEDGGQYSMFLNLVKKYGLIPKDLYGDLPYSTTASRKWNSLLTTKLREFAETLRTALKERSADDSIIVTLREQMQREIFRLMSLFMDIPPVQPNEQFTWEYVDKDKKIHTIKSTPLEFASKYAKLDPSTPVSLINDPRHPYGKLIKIDRLGNVLGGDAVIYLNVDNETLSKLVVKRLQNNKAVFFGSHTPKFMDKKTGVMDIELWNYPAIGYNLPQQKASRIRYHESLMTHAMLITGCHVDETSKLPLRYRVENSWGKDSGKDGLYVMTQKYFEEYCFQIVVDINELPKELASKFTSGKEEPIVLPIWDPMGALA

>d2cb5a\_ d.3.1.1 (A:) Bleomycin hydrolase {Human (Homo sapiens)}

SSSGLNSEKVAALIQKLNSDPQFVLAQNVGTTHDLLDICLKRATVQRAQHVFQHAVPQEGKPITNQKSSGRSWIFSCLNVMRLPFMKKLNIEEFEFSQSYLFFWDKVERCYFFLSAFVDTAQRKEPEDGRLVQFLLMNPANDGGQWDMLVNIVEKYGVIPKKCFPESYTTEATRRMNDILNHKMREFCIRLRNLVHSGATKGEISATQDVMMEEIFRVVCICLGNPPETFTWEYRDKDKNYEKIGPITPLEFYREHVKPLFNMEDKICLVNDPRPQHKHNKLYTVEYLSNMVGGRKTLYNNQPIDFLKKMVAASIKDGEAVWFGCDVGKHFNSKLGLSDMNLYDHELVFGVSLKNMNKAERLTFGESLMTHAMTFTAVSEKDDQDGAFTKWRVENSWGEDHGHKGYLCMTDEWFSEYVYEVVVDRKHVPEEVLAVLEQEPIILPAWDPMGALA

>d1f2aa\_ d.3.1.1 (A:) Cruzain {Trypanosoma cruzi}

APAAVDWRARGAVTAVKDQGQCGSCWAFSAIGNVECQWFLAGHPLTNLSEQMLVSCDKTDSGCSGGLMNNAFEWIVQENNGAVYTEDSYPYASGEGISPPCTTSGHTVGATITGHVELPQDEAQIAAWLAVNGPVAVAVDASSWMTYTGGVMTSCVSEQLDHGVLLVGYNDSAAVPYWIIKNSWTTQWGEEGYIRIAKGSNQCLVKEEASSAVVG

>d3pbh\_\_ d.3.1.1 (-) (Pro)cathepsin B {Human (Homo sapiens)}

MRSRPSFHPLSDELVNYVNKRNTTWQAGHNFYNVDMSYLKRLCGTFLGGPKPPQRVMFTEDLKLPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICIHTNAHVSVEVSAEDLLTCCGSMCGDGCNGGYPAEAWNFWTRKGLVSGGLYESHVGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYSPTYKQDKHYGYNSYSVSNSEKDIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMGGHAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEVVAGIPRTD

>g1huc.1 d.3.1.1 (A:,B:) (Pro)cathepsin B {Human (Homo sapiens)}

LPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICIHTNXVSVEVSAEDLLTCCGSMCGDGCNGGYPAEAWNFWTRKGLVSGGLYESHVGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYSPTYKQDKHYGYNSYSVSNSEKDIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVTGEMMGGHAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEVVAGIPRTD

>d1mira\_ d.3.1.1 (A:) (Pro)cathepsin B {Rat (Rattus norvegicus)}

SDDMINYINKQNTTWQAGRNFYNVDISYLKKLCGTVLGGPKLPERVGFSEDINLPESFDAREQWSNCPTIAQIRDQGSCGSSWAFGAVEAMSDRICIHTNGRVNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWNFWTRKGLVSGGVYNSHIGCLPYTIPPCEHHVNGARPPCTGEGDTPKCNKMCEAGYSTSYKEDKHYGYTSYSVSDSEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDVMGGHAIRILGWGIENGVPYWLVANSWNADWGDNGFFKILRGENHCGIESEIVAGIPRTQQYWGRF

>d1thea\_ d.3.1.1 (A:) (Pro)cathepsin B {Rat (Rattus norvegicus)}

LPESFDAREQWSNCPTIAQIRDQGSCGSCWAFGAVEAMSDRICIHTNGRVNVEVSAEDLLTCCGIQCGDGCNGGYPSGAWNFWTRKGLVSGGVYNSHIGCLPYTIPPCEHHVNGARPPCTGEGDTPKCNKMCEAGYSTSYKEDKHYGYTSYSVSDSEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDVMGGHAIRILGWGIENGVPYWLVANSWNADWGDNGFFKILRGENHCGIESEIVAGIPRT

>d1qdqa\_ d.3.1.1 (A:) (Pro)cathepsin B {Cow (Bos taurus)}

LPESFDAREQWPNCPTIKEIRDQGSCGSCWAFGAVEAISDRICIHSNGRVNVEVSAEDMLTCCGGECGDGCNGGEPSGAWNFWTKKGLVSGGLYNSHVGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKTCEPGYSPSYKEDKHFGCSSYSVANNEKEIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVSGEIMGGHAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEIVAGMPCT

>d1cs8a\_ d.3.1.1 (A:) (Pro)cathepsin L {Human (Homo sapiens)}

SLTFDHSLEAQWTKWKAMHNRLYGMNEEGWRRAVWEKNMKMIELHNQEYREGKHSFTMAMNAFGDMTSEEFRQVMNGFQNRKPRKGKVFQEPLFYEAPRSVDWREKGYVTPVKNQGQCGSCWAFSATGALEGQMFRKTGRLISLSEQNLVDCSGPQGNEGCNGGLMDYAFQYVQDNGGLDSEESYPYEATEESCKYNPKYSVANDAGFVDIPKQEKALMKAVATVGPISVAIDAGHESFLFYKEGIYFEPDCSSEDMDHGVLVVGYGFESTESDNNKYWLVKNSWGEEWGMGGYVKMAKDRRNHCGIASAASYPTV

>g1icf.1 d.3.1.1 (A:,B:) (Pro)cathepsin L {Human (Homo sapiens)}

APRSVDWREKGYVTPVKNQGQCGSCWAFSATGALEGQMFRKTGRLISLSEQNLVDCSGPQGNEGCNGGLMDYAFQYVQDNGGLDSEESYPYEATEESCKYNPKYSVANDTGFVDIPKQEKALMKAVATVGPISVAIDAGHESFLFYKEGIYFEPDCSSEDMDHGVLVVGYGFESTXNNKYWLVKNSWGEEWGMGGYVKMAKDRRNHCGIASAASYPTV

>d1mema\_ d.3.1.1 (A:) (Pro)cathepsin K {Human (Homo sapiens)}

APDSVDYRKKGYVTPVKNQGQCGSCWAFSSVGALEGQLKKKTGKLLNLSPQNLVDCVSENDGCGGGYMTNAFQYVQKNRGIDSEDAYPYVGQEESCMYNPTGKAAKCRGYREIPEGNEKALKRAVARVGPVSVAIDASLTSFQFYSKGVYYDESCNSDNLNHAVLAVGYGIQKGNKHWIIKNSWGENWGNKGYILMARNKNNACGIANLASFPKM

>d7pcka\_ d.3.1.1 (A:) (Pro)cathepsin K {Human (Homo sapiens)}

LYPEEILDTHWELWKKTHRKQYNNKVDEISRRLIWEKNLKYISIHNLEASLGVHTYELAMNHLGDMTSEEVVQKMTGLKVPLSHSRSNDTLYIPEWEGRAPDSVDYRKKGYVTPVKNQGQCGSCWAFSSVGALEGQLKKKTGKLLNLSPQNLVDCVSENDGCGGGYMTNAFQYVQKNRGIDSEDAYPYVGQEESCMYNPTGKAAKCRGYREIPEGNEKALKRAVARVGPVSVAIDASLTSFQFYSKGVYYDESCNSDNLNHAVLAVGYGIQKGNKHWIIKNSWGENWGNKGYILMARNKNNACGIANLASFPKM

>d8pcha\_ d.3.1.1 (A:) (Pro)cathepsin K {Pig (Sus scrofa)}

YPPSMDWRKKGNFVSPVKNQGSCGSCWTFSTTGALESAVAIATGKMLSLAEQQLVDCAQNFNNHGCQGGLPSQAFEYIRYNKGIMGEDTYPYKGQDDHCKFQPDKAIAFVKDVANITMNDEEAMVEAVALYNPVSFAFEVTNDFLMYRKGIYSSTSCHKTPDKVNHAVLAVGYGEENGIPYWIVKNSWGPQWGMNGYFLIERGKNMCGLAACASYPIPLV

>d1fh0a\_ d.3.1.1 (A:) (Pro)cathepsin V {Human (Homo sapiens)}

LPKSVDWRKKGYVTPVKNQKQCGSCWAFSATGALEGQMFRKTGKLVSLSEQNLVDCSRPQGNQGCNGGFMARAFQYVKENGGLDSEESYPYVAVDEICKYRPENSVAQDTGFTVVAPGKEKALMKAVATVGPISVAMDAGHSSFQFYKSGIYFEPDCSSKNLDHGVLVVGYGFEGANSDNSKYWLVKNSWGPEWGSNGYVKIAKDKNNHCGIATAASYPNV

>d1deua\_ d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}

RGQTCYRPLRGDGLAPLGRTTYPRPHEYLSPADLPKSWDWRNVDGVNYASITRNQHIPQYCGSCWAHASTSAMADRINIKRKGAWPSTLLSVQNVIDCGNAGSCEGGNDLSVWDYAHQHGIPDETCNNYQAKDQECDKFNQCGTCNEFKECHAIRNYTLWRVGDYGSLSGREKMMAEIYANGPISCGIMATERLANYTGGIYAEYQDTTYINHVVSVAGWGISDGTEYWIVRNSWGEPWGERGWLRIVTSTYKDGKGARYNLAIEEHCTFGDPIV

>d1ef7a\_ d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}

LPKSWDWRNVDGVNYASITRNQHIPQYCGSCWAHASTSAMADRINIKRKGAWPSTLLSVQNVIDCGNAGSCEGGNDLSVWDYAHQHGIPDETCNNYQAKDQECDKFNQCGTCNEFKECHAIRNYTLWRVGDYGSLSGREKMMAEIYANGPISCGIMATERLANYTGGIYAEYQDTTYINHVVSVAGWGISDGTEYWIVRNSWGEPWGERGWLRIVTSTYKDGKGARYNLAIEEHCTFGDPIV

>d1cv8\_\_ d.3.1.1 (-) Staphopain {Staphylococcus aureus}

NEQYVNKLENFKIRETQGNNGWCAGYTMSALLNATYNTNKYHAEAVMRFLHPNLQGQQFQFTGLTPREMIYFGQTQGRSPQLLNRMTTYNEVDNLTKNNKGIAILGSRVESRNGMHAGHAMAVVGNAKLNNGQEVIIIWNPWDNGFMTQDAKNNVIPVSNGDHYQWYSSIYGY

>d1dkia\_ d.3.1.1 (A:) Streptococcal pyrogenic exotoxin B {Streptococcus pyogenes}

LDKVNLGGELSGSNMYVYNISTGGFVIVSGDKRSPEILGYSTSGSFDVNGKENIASFMESYVEQIKENKKLDSTYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGSVATATAQIMKYHNYPNKGLKDYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQINRGDFSKQDWEAQIDKELSQNQPVYYQGVGKVGGHAFVIDGADGRNFYHVNWGWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVGIKP

>d1qmya\_ d.3.1.2 (A:) FMDV leader protease {Foot-and-mouth disease virus}

MELTLYNGEKKTFYSRPNNHDNAWLNAILQLFRYVEEPFFDWVYSSPENLTLEAIKQLEDLTGLELHEGGPPALVIWNIKHLLHTGIGTASRPSEVCVVDGTDMSLADFHAGIFLKGQEHAVFACVTSNGWYAIDDEDFYPWTPDPSDVLVFVPYD

>d1qola\_ d.3.1.2 (A:) FMDV leader protease {Foot-and-mouth disease virus}

MELTLYNGEKKTFYSRPNNHDNAWLNAILQLFRYVEEPFFDWVYSSPENLTLEAIKQLEDLTGLELHEGGPPALVIWNIKHLLHTGIGTASRPSEVCVVDGTDMCLADFHAGIFLKGQEHAVFACVTSNGWYAIDDEDFYPWTPDPSDVLVFVPYDQEPLNGEWKAKVQRKLK

>d1kful3 d.3.1.3 (L:2-355) Calpain large subunit, catalytic domain (domain II) {Human (Homo sapiens)}

AGIAAKLAKDREAAEGLGSHERAIKYLNQDYEALRNECLEAGTLFQDPSFPAIPSALGFKELGPYSSKTRGMRWKRPTEICADPQFIIGGATRTDICQGALGDCWLLAAIASLTLNEEILARVVPLNQSFQENYAGIFHFQFWQYGEWVEVVVDDRLPTKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEGFEDFTGGIAEWYELKKPPPNLFKIIQKALQKGSLLGCSIDITSAADSEAITFQKLVKGHAYSVTGAEEVESNGSLQKLIRIRNPWGEVEWTGRWNDNCPSWNTIDPEERERLTRRHEDGEFWMSFSDFLRHYSRLEICNLTPDTLTSDTYKK

>d1df0a3 d.3.1.3 (A:2-355) Calpain large subunit, catalytic domain (domain II) {Rat (Rattus norvegicus)}

AGIAMKLAKDREAAEGLGSHERAIKYLNQDYETLRNECLEAGALFQDPSFPALPSSLGFKELGPYSSKTRGIEWKRPTEICADPQFIIGGATRTDICQGALGDSWLLAAIASLTLNEEILARVVPLDQSFQENYAGIFHFQFWQYGEWVEVVVDDRLPTKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEGFEDFTGGIAEWYELRKPPPNLFKIIQKALEKGSLLGCSIDITSAADSEAVTYQKLVKGHAYSVTGAEEVESSGSLQKLIRIRNPWGQVEWTGKWNDNCPSWNTVDPEVRANLTERQEDGEFWMSFSDFLRHYSRLEICNLTPDTLTCDSYKK

>d1f13a4 d.3.1.4 (A:191-515) Transglutaminase catalytic domain {Human (Homo sapiens)}

DAVYLDNEKEREEYVLNDIGVIFYGEVNDIKTRSWSYGQFEDGILDTCLYVMDRAQMDLSGRGNPIKVSRVGSAMVNAKDDEGVLVGSWDNIYAYGVPPSAWTGSVDILLEYRSSENPVRYGQCWVFAGVFNTFLRCLGIPARIVTNYFSAHDNDANLQMDIFLEEDGNVNSKLTKDSVWNYHCWNEAWMTRPDLPVGFGGWQAVDSTPQENSDGMYRCGPASVQAIKHGHVCFQFDAPFVFAEVNSDLIYITAKKDGTHVVENVDATHIGKLIVTKQIGGDGMMDITDTYKFQEGQEEERLALETALMYGAKKPLNTEGVMKSR

>d1g0da4 d.3.1.4 (A:141-461) Transglutaminase catalytic domain {Red sea bream (Chrysophrys major)}

DMVYLPDESKLQEYVMNEDGVIYMGTWDYIRSIPWNYGQFEDYVMDICFEVLDNSPAALKNSEMDIEHRSDPVYVGRTITAMVNSNGDRGVLTGRWEEPYTDGVAPYRWTGSVPILQQWSKAGVRPVKYGQCWVFAAVACTVLRCLGIPTRPITNFASAHDVDGNLSVDFLLNERLESLDSRQRSDSSWNFHCWVESWMSREDLPEGNDGWQVLDPTPQELSDGEFCCGPCPVAAIKEGNLGVKYDAPFVFAEVNADTIYWIVQKDGQRRKITEDHASVGKNISTKSVYGNHREDVTLHYKYPEGSQKEREVYKKAGRRVT

>d1e2ta\_ d.3.1.5 (A:) Arylamine N-acetyltransferase {Salmonella typhimurium}

HMTSFLHAYFTRLHCQPLGVPTVEALRTLHLAHNCAIPFENLDVLLPREIQLDETALEEKLLYARRGGYCFELNGLFERALRDIGFNVRSLLGRVILSHPASLPPRTHRLLLVDVEDEQWIADVGFGGQTLTAPLRLQAEIAQQTPHGEYRLMQEGSTWILQFRHHEHWQSMYCFDLGVQQQSDHVMGNFWSAHWPQSHFRHHLLMCRHLPDGGKLTLTNFHFTRYHQGHAVEQVNVPDVPSLYQLLQQQFGLGVNDVKHGFTEAELAAVMAAF

>d1uch\_\_ d.3.1.6 (-) Ubiquitin C-terminal hydrolase UCH-l3 {Human (Homo sapiens)}

RWLPLEANPEVTNQFLKQLGLHPNWQFVDVYGMDPELLSMVPRPVCAVLLLFPITEKYEVFRTEEEEKIKSQGQDVTSSVYFMKQTISNACGTIGLIHAIANNKDKMHFESGSTLKKFLEESVSMSPEERARYLENYDAIRVTHETSAHEGQTEAPSIDEKVDLHFIALVHVDGHLYELDGRKPFPINHGETSDETLLEDAIEVCKKFMERDPDELRFNAIALSAA

>d1cmxa\_ d.3.1.6 (A:) Ubiquitin C-terminal hydrolase UCH-l3 {Synthetic, based on Saccharomyces cerevisiae sequence}

RAVVPIESNPEVFTNFAHKLGLKNEWAYFDIYSLTEPELLAFLPRPVKAIVLLFPINEDRKSSTSQQITSSYDVIWFKQSVKNACGLYAILHSLSNNQSLLEPGSDLDNFLKSQSDTSSSKNRFDDVTTDQFVLNVIKENVQTFSTGQSEAPEATADTNLHYITYVEENGGIFELDGRNLSGPLYLGKSDPTATDLIEQELVRVRVASYMENANEEDVLNFAMLGLGPN

>d1avpa\_ d.3.1.7 (A:) Human adenovirus 2 proteinase {Mastadenovirus H2}

MGSSEQELKAIVKDLGCGPYFLGTYDKRFPGFVSPHKLACAIVNTAGRETGGVHWMAFAWNPRSKTCYLFEPFGFSDQRLKQVYQFEYESLLRRSAIASSPDRCITLEKSTQSVQGPNSAACGLFCCMFLHAFANWPQTPMDHNPTMNLITGVPNSMLNSPQVQPTLRRNQEQLYSFLERHSPYFRSHSAQIRSATSFCHLKNM

>d1euva\_ d.3.1.7 (A:) Ulp1 protease C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

GSLVPELNEKDDDQVQKALASRENTQLMNRDNIEITVRDFKTLAPRRWLNDTIIEFFMKYIEKSTPNTVAFNSFFYTNLSERGYQGVRRWMKRKKTQIDKLDKIFTPINLNQSHWALGIIDLKKKTIGYVDSLSNGPNAMSFAILTDLQKYVMEESKHTIGEDFDLIHLDCPQQPNGYDCGIYVCMNTLYGSADAPLDFDYKDAIRMRRFIAHLILTDALK

>d7ceib\_ d.4.1.1 (B:) DNase domain of colicin E7 {Escherichia coli}

RNKPGKATGKGKPVNNKWLNNAGKDLGSPVPDRIANKLRDKEFKSFDDFRKKFWEEVSKDPELSKQFSRNNNDRMKVGKAPKTRTQDVSGKRTSFELHHEKPISQNGGVYDMDNISVVTPKRHIDIH

>d1emvb\_ d.4.1.1 (B:) DNase domain of colicin E9 {Escherichia coli}

MESKRNKPGKATGKGKPVGDKWLDDAGKDSGAPIPDRIADKLRDKEFKSFDDFRKAVWEEVSKDPELSKNLNPSNKSSVSKGYSPFTPKNQQVGGRKVYELHHDKPISQGGEVYDMDNIRVTTPKRHIDIH

>d1ql0a\_ d.4.1.2 (A:) Sm endonuclease {Serratia marcescens}

SIDNCAVGCPTGGSSKVSIVRHAYTLNNNSTTKFANWVAYHITKDTPASGKTRNWKTDPALNPADTLAPADYTGANAALKVDRGHQAPLASLAGVSDWESLNYLSNITPQKSDLNQGAWARLEDQERKLIDRADISSVYTVTGPLYERDMGKLPGTQKAHTIPSAYWKVIFINNSPAVNHYAAFLFDQNTPKGADFCQFRVTVDEIEKRTGLIIWAGLPDDVQASLKSKPGVLPELMGCKN

>d1a73a\_ d.4.1.3 (A:) Intron-encoded homing endonuclease I-PpoI {Slime mold (Physarum polycephalum)}

ALTNAQILAVIDSWEETVGQFPVITHHVPLGGGLQGTLHCYEIPLAAPYGVGFAKNGPTRWQYKRTINQVVHRWGSHTVPFLLEPDNINGKTCTASHLCHNTRCHNPLHLCWESLDDNKGRNWCPGPNGGCVHAVVCLRQGPLYGPGATVAGPQQRGSHFVV

>d1e7la2 d.4.1.5 (A:1-103) Recombination endonuclease VII, C-terminal and dimerization domains {Bacteriophage T4}

MLLTGKLYKEEKQKFYDAQNGKCLICQRELNPDVQANHLDHDHELNGPKAGKVRGLLCNLCDAAEGQMKHKFNRSGLKGQGVDYLEWLENLLTYLKSDYTQNN

>d1dy5a\_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KETAAAKFERQHMDSSTSAASSSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTNCYQSYSTMSITDCRETGSSKYPNCAYKTTQANKHIIVACEGNPYVPVHFDASV

>d1h8xa\_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KESAAAKFERQHMDSGNSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNVCFQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSQKERHIIVACEGSPYVPVHFDASVE

>d1rbd\_\_ d.5.1.1 (-) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

SSSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTNCYQSYSTMSITDCRETGSSKYPNCAYKTTQANKHIIVACEGNPYVPVHFDASV

>g1d5d.1 d.5.1.1 (A:,B:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KETAAAKMERQHLDSXNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTNCYQSYSTMSITDCRETGSSKYPNCAYKTTQANKHIIVACEGNPYVPVHFDASV

>d1e21a\_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Human (Homo sapiens), des1-7}

AFQRQHMDSDSSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNVCFQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSPKERHIIVACEGSPYVPVHFDASVE

>d1rraa\_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Rat (Rattus norvegicus)}

AESSADKFKRQHMDTEGPSKSSPTYCNQMMKRQGMTKGSCKPVNTFVHEPLEDVQAICSQGQVTCKNGRNNCHKSSSTLRITDCRLKGSSKYPNCDYTTTDSQKHIIIACDGNPYVPVHFDASV

>d1onc\_\_ d.5.1.1 (-) P-30 protein {Frog (Rana pipiens)}

EDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTTSEFYLSDCNVTSRPCKYKLKKSTNKFCVTCENQAPVHFVGVGSC

>d1bc4\_\_ d.5.1.1 (-) Cytotoxic ribonuclease {Bullfrog (Rana catesbeiana)}

ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFIISSATTVKAICTGVINMNVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP

>d11bga\_ d.5.1.1 (A:) Seminal ribonucleasease {Cow (Bos taurus)}

KESAAAKFERQHMDSGNSPSSSSNYCNLMMCCRKMTQGKCKPVNTFVHESLADVKAVCSQKKVTCKNGQTNCYQSKSTMRITDCRETGSSKYPNCAYKTTQVEKHIIVACGGKPSVPVHFDASV

>d1b6va\_ d.5.1.1 (A:) Hybrid between ribonuclease A and seminal ribonuclease {Cow (Bos taurus)}

KETAAAKFERQHMDSSTSAASSSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVKAVCSQKKVTCKNGQTNCYQSKSTMRITDCRETGSSKYPNCAYKTTQANKHIIVACGGKPYVPVHFDASV

>d1dyta\_ d.5.1.1 (A:) Eosinophil cationic protein (ECP), ribonuclease 3 {Human (Homo sapiens)}

RPPQFTRAQWFAIQHISLNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSRFRVPLLHCDLINPGAQNISNCRYADRPGRRFYVVACDNRDPRDSPRYPVVPVHLDTTI

>d1hi2a\_ d.5.1.1 (A:) Eosinophil-derived neurotoxin (EDN) {Human (Homo sapiens)}

MKPPQFTWAQWFETQHINMTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGNPNMTCPSNKTRKNCHHSGSQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRRDPPQYPVVPVHLDRII

>d1rnfa\_ d.5.1.1 (A:) Ribonuclease 4 {Human (Homo sapiens)}

MQDGMYQRFLRQHVHPEETGGSDRYCNLMMQRRKMTLYHCKRFNTFIHEDIWNIRSICSTTNIQCKNGKMNCHEGVVKVTDCRDTGSSRAPNCRYRAIASTRRVVIACEGNPQVPVHFDG

>d1b1ia\_ d.5.1.1 (A:) Angiogenin {Human (Homo sapiens)}

EDNSRYTHFLTQHYDAKPQGRDDRYCESIMRRRGLTSPCKDINTFIHGNKRSIKAICENKNGNPHRENLRISKSSFQVTTCKLHGGSPWPPCQYRATAGFRNVVVACENGLPVHLDQSIFRRP

>d1agi\_\_ d.5.1.1 (-) Angiogenin {Cow (Bos taurus)}

AQDDYRYIHFLTQHYDAKPKGRNDEYCFNMMKNRRLTRPCKDRNTFIHGNKNDIKAICEDRNGQPYRGDLRISKSEFQITICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHFDESFITPRH

>d1ag2\_\_ d.6.1.1 (-) Prion protein domain {Mouse (Mus musculus)}

GLGGYMLGSAMSRPMIHFGNDWEDRYYRENMYRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCVTQYQKESQAYY

>d1b10a\_ d.6.1.1 (A:) Prion protein domain {Golden hamster (Mesocricetus auratus)}

LGGYMLGSAMSRPMMHFGNDWEDRYYRENMNRYPNQVYYRPVDQYNNQNNFVHDCVNITIKQHTVTTTTKGENFTETDIKIMERVVEQMCTTQYQKESQAYYDG

>d1fo7a\_ d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}

LGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTVTTTTKGENFTKTDVKMMERVVEQMCITQYERESQAYYQRGSS

>d1i4ma\_ d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}

GAVVGGLGGYMLGSAMSRPIIHFGSDYEDRYYRENMHRYPNQVYYRPMDEYSNQNNFVHDCVNITIKQHTVTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYY

>d1dwya\_ d.6.1.1 (A:) Prion protein domain {Cow (Bos taurus)}

GLGGYMLGSAMSRPLIHFGSDYEDRYYRENMHRYPNQVYYRPVDQYSNQNNFVHDCVNITVKEHTVTTTTKGENFTETDIKMMERVVEQMCITQYQRESQAYYQ

>d1i17a\_ d.6.1.1 (A:) Prion-like protein Doppel {Mouse (Mus musculus)}

RVAENRPGAFIKQGRKLDIDFGAEGNRYYAANYWQFPDGIYYEGCSEANVTKEMLVTSCVNATQAANQAEFSREKQDSKLHQRVLWRLIKEICSAKHCDFWLERGAA

>d1e01a\_ d.7.1.1 (A:) Membrane-bound lytic murein transclycosylase D, MltD {Escherichia coli}

DSITYRVRKGDSLSSIAKRHGVNIKDVMRWNSDTANLQPGDKLTLFVK

>d1hywa\_ d.186.1.1 (A:) Head-to-tail joining protein W, gpW {Bacteriophage lambda}

MTRQEELAAARAALHDLMTGKRVATVQKDGRRVEFTATSVSDLKKYIAELEVQTGMTQ

>d1ejra\_ d.8.1.1 (A:) Urease, gamma-subunit {Klebsiella aerogenes}

MELTPREKDKLLLFTAALVAERRLARGLKLNYPESVALISAFIMEGARDGKSVASLMEEGRHVLTREQVMEGVPEMIPDIQVEATFPDGSKLVTVHNPII

>d4ubpa\_ d.8.1.1 (A:) Urease, gamma-subunit {Bacillus pasteurii}

MHLNPAEKEKLQIFLASELLLRRKARGLKLNYPEAVAIITSFIMEGARDGKTVAMLMEEGKHVLTRDDVMEGVPEMIDDIQAEATFPDGTKLVTVHNPIS

>d1e9ya2 d.8.1.1 (A:1-105) Urease, gamma-subunit {Helicobacter pylori}

MKLTPKELDKLMLHYAGELAKKRKEKGIKLNYVEAVALISAHIMEEARAGKKTAAELMQEGRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGK

>d1qe6b\_ d.9.1.1 (B:) Interleukin-8, IL-8 {Human (Homo sapiens)}

AKECRCQCIKTYSKPFHPKFIKELRVIESGPCCANTEIIVKLSDGRELCLDPKENWVQRVVEKFLKRAENS

>d3il8\_\_ d.9.1.1 (-) Interleukin-8, IL-8 {Human (Homo sapiens)}

LRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVEKFLKRAENS

>d1plfa\_ d.9.1.1 (A:) Platelet factor 4, PF4 {Cow (Bos taurus)}

LQCVCLKTTSGINPRHISSLEVIGAGLHCPSPQLIATLKTGRKICLDQQNPLYKKIIKRLLKS

>d1pfma\_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}

MSAKELRCQCVKTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNGRKICLDLQAPLYKKIIKKLLES

>d1rhpa\_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}

DLQCLCVKTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNGRKICLDLQAPLYKKIIKKLLES

>d1mgsa\_ d.9.1.1 (A:) Melanoma growth stimulating activity (MGSA) {Human (Homo sapiens)}

ASVATELRCQCLQTLQGIHPKNIQSVNVKSPGPHCAQTEVIATLKNGRKACLNPASPIVKKIIEKMLNSDKSN

>d1roda\_ d.9.1.1 (A:) IL-8/MGSA chimeric protein CIL-8M {Human (Homo sapiens)}

SAKELRCQCIKTYSKPFHPKFIKELRVIESGPHCANTEIIVKLSDGRELCLDPASPIVKKIIEKMLNSDKSN

>d1huna\_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens), 1-beta}

APMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQEYVYDLELN

>d1b50a\_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens), 1-alpha}

SLAADTPTACCFSYTSRQIPQNFIAAYFETSSQCSKPGVIFLTKRSRQVCADPSEEWVQKYVSDLELSA

>d1ha6a\_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Mouse (Mus musculus), ccl20/mip-3a}

ASNYDCCLSYIQTPLPSRAIVGFTRQMADEACDINAIIFHTKKRKSVCADPKQNWVKRAVNLLSLRVKKM

>d1cm9a\_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Kaposi's sarcoma herpes virus, VMIP-II}

SWHRPDKCCLGYQKRPLPQVLLSSWYPTSQLCSKPGVIFLTKRGRQVCADKSKDWVKKLMQQLPVTAR

>d1b3aa\_ d.9.1.1 (A:) RANTES (regulated upon activation, normal T-cell expressed and secreted) {Human (Homo sapiens)}

PYSSDTTPCCFAYIARPLPRAHIKEYFYTSGKCSNPAVVFVTRKNRQVCANPEKKWVREYINSLEMS

>d1doka\_ d.9.1.1 (A:) Monocyte chemoattractant protein-1 (MCP-1, MCAF) {Human (Homo sapiens)}

MQPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWVQDSMDHLDKQT

>d1esra\_ d.9.1.1 (A:) Monocyte chemoattractant protein-2 (MCP-2) {Human (Homo sapiens)}

EPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTQRGKEVCADPKERWVRDSMKHLDQIFQNLKP

>d1el0a\_ d.9.1.1 (A:) CC chemokine I-309 {Human (Homo sapiens)}

SKSMQVPFSRCCFSFAEQEIPLRAILCYRNTSSICSNEGLIFKLKRGKEACALDTVGWVQRHRKMLRHCPSKRK

>d1eot\_\_ d.9.1.1 (-) Eotaxin {Human (Homo sapiens)}

GPASVPTTCCFNLANRKIPLQRLESYRRITSGKCPQKAVIFKTKLAKDICADPKKKWVQDSMKYLDQKSPTPKP

>d1eiha\_ d.9.1.1 (A:) Eotaxin-2 {Human (Homo sapiens)}

VVIPSPCCMFFVSKRIPENRVVSYQLSSRSTCLKAGVIFTTKKGQQSCGDPKQEWVQRYMKNLDAKQKKASPR

>d1j9oa\_ d.9.1.1 (A:) Lymphotactin {Human (Homo sapiens)}

VGSEVSDKRTCVSLTTQRLPVSRIKTYTITEGSLRAVIFITKRGLKVCADPQATWVRDVVRSMDRKSNTRNNMIQTKPTGTQQSTNTAVTLTG

>d1bo0\_\_ d.9.1.1 (-) Monocyte chemoattractant protein-3 (MCP-3) {Human (Homo sapiens)}

QPVGINTSTTCCYRFINKKIPKQRLESYRRTTSSHCPREAVIFKTKLDKEICADPTQKWVQDFMKHLDKKTQTPKL

>d1b2ta\_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}

MQHHGVTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAIILETRQHRLFCADPKEQWVKDAMQHLDRQAAALTRNG

>d1f2la\_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}

VTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAIILETRQHRLFCADPKEQWVKDAMQHLDRQ

>d1tvxa\_ d.9.1.1 (A:) Neutrophil-activating peptide-2 (NAP-2) {Human (Homo sapiens)}

LRCLCIKTTSGIHPKNIQSLEVIGKGTHCNQVEVIATLKDGRKICLDPDAPRIKKIVQKKLAGD

>d1tvxb\_ d.9.1.1 (B:) Neutrophil-activating peptide-2 (NAP-2) {Human (Homo sapiens)}

DSDLYAELRCLCIKTTSGIHPKNIQSLEVIGKGTHCNQVEVIATLKDGRKICLDPDAPRIKKIVQKKLAGD

>d1a15a\_ d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}

KPVSLSYRCPCRFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN

>d1a15b\_ d.9.1.1 (B:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}

RCPCRFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEK

>d1qg7a\_ d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}

SYRCPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN

>d1mi2a\_ d.9.1.1 (A:) Macrophage inflammatory protein-2 {Mouse (Mus musculus)}

AVVASELRCQCLKTLPRVDFKNIQSLSVTPPGPHCAQTEVIATLKGGQKVCLDPEAPLVQKIIQKILNKGKAN

>d2hcc\_\_ d.9.1.1 (-) Chemokine hcc-2 (macrophage inflammatory protein-5) {Human (Homo sapiens)}

HFAADCCTSYISQSIPCSLMKSYFETSSECSKPGVIFLTKKGRQVCAKPSGPGVQDCMKKLKPYSI

>d1qnka\_ d.9.1.1 (A:) Gro beta {Human (Homo sapiens)}

TELRCQCLQTLQGIHLKNIQSVKVKSPGPHCAQTEVIATLKNGQKACLNPASPMVKKIIEKMLKNGKSN

>d1g91a\_ d.9.1.1 (A:) Myeloid progenitor inhibitory factor-1 (MPIF-1) {Human (Homo sapiens)}

MDRFHATSADCCISYTPRSIPCSLLESYFETNSECSKPGVIFLTKKGRRFCANPSDKQVQVCMRMLKLDTRIKTRKN

>d1bf4a\_ d.9.2.1 (A:) DNA-binding protein {Archaeon Sulfolobus solfataricus, Sso7d}

ATVKFKYKGEEKEVDISKIKKVWRVGKMISFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK

>d1azpa\_ d.9.2.1 (A:) DNA-binding protein {Archaeon Sulfolobus acidocaldarius, Sac7d}

MVKVKFKYKGEEKEVDTSKIKKVWRVGKMVSFTYDDNGKTGRGAVSEKDAPKELLDMLARAEREKK

>d1ap0\_\_ d.9.2.2 (-) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}

HMVEEVLEEEEEEYVVEKVLDRRVVKGKVEYLLKWKGFSDEDNTWEPEENLDCPDLIAEFLQSQKTAHETDKS

>d1dz1a\_ d.9.2.2 (A:) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}

HMKEESEKPRGFARGLEPERIIGATDSSGELMFLMKWKNSDEADLVPAKEANVKCPQVVISFYEERLTWH

>d1e0ba\_ d.9.2.2 (A:) HP1 homologue SWI6 {Fission yeast (Schizosaccharomyces pombe)}

QVENYDSWEDLVSSIDTIERKDDGTLEIYLTWKNGAISHHPSTITNKKCPQKMLQFYESHL

>d1g6za\_ d.9.2.2 (A:) Histone methyltransferase clr4 chromo domain {Fission yeast (Schizosaccharomyces pombe)}

ISSPKQEEYEVERIVDEKLDRNGAVKLYRIRWLNYSSRSDTWEPPENLSGCSAVLAEWKRRKRRLKGSNS

>d1bb8\_\_ d.10.1.1 (-) DNA-binding domain from tn916 integrase {Enterococcus faecalis}

EKRRDNRGRILKTGESQRKDGRYLYKYIDSFGEPQFVYSWKLVATDRVPAGKRDCISLREKIAELQKDIHD

>d1gcca\_ d.10.1.2 (A:) GCC-box binding domain {Mouse-ear cress (Arabidopsis thaliana)}

KHYRGVRQRPWGKFAAEIRDPAKNGARVWLGTFETAEDAALAYDRAAFRMRGSRALLNFPLRV

>d1qk9a\_ d.10.1.3 (A:) Methyl-CpG-binding protein 2, MECP2 {Human (Homo sapiens)}

ASASPKQRRSIIRDRGPMYDDPTLPEGWTRKLKQRKSGRSAGKYDVYLINPQGKAFRSKVELIAYFEKVGDTSLDPNDFDFTVTGRGSGSGC

>d1d9na\_ d.10.1.3 (A:) Methylation-dependent transcriptional repressor MBD1/PCM1 {Human (Homo sapiens)}

MAEDWLDCPALGPGWKRREVFRKSGATCGRSDTYYQSPTGDRIRSKVELTRYLGPACDLTLFDFKQGILCYPAPK

>d1k25a1 d.11.1.1 (A:632-692) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}

TESSYAMPSIKDISPGELAEALRRNIVQPIVVGTGTKIKETSVEEGTNLAPNQQVLLLSDK

>d1k25a2 d.11.1.1 (A:693-750) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}

VEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLGD

>d1qmea1 d.11.1.1 (A:632-692) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}

QQSPYPMPSVKDISPGDLAEELRRNLVQPIVVGTGTKIKNSSAEEGKNLAPNQQVLILSDK

>d1qmea2 d.11.1.1 (A:693-750) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}

AEEVPDMYGWTKETAETLAKWLNIELEFQGSGSTVQKQDVRANTAIKDIKKITLTLGD

>d1jj2r\_ d.12.1.1 (R:) Ribosomal protein L23 {Archaeon Haloarcula marismortui}

SWDVIKHPHVTEKAMNDMDFQNKLQFAVDDRASKGEVADAVEEQYDVTVEQVNTQNTMDGEKKAVVRLSEDDDAQEVASRI

>d1ffki\_ d.12.1.2 (I:) Ribosomal protein L15e {Archaeon Haloarcula marismortui}

MKSMYAYIREAWKRPYEGYVGELMWHRLQKWRREPAVVRIPRPTRLDRARALGYKAKKGIIVVRVRIRRGGRRATRPNKGRKSKKMMVNRRPRKKNLQWIAEERANRKYPNMEVLNSYWVGEDGRYKWFEVILVDRDHPAIKSDPQLSWVSRTRGRVYRGLTSAGRKARGLRRKGRGAEKVRPSLRANFRKKRR

>d1jj2l\_ d.12.1.2 (L:) Ribosomal protein L15e {Archaeon Haloarcula marismortui}

ARSAYSYIREAWKRPKEGQIAELMWHRMQEWRNEPAVVRIERPTRLDRARSLGYKAKQGIIVVRVAIRKGSSRRTRFNKGRRSKRMMVNRITRKKNIQRIAEERANRKFPNLRVLNSYSVGEDGRHKWHEVILIDPDHPAIKSDDQLSWISRTRHRLRTFRGLTSAGRRCRGLRGQGKGSEKVRPSLRVNGAKA

>d4rhn\_\_ d.13.1.1 (-) Histidine triad nucleotide-binding protein (HINT) {Rabbit (Oryctolagus cuniculus)}

RPGGDTIFGKIIRKEIPAKIIFEDDQCLAFHDISPQAPTHFLVIPKKHISQISAAEDADESLLGHLMIVGKKCAADLGLKKGYRMVVNEGSDGGQSVYHVHLHVLGGRQMNWPPG

>d1fit\_\_ d.13.1.1 (-) FHIT (fragile histidine triad protein) {Human (Homo sapiens)}

SFRFGQHLIKPSVVFLKTELSFALVNRKPVVPGHVLVCPLRPVERFHDLRPDEVADLFQTTQRVGTVVEKHFHGTSLTFSMQDGPEAGQTVKHVHVHVLPRKAGDFHRNDSIYEELQKHDKEDFPASWRSEEEMAAEAAALRVYFQ

>d1kpf\_\_ d.13.1.1 (-) Protein kinase C inhibitor-1, PKCI-1 {Human (Homo sapiens)}

DTIFGKIIRKEIPAKIIFEDDRCLAFHDISPQAPTHFLVIPKKHISQISVAEDDDESLLGHLMIVGKKCAADLGLNKGYRMVVNEGSDGGQSVYHVHLHVLGGRQMHWPPG

>d1emsa1 d.13.1.1 (A:281-440) NIT-FHIT fusion protein, C-terminal domain {Nematode (Caenorhabditis elegans)}

RSDLYTLHINEKSSETGGLKFARFNIPADHIFYSTPHSFVFVNLKPVTDGHVLVSPKRVVPRLTDLTDAETADLFIVAKKVQAMLEKHHNVTSTTICVQDGKDAGQTVPHVHIHILPRRAGDFGDNEIYQKLASHDKEPERKPRSNEQMAEEAVVYRNLM

>d1guqa1 d.13.1.2 (A:2-177) Galactose-1-phosphate uridylyltransferase {Escherichia coli}

TQFNPVDHPHRRYNPLTGQWILVSPHRAKRPWQGAQETPAKQVLPAHDPDCFLCAGNVRVTGDKNPDYTGTYVFTNDFAALMSDTPDAPESHDPLMRCQSARGTSRVICFSPDHSKTLPELSVAALTEIVKTWQEQTAELGKTYPWVQVFENKGAAMGCSNPHPGGQIWANSFLPN

>d1guqa2 d.13.1.2 (A:178-348) Galactose-1-phosphate uridylyltransferase {Escherichia coli}

EAEREDRLQKEYFAEQKSPMLVDYVQRELADGSRTVVETEHWLAVVPYWAAWPFETLLLPKAHVLRITDLTDAQRSDLALALKKLTSRYDNLFQCSFPYSMGWHGAPFNGEENQHWQLHAHFYPPLLRSATVRKFMVGYEMLAETQRDLTAEQAAERLRAVSDIHFRESGV

>d1jyaa\_ d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}

YSFEQAITQLFQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDEKETLLSHNIFSQDILKPILSWDEVGGHPVLWNRQPLNSLDNNSLYTQLEMLVQGAERLQ

>d1k6za\_ d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}

SFEQAITQLFQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDEKETLLSHNIFSQDILKPILSWDEVGGHPVLWNRQPLNSLDNNSLYTQLEMLVQGAERLQTSSLISPPRSFSHH

>d1jyoa\_ d.198.1.1 (A:) Virulence effector SptP secretion chaperone SicP {Salmonella typhimurium}

LQAHQDIIANIGEKLGLPLTFDDNNQCLLLLDSDIFTSIEAKDDIWLLNGMIIPLSPVCGDSIWRQIMVINGELAANNEGTLAYIDAAETLLLIHAITDLTNTYHIISQLESFVNQQEALKNILQEYAKV

>d1k3ea\_ d.198.1.1 (A:) Secretion chaperone CesT {Escherichia coli}

MSSRSELLLEKFAEKIGIGSISFNENRLCSFAIDEIYYISLSDANDEYMMIYGVCGKFPTDNSNFALEILNANLWFAENGGPYLCYEAGAQSLLLALRFPLDDATPEKLENEIEVVVKSMENLYLVLHNQGITLENEHMKIEEISS

>d1k3sa\_ d.198.1.1 (A:) Secretion chaperone SigE {Salmonella enterica}

MESLLNRLYDALGLDAPEDEPLLIIDDGIQVYFNESDHTLEMCCPFMPLPDDILTLQHFLRLNYTSAVTIGADADNTALVALYRLPQTSTEEEALTGFELFISNVKQLKEHYA

>d1k8kf\_ d.198.2.1 (F:) ARPC4 (20 kDa subunit) {Cow (Bos taurus)}

TATLRPYLSAVRATLQAALCLENFSSQVVERHNKPEVEVRSSKELLLQPVTISRNEKEKVLIEGSINSVRVSIAVKQADEIEKILCHKFMRFMMMRAENFFILRRKPVEGYDISFLITNFHTEQMYKHKLVDFVIHFMEEIDKEISEMKLSVNARARIVAEEFLKNF

>d1k8kd1 d.198.2.1 (D:1-120) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

MILLEVNNRIIEETLALKFENAAAGNKPEAVEVTFADFDGVLYHISNPNGDKTKVMVSISLKFYKELQAHGADELLKRVYGSYLVNPESGYNVSLLYDLENLPASKDSIVHQAGMLKRNC

>d1k8kd2 d.198.2.1 (D:121-284) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

FASVFEKYFQFQEEGKEGENRAVIHYRDDETMYVESKKDRVTVVFSTVFKDDDDVVIGKVFMQEFKEGRRASHTAPQVLFSHREPPLELKDTDAAVGDNIGYITFVLFPRHTNASARDNTINLIHTFRDYLHYHIKCSKAYIHTRMRAKTSDFLKVLNRARPDA

>d1kafa\_ d.199.1.1 (A:) DNA-binding C-terminal domain of the transcription factor MotA {Bacteriophage T4}

MEITSDMEEDKDLMLKLLDKNGFVLKKVEIYRSNYLAILEKRTNGIRNFEINNNGNMRIFGYKMMEHHIQKFTDIGMSCKIAKNGNVYLDIKRSAENIEAVITVASEL

>d1dar\_3 d.14.1.1 (476-599) Elongation factor G (EF-G), domain IV {Thermus thermophilus}

VGKPQVAYRETITKPVDVEGKFIRQTGGRGQYGHVKIKVEPLPRGSGFEFVNAIVGGVIPKEYIPAVQKGIEEAMQSGPLIGFPVVDIKVTLYDGSYHEVDSSEMAFKIAGSMAIKEAVQKGDP

>d1pkp\_1 d.14.1.1 (78-148) Ribosomal protein S5, C-terminal domain {Bacillus stearothermophilus}

GTTIPHEVIGHFGAGEIILKPASEGTGVIAGGPARAVLELAGISDILSKSIGSNTPINMVRATFDGLKQLK

>d1fjge1 d.14.1.1 (E:74-154) Ribosomal protein S5, C-terminal domain {Thermus thermophilus}

GTIPHEIEVEFGASKIVLKPAAPGTGVIAGAVPRAILELAGVTDILTKELGSRNPINIAYATMEALRQLRTKADVERLRKG

>d1fjgi\_ d.14.1.1 (I:) Ribosomal protein S9 {Thermus thermophilus}

EQYYGTGRRKEAVARVFLRPGNGKVTVNGQDFNEYFQGLVRAVAALEPLRAVDALGRFDAYITVRGGGKSGQIDAIKLGIARALVQYNPDYRAKLKPLGFLTRDARVVERKKYGKHKARRAPQYSKR

>d1a6f\_\_ d.14.1.2 (-) RNase P protein {Bacillus subtilis}

AHLKKRNRLKKNEDFQKVFKHGTSVANRQFVLYTLDQPENDELRVGLSVSKKIGNAVMRNRIKRLIRQAFLEEKERLKEKDYIIIARKPASQLTYEETKKSLQHLFRKSSLYK

>d1d6ta\_ d.14.1.2 (A:) RNase P protein {Staphylococcus aureus}

MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVSKKLGNAVLRNKIKRAIRENFKVHKSHILAKDIIVIARQPAKDMTTLQIQNSLEHVLKIAKVFNKKIK

>d1b63a1 d.14.1.3 (A:217-331) DNA mismatch repair protein MutL {Escherichia coli}

GTAFLEQALAIEWQHGDLTLRGWVADPNHTTPALAEIQYCYVNGRMMRDRLINHAIRQACEDKLGADQQPAFVLYLEIDPHQVDVNVHPAKHEVRFHQSRLVHDFIYQGVLSVLQ

>d1h7sa1 d.14.1.3 (A:232-365) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}

GQKQLQSLIPFVQLPPSDSVCEEYGLSCSDALHNLFYISGFISQCTHGVGRSSTDRQFFFINRRPCDPAKVCRLVNEVYHMYNRHQYPFVVLNISVDSECVDINVTPDKRQILLQEEKLLLAVLKTSLIGMFDS

>d1ei1a1 d.14.1.3 (A:221-392) DNA gyrase B {Escherichia coli}

GIKAFVEYLNKNKTPIHPNIFYFSTEKDGIGVEVALQWNDGFQENIYCFTNNIPQRDGGTHLAGFRAAMTRTLNAYMDKEGYSKKAKVSATGDDAREGLIAVVSVKVPDPKFSSQTKDKLVSSEVKSAVEQQMNELLAEYLLENPTDAKIVVGKIIDAARAREAARRAREMT

>d1e3ha2 d.14.1.4 (A:3-151) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}

NETHYAEAVIDNGAFGTRTIRFETGRLARQAAGSAVAYLDDDTMVLSATTASKNPKDQLDFFPLTVDVEERMYAAGKIPGSFFRREGRPSEDAILTCRLIDRPLRPSFKKGLRNEIQVVATIMALNPDHLYDVVAINAASASTQLAGLP

>d1e3ha3 d.14.1.4 (A:346-482) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}

TDIRTLAAEVEAIPRVHGSALFERGETQILGVTTLNMLRMEQQLDTLSPVTRKRYMHNYNFPPYSVGETGRVGSPKRREIGHGALAERAIVPVLPTREEFPYAIRQVSEALGSNGSTSMGSVCASTMSLLNAGVPLK

>d1h72c1 d.14.1.5 (C:5-167) Homoserine kinase {Archaeon Methanococcus jannaschii}

MKVRVKAPCTSANLGVGFDVFGLCLKEPYDVIEVEAIDDKEIIIEVDDKNIPTDPDKNVAGIVAKKMIDDFNIGKGVKITIKKGVKAGSGLGSSAASSAGTAYAINELFKLNLDKLKLVDYASYGELASSGAKHADNVAPAIFGGFTMVTNYEPLEVLHIPID

>d1fi4a1 d.14.1.5 (A:3-190) Mevalonate 5-diphosphate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

VYTASVTAPVNIATLKYWGKRDTKLNLPTNSSISVTLSQDDLRTLTSAATAPEFERDTLWLNGEPHSIDNERTQNCLRDLRQLRKEMESKDASLPTLSQWKLHIVSENNFPTAAGLASSAAGFAALVSAIAKLYQLPQSTSEISRIARKGSGSACRSLFGGYVAWEMGKAEDGHDSMAVQIADSSDWP

>d1c3ta\_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}

MQLFVKTLTGKTLTVELEPSDTVENLKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNLQKESTIHLVLRLRGG

>d1gjza\_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}

GSMQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLE

>d1ubi\_\_ d.15.1.1 (-) Ubiquitin {Human (Homo sapiens)}

MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTLHLVLRLRGG

>d1ud7a\_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}

MQVFLKTLTGKTVTIEVEPSDTVENFKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDYNIQKESTIHLVLRLRGG

>d1a5r\_\_ d.15.1.1 (-) SUMO-1 (smt3 homologue) {Human (Homo sapiens)}

GSMSDQEAKPSTEDLGDKKEGEYIKLKVIGQDSSEIHFKVKMTTHLKKLKESYCQRQGVPMNSLRFLFEGQRIADNHTPKELGMEEEDVIEVYQEQTGGHSTV

>d1euvb\_ d.15.1.1 (B:) SUMO-1 (smt3 homologue) {Baker's yeast (Saccharomyces cerevisiae)}

PETHINLKVSDGSSEIFFKIKKTTPLRRLMEAFAKRQGKEMDSLRFLYDGIRIQADQTPEDLDMEDNDIIEAHREQIGG

>d1ndda\_ d.15.1.1 (A:) Nedd8 {Human (Homo sapiens)}

MLIKVKTLTGKEIEIDIEPTDKVERIKERVEEKEGIPPQQQRLIYSGKQMNDEKTAADYKILGGSVLHLVLALR

>d1vcba\_ d.15.1.1 (A:) Elongin B {Human (Homo sapiens)}

MDVFLMIRRHKTTIFTDAKESSTVFELKRIVEGILKRPPDEQRLYKDDQLLDDGKTLGECGFTSQTARPQAPATVGLAFRADDTFEALCIEPFSSPPE

>d1bt0a\_ d.15.1.1 (A:) Rub1 {Mouse-ear cress (Arabidopsis thaliana)}

MLIKVKTLTGKEIEIDIEPTDTIDRIKERVEEKEGIPPVQQRLIYAGKQLADDKTAKDYNIEGGSVLHLVLAL

>d1h8ca\_ d.15.1.2 (A:) Fas-assosiated factor 1, Faf1 {Human (Homo sapiens)}

NAEPVSKLRIRTPSGEFLERRFLASNKLQIVFDFVASKGFPWDEYKLLSTFPRRDVTQLDPNKSLLEVKLFPQETLFLEAKE

>d1i42a\_ d.15.1.2 (A:) p47 {Rat (Rattus norvegicus)}

KASSSILINEAEPTTNIQIRLADGGRLVQKFNHSHRISDIRLFIVDARPAMAATSFVLMTTFPNKELADENQTLKEANLLNAVIVQRLT

>d1eo6a\_ d.15.1.3 (A:) Golgi-associated ATPase enhancer of 16 kD, Gate-16 {Cow (Bos taurus)}

MKWMFKEDHSLEHRCVESAKIRAKYPDRVPVIVEKVSGSQIVDIDKRKYLVPSDITVAQFMWIIRKRIQLPSEKAIFLFVDKTVPQSSLTMGQLYEKEKDEDGFLYVAYSGENTFG

>d1gnua\_ d.15.1.3 (A:) GABA(A) receptor associated protein GABARAP {Human (Homo sapiens)}

MKFVYKEEHPFEKRRSEGEKIRKKYPDRVPVIVEKAPKARIGDLDKKKYLVPSDLTVGQFYFLIRKRIHLRAEDALFFFVNNVIPPTSATMGQLYQEHHEEDFFLYIAYSDESVYGL

>d1ef1a3 d.15.1.4 (A:4-87) Moesin {Human (Homo sapiens)}

TISVRVTTMDAELEFAIQPNTTGKQLFDQVVKTIGLREVWFFGLQYQDTKGFSTWLKLNKKVTAQDVRKESPLLFKFRAKFYPE

>d1gc7a3 d.15.1.4 (A:1-87) Radixin {Mouse (Mus musculus)}

MPKPINVRVTTMDAELEFAIQPNTTGKQLFDQVVKTVGLREVWFFGLQYVDSKGYSTWLKLNKKVTQQDVKKENPLQFKFRAKFFPE

>d1gg3a3 d.15.1.4 (A:1-81) Erythroid membrane protein 4.1R {Human (Homo sapiens)}

MHCKVSLLDDTVYECVVEKHAKGQDLLKRVCEHLNLLEEDYFGLAIWDNATSKTWLDSAKEIKKQVRGVPWNFTFNVKFYP

>d1h4ra3 d.15.1.4 (A:20-103) Merlin {Human (Homo sapiens)}

KTFTVRIVTMDAEMEFNCEMKWKGKDLFDLVCRTLGLRETWFFGLQYTIKDTVAWLKMDKKVLDHDVSKEEPVTFHFLAKFYPE

>d1c1yb\_ d.15.1.5 (B:) c-Raf1 RBD {Human (Homo sapiens)}

SNTIRVFLPNKQRTVVNVRNGMSLHDCLMKALKVRGLQPECCAVFRLLHEHKGKKARLDWNTDAASLIGEELQVDFL

>d1lfda\_ d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RalGDS {Rat (Rattus norvegicus)}

GDCCIIRVSLDVDNGNMYKSILVTSQDKAPTVIRKAMDKHNLDEDEPEDYELLQIISEDHKLKIPENANVFYAMNSAANYDFILKKR

>d1raxa\_ d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RalGDS {Human (Homo sapiens)}

QQVGDCCIIRVSLDVDNGNMYKSILVTSQDKAPAVIRKAMDKHNLEEEEPEDYELLQILSDDRKLKIPENANVFYAMNSTANYDFVLKKRTFT

>d1rlf\_\_ d.15.1.5 (-) RalGDS-like factor, Rlf {Mouse (Mus musculus)}

GSSDCRIIRVQMELGEDGSVYKSILVTSQDKAPSVISRVLKKNNRDSAVASEFELVQLLPGDRELTIPHSANVFYAMDGASHDFLLRQRR

>d1ef5a\_ d.15.1.5 (A:) Rgl {Mouse (Mus musculus)}

EDTCIIRISVEDNNGNMYKSIMLTSQDKTPAVIQRAMSKHNLESDPAEEYELVQVISEDKELVIPDSANVFYAMNSQVNFDFILRKKN

>d1e8xa3 d.15.1.5 (A:142-321) Phoshoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}

AASEETLAFQRQLNALIGYDVTDVSNVHDDELEFTRRRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKITNNCVFIVIHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIPESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDTPPDPALDEVRKE

>d1e8ya3 d.15.1.5 (A:143-322) Phoshoinositide 3-kinase (PI3K) {Human (Homo sapiens)}

MSEESQAFQRQLTALIGYDVTDVSNVHDDELEFTRRGLVTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKKIANNCIFIVIHRSTTSQTIKVSPDDTPGAILQSFFTKMAKKKSLMDIPESQSEQDFVLRVCGRDEYLVGETPIKNFQWVRHCLKNGEEIHVVLDTPPDPALDEVRKEE

>d1i35a\_ d.15.1.5 (A:) Protein kinase byr2 {Yest (Schizosaccharomyces pombe)}

CILRFIACNGQTRAVQSRGDYQKTLAIALKKFSLEDASKFIVCVSQSSRIKLITEEEFKQICFNSSSPERDRLIIVPKEKPCPSFEDLRRSWEIE

>d1d4ba\_ d.15.2.1 (A:) Cell death-inducing effector B (CIDE-B), N-terminal domain {Human (Homo sapiens)}

MEYLSALNPSDLLRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATRQELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLMVLQSGQSWSPTRSGVLHHHHHH

>d1c9fa\_ d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Mouse (Mus musculus)}

MCAVLRQPKCVKLRALHSACKFGVAARSCQELLRKGCVRFQLPMPGSRLCLYEDGTEVTDDCFPGLPNDAELLLLTAGETWHGYVSD

>d1ibxa\_ d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Human (Homo sapiens)}

MLQKPKSVKLRALRSPRKFGVAGRSCQEVLRKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTLGQAWQGH

>d1f2ri\_ d.15.2.1 (I:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Mouse (Mus musculus)}

MELSRGASAPDPDDVRPLKPCLLRRNHSRDQHGVAASSLEELRSKACELLAIDKSLTPITLVLAEDGTIVDDDDYFLCLPSNTKFVALACNEKWTYNDSD

>d1ibxb\_ d.15.2.1 (B:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Human (Homo sapiens)}

SGEIRTLKPCLLRRNYSREQHGVAASCLEDLRSKACDILAIDKSLTPVTLVLAEDGTIVDDDDYFLCLPSNTKFVALASNEKWAYNNSD

>d1ip9a\_ d.15.2.2 (A:) Bud emergence mediator Bemp1 {Baker's yeast (Saccharomyces cerevisiae)}

GAMGSSTSGLKTTKIKFYYKDDIFALMLKGDTTYKELRSKIAPRIDTDNFKLQTKLFDGSGEEIKTDSQVSNIIQAKLKISVHDI

>d1fm0d\_ d.15.3.1 (D:) Molybdopterin synthase subunit MoaD {Escherichia coli}

MIKVLFFAQVRELVGTDATEVAADFPTVEALRQHMAAQSDRWALALEDGKLLAAVNQTLVSFDHPLTDGDEVAFFPPVTGG

>d1f0za\_ d.15.3.2 (A:) Thiamin biosynthesis sulfur carrier protein ThiS {Escherichia coli}

MQILFNDQAMQCAAGQTVHELLEQLDQRQAGAALAINQQIVPREQWAQHIVQDGDQILLFQVIAGG

>d1jsba\_ d.15.3.2 (A:) Hypothetical protein MTH1743 {Archaeon Methanobacterium thermoautotrophicum}

MVIGMKFTVITDDGKKILESGAPRRIKDVLGELEIPIETVVVKKNGQIVIDEEEIFDGDIIEVIRVIYGG

>d1czpa\_ d.15.4.1 (A:) 2Fe-2S ferredoxin {Cyanobacterium (Anabaena sp.), pcc 7119 and 7120}

ATFKVTLINEAEGTKHEIEVPDDEYILDAAEEQGYDLPFSCRAGACSTCAGKLVSGTVDQSDQSFLDDDQIEAGYVLTCVAYPTSDVVIQTHKEEDLY

>d1frd\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Cyanobacterium (Anabaena sp.), pcc 7119 and 7120}

ASYQVRLINKKQDIDTTIEIDEETTILDGAEENGIELPFSCHSGSCSSCVGKVVEGEVDQSDQIFLDDEQMGKGFALLCVTYPRSNCTIKTHQEPYLA

>d4fxc\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Spirulina platensis}

ATYKVTLINEAEGINETIDCDDDTYILDAAEEAGLDLPYSCRAGACSTCAGTITSGTIDQSDQSFLDDDQIEAGYVLTCVAYPTSDCTIKTHQEEGLY

>d1fxia\_ d.15.4.1 (A:) 2Fe-2S ferredoxin {Cyanobacterium (Aphanothece sacrum)}

ASYKVTLKTPDGDNVITVPDDEYILDVAEEEGLDLPYSCRAGACSTCAGKLVSGPAPDEDQSFLDDDQIQAGYILTCVAYPTGDCVIETHKEEALY

>d1dox\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Synechocystis sp., pcc 6803}

ASYTVKLITPDGESSIECSDDTYILDAAEEAGLDLPYSCRAGACSTCAGKITAGSVDQSDQSFLDDDQIEAGYVLTCVAYPTSDCTIETHKEEDLY

>d2cjn\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Synechococcus elongatus}

ATYKVTLVRPDGSETTIDVPEDEYILDVAEEQGLDLPFSCRAGACSTCAGKLLEGEVDQSDQSFLDDDQIEKGFVLTCVAYPRSDCKILTNQEEELY

>d1awd\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Chlorella fusca}

YKVTLKTPSGEETIECPEDTYILDAAEEAGLDLPYSCRAGACSSCAGKVESGEVDQSDQSFLDDAQMGKGFVLTCVAYPTSDVTILTHQEAALY

>d1frra\_ d.15.4.1 (A:) 2Fe-2S ferredoxin {Equisetum arvense}

AYKTVLKTPSGEFTLDVPEGTTILDAAEEAGYDLPFSCRAGACSSCLGKVVSGSVDESEGSFLDDGQMEEGFVLTCIAIPESDLVIETHKEEELF

>d1doi\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Archaeon Haloarcula marismortui}

PTVEYLNYEVVDDNGWDMYDDDVFGEASDMDLDDEDYGSLEVNEGEYILEAAEAQGYDWPFSCRAGACANCAAIVLEGDIDMDMQQILSDEEVEDKNVRLTCIGSPDADEVKIVYNAKHLDYLQNRVI

>d1e0za\_ d.15.4.1 (A:) 2Fe-2S ferredoxin {Archaeon Halobacterium halobium}

PTVEYLNYETLDDQGWDMDDDDLFEKAADAGLDGEDYGTMEVAEGEYILEAAEAQGYDWPFSCRAGACANCASIVKEGEIDMDMQQILSDEEVEEKDVRLTCIGSPAADEVKIVYNAKHLDYLQNRVI

>d1pfd\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Parsley (Petroselinum crispum)}

ATYNVKLITPDGEVEFKCDDDVYVLDQAEEEGIDIPYSCRAGSCSSCAGKVVSGSIDQSDQSFLDDEQMDAGYVLTCHAYPTSDVVIETHKEEEIV

>d1a70\_\_ d.15.4.1 (-) 2Fe-2S ferredoxin {Spinach (Spinacia oleracea)}

AAYKVTLVTPTGNVEFQCPDDVYILDAAEEEGIDLPYSCRAGSCSSCAGKLKTGSLNQDDQSFLDDDQIDEGWVLTCAAYPVSDVTIETHKKEELTA

>d1gaqb\_ d.15.4.1 (B:) 2Fe-2S ferredoxin {Maize (Zea mays)}

ATYNVKLITPEGEVELQVPDDVYILDQAEEDGIDLPYSCRAGSCSSCAGKVVSGSVDQSDQSYLDDGQIADGWVLTCHAYPTSDVVIETHKEEELTGA

>d1e9ma\_ d.15.4.1 (A:) Ferredoxin VI {Rhodobacter capsulatus}

AKIIFIEHNGTRHEVEAKPGLTVMEAARDNGVPGIDADCGGACACSTCHAYVDPAWVDKLPKALPTETDMIDFAYEPNPATSRLTCQIKVTSLLDGLVVHLPEKQI

>d1put\_\_ d.15.4.1 (-) Putidaredoxin {Pseudomonas putida}

SKVVYVSHDGTRRQLDVADGVSLMQAAVSNGIYDIVGDCGGSASCATCHVYVNEAFTDKVPAANEREIGMLECVTAELKPNSRLCCQIIMTPELDGIVVDVPDRQW

>d1b9ra\_ d.15.4.1 (A:) Terpredoxin {Pseudomonas sp.}

PRVVFIDEQSGEYAVDAQDGQSLMEVATQNGVPGIVAECGGSCVCATCRIEIEDAWVEIVGEANPDENDLLQSTGEPMTAGTRLSCQVFIDPSMDGLIVRVPLPA

>d1ayfa\_ d.15.4.1 (A:) Adrenodoxin {Cow (Bos taurus)}

KITVHFINRDGETLTTKGKIGDSLLDVVVQNNLDIDGFGACEGTLACSTCHLIFEQHIFEKLEAITDEENDMLDLAYGLTDRSRLGCQICLTKAMDNMTVRVP

>d1feha2 d.15.4.2 (A:1-126) Fe-only hydrogenase, N-terminal domain {Clostridium pasteurianum}

MKTIIINGVQFNTDEDTTILKFARDNNIDISALCFLNNCNNDINKCEICTVEVEGTGLVTACDTLIEDGMIINTNSDAVNEKIKSRISQLLDIHEFKCGPCNRRENCEFLKLVIKYKARASKPFLP

>d1hlra2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio gigas}

MIQKVITVNGIEQNLFVDAEALLSDVLRQQLGLTGVKVGCEQGQCGACSVILDGKVVRACVTKMKRVADGAQITTIEGVG

>d1dgja2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio desulfuricans}

METKTLIVNGMARRLLVSPNDLLVDVLRSQLQLTSVKVGCGKGQCGACTVILDGKVVRACIIKMSRVAENASVTTLEGIG

>d1fo4a2 d.15.4.2 (A:3-92) Xanthine oxidase, N-terminal domain {Cow (Bos taurus)}

ADELVFFVNGKKVVEKNADPETTLLAYLRRKLGLRGTKLGCGEGGCGACTVMLSKYDRLQDKIIHFSANACLAPICTLHHVAVTTVEGIG

>d1jroa2 d.15.4.2 (A:1-84) Xanthine dehydrogenase chain A, N-terminal domain {Rhodobacter capsulatus}

MEIAFLLNGETRRVRIEDPTQSLLELLRAEGLTGTKEGCNEGDCGACTVMIRDAAGSRAVNACLMMLPQIAGKALRTIEGIAAP

>d1qj2a2 d.15.4.2 (A:3-81) Carbone monoxide (CO) dehydrogenase iron-sulfur protein, N-domain {Pseudomonas carboxydovorans}

KAHIELTINGHPVEALVEPRTLLIHFIREQQNLTGAHIGCDTSHCGACTVDLDGMSVKSCTMFAVQANGASITTIEGMA

>d1ffva2 d.15.4.2 (A:3-81) Carbone monoxide (CO) dehydrogenase iron-sulfur protein, N-domain {Hydrogenophaga pseudoflava}

KKIITVNVNGKAQEKAVEPRTLLIHFLREELNLTGAHIGCETSHCGACTVDIDGRSVKSCTHLAVQCDGSEVLTVEGLA

>d2pia\_3 d.15.4.2 (224-321) Phthalate dioxygenase reductase, C-terminal domain {Pseudomonas cepacia, db01}

SFGATNTNARENTPFTVRLSRSGTSFEIPANRSILEVLRDANVRVPSSCESGTCGSCKTALCSGEADHRDMVLRDDEKGTQIMVCVSRAKSAELVLDL

>d1fumb2 d.15.4.2 (B:1-105) Fumarate reductase iron-sulfur protein, N-terminal domain {Escherichia coli}

AEMKNLKIEVVRYNPEVDTAPHSAFYEVPYDATTSLLDALGYIKDNLAPDLSYRWSCRMAICGSCGMMVNNVPKLACKTFLRDYTDGMKVEALANFPIERDLVVD

>d1qlab2 d.15.4.2 (B:1-106) Fumarate reductase iron-sulfur protein, N-terminal domain {Wolinella succinogenes}

MGRMLTIRVFKYDPQSAVSKPHFQEYKIEEAPSMTIFIVLNMIRETYDPDLNFDFVCRAGICGSCGMMINGRPSLACRTLTKDFEDGVITLLPLPAFKLIKDLSVD

>d1jq4a\_ d.15.4.2 (A:) Methane monooxygenase reductase N-terminal domain {Methylococcus capsulatus}

MQRVHTITAVTEDGESLRFECRSDEDVITAALRQNIFLMSSCREGGCATCKALCSEGDYDLKGCSVQALPPEEEEEGLVLLCRTYPKTDLEIELPYTH

>d1ssn\_\_ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}

SSSFDKGKYKKGDDASYFEPTGPYLMVNVTGVDSKGNELLSPHYVEFPIKPGTTLTKEKIEYYVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSFPITEKGFVVPDLSEHIKNPGFNLITKVVIEKK

>d2sak\_\_ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}

SYFEPTGPYLMVNVTGVDSKGNELLSPHYVEFPIKPGTTLTKEKIEYYVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSFPITEKGFVVPDLSEHIKNPGFNLITKVVIEKK

>d1bmlc1 d.15.5.1 (C:12-148) Streptokinase {Streptococcus equisimilis}

SVNNSQLVVSVAGTVEGTNQDISLKFFEIDLTSRPAHGGKTEQGLSPKSKPFATDSGAMPHKLEKADLLKAIQEQLIANVHSNDDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPVQEFLLSGHVRVRPYKE

>d1bmlc3 d.15.5.1 (C:285-372) Streptokinase {Streptococcus equisimilis}

DPFDRSHLKLFTIKYVDVNTNELLKSEQLLTASERNLDFRDLYDPRDKAKLLYNNLDAFGIMDYTLTGKVEDNHDDTNRIITVYMGKR

>d1c4pc\_ d.15.5.1 (C:) Streptokinase {Streptococcus equisimilis}

KPIQNQAKSVDVEYTVQFTPLNPDDDFRPGLKDTKLLKTLAIGDTITSQELLAQAQSILNKTHPGYTIYERDSSIVTHDNDIFRTILPMDQEFTYHVKNREQAYEINKKSGLNEEINNTDLISEKYYVLKKG

>d1qqra\_ d.15.5.1 (A:) Streptokinase {Streptococcus equisimilis}

IQNQAKSVDVEYTVQFTPLNPDDDFRPGLKLTKLLKTLAIGDTITSQELLAQAQSILNKNHPGYTIYERDSSIVTHDNDIFRTILPMDQEFTYRVKNREQAYRINKKSGLNEEINNTDLISEKYYVLKKGEKPYDPFD

>d1esfa2 d.15.6.1 (A:121-233) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}

EEKKVPINLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQEKYNLYNSDVFDGKVQRGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS

>d1i4pa2 d.15.6.1 (A:121-239) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}

NHFDNGNLQNVLIRVYENKRNTISFEVQTDKKSVTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSKSVKIEVHLTTKNG

>d3tss\_2 d.15.6.1 (94-194) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}

LPTPIELPLKVKVHGKDSPLKYWPKFDKKQLAISTLDFKIRHQLTQTHGLYRSSDKTGGYWKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN

>d1sebd2 d.15.6.1 (D:127-235) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

DKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYETGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLT

>d3seb\_2 d.15.6.1 (122-238) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKKVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMPAPGDKFDQSKYLMMYNDNKMVDSKDVKIEVYLTTKK

>d1enfa2 d.15.6.1 (A:102-213) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}

EKLAQERVIGANVWVDGIQKETELIRTNKKNVTLQELDIKIRKILSDKYKIYYKDSEISKGLIEFDMKTPRDYSFDIYDLKGENDYEIDKIYEDNKTLKSDDISHIDVNLYT

>d1an8\_2 d.15.6.1 (96-208) Streptococcal superantigen Spe-C {Streptococcus pyogenes}

NKVNHKLLGNLFISGESQQNLNNKIILEKDIVTFQEIDFKIRKYLMDNYKIYDATSPYVSGRIEIGTKDGKHEQIDLFDSPNEGTRSDIFAKYKDNRIINMKNFSHFDIYLEK

>d1et9a2 d.15.6.1 (A:96-204) Streptococcal superantigen Spe-H {Streptococcus pyogenes}

EKKEIKVPVNVWDKSKQQPPMFITVNKPKVTAQEVDIKVRKLLIKKYDIYNNREQKYSKGTVTLDLNSGKDIVFDLYYFGNGDFNSMLKIYSNNERIDSTQFHVDVSIS

>d1eu3a2 d.15.6.1 (A:97-209) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}

TSIPKNIPVNLWINGKQISVPYNEISTNKTTVTAQEIDLKVRKFLIAQHQLYSSGSSYKSGRLVFHTNDNSDKYSFDLFYVGYRDKESIFKVYKDNKSFNIDKIGHLDIEIDS

>d1bxta2 d.15.6.1 (A:120-234) Streptococcal superantigen SSA {Streptococcus pyogenes}

QIEGKFPNITVKVYEDNENILSFDITTNKKQVTVQELDCKTRKILVSRKNLYEFNNSPYETGYIKFIESSGDSFWYDMMPAPGAIFDQSKYLMLYNDNKTVSSSAIAIEVHLTKK

>d1fnua2 d.15.6.1 (A:108-221) Streptococcal pyrogenic exotoxin A1 {Streptococcus pyogenes}

GNHLEIPKKIVVKVSIDGIQSLSFDIETNKKMVTAQELDYKVRKYTIDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMIYKDNETLDNKTSQIEVYLTTK

>d1fcla\_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

TTFKLIINGKTLKGETTTEAVDAATAEKVLKQYINDNGIDGEWTYDDATKTWTVTE

>d1fd6a\_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

MTTFKLIINGKTLKGETTTEAVDAATAEKVFKQYANDNGIDGEWTYDDATKTFTVTE

>d1gb4\_\_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

MTTFKLIINGKTLKGEITIEAVDAAEAEKIFKQYANDNGIDGEWTYDDATKTFTVTE

>d1pgb\_\_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

MTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTE

>d1pgx\_\_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

ELTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTEMVTEVPVA

>d1qkza\_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

VTTYKLVINGKTLKGETTTKAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEK

>d2igd\_\_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

MTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTE

>d2igg\_\_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

LTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTFTVTEKPE

>d1heze\_ d.15.7.1 (E:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

EVTIKVNLIFADGKIQTAEFKGTFEEATAEAYRYADLLAKVNGEYTADLEDGGNHMNIKFA

>d1hz6a\_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

HHAMEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVADKGYTLNIKFAG

>d1jmla\_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

MHHHHHHGMEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVVPKAYTLNIKFAG

>d1k52a\_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

MHHHHHHAMEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVADGGYTLNIKFAG

>d1kh0a\_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

EEVTIKANLIFANGSTQTAEFKGTKEKALSEVLAYADTLKKDNGEWTIDKRVTNGVIILNIKFAG

>d2ptl\_\_ d.15.7.1 (-) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAG

>d1tif\_\_ d.15.8.1 (-) Translation initiation factor IF3, N-terminal domain {Bacillus stearothermophilus}

KDFIINEQIRAREVRLIDQNGDQLGIKSKQEALEIAARRNLDLVLVAPNAKPPVCRIMDYGKFRFEQQKKEKEARK

>d1f52a1 d.15.9.1 (A:1-100) Glutamine synthetase, N-terminal domain {Salmonella typhimurium}

SAEHVLTMLNEHEVKFVDLRFTDTKGKEQHVTIPAHQVNAEFFEEGKMFDGSSIGGWKGINESDMVLMPDASTAVIDPFFADSTLIIRCDILEPGTLQGY

>d1coy\_2 d.16.1.1 (319-450) Cholesterol oxidase {Brevibacterium sterolicum}

GNNGNIMVGRANHMWDATGSKQATIPTMGIDNWADPTAPIFAEIAPLPAGLETYVSLYLAITKNPERARFQFNSGTGKVDLTWAQSQNQKGIDMAKKVFDKINQKEGTIYRTDLFGVYYKTWGDDFTYHPLG

>d1ijha2 d.16.1.1 (A:319-450) Cholesterol oxidase {Streptomyces sp.}

GPNGNIMTARANHMWNPTGAHQSSIPALGIDAWDNSDSSVFAEIAPMPAGLETWVSLYLAITKNPQRGTFVYDAATDRAKLNWTRDQNAPAVNAAKALFDRINKANGTIYRYDLFGTQLKAFADDFCYHPLG

>d1k0ia2 d.16.1.2 (A:174-275) p-Hydroxybenzoate hydroxylase (PHBH) {Pseudomonas aeruginosa}

LKVFERVYPFGWLGLLADTPPVSHELIYANHPRGFALCSQRSATRSQYYVQVPLSEKVEDWSDERFWTELKARLPSEVAEKLVTGPSLEKSIAPLRSFVVEP

>d1foha4 d.16.1.2 (A:241-341) Phenol hydroxylase {Soil-living yeast (Trichosporon cutaneum)}

GEQTDYIWGVLDAVPASNFPDIRSRCAIHSAESGSIMIIPRENNLVRFYVQLQARAEKGGRVDRTKFTPEVVIANAKKIFHPYTFDVQQLDWFTAYHIGQR

>d1an9a2 d.16.1.3 (A:195-287) D-amino acid oxidase {Pig (Sus scrofa)}

LQPGRGQIIKVDAPWLKNFIITHDLERGIYNSPYIIPGLQAVTLGGTFQVGNWNEINNIQDHNTIWEGCCRLEPTLKDAKIVGEYTGFRPVRP

>d1c0pa2 d.16.1.3 (A:1194-1288) D-amino acid oxidase {Yeast (Rhodotorula gracilis)}

AEPIRGQTVLVKSPCKRCTMDSSDPASPAYIIPRPGGEVICGGTYGVGDWDLSVNPETVQRILKHCLRLDPTISSDGTIEGIEVLRHNVGLRPAR

>d1el8a2 d.16.1.3 (A:218-321) Sarcosine oxidase {Bacillus sp., strain b0618}

LQPYRQVVGFFESDESKYSNDIDFPGFMVEVPNGIYYGFPSFGGCGLKLGYHTFGQKIDPDTINREFGVYPEDESNLRAFLEEYMPGANGELKRGAVCMYTKTL

>d1i8ta2 d.16.1.7 (A:245-313) UDP-galactopyranose mutases {Escherichia coli}

EYRSLKFETERHEFPNFQGNAVINFTDANVPYTRIIEHKHFDYVETKHTVVTKEYPLEWKVGDEPYYPV

>d1cf3a2 d.16.1.4 (A:325-520) Glucose oxidase {Aspergillus niger}

NLQDQTTATVRSRITSAGAGQGQAAWFATFNETFGDYSEKAHELLNTKLEQWAEEAVARGGFHNTTALLIQYENYRDWIVNHNVAYSELFLDTAGVASFDVWDLLPFTRGYVHILDKDPYLHHFAYDPQYFLNELDLLGQAAATQLARNISNSGAMQTYFAGETIPGDNLAYDADLSAWTEYIPYHFRPNYHGVGT

>d1gpea2 d.16.1.4 (A:329-524) Glucose oxidase {Penicillium amagasakiense}

NMQDQTTTTVSSRASSAGAGQGQAVFFANFTETFGDYAPQARDLLNTKLDQWAEETVARGGFHNVTALKVQYENYRNWLLDEDVAFAELFMDTEGKINFDLWDLIPFTRGSVHILSSDPYLWQFANDPKFFLNEFDLLGQAAASKLARDLTSQGAMKEYFAGETLPGYNLVQNATLSQWSDYVLQNFRPNWHAVSS

>d1b5qa2 d.16.1.5 (A:294-405) Polyamine oxidase {Maize (Zea mays)}

DMAVYTKIFLKFPRKFWPEGKGREFFLYASSRRGYYGVWQEFEKQYPDANVLLVTVTDEESRRIEQQSDEQTKAEIMQVLRKMFPGKDVPDATDILVPRWWSDRFYKGTFSN

>d1f8ra2 d.16.1.5 (A:320-432) L-amino acid oxidase {Malayan pit viper (Calloselasma rhodostoma)}

HYRSGTKIFLTCTTKFWEDDGIHGGKSTTDLPSRFIYYPNHNFTNGVGVIIAYGIGDDANFFQALDFKDCADIVFNDLSLIHQLPKKDIQSFCYPSVIQKWSLDKYAMGGITT

>d1gosa2 d.16.1.5 (A:290-401) Monoamine oxidase B {Human (Homo sapiens)}

PLGSVIKCIVYYKEPFWRKKDYCGTMIIDGEEAPVAYTLDDTKPEGNYAAIMGFILAHKARKLARLTKEERLKKLCELYAKVLGSLEALEPVHYEEKNWCEEQYSGGCYTTY

>d1d5ta2 d.16.1.6 (A:292-388) Guanine nucleotide dissosiation inhibitor, GDI {Cow (Bos taurus)}

RKAGQVIRIICILSHPIKNTNDANSCQIIIPQNQVNRKSDIYVCMISYAHNVAAQGKYIAIASTTVETTDPEKEVEPALGLLEPIDQKFVAISDLYE

>d1mola\_ d.17.1.1 (A:) Monellin, B & A chains together {Serendipity berry (Dioscoreophyllum cumminsii)}

GEWEIIDIGPFTQNLGKFAVDEENKIGQYGRLTFNKVIRPCMKKTIYENEREIKGYEYQLYVYASDKLFRADISEDYKTRGRKLLRFNGPVPPP

>d1eqka\_ d.17.1.2 (A:) Phytocystatin {Japanese rice (Oryza sativa), subsp. japonica, oryzacystatin-I}

MSSDGGPVLGGVEPVGNENDLHLVDLARFAVTEHNKKANSLLEFEKLVSVKQQVVAGTLYYFTIEVKEGDAKKLYEAKVWEKPWMDFKELQEFKPVDASANA

>d1cewi\_ d.17.1.2 (I:) Cystatin {Chicken (Gallus gallus)}

GAPVPVDENDEGLQRALQFAMAEYNRASNDKYSSRVVRVISAKRQLVSGIKYILQVEIGRTTCPKSSGDLQSCEFHDEPEMAKYTTCTFVVYSIPWLNQIKLLESKCQ

>d1dvd\_\_ d.17.1.2 (-) Cystatin A (stefin A) {Human (Homo sapiens)}

MIPGGLSEAKPATPEIQEIVDKVKPQLEEKTNETYGKLEAVQYKTQVVAGTNYYIKVRAGDNKYMHLKVFKSLPGQNEDLVLTGYQVDKNKDDELTGF

>d1stfi\_ d.17.1.2 (I:) Cystatin B (stefin B) {Human (Homo sapiens)}

MMSGAPSATQPATAETQHIADQVRSQLEEKYNKKFPVFKAVSFKSQVVAGTNYFIKVHVGDEDFVHLRVFQSLPHENKPLTLSNYQTNKAKHDELTYF

>d1g96a\_ d.17.1.2 (A:) Cystatin C {Human (Homo sapiens)}

VGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNYFLDVELGRTTCTKTQPNLDNCPFHDQPHLKRKAFCSFQIYAVPWQGTMTLSKSTCQDA

>d1oaca2 d.17.2.1 (A:91-185) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

KRPHPLNALTADEIKQAVEIVKASADFKPNTRFTEISLLPPDKEAVWAFALENKPVDQPRKADVIMLDGKHIIEAVVDLQNNKLLSWQPIKDAHG

>d1oaca3 d.17.2.1 (A:186-300) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

MVLLDDFASVQNIINNSEEFAAAVKKRGITDAKKVITTPLTVGYFDGKDGLKQDARLLKVISYLDVGDGNYWAHPIENLVAVVDLEQKKIVKIEEGPVVPVPMTARPFDGRDRVA

>d1ksia2 d.17.2.1 (A:6-98) Copper amine oxidase, domains 1 and 2 {Pea seedling (Pisum sativum)}

VQHPLDPLTKEEFLAVQTIVQNKYPISNNRLAFHYIGLDDPEKDHVLRYETHPTLVSIPRKIFVVAIINSQTHEILINLRIRSIVSDNIHNGY

>d1ksia3 d.17.2.1 (A:99-206) Copper amine oxidase, domains 1 and 2 {Pea seedling (Pisum sativum)}

GFPILSVDEQSLAIKLPLKYPPFIDSVKKRGLNLSEIVCSSFTMGWFGEEKNVRTVRLDCFMKESTVNIYVRPITGITIVADLDLMKIVEYHDRDIEAVPTAENTEYQ

>d1av4\_2 d.17.2.1 (9-96) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ASPFRLASAGEISEVQGILRTAGLLGPEKRIAYLGVLDPARGAGSEAEDRRFRVFIHDVSGARPQEVTVSVTNGTVISAVELDTAATG

>d1av4\_3 d.17.2.1 (97-211) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ELPVLEEEFEVVEQLLATDERWLKALAARNLDVSKVRVAPLSAGVFEYAEERGRRILRGLAFVQDFPEDSAWAHPVDGLVAYVDVVSKEVTRVIDTGVFPVPAEHGNYTDPELTG

>d1a2va2 d.17.2.1 (A:18-115) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula polymorpha)}

PARPAHPLDPLSTAEIKAATNTVKSYFAGKKISFNTVTLREPARKAYIQWKEQGGPLPPRLAYYVILEAGKPGVKEGLVDLASLSVIETRALETVQPI

>d1a2va3 d.17.2.1 (A:116-236) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula polymorpha)}

LTVEDLCSTEEVIRNDPAVIEQCVLSGIPANEMHKVYCDPWTIGYDERWGTGKRLQQALVYYRSDEDDSQYSHPLDFCPIVDTEEKKVIFIDIPNRRRKVSKHKHANFYPKHMIEKVGAMR

>d1eeja2 d.17.3.1 (A:1-60) Disulfide bond isomerase, DsbC, N-terminal domain {Escherichia coli}

DDAAIQQTLAKMGIKSSDIQPAPVAGMKTVLTNSGVLYITDDGKHIIQGPMYDVSGTAPV

>d3stda\_ d.17.4.1 (A:) Scytalone dehydratase {Fungus (Magnaporthe grisea)}

GEITFSDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEEFVGMVSSKQVLGDPTLRTQHFIGGTRWEKVSEDEVIGYHQLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKFAGLKPDIRWGEFDFDRIFEDGRETFG

>d1ouna\_ d.17.4.2 (A:) Nuclear transport factor-2 (NTF2) {Rat (Rattus norvegicus)}

GDKPIWEQIGSSFIQHYYQLFDNDRTQLGAIYIDASCLTWEGQQFQGKAAIVEKLSSLPFQKIQHSITAQDHQPTPDSCIISMVVGQLKADEDPIMGFHQMFLLKNINDAWVCTNDMFRLALHNF

>d1jkga\_ d.17.4.2 (A:) NTF2-related export protein 1 (p15) {Human (Homo sapiens)}

ASVDFKTYVDQACRAAEEFVNVYYTTMDKRRRLLSRLYMGTATLVWNGNAVSGQESLSEFFEMLPSSEFQISVVDCQPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASPSNTVWKIASDCFRFQDWAS

>d1jkgb\_ d.17.4.2 (B:) NTF2-like domain of Tip associating protein, TAP {Human (Homo sapiens)}

APPCKGSYFGTENLKSLVLHFLQQYYAIYDSGDRQGLLDAYHDGACCSLSIPFIPQNPARSSLAEYFKDSRNVKKLKDPTLRFRLLKHTRLNVVAFLNELPKTQHDVNSFVVDISAQTSTLLCFSVNGVFKEVDGKSRDSLRAFTRTFIAVPASNSGLCIVNDELFVRNASSEEIQRAFAMPAPTP

>d1qjga\_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Comamonas testosteroni and Pseudomonas testosteroni}

MNTPEHMTAVVQRYVAALNAGDLDGIVALFADDATVENPVGSEPRSGTAAIREFYANSLKLPLAVELTQEVRAVANEAAFAFIVSFEYQGRKTVVAPIDHFRFNGAGKVVSMRALFGEKNIHAGA

>d1ea2a\_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Pseudomonas putida}

NLPTAQEVQGLMARFIELVDVGDIEAIVQMYADDATVEDPFGQPPIHGREQIAAFYRQGLGGGKVRACLTGPVRASHNGCGAMPFRVEMVWNGQPCALDVIDVMRFDEHGRIQTMQAYWSEVNLSV

>d1eg9b\_ d.17.4.4 (B:) Naphthalene 1,2-dioxygenase beta subunit {Pseudomonas putida}

MINIQEDKLVSAHDAEEILRFFNCHDSALQQEATTLLTQEAHLLDIQAYRAWLEHCVGSEVQYQVISRELRAASERRYKLNEAMNVYNENFQQLKVRVEHQLDPQNWGNSPKLRFTRFITNVQAAMDVNDKELLHIRSNVILHRARRGNQVDVFYAAREDKWKRGEGGVRKLVQRFVDYPERILQTHNLMVFL

>d1euic\_ d.17.5.1 (C:) Uracil-DNA glycosylase inhibitor protein {Bacteriophage pbs2}

QLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

>d1ugia\_ d.17.5.1 (A:) Uracil-DNA glycosylase inhibitor protein {Bacteriophage pbs2}

TNLSDIIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKML

>d1pcfa\_ d.18.1.1 (A:) Transcriptional coactivator PC4 C-terminal domain {Human (Homo sapiens)}

AMFQIGKMRYVSVRDFKGKVLIDIREYWMDPEGEMKPGRKGISLNPEQWSQLKEQISDIDDAVRKL

>d1jb0d\_ d.187.1.1 (D:) Photosystem I subunit PsaD {Synechococcus elongatus}

TTLTGQPPLYGGSTGGLLSAADTEEKYAITWTSPKEQVFEMPTAGAAVMREGENLVYFARKEQCLALAAQQLRPRKINDYKIYRIFPDGETVLIHPKDGVFPEKVNKGREAVNSVPRSIGQNPNPSQLKFTGKKPYDP

>d3frua2 d.19.1.1 (A:1-178) Fc (IgG) receptor, alpha-1 and alpha-2 domains {Rat (Rattus norvegicus)}

AEPRLPLMYHLAAVSDLSTGLPSFWATGWLGAQQYLTYNNLRQEADPCGAWIWENQVSWYWEKETTDLKSKEQLFLEAIRTLENQINGTFTLQGLLGCELAPDNSSLPTAVFALNGEEFMRFNPRTGNWSGEWPETDIVGNLWMKQPEAARKESEFLLTSCPERLLGHLERGRQNLEW

>d1cd1a2 d.19.1.1 (A:7-185) CD1, alpha-1 and alpha-2 domains {Mouse (Mus musculus)}

NYTFRCLQMSSFANRSWSRTDSVVWLGDLQTHRWSNDSATISFTKPWSQGKLSNQQWEKLQHMFQVYRVSFTRDIQELVKMMSPKEDYPIEIQLSAGCEMYPGNASESFLHVAFQGKYVVRFWGTSWQTVPGAPSWLDLPIKVLNADQGTSATVQMLLNDTCPLFVRGLLEAGKSDLEK

>d1hdma2 d.19.1.1 (A:13-93) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}

LQNHTFLHTVYCQDGSPSVGLSEAYDEDQLFFFDFSQNTRVPRLPEFADWAQEQGDAILFDKEFCEWMIQQIPKLDGKIPV

>d1hdmb2 d.19.1.1 (B:3-87) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}

FVAHVESTCLLDDAGTPKDFTYCISFNKDLLTCWDPEENKMAPCNSLANVLSQHLNQKDTLMQRLNGLQNCATHTQPFWGSLTNR

>d1aqdb2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR1}

RPRFLWQLKFECHFFNGTERVRLLERCIYNQEESVRFDSDVGEYRAVTELGRPDAEYWNSQKDLLEQRRAAVDTYCRHNYGVGESFTVQ

>d1bx2b2 d.19.1.1 (B:3-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

TRPRFLWQPKRECHFFNGTERVRFLDRYFYNQEESVRFDSDVGEFRAVTELGRPDAEYWNSQKDILEQARAAVDTYCRHNYGVVESFTVQ

>d1fv1a2 d.19.1.1 (A:3-81) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

EEHVIIQAEFYLNPDQSGEFMFDFDGDEIFHVDMAKKETVWRLEEFGRFASFEAQGALANIAVDKANLEIMTKRSNYTP

>d1fv1b2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

GDTRPRFLQQDKYECHFFNGTERVRFLHRDIYNQEEDLRFDSDVGEYRAVTELGRPDAEYWNSQKDFLEDRRAAVDTYCRHNYGVGESFTVQ

>d1a6ab2 d.19.1.1 (B:5-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR3}

PRFLEYSTSECHFFNGTERVRYLDRYFHNQEENVRFDSDVGEFRAVTELGRPDAEYWNSQKDLLEQKRGRVDNYCRHNYGVVESFTVQ

>d1d5zb2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR4}

GDTRPRFLEQVKHECHFFNGTERVRFLDRYFYHQEEYVRFDSDVGEYRAVTELGRPDAEYWNSQKDLLEQKRAAVDTYCRHNYGVGESFTVQ

>d1jk8a2 d.19.1.1 (A:2-84) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}

VADHVASYGVNLYQSYGPSGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTNIAVLKHNLNIVIKRSNSTAATN

>d1jk8b2 d.19.1.1 (B:3-94) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}

SPEDFVYQFKGMCYFTNGTERVRLVTRYIYNREEYARFDSDVGVYRAVTPLGPPAAEYWNSQKEVLERTRAELDTVCRHNYQLELRTTLQRR

>d1iaka2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}

IEADHVGSYGITVYQSPGDIGQYTFEFDGDELFYVDLDKKETVWMLPEFAQLRRFEPQGGLQNIATGKHNLEILTKRSNSTP

>d1iakb2 d.19.1.1 (B:5-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}

GSFVHQFQPFCYFTNGTQRIRLVIRYIYNREEYVRFDSDVGEYRAVTELGRPDAEYWNKQYLERTRAELDTVCRHNYEKTETPTSLR

>d1fnga2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

IKEEHTIIQAEFYLLPDKRGEFMFDFDGDEIFHVDIEKSETIWRLEEFAKFASFEAQGALANIAVDKANLDVMKERSNNTP

>d1fngb2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

RPWFLEYCKSECHFYNGTQRVRLLVRYFYNLEENLRFDSDVGEFRAVTELGRPDAENWNSQPEFLEQKRAEVDTVCRHNYEIFDNFLVP

>d1i3rb2 d.19.1.1 (B:1-120) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

GKKVITAFNEGLKGGGGSLVGGGSGGGGSRPWFLEYCKSECHFYNGTQRVRLLVRYFYNLEENLRFDSDVGEFRAVTELGRPDAENWNSQPEFLEQKRAEVDTVCRHNYEIFDNFLVPRR

>d2iadb2 d.19.1.1 (B:5-93) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AD}

RHFVVQFKGECYYTNGTQRIRLVTRYIYNREEYVRYDSDVGEYRAVTELGRPDAEYWNSQPEILERTRAEVDTACRHNYEGPETSTSLR

>d1es0a2 d.19.1.1 (A:1B-82) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-A(G7)}

DIEADHVGFYGTTVYQSPGDIGQYTHEFDGDELFYVDLDKKKTVWRLPEFGQLILFEPQGGLQNIAAEKHNLGILTKRSNFTPA

>d1es0b2 d.19.1.1 (B:5-93) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-A(G7)}

RHFVHQFKGECYFTNGTQRIRLVTRYIYNREEYLRFDSDVGEYRAVTELGRHSAEYYNKQYLERTRAELDTACRHNYEETEVPTSLR

>d1k8ia2 d.19.1.1 (A:11-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

QNHTFRHTLFCQDGIPNIGLSETYDEDELFSFDFSQNTRVPRLPDFAEWAQGQGDASAIAFDKSFCEMLMREVSPKLEGQIP

>d1k8ib2 d.19.1.1 (B:1-94) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

GFVAHVESTCVLNDAGTPQDFTYCVSFNKDLLACWDPDVGKIVPCEFGVLSRLAEIISNILNEQESLIHRLQNGLQDCATHTQPFWDVLTHRTR

>d1i4fa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-A2.1}

GSHSMRYFFTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDVGSDWRFLRGYHQYAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQLRAYLEGTCVEWLRRYLENGKETLQR

>d1hsaa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B2705}

GSHSMRYFHTSVSRPGRGEPRFITVGYVDDTLFVRFDSDAASPREEPRAPWIEQEGPEYWDRETQICKAKAQTDREDLRTLLRYYNQSEAGSHTLQNMYGCDVGPDGRLLRGYHQDAYDGKDYIALNEDLSSWTAADTAAQITQRKWEAARVAEQLRAYLEGECVEWLRRYLENGKETLQR

>d1hsba2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-AW68}

GSHSMRYFYTSVSRPGRGEPRFIAVGYVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEYWDRNTRNVKAQSQTDRVDLGTLRGYYNQSEAGSHTIQMMYGCDVGSDGRFLRGYRQDAYDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQWRAYLEGTCVEWLRRYLENGKETLQR

>d1agda2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B0801}

GSHSMRYFDTAMSRPGRGEPRFISVGYVDDTQFVRFDSDAASPREEPRAPWIEQEGPEYWDRNTQIFKTNTQTDRESLRNLRGYYNQSEAGSHTLQSMYGCDVGPDGRLLRGHNQYAYDGKDYIALNEDLRSWTAADTAAQITQRKWEAARVAEQDRAYLEGTCVEWLRRYLENGKDTLER

>d1a1na2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B\*3501}

GSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRTEPRPPWIEQEGPEYWDRNTQIFKTNTQTYRESLRNLRGYYNQSEAGSHIIQRMYGCDLGPDGRLLRGHDQSAYDGKDYIALNEDLSSWTAADTAAQITQRKWEAARVAEQLRAYLEGLCVEWLRRYLENGKETLQR

>d1e27a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B\*5101}

GSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRTEPRAPWIEQEGPEYWDRNTQIFKTNTQTYRENLRIALRYYNQSEAGSHTWQTMYGCDVGPDGRLLRGHNQYAYDGKDYIALNEDLSSWTAADTAAQITQRKWEAAREAEQLRAYLEGLCVEWLRRHLENGKETLQR

>d1efxa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-CW3}

GSHSMRYFYTAVSRPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPRAPWVEQEGPEYWDRETQKYKRQAQTDRVSLRNLRGYYNQSEAGSHIIQRMYGCDVGPDGRLLRGYDQYAYDGKDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQLRAYLEGLCVEWLRRYLKNGKETLQR

>d1qqda2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-CW4}

SHSMRYFSTSVSWPGRGEPRFIAVGYVDDTQFVRFDSDAASPRGEPREPWVEQEGPEYWDRETQKYKRQAQADRVNLRKLRGYYNQSEDGSHTLQRMFGCDLGPDGRLLRGYNQFAYDGKDYIALNEDLRSWTAADTAAQITQRKWEAAREAEQRRAYLEGTCVEWLRRYLENGKETLQR

>d1mhea2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-E}

SHSLKYFHTSVSRPGRGEPRFISVGYVDDTQFVRFDNDAASPRMVPRAPWMEQEGSEYWDRETRSARDTAQIFRVNLRTLRGYYNQSEAGSHTLQWMHGCELGPDRRFLRGYEQFAYDGKDYLTLNEDLRSWTAVDTAAQISEQKSNDASEAEHQRAYLEDTCVEWLHKYLEKGKETLLH

>d1de4a2 d.19.1.1 (A:4-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), hemochromatosis protein Hfe}

RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKYGYDGQDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLLELGRGVLD

>d1fzka2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2KB}

GPHSLRYFVTAVSRPGLGEPRYMEVGYVDDTEFVRFDSDAENPRYEPRARWMEQEGPEYWERETQKAKGNEQSFRVDLRTLLGYYNQSKGGSHTIQVISGCEVGSDGRLLRGYQQYAYDGCDYIALNEDLKTWTAADMAALITKHKWEQAGAAEYYRAYLEGTCVEWLRRYLKNGNATLLR

>d1jpfa2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2DB}

PHSMRYFETAVSRPGLEEPRYISVGYVDNKEFVRFDSDAENPRYEPRAPWMEQEGPEYWERETQKAKGQEQWFRVSLRNLLGYYNQSAGGSHTLQQMSGCDLGSDWRLLRGYLQFAYEGRDYIALNEDLKTWTAADMAAQITRRKWEQSGAAEHYKAYLEGECVEWLHRYLKNGNATLLR

>d1mhca2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2M3}

GSHSLRYFHTAVSRPGRGEPQYISVGYVDDVQFQRCDSIEEIPRMEPRAPWMEKERPEYWKELKLKVKNIAQSARANLRTLLRYYNQSEGGSHILQWMVSCEVGPDMRLLGAHYQAAYDGSDYITLNEDLSSWTAVDMVSQITKSRLESAGTAEYFRAYVEGECLELLHRFLRNGKEILQR

>d1ld9a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2LD}

GPHSMRYFETAVSRPGLGEPRYISVGYVDNKEFVRFDSDAENPRYEPQAPWMEQEGPEYWERITQIAKGQEQWFRVNLRTLLGYYNQSAGGTHTLQWMYGCDVGSDGRLLRGYEQFAYDGCDYIALNEDLKTWTAADMAAQITRRKWEQAGAAEYYRAYLEGECVEWLHRYLKNGNATLLR

>d1qo3a2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2DD}

SHSLRYFVTAVSRPGFGEPRYMEVGYVDNTEFVRFDSDAENPRYEPRARWIEQEGPEYWERETRRAKGNEQSFRVDLRTALRYYNQSAGGSHTLQWMAGCDVESDGRLLRGYWQFAYDGCDYIALNEDLKTWTAADMAAQITRRKWEQAGAAERDRAYLEGECVEWLRRYLKNGNATLLR

>d1k8da2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), IB QA-2}

GQHSLQYFHTAVSRPGLGEPWFISVGYVDDTQFVRFDSDAENPRMEPRARWMEQEGPEYWERETQIAKGHEQSFRGSLRTAQSYYNQSKGGSHTLQWMYGCDMGSDGRLLRGYLQFAYEGRDYIALNEDLKTWTAVDMAAQITRRKWEQAGIAEKDQAYLEGTCMQSLRRYLELGKETLLR

>d1ed3a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Rat (Rattus norvegicus), RT1-AA}

GSHSLRYFYTAVSRPGLGEPRFIAVGYVDDTEFVRFDSDAENPRMEPRARWMEREGPEYWEQQTRIAKEWEQIYRVDLRTLRGYYNQSEGGSHTIQEMYGCDVGSDGSLLRGYRQDAYDGRDYIALNEDLKTWTAADFAAQITRNKWERARYAERLRAYLEGTCVEWLSRYLELGKETLLR

>d1zaga2 d.19.1.1 (A:5-183) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}

DGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGMEDWKQDSQLQKAREDIFMETLKDIVEYYNDSNGSHVLQGRFGCEIENNRSSGAFWKYYYDGKDYIEFNKEIPAWVPFDPAAQITKQKWEAEPVYVQRAKAYLEEECPATLRKYLKYSKNILDR

>d1hyrc2 d.19.1.1 (C:0-180) MHC I homolog {Human (Homo sapiens), Mic-a}

MEPHSLRYNLTVLSWDGSVQSGFLTEVHLDGQPFLRCDRQKCRAKPQGQWAEDVLGNKTWDRETRDLTGNGKDLRMTLAHIKDQKEGLHSLQEIRVCEIHEDNSTRSSQHFYYDGELFLSQNLETKEWTMPQSSRAQTLAMNVRNFLKEDAMKTKTHYHAMHADCLQELRRYLKSGVVLRR

>d1c16a2 d.19.1.1 (A:1-180) MHC I homolog {Mouse (Mus musculus), t22}

GSHSLRYFYTAVSRPGLGEPWFIIVGYVDDMQVLRFSSKEETPRMAPWLEQEEADNWEQQTRIVTIQGQLSERNLMTLVHFYNKSMDDSHTLQWLQGCDVEPDRHLCLWYNQLAYDSEDLPTLNENPSSCTVGNSTVPHISQDLKSHCSDLLQKYLEKGKERLL

>d1exua2 d.19.1.1 (A:4-176) Class I MHC-related Fc receptor {Human (Homo sapiens)}

HLSLLYHLTAVSSPAPGTPAFWVSGWLGPQQYLSYNSLRGEAEPCGAWVWENQVSWYWEKETTDLRIKEKLFLEAFKALGGKGPYTLQGLLGCELGPDNTSVPTAKFALNGEEFMNFDLKQGTWGGDWPEALAISQRWQQQDKAANKELTFLLFSCPHRLREHLERGRGNLEW

>d1kcgc\_ d.19.1.1 (C:) Class I MHC-related molecule Ulbp3 {Human (Homo sapiens)}

DAHSLWYNFTIIHLPRHGQQWCEVQSQVDQKNFLSYDCGSDKVLSMGHLEEQLYATDAWGKQLEMLREVGQRLRLELADTELEDFTPSGPLTLQVRMSCECEADGYIRGSWQFSFDGRKFLLFDSNNRKWTVVHAGARRMKEKWEKDSGLTTFFKMVSMRDCKSWLRDFLMHRKKRLE

>d1jfma\_ d.19.1.1 (A:) NK cell ligand RAE-1 beta {Mouse (Mus musculus)}

DAHSLRCNLTIKDPTPADPLWYEAKCFVGEILILHLSNINKTMTSGDPGETANATEVKKCLTQPLKNLCQKLRNKVSNTKVDTHKTNGYPHLQVTMIYPQSQGRTPSATWEFNISDSYFFTFYTENMSWRSANDESGVIMNKWKDDGEFVKQLKFLIHECSQKMDEFLKQSKEK

>d2aak\_\_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Arabidopsis thaliana}

MSTPARKRLMRDFKRLQQDPPAGISGAPQDNNIMLWNAVIFGPDDTPWDGGTFKLSLQFSEDYPNKPPTVRFVSRMFHPNIYADGSICLDILQNQWSPIYDVAAILTSIQSLLCDPNPNSPANSEAARMYSESKREYNRRVRDVVEQSWT

>d1fzya\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc1}

SRAKRIMKEIQAVKDDPAAHITLEFVSESDIHHLKGTFLGPPGTPYEGGKFVVDIEVPMEYPFKPPKMQFDTKVYHPNISSVTGAICLDILKNAWSPVITLKSALISLQALLQSPEPNDPQDAEVAQHYLRDRESFNKTAALWTRLYAS

>d1ayza\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc2 (RAD6)}

STPARRRLMRDFKRMKEDAPPGVSASPLPDNVMVWNAMIIGPADTPYEDGTFRLLLEFDEEYPNKPPHVKFLSEMFHPNVYANGEICLDILQNRWTPTYDVASILTSIQSLFNDPNPASPANVEAATLFKDHKSQYVKRVKETVEKSWEDDMD

>d1qcqa\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc4}

MSSSKRIAKELSDLERDPPTSCSAGPVGDDLYHWQASIMGPADSPYAGGVFFLSIHFPTDYPFKPPKISFTTKIYHPNINANGNICLDILKDQWSPALTLSKVLLSICSLLTDANPDDPLVPEIAHIYKTDRPKYEATAREWTKKYAV

>d2ucz\_\_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc7}

SKTAQKRLLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPPDTPYADGVFNAKLEFPKDYPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKILLSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

>d1jata\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc13}

AASLPKRIIKETEKLVSDPVPGITAEPHDDNLRYFQVTIEGPEQSPYEDGIFELELYLPDDYPMEAPKVRFLTKIYHPNIDRLGRICLDVLKTNWSPALQIRTVLLSIQALLASPNPNDPLANDVAEDWIKNEQGAKAKAREWTKLYAKKKP

>d1j7db\_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc13}

AGLPRRIIKETQRLLAEPVPGIKAEPDESNARYFHVVIAGPQDSPFEGGTFKLELFLPEEYPMAAPKVRFMTKIYHPNVDKLGRICLDILKDKWSPALQIRTVLLSIQALLSAPNPDDPLANDVAEQWKTNEAQAIETARAWTRLYAMN

>d1jatb\_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), mms2}

SKVPRNFRLLEELEKGEKGFGPESCSYGLADSDDITMTKWNGTILGPPHSNHENRIYSLSIDCGPNYPDSPPKVTFISKINLPCVNPTTGEVQTDFHTLRDWKRAYTMETLLLDLRKEMATPANKKLRQPKEGETF

>d1j7da\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), mms2}

GVKVPRNFRLLEELEEGQKGVGDGTVSWGLEDDEDMTLTRWTGMIIGPPRTNYENRIYSLKVECGPKYPEAPPSVRFVTKINMNGINNSSGMVDARSIPVLAKWQNSYSIKVVLQELRRLMMSKENMKLPQPPEGQTYNN

>d1c4zd\_ d.20.1.1 (D:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch7}

SRRLMKELEEIRKCGMKNFRNIQVDEANLLTWQGLIVPDNPPYDKGAFRIEINFPAEYPFKPPKITFKTKIYHPNIDEKGQVCLPVISAENWKPATKTDQVIQSLIALVNDPQPEHPLRADLAEEYSKDRKKFCKNAEEFTKKY

>d1u9aa\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc9}

LNMSGIALSRLAQERKAWRKDHPFGFVAVPTKNPDGTMNLMNWECAIPGKKGTPWEGGLFKLRMLFKDDYPSSPPKCKFEPPLFHPNVYPSGTVCLSILEEDKDWRPAITIKQILLGIQELLNEPNIQDPAQAEAYTIYCQNRVEYEKRVRAQAKKFAPS

>d1i7ka\_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch10}

PVGKRLQQELMTLMMSGDKGISAFPESDNLFKWVGTIHGAAGTVYEDLRYKLSLEFPSGYPYNAPTVKFLTPCYHPNVDTQGNISLDILKEKWSALYDVRTILLSIQSLLGEPNIDSPLNTHAAELWKNPTAFKKYLQETYSKQVT

>d2e2c\_\_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Clam (Spisula solidissima), E-2C}

MTTSKERHSVSKRLQQELRTLLMSGDPGITAFPDGDNLFKWVATLDGPKDTVYESLKYKLTLEFPSDYPYKPPVVKFTTPCWHPNVDQSGNICLDILKENWTASYDVRTILLSLQSLLGEPNNASPLNAQAADMWSNQTEYKKVLHEKYKTAQSDK

>d1bwza1 d.21.1.1 (A:1-130) Diaminopimelate epimerase {Haemophilus influenzae}

MQFSKMHGLGNDFVVVDGVTQNVFFTPETIRRLANRHCGIGFDQLLIVEAPYDPELDFHYRIFNADGSEVSQCGNGARCFARFVTLKGLTNKKDISVSTQKGNMVLTVKDMNQIRVNMGEPIWEPAKIPF

>d1bwza2 d.21.1.1 (A:131-274) Diaminopimelate epimerase {Haemophilus influenzae}

TANKFEKNYILRTDIQTVLCGAVSMGNPHCVVQVDDIQTANVEQLGPLLESHERFPERVNAGFMQIINKEHIKLRVYERGAGETQACGSGACAAVAVGIMQGLLNNNVQVDLPGGSLMIEWNGVGHPLYMTGEATHIYDGFITL

>d1h6ra\_ d.22.1.1 (A:) Green fluorescent protein, GFP {Jellyfish (Aequorea victoria)}

SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFIVTTGKLPVPWPTLVTTFAYGLQCFARYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHCVYIVADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLCYQSALSKDPNEKRDHMVLLEFVTAAGITH

>d2emd\_\_ d.22.1.1 (-) Green fluorescent protein, GFP {Jellyfish (Aequorea victoria)}

ELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTLSYGVQCFSRYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNYNSHNVYIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLLEFVTAAGIT

>d1ggxa\_ d.22.1.1 (A:) Red fluorescent protein (fp583 or dsred(clontech)) {Coral (Discosoma sp.)}

VIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL

>d1gl4a1 d.22.1.2 (A:399-631) Domain G2 of nidogen-1 {Mouse (Mus musculus)}

GSPQRVNGKVKGRIFVGSSQVPVVFENTDLHSYVVMNHGRSYTAISTIPETVGYSLLPLAPIGGIIGWMFAVEQDGFKNGFSITGGEFTRQAEVTFLGHPGKLVLKQQFSGIDEHGHLTISTELEGRVPQIPYGASVHIEPYTELYHYSSSVITSSSTREYTVMEPDQDGAAPSHTHIYQWRQTITFQECAHDDARPALPSTQQLSVDSVFVLYNKEERILRYALSNSIGPVR

>d1c8za\_ d.23.1.1 (A:) Transcriptional factor tubby, C-terminal domain {Mouse (Mus musculus)}

GSVDIEVQDLEEFALRPAPQGITIKCRITRDKKGMDRGMFPTYFLHLDREDGKKVFLLAGRKRKKSKTSNYLISVDPTDLSRGGDSYIGKLRSNLMGTKFTVYDNGVNPQKASSSTLESGTLRQELAAVCYETNVLGFKGPRKMSVIVPGMNMVHERVCIRPRNEHETLLARWQNKNTESIIELQNKTPVWNDDTQSYVLNFHGRVTQASVKNFQIIHGNDPDYIVMQFGRVAEDVFTMDYNYPLCALQAFAIALSSFDSKLACE

>d2pil\_\_ d.24.1.1 (-) Pilin {Gc (Neisseria gonorrhoeae)}

FTLIELMIVIAIVGILAAVALPAYQDYTARAQVSEAILLAEGQKSAVTEYYLNHGKWPENNTSAGVASPPSDIKGKYVKEVEVKNGVVTATMLSSGVNNEIKGKKLSLWARRENGSVKWFCGQPVTRTDDDTVADAKDGKEIDTKHLPSTCRDNFDAK

>d1hpwa\_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa}

ALEGTEFARAQLSEAMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKVTTGGTAAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNADNKYLPKTCQTATTTTP

>d1dzoa\_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa, type IV pilin, pak pilin}

GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLTRTAADGLWKCTSDQDEQFIPKGCSR

>d1p32a\_ d.25.1.1 (A:) Acidic mitochondrial matrix protein p32 {Human (Homo sapiens)}

MHTDGDKAFVDFLSDEIKEERKIQKHKTLPKMSGGWELELNGTEAKLVRKVAGEKITVTFNINNSIPPTFDGEEEPSQGQKVEEQEPELTSTPNFVVEVIKNDDGKKALVLDCHYPEDEVGQEDEAESDIFSIREVSFQSTGESEWKDTNYTLNTDSLDWALYDHLMDFLADRGVDNTFADELVELSTALEHQEYITFLEDLKSFVKSQ

>d1bkf\_\_ d.26.1.1 (-) FK-506 binding protein (FKBP12), an immunophilin {Human (Homo sapiens)}

GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDKNKPFKFMLGKQEVIRGWEEGVAQMSVGQRAKLTISPDYAYGATGVPGIIPPHATLVFDVELLKLE

>d1c9ha\_ d.26.1.1 (A:) Calcineurin (FKBP12.6) {Human (Homo sapiens)}

GVEIETISPGDGRTFPKKGQTCVVHYTGMLQNGKKFDSSRDRNKPFKFRIGKQEVIKGFEEGAAQMSLGQRAKLTCTPDVAYGATGHPGVIPPNATLIFDVELLNLE

>d1yat\_\_ d.26.1.1 (-) Calcineurin (FKBP12.6) {Baker's yeast (Saccharomyces cerevisiae)}

SEVIEGNVKIDRISPGDGATFPKTGDLVTIHYTGTLENGQKFDSSVDRGSPFQCNIGVGQVIKGWDVGIPKLSVGEKARLTIPGPYAYGPRGFPGLIPPNSTLVFDVELLKVN

>d1pbk\_\_ d.26.1.1 (-) FKBP25 {Human (Homo sapiens)}

PKYTKSVLKKGDKTNFPKKGDVVHCWYTGTLQDGTVFDTNIQTSAKKKKNAKPLSFKVGVGKVIRGWDEALLTMSKGEKARLEIEPEWAYGKKGQPDAKIPPNAKLTFEVELVDID

>d1rot\_\_ d.26.1.1 (-) FKBP59-I, N-terminal domain {Rabbit (Oryctolagus cuniculus)}

GVDISPKQDEGVLKVIKREGTGTETPMIGDRVFVHYTGWLLDGTKFDSSLDRKDKFSFDLGKGEVIKAWDIAVATMKVGELCRITCKPEYAYGSAGSPPKIPPNATLVFEVELFEFKG

>d1pina2 d.26.1.1 (A:45-163) Mitotic rotamase PIN1, domain 2 {Human (Homo sapiens)}

GKNGQGEPARVRCSHLLVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKARGDLGAFSRGQMQKPFEDASFALRTGEMSGPVFTDSGIHIILRTE

>d1eq3a\_ d.26.1.1 (A:) Parvulin {Human (Homo sapiens), hpar14}

NAVKVRHILCEKHGKIMEAMEKLKSGMRFNEVAAQYSEDKARQGGDLGWMTRGSMVGPFQEAAFALPVSGMDKPVFTDPPVKTKFGYHIIMVEGRK

>d1fd9a\_ d.26.1.1 (A:) Macrophage infectivity potentiator protein (MIP) {Legionella pneumophila}

TDKDKLSYSIGADLGKNFKNQGIDVNPEAMAKGMQDAMSGAQLALTEQQMKDVLNKFQKDLMAKRTAEFNKKADENKVKGEAFLTENKNKPGVVVLPSGLQYKVINSGNGVKPGKSDTVTVEYTGRLIDGTVFDSTEKTGKPATFQVSQVIPGWTEALQLMPAGSTWEIYVPSGLAYGPRSVGGPIGPNETLIFKIHLISVKKS

>d1grj\_2 d.26.1.2 (80-158) GreA transcript cleavage factor, C-terminal domain {Escherichia coli}

MPNNGRVIFGATVTVLNLDSDEEQTYRIVGDDEADFKQNLISVNSPIARGLIGKEEDDVVVIKTPGGEVEFEVIKVEYL

>d3eipa\_ d.26.2.1 (A:) Colicin E3 immunity protein {Escherichia coli}

GLKLDLTWFDKSTEDFKGEEYSKDFGDDGSVMESLGVPFKDNVNNGCFDVIAEWVPLLQPYFNHQIDISDNEYFVSFDYRDGDW

>d1edqa3 d.26.3.1 (A:444-516) Chitinase A {Serratia marcescens}

YGRGWTGVNGYQNNIPFTGTATGPVKGTWENGIVDYRQIAGQFMSGEWQYTYDATAEAPYVFKPSTGDLITFD

>d1goia3 d.26.3.1 (A:292-379) Chitinase B {Serratia marcescens}

YGRAFKGVSGGNGGQYSSHSTPGEDPYPSTDYWLVGCEECVRDKDPRIASYRQLEQMLQGNYGYQRLWNDKTKTPYLYHAQNGLFVTY

>d1d2ka2 d.26.3.1 (A:293-354) Chitinase 1 {Fungus (Coccidioides immitis)}

YGRAFASTDGIGTSFNGVGGGSWENGVWDYKDMPQQGAQVTELEDIAASYSYDKNKRYLISY

>d1e9la2 d.26.3.1 (A:267-336) Chitinase-like lectin ym1 {Mouse (Mus musculus)}

YGHTFILSDPSKTGIGAPTISTGPPGKYTDESGLLAYYEVCTFLNEGATEVWDAPQEVPYAYQGNEWVGY

>d1fjgp\_ d.27.1.1 (P:) Ribosomal protein S16 {Thermus thermophilus}

MVKIRLARFGSKHNPHYRIVVTDARRKRDGKYIEKIGYYDPRKTTPDWLKVDVERARYWLSVGAQPTDTARRLLRQAGVFRQE

>d1fjgs\_ d.28.1.1 (S:) Ribosomal protein S19 {Thermus thermophilus}

PRSLKKGVFVDDHLLEKVLELNAKGEKRLIKTWSRRSTIVPEMVGHTIAVYNGKQHVPVYITENMVGHKLGEFAPTRTYRGHGK

>d1qkha\_ d.28.1.1 (A:) Ribosomal protein S19 {Thermus thermophilus}

GVFVDDHLLEKVLELNAKGEKRLIKTWSRRSTIVPEMVGHTIAVYNGKQHVPVYITENMVGHKLGEFAPTRTY

>d1jj2w\_ d.29.1.1 (W:) Ribosomal protein L31e {Archaeon Haloarcula marismortui}

ERVVTIPLRDARAEPNHKRADKAMILIREHLAKHFSVDEDAVRLDPSINEAAWARGRANTPSKIRVRAARFEEEGEAIVEAE

>d1b33n\_ d.30.1.1 (N:) Allophycocyanin linker chain (domain) {Mastigocladus laminosus}

GRLFKITACVPSQTRIRTQRELQNTYFTKLVPYENWFREQQRIQKMGGKIVKVELATGKQGINTGLA

>d1qcsa2 d.31.1.1 (A:86-201) C-terminal domain of NSF-N, NSF-Nc {Hamster (Cricetulus griseus)}

DKAKQCIGTMTIEIDFLQKKNIDSNPYDTDKMAAEFIQQFNNQAFSVGQQLVFSFNDKLFGLLVKDIEAMDPSILKGEPASGKRQKIEVGLVVGNSQVAFEKAENSSLNLIGKAKT

>d1cr5a2 d.31.1.1 (A:108-210) C-terminal domain of NSF-N, NSF-Nc {Baker's yeast (Saccharomyces cerevisiae), sec18p}

SGKQSYLGSIDIDISFRARGKAVSTVFDQDELAKQFVRCYESQIFSPTQYLIMEFQGHFFDLKIRNVQAIDLGDIEPTSAVATGIETKGILTKQTQINFFKGR

>d1cz4a2 d.31.1.1 (A:92-185) C-terminal domain of VAT-N, VAT-Nc {Archaeon Thermoplasma acidophilum}

TEIAKKVTLAPIIRKDQRLKFGEGIEEYVQRALIRRPMLEQDNISVPGLTLAGQTGLLFKVVKTLPSKVPVEIGEETKIEIREEPASEVLEEGG

>d1e32a3 d.31.1.1 (A:107-200) Membrane fusion atpase p97 domain 2, P97-Nc {Mouse (Mus musculus)}

DVKYGKRIHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIRKGDIFLVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGEPIKREDEEESLNE

>d1qipa\_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Human (Homo sapiens)}

GGLTDEAALSCCSDADPSTKDFLLQQTMLRVKDPKKSLDFYTRVLGMTLIQKCDFPIMKFSLYFLAYEDKNDIPKEKDEKIAWALSRKATLELTHNWGTEDDETQSYHNGNSDPRGFGHIGIAVPDVYSACKRFEELGVKFVKKPDDGKMKGLAFIQDPDGYWIEILNPNKMATLM

>d1f9za\_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Escherichia coli}

MRLLHTMLRVGDLQRSIDFYTKVLGMKLLRTSENPEYKYSLAFVGYGPETEEAVIELTYNWGVDKYELGTAYGHIALSVDNAAEACEKIRQNGGNVTREAGPVKGGTTVIAFVEDPDGYKIELIEEKDAGRGLGN

>d1qtoa\_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptomyces verticillus}

MVKFLGAVPVLTAVDVPANVSFWVDTLGFEKDFGDRDFAGVRRGDIRLHISRTEHQIVADNTSAWIEVTDPDALHEEWARAVSTDYADTSGPAMTPVGESPAGREFAVRDPAGNCVHFTAGE

>d1byla\_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptoalloteichus hindustanus}

FMAKLTSAVPVLTARDVAGAVEFWTDRLGFSRDFVEDDFAGVVRDDVTLFISAVQDQVVPDNTLAWVWVRGLDELYAEWSEVVSTNFRDASGPAMTEIGEQPWGREFALRDPAGNCVHFVAE

>d1ecsa\_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Klebsiella pneumoniae}

TDQATPNLPSRDFDSTAAFYERLGFGIVFRDAGWMILQRGDLMLEFFAHPGLDPLASWFSCCLRLDDLAEFYRQCKSVGIQETSSGYPRIHAPELQGWGGTMAALVDPDGTLLRLIQNEL

>d1jc4a\_ d.32.1.4 (A:) Methylmalonyl-CoA epimerase {Propionibacterium shermanii}

NEDLFICIDHVAYACPDADEASKYYQETFGWHELHREENPEQGVVEIMMAPAAKLTEHMTQVQVMAPLNDESTVAKWLAKHNGRAGLHHMAWRVDDIDAVSATLRERGVQLLYDEPKLGTGGNRINFMHPKSGKGVLIELTQYPK

>d1gdga1 d.32.1.3 (A:1-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Pseudomonas sp.}

SIERLGYLGFAVKDVPAWDHFLTKSVGLMAAGSAGDAALYRADQRAWRIAVQPGELDDLAYAGLEVDDAAALERMADKLRQAGVAFTRGDEALMQQRKVMGLLCLQDPFGLPLEIYYGPAEIFHEPFLPSAP

>d1gdga2 d.32.1.3 (A:133-288) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Pseudomonas sp.}

VSGFVTGDQGIGHFVRCVPDTAKAMAFYTEVLGFVLSDIIDIQMGPETSVPAHFLHCNGRHHTIALAAFPIPKRIHHFMLQANTIDDVGYAFDRLDAAGRITSLLGRHTNDQTLSFYADTPSPMIEVEFGWGPRTVDSSWTVARHSRTAMWGHKSV

>d1han\_1 d.32.1.3 (2-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Burkholderia cepacia (formerly Pseudomonas cepacia)}

SIRSLGYMGFAVSDVAAWRSFLTQKLGLMEAGTTDNGDLFRIDSRAWRIAVQQGEVDDLAFAGYEVADAAGLAQMADKLKQAGIAVTTGDASLARRRGVTGLITFADPFGLPLEIYYGASEVFEKPFLPGA

>d1han\_2 d.32.1.3 (133-289) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Burkholderia cepacia (formerly Pseudomonas cepacia)}

AVSGFLTGEQGLGHFVRCVPDSDKALAFYTDVLGFQLSDVIDMKMGPDVTVPAYFLHCNERHHTLAIAAFPLPKRIHHFMLEVASLDDVGFAFDRVDADGLITSTLGRHTNDHMVSFYASTPSGVEVEYGWSARTVDRSWVVVRHDSPSMWGHKSVR

>d1mpya1 d.32.1.3 (A:1-145) Catechol 2,3-dioxygenase (metapyrocatechase) {Pseudomonas putida, mt2}

MNKGVMRPGHVQLRVLDMSKALEHYVELLGLIEMDRDDQGRVYLKAWTEVDKFSLVLREADEPGMDFMGFKVVDEDALRQLERDLMAYGCAVEQLPAGELNSCGRRVRFQAPSGHHFELYADKEYTGKWGLNDVNPEAWPRDLKG

>d1mpya2 d.32.1.3 (A:146-307) Catechol 2,3-dioxygenase (metapyrocatechase) {Pseudomonas putida, mt2}

MAAVRFDHALMYGDELPATYDLFTKVLGFYLAEQVLDENGTRVAQFLSLSTKAHDVAFIHHPEKGRLHHVSFHLETWEDLLRAADLISMTDTSIDIGPTRHGLTHGKTIYFFDPSGNRNEVFCGGDYNYPDHKPVTWTTDQLGKAIFYHDRILNERFMTVLT

>d1cjxa1 d.32.1.3 (A:4-153) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas fluorescens}

YENPMGLMGFEFIEFASPTPGTLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILNNEPNSIASYFAAEHGPSVCGMAFRVKDSQKAYNRALELGAQPIHIDTGPMELNLPAIKGIGGAPLYLIDRFGEGSSIYDIDFVYLEGVERNPVG

>d1cjxa2 d.32.1.3 (A:154-356) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas fluorescens}

AGLKVIDHLTHNVYRGRMVYWANFYEKLFNFREARYFDIKGEYTGLTSKAMSAPDGMIRIPLNEESSKGAGQIEEFLMQFNGEGIQHVAFLTDDLVKTWDALKKIGMRFMTAPPDTYYEMLEGRLPDHGEPVDQLQARGILLDGSSVEGDKRLLLQIFSETLMGPVFFEFIQRKGDDGFGEGNFKALFESIERDQVRRGVLAT

>d1fx3a\_ d.33.1.1 (A:) Bacterial protein-export protein SecB {Haemophilus influenzae}

QPVLQIQRIYVKDVSFEAPNLPHIFQQEWKPKLGFDLSTETTQVGDDLYEVVLNISVETTLEDSGDVAFICEVKQAGVFTISGLEDVQMAHCLTSQCPNMLFPYARELVSNLVNRGTFPALNLSPVNFDALFVEYMNRQQAEN

>d1bm8\_\_ d.34.1.1 (-) DNA-binding domain of Mlu1-box binding protein MBP1 {Baker's yeast (Saccharomyces cerevisiae)}

QIYSARYSGVDVYEFIHSTGSIMKRKKDDWVNATHILKAANFAKAKRTRILEKEVLKETHEKVQGGFGKYQGTWVPLNIAKQLAEKFSVYDQLKPLFDF

>d1dk0a\_ d.35.1.1 (A:) Heme-binding protein A (HasA) {Serratia marcescens}

AFSVNYDSSFGGYSIHDYLGQWASTFGDVNHTNGNVTDANSGGFYGGSLSGSQYAISSTANQVTAFVAGGNLTYTLFNEPAHTLYGQLDSLSFGDGLSGGDTSPYSIQVPDVSFGGLNLSSLQAQGHDGVVHQVVYGLMSGDTGALETALNGILDDYGLSVNSTFDQVAAATA

>d1eyqa\_ d.36.1.1 (A:) Chalcone isomerase {Alfalfa (Medicago sativa)}

SITAITVENLEYPAVVTSPVTGKSYFLGGAGERGLTIEGNFIKFTAIGVYLEDIAVASLAAKWKGKSSEELLETLDFYRDIISGPFEKLIRGSKIRELSGPEYSRKVMENCVAHLKSVGTYGDAEAEAMQKFAEAFKPVNFPPGASVFYRQSPDGILGLSFSPDTSIPEKEAALIENKAVSSAVLETMIGEHAVSPDLKRCLAARLPALLNE

>d1b3ob2 d.37.1.1 (B:112-159) Type II inosine monophosphate dehydrogenase {Human (Homo sapiens)}

QGFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIIS

>d1jr1a2 d.37.1.1 (A:113-155) Type II inosine monophosphate dehydrogenase {Chinese hamster (Cricetulus griseus)}

GFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLV

>d1jr1a3 d.37.1.1 (A:178-232) Type II inosine monophosphate dehydrogenase {Chinese hamster (Cricetulus griseus)}

IMTKREDLVVAPAGITLKEANEILQRSKKGKLPIVNENDELVAIIARTDLKKNRD

>d1zfja2 d.37.1.1 (A:95-158) Type II inosine monophosphate dehydrogenase {Streptococcus pyogenes}

NGVIIDPFFLTPEHKVSEAEELMQRYRISGVPIVETLANRKLVGIITNRDMRFISDYNAPISEH

>d1zfja3 d.37.1.1 (A:159-220) Type II inosine monophosphate dehydrogenase {Streptococcus pyogenes}

MTSEHLVTAAVGTDLETAERILHEHRIEKLPLVDNSGRLSGLITIKDIEKVIEFPHAAKDEF

>d1bvqa\_ d.38.1.1 (A:) 4-hydroxybenzoyl-CoA thioesterase {Pseudomonas sp., CBS-3}

ARSITMQQRIEFGDCDPAGIVWYPNYHRWLDAASRNYFIKCGLPPWRQTVVERGIVGTPIVSCNASFVCTASYDDVLTIETCIKEWRRKSFVQRHSVSRTTPGGDVQLVMRADEIRVFAMNDGERLRAIEVPADYIELC

>d1mkaa\_ d.38.1.2 (A:) beta-Hydroxydecanol thiol ester dehydrase {Escherichia coli}

VDKRESYTKEDLLASGRGELFGAKGPQLPAPNMLMMDRVVKMTETGGNFDKGYVEAELDINPDLWFFGCHFIGDPVMPGCLGLDAMWQLVGFYLGWLGGEGKGRALGVGEVKFTGQVLPTAKKVTYRIHFKRIVNRRLIMGLADGEVLVDGRLIYTASDLKVGLFQDTSAF

>d1c8ua1 d.38.1.3 (A:2-115) Thioesterase II (TesB) {Escherichia coli}

SQALKNLLTLLNLEKIEEGLFRGQSEDLGLRQVFGGQVVGQALYAAKETVPEERLVHSFHSYFLRPGDSKKPIIYDVETLRDGNSFSARRVAAIQNGKPIFYMTASFQAPEAGF

>d1c8ua2 d.38.1.3 (A:116-286) Thioesterase II (TesB) {Escherichia coli}

EHQKTMPSAPAPDGLPSETQIAQSLAHLLPPVLKDKFICDRPLEVRPVEFHNPLKGHVAEPHRQVWIRANGSVPDDLRVHQYLLGYASDLNFLPVALQPHGIGFLEPGIQIATIDHSMWFHRPFNLNEWLLYSVESTSASSARGFVRGEFYTQDGVLVASTVQEGVMRNHN

>d1cmia\_ d.39.1.1 (A:) Dynein light chain 8 (DLC8) {Human (Homo sapiens)}

KAVIKNADMSEEMQQDSVECATQALEKYNIEKDIAAHIKKEFDKKYNPTWHCIVGRNFGSYVTHETKHFIYFYLGQVAILLFKSG

>d1csei\_ d.40.1.1 (I:) Eglin C {Leech (Hirudo medicinalis)}

KSFPEVVGKTVDQAREYFTLHYPQYNVYFLPEGSPVTLDLRYNRVRVFYNPGTNVVNHVPHVG

>d1egl\_\_ d.40.1.1 (-) Eglin C {Leech (Hirudo medicinalis)}

TEFGSELKSFPEVVGKTVDQAREYFTLHYPQYDVYFLPEGSPVTLDLRYNRVRVFYNPGTNVVNHVPHVG

>d1ypci\_ d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}

MKTEWPELVGKSVAAAKKVILQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAQVPRVG

>d2snii\_ d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}

LKTEWPELVGKSVEEAKKVILQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAEVPRVG

>g1cq4.1 d.40.1.1 (A:,B:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}

KTEWPELVGKSVEEAKKVILQDKPEAQIIVLPVGTIVXYRIDRVRLFVDKLDNIAQVPRVG

>d1tin\_\_ d.40.1.1 (-) Trypsin inhibitor V {Pumpkin (Cucurbita maxima)}

SSCPGKSSWPHLVGVGGSVAKAIIERQNPNVKAVILEEGTPVTKDFRCNRVRIWVNKRGLVVSPPRIG

>d1dwma\_ d.40.1.1 (A:) Trypsin inhibitor LUTI {Flax (Linum usitatissimum)}

SRRCPGKNAWPELVGKSGNMAAATVERENRNVHAIVLKEGSAMTKDFRCDRVWVIVNDHGVVTSVPHIT

>d1jv2b3 d.200.1.1 (B:606-690) Integrin beta tail domain {Human (Homo sapiens)}

DACTFKKECVECKKFDREPYMTENTCNRYCRDEIESVKELKDTGKDAVNCTYKNEDDCVVRFQYYEDSSGKSILYVVEEPECPKG

>d1hlra3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio gigas}

DYGADLGLKMPAGTLHLAMVQAKVSHANIKGIDTSEALTMPGVHSVITHKDVKGKNRITGLITFPTNKGDGWDRPILCDEKVFQYGDCIALVCADSEANARAAAEKVKVDLEELPAY

>d1dgja3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio desulfuricans}

EFGADAALRMPENTLHLALAQAKVSHALIKGIDTSEAEKMPGVYKVLTHKDVKGKNRITGLITFPTNKGDGWERPILNDSKIFQYGDALAIVCADSEANARAAAEKVKFDLELLPEY

>d1fiqc1 d.41.1.1 (C:571-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}

DTVGRPLPHLAAAMQASGEAVYCDDIPRYENELFLRLVTSTRAHAKIKSIDVSEAQKVPGFVCFLSADDIPGSNETGLFNDETVFAKDTVTCVGHIIGAVVADTPEHAERAAHVVKVTYEDLPA

>d1fo4a3 d.41.1.1 (A:537-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}

KLDPTYTSATLLFQKHPPANIQLFQEVPNGQSKEDTVGRPLPHLAAAMQASGEAVYCDDIPRYENELFLRLVTSTRAHAKIKSIDVSEAQKVPGFVCFLSADDIPGSNETGLFNDETVFAKDTVTCVGHIIGAVVADTPEHAERAAHVVKVTYEDLPA

>d1jrob1 d.41.1.1 (B:2-123) Xanthine dehydrogenase chain B, N-terminal domain {Rhodobacter capsulatus}

SVGKPLPHDSARAHVTGQARYLDDLPCPANTLHLAFGLSTEASAAITGLDLEPVRESPGVIAVFTAADLPHDNDASPAPSPEPVLATGEVHFVGQPIFLVAATSHRAARIAARKARITYAPR

>d1qj2b1 d.41.1.1 (B:10-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {Pseudomonas carboxydovorans}

TSAERAEKLQGMGCKRKRVEDIRFTQGKGNYVDDVKLPGMLFGDFVRSSHAHARIKSIDTSKAKALPGVFAVLTAADLKPLNLHYMPTLAGDVQAVLADEKVLFQNQEVAFVVAKDRYVAADAIELVEVDYEPLPVL

>d1ffvb1 d.41.1.1 (B:7-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {Hydrogenophaga pseudoflava}

DAEARELALAGMGASRLRKEDARFIQGKGNYVDDIKMPGMLHMDIVRAPIAHGRIKKIHKDAALAMPGVHAVLTAEDLKPLKLHWMPTLAGDVAAVLADEKVHFQMQEVAIVIADDRYIAADAVEAVKVEYDELPVVIDP

>d1qapa2 d.41.2.1 (A:8-129) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Salmonella typhimurium}

DDRRDALLERINLDIPAAVAQALREDLGGEVDAGNDITAQLLPADTQAHATVITREDGVFCGKRWVEEVFIQLAGDDVRLTWHVDDGDAIHANQTVFELQGPARVLLTGERTALNFVQTLSG

>d1qpoa2 d.41.2.1 (A:2-116) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Mycobacterium tuberculosis}

GLSDWELAAARAAIARGLDEDLRYGPDVTTLATVPASATTTASLVTREAGVVAGLDVALLTLNEVLGTNGYRVLDRVEDGARVPPGEALMTLEAQTRGLLTAERTMLNLVGHLSG

>d2tpt\_3 d.41.3.1 (336-440) Thymidine phosphorylase {Escherichia coli}

TAMLTKAVYADTEGFVSEMDTRALGMAVVAMGGGRRQASDTIDYSVGFTDMARLGDQVDGQRPLAVIHAKDENNWQEAAKAVKAAIKLADKAPESTPTVYRRISE

>d1brwa3 d.41.3.1 (A:331-433) Pyrimidine nucleoside phosphorylase {Bacillus stearothermophilus}

KAAYTSTVTAAADGYVAEMAADDIGTAAMWLGAGRAKKEDVIDLAVGIVLHKKIGDRVQKGEALATIHSNRPDVLDVKEKIEAAIRLSPQPVARPPLIYETIV

>d1ffkf\_ d.41.4.1 (F:) Ribosomal protein L10e {Archaeon Haloarcula marismortui}

KPGAHFRNSIKPAYTRREYISGIPGKGIAQFKMGNNGAGPTYPAQVENVVEKPVQIRHNALEAARNAANRFVQNSGAAANYKFRIRKFPFHVIREQDGDGMRAPFGKSVGTAARSHGANHDFIAWVNPDPAVEFAWRRAYMKVTPTVNIDSSPAGNA

>d1jj2h\_ d.41.4.1 (H:) Ribosomal protein L10e {Archaeon Haloarcula marismortui}

KPGAMYRNSSKPAYTRREYISGIPGKKIAQFDMGNNGAGPTYPAQVELVVEKPVQIRHNALEAARVAANRYVQNSGAAANYKFRIRKFPFHVIRENKAAAAAAAAAAADGMRAPFGKPVGTAARVHGANHIFIAWVNPDPNVEEAWRRAKMKVTPTINIDSSPAGNA

>d1fm0e\_ d.41.5.1 (E:) Molybdopterin synthase subunit MoaE {Escherichia coli}

AETKIVVGPQPFSVGEEYPWLAERDEDGAVVTFTGKVRNHNLGDSVNALTLEHYPGMTEKALAEIVDEARNRWPLGRVTVIHRIGELWPGDEIVFVGVTSAHRSSAFEAGQFIMDYLKTRAPFWKREATPEGDRWVEARESDQQAAKRW

>d1buoa\_ d.42.1.1 (A:) Promyelocytic leukemia zinc finger (PLZF) protein BTB domain {Human (Homo sapiens)}

MGMIQLQNPSHPTGLLCKANQMRLAGTLCDVVIMVDSQEFHAHRTVLACTSKMFEILFHRNSQHYTLDFLSPKTFQQILEYAYTATLQAKAEDLDDLLYAAEILEIEYLEEQCLKMLETIQ

>d1vcbb\_ d.42.1.1 (B:) Elongin C {Human (Homo sapiens)}

MYVKLISSDGHEFIVKREHALTSGTIKAMLSGPGQFAENETNEVNFREIPSHVLSKVCMYFTYKVRYTNSSTEIPEFPIAPEIALELLMAANFLDC

>d1hv2a\_ d.42.1.1 (A:) Elongin C {Baker's yeast (Saccharomyces cerevisiae)}

MSQDFVTLVSKDDKEYEISRSAAMISPTLKAMIEGPFRESKGRIELKQFDSHILEKAVEYLNYNLKYSGVSEDDDEIPEFEIPTEMSLELLLAADYLSI

>d1a68\_\_ d.42.1.2 (-) Shaker potassium channel {California sea hare (Aplysia californica)}

ERVVINVSGLRFETQLKTLNQFPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGRLRRPVNVPLDVFSEEIKFYELG

>d1t1da\_ d.42.1.2 (A:) Shaker potassium channel {California sea hare (Aplysia californica)}

ERVVINVSGLRFETQLKTLNQFPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGRLRRPVNVPLDVFSEEIKFYELGENAFERYREDEGF

>d3kvt\_\_ d.42.1.2 (-) akv3.1 voltage-gated potassium channel {California sea hare (Aplysia californica)}

ENRVIINVGGIRHETYKATLKKIPATRLSRLTEGMLNYDPVLNEYFFDRHPGVFAQIINYYRSGKLHYPTDVCGPLFEEELEFWGLDSNQVEPCCWMTYTAHR

>d1exbe\_ d.42.1.2 (E:) KV1.1 {Rat (Rattus norvegicus)}

CERVVINISGLRFETQLKTLAQFPNTLLGNPKKRMRYFDPLRNEYFFDRNRPSFDAILYYYQSGGRLRRPVNVPLDMFSEEIKFYELGEEA

>d1dsxa\_ d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}

ERVVINISGLRFEVQLKTLAQFPETLLGDPKKRMRYFDPLRNEYFFDRNRPSFDAILYYYQSGGRLRRPVNVPLDIFSEEIRFYELG

>d1qdva\_ d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}

ERVVINISGLRFETQLKTLAQFPETLLGDPKKRMRYFDPLRNEYFFDRNRPSFDAILYYYQSGGRLRRPVNVPLDIFSEEIRFYELGEEAMEMFREDEG

>d1fs1b2 d.42.1.2 (B:2-68) Cyclin A/CDK2-associated p45, Skp1 {Human (Homo sapiens)}

PSIKLQSSDGEIFEVDVEIAKQSVTIKTMLEDLGMDPVPLPNVNAAILKKVIQWCTHHKDD

>d1efub2 d.43.1.1 (B:140-282) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}

DVLGSYQHGARIGVLVAAKGADEELVKHIAMHVAASKPEFIKPEDVSAEVVEKEYQVQLDIAMQSGKPKEIAEKMVEGRMKKFTGEVSLTGQPFVMEPSKTVGQLLKEHNAEVTGFIRFEVGEGIEKVETDFAAEVAAMSKQS

>d1efub4 d.43.1.1 (B:55-139) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}

VAADGVIKTKIDGNYGIILEVNCQTDFVAKDAGFQAFADKVLDAAVAGKITDVEVLKAQFEEERVALVAKIGENINIRRVAALEG

>d1tfe\_\_ d.43.1.1 (-) Elongation factor Ts (EF-Ts), dimerisation domain {Thermus thermophilus}

AREGIIGHYIHHNQRVGVLVELNCETDFVARNELFQNLAKDLAMHIAMMNPRYVSAEEIPAEELEKERQIYIQAALNEGKPQQIAEKIAEGRLKKYLEEVVLLEQPFVKDDKVKVKELIQQAIAKIGENIVVRRFCRFELGA

>d1i0ha2 d.44.1.1 (A:91-205) Mn superoxide dismutase (MnSOD) {Escherichia coli}

GTTLQGDLKAAIERDFGSVDNFKAEFEKAAASRFGSGWAWLVLKGDKLAVVSTANQDSPLMGEAISGASGFPIMGLDVWEHAYFLKFQNRRPDYIKEFWNVVNWDEAAARFAAKK

>d1mnga2 d.44.1.1 (A:93-203) Mn superoxide dismutase (MnSOD) {Thermus thermophilus}

GGAKEPVGELKKAIDEQFGGFQALKEKLTQAAMGRFGSGWAWLVKDPFGKLHVLSTPNQDNPVMEGFTPIVGIDVWEHAYYLKYQNRRADYLQAIWNVLNWDVAEEFFKKA

>d1ap6a2 d.44.1.1 (A:84-198) Mn superoxide dismutase (MnSOD) {Human (Homo sapiens)}

NGGGEPKGELLEAIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNKERGHLQIAACPNQDPLQGTTGLIPLLGIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYMACKK

>d1kkca2 d.44.1.1 (A:98-213) Mn superoxide dismutase (MnSOD) {Aspergillus fumigatus}

EKSGGGKIDQAPVLKAAIEQRWGSFDKFKDAFNTTLLGIQGSGWGWLVTDGPKGKLDITTTHDQDPVTGAAPVFGVDMWEHAYYLQYLNDKASYAKGIWNVINWAEAENRYIAGDK

>d1dt0a2 d.44.1.1 (A:84-197) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}

AGGQPTGALADAINAAFGSFDKFKEEFTKTSVGTFGSGWGWLVKKADGSLALASTIGAGCPLTIGDTPLLTCDVWEHAYYIDYRNLRPKYVEAFWNLVNWAFVAEQFEGKTYKV

>d3sdpa2 d.44.1.1 (A:84-190) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}

DAGGQPTGALADAINAAFGSFDKFKEEFTKTSVGTFGSGWAWLVKADGSLALCSTIGAGAPLTSGDTPLLTCDVWEHAYYIDYRNLRPKYVEAFWNLVNWAFVAEEG

>d1isaa2 d.44.1.1 (A:83-192) Fe superoxide dismutase (FeSOD) {Escherichia coli}

NAGGEPTGKVAEAIAASFGSFADFKAQFTDAAIKNFGSGWTWLVKNSDGKLAIVSTSNAGTPLTTDATPLLTVDVWEHAYYIDYRNARPGYLEHFWALVNWEFVAKNLAA

>d1idsa2 d.44.1.1 (A:86-199) Fe superoxide dismutase (FeSOD) {Mycobacterium tuberculosis}

NGGDKPTGELAAAIADAFGSFDKFRAQFHAAATTVQGSGWAALGWDTLGNKLLIFQVYDHQTNFPLGIVPLLLLDMWEHAFYLQYKNVKVDFAKAFWNVVNWADVQSRYAAATS

>d1coja2 d.44.1.1 (A:91-212) Fe superoxide dismutase (FeSOD) {Aquifex pyrophilus}

GGKGEPSEALKKKIEEDIGGLDACTNELKAAAMAFRGWAILGLDIFSGRLVVNGLDAHNVYNLTGLIPLIVIDTYEHAYYVDYKNKRPPYIDAFFKNINWDVVNERFEKAMKAYEALKDFIK

>d1sssa2 d.44.1.1 (A:93-208) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus solfataricus}

PSGKGGGKPGGALADLINKQYGSFDRFKQVFTETANSLPGTGWAVLYYDTESGNLQIMTFENHFQNHIAEIPIILILDEFEHAYYLQYKNKRADYVNAWWNVVNWDAAEKKLQKYL

>d1b06a2 d.44.1.1 (A:93-210) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus acidocaldarius}

PAGKGGGKPGGALADLIDKQYGSFDRFKQVFSESANSLPGSGWTVLYYDNESGNLQIMTVENHFMNHIAELPVILIVDEFEHAYYLQYKNKRGDYLNAWWNVVNWDDAEKRLQKYLNK

>d1bsma2 d.44.1.1 (A:87-201) Cambialistic superoxide dismutase {Propionibacterium shermanii}

SAPERPTDELGAAIDEFFGSFDNMKAQFTAAATGIQGSGWASLVWDPLGKRINTLQFYDHQNNLPAGSIPLLQLDMWEHAFYLQYKNVKGDYVKSWWNVVNWDDVALRFSEARVA

>d1qnna2 d.44.1.1 (A:85-191) Cambialistic superoxide dismutase {Porphyromonas gingivalis}

KGGAPKGKLGEAIDKQFGSFEKFKEEFNTAGTTLFGSGWVWLASDANGKLSIEKEPNAGNPVRKGLNPLLGFDVWEHAYYLTYQNRRADHLKDLWSIVDWDIVESRY

>d1ctf\_\_ d.45.1.1 (-) Ribosomal protein L7/12, C-terminal domain {Escherichia coli}

EFDVILKAAGANKVAVIKAVRGATGLGLKEAKDLVESAPAALKEGVSKDDAEALKKALEEAGAEVEVK

>d1dd3a2 d.45.1.1 (A:58-128) Ribosomal protein L7/12, C-terminal domain {Thermotoga maritima}

EFDVVLKSFGQNKIQVIKVVREITGLGLKEAKDLVEKAGSPDAVIKSGVSKEEAEEIKKKLEEAGAEVELK

>d1ekta\_ d.46.1.1 (A:) Transcription-state regulator AbrB, the N-terminal DNA recognition domain {Bacillus subtilis}

MKSTGIVRKVDELGRVVIPIELRRTLGIAEKDALEIYVDDEKIILKKYKPNMT

>d1mmsa2 d.47.1.1 (A:8-70) Ribosomal protein L11, N-terminal domain {Thermotoga maritima}

QIKLQLPAGKATPAPPVGPALGQHGVNIMEFCKRFNAETADKAGMILPVVITVYEDKSFTFII

>d2reb\_2 d.48.1.1 (269-328) RecA protein, C-terminal domain {Escherichia coli}

NFYGELVDLGVKEKLIEKAGAWYSYKGEKIGQGKANATAWLKDNPETAKEIEKKVRELLL

>d1g19a2 d.48.1.1 (A:270-329) RecA protein, C-terminal domain {Mycobacterium tuberculosis}

SREGSLIDMGVDQGLIRKSGAWFTYEGEQLGQGKENARNFLVENADVADEIEKKIKEKLG

>d1e8oa\_ d.49.1.1 (A:) Signal recognition particle alu RNA binding heterodimer, SRP9/14 {Human (Homo sapiens)}

PQYQTWEEFSRAAEKLYLADPMKARVVLKYRHSDGNLCVKVTDDLVCLVYKTDQAQDVKKIEKFHSQLMRLMVA

>d1e8ob\_ d.49.1.1 (B:) Signal recognition particle alu RNA binding heterodimer, SRP9/14 {Human (Homo sapiens)}

VLLESEQFLTELTRLFQKCRTSGSVYITLKKYDGRTKPIPKKGTVEGFEPADNKCLLRATDGKKKISTVVSSKEVNKFQMAYSNLLRANMDGLK

>d1914\_\_ d.49.1.1 (-) Signal recognition particle alu RNA binding heterodimer, SRP9/14 {Mouse (Mus musculus)}

MVLLESEQFLTELTRLFQKCRSSGSVFITLKKYDGRTKPIPRKSSVEGLEPAENKCLLRATDGKRKISTVVSSKEVNKFQMAYSNLLRANMDGLKKRDKKNKSKKSKPAQGGEQKLISEEDDSAGSPMPQFQTWEEFSRAAEKLYLADPMKVRVVLKYRHVDGNLCIKVTDDLVCLVYRTDQAQDVKKIEKFHSQLMRLMVAKESRNV

>d1di2a\_ d.50.1.1 (A:) Double-stranded RNA-binding protein A, second dsRBD {Xenopus laevis}

MPVGSLQELAVQKGWRLPEYTVAQESGPPHKREFTITCRVETFVETGSGTSKQVAKRVAAEKLLTKFKT

>d1ekza\_ d.50.1.1 (A:) Staufen, domain III {Fruit fly (Drosophila melanogaster)}

MDEGDKKSPISQVHEIGIKRNMTVHFKVLREEGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAEKMLVELQKL

>d1stu\_\_ d.50.1.1 (-) Staufen, domain III {Fruit fly (Drosophila melanogaster)}

PISQVHEIGIKRNMTVHFKVLREEGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAEKMLVELQKL

>d1qu6a1 d.50.1.1 (A:1-90) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}

GSHMEMAGDLSAGFFMEELNTYRQKQGVVLKYQELPNSGPPHDRRFTFQVIIDGREFPEGEGRSKKEAKNAAAKLAVEILNKEKKAVSPL

>d1qu6a2 d.50.1.1 (A:91-179) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}

LLTTTNSSEGLSMGNYIGLINRIAQKKRLTVNYEQCASGVHGPEGFHYKCKMGQKEYSIGTGSTKQEAKQLAAKLAYLQILSEETGSGC

>d1pkp\_2 d.50.1.2 (4-77) Ribosomal S5 protein, N-terminal domain {Bacillus stearothermophilus}

INPNKLELEERVVAVNRVAKVVKGGRRLRFSALVVVGDKNGHVGFGTGKAQEVPEAIRKAIEDAKKNLIEVPIV

>d1fjge2 d.50.1.2 (E:5-73) Ribosomal S5 protein, N-terminal domain {Thermus thermophilus}

DFEEKMILIRRTARMQAGGRRFRFGALVVVGDRQGRVGLGFGKAPEVPLAVQKAGYYARRNMVEVPLQN

>d1ah5\_2 d.50.2.1 (220-313) Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}

NHHETALRVTAERAMNTRLEGGCQVPIGSYAELIDGEIWLRALVGAPDGSQIIRGERRGAPQDAEQMGISLAEELLNNGAREILAEVYNGDAPA

>d1pda\_2 d.50.2.1 (220-307) Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}

NHHETALRVTAERAMNTRLEGACQVPIGSYAELIDGEIWLRGLVGAPDGSQIIRGERRGAPQDAEQMGISLAEELLNNGAREILAEVY

>d1dq3a2 d.50.3.1 (A:336-414) PI-Pfui intein middle domain {Archaeon Pyrococcus furiosus}

GNFGLPLNFNAFKEWASEYGVEFKTNGSQTIAIINDERISLGQWHTRNRVSKAVLVKMLRKLYEATKDEEVKRMLHLIE

>d1jida\_ d.201.1.1 (A:) SRP19 {Human (Homo sapiens)}

AARSPADQDRFICIYPAYLNNKKTIAEGRRIPISKAVENPTATEIQDVCSAVGLNVFLEKNKMYSREWNRDVQYRGRVRVQLKQEDGSLCLVQFPSRKSVMLYAAEMIPKLKTR

>d1dt4a\_ d.51.1.1 (A:) Neuro-oncological ventral antigen 1, nova-1, KH3 {Human (Homo sapiens)}

MKDVVEIAVPENLVGAILGKGGKTLVEYQELTGCRIQISKKGEFLPGTRNRKVTITGTPAATQAAQYLITQRI

>d1dtja\_ d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}

MKELVEMAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGEFLPGTRNRRVTITGSPAATQAAQYLISQRVT

>d1ec6a\_ d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}

MKELVEIAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGEFLPGTRNRRVTITGSPAATQAAQYLISQRVTYEQGVRASNPQKV

>d1vig\_\_ d.51.1.1 (-) Vigilin, KH6 {Human (Homo sapiens)}

INRMDYVEINIDHKFHRHLIGKSGANINRIKDQYKVSVRIPPDSEKSNLIRIEGDPQGVQQAKRELLELAS

>d2fmr\_\_ d.51.1.1 (-) Fragile X protein, KH1 {Human (Homo sapiens)}

ASRFHEQFIVREDLMGLAIGTHGANIQQARKVPGVTAIDLDEDTCTFHIYGEDQDAVKKARSFLE

>d1khma\_ d.51.1.1 (A:) HnRNP K, KH3 {Human (Homo sapiens)}

GSPNSYGDLGGPIITTQVTIPKDLARSIIGKGGQRIKQIRHESGASIKIDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVKQYSGKFF

>d1k1ga\_ d.51.1.1 (A:) RNA splicing factor 1 {Human (Homo sapiens)}

TRVSDKVMIPQDEYPEINFVGLLIGPRGNTLKNIEKECNAKIMIRGKGSVKEGKVGRKDGQMLPGEDEPLHALVTANTMENVKKAVEQIRNILKQGIETPEDQNDLRKMQLRELARLNGTLR

>d2proc1 d.52.1.1 (C:18-85) Alpha-lytic protease prodomain {Lysobacter enzymogenes}

IFPTQLPQYLQTEKLARTQAAAIEREFGAQFAGSWIERNEDGSFKLVAATSGARKSSTLGGVEVRNVR

>d3proc1 d.52.1.1 (C:6-85) Alpha-lytic protease prodomain {Lysobacter enzymogenes}

PQLKFAMQRDLGIFPTQLPQYLQTEKLARTQAAAIEREFGAQFAGSWIERNEDGSFKLVAATSGARKSSTLGGVEVRNVR

>d3proc2 d.52.1.1 (C:86-163) Alpha-lytic protease prodomain {Lysobacter enzymogenes}

YSLKQLQSAMEQLDAGANARVKGVSKPLDGVQSWYVDPRSNAVVVKVDDGATDAGVDFVALSGADSAQVRIESSPGKL

>d1gpma3 d.52.2.1 (A:405-525) GMP synthetase, C-terminal, dimerisation domain {Escherichia coli}

GPGLGVRVLGEVKKEYCDLLRRADAIFIEELRKADLYDKVSQAFTVFLPVRSVGVMGDGRKYDWVVSLRAVETIDFMTAHWAHLPYDFLGRVSNRIINEVNGISRVVYDISGKPPATIEWE

>d1fjgc1 d.52.3.1 (C:2-106) Ribosomal protein S3 N-terminal domain {Thermus thermophilus}

GNKIHPIGFRLGITRDWESRWYAGKKQYRHLLLEDQRIRGLLEKELYSAGLARVDIERAADNVAVTVHVAKPGVVIGRGGERIRVLREELAKLTGKNVALNVQEV

>d1egaa2 d.52.3.1 (A:183-295) GTPase Era C-terminal domain {Escherichia coli}

DYITDRSQRFMASEIIREKLMRFLGAELPYSVTVEIERFVSNERGGYDINGLILVEREGQKKMVIGNKGAKIKTIGIEARKDMQEMFEAPVHLELWVKVKSGWADDERALRSL

>d1hh2p2 d.52.3.1 (P:199-276) Transcription factor NusA, C-terminal domains {Thermotoga maritima}

RVPEFVIGLMKLEIPEVENGIVEIKAIAREPGVRTKVAVASNDPNVDPIGACIGEGGSRIAAILKELKGEKLDVLKWS

>d1hh2p3 d.52.3.1 (P:277-344) Transcription factor NusA, C-terminal domains {Thermotoga maritima}

DDPKQLIANALAPATVIEVEILDKENKAARVLVPPTQLSLAIGKGGQNARLAAKLTGWKIDIKPIMNL

>d1k0ra2 d.52.3.1 (A:184-262) Transcription factor NusA, C-terminal domains {Mycobacterium tuberculosis}

THPNLVRKLFSLEVPEIADGSVEIVAVAREAGHRSKIAVRSNVAGLNAKGACIGPMGQRVRNVMSELSGEKIDIIDYDD

>d1k0ra3 d.52.3.1 (A:263-329) Transcription factor NusA, C-terminal domains {Mycobacterium tuberculosis}

DPARFVANALSPAKVVSVSVIDQTARAARVVVPDFQLSLAIGKEGQNARLAARLTGWRIDIRGDAPP

>d1e3ha4 d.52.3.1 (A:579-632) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 6 {Streptomyces antibioticus}

APRIITVKIPVDKIGEVIGPKRQMINQIQEDTGAEITIEDDGTIYIGAADGPAA

>d1fjgc2 d.53.1.1 (C:107-207) Ribosomal protein S3 C-terminal domain {Thermus thermophilus}

QNPNLSAPLVAQRVAEQIERRFAVRRAIKQAVQRVMESGAKGAKVIVSGRIGGAEQARTEWAAQGRVPLHTLRANIDYGFALARTTYGVLGVKAYIFLGEV

>d1hh2p4 d.202.1.1 (P:1-126) Transcription factor NusA, N-terminal domain {Thermotoga maritima}

MNIGLLEALDQLEEEKGISKEEVIPILEKALVSAYRKNFGNSKNVEVVIDRNTGNIKVYQLLEVVEEVEDPATQISLEEAKKIDPLAEVGSIVKKELNVKNFGRIAAQTAKQVLIQRIRELEKEKQ

>d1k0ra4 d.202.1.1 (A:-4-99) Transcription factor NusA, N-terminal domain {Mycobacterium tuberculosis}

VSRRHMNIDMAALHAIEVDRGISVNELLETIKSALLTAYRHTQGHQTDARIEIDRKTGVVRVIARETDEAGNLISEWDDTPEGFGRIAATTARQVMLQRFRDAE

>d1onea2 d.54.1.1 (A:1-141) Enolase {Baker's yeast (Saccharomyces cerevisiae)}

AVSKVYARSVYDSRGNPTVEVELTTEKGVFRSIVPSGASTGVHEALEMRDGDKSKWMGKGVLHAVKNVNDVIAPAFVKANIDVKDQKAVDDFLISLDGTANKSKLGANAILGVSLAASRAAAAEKNVPLYKHLADLSKSKT

>d1pdz\_2 d.54.1.1 (1-139) Enolase {Lobster (Homarus vulgaris)}

SITKVFARTIFDSRGNPTVEVDLYTSKGLFRAAVPSGASTGVHEALEMRDGDKSKYHGKSVFNAVKNVNDVIVPEIIKSGLKVTQQKECDEFMCKLDGTENKSSLGANAILGVSLAICKAGAAELGIPLYRHIANLANY

>d1e9ia2 d.54.1.1 (A:1-139) Enolase {Escherichia coli}

SKIVKIIGREIIDSRGNPTVEAEVHLEGGFVGMAAAPSGASTGSREALELRDGDKSRFLGKGVTKAVAAVNGPIAQALIGKDAKDQAGIDKIMIDLDGTENKSKFGANAILAVSLANAKAAAAAKGMPLYEHIAELNGT

>d1bqg\_2 d.54.1.1 (12-143) D-glucarate dehydratase {Pseudomonas putida}

GAPVITDLKVVPVAGHDSMLLNLSGAHGPLFTRNILILTDSSGHVGVGEVPGGEGIRKTLEDARHLLINQSIGNYQSLLNKVRNAFADRDVGGRGLQTFDLRIAVHAVTAVESALLDLLGQHLQVPVAALLG

>d1ec7a2 d.54.1.1 (A:5-137) D-glucarate dehydratase {Escherichia coli}

FTTPVVTEMQVIPVAGHDSMLMNLSGAHAPFFTRNIVIIKDNSGHTGVGEIPGGEKIRKTLEDAIPLVVGKTLGEYKNVLTLVRNTFADRDAGGRGLQTFDLRTTIHVVTGIEAAMLDLLGQHLGVNVASLLG

>d1fhua2 d.54.1.1 (A:1-99) O-succinylbenzoate synthase {Escherichia coli}

MRSAQVYRWQIPMDAGVVLRDRRLKTRDGLYVCLREGEREGWGEISPLPGFSQETWEEAQSVLLAWVNNWLAGDCELPQMPSVAFGVSCALAELTDTLP

>d1muca2 d.54.1.1 (A:4-130) Muconate-lactonizing enzyme (cis muconate cycloisomerase) {Pseudomonas putida}

ALIERIDAIIVDLPTIRPHKLAMHTMQQQTLVVLRVRCSDGVEGIGEATTIGGLAYGYESPEGIKANIDAHLAPALIGLAADNINAAMLKLDKLAKGNTFAKSGIESALLDAQGKRLGLPVSELLGG

>d2mnr\_2 d.54.1.1 (3-132) Mandelate racemase {Pseudomonas putida}

EVLITGLRTRAVNVPLAYPVHTAVGTVGTAPLVLIDLATSAGVVGHSYLFAYTPVALKSLKQLLDDMAAMIVNEPLAPVSLEAMLAKRFCLAGYTGLIRMAAAGIDMAAWDALGKVHETPLVKLLGANAR

>d2chr\_2 d.54.1.1 (1-126) Chlormuconate cycloisomerase {Alcaligenes eutrophus}

MKIDAIEAVIVDVPTKRPIQMSITTVHQQSYVIVRVYSEGLVGVGEGGSVGGPVWSAECAETIKIIVERYLAPHLLGTDAFNVSGALQTMARAVTGNASAKAAVEMALLDLKARALGVSIAELLGG

>d1jpdx2 d.54.1.1 (X:-2-113) L-Ala-D/L-Glu epimerase {Escherichia coli}

GSHMRTVKVFEEAWPLHTPFVIARGSRSEARVVVVELEEEGIKGTGECTPYPRYGESDASVMAQIMSVVPQLEKGLTREELQKILPAGAARNALDCALWDLAARRQQQSLADLIGI

>d1jpma2 d.54.1.1 (A:1-125) L-Ala-D/L-Glu epimerase {Bacillus subtilis}

MKIIRIETSRIAVPLTKPFKTALRTVYTAESVIVRITYDSGAVGWGEAPPTLVITGDSMDSIESAIHHVLKPALLGKSLAGYEAILHDIQHLLTGNMSAKAAVEMALYDGWAQMCGLPLYQMLGG

>d1kcza2 d.54.1.1 (A:1-160) beta-Methylaspartase {Clostridium tetanomorphum}

MKIVDVLCTPGLTGFYFDDQRAIKKGAGHDGFTYTGSTVTEGFTQVRQKGESISVLLVLEDGQVAHGDCAAVQYSGAGGRDPLFLAKDFIPVIEKEIAPKLIGREITNFKPMAEEFDKMTVNGNRLHTAIRYGITQAILDAVAKTRKVTMAEVIRDEYNP

>d1kkoa2 d.54.1.1 (A:1-160) beta-Methylaspartase {Citrobacter amalonaticus}

MKIKQALFTAGYSSFYFDDQQAIKNGAGHDGFIYTGDPVTPGFTSVRQAGECVSVQLILENGAVAVGDCAAVQYSGAGGRDPLFLAEHFIPFLNDHIKPLLEGRDVDAFLPNARFFDKLRIDGNLLHTAVRYGLSQALLDATALASGRLKTEVVCDEWQL

>d1bxea\_ d.55.1.1 (A:) Ribosomal protein L22 {Thermus aquaticus, subsp. Thermus thermophilus}

MEAKAIARYVRISPRKVRLVVDLIRGKSLEEARNILRYTNKRGAYFVAKVLESAAANAVNNHDMLEDRLYVKAAYVDEGPALKRVLPRARGRADIIKKRTSHITVILGEK

>d1jj2q\_ d.55.1.1 (Q:) Ribosomal protein L22 {Archaeon Haloarcula marismortui}

GISYSVEADPDTTAKAMLRERQMSFKHSKAIAREIKGKTAGEAVDYLEAVIEGDQPVPFKQHNSGVGHKSKVDGWDAGRYPEKASKAFLDLLENAVGNADHQGFDGEAMTIKHVAAHKVGEQQGRKPRAMGRASAWNSPQVDVELILEEP

>d1gd8a\_ d.188.1.1 (A:) Prokaryotic ribosomal protein L17 {Thermus thermophilus}

SSHRLALYRNQAKSLLTHGRITTTVPKAKELRGFVDHLIHLAKRGDLHARRLVLRDLQDVKLVRKLFDEIAPRYRDRQGGYTRVLKLAERRRGDGAPLALVELVE

>d1oela3 d.56.1.1 (A:137-190,A:367-409) GroEL {Escherichia coli}

PCSDSKAIAQVGTISANSDETVGKLIAEAMDKVGKEGVITVEDGTGLQDELDVVXERVAKLAGGVAVIKVGAATEVEMKEKKARVEDALHATRAAVEE

>d1ioka3 d.56.1.1 (A:137-190,A:367-409) GroEL {Paracoccus denitrificans}

PVNDSSEVAQVGTISANGESFIGQQIAEAMQRVGNEGVITVEENKGMETEVEVVXERVAKLAGGVAVIRVGGMTEIEVKERKDRVDDALNATRAAVQE

>d1a6da3 d.56.1.2 (A:146-214,A:368-403) Thermosome {Archaeon Thermoplasma acidophilum}

TDDATLRKIALTALSGKNTGLSNDFLADLVVKAVNAVAEVRDGKTIVDTANIKVDKKNGGSVNDTQFISXAVSILIRGGTDHVVSEVERALNDAIRVVAITKEDGK

>d1a6db3 d.56.1.2 (B:145-215,B:368-403) Thermosome {Archaeon Thermoplasma acidophilum}

GADEKALLLKMAQTSLNSKSASVAKDKLAEISYEAVKSVAELRDGKYYVDFDNIQVVKKQGGAIDDTQLINXKAVSILVRGETEHVVDEMERSITDSLHVVASALEDG

>d1h6ha\_ d.189.1.1 (A:) p40phox NADPH oxidase {Human (Homo sapiens)}

AVAQQLRAESDFEQLPDDVAISANIADIEEKRGFTSHFVFVIEVKTKGGSKYLIYRRYRQFHALQSKLEERFGPDSKSSALACTLPTLPAKVYVGVKQEIAEMRIPALNAYMKSLLSLPVWVLMDEDVRIFFYQSPYDSEQVP

>d1gd5a\_ d.189.1.1 (A:) p47phox NADPH oxidase {Human (Homo sapiens)}

GSMGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVVYRRFTEIYEFHKTLKEMFPIEAGAINPENRIIPHLPAPKWFDGQRAAENRQGTLTEYCSTLMSLPTKISRCPHLLDFFKVRPDDLKLP

>d1ji8a\_ d.203.1.1 (A:) DsrC, the gamma subunit of dissimilatory sulfite reductase {Archaeon Pyrobaculum aerophilum}

MPVKCPGEYQVDGKKVILDEDCFMQNPEDWDEKVAEWLARELEGIQKMTEEHWKLVKYLREYWETFGTCPPIKMVTKETGFSLEKIYQLFPSGPAHGACKVAGAPKPTGCV

>d1ghha\_ d.57.1.1 (A:) DNA damage-inducible protein DinI {Escherichia coli}

MRIEVTIAKTSPLPAGAIDALAGELSRRIQYAFPDNEGHVSVRYAAANNLSVIGATKEDKQRISEILQETWESADDWFVSE

>d1fxd\_\_ d.58.1.1 (-) Ferredoxin II {Desulfovibrio gigas}

PIEVNDDCMACEACVEICPDVFEMNEEGDKAVVINPDSDLDCVEEAIDSCPAEAIVRS

>d1dura\_ d.58.1.1 (A:) Ferredoxin II {Peptostreptococcus asaccharolyticus}

AYVINDSCIACGACKPECPVNCIQEGSIYAIDADSCIDCGSCASVCPVGAPNPED

>d1fca\_\_ d.58.1.1 (-) Ferredoxin II {Clostridium acidi-urici}

AYVINEACISCGACEPECPVDAISQGGSRYVIDADTCIDCGACAGVCPVDAPVQA

>d2fdn\_\_ d.58.1.1 (-) Ferredoxin II {Clostridium acidi-urici}

AYVINEACISCGACEPECPVNAISSGDDRYVIDADTCIDCGACAGVCPVDAPVQA

>d1clf\_\_ d.58.1.1 (-) Ferredoxin II {Clostridium pasteurianum}

AYKIADSCVSCGACASECPVNAISQGDSIFVIDADTCIDCGNCANVCPVGAPVQE

>d1blu\_\_ d.58.1.1 (-) Ferredoxin II {Chromatium vinosum}

ALMITDECINCDVCEPECPNGAISQGDETYVIEPSLCTECVGHYETSQCVEVCPVDCIIKDPSHEETEDELRAKYERITG

>d7fd1a\_ d.58.1.2 (A:) Ferredoxin {Azotobacter vinelandii}

AFVVTDNCIKCKYTDCVEVCPVDCFYEGPNFLVIHPDECIDCALCEPECPAQAIFSEDEVPEDMQEFIQLNAELAEVWPNITEKKDPLPDAEDWDGVKGKLQHLER

>d1bc6\_\_ d.58.1.2 (-) Ferredoxin {Bacillus schlegelii}

AYVITEPCIGTKDASCVEVCPVDCIHEGEDQYYIDPDVCIDCGACEAVCPVSAIYHEDFVPEEWKSYIQKNRDFFKK

>d1h98a\_ d.58.1.2 (A:) Ferredoxin {Thermus thermophilus}

PHVICEPCIGVKDQSCVEVCPVECIYDGGDQFYIHPEECIDCGACVPACPVNAIYPEEDVPEQWKSYIEKNRKLAGL

>d1xer\_\_ d.58.1.3 (-) Ferredoxin {Archaeon Sulfolobus sp.}

GIDPNYRTNRQVVGEHSGHKVYGPVEPPKVLGIHGTIVGVDFDLCIADGSCINACPVNVFQWYDTPGHPASEKKADPVNEQACIFCMACVNVCPVAAIDVKPP

>d1vjw\_\_ d.58.1.4 (-) Ferredoxin {Thermotoga maritima}

MKVRVDADACIGCGVCENLCPDVFQLGDDGKAKVLQPETDLPCAKDAADSCPTGAISVE

>d1fxra\_ d.58.1.4 (A:) Ferredoxin I {Sulfate-reducing bacteria (Desulfovibrio africanus)}

ARKFYVDQDECIACESCVEIAPGAFAMDPEIEKAYVKDVEGASQEEVEEAMDTCPVQCIHWEDE

>d1iqza\_ d.58.1.4 (A:) Ferredoxin {Bacillus thermoproteolyticus}

PKYTIVDKETCIACGACGAAAPDIYDYDEDGIAYVTLDDNQGIVEVPDILIDDMMDAFEGCPTDSIKVADEPFDGDPNKFE

>d1jb0c\_ d.58.1.4 (C:) Photosystem I iron-sulfur protein PsaC {Synechococcus elongatus}

AHTVKIYDTCIGCTQCVRACPTDVLEMVPWDGCKAGQIASSPRTEDCVGCKRCETACPTDFLSIRVYLGAETTRSMGLAY

>d1feha3 d.58.1.5 (A:127-209) Fe-only hydrogenase, second domain {Clostridium pasteurianum}

KDKTEYVDERSKSLTVDRTKCLLCGRCVNACGKNTETYAMKFLNKNGKTIIGAEDEKCFDDTNCLLCGQCIIACPVAALSEKS

>d1hfel2 d.58.1.5 (L:2-86) Fe-only hydrogenase larger subunit, N-domain {Desulfovibrio desulfuricans}

SRTVMERIEYEMHTPDPKADPDKLHFVQIDEAKCIGCDTCSQYCPTAAIFGEMGEPHSIPHIEACINCGQCLTHCPENAIYEAQS

>d1keka5 d.58.1.5 (A:669-785) Pyruvate-ferredoxin oxidoreductase, PFOR, domain V {Desulfovibrio africanus}

TSQFEKRGVAINVPQWVPENCIQCNQCAFVCPHSAILPVLAKEEELVGAPANFTALEAKGKELKGYKFRIQINTLDCMGCGNCADICPPKEKALVMQPLDTQRDAQVPNLEYAARIP

>d1h7wa5 d.58.1.5 (A:845-1017) Dihydropyrimidine dehydrogenase, C-terminal domain {Pig (Sus scrofa)}

ELQGWDGQSPGTESHQKGKPVPRIAELMGKKLPNFGPYLEQRKKIIAEEKMRLKEQNAAFPPLERKPFIPKKPIPAIKDVIGKALQYLGTFGELSNIEQVVAVIDEEMCINCGKCYMTCNDSGYQAIQFDPETHLPTVTDTCTGCTLCLSVCPIIDCIRMVSRTTPYEPKRGL

>d1jnrb\_ d.58.1.5 (B:) Adenylylsulfate reductase B subunit {Archaeon Archaeoglobus fulgidus}

PSFVNPEKCDGCKALERTACEYICPNDLMTLDKEKMKAYNREPDMCWECYSCVKMCPQGAIDVRGYVDYSPLGGACVPMRGTSDIMWTVKYRNGKVLRFKFAIRTTPWGSIQPFEGFPEPTEEALKSELLAGEPEIIGTSEFPQVKKKA

>d1d09b1 d.58.2.1 (B:1-100) Aspartate carbamoyltransferase {Escherichia coli}

MTHDNKLQVEAIKRGTVIDHIPAQIGFKLLSLFKLTETDQRITIGLNLPSGEMGRKDLIKIENTFLSEDQVDQLALYAPQATVNRIDNYEVVGKSRPSLP

>d2atcb1 d.58.2.1 (B:1-100) Aspartate carbamoyltransferase {Escherichia coli}

MTHNDKLQVAEIKRGTVINHIPAEIGFKLLSLFKLTETQDRITIGLNLPSGEMGRKDLIKIENTFLSEDEVDELALYAPQATVNRINDYEVVGKSRPSLP

>d1pca\_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Pig (Sus scrofa)}

KEDFVGHQVLRISVDDEAQVQKVKELEDLEHLQLDFWRGPARPGFPIDVRVPFPSIQAVKVFLEAHGIRYTIMIEDVQLLLDEEQEQMFASQGR

>d1pyta\_ d.58.3.1 (A:) Procarboxypeptidase A {Cow (Bos taurus)}

KEDFVGHQVLRITAADEAEVQTVKELEDLEHLQLDFWRGPGQPGSPIDVRVPFPSLQAVKVFLEAHGIRYRIMIEDVQSLLDEEQEQMFASQSR

>d1aye\_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Human (Homo sapiens)}

LETFVGDQVLEIVPSNEEQIKNLLQLEAQEHLQLDFWKSPTTPGETAHVRVPFVNVQAVKVFLESQGIAYSIMIEDVQVLLDKENEEMLFNRRR

>d1nsa\_2 d.58.3.1 (7A-95A) Procarboxypeptidase B {Pig (Sus scrofa)}

FEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVEDFLEQNELQYEVLINNLRSVLEAQFDSVSR

>d1pba\_\_ d.58.3.1 (-) Procarboxypeptidase B {Pig (Sus scrofa)}

HHSGEHFEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVEDFLEQNELQYEVLINN

>d1spbp\_ d.58.3.2 (P:) Subtilisin prosegment {Bacillus amyloliquefaciens}

EKKYIVGFKQTMSTMSAAKKKDVISEKGGKVQKQFKYVDAASATLNEKAVKELKKDPSVAYVEEDHVAHAY

>d1scjb\_ d.58.3.2 (B:) Subtilisin prosegment {Bacillus subtilis}

EKKYIVGFKQTMSAMSSAKKKDVISQKGGKVEKQFKYVNAAAATLDEKAVKELKKDPSVAYVEEDHIAHEY

>d1itpa\_ d.58.3.2 (A:) Proteinase A inhibitor 1, POIA1 {Oyster mushroom (Pleurotus ostreatus)}

GSAGKFIVIFKNDVSEDKIRETKDEVIAEGGTITNEYNMPGMKGFAGELTPQSLTKFQGLQGDLIDSIEEDGIVTTQ

>d1mli\_\_ d.58.4.1 (-) Muconalactone isomerase {Pseudomonas putida}

MLFHVKMTVKLPVDMDPAKATQLKADEKELAQRLQREGTWRHLWRIAGHYANYSVFDVPSVEALHDTLMQLPLFPYMDIEVDGLCRHPSSIHSDDR

>d2pii\_\_ d.58.5.1 (-) PII (product of glnB) {Escherichia coli}

MKKIDAIIKPFKLDDVREALAEVGITGMTVTEVKGFGRQKGHTELYRGAEYMVDFLPKVKIEIVVPDDIVDTCVDTIIRTAQTGKIGDGKIFVFDVARVIRIRTGEEDDAAI

>d1gnka\_ d.58.5.1 (A:) PII-homolog GlnK {Escherichia coli}

MKLVTVIIKPFKLEDVREALSSIGIQGLTVTEVKGFGRQKGHAELYRGAEYSVNFLPKVKIDVAIADDQLDEVIDIVSKAAYTGKIGDGKIFVAELQRVIRIRTGEADEAAL

>d1nuea\_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo sapiens)}

ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRASEEHLKQHYIDLKDRPFFPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVKSAEKEISLWFKPEELVDYKSCAHDWVYE

>d1ehwa\_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo sapiens), NDK4}

HMGTRERTLVAVKPDGVQRRLVGDVIQRFERRGFTLVGMKMLQAPESVLAEHYQDLRRKPFYPALIRYMSSGPVVAMVWEGYNVVRASRAMIGHTDSAEAAPGTIRGDFSVHISRNVIHASDSVEGAQREIQLWFQSSELVSW

>d1be4a\_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Cow (Bos taurus)}

ANSERTFIAIKPDGVQRGLMGEIIKRFEQKGFRLVAMKFMRASEDLLKEHYIDLKDRPFFAGLVKYMHSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVESAEKEIALWFRPEELVNYKSCAQNWIYE

>d1hlwa\_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Dictyostelium discoideum}

VNKERTFLAVKPDGVARGLVGEIIARYEKKGFVLVGLKQLVPTKDLAESHYAEHKERPFFGGLVSFITSGPVVAMVFEGKGVVASARLMIGVTNPLASAPGSIRGDFGVDVGRNIIAGSDSVESANREIALWFKPEELLTEVKPNPNLYE

>d1nsqa\_ d.58.6.1 (A:) Nucleoside diphosphate kinases {Drosophila melanogaster}

AANKERTFIMVKPDGVQRGLVGKIIERFEQKGFKLVALKFTWASKELLEKHYADLSARPFFPGLVNYMNSGPVVPMVWEGLNVVKTGRQMLGATNPADSLPGTIRGDFCIQVGRNIIHGSDAVESAEKEIALWFNEKELVTWTPAAKDWIYE

>d1nhkl\_ d.58.6.1 (L:) Nucleoside diphosphate kinases {Myxococcus xanthus}

AIERTLSIIKPDGLEKGVIGKIISRFEEKGLKPVAIRLQHLSQAQAEGFYAVHKARPFFKDLVQFMISGPVVLMVLEGENAVLANRDIMGATNPAQAAEGTIRKDFATSIDKNTVHGSDSLENAKIEIAYFFRETEIHSYPYQ

>d1ha1\_1 d.58.7.1 (8-92) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}

EPEQLRKLFIGGLSFETTDESLRSHFEQWGTLTDCVVMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDGRVVEPKRAVSRE

>d1ha1\_2 d.58.7.1 (99-180) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}

AHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIVIQKYHTVNGHNCEVRKAL

>d2up1a2 d.58.7.1 (A:99-190) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}

GAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIVIQKYHTVNGHNCEVRKALSKQEMASAS

>d1fht\_\_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}

AVPETRPNHTIYINNLNEKIKKDELKKSLYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSATNALRSMQGFPFYDKPMRIQYAKTDSDIIAKMKGTFVERDRKREKRKPKSQE

>d1nrca\_ d.58.7.1 (A:) Splicesomal U1A protein {Human (Homo sapiens)}

TRPNHTIYINNLNEKIKKDELKKSLYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSATNALRSMQGFPFYDKPMRICYAKTD

>d1urna\_ d.58.7.1 (A:) Splicesomal U1A protein {Human (Homo sapiens)}

AVPETRPNHTIYINNLNEKIKKDELKKSLHAIFSRFGQILDILVSRSLKMRGQAFVIFKEVSSATNALRSMQGFPFYDKPMRIQYAKTDSDIIAKM

>d2u1a\_\_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}

MAPAQPLSENPPNHILFLTNLPEETNELMLSMLFNQFPGFKEVRLVPGRHDIAFVEFDNEVQAGAARDALQGFKITQNNAMKISFAKK

>d1a9nb\_ d.58.7.1 (B:) Splicing factor U2B'' {Human (Homo sapiens)}

IRPNHTIYINNMNDKIKKEELKRSLYALFSQFGHVVDIVALKTMKMRGQAFVIFKELGSSTNALRQLQGFPFYGKPMRIQYAKTDSDIISKMRG

>d1u2fa\_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}

ARRLYVGNIPFGITEEAMMDFFNAQMRLGGLTQAPGNPVLAVQINQDKNFAFLEFRSVDETTQAMAFDGIIFQGQSLKIRRPHDYQPLPG

>d2u2fa\_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}

AHKLFIGGLPNYLNDDQVKELLTSFGPLKAFNLVKDSATGLSKGYAFCEYVDINVTDQAIAGLNGMQLGDKKLLVQRASVGAKNA

>d1b7fa1 d.58.7.1 (A:123-204) Sex-lethal protein {Drosophila melanogaster}

SNTNLIVNYLPQDMTDRELYALFRAIGPINTCRIMRDYKTGYSYGYAFVDFTSEMDSQRAIKVLNGITVRNKRLKVSYARPG

>d1b7fa2 d.58.7.1 (A:205-289) Sex-lethal protein {Drosophila melanogaster}

GESIKDTNLYVTNLPRTITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRYNKREEAQEAISALNNVIPEGGSQPLSVRLA

>d1sxl\_\_ d.58.7.1 (-) Sex-lethal protein {Drosophila melanogaster}

MSYARPGGESIKDTNLYVTNLPRTITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRYNKREEAQEAISALNNVIPEGGSQPLSVRLAEEHGK

>d1d8za\_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}

MDSKTNLIVNYLPQNMTQDEFKSLFGSIGDIESCKLVRDKITGQSLGYGFVNYSDPNDADKAINTLNGLKLQTKTIKVSYARPSSASIR

>d1d9aa\_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}

DANLYVSGLPKTMSQKEMEQLFSQYGRIITSRILLDQATGVSRGVGFIRFDKRIEAEEAIKGLNGQKPLGAAEPITVKFANNPSQ

>d1fxla1 d.58.7.1 (A:37-118) Hu antigen D (Hud) {Human (Homo sapiens)}

SKTNLIVNYLPQNMTQEEFRSLFGSIGEIESCKLVRDKITGQSLGYGFVNYIDPKDAEKAINTLNGLRLQTKTIKVSYARPS

>d1fxla2 d.58.7.1 (A:119-203) Hu antigen D (Hud) {Human (Homo sapiens)}

SASIRDANLYVSGLPKTMTQKELEQLFSQYGRIITSRILVDQVTGVSRGVGFIRFDKRIEAEEAIKGLNGQKPSGATEPITVKFA

>d1hd1a\_ d.58.7.1 (A:) Heterogeneous nuclear ribonucleoprotein d0 {Human (Homo sapiens)}

KMFIGGLSWDTTKKDLKDYFSKFGEVVDCTLKLDPITGRSRGFGFVLFKESESVDKVMDQKEHKLNGKVIDPKRA

>d2msta\_ d.58.7.1 (A:) Neural RNA-binding protein Musashi-1 {Mouse (Mus musculus)}

KIFVGGLSVNTTVEDVKHYFEQFGKVDDAMLMFDKTTNRHRGFGFVTFESEDIVEKVCEIHFHEINNKMVECKKA

>d1cvja1 d.58.7.1 (A:11-90) Poly(A)-binding protein {Human (Homo sapiens)}

ASLYVGDLHPDVTEAMLYEKFSPAGPILSIRVCRDMITRRSLGYAYVNFQQPADAERALDTMNFDVIKGKPVRIMWSQRD

>d1cvja2 d.58.7.1 (A:91-179) Poly(A)-binding protein {Human (Homo sapiens)}

PSLRKSGVGNIFIKNLDKSIDNKALYDTFSAFGNILSCKVVCDENGSKGYGFVHFETQEAAERAIEKMNGMLLNDRKVFVGRFKSRKER

>d1qm9a1 d.58.7.1 (A:1-110) Polypyrimidine tract-binding protein {Human (Homo sapiens)}

MGNSVLLVSNLNPERVTPQSLFILFGVYGDVQRVKILFNKKENALVQMADGNQAQLAMSHLNGHKLHGKPIRITLSKHQNVQLPREGQEDQGLTKDYGNSPLHRFKKPGS

>d1qm9a2 d.58.7.1 (A:111-198) Polypyrimidine tract-binding protein {Human (Homo sapiens)}

KNFQNIFPPSATLHLSNIPPSVSEEDLKVLFSSNGGVVKGFKFFQKDRKMALIQMGSVEEAVQALIDLHNHDLGENHHLRVSFSKSTI

>d1fj7a\_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}

GSHMLEDPVEGSESTTPFNLFIGNLNPNKSVAELKVAISELFAKNDLAVVDVRTGTNRKFGYVDFESAEDLEKALELTGLKVFGNEIKLEKPKGRDGTRGC

>d1fjca\_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}

SHMLEDPCTSKKVRAARTLLAKNLSFNITEDELKEVFEDALEIRLVSQDGKSKGIAYIEFKSEADAEKNLEEKQGAEIDGRSVSLYYTGEKGGTRG

>d1fjeb1 d.58.7.1 (B:1-91) Nucleolin {Golden hamster (Mesocricetus auratus)}

GSHMVEGSESTTPFNLFIGNLNPNKSVAELKVAISELFAKNDLAVVDVRTGTNRKFGYVDFESAEDLEKALELTGLKVFGNEIKLEKPKGR

>d1fjeb2 d.58.7.1 (B:92-175) Nucleolin {Golden hamster (Mesocricetus auratus)}

DSKKVRAARTLLAKNLSFNITEDELKEVFEDALEIRLVSQDGKSKGIAYIEFKSEADAEKNLEEKQGAEIDGRSVSLYYTGEKG

>d1h6kx\_ d.58.7.1 (X:) CBP20, 20KDa nuclear cap-binding protein {Human (Homo sapiens)}

KSCTLYVGNLSFYTTEEQIYELFSKSGDIKKIIMGLDKMTACGFCFVEYYSRADAENAMRYINGTRLDDRIIRTDWDAG

>d1fo1a2 d.58.7.2 (A:123-191) mRNA export factor tap {Human (Homo sapiens)}

TIPYGRKYDKAWLLSMIQSKCSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRISIII

>d1ft8a2 d.58.7.2 (A:118-199) mRNA export factor tap {Human (Homo sapiens)}

NWFKITIPYGRKYDKAWLLSMIQSKCSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRISIIINSSAPPHT

>d1ft8e1 d.58.7.2 (E:) mRNA export factor tap {Human (Homo sapiens)}

WFKITIPYGRKYDKAWLLSMIQSKCSVPFTPIEFHYENTRAQFFVEDASTASALKAV

>d1koha2 d.58.7.2 (A:105-200) mRNA export factor tap {Human (Homo sapiens)}

RGGAGTSQDGTSKNWFKITIPYGRKYDKAWLLSMIQSKSSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRISIIINSSAPPHTI

>d1jmta\_ d.58.7.3 (A:) U2AF35 (35 KDa subunit) {Human (Homo sapiens)}

SQTIALLNIYRNPQNSSQSADGLRSAVSDVEMQEHYDEFFEEVFTEMEEKYGEVEEMNVCDNLGDHLVGNVYVKFRREEDAEKAVIDLNNRWFNGQPIHAELSP

>d1dbda\_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}

RRTTNDGFHLLKAGGSCFALISGTANQVKCYRFRVKKNHRHRYENCTTTWFTVADNGAERQGQAQILITFGSPSQRQDFLKHVPLPPGMNISGFTASLDF

>d2bopa\_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}

SCFALISGTANQVKCYRFRVKKNHRHRYENCTTTWFTVADNGAERQGQAQILITFGSPSQRQDFLKHVPLPPGMNISGFTASLDF

>d1a7ge\_ d.58.8.1 (E:) Papillomavirus-1 E2 protein {Human papillomavirus type 31}

ATTPIIHLKGDANILKCLRYRLSKYKQLYEQVSSTWHWTCTDGKHKNAIVTLTYISTSQRDDFLNTVVIPNTVSVSTGYMTI

>d1by9\_\_ d.58.8.1 (-) Papillomavirus-1 E2 protein {Human papillomavirus type 16}

TTPIVHLKGDANTLKCLRYRFKKHCTLYTAVSSTWHWTGHNVKHKSAIVTLTYDSEWQRDQFLSQVKIPKTITVSTGFMS

>d1f9fa\_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Human papillomavirus type 18}

HMTPIIHLKGDRNSLKCLRYRLRKHSDHYRDISSTWHWTGAGNEKTGILTVTYHSETQRTKFLNTVAIPDSVQILVGYMTM

>d1b3ta\_ d.58.8.1 (A:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}

KGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLP

>d1vhib\_ d.58.8.1 (B:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}

PKFENIAEGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYNLRRGTALAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRVTVCSFDDGVDLP

>d3rubl2 d.58.9.1 (L:22-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}

LTYYTPEYQTKDTDILAAFRVTPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYRIERVVGEKDQYIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPPAYVKT

>d1bura2 d.58.9.1 (A:12-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

EFKAGVKDYKLTYYTPEYETLDTDILAAFRVSPQPGVPPEEAGAAVAAESSTGTWTTVWTDGLTNLDRYKGRCYHIEPVAGEENQYICYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPVAYVKT

>d1bwva2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

RIKNSRYESGVIPYAKMGYWNPDYQVKDTDVLALFRVTPQPGVDPIEAAAAVAGESSTATWTVVWTDLLTAADLYRAKAYKVDQVPNNPEQYFAYIAYELDLFEEGSIANLTASIIGNVFGFKAVKALRLEDMRLPLAYLKTFQ

>d1gk8a2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}

TKAGAGFKAGVKDYRLTYYTPDYVVRDTDILAAFRMTPQPGVPPEECGAAVAAESSTGTWTTVWTDGLTSLDRYKGRCYDIEPVPGEDNQYIAYVAYPIDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPPAYVKTFV

>d1bxna2 d.58.9.1 (A:22-150) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}

YKMGYWDGDYVPKDTDLLALFRITPQDGVDPVEAAAAVAGESSTATWTVVWTDRLTACDMYRAKAYRVDPVPNNPEQFFCYVAYDLSLFEEGSIANLTASIIGNVFSFKPIKAARLEDMRFPVAYVKT

>d1rbla2 d.58.9.1 (A:9-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}

SAAGYKAGVKDYKLTYYTPDYTPKDTDLLAAFRFSPQPGVPADEAGAAIAAESSTGTWTTVWTDLLTDMDRYKGKCYHIEPVAGEENSYFAFIAYPLDLFEEGSVTNILTSIVGNVFGFKAIRSLRLEDIRFPVALVKT

>d5ruba2 d.58.9.1 (A:2-137) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Rhodospirillum rubrum}

DQSSRYVNLALKEEDLIAGGEHVLCAYIMKPKAGYGYVATAAHFAAESSTGTNVEVCTTDDFTRGVDALVYEVDEARELTKIAYPVALFDRNITDGKAMIASFLTLTMGNNQGMGDVEYAKMHDFYVPEAYRALFD

>d1geha2 d.58.9.1 (A:12-136) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Archaeon Thermococcus kodakaraensis}

YVDKGYEPSKKRDIIAVFRVTPAEGYTIEQAAGAVAAESSTGTWTTLYPWYEQERWADLSAKAYDFHDMGDGSWIVRIAYPFHAFEEANLPGLLASIAGNIFGMKRVKGLRLEDLYFPEKLIREF

>d2acy\_\_ d.58.10.1 (-) Acylphosphatase {Cow (Bos taurus)}

AEGDTLISVDYEIFGKVQGVFFRKYTQAEGKKLGLVGWVQNTDQGTVQGQLQGPASKVRHMQEWLETKGSPKSHIDRASFHNEKVIVKLDYTDFQIVK

>d1aps\_\_ d.58.10.1 (-) Acylphosphatase {Horse (Equus caballus)}

STARPLKSVDYEVFGRVQGVCFRMYAEDEARKIGVVGWVKNTSKGTVTGQVQGPEEKVNSMKSWLSKVGSPSSRIDRTNFSNEKTISKLEYSNFSVRY

>d1i1ga2 d.58.37.1 (A:62-141) LprA {Archaeon Pyrococcus furiosus}

YSLVTITGVDTKPEKLFEVAEKLKEYDFVKELYLSSGDHMIMAVIWAKDGEDLAEIISNKIGKIEGVTKVCPAIILEKLK

>d1dar\_4 d.58.11.1 (600-689) Elongation factor G (EF-G), domains III and V {Thermus thermophilus}

VILEPIMRVEVTTPEEYMGDVIGDLNARRGQILGMEPRGNAQVIRAFVPLAEMFGYATDLRSKTQGRGSFVMFFDHYQEVPKQVQEKLIK

>d1fnma4 d.58.11.1 (A:404-482) Elongation factor G (EF-G), domains III and V {Thermus thermophilus}

VPEPVIDVAIEPKTKADQEKLSQALARLAEEDPTFRVSTHPETGQTIISGMGELHLEIIVDRLKREFKVDANVGKPQVA

>d1b64\_\_ d.58.12.1 (-) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Human (Homo sapiens)}

MLVAKSSILLDVKPWDDETDMAKLEECVRSIQADGLVWGSSKLVPVGYGIKKLQIQCVVEDDKVGTDMLEEQITAFEDYVQSMDVAAFNKI

>d1f60b\_ d.58.12.1 (B:) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Baker's yeast (Saccharomyces cerevisiae)}

PAAKSIVTLDVKPWDDETNLEEMVANVKAIEMEGLTWGAHQFIPIGFGIKKLQINCVVEDDKVSLDDLQQSIEEDEDHVQSTDIAAMQKL

>d1gh8a\_ d.58.12.1 (A:) aEF-1beta {Archaeon Methanobacterium thermoautotrophicum}

MGDVVATIKVMPESPDVDLEALKKEIQERIPEGTELHKIDEEPIAFGLVALNVMVVVGDAEGGTEAAEESLSGIEGVSNIEVTDVRRLM

>d1b7yb4 d.58.13.1 (B:682-775) Phenylalanyl-tRNA synthetase {Thermus thermophilus (Thermus aquaticus)}

LAFQDPSRHPAAFRDLAVVVPAPTPYGEVEALVREAAGPYLESLALFDLYQGPPLPEGHKSLAFHLRFRHPKRTLRDEEVEEAVSRVAEALRAR

>d1jjcb4 d.58.13.1 (B:682-785) Phenylalanyl-tRNA synthetase {Thermus thermophilus (Thermus aquaticus)}

LAFQDPSRHPAAFRDLAVVVPAPTPYGEVEALVREAAGPYLESLALFDLYQGPPLPEGHKSLAFHLRFRHPKRTLRDEEVEEAVSRVAEALRARGFGLRGLDTP

>d1loua\_ d.58.14.1 (A:) Ribosomal protein S6 {Thermus thermophilus}

MRRYEVNIVLNPNLDQSQLALEKEIIQRAAENYGARVEKVEELGLRRLAYPIAKDPQGYFLWYQVEMPEDRVNDLARELRIRDNVRRVMVVKSQEPF

>d1qjha\_ d.58.14.1 (A:) Ribosomal protein S6 {Thermus thermophilus}

MRRYEVNIVLNPNLDQSQLALEKEIIQRALENYGARVEKVAILGLMVLAYPIAKDPQGYFLWYQVEMPEDRVNDLARELRIRDNVRRVMVVKS

>d1fjgj\_ d.58.15.1 (J:) Ribosomal protein S10 {Thermus thermophilus}

KIRIKLRGFDHKTLDASAQKIVEAARRSGAQVSGPIPLPTRVRRFTVIRGPFKHKDSREHFELRTHNRLVDIINPNRKTIEQLMTLDLPTGVEIEIKT

>d1fa0a1 d.58.16.1 (A:352-523) Poly(A) polymerase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

NDFFFRYKFYLEITAYTRGSDEQHLKWSGLVESKVRLLVMKLEVLAGIKIAHPFTKPFESSYCCPTEDDYEMIQDKYGSHKTETALNALKLVTDENKEEESIKDAPKAYLSTMYIGLDFNIENKKEKVDIHIPCTEFVNLCRSFNEDYGDHKVFNLALRFVKGYDLPDEVFD

>d1f5aa1 d.58.16.1 (A:365-498) Poly(A) polymerase, C-terminal domain {Cow (Bos taurus)}

PNFFQKYKHYIVLLASAPTEKQRLEWVGLVESKIRILVGSLEKNEFITLAHVNPQSFPAPKENPDKEEFRTMWVIGLVFKKTENSENLSVDLTYDIQSFTDTVYRQAINSKMFEVDMKIAAMHVKRKQLHQLLP

>d1afj\_\_ d.58.17.1 (-) Mercuric ion binding protein MerP {Shigella flexneri}

ATQTVTLAVPGMTCAACPITVKKALSKVEGVSKVDVGFEKREAVVTFDDTKASVQKLTKATADAGYPSSVKQ

>d1fvqa\_ d.58.17.1 (A:) Copper transporter domain ccc2a {Baker's yeast (Saccharomyces cerevisiae)}

AREVILAVHGMTCSACTNTINTQLRALKGVTKCDISLVTNECQVTYDNEVTADSIKEIIEDCGFDCEILRDS

>d1aw0\_\_ d.58.17.1 (-) Menkes copper-transporting ATPase {Human (Homo sapiens)}

LTQETVINIDGMTCNSCVQSIEGVISKKPGVKSIRVSLANSNGTVEYDPLLTSPETLRGAIEDMGFDATLSD

>d1cc8a\_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Baker's yeast (Saccharomyces cerevisiae)}

AEIKHYQFNVVMTCSGCSGAVNKVLTKLEPDVSKIDISLEKQLVDVYTTLPYDFILEKIKKTGKEVRSGKQL

>d1fe0a\_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Human (Homo sapiens), HAH1}

PKHEFSVDMTCGGCAEAVSRVLNKLGGVKYDIDLPNKKVCIESEHSMDTLLATLKKTGKTVSYLGL

>d1cpza\_ d.58.17.1 (A:) Copper chaperone {Enterococcus hirae}

AQEFSVKGMSCNHCVARIEEAVGRISGVKKVKVQLKKEKAVVKFDEANVQATEICQAINELGYQAEVI

>d1k0va\_ d.58.17.1 (A:) Copper chaperone {Bacillus subtilis, CopZ}

MEQKTLQVEGMSCQHCVKAVETSVGELDGVSAVHVNLEAGKVDVSFDADKVSVKDIADAIEDQGYDVAKIEGR

>d1qupa2 d.58.17.1 (A:2-73) Copper chaperone for superoxide dismutase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

TTNDTYEATYAIPMHCENCVNDIKACLKNVPGINSLNFDIEQQIMSVESSVAPSTIINTLRNCGKDAIIRGA

>d1gmua2 d.58.38.1 (A:71-138) Urease metallochaperone UreE, C-terminal domain {Klebsiella aerogenes}

DEEVSVVRCDDPFMLAKACYALGNRHVPLQIMPGELRYHHDHVLDDMLRQFGLTVTFGQLPFEPEAGA

>d1eara2 d.58.38.1 (A:75-142) Urease metallochaperone UreE, C-terminal domain {Bacillus pasteurii}

LEKVYVIKPQTMQEMGKMAFEIGNRHTMCIIEDDEILVRYDKTLEKLIDEVGVSYEQSERRFKEPFKY

>d1psda3 d.58.18.1 (A:327-410) Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain {Escherichia coli}

FPEVSLPLHGGRRLMHIHENRPGVLTALNKIFAEQGVNIAAQYLQTSAQMGYVVIDIEADEDVAEKALQAMKAIPGTIRARLLY

>d1tdj\_2 d.58.18.2 (336-423) Allosteric threonine deaminase C-terminal domain {Escherichia coli}

QREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNYRFADAKNACIFVGVRLSRGLEERKEILQMLNDGGYSVVDLSDDEMAKLHVRYMV

>d1tdj\_3 d.58.18.2 (424-514) Allosteric threonine deaminase C-terminal domain {Escherichia coli}

GGRPSHPLQERLYSFEFPESPGALLRFLNTLGTYWNISLFHYRSHGTDYGRVLAAFELGDHEPDFETRLNELGYDCHDETNNPAFRFFLAG

>d1phza1 d.58.18.3 (A:19-115) Phenylalanine hydroxylase N-terminal domain {Rat (Rattus norvegicus)}

GQETSYIEDNSNQNGAISLIFSLKEEVGALAKVLRLFEENDINLTHIESRPSRLNKDEYEFFTYLDKRTKPVLGSIIKSLRNDIGATVHELSRDKEK

>d1cg2a2 d.58.19.1 (A:214-326) Carboxypeptidase G2, dimerisation domain {Pseudomonas sp., strain rs-16}

SGIAYVQVNITGKASHAGAAPELGVNALVEASDLVLRTMNIDDKAKNLRFNWTIAKAGNVSNIIPASATLNADVRYARNEDFDAAMKTLEERAQQKKLPEADVKVIVTRGRPA

>d1dqaa1 d.58.20.1 (A:587-703) NAD-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

GMTRGPVVRLPRACDSAEVKAWLETSEGFAVIKEAFDSTSRFARLQKLHTSIAGRNLYIRFQSRSGDAMGMNMISKGTEKALSKLHEYFPEMQILAVSGNYCTDKKPAAINWIEGRG

>d1qaxa1 d.58.20.1 (A:111-220) NAD-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

LMHAQVQIVGIQDPLNARLSLLRRKDEIIELANRKDQLLNSLGGGCRDIEVHTFADTPRGPMLVAHLIVDVRDAMGANTVNTMAEAVAPLMEAITGGQVRLRILSNLADL

>d1ekra\_ d.58.21.1 (A:) Molybdenum cofactor biosynthesis protein C, MoaC {Escherichia coli}

GEAHMVDVSAKAETVREARAEAFVTMRSETLAMIIDGRHHKGDVFATARIAGIQAAKRTWDLIPLCHPLMLSKVEVNLQAEPEHNRVRIETLCRLTGKTGVEMEALTAASVAALTIYDMCKAVQKDMVIGPVRLLAKSGGKSGDFK

>d1f3va\_ d.58.22.1 (A:) TRADD, N-terminal domain {Human (Homo sapiens)}

HEEWVGSAYLFVESSLDKVVLSDAYAHPQQKVAVYRALQAALAESGGSPDVLQMLKIHRSDPQLIVQLRFCGRQPCGRFLRAYREGALRAALQRSLAAALAQHSVPLQLELRAGAERLDALLADEERCLSCILAQQPDRLRDEELAELEDALRNLKCG

>d1mla\_2 d.58.23.1 (128-197) Probable ACP-binding domain of malonyl-CoA ACP transacylase {Escherichia coli}

GTGAMAAIIGLDDASIAKACEEAAEGQVVSPVNFNSPGQVVIAGHKEAVERAGAACKAAGAKRALPLPVS

>d1ffgb\_ d.58.24.1 (B:) CheY-binding domain of CheA {Escherichia coli}

PRRIILSRLKAGEVDLLEEELGHLTTLTDVVKGADSLSAILPGDIAEDDITAVLCFVIEADQITFETV

>d1kp6a\_ d.58.25.1 (A:) Killer toxin KP6 alpha-subunit {Smut fungus (Ustilago maydis)}

NNAFCAGFGLSCKWECWCTAHGTGNELRYATAAGCGDHLSKSYYDARAGHCLFSDDLRNQFYSHCSSLNNNMSCRSLSK

>d1h72c2 d.58.26.1 (C:168-300) Homoserine kinase, C-terminal domain {Archaeon Methanococcus jannaschii}

FKLDILIAIPNISINTKEAREILPKAVGLKDLVNNVGKACGMVYALYNKDKSLFGRYMMSDKVIEPVRGKLIPNYFKIKEEVKDKVYGITISGSGPSIIAFPKEEFIDEVENILRDYYENTIRTEVGKGVEVV

>d1fi4a2 d.58.26.2 (A:191-393) Mevalonate 5-diphosphate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

QMKACVLVVSDIKKDVSSTQGMQLTVATSELFKERIEHVVPKRFEVMRKAIVEKDFATFAKETMMDSNSFHATCLDSFPPIFYMNDTSKRIISWCHTINQFYGETIVAYTFDAGPNAVLYYLAENESKLFAFIYKLFGSVPGWDKKFTTEQLEAFNHQFESSNFTARELDLELQKDVARVILTQVGSGPQETNESLIDAKTGL

>d1regx\_ d.58.27.1 (X:) Translational regulator protein regA {Bacteriophage T4}

MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKKGLYYIVHFKEMLRMDGRQVEMTEEDEVRRDSIAWLLEDWGLIEIVPGQRTFMKDLTNNFRVISFKQKHEWKLVPKYTIGN

>d1fvga\_ d.58.28.1 (A:) Peptide methionine sulfoxide reductase {Cow (Bos taurus)}

KIVSPQEALPGRKEPLVVAAKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWTLKGVYSTQVGFAGGYTPNPTYKEVCSGKTGHAEVVRVVFQPEHISFEELLKVFWENHDPTQGMRQGNDHGSQYRSAIYPTSAEHVGAALKSKEDYQKVLSEHGFGLITTDIREGQTFYYAEDYHQQYLSKDPDGYC

>d1ff3a\_ d.58.28.1 (A:) Peptide methionine sulfoxide reductase {Escherichia coli}

SLFDKKHLVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMEIAIFAMGCFWGVERLFWQLPGVYSTAAGYTGGYTPNPTYREVCSGDTGHAEAVRIVYDPSVISYEQLLQVFWENHDPAQGMRQGNDHGTQYRSAIYPLTPEQDAAARASLERFQAAMLAADDDRHITTEIANATPFYYAEDDHQQYLHKNPYGYCGIGGIGVCLPPEA

>d1ff3c\_ d.58.28.1 (C:) Peptide methionine sulfoxide reductase {Escherichia coli}

LVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMEIAIFAMGCFWGVERLFWQLPGVYSTAAGYTGGYTPNPTYREVCSGDTGHAEAVRIVYDPSVISYEQLLQVFWENHDPAQGMRQGNDHGTQYRSAIYPLTPEQDAAARASLERFQAAMLAADDDRHITTEIANATPFYYAEDDHQQYLHK

>d1azsa\_ d.58.29.1 (A:) Adenylyl cyclase VC1, domain C1a {Dog (Canis familiaris)}

DMMFHKIYIQKHDNVSILFADIEGFTSLASQCTAQELVMTLNELFARFDKLAAENHCLRIKILGDCYYCVSGLPEARADHAHCCVEMGMDMIEAISLVREMTGVNVNMRVGIHSGRVHCGVLGLRKWQFDVWSNDVTLANHMEAGGKAGRIHITKATLSYLNGDYEVEPGCGGERNAYLKEHSIETFLIL

>d1azsb\_ d.58.29.1 (B:) Adenylyl cyclase IIC1, domain C2a {Rat (Rattus norvegicus)}

HQSYDCVCVMFASIPDFKEFYTESDVNKEGLECLRLLNEIIADFDDLLSKPKFSGVEKIKTIGSTYMAATGLSAIPSQEHAQEPERQYMHIGTMVEFAYALVGKLDAINKHSFNDFKLRVGINHGPVIAGVIGAQKPQYDIWGNTVNVASRMDSTGVLDKIQVTEETSLILQTLGYTCTCRGIINVKGKGDLKTYFVNT

>d1fx2a\_ d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma brucei), different isoform}

NNNRAPKEPTDPVTLIFTDIESSTALWAAHPDLMPDAVAAHHRMVRSLIGRYKCYEVKTVGDSFMIASKSPFAAVQLAQELQLCFLHHDWGTNALDDSYREFEEQRAEGECEYTPPTAHMDPEVYSRLWNGLRVRVGIHTGLCDIRHDEVTKGYDYYGRTPNMAARTESVANGGQVLMTHAAYMSLSAEDRKQIDVTALGDVALRGVSDPVKMYQLNTVPSRNFAALRLDREYFD

>d1fx4a\_ d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma brucei), different isoform}

DNDSAPKEPTGPVTLIFTDIESSTALWAAHPDLMPDAVATHHRLIRSLITRYECYEVKTVGDSFMIASKSPFAAVQLAQELQLCFLRLDWETNAVDESYREFEEQRAEGECEYTPPTASLDPEVYSRLWNGLRVRVGIHTGLCDIRYDEVTKGYDYYGRTSNMAARTESVANGGQVLMTHAAYMSLSGEDRNQLDVTTLGATVLRGVPEPVRMYQLNAVPGRNFAALRLDR

>d1eqoa\_ d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK {Escherichia coli}

TVAYIAIGSNLASPLEQVNAALKALGDIPESHILTVSSFYRTPPLGPQDQPDYLNAAVALETSLAPEELLNHTQRIELQQGRVRKAERWGPRTLDLDIMLFGNEVINTERLTVPHYDMKNRGFMLWPLFEIAPELVFPDGEMLRQILHTRAFDKLNKW

>d1cbka\_ d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK {Haemophilus influenzae}

MITAYIALGSNLNTPVEQLHAALKAISQLSNTHLVTTSSFYKSKPLGPQDQPDYVNAVAKIETELSPLKLLDELQRIENEQGRVRLRRWGERTLDLDILLYGNEIIQNERLTIPHYDMHNREFVIVPLFEIASDLVLPNSQIITELVKQFADHKMIKLNP

>d1gpja3 d.58.39.1 (A:1-143) Glutamyl tRNA-reductase catalytic, N-terminal domain {Archaeon Methanopyrus kandleri}

MEDLVSVGITHKEAEVEELEKARFESDEAVRDIVESFGLSGSVLLQTSNRVEVYASGARDRAEELGDLIHDDAWVKRGSEAVRHLFRVASGLESMMVGEQEILRQVKKAYDRAARLGTLDEALKIVFRRAINLGKRAREETRI

>d1hbnc\_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanobacterium thermoautotrophicum}

AQYYPGTTKVAQNRRNFCNPEYELEKLREISDEDVVKILGHRAPGEEYPSVHPPLEEMDEPEDAIREMVEPIDGAKAGDRVRYIQFTDSMYFAPAQPYVRSRAYLCRYRGADAGTLSGRQIIETRERDLEKISKELLETEFFDPARSGVRGKSVHGHSLRLDEDGMMFDMLRRQIYNKDTGRVEMVKNQIGDELDEPVDLGEPLDEETLMEKTTIYRVDGEAYRDDVEAVEIMQRIHVLRSQGGFNL

>d1e6vc\_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanopyrus kandleri}

FYYPGETDVAENRRKYMNPNYELKKLREIPDEDIVRLMGHREPGEEYPSVHPPLEEMEEPECPIRELVEPTEGAKAGDRIRYIQFTDSVYFAPIHPYIRARMYMWRYRGVDTGSLSGRQIIEVRERDLEKIAKELLETEIFDPARSGVRGATVHGHALRLDENGLMLHALRRYRLNEETGEVEYVKDQVGIELDEPIPVGAPADEDDLKERTTIYRIDGTPYREDEELLQVVQRIHELRTLAGYRPEE

>d1e6yc\_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanosarcina barkeri}

AYERQYYPGATSVAANRRKHMSGKLEKLREISDEDLTAVLGHRAPGSDYPSTHPPLAEMGEPACSTRENVAATPGAAAGDRVRYIQFADSMYNAPATPYFRSYFAAINFRGVDPGTLSGRQIVEARERDMEQCAKVQMETEITDHALAGVRGATVHGHSVRLQEDGVMFDMLDRRRLENGTIIMDKDQVAIPLDRKVDLGKPMSSEEAAKRTTIYRVDNVAFRDDAEVVEWVHRIFDQRTKFGFQPK

>d1hbna2 d.58.31.2 (A:2-269) Alpha chain {Archaeon Methanobacterium thermoautotrophicum}

ADKLFINALKKKFEESPEEKKTTFYTLGGWKQSERKTEFVNAGKEVAAKRGIPQYNPDIGTPLGQRVLMPYQVSTTDTYVEGDDLHFVNNAAMQQMWDDIRRTVIVGLNHAHAVIEKRLGKEVTPETITHYLETVNHAMPGAAVVQEHMVETHPALVADSYVKVFTGNDEIADEIDPAFVIDINKQFPEDQAETLKAEVGDGIWQVVRIPTIVSRTCDGATTSRWSAMQIGMSMISAYKQAAGEAATGDFAYAAKHAEVIHMGTYLPV

>d1e6va2 d.58.31.2 (A:8-272) Alpha chain {Archaeon Methanopyrus kandleri}

LFMKALKEKFEESPEEKYTKFYIFGGWKQSERKKEFKEWADKIVEERGVPHYNPDIGVPLGQRKLMSYQVSGTDVFVEGDDLTFVNNAAMQQMWDDIRRTVIVGMDTAHRVLERRLGKEVTPETINEYMETLNHALPGGAVVQEHMVEIHPGLTWDCYAKIITGDLELADEIDDKFLIDIEKLFPEEQAEQLIKAIGNRTYQVCRMPTIVGHVCDGATMYRWAAMQIAMSFICAYKIAAGEAAVSDFAFASKHAEVINMGEMLPA

>d1e6ya2 d.58.31.2 (A:1002-1283) Alpha chain {Archaeon Methanosarcina barkeri}

AADIFSKFKKDMEVKFAQEFGSNKQTGGDITDKTAKFLRLGPEQDPRKVEMIKAGKEIAEKRGIAFYNPMMHSGAPLGQRAITPYTISGTDIVCEPDDLHYVNNAAMQQMWDDIRRTCIVGLDMAHETLEKRLGKEVTPETINHYLEVLNHAMPGAAVVQEMMVETHPALVDDCYVKVFTGDDALADEIDKQFLIDINKEFSEEQAAQIKASIGKTSWQAIHIPTIVSRTTDGAQTSRWAAMQIGMSFISAYAMCAGEAAVADLSFAAKHAALVSMGEMLPA

>d1hbnb2 d.58.31.2 (B:2-188) Beta chain {Archaeon Methanobacterium thermoautotrophicum}

AKFEDKVDLYDDRGNLVEEQVPLEALSPLRNPAIKSIVQGIKRTVAVNLEGIENALKTAKVGGPACKIMGRELDLDIVGNAESIAAAAKEMIQVTEDDDTNVELLGGGKRALVQVPSARFDVAAEYSAAPLVTATAFVQAIINEFDVSMYDANMVKAAVLGRYPQSVEYMGANIATMLDIPQKLEGP

>d1e6vb2 d.58.31.2 (B:7-189) Beta chain {Archaeon Methanopyrus kandleri}

DTVDLYDDRGNCVAEEVPIEVLSPMRNEAIQSIVNDIKRTVAVDLEGIENALQNATVGGKGMKIPGREMDVDIVDNAEAIADEIEKMIRVYQDDDTNVEPMYDGKRLLVQLPSERVKVMADPYSGTLQAGMAVVHAIIDVCEVDMWDANMVKAAVFGRYPQTIDYFGGNVASMLDVPMKQEGV

>d1e6yb2 d.58.31.2 (B:2002-2185) Beta chain {Archaeon Methanosarcina barkeri}

SDTVDIYDDRGKLLESNVDIMSLAPTRNAAIQSIIMDTKRSVAVNLAGIQGALASGKMGGKGRQILGRGLNYDIVGNADAIAENVKKLVQVDEGDDTNVIKVKGGKSLLIQSPKSRIIAGADFMSATTVGAAAVTQTIMDMFGTDPYDAPIVKSAVWGSYPQTMDLMGGQVQGILSIPQNNEGL

>d1e8ga1 d.58.32.1 (A:274-560) Vanillyl-alcohol oxidase {Fungus (Penicillium simplicissimum)}

GGYQSYLITLPKDGDLKQAVDIIRPLRLGMALQNVPTIRHILLDAAVLGDKRSYSSRTEPLSDEELDKIAKQLNLGRWNFYGALYGPEPIRRVLWETIKDAFSAIPGVKFYFPEDTPENSVLRVRDKTMQGIPTYDELKWIDWLPNGAHLFFSPIAKVSGEDAMMQYAVTKKRCQEAGLDFIGTFTVGMREMHHIVCIVFNKKDLIQKRKVQWLMRTLIDDCAANGWGEYRTHLAFMDQIMETYNWNNSSFLRFNEVLKNAVDPNGIIAPGKSGVWPSQYSHVTWKL

>d1diqa1 d.58.32.1 (A:243-521) Flavoprotein subunit of p-cresol methylhydroxylase {Pseudomonas putida}

PVFKPFEVIFEDEADIVEIVDALRPLRMSNTIPNSVVIASTLWEAGSAHLTRAQYTTEPGHTPDSVIKQMQKDTGMGAWNLYAALYGTQEQVDVNWKIVTDVFKKLGKGRIVTQEEAGDTQPFKYRAQLMSGVPNLQEFGLYNWRGGGGSMWFAPVSEARGSECKKQAAMAKRVLHKYGLDYVAEFIVAPRDMHHVIDVLYDRTNPEETKRADACFNELLDEFEKEGYAVYRVNTRFQDRVAQSYGPVKRKLEHAIKRAVDPNNILAPGRSGIDLNNDF

>d1f0xa1 d.58.32.2 (A:274-567) D-lactate dehydrogenase {Escherichia coli}

KNQQVFYIGTNQPEVLTEIRRHILANFENLPVAGEYMHRDIYDIAEKYGKDTFLMIDKLGTDKMPFFFNLKGRTDAMLEKVKFFRPHFTDRAMQKFGHLFPSHLPPRMKNWRDKYEHHLLLKMAGDGVGEAKSWLVDYFKQAEGDFFVCTPEEGSKAFLHRFAAAGAAIRYQAVHSDEVEDILALDIALRRNDTEWYEHLPPEIDSQLVHKLYYGHFMCYVFHQDYIVKKGVDVHALKEQMLELLQQRGAQYPAEHNVGHLYKAPETLQKFYRENDPTNSMNPGIGKTSKRKNW

>d1i19a1 d.58.32.3 (A:274-613) Cholesterol oxidase {Brevibacterium sterolicum}

FRQRCQSYTDIPWRELFAPKGADGRTFEKFVAESGGAEAIWYPFTEKPWMKVWTVSPTKPDSSNEVGSLGSAGSLVGKPPQAREVSGPYNYIFSDNLPEPITDMIGAINAGNPGIAPLFGPAMYEITKLGLAATNANDIWGWSKDVQFYIKATTLRLTEGGGAVVTSRANIATVINDFTEWFHERIEFYRAKGEFPLNGPVEIRCCGLDQAADVKVPSVGPPTISATRPRPDHPDWDVAIWLNVLGVPGTPGMFEFYREMEQWMRSHYNNDDATFRPEWSKGWAFGPDPYTDNDIVTNKMRATYIEGVPTTENWDTARARYNQIDPHRVFTNGFMDKLLP

>d1ftra1 d.58.33.1 (A:1-148) Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon Methanopyrus kandleri}

MEINGVEIEDTFAEAFEAKMARVLITAASHKWAMIAVKEATGFGTSVIMCPAEAGIDCGYVPPEETPDGRPGVTIMIGHNDEDELKEQLLDRIGQCVMTAPTASAFDAMPEAEKEDEDRVGYKLSFFGDGYQEEDELDGRKVWKIPVV

>d1ftra2 d.58.33.1 (A:149-296) Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon Methanopyrus kandleri}

EGEFIVEDSFGITTGVAGGNFYIMAESQPAGLQAAEAAVDAIKGVEGAYAPFPGGIVASASKVGSKQYDFLPASTNDAYCPTVEDNELPEGVKCVYEIVINGLNEEAVKEAMRVGIEAACQQPGVVKISAGNFGGKLGQYEIHLHDLF

>d1qd1a1 d.58.34.1 (A:2-180) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}

SQLVECVPNFSEGKNQEVIDAISRAVAQTPGCVLLDVDSGPSTNRTVYTFVGRPEDVVEGALNAARAAYQLIDMSRHHGEHPRMGALDVCPFIPVRGVTMDECVRCAQAFGQRLAEELGVPVYLYGEAARTAGRQSLPALRAGEYEALPEKLKQAEWAPDFGPSAFVPSWGATVAGARK

>d1qd1a2 d.58.34.1 (A:181-326) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}

FLLAFNINLLSTREQAHRIALDLREQGRGKDQPGRLKKVQAIGWYLDEKNLAQVSTNLLDFEVTGLHTVFEETCREAQELSLPVVGSQLVGLVPLKALLDAAAFYCEKENLFLLQDEHRIRLVVNRLGLDSLAPFKPKERIIEYLV

>d1dj0a1 d.58.35.1 (A:7-114) Pseudouridine synthase I {Escherichia coli}

PPVYKIALGIEYDGSKYYGWQRQNEVRSVQEKLEKALSQVANEPITVFCAGRTDAGVHGTGQVVHFETTALRKDAAWTLGVNANLPGDIAVRWVKTVPDDFHARFSAT

>d1dj0a2 d.58.35.1 (A:115-270) Pseudouridine synthase I {Escherichia coli}

ARRYRYIIYNHRLRPAVLSKGVTHFYEPLDAERMHRAAQCLLGENDFTSFRAVQCQSRTPWRNVMHINVTRHGPYVVVDIKANAFVHHMVRNIVGSLMEVGAHNQPESWIAELLAAKDRTLAAATAKAEGLYLVAVDYPDRYDLPKPPMGPLFLAD

>d1k8wa1 d.58.35.2 (A:9-73) Pseudouridine synthase II TruB {Escherichia coli}

MDINGVLLLDKPQGMSSNDALQKVKRIYNANRAGHTGALDPLATGMLPICLGEATKFSQYLLDSD

>d1k8wa2 d.58.35.2 (A:74-312) Pseudouridine synthase II TruB {Escherichia coli}

KRYRVIARLGQRTDTSDADGQIVEERPVTFSAEQLAAALDTFRGDIEQIPSMYSALKYQGKKLYEYARQGIEVPREARPITVYELLFIRHEGNELELEIHCSKGTYIRTIIDDLGEKLGCGAHVIYLRRLAVSKYPVERMVTLEHLRELVEQAEQQDIPAAELLDPLLMPMDSPASDYPVVNLPLTSSVYFKNGNPVRTSGAPLEGLVRVTEGENGKFIGMGEIDDEGRVAPRRLVVEY

>d1aop\_1 d.58.36.1 (81-145) Sulfite reductase, domains 1 and 3 {Escherichia coli}

LLRCRLPGGVITTKQWQAIDKFAGENTIYGSIRLTNRQTFQFHGILKKNVKPVHQMLHSVGLDAL

>d1aop\_2 d.58.36.1 (346-425) Sulfite reductase, domains 1 and 3 {Escherichia coli}

IGWVKGIDDNWHLTLFIENGRILDYPARPLKTGLLEIAKIHKGDFRITANQNLIIAGVPESEKAKIEKIAKESGLMNAVT

>d1bxya\_ d.59.1.1 (A:) Prokaryotic ribosomal protein L30 {Thermus thermophilus}

MPRLKVKLVKSPIGYPKDQKAALKALGLRRLQQERVLEDTPAIRGNVEKVAHLVRVEVVE

>d1jj2v\_ d.59.1.1 (V:) Archaeal L30 (L30a) {Archaeon Haloarcula marismortui}

MHALVQLRGEVNMHTDIQDTLEMLNIHHVNHCTLVPETDAYRGMVAKVNDFVAFGEPSQETLETVLATRAEPLEGDADVDDEWVAEHTDYDDISGLAFALLSEETTLREQGLSPTLRLHPPRGGHDGVKHPVKEGGQLGKHDTEGIDDLLEAMR

>d1fw9a\_ d.190.1.1 (A:) Chorismate lyase {Escherichia coli}

SHPALTQLRALRYSKEIPALDPQLLDWLLLEDSMTKRFEQQGKTVSVTMIREGFVEQNEIPEELPLLPKESRYWLREILLSADGEPWLAGRTVVPVSTLSGPELALQKLGKTPLGRYLFTSSTLTRDFIEIGRDAGLWGRRSRLRLSGKPLLLTELFLPASPLY

>d1bowa\_ d.60.1.1 (A:) Multidrug-binding domain of transcription activator BmrR {Bacillus subtilis}

RLGEVFVLDEEEIRIIQTEAEGIGPENVLNASYSKLKKFIESADGFTNNSYGATFSFQPYTSIDEMTYRHIFTPVLTNKQISSITPDMEITTIPKGRYACIAYNFSPEHYFLNLQKLIKYIADRQLTVVSDVYELIIPIHYSPKKQEEYRVEMKIRIL

>d1d5ya3 d.60.1.2 (A:122-294) Rob transcription factor, C-terminal domain {Escherichia coli}

EFTMPEHKFVTLEDTPLIGVTQSYSCSLEQISDFRHEMRYQFWHDFLGNAPTIPPVLYGLNETRPSQDKDDEQEVFYTTALAQDQADGYVLTGHPVMLQGGEYVMFTYEGLGTGVQEFILTVYGTCMPMLNLTRRKGQDIERYYPAEDAKAGDRPINLRCELLIPIRRKLAAA

>d1jh6a\_ d.61.1.1 (A:) tRNA splicing product Apprp cyclic nucleotide phosphodiesterase {Thale cress (Arabidopsis thaliana)}

MEEVKKDVYSVWALPDEESEPRFKKLMEALRSEFTGPRFVPHVTVAVSAYLTADEAKKMFESACDGLKAYTATVDRVSTGTFFFQCVFLLLQTTPEVMEAGEHCKNHFNCSTTTPYMPHLSLLYAELTEEEKKNAQEKAYTLDSSLDGLSFRLNRLALCKTDTEDKTLETWETVAVCNLNP

>d1f32a\_ d.62.1.1 (A:) Pepsin inhibitor-3 {Pig roundworm (Ascaris suum)}

FLFSMSTGPFICTVKDNQVFVANLPWTMLEGDDIQVGKEFAARVEDCTNVKHDMAPTCTKPPPFCGPQDMKMFNFVGCSVLGNKLFIDQKYVRDLTAKDHAEVQTFREKIAAFEEQQENQPPSSGMPHGAVPAGGLSPPPPPSFCTV

>d1d8ia\_ d.63.1.1 (A:) mRNA triphosphatase CET1 {Baker's yeast (Saccharomyces cerevisiae)}

HMYRNVPIWAQKWKPTIKALQSINVKDLKIDPSFLNIIPDDDLTKSVQDWVYATIYSIAPELRSFIELEMKFGVIIDAKGPDRVNPPVSSQCVFTELDAHLTPNIDASLFKELSKYIRGISEVTENTGKFSIIESQTRDSVYRVGLSTQRPRFLRMSTDIKTGRVGQFIEKRHVAQLLLYSPKDSYDVKISLNLELPVPDNDPPEKYKSQSPISERTKDRVSYIHNDSCTRIDITKVENHNQNSKSRQSETTHEVELEINTPALLNAFDNITNDSKEYASLIRTFLNNGTIIRRKLSSLSY

>d2if1\_\_ d.64.1.1 (-) Eukaryotic translation initiation factor eIF-1 (SUI1) {Human (Homo sapiens)}

MRGSHHHHHHTDPMSAIQNLHSFDPFADASKGDDLLPAGTEDYIHIRIQQRNGRKTLTTVQGIADDYDKKKLVKAFKKKFACNGTVIEHPEYGEVIQLQGDQRKNICQFLVEIGLAKDDQLKVHGF

>d1d1ra\_ d.64.1.1 (A:) YciH {Escherichia coli}

KGDGVVRIQRQTSGRKGKGVCLITGVDLDDAELTKLAAELKKKCGCGGAVKDGVIEIQGDKRDLLKSLLEAKGMKVKLAGGLE

>d1lbu\_2 d.65.1.1 (84-213) Zn2+ DD-carboxypeptidase, C-terminal, catalytic domain {Streptomyces albus G}

VNFTYAELNRCNSDWSGGKVSAATARANALVTMWKLQAMRHAMGDKPITVNGGFRSVTCNSNVGGASNSRHMYGHAADLGAGSQGFCALAQAARNHGFTEILGPGYPGHNDHTHVAGGDGRFWSAPSCGI

>d1vhh\_\_ d.65.1.2 (-) Sonic hedgehog {Mouse (Mus musculus)}

KLTPLAYKQFIPNVAEKTLGASGRYEGKITRNSERFKELTPNYNPDIIFKDEENTGADRLMTQRCKDKLNALAISVMNQWPGVKLRVTEGWDEDGHHSEESLHYEGRAVDITTSDRDRSKYGMLARLAVEAGFDWVYYESKAHIHCSVKAENSVAAK

>d1qf6a2 d.66.1.1 (A:2-62) Threonyl-tRNA synthetase (ThrRS), N-terminal 'additional' domain {Escherichia coli}

PVITLPDGSQRHYDHAVSPMDVALDIGPGLAKACIAGRVNGELVDACDLIENDAQLSIITA

>d1fjgd\_ d.66.1.2 (D:) Ribosomal protein S4 {Thermus thermophilus}

GRYIGPVCRLCRREGVKLYLKGERCYSPKCAMERRPYPPGQHGQKRARRPSDYAVRLREKQKLRRIYGISERQFRNLFEEASKKKGVTGSVFLGLLESRLDNVVYRLGFAVSRRQARQLVRHGHITVNGRRVDLPSYRVRPGDEIAVAEKSRNLELIRQNLEAMKGRKVGPWLSLDVEGMKGKFLRLPDREDLALPVQENLVIEFYSR

>d1c06a\_ d.66.1.2 (A:) Ribosomal protein S4 {Bacillus stearothermophilus}

MKLSEYGLQLQEKQKLRHMYGVNERQFRKTFEEAGKMPGKHGENFMILLESRLDNLVYRLGLARTRRQARQLVTHGHILVDGSRVNIPSYRVKPGQTIAVREKSRNLQVIKEALEANNYIPDYLSFDPEKMEGTYTRLPERSELPAEINEALIVEFYSR

>d1dm9a\_ d.66.1.3 (A:) Heat shock protein 15 kD {Escherichia coli}

PAVEVRLDKWLWAARFYKTRALAREMIEGGKVHYNGQRSKPSKIVELNATLTLRQGNDERTVIVKAITEQRRPASEAALLYEETAESVEKREKMALARKLNALT

>d1qf6a3 d.67.1.1 (A:63-241) Threonyl-tRNA synthetase (ThrRS), second 'additional' domain {Escherichia coli}

KDEEGLEIIRHSCAHLLGHAIKQLWPHTKMAIGPVIDNGFYYDVDLDRTLTQEDVEALEKRMHELAEKNYDVIKKKVSWHEARETFANRGESYKVSILDENIAHDDKPGLYFHEEYVDMCRGPHVPNMRFCHHFKLMKTAGAYWRGDSNNKMLQRIYGTAWADKKALNAYLQRLEEAAK

>d1f7ua3 d.67.2.1 (A:2-135) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Baker's yeast (Saccharomyces cerevisiae)}

ASTANMISQLKKLSIAEPAVAKDSHPDVNIVDLMRNYISQELSKISGVDSSLIFPALEWTNTMERGDLLIPIPRLRIKGANPKDLAVQWAEKFPCGDFLEKVEANGPFIQFFFNPQFLAKLVIPDILTRKEDYG

>d1iq0a3 d.67.2.1 (A:1-96) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Thermus thermophilus}

MLRRALEEAIAQALKEMGVPVRLKVARAPKDKPGDYGVPLFALAKELRKPPQAIAQELKDRLPLPEFVEEAVPVGGYLNFRLRTEALLREALRPKA

>d1dd5a\_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermotoga maritima}

VNPFIKEAKEKMKRTLEKIEDELRKMRTGKPSPAILEEIKVDYYGVPTPVNQLATISISEERTLVIKPWDKSVLSLIEKAINASDLGLNPINDGNVIRLVFPSPTTEQREKWVKKAKEIVEEGKIAIRNIRREILKKIKEDQKEGLIPEDDAKRLENEIQKLTDEFIEKLDEVFEIKKEEIMEF

>d1eh1a\_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermus thermophilus}

MTLKELYAETRSHMQKSLEVLEHNLAGLRTGRANPALLLHLKVEYYGAHVPLNQIATVTAPDPRTLVVQSWDQNALKAIEKAIRDSDLGLNPSNKGDALYINIPPLTEERRKDLVRAVRQYAEEGRVAIRNIRREALDKLKKLAKELHLSEDETKRAEAEIQKITDEFIAKADQLAEKKEQEILG

>d1ek8a\_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Escherichia coli}

MISDIRKDAEVRMDKCVEAFKTQISKIRTGRASPSLLDGIVVEYYGTPTPLRQLASVTVEDSRTLKINVFDRSMSPAVEKAIMASDLGLNPNSAGSDIRVPLPPLTEERRKDLTKIVRGEAEQARVAVRNVRRDANDKVKALLKDKEISEDDDRRSQDDVQKLTDAAIKKIEAALADKEAELMQF

>d1ge9a\_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Aquifex aeolicus}

MIKELEDIFKEAEKDMKKAVEYYKNEIAGLRTSRASTALVEEIKVEYYGSKVPIKQLGTISVPEHNQIVIQVWDQNAVPAIEKAIREELNLNPTVQGNVIRVTLPPLTEERRRELVRLLHKITEEARVRVRNVRREAKEMIEELEGISEDEKKRALERLQKLTDKYIDEINKLMEAKEKEIMSV

>d1j98a\_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Bacillus subtilis}

VESFELDHNAVVAPYVRHCGVHKVGTDGVVNKFDIRFCQPNKQAMKPDTIHTLEHLLAFTIRSHAEKYDHFDIIDISPMGCQTGYYLVVSGETTSAEIVDLLEDTMKEAVEITEIPAANEKQCGQAKLHDLEGAKRLMRFWLSQDKEELLKVFG

>d1inna\_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Deinococcus radiodurans}

NVESFDLDHTKVKAPYVRLAGVKTTPKGDQISKYDLRFLQPNQGAIDPAAIHTLEHLLAGYMRDHLEGVVDVSPMGCRTGMYMAVIGEPDEQGVMKAFEAALKDTAGHDQPIPGVSELECGNYRDHDLAAARQHARDVLDQGLKVQETILL

>d1j6wa\_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Haemophilus influenzae}

LLDSFKVDHTKMNAPAVRIAKTMLTPKGDNITVFDLRFCIPNKEILSPKGIHTLEHLFAGFMRDHLNGDSIEIIDISPMGCRTGFYMSLIGTPNEQKVSEAWLASMQDVLGVQDQASIPELNIYQCGSYTEHSLEDAHEIAKNVIARGIGVNKNEDLSLDN

>d1j6xa\_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Helicobacter pylori}

MKMNVESFNLDHTKVKAPYVRIADRKKGVNGDLIVKYDVRFKQPNRDHMDMPSLHSLEHLVAEIIRNHANYVVDWSPMGCQTGFYLTVLNHDNYTEILEVLEKTMQDVLKAKEVPASNEKQCGWAANHTLEGAQNLARAFLDKRAEWSEVG

>d1hr6b1 d.185.1.1 (B:24-245) Mitochondrial processing peptidase (MPP) beta chain {Baker's yeast (Saccharomyces cerevisiae)}

PGTRTSKLPNGLTIATEYIPNTSSATVGIFVDAGSRAENVKNNGTAHFLEHLAFKGTQNRPQQGIELEIENIGSHLNAYTSRENTVYYAKSLQEDIPKAVDILSDILTKSVLDNSAIERERDVIIRESEEVDKMYDEVVFDHLHEITYKDQPLGRTILGPIKNIKSITRTDLKDYITKNYKGDRMVLAGAGAVDHEKLVQYAQKYFGHVPKSESPVPLGSPR

>d1hr6b2 d.185.1.1 (B:246-462) Mitochondrial processing peptidase (MPP) beta chain {Baker's yeast (Saccharomyces cerevisiae)}

GPLPVFCRGERFIKENTLPTTHIAIALEGVSWSAPDYFVALATQAIVGNWDRAIGTGTNSPSPLAVAASQNGSLANSYMSFSTSYADSGLWGMYIVTDSNEHNVRLIVNEILKEWKRIKSGKISDAEVNRAKAQLKAALLLSLDGSTAIVEDIGRQVVTTGKRLSPEEVFEQVDKITKDDIIMWANYRLQNKPVSMVALGNTSTVPNVSYIEEKLNQ

>d1hr6a1 d.185.1.1 (A:14-233) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}

ARTDNFKLSSLANGLKVATSNTPGHFSALGLYIDAGSRFEGRNLKGCTHILDRLAFKSTEHVEGRAMAETLELLGGNYQCTSSRENLMYQASVFNQDVGKMLQLMSETVRFPKITEQELQEQKLSAEYEIDEVWMKPELVLPELLHTAAYSGETLGSPLICPRGLIPSISKYYLLDYRNKFYTPENTVAAFVGVPHEKALELTGKYLGDWQSTHPPITKK

>d1hr6a2 d.185.1.1 (A:234-470) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}

VAQYTGGESCIPPAPVFGNLPELFHIQIGFEGLPIDHPDIYALATLQTLLGGGGSFSAGGPGKGMYSRLYTHVLNQYYFVENCVAFNHSYSDSGIFGISLSCIPQAAPQAVEVIAQQMYNTFANKDLRLTEDEVSRAKNQLKSSLLMNLESKLVELEDMGRQVLMHGRKIPVNEMISKIEDLKPDDISRVAEMIFTGNVNNAGNGKGRATVVMQGDRGSFGDVENVLKAYGLGNSSS

>d1be3a1 d.185.1.1 (A:1-233) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}

TATYAQALQSVPETQVSQLDNGLRVASEQSSQPTCTVGVWIDAGSRYESEKNNGAGYFVEHLAFKGTKNRPGNALEKEVESMGAHLNAYSTREHTAYYIKALSKDLPKAVELLADIVQNCSLEDSQIEKERDVILQELQENDTSMRDVVFNYLHATAFQGTPLAQSVEGPSENVRKLSRADLTEYLSRHYKAPRMVLAAAGGLEHRQLLDLAQKHFSGLSGTYDEDAVPTLSP

>d1be3a2 d.185.1.1 (A:234-446) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}

CRFTGSQICHREDGLPLAHVAIAVEGPGWAHPDNVALQVANAIIGHYDCTYGGGAHLSSPLASIAATNKLCQSFQTFNICYADTGLLGAHFVCDHMSIDDMMFVLQGQWMRLCTSATESEVLRGKNLLRNALVSHLDGTTPVCEDIGRSLLTYGRRIPLAEWESRIAEVDARVVREVCSKYFYDQCPAVAGFGPIEQLPDYNRIRSGMFWLRF

>d1bcca1 d.185.1.1 (A:4-232) Cytochrome bc1 core subunit 1 {Chicken (Gallus gallus)}

YAQALQSVPETQVSQLDNGVRVASEQSSQPTCTVGVWIDAGSRYESEKNNGAGYFLEHLAFKGTKNRPQNALEKEVESMGAHLNAYSSREHTAYYIKALSKDVPKAVELLADIVQNCSLEDSQIEKERDVIVRELQENDTSMREVVFNYLHATAFQGTGLAQSVEGPSENIRKLSRADLTEYLSTHYTAPRMVLAAAGGVEHQQLLELAQKHFGGVPFTYDDDAVPTLS

>d1bcca2 d.185.1.1 (A:233-445) Cytochrome bc1 core subunit 1 {Chicken (Gallus gallus)}

KCRFTGSQIRHREDGLPLAHVAIAVEGPGWAHPDLVALQVANAIIGHYDRTYGGGLHSSSPLASIAVTNKLCQSFQTFSICYSETGLFGFYFVCDRMSIDDMMFVLQGQWMRLCTSISESEVLRGKNFLRNALVSHLDGTTPVCEDIGRELLTYGRRIPLEEWEERLAEVDARMVREVCSKYIYDQCPAVAGPGPIEQLPDYNRIRSGMFWLR

>d1ezva1 d.185.1.1 (A:27-239) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}

AEVTQLSNGIVVATEHNPAHTASVGVVFGSGAANENPYNNGVSNLWKNIFLSKENSAVAAKEGLALSSNISRDFQSYIVSSLPGSTDKSLDFLNQSFIQQKANLLSSSNFEATKKSVLKQVQDFEDNDHPNRVLEHLHSTAFQNTPLSLPTRGTLESLENLVVADLESFANNHFLNSNAVVVGTGNIKHEDLVNSIESKNLSLQTGTKPVLKK

>d1ezva2 d.185.1.1 (A:240-456) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}

KAAFLGSEVRLRDDTLPKAWISLAVEGEPVNSPNYFVAKLAAQIFGSYNAFEPASRLQGIKLLDNIQEYQLCDNFNHFSLSYKDSGLWGFSTATRNVTMIDDLIHFTLKQWNRLTISVTDTEVERAKSLLKLQLGQLYESGNPVNDANLLGAEVLIKGSKLSLGEAFKKIDAITVKDVKAWAGKRLWDQDIAIAGTGQIEGLLDYMRIRSDMSMMRW

>d1be3b1 d.185.1.1 (B:21-235) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}

PQDLEFTRLPNGLVIASLENYAPASRIGLFIKAGSRYENSNNLGTSHLLRLASSLTTKGASSFKITRGIEAVGGKLSVTSTRENMAYTVECLRDDVDILMEFLLNVTTAPEFRRWEVAALQPQLRIDKAVALQNPQAHVIENLHAAAYRNALANSLYCPDYRIGKVTPVELHDYVQNHFTSARMALIGLGVSHPVLKQVAEQFLNIRGGLGLSGA

>d1be3b2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}

KAKYHGGEIREQNGDSLVHAALVAESAAIGSAEANAFSVLQHVLGAGPHVKRGSNATSSLYQAVAKGVHQPFDVSAFNASYSDSGLFGFYTISQAASAGDVIKAAYNQVKTIAQGNLSNPDVQAAKNKLKAGYLMSVESSEGFLDEVGSQALAAGSYTPPSTVLQQIDAVADADVINAAKKFVSGRKSMAASGNLGHTPFIDEL

>d1bccb1 d.185.1.1 (B:18-235) Cytochrome bc1 core subunit 2 {Chicken (Gallus gallus)}

PPHPQDLEITKLPNGLVIASLENYSPGSTIGVFIKAGSRYENSSNLGTSHLLRLASSLTTKGASSFKITRGIEAVGGKLSVESTRENMAYTVECLRDDVEILMEFLLNVTTAPEFRPWEVADLQPQLKIDKAVAFQNPQTHVIENLHAAAYRNALADSLYCPDYRIGKVTSVELHDFVQNHFTSARMALVGLGVSHPVLKNVAEQLLNIRGGLGLSGA

>d1bccb2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Chicken (Gallus gallus)}

KAKYRGGEIREQNGDSLVHAAIVAESAAIGGAEANAFSVLQHVLGANPHVKRGLNATSSLYQAVAKGVHQPFDVSAFNASYSDSGLFGFYTISQAAYAGQVIKAAYNQVKTIAQGNVSNENVQAAKNKLKAKYLMSVESSEGFLEEVGSQALAAGSYNPPSTVLQQIDAVADADVIKAAKKFVSRQKSMAASGNLGHTPFVDEL

>d1ezvb1 d.185.1.1 (B:17-218) Cytochrome bc1 core subunit 2 {Baker's yeast (Saccharomyces cerevisiae)}

LTVSARDAPTKISTLAVKVHGGSRYATKDGVAHLLNRFNFQNTNTRSALKLVRESELLGGTFKSTLDREYITLKATFLKDDLPYYVNALADVLYKTAFKPHELTESVLPAARYDYAVAEQCPVKSAEDQLYAITFRKGLGNPLLYDGVERVSLQDIKDFADKVYTKENLEVSGENVVEADLKRFVDESLLSTLPAGKSLVSK

>d1ezvb2 d.185.1.1 (B:219-368) Cytochrome bc1 core subunit 2 {Baker's yeast (Saccharomyces cerevisiae)}

SEPKFFLGEENRVRFIGDSVAAIGIPVNKASLAQYEVLANYLTSALSELSGLISSAKLDKFTDGGLFTLFVRDQDSAVVSSNIKKIVADLKKGKDLSPAINYTKLKNAVQNESVSSPIELNFDAVKDFKLGKFNYVAVGDVSNLPYLDEL

>d1tig\_\_ d.68.1.1 (-) Translation initiation factor IF3, C-terminal domain {Bacillus stearothermophilus}

INVKEVRLSPTIEEHDFNTKLRNARKFLEKGDKVKATIRFKGRAITHKEIGQRVLDRLSEACADIAVVETAPKMDGRNMFLVLAPKND

>d2ifea\_ d.68.1.1 (A:) Translation initiation factor IF3, C-terminal domain {Escherichia coli}

VIQVKEIKFRPGTDEGDYQVKLRSLIRFLEEGDKAKITLRFRGREMAHQQIGMEVLNRVKDDLQELAVVESFPTKIEGRQMIMVLAPKKKQ

>d1i96v\_ d.68.1.1 (V:) Translation initiation factor IF3, C-terminal domain {Thermus thermophilus}

EVKSIKFRVKIDEHDYQTKLGHIKRFLQEGHKVKVTIMFRGREVAHPELGERILNRVTEDLKDLAVVEMKPEMLGRDMNMLLAPVK

>d1dcja\_ d.68.3.1 (A:) SirA {Escherichia coli}

MTDLFSSPDHTLDALGLRCPEPVMMVRKTVRNMQPGETLLIIADDPATTRDIPGFCTFMEHELVAKETDGLPYRYLIRKGG

>d1jdqa\_ d.68.3.2 (A:) Hypothetical protein TM0983 {Thermotoga maritima}

GSSHHHHHHSSGLVPRGSHMAKYQVTKTLDVRGEVCPVPDVETKRALQNMKPGEILEVWIDYPMSKERIPETVKKLGHEVLEIEEVGPSEWKIYIKVK

>d1qmha2 d.68.2.1 (A:5-184,A:280-338) RNA 3'-terminal phosphate cyclase, RPTC {Escherichia coli}

MIALDGAQGEGGGQILRSALSLSMITGQPFTITSIRAGRAKPGLLRQHLTAVKAATEICGATVEGAELGSQRLLFRPGTVRGGDYRFAIGSAGSCTLVLQTVLPALWFADGPSRVEVSGGTDNPSAPPADFIRRVLEPLLAKIGIHQQTTLLRHGFYPAGGGVVATEVSPVASFNTLQLGXAVGEYLADQLVLPMALAGAGEFTVAHPSCHLLTNIAVVERFLPVRFSLIETDGVTRVSI

>d1uae\_\_ d.68.2.2 (-) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT, MurA, MurZ) {Escherichia coli}

MDKFRVQGPTKLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVDTSMKLLSQLGAKVERNGSVHIDARDVNVFCAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCTIGARPVDLHISGLEQLGATIKLEEGYVKASVDGRLKGAHIVMDKVSVGATVTIMCAATLAEGTTIIENAAREPEIVDTANFLITLGAKISGQGTDRIVIEGVERLGGGVYRVLPDRIETGTFLVAAAISRGKIICRNAQPDTLDAVLAKLRDAGADIEVGEDWISLDMHGKRPKAVNVRTAPHPAFPTDMQAQFTLLNLVAEGTGFITETVFENRFMHVPELSRMGAHAEIESNTVICHGVEKLSGAQVMATDLRASASLVLAGCIAEGTTVVDRIYHIDRGYERIEDKLRALGANIERVKG

>d1ejda\_ d.68.2.2 (A:) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT, MurA, MurZ) {Enterobacter cloacae}

MDKFRVQGPTRLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLTQLGTKVERXGSVWIDASNVNNFSAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCAIGARPVDLHIFGLEKLGAEIKLEEGYVKASVNGRLKGAHIVMDKVSVGATVTIMSAATLAEGTTIIENAAREPEIVDTANFLVALGAKISGQGTDRITIEGVERLGGGVYRVLPDRIETGTFLVAAAISGGKIVCRNAQPDTLDAVLAKLREAGADIETGEDWISLDMHGKRPKAVTVRTAPHPAFPTDMQAQFTLLNLVAEGTGVITETIFENRFMHVPELIRMGAHAEIESNTVICHGVEKLSGAQVMATDLRASASLVLAGCIAEGTTVVDRIYHIDRGYERIEDKLRALGANIERVKGE

>d1g6sa\_ d.68.2.2 (A:) 5-enol-pyruvyl shikimate-3-phosphate(EPSP) synthase {Escherichia coli}

MESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDDVRHMLNALTALGVSYTLSADRTRCEIIGNGGPLHAEGALELFLGNAGTAMRPLAAALCLGSNDIVLTGEPRMKERPIGHLVDALRLGGAKITYLEQENYPPLRLQGGFTGGNVDVDGSVSSQFLTALLMTAPLAPEDTVIRIKGDLVSKPYIDITLNLMKTFGVEIENQHYQQFVVKGGQSYQSPGTYLVEGDASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDYISCTRGELNAIDMDMNHIPDAAMTIATAALFAKGTTTLRNIYNWRVKETDRLFAMATELRKVGAEVEEGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILDPKCTAKTFPDYFEQLARISQAA

>d1imua\_ d.204.1.1 (A:) Ribosome binding protein Y (HI0257, YfiA homologue) {Haemophilus influenzae}

MTLNITSKQMDITPAIREHLEERLAKLGKWQTQLISPHFVLNKVPNGFSVEASIGTPLGNLLASATSDDMYKAINEVEEKLERQLNKLQHKSESRRADERLKDSFEN

>d1tola2 d.69.1.1 (A:125-216) C-terminal domain of TolA {Escherichia coli}

SGADINNYAGQIKSAIESKFYDASSYAGKTCTLRIKLAPDGMLLDIKPEGGDPALCQAALAAAKLAKIPKPPSQAVYEVFKNAPLDFKPAAA

>d1kpta\_ d.70.1.1 (A:) Virally encoded KP4 toxin {Ustilago maydis, P4 strain}

LGINCRGSSQCGLSGGNLMVRIRDQACGNQGQTWCPGERRAKVCGTGNSISAYVQSTNNCISGTEACRHLTNLVNHGCRVCGSDPLYAGNDVSRGQLTVNYVNSC

>g1kve.1 d.70.1.2 (A:,B:) SMK toxin {Halotolerant yeast (Pichia farinosa)}

WSLRWRMQKSTTIAAIAGCSGAATFGGLAGGIVGCIAAGILAILQGFEVNWHNGGGGDRSNPVXGEATTIWGVGADEAIDKGTPSKNDLQNMSADLAKNGFKGHQGVACSTVKDGNKDVYMIKFSLAGGSNDPGGSPCSDD

>d1ev0a\_ d.71.1.1 (A:) Cell division protein MinE topological specificity domain {Escherichia coli}

RSDAEPHYLPQLRKDILEVICKYVQIDPEMVTVQLEQKDGDISILELNVTLPEAEELK

>d1dw9a2 d.72.1.1 (A:87-156) Cyanase C-terminal domain {Escherichia coli}

RIPTDPTMYRFYEMLQVYGTTLKALVHEKFGDGIISAINFKLDVKKVADPEGGERAVITLDGKYLPTKPF

>d3rubs\_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}

MQVWPPINKKKYETLSYLPDLSQEQLLSEVEYLLKNGWVPCLEFETEHGFVYRENNKSPGYYDGRYWTMWKLPMFGCTDATQVLAEVEEAKKAYPQAWIRIIGFDNVRQVQCISFIAYKPEGY

>d1burs\_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

MQVWPILGMKKYETLSYLPPLTTEQLLAEVNYLLVNNWIPCLEFEVKDGFVYREHLKSPGYYDGRYWTMWKLPMFGCTDPAQVLNELEECKKAYPDAFIRIIGFDNKRQVQCISFIAYKPAGY

>d8ruci\_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

MQVWPILNLKKYETLSYLPPLTTDQLARQVDYLLNNKWVPCLEFETDHGFVYREHHNSPGYYDGRYWTMWKLPMFGCTDPAQVLNELEECKKEYPNAFIRIIGFDSNREVQCISFIAYKPAGY

>d1bwvs\_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

VRITQGTFSFLPDLTDEQIKKQIDYMISKKLAIGIEYTNDIHPRNAYWEIWGLPLFDVTDPAAVLFEINACRKARSNFYIKVVGFSSVRGIESTIISFIVNRPKHEPGFNLMRQEDKSRSIKYTIHSYESYKPEDERY

>d1gk8i\_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}

MVWTPVNNKMFETFSYLPPLTDEQIAAQVDYIVANGWIPCLEFAEADKAYVSNESAIRFGSVSCLYYDNRYWTMWKLPMFGCRDPMQVLREIVACTKAFPDAYVRLVAFDNQKQVQIMGFLVQRP

>d1bxni\_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}

MRITQGTFSFLPELTDEQITKQLEYCLNQGWAVGLEYTDDPHPRNTYWEMFGLPMFDLRDAAGILMEINNARNTFPNHYIRVTAFDSTHTVESVVMSFIVNRPADEPGFRLVRQEEPGRTLRYSIESYA

>d1rblm\_ d.73.1.1 (M:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}

SMKTLPKERRFETFSYLPPLSDRQIAAQIEYMIEQGFHPLIEFNEHSNPEEFYWTMWKLPLFACAAPQQVLDEVRECRSEYGDCYIRVAGFDNIKECQTSSFIVHRPGR

>d1dcpa\_ d.74.1.1 (A:) Pterin-4a-carbinolamine dehydratase (PCD)/dimerization cofactor of HNF1 (DCoH) {Rat (Rattus norvegicus)}

HRLSAEERDQLLPNLRAVGWNELEGRDAIFKQFHFKDFNRAFGFMTRVALQAEKLDHHPEWFNVYNKVHITLSTHECAGLSERDINLASFIEQVAVSMT

>d1xxaa\_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Escherichia coli}

LKNLVLDIDYNDAVVVIHTSPGAAQLIARLLDSLGKAEGILGTIAGDDTIFTTPANGFTVKDLYEAILELF

>d1b4ba\_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Bacillus stearothermophilus}

ALVDVFIKLDGTGNLLVLRTLPGNAHAIGVLLDNLDWDEIVGTICGDDTCLIICRTPKDAKKVSNQLLSML

>d1f9na2 d.74.2.1 (A:79-149) C-terminal domain of arginine repressor {Bacillus subtilis}

ALMDAFVKIDSASHMIVLKTMPGNAQAIGALMDNLDWDEMMGTICGDDTILIICRTPEDTEGVKNRLLELL

>d1i50k\_ d.74.3.2 (K:) RPB11 {Baker's yeast (Saccharomyces cerevisiae)}

MNAPDRFELFLLGEGESKLKIDPDTKAPNAVVITFEKEDHTLGNLIRAELLNDRKVLFAAYKVEHPFFARFKLRIQTTEGYDPKDALKNACNSIINKLGALKTNFETEWNLQTL

>d1bdfa1 d.74.3.1 (A:2-52,A:179-232) RNA polymerase alpha {Escherichia coli}

QGSVTEFLKPRLVDIEQVSSTHAKVTLEPLERGFGHTLGNALRAILLSSMPXPVERIAYNVEAARVEQRTDLDKLVIEMETNGTIDPEEAIRRAATILAEQLEAFV

>d1i6va1 d.74.3.1 (A:6-49,A:173-229) RNA polymerase alpha {Thermus aquaticus}

LKAPVFTATTQGDHYGEFVLEPLERGFGVTLGNPLRRILLSSIPXPVRRVAFQVEDTRLGQRTDLDKLTLRIWTDGSVTPLEALNQAVAILKEHLNYFANPE

>d1i50c1 d.74.3.1 (C:3-41,C:173-268) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

EEGPQVKIREASKDNVDFILSNVDLAMANSLRRVMIAEIXAAAIEFEYDPWNKLKHTDYWYEQDSAKEWPQSKNCEYEDPPNEGDPFDYKAQADTFYMNVESVGSIPVDQVVVRGIDTLQKKVASILLALTQMDQD

>d1c0aa2 d.74.4.1 (A:288-420) Prokaryotic AspRS, insert domain {Escherichia coli}

NPMELTDVADLLKSVEFAVFAGPANDPKGRVAALRVPGGASLTRKQIDEYGNFVKIYGAKGLAYIKVNERAKGLEGINSPVAKFLNAEIIEDILDRTAAQDGDMIFFGADNKKIVADAMGALRLKVGKDLGLT

>d1g51a2 d.74.4.1 (A:295-414) Prokaryotic AspRS, insert domain {Thermus thermophilus}

FGLELKEVGPLFRQSGFRVFQEAESVKALALPKALSRKEVAELEEVAKRHKAQGLAWARVEEGGFSGGVAKFLEPVREALLQATEARPGDTLLFVAGPRKVAATALGAVRLRAADLLGLK

>d1a79a2 d.75.1.1 (A:9-82) tRNA splicing endonuclease EdnA, N-terminal domain {Archaeon Methanococcus jannaschii}

KITGLLDGDRVIVFDKNGISKLSARHYGNVEGNFLSLSLVEALYLINLGWLEVKYKDNKPLSFEELYEYARNVE

>d1ewqa4 d.75.2.1 (A:1-120) DNA repair protein MutS, domain I {Thermus aquaticus}

MEGMLKGEGPGPLPPLLQQYVELRDQYPDYLLLFQVGDFYECFGEDAERLARALGLVLTHKTSKDFTTPMAGIPLRAFEAYAERLLKMGFRLAVADQVEPAEEAEGLVRREVTQLLTPGT

>d1e3ma4 d.75.2.1 (A:2-116) DNA repair protein MutS, domain I {Escherichia coli}

SAIENFDAHTPMMQQYLRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPIPMAGIPYHAVENYLAKLVNQGESVAICEQIGDPATSKGPVERKVVRIVTP

>d1e3mb4 d.75.2.1 (B:14-116) DNA repair protein MutS, domain I {Escherichia coli}

MQQYLRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPIPMAGIPYHAVENYLAKLVNQGESVAICEQIGDPATSKGPVERKVVRIVTP

>d1gyfa\_ d.76.1.1 (A:) GYF domain from cd2bp2 protein {Human (Homo sapiens)}

DVMWEYKWENTGDAELYGPFTSAQMQTWVSEGYFPDGVYCRKLDPPGGQFYNSKRIDFDLYT

>d1jg5a\_ d.205.1.1 (A:) GTP cyclohydrolase I feedback regulatory protein, GFRP {Rat (Rattus norvegicus)}

PYLLISTQIRMEVGPTMVGDEHSDPELMQQLGASKRRVLGNNFYEYYVNDPPRIVLDKLECRGFRVLSMTGVGQTLVWCLHKE

>d1iq4a\_ d.77.1.1 (A:) Ribosomal protein L5 {Bacillus stearothermophilus}

MNRLKEKYLNEVVPALMSKFNYKSIMQVPKIEKIVINMGVGDAVQNPKALDSAVEELTLIAGQRPVVTRAKKSIAGFRLRQGMPIGAKVTLRGERMYEFLDKLISVSLPRARDFRGVSKKSFDGRGNYTLGIKEQLIFPEIDYDKVNKVRGMDIVIVTTANTDEEARELLALLGMPFQK

>d1jj2d\_ d.77.1.1 (D:) Ribosomal protein L5 {Archaeon Haloarcula marismortui}

FHEMREPRIEKVVVHMGIGHGGRDLANAEDILGEITGQMPVRTKAKRTVGEFDIREGDPIGAKVTLRDEMAEEFLQTALPLAELATSQFDDTGNFSFGVEEHTEFPSQEYDPSIGIYGLDVTVNLVRPGYRVAKRDKASRSIPTKHRLNPADAVAFIESTYDVEV

>d1eika\_ d.78.1.1 (A:) RNA polymerase subunit RBP5 (RNA polymerase subunit H) {Archaeon Methanobacterium thermoautotrophicum}

MKREILKHQLVPEHVILNESEAKRVLKELDAHPEQLPKIKTTDPVAKAIGAKRGDIVKIIRKSPTAEEFVTYRLVQD

>d1hmja\_ d.78.1.1 (A:) RNA polymerase subunit RBP5 (RNA polymerase subunit H) {Archaeon Methanococcus jannaschii}

PKHEIVPKEEVEEILKRYNIKIQQLPKIYEDDPVIQEIGAKEGDVVRVIRKSPTAGVSIAYRLVIKRI

>d1dzfa2 d.78.1.1 (A:144-215) Eukaryotic RPB5 C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

ITHHELVPKHIRLSSDEKRELLKRYRLKESQLPRIQRADPVALYLGLKRGEVVKIIRKSETSGRYASYRICM

>d1qkla\_ d.78.1.2 (A:) RPB6 {Human (Homo sapiens)}

MSDNEDNFDGDDFDDVEEDEGLDDLENAEEEGQENVEILPSGERPQANQKRITTPYMTKYERARVLGTRALQIAMCAPVMVELEGETDPLLIAMKELKARKIPIIIRRYLPDGSYEDWGVDELIITD

>d1i50f\_ d.78.1.2 (F:) RPB6 {Baker's yeast (Saccharomyces cerevisiae)}

KAIPKDQRATTPYMTKYERARILGTRALQISMNAPVFVDLEGETDPLRIAMKELAEKKIPLVIRRYLPDGSFEDWSVEELIVDL

>d1qu9a\_ d.79.1.1 (A:) Conserved 'hypothetical' protein YjgF {Escherichia coli}

SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPKTGEVPADVAAQARQSLDNVKAIVEAAGLKVGDIVKTTVFVKDLNDFATVNATYEAFFTEHNATFPARSCVEVARLPKDVKIEIEAIAVRR

>d1qd9a\_ d.79.1.1 (A:) Purine regulatory protein YabJ {Bacillus subtilis}

TKAVHTKHAPAAIGPYSQGIIVNNMFYSSGQIPLTPSGEMVNGDIKEQTHQVFSNLKAVLEEAGASFETVVKATVFIADMEQFAEVNEVYGQYFDTHKPARSCVEVARLPKDALVEIEVIALVK

>d1jd1a\_ d.79.1.1 (A:) Highdosage growth inhibitor YER057cp (YEO7\_YEAST) {Baker's yeast (Saccharomyces cerevisiae)}

TTLTPVICESAPAAAASYSHAMKVNNLIFLSGQIPVTPDNKLVEGSIADKAEQVIQNIKNVLEASNSSLDRVVKVNIFLADINHFAEFNSVYAKYFNTHKPARSCVAVAALPLGVDMEMEAIAAER

>d1dbfa\_ d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}

MMIRGIRGATTVERDTEEEILQKTKQLLEKIIEENHTKPEDVVQMLLSATPDLHAVFPAKAVRELSGWQYVPVTCMQEMDVTGGLKKCIRVMMTVQTDVPQDQIRHVYLEKAVVLRPDLSLTKNTEL

>d1fnja\_ d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}

MIRGIRGATTVERDTEEEILQKTKQLLEKIIEENHTKPEDVVQMLLSATPDLHAVFPAKAVRELSGWQYVPVTCMQEMDVTGGLKKSIKVMMTVQTDVPQDQIRHVYLEKAVVLR

>d1jy8a\_ d.79.5.1 (A:) 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF {Escherichia coli}

MRIGHGFDVHAFGGEGPIIIGGVRIPYEKGLLAHSDGDVALHALTDALLGAAALGDIGKLFPDTDPAFKGADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMRVFIAEDLGCHMDDVNVKATTTEKLGFTGRGEGIACEAVALLI

>d1fsz\_2 d.79.2.1 (232-356) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}

INVDFADVKAVMNNGGLAMIGIGESDSEKRAKEAVSMALNSPLLDVDIDGATGALIHVMGPEDLTLEEAREVVATVSSRLDPNATIIWGATIDENLENTVRVLLVITGVQSRIEFTDTGLKRKKL

>d1tuba2 d.79.2.1 (A:246-440) Tubulin alpha-subunit {Pig (Sus scrofa)}

GALNVDLTEFQTNLVPYPRGHFPLATYAPVISAEKAYHEQLSVAEITNACFEPANQMVKCDPRHGKYMACCLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYEPPTVVPGGDLAKVQRAVCMLSNTTAIAEAWARLDHKFDLMYAKRAFVHWYVGEGMEEGEFSEAREDMAALEKDYEEVGVDSV

>d1tubb2 d.79.2.1 (B:246-437) Tubulin beta-subunit {Pig (Sus scrofa)}

GQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDAKNMMAACDPRHGRYLTVAAVFRGRMSMKEVDEQMLNVQNKNSSYFVEWIPNNVKTAVCDIPPRGLKMSATFIGNSTAIQELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSEYQQYQD

>d1ck9a\_ d.79.3.1 (A:) Eukaryotic ribosomal protein L30 (L30e) {Baker's yeast (Saccharomyces cerevisiae)}

APVKSQESINQKLALVIKSGKYTLGYKSTVKSLRQGKSKLIIIAANTPVLRKSELEYYAMLSKTKVYYFQGGNNELGTAVGKLFRVGVVSILEAGDSDILTTLA

>d1jj2f\_ d.79.3.1 (F:) Ribosomal protein L7ae {Archaeon Haloarcula marismortui}

PVYVDFDVPADLEDDALEALEVARDTGAVKKGTNETTKSIERGSAELVFVAEDVQPEEIVMHIPELADEKGVPFIFVEQQDDLGHAAGLEVGSAAAAVTDAGAAATVLEEIADKVEELR

>d1e7ka\_ d.79.3.1 (A:) Spliceosomal 15.5kd protein {Human (Homo sapiens)}

ADVNPKAYPLADAHLTKKLLDLVQQSCNYKQLRKGANEATKTLNRGISEFIVMAADAEPLEIILHLPLLCEDKNVPYVFVRSKQALGRACGVSRPVIACSVTIKEGSQLKQQIQSIQQSIERLLV

>d1dt9a2 d.79.3.2 (A:277-422) C-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 {Human (Homo sapiens)}

NVKFIQEKKLIGRYFDEISQDTGKYCFGVEDTLKALEMGAVEILIVYENLDIMRYVLHCQGTEEEKILYLTPEQEKDKSHFTDKETGQEHELIESMPLLEWFANNYKKFGATLEIVTDKSQEGSQFVKGFGGIGGILRYRVDFQGM

>d1clia1 d.79.4.1 (A:5-170) Aminoimidazole ribonucleotide synthetase (PurM) N-terminal domain {Escherichia coli}

TSLSYKDAGVDIDAGNALVGRIKGVVKKTRRPEVMGGLGGFGALCALPQKYREPVLVSGTDGVGTKLRLAMDLKRHDTIGIDLVAMCVNDLVVQGAEPLFFLDYYATGKLDVDTASAVISGIAEGCLQSGCSLVGGETAEMPGMYHGEDYDVAGFCVGVVEKSEII

>d1clib1 d.79.4.1 (B:1021-1170) Aminoimidazole ribonucleotide synthetase (PurM) N-terminal domain {Escherichia coli}

ALVGRIKGVVKKTRRPEVMGGLGGFGALCALPQKYREPVLVSGTDGVGTKLRLAMDLKRHDTIGIDLVAMCVNDLVVQGAEPLFFLDYYATGKLDVDTASAVISGIAEGCLQSGCSLVGGETAEMPGMYHGEDYDVAGFCVGVVEKSEII

>d1otfa\_ d.80.1.1 (A:) 4-oxalocrotonate tautomerase {Pseudomonas sp., DmpI}

PIAQLYIIEGRTDEQKETLIRQVSEAMANSLDAPLERVRVLITEMPKNHFGIGGEPASK

>d1bjpa\_ d.80.1.1 (A:) 4-oxalocrotonate tautomerase {Pseudomonas putida, XylH}

PIAQIHILEGRSDEQKETLIREVSEAISRSLDAPLTSVRVIITEMAKGHFGIGGELASKVRR

>d1otga\_ d.80.1.2 (A:) 5-carboxymethyl-2-hydroxymuconate isomerase (CHMI) {Escherichia coli}

PHFIVECSDNIREEADLPGLFAKVNPTLAATGIFPLAGIRSRVHWVDTWQMADGQHDYAFVHMTLKIGAGRSLESRQQAGEMLFELIKTHFAALMESRLLALSFEIEELHPTLNFKQNNVHALFK

>d1gd0a\_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Human (Homo sapiens)}

PMFIVNTNVPRASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGGSSEPCALCSLHSIGKIGGAQNRSYSKLLCGLLAERLRISPDRVYINYYDMNAANVGWNNSTFALEHH

>d1fim\_\_ d.80.1.3 (-) Microphage migration inhibition factor (MIF) {Rat (Rattus norvegicus)}

PAFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQNRNYSKLLCGLLSDRLHISPDRVYINYYDANA

>d1mfia\_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Mouse (Mus musculus)}

PMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTNDPCALCSLHSIGKIGGAQNRNYSKLLCGLLSDRLHISPDRVYINYYDMNAANVGWNGSTFA

>d1hfoa\_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Trichina (Trichinella spiralis)}

PIFTLNTNIKATDVPSDFLSSTSALVGNILSKPGSYVAVHINTDQQLSFGGSTNPAAFGTLMSIGGIEPSRNRDHSAKLFDHLNTKLGIPKNRMYIHFVNLNGDDVGWNGTTF

>d1dpta\_ d.80.1.3 (A:) D-dopachrome tautomerase {Human (Homo sapiens)}

PFLELDTNLPANRVPAGLEKRLCAAAASILGKPADRVNVTVRPGLAMALSGSTEPCAQLSISSIGVVGTAEDNRSHSAHFFEFLTKELALGQDRILIRFFPLESWQIGKIGTVMTFL

>d1gado2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Escherichia coli}

CTTNCLAPLAKVINDNFGIIEGLMTTVHATTATQKTVDGPSHKDWRGGRGASQNIIPSSTGAAKAVGKVLPELNGKLTGMAFRVPTPNVSVVDLTVRLEKAATYEQIKAAVKAAAEGEMKGVLGYTEDDVVSTDFNGEVCTSVFDAKAGIALNDNFVKLVSWYD

>d1gd1o2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Bacillus stearothermophilus, nca 1503}

CTTNCLAPFAKVLHEQFGIVRGMMTTVHSYTNDQRILDLPHKDLRRARAAAESIIPTTTGAAKAVALVLPELKGKLNGMAMRVPTPNVSVVDLVAELEKEVTVEEVNAALKAAAEGELKGILAYSEEPLVSRDYNGSTVSSTIDALSTMVIDGKMVKVVSWYD

>d1cero2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermus aquaticus}

CTTNSLAPVMKVLEEAFGVEKALMTTVHSYTNDQRLLDLPHKDLRRARAAAINIIPTTTGAAKATALVLPSLKGRFDGMALRVPTATGSISDITALLKREVTAEEVNAALKAAAEGPLKGILAYTEDEIVLQDIVMDPHSSIVDAKLTKALGNMVKVFAWYD

>d1hdgo2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermotoga maritima}

CTTNSIAPIVKVLHEKFGIVSGMLTTVHSYTNDQRVLDLPHKDLRRARAAAVNIIPTTTGAAKAVALVVPEVKGKLDGMAIRVPTPDGSITDLTVLVEKETTVEEVNAVMKEATEGRLKGIIGYNDEPIVSSDIIGTTFSGIFDATITNVIGGKLVKVASWYD

>d1b7go2 d.81.1.1 (O:139-300) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Sulfolobus solfataricus}

CNTTALLRTICTVNKVSKVEKVRATIVRRAADQKEVKKGPINSLVPDPATVPSHHAKDVNSVIRNLDIATMAVIAPTTLMHMHFINITLKDKVEKKDILSVLENTPRIVLISSKYDAEATAELVEVARDLKRDRNDIPEVMIFSDSIYVKDDEVMLMYAVHQ

>d1cf2o2 d.81.1.1 (O:139-303) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Methanothermus fervidus}

SCNTTGLCRTLKPLHDSFGIKKVRAVIVRRGADPAQVSKGPINAIIPNPPKLPSHHGPDVKTVLDINIDTMAVIVPTTLMHQHNVMVEVEETPTVDDIIDVFEDTPRVILISAEDGLTSTAEIMEYAKELGRSRNDLFEIPVWRESITVVDNEIYYMQAVHQESD

>d1ggaa2 d.81.1.1 (A:165-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Trypanosoma brucei brucei, glycosome}

CTTNCLAPLVHVLVKEGFGISTGLMTTVHSYTATQKTVDGVSVKDWRGGRAAALNIIPSTTGAAKAVGMVIPSTQGKLTGMAFRVPTADVSVVDLTFIATRDTSIKEIDAALKRASKTYMKNILGYTDEELVSADFISDSRSSIYDSKATLQNNLPNERRFFKIVSWYD

>d1i32a2 d.81.1.1 (A:166-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Leishmania mexicana}

CTTNCLAPIVHVLTKENFGIETGLMTTIHSYTATQKTVDGVSLKDWRGGRAAAVNIIPSTTGAAKAVGMVIPSTKGKLTGMSFRVPTPDVSVVDLTFRATRDTSIQEIDKAIKKAAQTYMKGILGFTDEELVSADFINDNRSSVYDSKATLQNNLPGEKRFFKVVSWYD

>d1dssg2 d.81.1.1 (G:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Lobster (Palinurus versicolor)}

CTTNCLAPVAKVLHENFEIVEGLMTTVHAVTATQKTVDGPSAKDWRGGRGAAQNIIPSSTGAAKAVGKVIPELDGKLTGMAFRVPTPNVSVVDLTVRLGKECSYDDIKAAMKAASEGPLQGVLGYTEDDVVSCDFTGDNRSSIFDAKAGIQLSKTFVKVVSWYD

>d3gpdg2 d.81.1.1 (G:151-314) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Human (Homo sapiens)}

CTTNCLAPLAKVIHDHFGIVEGLMTTVHAITATQKTVDSPSGKLWRGGRGAAQNLIPASTGAAKAVGKVIPELDGKLTGMAFRVPTANVSVLDLTCRLEKPAKYDDIKKVVKEASEGPLKGILGYTEDEVVSDDFNGSNHSSIFDAGAGIELNDTFVKLVSWYD

>d1jn0a2 d.81.1.1 (A:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Spinach (Spinacia oleracea)}

CTTNCLAPFVKVLDQKFGIIKGTMTTTHSYTGDQRLLDASHRDLRRARAACLNIVPTSTGAAKAVALVLPQLKGKLNGIALRVPTPNVSVVDLVVQVSKKTFAEEVNAAFRESADQELKGILSVCDEPLVSIDFRCTDVSSTIDSSLTMVMGDDMVKVIAWYD

>d1gl3a2 d.81.1.1 (A:134-354) Aspartate beta-semialdehyde dehydrogenase {Escherichia coli}

NCTVSLMLMSLGGLFANDLVDWVSVATYQAASGGGARHMRELLTQMGHLYGHVADELATPSSAILDIERKVTTLTRSGELPVDNFGVPLAGSLIPWIDKQLDNGQSREEWKGQAETNKILNTSSVIPVDGLCVRVGALRCHSQAFTIKLKKDVSIPTVEELLAAHNPWAKVVPNDREITMRELTPAAVTGTLTTPVGRLRKLNMGPEFLSAFTVGDQLLWG

>d1ebfa2 d.81.1.2 (A:151-340) Homoserine dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

PIISFLREIIQTGDEVEKIEGIFSGTLSYIFNEFSTSQANDVKFSDVVKVAKKLGYTEPDPRDDLNGLDVARKVTIVGRISGVEVESPTSFPVQSLIPKPLESVKSADEFLEKLSDYDKDLTQLKKEAATENKVLRFIGKVDVATKSVSVGIEKYDYSHPFASLKGSDNVISIKTKRYTNPVVIQGAGAG

>d1e5qa2 d.81.1.2 (A:125-391) Saccharopine reductase {Rice blast fungus (Magnaporthe grisea)}

LDPGIDHLYAIKTIEEVHAAGGKIKTFLSYCGGLPAPESSDNPLGYKFSWSSRGVLLALRNAASFYKDGKVTNVAGPELMATAKPYFIYPGFAFVAYPNRDSTPYKERYQIPEADNIVRGTLRYQGFPQFIKVLVDIGFLSDEEQPFLKEAIPWKEATQKIVKASSASEQDIVSTIVSNATFESTEEQKRIVAGLKWLGIFSDKKITPRGNALDTLCATLEEKMQFEEGERDLVMLQHKFEIENKDGSRETRTSSLCEYGAPIGSGG

>d1f06a2 d.81.1.3 (A:119-268) Diaminopimelic acid dehydrogenase (DAPDH) {Corynebacterium glutamicum}

WDPGMFSINRVYAAAVLAEHQQHTFWGPGLSQGHSDALRRIPGVQKAVQYTLPSEDALEKARRGEAGDLTGKQTHKRQCFVVADAADHERIENDIRTMPDYFVGYEVEVNFIDEATFDSEHTGMPHGGHVITTGDTGGFNHTVEYILKLD

>d1dih\_2 d.81.1.3 (131-240) Dihydrodipicolinate reductase {Escherichia coli}

VGVNVMLKLLEKAAKVMGDYTDIEIIEAHHRHKVDAPSGTALAMGEAIAHALDKDLKDCAVYSREGHTGERVPGTIGFATVRAGDIVGEHTAMFADIGERLEITHKASSR

>d1k5ha3 d.81.1.3 (A:126-274) 1-deoxy-D-xylulose-5-phosphate reductoisomerase {Escherichia coli}

ESLVTCGRLFMDAVKQSKAQLLPVDSEHNAIFQSLPQPIQHNLGYADLEQNGVVSILLTGSGGPFRETPLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIEARWLFNASASQMEVLIHPQSVIHSMVRYQDGSVLAQLGEP

>d1gcua2 d.81.1.4 (A:129-246) Biliverdin reductase {Rat (Rattus norvegicus)}

MEEFEFLRREVLGKELLKGSLRFTASPLEEERFGFPAFSGISRLTWLVSLFGELSLISATLEERKEDQYMKMTVQLETQNKGLLSWIEEKGPGLKRNRYVNFQFTSGSLEEVPSVGVN

>d1h6da2 d.81.1.5 (A:213-374) Glucose-fructose oxidoreductase {Zymomonas mobilis}

DPMNRAAVKLIRENQLGKLGMVTTDNSDVMDQNDPAQQWRLRRELAGGGSLMDIGIYGLNGTRYLLGEEPIEVRAYTYSDPNDERFVEVEDRIIWQMRFRSGALSHGASSYSTTTTSRFSVQGDKAVLLMDPATGYYQNLISVQTPGHANQSMMPQFIMPAN

>d1dpga2 d.81.1.5 (A:182-412,A:427-485) Glucose 6-phosphate dehydrogenase {Leuconostoc mesenteroides}

KEMVQNIAALRFGNPIFDAAWNKDYIKNVQVTLSEVLGVEERAGYYDTAGALLDMIQNHTMQIVGWLAMEKPESFTDKDIRAAKNAAFNALKIYDEAEVNKYFVRAQYGAGDSADFKPYLEELDVPADSKNNTFIAGELQFDLPRWEGVPFYVRSGKRLAAKQTRVDIVFKAGTFNFGSEQEAQEAVLSIIIDPKGAIELKLNAKSVEDAFNTRTIDLGWTVSDEDKKNTPXGSNFADWNGVSIAWKFVDAISAVYTADKAPLETYKSGSMGPEASDKLLAANGDAWVFKG

>d1qkia2 d.81.1.5 (A:200-434,A:450-511) Glucose 6-phosphate dehydrogenase {Human (Homo sapiens)}

DHYLGKEMVQNLMVLRFANRIFGPIWNRDNIACVILTFKEPFGTEGRGGYFDEFGIIRDVMQNHLLQMLCLVAMEKPASTNSDDVRDEKVKVLKCISEVQANNVVLGQYVGNPDGEGEATKGYLDDPTVPRGSTTATFAAVVLYVENERWDGVPFILRCGKALNERKAEVRLQFHDVAGDIFHQQCKRNELVIRVQPNEAVYTKMMTKKPGMFFNPEESELDLTYGNRYKNVKLPXMHFVRSDELLEAWRIFTPLLHQIELEKPKPIPYIYGSRGPTEADELMKRVGFQYEGTYKWVN

>d1oaca4 d.82.1.1 (A:5-90) Copper amine oxidase, domain N {Escherichia coli}

AHMVPMDKTLKEFGADVQWDDYAQLFTLIKDGAYVKVKPGAQTAIVNGQPLALQVPVVMKDNKAWVSDTFINDVFQSGLDQTFQVE

>d1ekga\_ d.82.2.1 (A:) C-terminal domain of frataxin {Human (Homo sapiens)}

LDETTYERLAEETLDSLAEFFEDLADKPYTFEDYDVSFGSGVLTVKLGGDLGTYVINKQTPNKQIWLSSPSSGPKRYDWTGKNWVYSHDGVSLHELLAAELTKALKTKLDLSSLAYSGK

>d1ew4a\_ d.82.2.1 (A:) CyaY {Escherichia coli}

MNDSEFHRLADQLWLTIEERLDDWDGDSDIDCEINGGVLTITFENGSKIIINRQEPLHQVWLATKQGGYHFDLKGDEWICDRSGETFWDLLEQAATQQAGETVSFR

>d1ewfa1 d.83.1.1 (A:1-217) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

VNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREFQLPSSQISMVPNVGLKFSISNANIKISGKWKAQKRFLKMSGNFDLSIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNSVSSELQPYFQTLPVMTKIDSVAGINYGLVAPPATTA

>d1ewfa2 d.83.1.1 (A:218-456) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

ETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAFAVLPNSALASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLLELKHSNIGPFPVELLQDIMNYIVPILVLPRVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLLFGADVVYK

>d1ihra\_ d.191.1.1 (A:) Dimeric C-terminal domain of membrane protein TonB {Escherichia coli}

ARAQALRIEGQVKVKFDVTPDGRVDNVQILSAKPANMFEREVKNAMRRWRYEPGKPGSGIVVNILFKINGTTE

>d2sici\_ d.84.1.1 (I:) Subtilisin inhibitor {Streptomyces albogriseolus, s-3253}

YAPSALVLTVGKGVSATTAAPERAVTLTCAPGPSGTHPAAGSACADLAAVGGDLNALTRGEDVMCPMVYDPVLLTVDGVWQGKRVSYERVFSNECEMNAHGSSVFAF

>d1e6ta\_ d.85.1.1 (A:) MS2 virus coat protein {Bacteriophage MS2}

ASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQNRKYTIKVEVPKVATQTVGGVELPVAAWRSYLNMELTIPIFATNSDCELIVKAMQGLLKDGNPIPSAIAANSGIY

>d1unaa\_ d.85.1.1 (A:) GA coat protein {Bacteriophage GA}

ATLHSFVLVDNGGTGNVTVVPVSNANGVAEWLSNNSRSQAYRVTASYRASGADKRKYTIKLEVPKIVTQVVNGVELPVSAWKAYASIDLTIPIFAATDDVTVISKSLTGLFKVGNPIAEAISSQSGFYA

>d1frsa\_ d.85.1.1 (A:) fr coat protein {Bacteriophage FR}

ASNFEEFVLVDNGGTGDVKVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSANNRKYTVKVEVPKVATQVQGGVELPVAAWRSYMNMELTIPVFATNDDCALIVKALQGTFKTGNPIATAIAANSGIY

>d1qbea\_ d.85.1.1 (A:) Qbeta coat protein {Bacteriophage Qbeta}

AKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFVRTELAALLASPLLIDAIDQLNPAY

>d1dwna\_ d.85.1.1 (A:) PP7 coat protein {Bacteriophage PP7}

SKTIVLSVGEATRTLTEIQSTADRQIFEEKVGPLVGRLRLTASLRQNGAKTAYRVNLKLDQADVVDCSTSVCGELPKVRYTQVWSHDVTIVANSTEASRKSLYDLTKSLVATSQVEDLVVNLVPLGR

>d1ej1a\_ d.86.1.1 (A:) Translation initiation factor eIF4e {Mouse (Mus musculus)}

KHPLQNRWALWFFKNDKSKTWQANLRLISKFDTVEDFWALYNHIQLSSNLMPGCDYSLFKDGIEPMWEDEKNKRGGRWLITLNKQQRRSDLDRFWLETLLCLIGESFDDYSDDVCGAVVNVRAKGDKIAIWTTECENRDAVTHIGRVYKERLGLPPKIVIGYQSHADTATKSGSTTKNRFVV

>d1ap8\_\_ d.86.1.1 (-) Translation initiation factor eIF4e {Baker's yeast (Saccharomyces cerevisiae)}

MSVEEVSKKFEENVSVDDTTATPKTVLSDSAHFDVKHPLNTKWTLWYTKPAVDKSESWSDLLRPVTSFQTVEEFWAIIQNIPEPHELPLKSDYHVFRNDVRPEWEDEANAKGGKWSFQLRGKGADIDELWLRTLLAVIGETIDEDDSQINGVVLSIRKGGNKFALWTKSEDKEPLLRIGGKFKQVLKLTDDGHLEFFPHSSANGRHPQPSITL

>d3grs\_3 d.87.1.1 (364-478) Glutathione reductase {Human (Homo sapiens)}

YNNIPTVVFSHPPIGTVGLTEDEAIHKYGIENVKTYSTSFTPMYHAVTKRKTKCVMKMVCANKEEKVVGIHMQGLGCDEMLQGFAVAVKMGATKADFDNTVAIHPTSSEELVTLR

>d1gesa3 d.87.1.1 (A:336-450) Glutathione reductase {Escherichia coli}

YSNIPTVVFSHPPIGTVGLTEPQAREQYGDDQVKVYKSSFTAMYTAVTTHRQPCRMKLVCVGSEEKIVGIHGIGFGMDEMLQGFAVALKMGATKKDFDNTVAIHPTAAEEFVTMR

>d1feca3 d.87.1.1 (A:358-485) Trypanothione reductase {Crithidia fasciculata}

HTKVACAVFSIPPMGVCGYVEEDAAKKYDQVAVYESSFTPLMHNISGSTYKKFMVRIVTNHADGEVLGVHMLGDSSPEIIQSVAICLKMGAKISDFYNTIGVHPTSAEELCSMRTPAYFYEKGKRVEK

>d1aoga3 d.87.1.1 (A:358-487) Trypanothione reductase {Trypanosoma cruzi}

DHTRVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSFTPLMHKVSGSKYKTFVAKIITNHSDGTVLGVHLLGDNAPEIIQGIGICLKLNAKISDFYNTIGVHPTSAEELCSMRTPSYYYVKGEKMEKP

>d1h6va3 d.87.1.1 (A:367-499) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}

YDNVPTTVFTPLEYGCCGLSEEKAVEKFGEENIEVYHSFFWPLEWTVPSRDNNKCYAKVICNLKDNERVVGFHVLGPNAGEVTQGFAAALKCGLTKQQLDSTIGIHPVCAEIFTTLSVTKRSGGDILQSGCCG

>d1nhp\_3 d.87.1.1 (322-447) NADH peroxidase {Enterococcus faecalis}

GVQGSSGLAVFDYKFASTGINEVMAQKLGKETKAVTVVEDYLMDFNPDKQKAWFKLVYDPETTQILGAQLMSKADLTANINAISLAIQAKMTIEDLAYADFFFQPAFDKPWNIINTAALEAVKQER

>d1d7ya3 d.87.1.1 (A:309-405) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}

TAPGYAELPWYWSDQGALRIQVAGLASGDEEIVRGEVSLDAPKFTLIELQKGRIVGATCVNNARDFAPLRRLLAVGAKPDRAALADPATDLRKLAAA

>d1lvl\_3 d.87.1.1 (336-458) Dihydrolipoamide dehydrogenase {Pseudomonas putida}

PAAIAAVCFTDPEVVVVGKTPEQASQQGLDCIVAQFPFAANGRAMSLESKSGFVRVVARRDNHLILGWQAVGVAVSELSTAFAQSLEMGACLEDVAGTIHAHPTLGEAVQEAALRALGHALHI

>d1lpfa3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}

YDLIPSVIYTHPEIAWVGKTEQTLKAEGVEVNVGTFPFAASGRAMAANDTTGLVKVIADAKTDRVLGVHVIGPSAAELVQQGAIGMEFGTSAEDLGMMVFSHPTLSEALHEAALAVNGHAIHIA

>d3lada3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}

YDLIPAVIYTHPEIAGVGKTEQALKAEGVAINVGVFPFAASGRAMAANDTAGFVKVIADAKTDRVLGVHVIGPSAAELVQQGAIAMEFGTSAEDLGMMVFAHPALSEALHEAALAVSGHAIHVA

>d1ebda3 d.87.1.1 (A:347-461) Dihydrolipoamide dehydrogenase {Bacillus stearothermophilus}

AIPAVVFSDPECASVGYFEQQAKDEGIDVIAAKFPFAANGRALALNDTDGFLKLVVRKEDGVIIGAQIIGPNASDMIAELGLAIEAGMTAEDIALTIHAHPTLGEIAMEAAEVAL

>d1ojt\_3 d.87.1.1 (471-598) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

ARVIPGVAYTSPEVAWVGETELSAKASARKITKANFPWAASGRAIANGCDKPFTKLIFDAETGRIIGGGIVGPNGGDMIGEVCLAIEMGCDAADIGKTIHPHPTLGESIGMAAEVALGTCTDLPPQKK

>d1jeha3 d.87.1.1 (A:356-478) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

YNNIPSVMYSHPEVAWVGKTEEQLKEAGIDYKIGKFPFAANSRAKTNQDTEGFVKILIDSKTERILGAHIIGPNAGEMIAEAGLALEYGASAEDVARVCHAHPTLSEAFKEANMAAYDKAIHC

>d1dxla3 d.87.1.1 (A:348-470) Dihydrolipoamide dehydrogenase {Garden pea (Pisum sativum)}

YDKVPGVVYTNPEVASVGKTEEQVKETGVEYRVGKFPFMANSRAKAIDNAEGLVKIIAEKETDKILGVHIMAPNAGELIHEAAIALQYDASSEDIARVCHAHPTMSEAIKEAAMATYDKPIHI

>d1fcda3 d.87.1.1 (A:328-401) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (Chromatium vinosum)}

PGTPSYLNTCYSILAPAYGISVAAIYRPNADGSAIESVPDSGGVTPVDAPDWVLEREVQYAYSWYNNIVHDTFG

>d1qj2c1 d.87.2.1 (C:178-285) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal domain {Pseudomonas carboxydovorans}

GHGYAYEKLKRKIGDYATAAAAVVLTMSGGKCVTASIGLTNVANTPLWAEEAGKVLVGTALDKPALDKAVALAEAITAPASDGRGPAEYRTKMAGVMLRRAVERAKAR

>d1ffvc1 d.87.2.1 (C:178-287) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal domain {Hydrogenophaga pseudoflava}

GTGWAYEKLKRKTGDWATAGCAVVMRKSGNTVSHIRIALTNVAPTALRAEAAEAALLGKAFTKEAVQAAADAAIAICEPAEDLRGDADYKTAMAGQMVKRALNAAWARCA

>d1fo4a4 d.87.2.1 (A:415-531) Xanthine oxidase, domain 4 (?) {Cow (Bos taurus)}

DEFFSAFKQASRREDDIAKVTCGMRVLFQPGSMQVKELALCYGGMADRTISALKTTQKQLSKFWNEKLLQDVCAGLAEELSLSPDAPGGMIEFRRTLTLSFFFKFYLTVLKKLGKDS

>d1jroa3 d.87.2.1 (A:346-462) Xanthine dehydrogenase chain A, domain 4 {Rhodobacter capsulatus}

PGLRCYKLSKRFDQDISAVCGCLNLTLKGSKIETARIAFGGMAGVPKRAAAFEAALIGQDFREDTIAAALPLLAQDFTPLSDMRASAAYRMNAAQAMALRYVRELSGEAVAVLEVMP

>d1srsa\_ d.88.1.1 (A:) Serum response factor (SRF) core {Human (Homo sapiens)}

TRGRVKIKMEFIDNKLRRYTTFSKRKTGIMKKAYELSTLTGTQVLLLVASETGHVYTFATRKLQPMITSETGKALIQTCLNSPD

>d1mnma\_ d.88.1.1 (A:) MCM1 transcriptional regulator {Baker's yeast (Saccharomyces cerevisiae)}

QKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFELSVLTGTQVLLLVVSETGLVYTFSTPKFEPIVTQQEGRNLIQACLNAPDD

>d1egwa\_ d.88.1.1 (A:) Mef2a core {Human (Homo sapiens)}

GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLFQYASTDMDKVLLKYTEY

>d1tbd\_\_ d.89.1.1 (-) The origin DNA-binding domain of SV40 T-antigen {Simian virus 40}

GSKVEDPKDFPSELLSFLSHAVFSNRTLACFAIYTTKEKAALLYKKIMEKYSVTFISRHNSYNHNILFFLTPHRHRVSAINNYAQKLCTFSFLICKGVNKEYLMYSALTRDPFSVIEESLPGGLKEHDFNPESS

>d1f08a\_ d.89.1.2 (A:) Replication initiation protein E1 {Bovine papillomavirus}

GSRATVFKLGLFKSLFLCSFHDITRLFKNDKTTNQQWVLAVFGLAEVFFEASFELLKKQCSFLQMQKRSHEGGTCAVYLICFNTAKSRETVRNLMANMLNVREECLMLQPPKIRGLSAALFWFKSSLSPATLKHGALPEWIRAQTTLN

>d1nox\_\_ d.90.1.1 (-) NADH oxidase {Thermus thermophilus, HB8}

PVLDAKTAALKRRSIRRYRKDPVPEGLLREILEAALRAPSAWNLQPWRIVVVRDPATKRALREAAFGQAHVEEAPVVLVLYADLEDALAHLDEVIHPGVQGERREAQKQAIQRAFAAMGQEARKAWASGQSYILLGYLLLLLEAYGLGSVPMLGFDPERVRAILGLPSRAAIPALVALGYPAEEGYPSHRLPLERVVLWR

>d1bkja\_ d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio harveyi}

NNTIETILAHRSIRKFTAVPITDEQRQTIIQAGLAASSSSMLQVVSIVRVTDSEKRNELAQFAGNQAYVESAAEFLVFCIDYQRHATINPDVQADFTELTLIGAVDSGIMAQNCLLAAESMGLGGVYIGGLRNSAAQVDELLGLPENSAVLFGMCLGHPDQNPEVKPRLPAHVVVHENQYQELNLDDIQSYDQTMQAYYASRTSNQKLSTWSQEVTGKLAGESRPHILPYLNSKGLAKR

>d1vfra\_ d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio fischeri}

THPIIHDLENRYTSKKYDPSKKVSQEDLAVLLEALRLSASSINSQPWKFIVIESDAAKQRMHDSFANMHQFNQPHIKACSHVILFANKLSYTRDDYDVVLSKAVADKRITEEQKEAAFASFKFVELNCDENGEHKAWTKPQAYLALGNALHTLARLNIDSTTMEGIDPELLSEIFADELKGYECHVALAIGYHHPSEDYNASLPKSRKAFEDVITIL

>d1kqba\_ d.90.1.1 (A:) Nitroreductase {Enterobacter cloacae}

DIISVALKRHSTKAFDASKKLTAEEAEKIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGTYVFNERKMLDASHVVVFCAKTAMDDAWLERVVDQEEADGRFNTPEAKAANHKGRTYFADMHRVDLKDDDQWMAKQVYLNVGNFLLGVGAMGLDAVPIEGFDAAILDEEFGLKEKGFTSLVVVPVGHHSVEDFNATLPKSRLPLSTIVTEC

>d1icra\_ d.90.1.1 (A:) Nitroreductase {Escherichia coli, minor form}

DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADMHRKDLHDDAEWMAKQVYLNVGNFLLGVAALGLDAVPIEGFDAAILDAEFGLKEKGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV

>d1f5va\_ d.90.1.1 (A:) Nitroreductase {Escherichia coli, oxygen-insensitive form}

MTPTIELICGHRSIRHFTDEPISEAQREAIINSARATSSSSFLQCSSIIRITDKALREELVTLTGGQKHVAQAAEFWVFCADFNRHLQICPDAQLGLAEQLLLGVVDTAMMAQNALIAAESLGLGGVYIGGLRNNIEAVTKLLKLPQHVLPLFGLCLGWPADNPDLKPRLPASILVHENSYQPLDKGALAQYDEQLAEYYLTRGSNNRRDTWSDHIRRTIIKESRPFILDYLHKQGWATR

>d1dt9a3 d.91.1.1 (A:5-142) N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 {Human (Homo sapiens)}

PSAADRNVEIWKIKKLIKSLEAARGNGTSMISLIIPPKDQISRVAKMLADEFGTASNIKSRVNRLSVLGAITSVQQRLKLYNKVPPNGLVVYCGTIVTEEGKEKKVNIDFEPFKPINTSLYLCDNKFHTEALTALLSD

>d1c7ka\_ d.92.1.1 (A:) Zinc protease {Streptomyces caespitosus}

TVTVTYDPSNAPSFQQEIANAAQIWNSSVRNVQLRAGGNADFSYYEGNDSRGSYAQTDGHGRGYIFLDYQQNQQYDSTRVTAHETGHVLGLPDHYQGPCSELMSGGGPGPSCTNPYPNAQERSRVNALWANG

>d1g12a\_ d.92.1.12 (A:) Fungal zinc peptidase {Grifola frondosa}

TYNGCSSSEQSALAAAASAAQSYVAESLSYLQTHTAATPRYTTWFGSYISSRHSTVLQHYTDMNSNDFSSYSFDCTCTAAGTFAYVYPNRFGTVYLCGAFWKAPTTGTDSQAGTLVHESSHFTRNGGTKDYAYGQAAAKSLATMDPDKAVMNADNHEYFSENNPAQS

>d1eb6a\_ d.92.1.12 (A:) Fungal zinc peptidase {Aspergillus oryzae, deuterolysin}

TEVTDCKGDAESSLTTALSNAAKLANQAAEAAESGDESKFEEYFKTTDQQTRTTVAERLRAVAKEAGSTSGGSTTYHCNDPYGYCEPNVLAYTLPSKNEIANCDIYYSELPPLAQKCHAQDQATTTLHEFTHAPGVYQPGTEDLGYGYDAATQLSAQDALNNADSYALYANAIELKC

>d1ezm\_\_ d.92.1.2 (-) Elastase {Pseudomonas aeruginosa}

AEAGGPGGNQKIGKYTYGSDYGPLIVNDRCEMDDGNVITVDMNSSTDDSKTTPFRFACPTNTYKQVNGAYSPLNDAHFFGGVVFKLYRDWFGTSPLTHKLYMKVHYGRSVENAYWDGTAMLFGDGATMFYPLVSLDVAAHEVSHGFTEQNSGLIYRGQSGGMNEAFSDMAGEAAEFYMRGKNDFLIGYDIKKGSGALRYMDQPSRDGRSIDNASQYYNGIDVHHSSGVYNRAFYLLANSPGWDTRKAFEVFVDANRYYWTATSNYNSGACGVIRSAQNRNYSAADVTRAFSTVGVTCP

>d8tlne\_ d.92.1.2 (E:) Thermolysin {Bacillus thermoproteolyticus}

ITGTSTVGVGRGVLGDQKNINTTYSTYYYLQDNTRGDGIFTYDAKYRTTLPGSLWADADNQFFASYDAPAVDAHYYAGVTYDYYKNVHNRLSYDGNNAAIRSSVHYSQGYNNAFWNGSEMVYGDGDGQTFIPLSGGIDVVAHELTHAVTDYTAGLIYQNESGAINEAISDIFGTLVEFYANKNPDWEIGEDVYTPGISGDSLRSMSDPAKYGDPDHYSKRYTGTQDNGGVHINSGIINKAAYLISQGGTHYGVSVVGIGRDKLGKIFYRALTQYLTPTSNFSQLRAAAVQSATDLYGSTSQEVASVKQAFDAVGVK

>d1npc\_\_ d.92.1.2 (-) Neutral protease {Bacillus cereus, strain dsm 3101}

VTGTNKVGTGKGVLGDTKSLNTTLSGSSYYLQDNTRGATIFTYDAKNRSTLPGTLWADADNVFNAAYDAAAVDAHYYAGKTYDYYKATFNRNSINDAGAPLKSTVHYGSNYNNAFWNGSQMVYGDGDGVTFTSLSGGIDVIGHELTHAVTENSSNLIYQNESGALNEAISDIFGTLVEFYDNRNPDWEIGEDIYTPGKAGDALRSMSDPTKYGDPDHYSKRYTGSSDNGGVHTNSGIINKQAYLLANGGTHYGVTVTGIGKDKLGAIYYRANTQYFTQSTTFSQARAGAVQAAADLYGANSAEVAAVKQSFSAVGVN

>d1bqba\_ d.92.1.2 (A:) Aureolysin {Staphylococcus aureus}

AAATGTGKGVLGDTKDININSIDGGFSLEDLTHQGKLSAYNFNDQTGQATLITNEDENFVKDDQRAGVDANYYAKQTYDYYKNTFGRESYDNHGSPIVSLTHVNHYGGQDNRNNAAWIGDKMIYGDGDGRTFTNLSGANDVVAHEITHGVTQQTANLEYKDQSGALNESFSDVFGYFVDDEDFLMGEDVYTPGKEGDALRSMSNPEQFGQPSHMKDYVYTEKDNGGVHTNSGIPNKAAYNVIQAIGKSKSEQIYYRALTEYLTSNSNFKDLKDALYQAAKDLYEQQTAEQVYEAWNEVGVE

>d1hs6a3 d.92.1.13 (A:209-460) Leukotriene A4 hydrolase catalytic domain {Human (Homo sapiens)}

LESRQIGPRTLVWSEKEQVEKSAYEFSETESMLKIAEDLGGPYVWGQYDLLVLPPSFPYGGMENPCLTFVTPTLLAGDKSLSNVIAHEISHSWTGNLVTNKTWDHFWLNEGHTVYLERHICGRLFGEKFRHFNALGGWGELQNSVKTFGETHPFTKLVVDLTDIDPDVAYSSVPYEKGFALLFYLEQLLGGPEIFLGFLKAYVEKFSYKSITTDDWKDFLYSYFKDKVDVLNQVDWNAWLYSPGLPPIKPNY

>d1dmta\_ d.92.1.4 (A:) Neutral endopeptidase (neprilysin) {Human (Homo sapiens)}

GICKSSDCIKSAARLIQNMDATTEPCTDFFKYACGGWLKRNVIPETSSRYGNFDILRDELEVVLKDVLQEPKTEDIVAVQKAKALYRSCINESAIDSRGGEPLLKLLPDIYGWPVATENWEQKYGASWTAEKAIAQLNSKYGKKVLINLFVGTDDKNSVNHVIHIDQPRLGLPSRDYYECTGIYKEACTAYVDFMISVARLIRQEERLPIDENQLALEMNKVMELEKEIANATAKPEDRNDPMLLYNKMTLAQIQNNFSLEINGKPFSWLNFTNEIMSTVNISITNEEDVVVYAPEYLTKLKPILTKYSARDLQNLMSWRFIMDLVSSLSRTYKESRNAFRKALYGTTSETATWRRCANYVNGNMENAVGRLYVEAAFAGESKHVVEDLIAQIREVFIQTLDDLTWMDAETKKRAEEKALAIKERIGYPDDIVSNDNKLNNEYLELNYKEDEYFENIIQNLKFSQSKQLKKLREKVDKDEWISGAAVVNAFYSSGRNQIVFPAGILQPPFFSAQQSNSLNYGGIGMVIGHEITHGFDDNGRNFNKDGDLVDWWTQQSASNFKEQSQCMVYQYGNFSWDLAGGQHLNGINTLGENIADNGGLGQAYRAYQNYIKKNGEEKLLPGLDLNHKQLFFLNFAQVWCGTYRPEYAVNSIKTDVHSPGNFRIIGTLQNSAEFSEAFHCRKNSYMNPEKKCRVW

>d1i1ip\_ d.92.1.5 (P:) Neurolysin (endopeptidase 24.16) {Rat (Rattus norvegicus)}

MSSYTAAGRNVLRWDLSPEQIKTRTEQLIAQTKQVYDTVGTIALKEVTYENCLQVLADIEVTYIVERTMLDFPQHVSSDREVRAASTEADKKLSRFDIEMSMREDVFQRIVHLQETCDLEKIKPEARRYLEKSIKMGKRNGLHLSEHIRNEIKSMKKRMSELCIDFNKNLNEDDTSLVFSKAELGALPDDFIDSLEKTDEDKYKVTLKYPHYFPVMKKCCVPETRRKMEMAFHTRCKQENTAILQQLLPLRAQVAKLLGYNTHADFVLELNTAKSTSRVAAFLDDLSQKLKPLGEAEREFILSLKKKECEERGFEYDGKINAWDLHYYMTQTEELKYSVDQESLKEYFPIEVVTEGLLSIYQELLGLSFEQVPDAHVWNKSVSLYTVKDKATGEVLGQFYLDLYPREGKYNHAACFGLQPGCLLPDGSRMMSVAALVVNFSQPVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTDFARFSGTNVETDFVEVPSQMLENWVWDVDSLRKLSKHYKDGHPITDELLEKLVASRLVNTGLLTLRQIVLSKVDQSLHTNATLDAASEYAKYCTEILGVAATPGTNMPATFGHLAGGYDGQYYGYLWSEVFSMDMFHSCFKKEGIMNPEVGMKYRNLILKPGGSLDGMDMLQNFLQREPNQKAFLMSRGL

>d1j7na1 d.92.1.14 (A:27-263) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}

ERNKTQEEHLKEIMKHIVKIEVKGEEAVKKEAAEKLLEKVPSDVLEMYKAIGGKIYIVDGDITKHISLEALSEDKKKIKDIYGKDALLHEHYVYAKEGYEPVLVIQSSEDYVENTEKALNVYYEIGKILSRDILSKINQPYQKFLDVLNTIKNASDSDGQDLLFTNQLKEHPTDFSVEFLEQNSNEVQEVFAKAFAYYIEPQHRDVLQLYAPEAFNYMDKFNEQEINLSLEELKDQR

>d1j7na2 d.92.1.14 (A:551-773) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}

PKSKIDTKIQEAQLNINQEWNKALGLPKYTKLITFNVHNRYASNIVESAYLILNEWKNNIQSDLIKKVTNYLVDGNGRFVFTDITLPNIAEQYTHQDEIYEQVHSKGLYVPESRSILLHGPSKGVELRNDSEGFIHEFGHAVDDYAGYLLDKNQSDLVTNSKKFIDIFKEEGSNLTSYGRTNEAEFFAEAFRLMHSTDHAERLKVQKNAPKTFQFINDQIKFI

>d1lml\_\_ d.92.1.3 (-) Leishmanolysin {Leishmania major}

VVRDVNWGALRIAVSTEDLTDPAYHCARVGQHVKDHAGAIVTCTAEDILTNEKRDILVKHLIPQAVQLHTERLKVQQVQGKWKVTDMVGDICGDFKVPQAHITEGFSNTDFVMYVASVPSEEGVLAWATTCQTFSDGHPAVGVINIPAANIASRYDQLVTRVVTHEMAHALGFSGPFFEDARIVANVPNVRGKNFDVPVINSSTAVAKAREQYGCDTLEYLEVEDQGGAGSAGSHIKMRNAQDELMAPAAAAGYYTALTMAIFQDLGFYQADFSKAEVMPWGQNAGCAFLTNKCMEQSVTQWPAMFCNESEDAIRCPTSRLSLGACGVTRHPGLPPYWQYFTDPSLAGVSAFMDYCPVVVPYSDGSCTQRASEAHASLLPFNVFSDAARCIDGAFRPKATDGIVKSYAGLCANVQCDTATRTYSVQVHGSNDYTNCTPGLRVELSTVSNAFEGGGYITCPPYVEVCQGNVQAAKD

>d1kapp2 d.92.1.6 (P:1-246) Metallo protease, catalytic (N-terminal) domain {Pseudomonas aeruginosa, alkaline protease}

GRSDAYTQVDNFLHAYARGGDELVNGHPSYTVDQAAEQILREQASWQKAPGDSVLTLSYSFLTKPNDFFNTPWKYVSDIYSLGKFSAFSAQQQAQAKLSLQSWSDVTNIHFVDAGQGDQGDLTFGNFSSSVGGAAFAFLPDVPDALKGQSWYLINSSYSANVNPANGNYGRQTLTHEIGHTLGLSHPGDYNAGEGDPTYADATYAEDTRAYSVMSYWEEQNTGQDFKGAYSSAPLLDDIAAIQKLY

>d1sat\_2 d.92.1.6 (4-246) Metallo protease, catalytic (N-terminal) domain {Serratia marcescens}

TGYDAVDDLLHYHERGNGIQINGKDSFSNEQAGLFITRENQTWNGYKVFGQPVKLTFSFPDYKFSSTNVAGDTGLSKFSAEQQQQAKLSLQSWADVANITFTEVAAGQKANITFGNYSQDRPGHYDYGTQAYAFLPNTIWQGQDLGGQTWYNVNQSNVKHPATEDYGRQTFTHEIGHALGLSHPGDYNAGEGDPTYADVTYAEDTRQFSLMSYWSETNTGGDNGGHYAAAPLLDDIAAIQHLY

>d3btaa3 d.92.1.7 (A:1-546) Botulinum neurotoxin {Clostridium botulinum, serotype A}

PFVNKQFNYKDPVNGVDIAYIKIPNVGQMQPVKAFKIHNKIWVIPERDTFTNPEEGDLNPPPEAKQVPVSYYDSTYLSTDNEKDNYLKGVTKLFERIYSTDLGRMLLTSIVRGIPFWGGSTIDTELKVIDTNCINVIQPDGSYRSEELNLVIIGPSADIIQFECKSFGHEVLNLTRNGYGSTQYIRFSPDFTFGFEESLEVDTNPLLGAGKFATDPAVTLAHELIHAGHRLYGIAINPNRVFKVNTNAYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYYNKFKDIASTLNKAKSIVGTTASLQYMKNVFKEKYLLSEDTSGKFSVDKLKFDKLYKMLTEIYTEDNFVKFFKVLNRKTYLNFDKAVFKINIVPKVNYTIYDGFNLRNTNLAANFNGQNTEINNMNFTKLKNFTGLFEFYKLLCVRGIITSKTKSLDKGYNKALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSDTNIEAAEENISLDLIQQYYLTFNFDNEPENISIENLSSDIIGQLELMPNIERFPNGKKYELDK

>d1epwa3 d.92.1.7 (A:1-533) Botulinum neurotoxin {Clostridium botulinum, serotype B}

PVTINNFNYNDPIDNNNIIMMEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCEYYDPDYLNTNDKKNIFLQTMIKLFNRIKSKPLGEKLLEMIINGIPYLGDRRVPLEEFNTNIASVTVNKLISNPGEVERKKGIFANLIIFGPGPVLNENETIDIGIQNHFASREGFGGIMQMKFCPEYVSVFNNVQENKGASIFNRRGYFSDPALILMHELIHVLHGLYGIKVDDLPIVPNEKKFFMQSTDAIQAEELYTFGGQDPSIITPSTDKSIYDKVLQNFRGIVDRLNKVLVCISDPNININIYKNKFKDKYKFVEDSEGKYSIDVESFDKLYKSLMFGFTETNIAENYKIKTRASYFSDSLPPVKIKNLLDNEIYTIEEGFNISDKDMEKEYRGQNKAINKQAYEEISKEHLAVYKIQMCKSVKAPGICIDVDNEDLFFIADKNSFSDDLSKNERIEYNTQSNYIENDFPINELILDTDLISKIELPSENTESLTDFNVDVPVYEKQPAIKKIFTDE

>d1f83a\_ d.92.1.7 (A:) Botulinum neurotoxin {Clostridium botulinum, serotype B}

PVTINNFNYNDPIDNNNIIMMEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCEYYDPDYLNTNDKKNIFLQTMIKLFNRIKSKPLGEKLLEMIINGIPYLGDRRVPLEEFNTNIASVTVNKLISNPGEVERKKGIFANLIIFGPGPVLNENETIDIGIQNHFASREGFGGIMQMKFCPEYVSVFNNVQENKGASIFNRRGYFSDPALILMHELIHVLHGLYGIKVDDLPIVPNEKKFFMQSTDAIQAEELYTFGGQDPSIITPSTDKSIYDKVLQNFRGIVDRLNKVLVCISDPNININIYKNKFKDKYKFVEDSEGKYSIDVESFDKLYKSLMFGFTETNIAENYKIKTRASYFSDSLPPVKIKNLLDNEIYTIEEGFNISDKDMEKEYRGQNKAINKQAYEEISK

>d1ast\_\_ d.92.1.8 (-) Astacin {European fresh water crayfish (Astacus astacus)}

AAILGDEYLWSGGVIPYTFAGVSGADQSAILSGMQELEEKTCIRFVPRTTESDYVEIFTSGSGCWSYVGRISGAQQVSLQANGCVYHGTIIHELMHAIGFYHEHTRMDRDNYVTINYQNVDPSMTSNFDIDTYSRYVGEDYQYYSIMHYGKYSFSIQWGVLETIVPLQNGIDLTDPYDKAHMLQTDANQINNLYTNECSL

>d4aig\_\_ d.92.1.9 (-) Snake venom metalloprotease {Eastern diamondback rattlesnake (Crotalus adamanteus), adamalysin II}

NLPQRYIELVVVADRRVFMKYNSDLNIIRTRVHEIVNIINEFYRSLNIRVSLTDLEIWSGQDFITIQSSSSNTLNSFGEWRERVLLTRKRHDNAQLLTAINFEGKIIGKAYTSSMCNPRSSVGIVKDHSPINLLVAVTMAHELGHNLGMEHDGKDCLRGASLCIMRPGLTPGRSYEFSDDSMGYYQKFLNQYKPQCILNKP

>d1atla\_ d.92.1.9 (A:) Snake venom metalloprotease {Western diamonback rattlesnake (Crotalus atrox), atrolysin C}

LPQRYIELVVVADHRVFMKYNSDLNTIRTRVHEIVNFINGFYRSLNIHVSLTDLEIWSNEDQINIQSASSDTLNAFAEWRETDLLNRKSHDNAQLLTAIELDEETLGLAPLGTMCDPKLSIGIVQDHSPINLLMGVTMAHELGHNLGMEHDGKDCLRGASLCIMRPGLTKGRSYEFSDDSMHYYERFLKQYKPQCILNKP

>d1buda\_ d.92.1.9 (A:) Snake venom metalloprotease {Five-pace snake (Agkistrodon acutus), acutolysin A}

FQRYMEIVIVVDHSMVKKYNGDSDSIKAWVYEMINTITESYSYLKIDISLSGLEIWSGKDLIDVEASAGNTLKSFGEWRAKDLIHRISHDNAQLLTATDFDGATIGLAYVASMCNPKRSVGVIQDHSSVNRLVAITLAHEMAHNLGVSHDEGSCSCGGKSCIMSPSISDETIKYFSDCSYIQCRDYISKENPPCILN

>d1quaa\_ d.92.1.9 (A:) Snake venom metalloprotease {Chinese five-pace snake (Agkistrodon acutus), acutolysin C}

PAPQTSIELFLIVDHSMYAKYNSNSSKITTTLKARVNIMNAIYSSLNLVITLSGIEMWSAADLITVQSSSRNTLKLFASWRETDLLKRTSNDNAQLLTATNFNGNTVGLAYLKTMCNSKYSVGLIQDHSAIPLLMAVTMAHELGHNLGMNHDGAGCSCATCIMAPVLSSGPAKSFSDCSKHDYQSFLTIHKPQCLLN

>d1bkca\_ d.92.1.10 (A:) TNF-alpha converting enzyme, TACE, catalytic domain {Human (Homo sapiens)}

DPMKNTCKLLVVADHRFYRYMGRGEESTTTNYLIELIDRVDDIYRNTAWDNAGFKGYGIQIEQIRILKSPQEVKPGEKHYNMAKSYPNEEKDAWDVKMLLEQFSFDIAEEASKVCLAHLFTYQDFDMGTLGLAYVGSPRANSHGGVCPKAYYSPVGKKNIYLNSGLTSTKNYGKTILTKEADLVTTHELGHNFGAEHDPDGLAECAPNEDQGGKYVMYPIAVSGDHENNKMFSQCSKQSIYKTIESKAQECFQER

>d1cgla\_ d.92.1.11 (A:) Fibroblast collagenase (MMP-1) {Human (Homo sapiens)}

VLTEGNPRWEQTHLRYRIENYTPDLPRADVDHAIEKAFQLWSDVTPLTFTKVSEGQADIMISFVRGDHRDNSPFDGPGGNLAHAFDPGPGIGGDAHFDEDERWTNNFREYNLHRVAAHELGHSLGLSHSTDIGALMYPSYTFSGDVQLAQDDIDGIQAIYGRSQNPVQ

>d1hfc\_\_ d.92.1.11 (-) Fibroblast collagenase (MMP-1) {Human (Homo sapiens)}

PRWEQTHLTYRIENYTPDLPRADVDHAIEKAFQLWSNVTPLTFTKVSEGQADIMISFVRGDHRDNSPFDGPGGNLAHAFQPGPGIGGDAHFDEDERWTNNFREYNLHRVAAHELGHSLGLSHSTDIGALMYPSYTFSGDVQLAQDDIDGIQAIYGRS

>d1fbl\_2 d.92.1.11 (100-271) Fibroblast collagenase (MMP-1) {Pig (Sus scrofa)}

FVLTPGNPRWENTHLTYRIENYTPDLSREDVDRAIEKAFQLWSNVSPLTFTKVSEGQADIMISFVRGDHRDNSPFDGPGGNLAHAFQPGPGIGGDAHFDEDERWTKNFRDYNLYRVAAHELGHSLGLSHSTDIGALMYPNYIYTGDVQLSQDDIDGIQAIYGPSENPVQPSG

>d1hova\_ d.92.1.11 (A:) MMP-2 {Human (Homo sapiens)}

MYNFFPRKPKWDKNQITYRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRIHDGEADIMINFGRWEHGDGYPFDGKDGLLAHAFAPGTGVGGDSHFDDDELWTNTSANYSLFLVAAHEFGHAMGLEHSQDPGALMAPIYTYTKNFRLSQDDIKGIQELYG

>d1i76a\_ d.92.1.11 (A:) Neutrophil collagenase (MMP-8) {Human (Homo sapiens)}

MLTPGNPKWERTNLTYRIRNYTPQLSEAEVERAIKDAFELWSVASPLIFTRISQGEADINIAFYQRDHGDNSPFDGPNGILAHAFQPGQGIGGDAHFDAEETWTNTSANYNLFLVAAHEFGHSLGLAHSSDPGALMYPNYAFRETSNYSLPQDDIDGIQAIYG

>d1qiba\_ d.92.1.11 (A:) Gelatinase A {Human (Homo sapiens)}

RKPKWDKNQITYRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRIHDGEADIMINFGRWEHGDGYPFDGKDGLLAHAFAPGTGVGGDSHFDDDELWSLGKGVGYSLFLVAAHEFGHAMGLEHSQDPGALMAPIYTYTKNFRLSQDDIKGIQELYGASP

>d1hy7a\_ d.92.1.11 (A:) Stromelysin-1 (MMP-3) {Human (Homo sapiens), fibroblast}

FRTFPGIPKWRKTHLTYRIVNYTPDLPKDAVDSAVEKALKVWEEVTPLTFSRLYEGEADIMISFAVREHGDFYPFDGPGNVLAHAYAPGPGINGDAHFDDDEQWTKDTTGTNLFLVAAHEIGHSLGLFHSANTEALMYPLYHSLTDLTRFRLSQDDINGIQSLYGPPP

>d1mmq\_\_ d.92.1.11 (-) Matrilysin (MMP-9) {Human (Homo sapiens)}

YSLFPNSPKWTSKVVTYRIVSYTRDLPHITVDRLVSKALNMWGKEIPLHFRKVVWGTADIMIGFARGAHGDSYPFDGPGNTLAHAFAPGTGLGGDAHFDEDERWTDGSSLGINFLYAATHELGHSLGMGHSSDPNAVMYPTYGNGDPQNFKLSQDDIKGIQKLYGK

>d1hv5a\_ d.92.1.11 (A:) Stromelysin-3 (MMP-11) {Mouse (Mus musculus)}

MFVLSGGRWEKTDLTYRILRFPWQLVREQVRQTVAEALQVWSEVTPLTFTEVHEGRADIMIDFARYWHGDNLPFDGPGGILAHAFFPKTHREGDVHFDYDETWTIGDNQGTDLLQVAAHEFGHVLGLQHTTAAKALMSPFYTFRYPLSLSPDDRRGIQHLYG

>d1jk3a\_ d.92.1.11 (A:) Macrophage elastase (MMP-12) {Human (Homo sapiens)}

GPVWRKHYITYRINNYTPDMNREDVDYAIRKAFQVWSNVTPLKFSKINTGMADILVVFARGAHGDFHAFDGKGGILAHAFGPGSGIGGDAHFDEDEFWTTHSGGTNLFLTAVHAIGHSLGLGHSSDPKAVMFPTYKYVDINTFRLSADDIRGIQSLYG

>d830ca\_ d.92.1.11 (A:) Collagenase-3 (MMP-13) {Human (Homo sapiens)}

YNVFPRTLKWSKMNLTYRIVNYTPDMTHSEVEKAFKKAFKVWSDVTPLNFTRLHDGIADIMISFGIKEHGDFYPFDGPSGLLAHAFPPGPNYGGDAHFDDDETWTSSSKGYNLFLVAAHEFGHSLGLDHSKDPGALMFPIYTYTGKSHFMLPDDDVQGIQSLYGPGDE

>d1cxva\_ d.92.1.11 (A:) Collagenase-3 (MMP-13) {Mouse (Mus musculus)}

YNVFPRTLKWSQTNLTYRIVNYTPDMSHSEVEKAFRKAFKVWSDVTPLNFTRIYDGTADIMISFGTKEHGDFYPFDGPSGLLAHAFPPGPNYGGDAHFDDDETWTSSSKGYNLFIVAAHELGHSLGLDHSKDPGALMFPIYTYTGKSHFMLPDDDVQGIQFLYG

>d1bqqm\_ d.92.1.11 (M:) Membrane-type matrix metalloproteinase (CDMT1-MMP) {Human (Homo sapiens)}

IQGLKWQHNEITFCIQNYTPKVGEYATYEAIRKAFRVWESATPLRFREVPYAYIREGHEKQADIMIFFAEGFHGDSTPFDGEGGFLAHAYFPGPNIGGDTHFDSAEPWTVRNEDLNGNDIFLVAVHELGHALGLEHSSDPSAIMAPFYQWMDTENFVLPDDDRRGIQQLYGGES

>d1qba\_4 d.92.2.1 (201-337) Bacterial chitobiase, Domain 2 {Serratia marcescens}

SNADLQTLPAGALRGKIVPTPMQVKVHAQDADLRKGVALDLSTLVKPAADVVSQRFALLGVPVQTNGYPIKTDIQPGKFKGAMAVSGAYELKIGKKEAQVIGFDQAGVFYGLQSILSLVPSDGSGKIATLDASDAPR

>d1jaka2 d.92.2.1 (A:8-150) beta-N-acetylhexosaminidase, N-terminal domain {Streptomyces plicatus}

DRKAPVRPTPLDRVIPAPASVDPGGAPYRITRGTHIRVDDSREARRVGDYLADLLRPATGYRLPVTAHGHGGIRLRLAGGPYGDEGYRLDSGPAGVTITARKAAGLFHGVQTLRQLLPPAVEKDSAQPGPWLVAGGTIEDTPR

>d1cwdl\_ d.93.1.1 (L:) p56-lck tyrosine kinase {Human (Homo sapiens)}

GSWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSR

>d1lkka\_ d.93.1.1 (A:) p56-lck tyrosine kinase {Human (Homo sapiens)}

LEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESESTAGSFSLSVRDFDQNQGEVVKHYKIRNLDNGGFYISPRITFPGLHELVRHYTNASDGLCTRLSRPCQT

>d1bkl\_\_ d.93.1.1 (-) v-src tyrosine kinase {Rous sarcoma virus, Schmidt-ruppin strain a}

EEWYFGKITRRESESLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPTSKEFIVTD

>d1shaa\_ d.93.1.1 (A:) v-src tyrosine kinase {Rous sarcoma virus, Schmidt-ruppin strain a}

AEEWYFGKITRRESERLLLNPENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSGGFYITSRTQFSSLQQLVAYYSKHADGLCHRLTNVCPT

>d1a09a\_ d.93.1.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}

DSIQAEEWYFGKITRRESERLLLNAENPRGTFLVRESETTKGAYCLSVSDFDNAKGLNVKHYKIRKLDSGGFYITSRTQFNSLQQLVAYYSKHADGLCHRLTTVCP

>d1g83a2 d.93.1.1 (A:142-245) Tyrosine kinase Fyn {Human (Homo sapiens)}

DSIQAEEWYFGKLGRKDAERQLLSFGNPRGTFLIRESETTKGAYSLSIRDWDDMKGDHVKHYKIRKLDNGGYYITTRAQFETLQQLVQHYSERAAGLSSRLVVP

>d1ayaa\_ d.93.1.1 (A:) Tyrosine phosphatase Syp {Mouse (Mus musculus)}

MRRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDFTLSVRRNGAVTHIKIQNTGDYYDLYGGEKFATLAELVQYYMEHHGQLKEKNGDVIELKYPLN

>d1fhs\_\_ d.93.1.1 (-) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo sapiens)}

GIEMKPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKVLRDGAGKYFLWVVKFNSLNELVDYHRSTSVSRNQQIFLRDIEQVPQQPTYVQA

>d1zfpe\_ d.93.1.1 (E:) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo sapiens)}

KPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKVLRDGAGKYFLWVVKFNSLNELVDYHRSTSVSRNQQIFLRDIEQ

>d1qcfa2 d.93.1.1 (A:146-248) Hemopoetic cell kinase Hck {Human (Homo sapiens)}

EEWFFKGISRKDAERQLLAPGNMLGSFMIRDSETTKGSYSLSVRDYDPRQGDTVKHYKIRTLDNGGFYISPRSTFSTLQELVDHYKKGNDGLCQKLSVPCMSS

>d1mil\_\_ d.93.1.1 (-) Shc adaptor protein {Human (Homo sapiens)}

GSQLRGEPWFHGKLSRREAEALLQLNGDFLVRESTTTPGQYVLTGLQSGQPKHLLLVDPEGVVRTKDHRFESVSHLISYHMDNHLPIISAGSELCLQQPVERKL

>d1qada\_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Cow (Bos taurus)}

EDLPHHDEKTWNVGSSNRNKAENLLRGKRDGTFLVRESSKQGCYACSVVVDGEVKHCVINKTATGYGFAEPYNLYSSLKELVLHYQHTSLVQHNDSLNVTLAYPVYA

>d1pica\_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Human (Homo sapiens)}

GSPIPHHDEKTWNVGSSNRNKAENLLRGKRDGTFLVRESSKQGCYACSVVVDGEVKHCVINKTATGYGFAEPYNLYSSLKELVLHYQHTSLVQHNDSLNVTLAYPVYAQQRR

>d1fu6a\_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Rat (Rattus norvegicus)}

GMNNNMSLQDAEWYWGDISREEVNEKLRDTADGTFLVRDASTKMHGDYTLTLRKGGNNKSIKIFHRDGKYGFSDPLTFNSVVELINHYRNESLAQYNPKLDVKLLYPVSKY

>d1ab2\_\_ d.93.1.1 (-) Proto-oncogen tyrosine kinase {Human (Homo sapiens)}

GSGNSLEKHSWYHGPVSRNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLYVSSESRFNTLAELVHHHSTVADGLITTLHYPAPKRGIHRD

>d1a81a1 d.93.1.1 (A:9-137) Syk tyrosine kinase {Human (Homo sapiens)}

SANHLPFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHYTIERELNGTYAIAGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPQGVQPKTGPFEDLKENLIREYVKQTWN

>d1a81a2 d.93.1.1 (A:138-262) Syk tyrosine kinase {Human (Homo sapiens)}

LQGQALEQAIISQKPQLEKLIATTAHEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKVLHYRIDKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKI

>d1a81e1 d.93.1.1 (E:9-117) Syk tyrosine kinase {Human (Homo sapiens)}

SANHLPFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHYTIERELNGTYAIAGGRTHASPADLCHYHSQESDGLVCLLKKPFNRPQGVQPKT

>d1a81e2 d.93.1.1 (E:152-262) Syk tyrosine kinase {Human (Homo sapiens)}

PQLEKLIATTAHEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKVLHYRIDKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKI

>d1csya\_ d.93.1.1 (A:) Syk tyrosine kinase {Human (Homo sapiens)}

GSRRASVGSHEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKVLHYRIDKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKIGTQ

>d2plda\_ d.93.1.1 (A:) Phospholipase C-gamma-1 {Cow (Bos taurus)}

GSPGIHESKEWYHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYAISFRAEGKIKHCRVQQEGQTVMLGNSEFDSLVDLISYYEKHPLYRKMKLRYPINEENSS

>d1blk\_\_ d.93.1.1 (-) P55 Blk protein tyrosine kinase {Mouse (Mus musculus)}

GSVAPVETLEVEKWFFRTISRKDAERQLLAPMNKAGSFLIRESESNKGAFSLSVKDITTQGEVVKHYKIRSLDNGGYYISPRITFPTLQALVQHYSKKGDGLCQKLTLPCVNLA

>d2abl\_2 d.93.1.1 (140-237) Abl tyrosine kinase {Human (Homo sapiens)}

SLEKHSWYHGPVSRNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLYVSSESRFNTLAELVHHHSTVADGLITTLHYPAP

>d1jwoa\_ d.93.1.1 (A:) Csk homologous kinase Chk {Human (Homo sapiens)}

LSLMPWFHGKISGQEAVQQLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDGHLTIDEAVFFCNLMDMVEHYSKDKGAICTKLVRPKRK

>d1bf5a3 d.93.1.1 (A:569-710) STAT-1 {Human (Homo sapiens)}

LLPLWNDGCIMGFISKERERALLKDQQPGTFLLRFSESSREGAITFTWVERSQNGGEPDFHAVEPYTKKELSAVTFPDIIRNYKVMAAENIPENPLKYLYPNIDKDHAFGKYYSRGYIKTELISVS

>d1bg1a3 d.93.1.1 (A:576-716) STAT3b {Mouse (Mus musculus)}

ILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWVEKDISGSTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPGSAAPYLKTKFICVTPF

>d2cbla3 d.93.1.1 (A:264-351) Cbl {Human (Homo sapiens)}

THPGYMAFLTYDEVKARLQKFIHKPGSYIFRLSCTRLGQWAIGYVTADGNILQTIPHNKPLFQALIDGFREGFYLFPDGRNQNPDLTG

>d2shpa2 d.93.1.1 (A:2-110) Tyrosine phoshatase shp-2 {Human (Homo sapiens)}

KSRRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDLTLSVRRNGAVTHIKIQNTGDYYDLYGGEKFATLAELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSE

>d2shpa3 d.93.1.1 (A:111-218) Tyrosine phoshatase shp-2 {Human (Homo sapiens)}

RWFHGHLSGKEAEKLLTEKGKHGSFLVRESQSHPGDFVLSVRTGDDKGESNDGKSKVTHVMIRCQELKYDVGGGERFDSLTDLVEHYKKNPMVETLGTVLQLKQPLNT

>d1d4ta\_ d.93.1.1 (A:) The Xlp protein Sap {Human (Homo sapiens)}

MDAVAVYHGKISRETGEKLLLATGLDGSYLLRDSESVPGVYCLCVLYHGYIYTYRVSQTETGSWSAETAPGVHKRYFRKIKNLISAFQKPDQGIVIPLQYPVEK

>d1spha\_ d.94.1.1 (A:) Histidine-containing phosphocarrier protein (HPr) {Bacillus subtilis}

AQKTFKVTADSGIHARPATVLVQTASKYDADVNLEYNGKTVNLKDIMGVMSLGIAKGAEITISASGADENDALNALEETMKSEGLGE

>d1ptf\_\_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Enterococcus faecalis}

MEKKEFHIVAETGIHARPATLLVQTASKFNSDINLEYKGKSVNLKSIMGVMSLGVGQGSDVTITVDGADEAEGMAAIVETLQKEGLA

>d1opd\_\_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Escherichia coli}

MFEQEVTITAPNGLHTRPAAQFVKEAKGFTSEITVTSNGKSASAKDLFKLQTLGLTQGTVVTISAEGEDEQKAVEHLVKLMAELE

>d1pch\_\_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Mycoplasma capricolum}

AKFSAIITDKVGLHARPASVLAKEASKFSSNITIIANEKQGNLKSIMNVMAMAIKTGTEITIQADGNDADQAIQAIKQTMIDTALIQG

>d1zer\_\_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Staphylococcus aureus}

MEQNSYVIIDETGIHARPATMLVQTASKFDSDIQLEYNGKKVNLKSIMGVMSLGVGKDAEITIYADGSDESDAIQAISDVLSKEGLT

>d1qr5a\_ d.94.1.1 (A:) Histidine-containing phosphocarrier protein (HPr) {Staphylococcus carnosus}

MEQQSYTIIDETGIHARPATMLVQTASKFDSDIQLEYNGKKVNLKSIMGVMSLGVGKDAEITIYADGSDEADAIQAITDVLSKEGLTE

>d1k1ca\_ d.94.1.1 (A:) Crh, catabolite repression HPr-like protein {Bacillus subtilis}

VQQKVEVRLKTGLQARPAALFVQEANRFTSDVFLEKDGKKVNAKSIMGLMSLAVSTGTEVTLIAQGEDEQEALEKLAAYVQEEV

>d1jrma\_ d.206.1.1 (A:) Hypothetical protein MTH637 {Archaeon Methanobacterium thermoautotrophicum}

VITMDCLREVGDDLLVNIEVSPASGKFGIPSYNEWRKRIEVKIHSPPQKGKANREIIKEFSETFGRDVEIVSGQKSRQKTIRIQGMGRDLFLKLVSEKFGLEIP

>d1iba\_\_ d.95.1.1 (-) Glucose permease domain IIB {Escherichia coli}

MAPALVAAFGGKENITNLDACITRLRVSVADVSKVDQAGLKKLGAAGVVVAGSGVQAIFGTKSDNLKTEMDEYIRNFG

>d1af5\_\_ d.95.2.1 (-) DNA endonuclease I-CreI {Chlamydomonas reinhardtii}

KYNKEFLLYLAGFVDGDGSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLGKLVDEIGVGYVRDRGSVSDYILSEIKPLHNFLTQLQPFLKLKQKQANLVLKIIEQLPLEVCTWVDQIAALNDS

>d1g9za\_ d.95.2.1 (A:) DNA endonuclease I-CreI {Chlamydomonas reinhardtii}

NTKYNKEFLLYLAGFVDGDGSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLDKLVDEIGVGYVRDRGSVSDYILSEIKPLHNFLTQLQPFLKLKQKQANLVLKIIEQLPSAKESPDKFLEVCTWVDQIAALNDSKTRKTTSETVRAVLD

>d1b24a1 d.95.2.1 (A:7-99) I-dmoI {Archaeon Desulfurococcus mobilis}

VSGISAYLLGLIIGDGGLYKLKYKGNRSEYRVVITQKSENLIKQHIAPLMQFLIDELNVKSKIQIVKGDTRYELRVSSKKLYYYFANMLERIR

>d1b24a2 d.95.2.1 (A:100-179) I-dmoI {Archaeon Desulfurococcus mobilis}

LFNMREQIAFIKGLYVAEGDKTLKRLRIWNKNKALLEIVSRWLNNLGVRNTIHLDDHRHGVYVLNISLRDRIKFVHTILS

>d1dfaa2 d.95.2.2 (A:181-298) PI-SceI {Baker's yeast (Saccharomyces cerevisiae)}

PILYENDHFFDYMQKSKFHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAEKLNLCAEYKDRKEPQVAKTVNLYSKVVRGNGIRNNLNTENPLWDAIVGLGFLKD

>d1dfaa3 d.95.2.2 (A:299-415) PI-SceI {Baker's yeast (Saccharomyces cerevisiae)}

GVKNIPSFLSTDNIGTRETFLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGLVSLARSLGLVVSVNAEPAKVDMNGTKHKISYAIYMSGGDVLLNVLSKCAGSKKFRPAPAAAFARE

>d1dq3a3 d.95.2.2 (A:129-226) PI-Pfui intein {Archaeon Pyrococcus furiosus}

PDGEDYKFIFDYWLAGFIAGDGCFDKYHSHVKGHEYIYDRLRIYDYRIETFEIINDYLEKTFGRKYSIQKDRNIYYIDIKARNITSHYLKLLEGIDNG

>d1dq3a4 d.95.2.2 (A:227-335) PI-Pfui intein {Archaeon Pyrococcus furiosus}

IPPQILKEGKNAVLSFIAGLFDAEGHVSNKPGIELGMVNKRLIEDVTHYLNALGIKARIREKLRKDGIDYVLHVEEYSSLLRFYELIGKNLQNEEKREKLEKVLSNHKG

>d1a8ra\_ d.96.1.1 (A:) GTP cyclohydrolase I {Escherichia coli}

PSLSKEAALVHEALVARGLETPLRPPVHEMDNETRKSLIAGHMTEIMQLLNLDLADDSLMETPHRIAKMYVDEIFSGLDYANFPKITLIENKMKVDEMVTVRDITLTSTCESHFVTIDGKATVAYIPKDSVIGLSKINRIVQFFAQRPQVQERLTQQILIALQTLLGTNNVAVSIDAVHYCVKARGIRDATSATTTTSLGGLFKSSQNTRHEFLRAVRHHN

>d1is8a\_ d.96.1.1 (A:) GTP cyclohydrolase I {Rat (Rattus norvegicus)}

RPRSEEDNELNLPNLAAAYSSILRSLGEDPQRQGLLKTPWRAATAMQFFTKGYQETISDVLNDAIFDEDHDEMVIVKDIDMFSMCEHHLVPFVGRVHIGYLPNKQVLGLSKLARIVEIYSRRLQVQERLTKQIAVAITEALQPAGVGVVIEATHMCMVMRGVQKMNSKTVTSTMLGVFREDPKTREEFLTLIRS

>d1b66a\_ d.96.1.2 (A:) 6-pyruvoyl tetrahydropterin synthase {Rat (Rattus norvegicus)}

LRRRARLSRLVSFSASHRLHSPSLSAEENLKVFGKCNNPNGHGHNYKVVVTIHGEIDPVTGMVMNLTDLKEYMEEAIMKPLDHKNLDLDVPYFADVVSTTENVAVYIWENLQRLLPVGALYKVKVYETDNNIVVYKGE

>d1dhn\_\_ d.96.1.3 (-) 7,8-dihidroneopterin aldolase {Staphylococcus aureus}

MQDTIFLKGMRFYGYHGALSAENEIGQIFKVDVTLKVDLSEAGRTDNVIDTVHYGEVFEEVKSIMEGKAVNLLEHLAERIANRINSQYNRVMETKVRITKENPPIPGHYDGVGIEIVRENK

>d1b9la\_ d.96.1.3 (A:) 7,8-dihydroneopterin triphosphate epimerase {Escherichia coli}

AQPAAIIRIKNLRLRTFIGIKEEEINNRQDIVINVTIHYPADKARTSEDINDALNYRTVTKNIIQHVENNRFSLLEKLTQDVLDIAREHHWVTYAEVEIDKLHALRYADSVSMTLSWQR

>d1uox\_1 d.96.1.4 (1-136) Urate oxidase (uricase) {Aspergillus flavus}

SAVKAARYGKDNVRVYKVHKDEKTGVQTVYEMTVCVLLEGEIETSYTKADNSVIVATDSIKNTIYITAKQNPVTPPELFGSILGTHFIEKYNHIHAAHVNIVCHRWTRMDIDGKPHPHSFIRDSEEKRNVQVDVVE

>d1uox\_2 d.96.1.4 (137-295) Urate oxidase (uricase) {Aspergillus flavus}

GKGIDIKSSLSGLTVLKSTNSQFWGFLRDEYTTLKETWDRILSTDVDATWQWKNFSGLQEVRSHVPKFDATWATAREVTLKTFAEDNSASVQATMYKMAEQILARQQLIETVEYSLPNKHYFEIDLSWHKGLQNTGKNAEVFAPQSDPNGLIKCTVGRS

>d1puc\_\_ d.97.1.1 (-) suc1 {Fission yeast (Schizosaccharomyces pombe)}

SKSGVPRLLTASERERLEPFIDQIHYSPRYADDEYEYRHVMLPKAMLKAIPTDYFNPETGTLRILQEEEWRGLGITQSLGWEMYEVHVPEPHILLFKREKD

>d1qb3a\_ d.97.1.1 (A:) cks1 {Baker's yeast (Saccharomyces cerevisiae)}

HAFQGRKLTDQERARVLEFQDSIHYSPRYSDDNYEYRHVMLPKAMLKVIPSDYFNSEVGTLRILTEDEWRGLGITQSLGWEHYECHAPEPHILLFKRPLNYEAELRAATAAAQ

>d1cksa\_ d.97.1.1 (A:) CksHs2 {Human (Homo sapiens)}

AHKQIYYSDKYFDEHYEYRHVMLPRELSKQVPKTHLMSEEEWRRLGVQQSLGWVHYMIHEPEPHILLFRRPLPK

>d1buhb\_ d.97.1.1 (B:) CksHs1 {Human (Homo sapiens)}

QIYYSDKYDDEEFEYRHVMLPKDIAKLVPKTHLMSESEWRNLGVQQSQGWVHYMIHEPEPHILLFRRPLP

>d1jtgb\_ d.98.1.1 (B:) beta-lactamase-inhibitor protein, BLIP {Streptomyces clavuligerus}

AGVMTGAKFTQIQFGMTRQQVLDIAGAENCETGGSFGDSIHCRGHAAGDYYAYATFGFTSAAADAKVDSKSQEKLLAPSAPTLTLAKFNQVTVGMTRAQVLATVGQGSCTTWSEYYPAYPSTAGVTLSLSCFDVDGYSSTGFYRGSAHLWFTDGVLQGKRQWDLV

>d1div\_1 d.99.1.1 (56-149) Ribosomal protein L9 C-domain {Bacillus stearothermophilus}

RQAAEELANAKKLKEQLEKLTVTIPAKAGEGGRLFGSITSKQIAESLQAQHGLKLDKRKIELADAIRALGYTNVPVKLHPEVTATLKVHVTEQK

>d1div\_2 d.100.1.1 (1-55) Ribosomal protein L9 N-domain {Bacillus stearothermophilus}

MKVIFLKDVKGKGKKGEIKNVADGYANNFLFKQGLAIEATPANLKALEAQKQKEQ

>d1qhka\_ d.100.1.2 (A:) N-terminal domain of RNase HI {Baker's yeast (Saccharomyces cerevisiae)}

GNFYAVRKGRETGIYNTWNECKNQVDGYGGAIYKKFNSYEQAKSFLG

>d1e3ha5 d.101.1.1 (A:152-262) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5 {Streptomyces antibioticus}

FSGPIGGVRVALIRGQWVAFPTHTELEDAVFDMVVAGRVLEDGDVAIMMVEAEATEKTIQLVKDGAEAPTEEVVAAGLDAAKPFIKVLCKAQADLAAKAAKPTGEFPVFLD

>d1e3ha6 d.101.1.1 (A:483-578) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5 {Streptomyces antibioticus}

APVAGIAMGLISQEINGETHYVALTDILGAEDAFGDMDFKVAGTKEFVTALQLDTKLDGIPASVLAAALKQARDARLHILDVMMEAIDTPDEMSPN

>d1efnb\_ d.102.1.1 (B:) Regulatory factor Nef {Human immunodeficiency virus type 1}

RPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPGVRYPLTFGWCYKLVPVEPDKVEEANKGENTSLLHPVSLHGMDDPEREVLEWRFDSRLAFHHVARELHPEYF

>d2nef\_\_ d.102.1.1 (-) Regulatory factor Nef {Human immunodeficiency virus type 1}

AWLEAQEEEEVGFPVTPQVPLRPMTYKAAVDLSHFLKEKGGLEGLIHSQRRQDILDLWIYHTQGYFPDWQNYTPGPGIRYPLTFGWCYKLVPVEPEKLEEANKDDPEREVLEWRFDSRLAFHHMARELHPEYFKNA

>d1cby\_\_ d.103.1.1 (-) Mosquitocidal delta-endotoxin CytB {Bacillus thuringiensis, strain Kyushuensis}

CSAPIIRKPFKHIVLTVPSSDLDNFNTVFYVQPQYINQALHLANAFQGAIDPLNLNFNFEKALQIANGIPNSAIVKTLNQSVIQQTVEISVMVEQLKKIIQEVLGLVINSTSFWNSVEATIKGTFTNLDTQIDEAWIFWHSLSAHNTSYYYNILFSIQNEDTGAVMAVLPLAFEVSVDVEKQKVLFFTIKDSARYEVKMKALTLVQALHSSNAPIVDIFNVNNYNLY

>d1seta2 d.104.1.1 (A:111-421) Seryl-tRNA synthetase (SerRS) {Thermus thermophilus, strain hb27}

VGGEEANREIKRVGGPPEFSFPPLDHVALMEKNGWWEPRISQVSGSRSYALKGDLALYELALLRFAMDFMARRGFLPMTLPSYAREKAFLGTGHFPAYRDQVWAIAETDLYLTGTAEVVLNALHSGEILPYEALPLRYAGYAPAFRSEAGSFGKDVRGLMRVHQFHKVEQYVLTEASLEASDRAFQELLENAEEILRLLELPYRLVEVATGDMGPGKWRQVDIEVYLPSEGRYRETHSCSALLDWQARRANLRYRDPEGRVRYAYTLNNTALATPRILAMLLENHQLQDGRVRVPQALIPYMGKEVLEPCG

>d1e1oa2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysU}

DQEVRYRQRYLDLIANDKSRQTFVVRSKILAAIRQFMVARGFMEVETPMMQVIPGGASARPFITHHNALDLDMYLRIAPELYLKRLVVGGFERVFEINRNFRNEGISVRHNPEFTMMELYMAYADYHDLIELTESLFRTLAQEVLGTTKVTYGEHVFDFGKPFEKLTMREAIKKYRPETDMADLDNFDAAKALAESIGITVEKSWGLGRIVTEIFDEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGGREIGNGFSELNDAEDQAERFQEQVNAKAAGDDEAMFYDEDYVTALEYGLPPTAGLGIGIDRMIMLFTNSHTIRDVILFPAMRP

>d1bbua2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}

DQEARYRQRYLDLISNDESRNTFKVRSQILSGIRQFMVNRGFMEVETPMMQVIPGGAAARPFITHHNALDLDMYLRIAPELYLKRLVVGGFERVFEINRNFRNEGISVRHNPEFTMMELYMAYADYKDLIELTESLFRTLAQDILGKTEVTYGDVTLDFGKPFEKLTMREAIKKYRPETDMADLDNFDSAKAIAESIGIHVEKSWGLGRIVTEIFEEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGGREIGNGFSELNDAEDQAQRFLDQVAAKDAGDDEAMFYDEDYVTALEHGLPPTAGLGIGIDRMVMLFTNSHTIRDVILFPAMRP

>d1kmma2 d.104.1.1 (A:4-325) Histidyl-tRNA synthetase (HisRS) {Escherichia coli}

NIQAIRGMNDYLPGETAIWQRIEGTLKNVLGSYGYSEIRLPIVEQTPLFKRAIGEVTDVVEKEMYTFEDRNGDSLTLRPEGTAGCVRAGIEHGLLYNQEQRLWYIGPMFRHERPQKGRYRQFHQLGCEVFGLQGPDIDAELIMLTARWWRALGISEHVTLELNSIGSLEARANYRDALVAFLEQHKEKLDEDCKRRMYTNPLRVLDSKNPEVQALLNDAPALGDYLDEESREHFAGLCKLLESAGIAYTVNQRLVRGLDYYNRTVFEWVTNSLGSQGTVCAGGRYDGLVEQLGGRATPAVGFAMGLERLVLLVQAVNPEFKA

>d1qe0a2 d.104.1.1 (A:1-325) Histidyl-tRNA synthetase (HisRS) {Staphylococcus aureus}

MIKIPRGTQDILPEDSKKWRYIENQLDELMTFYNYKEIRTPIFESTDLFARGVGDSTDVVQKEMYTFKDKGDRSITLRPEGTAAVVRSYIEHKMQGNPNQPIKLYYNGPMFRYERKQKGRYRQFNQFGVEAIGAENPSVDAEVLAMVMHIYQSFGLKHLKLVINSVGDMASRKEYNEALVKHFEPVIHEFCSDCQSRLHTDPMRILDCKVDRDKEAIKTAPRITDFLNEESKAYYEQVKAYLDDLGIPYTEDPNLVRGLDYYTHTAFELMMDNPNYDGAITTLCGGGRYNGLLELLDGPSETGIGFALSIERLLLALEEEGIELD

>d1h4vb2 d.104.1.1 (B:2-325) Histidyl-tRNA synthetase (HisRS) {Thermus thermophilus}

TARAVRGTKDLFGKELRMHQRIVATARKVLEAAGALELVTPIFEETQVFEKGVGAATDIVRKEMFTFQDRGGRSLTLRPEGTAAMVRAYLEHGMKVWPQPVRLWMAGPMFRAERPQKGRYRQFHQVNYEALGSENPILDAEAVVLLYECLKELGLRRLKVKLSSVGDPEDRARYNAYLREVLSPHREALSEDSKERLEENPMRILDSKSERDQALLKELGVRPMLDFLGEEARAHLKEVERHLERLSVPYELEPALVRGLDYYVRTAFEVHHEEIGAQSALGGGGRYDGLSELLGGPRVPGVGFAFGVERVALALEAEGFGLPE

>d1atia2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}

AASSLDELVALCKRRGFIFQSSEIYGGLQGVYDYGPLGVELKNNLKQAWWRRNVYERDDMEGLDASVLTHRLVLHYSGHEATFADPMVDNRITKKRYRLDHLLKEQPEEVLKRLYRAMEVEEENLHALVQAMMQAPERAGGAMTAAGVLDPASGEPGDWTPPRYFNMMFQDLRGPRGGRGLLAYLRPETAQGIFVNFKNVLDATSRKLGFGIAQIGKAFRNEITPRNFIFRVREFEQMEIEYFVRPGEDEYWHRYWVEERLKWWQEMGLSRENLVPYQQPPESSAHYAKATVDILYRFPHGSLELEGIAQRTDFDLGSHTKDQEALGITARVLRNEHSTQRLAYRDPETGKWFVPYVIEPSAGVDRGVLALLAEAFTREELPNGEERIVLKLKP

>d1b76a2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}

AASSLDELVALCKRRGFIFQSSEIYGGLQGVYDYGPLGVELKNNLKQAWWRRNVYERDDMEGLDASVLTHRLVLHYSGHEATFADPMVDNAKARYWTPPRYFNMMFQDLRGPRGGRGLLAYLRPETAQGIFVNFKNVLDATSRKLGFGIAQIGKAFRNEITPRNFIFRVREFEQMEIEYFVRPGEDEYWHRYWVEERLKWWQEMGLSRENLVPYQQPPESSAHYAKATVDILYRFPHGSLELEGIAQRTDFDLGSHTKDQEALGITARVLRNEHSTQRLAYRDPETGKWFVPYVIEPSAGVDRGVLALLAEAFTREELPNGEERIVLKLKP

>d1qf6a4 d.104.1.1 (A:242-532) Threonyl-tRNA synthetase (ThrRS) {Escherichia coli}

RDHRKIGKQLDLYHMQEEAPGMVFWHNDGWTIFRELEVFVRSKLKEYQYQEVKGPFMMDRVLWEKTGHWDNYKDAMFTTSSENREYCIKPMNCPGHVQIFNQGLKSYRDLPLRMAEFGSCHRNEPSGSLHGLMRVRGFTQDDAHIFCTEEQIRDEVNGCIRLVYDMYSTFGFEKIVVKLSTRPEKRIGSDEMWDRAEADLAVALEENNIPFEYQLGEGAFYGPKIEFTLYDCLDRAWQCGTVQLDFSLPSRLSASYVGEDNERKVPVMIHRAILGSMERFIGILTEEFAGF

>d1eova2 d.104.1.1 (A:205-557) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}

PILLEDASRSEAEAEAAGLPVVNLDTRLDYRVIDLRTVTNQAIFRIQAGVCELFREYLATKKFTEVHTPKLLGAPSEGGSSVFEVTYFKGKAYLAQSPQFNKQQLIVADFERVYEIGPVFRAENSNTHRHMTEFTGLDMEMAFEEHYHEVLDTLSELFVFIFSELPKRFAHEIELVRKQYPVEEFKLPKDGKMVRLTYKEGIEMLRAAGKEIGDFEDLSTENEKFLGKLVRDKYDTDFYILDKFPLEIRPFYTMPDPANPKYSNSYDFFMRGEEILSGAQRIHDHALLQERMKAHGLSPEDPGLKDYCDGFSYGCPPHAGGGIGLERVVMFYLDLKNIRRASLFPRDPKRLRP

>d1b8aa2 d.104.1.1 (A:104-438) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus kodakaraensis}

PLPLDPTGKVKAELDTRLNNRFMDLRRPEVMAIFKIRSSVFKAVRDFFHENGFIEIHTPKIIATATEGGTELFPMKYFEEDAFLAESPQLYKEIMMASGLDRVYEIAPIFRAEEHNTTRHLNEAWSIDSEMAFIEDEEEVMSFLERLVAHAINYVREHNAKELDILNFELEEPKLPFPRVSYDKALEILGDLGKEIPWGEDIDTEGERLLGKYMMENENAPLYFLYQYPSEAKPFYIMKYDNKPEICRAFDLEYRGVEISSGGQREHRHDILVEQIKEKGLNPESFEFYLKAFRYGMPPHGGFGLGAERLIKQMLDLPNIREVILFPRDRRRLTP

>d1c0aa3 d.104.1.1 (A:107-287,A:421-585) Aspartyl-tRNA synthetase (AspRS) {Escherichia coli}

VLPLDSNHVNTEEARLKYRYLDLRRPEMAQRLKTRAKITSLVRRFMDDHGFLDIETPMLTKATPEGARDYLVPSRVHKGKFYALPQSPQLFKQLLMMSGFDRYYQIVKCFRDEDLRADRQPEFTQIDVETSFMTAPQVREVMEALVRHLWLEVKGVDLGDFPVMTFAEAERRYGSDKPDLRXDESKWAPLWVIDFPMFEDDGEGGLTAMHHPFTSPKDMTAAELKAAPENAVANAYDMVINGYEVGGGSVRIHNGDMQQTVFGILGINEEEQREKFGFLLDALKYGTPPHAGLAFGLDRLTMLLTGTDNIRDVIAFPKTTAAACLMTEAPSFANPTALAELSIQVVK

>d1g51a3 d.104.1.1 (A:105-294,A:415-580) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}

TPPFPVDAGWRGEEEKEASEELRLKYRYLDLRRRRMQENLRLRHRVIKAIWDFLDREGFVQVETPFLTKSTPEGARDFLVPYRHEPGLFYALPQSPQLFKQMLMVAGLDRYFQIARCFRDEDLRADRQPDFTQLDLEMSFVEVEDVLELNERLMAHVFREALGVELPLPFPRLSYEEAMERYGSDKPDLRXREGFRFLWVVDFPLLEWDEEEEAWTYMHHPFTSPHPEDLPLLEKDPGRVRALAYDLVLNGVEVGGGSIRIHDPRLQARVFRLLGIGEEEQREKFGFFLEALEYGAPPHGGIAWGLDRLLALMTGSPSIREVIAFPKNKEGKDPLTGAPSPVPEEQLRELGLMVVRP

>d1jjca\_ d.104.1.1 (A:) Phenyl-tRNA synthetase (PheRS) alpha subunit, PheS {Thermus thermophilus and (Thermus aquaticus)}

RVDVSLPGASLFSGGLHPITLMERELVEIFRALGYQAVEGPEVESEFFNFDALNIPEHHPARDMWDTFWLTGEGFRLEGPLGEEVEGRLLLRTHTSPMQVRYMVAHTPPFRIVVPGRVFRFEQTDATHEAVFHQLEGLVVGEGIAMAHLKGAIYELAQALFGPDSKVRFQPVYFPFVEPGAQFAVWWPEGGKWLELGGAGMVHPKVFQAVDAYRERLGLPPAYRGVTGFAFGLGVERLAMLRYGIPDIRYFFGGRLKFLEQFKGVL

>d1jjcb5 d.104.1.1 (B:475-681) Phenyl-tRNA synthetase (PheRS) beta subunit, PheT, central domain {Thermus thermophilus (Thermus aquaticus)}

ALPAFFPAPDNRGVEAPYRKEQRLREVLSGLGFQEVYTYSFMDPEDARRFRLDPPRLLLLNPLAPEKAALRTHLFPGLVRVLKENLDLDRPERALLFEVGRVFREREETHLAGLLFGEGVGLPWAKERLSGYFLLKGYLEALFARLGLAFRVEAQAFPFLHPGVSGRVLVEGEEVGFLGALHPEIAQELELPPVHLFELRLPLPDKP

>d1hc7a2 d.104.1.1 (A:5-276) Prolyl-tRNA synthetase (ProRS) {Thermus thermophilus}

KGLTPQSQDFSEWYLEVIQKAELADYGPVRGTIVVRPYGYAIWENIQQVLDRMFKETGHQNAYFPLFIPMSFLRKEAEHVEGFSPELAVVTHAGGEELEEPLAVRPTSETVIGYMWSKWIRSWRDLPQLLNQWGNVVRWEMRTRPFLRTSEFLWQEGHTAHATREEAEEEVRRMLSIYARLAREYAAIPVIEGLKTEKEKFAGAVYTTTIEALMKDGKALQAGTSHYLGENFARAFDIKFQDRDLQVKYVHTTSWGLSWRFIGAIIMTHGDD

>d1g5ha2 d.104.1.1 (A:41-330) The aaRS-like accessory subunit of mitochondrial polymerase gamma, N-terminal domain {Mouse (Mus musculus)}

EALVDLCRRRHFLSGTPQQLSTAALLSGCHARFGPLGVELRKNLASQWWSSMVVFREQVFAVDSLHQEPGSSQPRDSAFRLVSPESIREILQDREPSKEQLVAFLENLLKTSGKLRATLLHGALEHYVNCLDLVNRKLPFGLAQIGVCFHPVSNSNQTPSSVTRVGEKTEASLVWFTPTRTSSQWLDFWLRHRLLWWRKFAMSPSNFSSADCQDELGRKGSKLYYSFPWGKEPIETLWNLGDQELLHTYPGNVSTIQGRDGRKNVVPCVLSVSGDVDLGTLAYLYDSFQL

>d12asa\_ d.104.1.1 (A:) Asparagine synthetase {Escherichia coli}

AYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGAEKAVQVKVKALPDAQFEVVHSLAKWKRQTLGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDQWDWERVMGDGERQFSTLKSTVEAIWAGIKATEAAVSEEFGLAPFLPDQIHFVHSQELLSRYPDLDAKGRERAIAKDLGAVFLVGIGGKLSDGHRHDVRAPDYDDWSTPSELGHAGLNGDILVWNPVLEDAFELSSMGIRVDADTLKHQLALTGDEDRLELEWHQALLRGEMPQTIGGGIGQSRLTMLLLQLPHIGQVQAGVWPAAVRESVPSLL

>d1bia\_3 d.104.1.2 (64-270) Biotin repressor/biotin holoenzyme synthetase, catalytic (central) domain {Escherichia coli}

IQLLNAKQILGQLDGGSVAVLPVIDSTNQYLLDRIGELKSGDACIAEYQQAGRGRRGRKWFSPFGANLYLSMFWRLEQGPAAAIGLSLVIGIVMAEVLRKLGADKVRVKWPNDLYLQDRKLAGILVELTGKTGDAAQIVIGAGINMAMRRVEESVVNQGWITLQEAGINLDRNTLAAMLIRELRAALELFEQEGLAPYLSRWEKLDN

>d1qtsa2 d.105.1.1 (A:825-938) Alpa-adaptin AP2, C-terminal subdomain {Mouse (Mus musculus)}

FFQPTEMASQDFFQRWKQLSNPQQEVQNIFKAKHPMDTEITKAKIIGFGSALLEEVDPNPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKDTVSQRLCELLSEQF

>d1e42a2 d.105.1.1 (A:825-937) Beta2-adaptin AP2, C-terminal subdomain {Human (Homo sapiens)}

LFVEDGKMERQVFLATWKDIPNENELQFQIKECHLNADTVSSKLQNNNVYTIAKRNVEGQDMLYQSLKLTNGIWILAELRIQPGNPNYTLSLKCRAPEVSQYIYQVYDSILKN

>d1c44a\_ d.106.1.1 (A:) Sterol carrier protein 2 (SCP2) {Rabbit (Oryctolagus cuniculus)}

SSAGDGFKANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGPGGKEATWVVDVKNGKGSVLPNSDKKADCTITMADSDLLALMTGKMNPQSAFFQGKLKITGNMGLAMKLQNLQLQPGKAKL

>d1ikta\_ d.106.1.1 (A:) SCP2-like domain of MFE-2 {Human (Homo sapiens)}

LQSTFVFEEIGRRLKDIGPEVVKKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGPAKGAADTTIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIMLSQKLQMILKDYAKL

>d1eq6a\_ d.107.1.1 (A:) Ran-binding protein mog1p {Baker's yeast (Saccharomyces cerevisiae)}

SMNNKEVELYGGAITTVVPPGFIDASTLREVPDTQEVYVNSRRDEEEFEDGLATNESIIVDLLETVDKSDLKEAWQFHVEDLTELNGTTKWEALQEDTVQQGTKFTGLVMEVANKWGKPDLAQTVVIGVALIRLTQFDTDVVISINVPLTKEEASQASNKELPARCHAVYQLLQEMVRKFHVVDTSLFA

>d1b87a\_ d.108.1.1 (A:) Aminoglycoside 6'-N-acetyltransferase {Enterococcus faecium}

MIISEFDRNNPVLKDQLSDLLRLTWPEEYGDSSAEEVEEMMNPERIAVAAVDQDELVGFIGAIPQYGITGWELHPLVVESSRRKNQIGTRLVNYLEKEVASRGGITIYLGTDDLDHGTTLSQTDLYEHTFDKVASIQNLREHPYEFYEKLGYKIVGVLPNANGWDKPDIWMAKTIIPRPDS

>d1bo4a\_ d.108.1.1 (A:) Aminoglycoside 3-N-acetyltransferase {Serratia marcescens}

GIIRTCRLGPDQVKSMRAALDLFGREFGDVATYSQHQPDSDYLGNLLRSKTFIALAAFDQEAVVGALAAYVLPKFEQPRSEIYIYDLAVSGEHRRQGIATALINLLKHEANALGAYVIYVQADYGDDPAVALYTKLG

>d1cm0a\_ d.108.1.1 (A:) Histone acetyltransferase domain of P300/CBP associating factor, PCAF {Human (Homo sapiens)}

KVIEFHVVGNSLNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTLALIKDGRVIGGICFRMFPSQGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRI

>d1ygha\_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Baker's yeast (Saccharomyces cerevisiae)}

KIEFRVVNNDNTKENMMVLTGLKNIFQKQLPKMPKEYIARLVYDRSHLSMAVIRKPLTVVGGITYRPFDKREFAEIVFCAISSTEQVRGYGAHLMNHLKDYVRNTSNIKYFLTYADNYAIGYFKKQGFTKEITLDKSIWMGYIKDYEGGTLMQCSMLPRIRYLD

>d1qsta\_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Tetrahymena thermophila}

LDFDILTNDGTHRNMKLLIDLKNIFSRQLPKMPKEYIVKLVFDRHHESMVILKNKQKVIGGICFRQYKPQRFAEVAFLAVTANEQVRGYGTRLMNKFKDHMQKQNIEYLLTYADNFAIGYFKKQGFTKEHRMPQEKWKGYIKDYDGGTLMECYIHPYVDY

>d1qsma\_ d.108.1.1 (A:) Histone acetyltransferase HPA2 {Baker's yeast (Saccharomyces cerevisiae)}

DNITVRFVTENDKEGWQRLWKSYQDFYEVSFPDDLDDFNFGRFLDPNIKMWAAVAVESSSEKIIGMINFFNHMTTWDFKDKIYINDLYVDENSRVKGAGGKLIQFVYDEADKLGTPSVYWCTDESNHRAQLLYVKVGYKAPKILYKRKGY

>d1bob\_\_ d.108.1.1 (-) Histone acetyltransferase HAT1 {Baker's yeast (Saccharomyces cerevisiae)}

FKPETWTSSANEALRVSIVGENAVQFSPLFTYPIYGDSEKIYGYKDLIIHLAFDSVTFKPYVNVKYSAKLGDDNIVDVEKKLLSFLPKDDVIVRDEAKWVDCFAEERKTHNLSDVFEKVSEYSLNGEEFVVYKSSLVDDFARRMHRRVQIFSLLFIEAANYIDETDPSWQIYWLLNKKTKELIGFVTTYKYWHYLGAKSFDEDIDKKFRAKISQFLIFPPYQNKGHGSCLYEAIIQSWLEDKSITEITVEDPNEAFDDLRDRNDIQRLRKLGYDAVFQKHSDLSDEFLESSRKSLKLEERQFNRLVEMLLLLNNS

>d1fy7a\_ d.108.1.1 (A:) Histone acetyltransferase ESA1 {Baker's yeast (Saccharomyces cerevisiae)}

ARVRNLNRIIMGKYEIEPWYFSPYPIELTDEDFIYIDDFTLQYFGSKKQYERYRKKCTLRHPPGNEIYRDDYVSFFEIDGRKQRTWCRNLCLLSKLFLDHKTLYYDVDPFLFYCMTRRDELGHHLVGYFSKEKESADGYNVACILTLPQYQRMGYGKLLIEFSYELSKKENKVGSPEKPLSDLGLLSYRAYWSDTLITLLVEHQKEITIDEISSMTSMTTTDILHTAKTLNILRYYKGQHIIFLNEDILDRYNRLKAKKRRTIDPNRLIWKPP

>d1cjwa\_ d.108.1.1 (A:) Serotonin N-acetyltranferase {Sheep (Ovis aries)}

HTLPANEFRCLTPEDAAGVFEIEREAFISVSGNCPLNLDEVQHFLTLCPELSLGWFVEGRLVAFIIGSLWDEERLTQESLALHRPRGHSAHLHALAVHRSFRQQGKGSVLLWRYLHHVGAQPAVRRAVLMCEDALVPFYQRFGFHPAGPCAIVVGSLTFTEMHCSL

>d1i12a\_ d.108.1.1 (A:) Glucosamine-phoshate N-acetyltransferase GNA1 {Baker's yeast (Saccharomyces cerevisiae)}

LPDGFYIRRMEEGDLEQVTETLKVLTTVGTITPESFCKLIKYWNEATVWNDNEDKKIMQYNPMVIVDKRTETVAATGNIIIERKIIHELGLCGHIEDIAVNSKYQGQGLGKLLIDQLVTIGFDYGCYKIILDCDEKNVKFYEKCGFSNAGVEMQIRK

>d1iica1 d.108.1.2 (A:34-218) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces cerevisiae)}

AMKDHKFWRTQPVKDFDEKVVEEGPIDKPKTPEDISDKPLPLLSSFEWCSIDVDNKKQLEDVFVLLNENYVEDRDAGFRFNYTKEFFNWALKSPGWKKDWHIGVRVKETQKLVAFISAIPVTLGVRGKQVPSVEINFLCVHKQLRSKRLTPVLIKEITRRVNKCDIWHALYTAGIVLPAPVSTCR

>d1iica2 d.108.1.2 (A:219-455) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces cerevisiae)}

YTHRPLNWKKLYEVDFTGLPDGHTEEDMIAENALPAKTKTAGLRKLKKEDIDQVFELFKRYQSRFELIQIFTKEEFEHNFIGEESLPLDKQVIFSYVVEQPDGKITDFFSFYSLPFTILNNTKYKDLGIGYLYYYATDADFQFKDRFDPKATKALKTRLCELIYDACILAKNANMDVFNALTSQDNTLFLDDLKFGPGDGFLNFYLFNYRAKPITGGLNPDNSNDIKRRSNVGVVML

>d1nmta1 d.108.1.2 (A:60-224) N-myristoyl transferase, NMT {Yeast (Candida albicans)}

EGPIDKLKTPEDVPNDPLPLISDFEWSTLDIDDNLQLDELYKLLYDNYVEDIDATFRFKYSHEFFQWALKPPGWRKDWHVGVRVKSTGKLVAFIAATPVTFKLNKSNKVIDSVEINFLCIHKKLRNKRLAPVLIKEITRRVNKQNIWQALYTGGSILPTPLTTCR

>d1nmta2 d.108.1.2 (A:225-451) N-myristoyl transferase, NMT {Yeast (Candida albicans)}

YQHRPINWSKLHDVGFSHLPPNQTKSSMVASYTLPNNPKLKGLRPMTGKDVSTVLSLLYKYQERFDIVQLFTEEEFKHWMLGHDENSDSNVVKSYVVEDENGIITDYFSYYLLPFTVLDNAQHDELGIAYLFYYASDSFEKPNYKKRLNELITDALITSKKFGVDVFNCLTCQDNTYFLKDCKFGSGDGFLNYYLFNYRTFPMDGGIDKKTKEVVEDQTSGIGVVLL

>d2vik\_\_ d.109.1.1 (-) Villin, domain 1 (res. 1-126) {Chicken (Gallus gallus)}

VELSKKVTGKLDKTTPGIQIWRIENMEMVPVPTKSYGNFYEGDCYVLLSTRKTGSGFSYNIHYWLGKNSSQDEQGAAAIYTTQMDEYLGSVAVQHREVQGHESETFRAYFKQGLIYKQGGVASGMK

>d1svy\_\_ d.109.1.1 (-) Severin, domain 2 {Dictyostelium discoideum}

EYKPRLLHISGDKNAKVAEVPLATSSLNSGDCFLLDAGLTIYQFNGSKSSPQEKNKAAEVARAIDAERKGLPKVEVFCETDSDIPAEFWKLLGGKGAIAAKH

>d1d0na2 d.109.1.1 (A:153-262) Gelsolin {Horse (Equus caballus)}

VPNEVVVQRLLQVKGRRVVRATEVPVSWESFNNGDCFILDLGNNIYQWCGSKSNRFERLKATQVSKGIRDNERSGRAQVSVFEEGAEPEAMLQVLGPKPTLPEATEDTVK

>d1d0na3 d.109.1.1 (A:263-383) Gelsolin {Horse (Equus caballus)}

EDAANRKLAKLYKVSNGAGPMVVSLVADENPFAQGALRSEDCFILDHGKDGKIFVWKGKQANMEERKAALKTASDFISKMDYPKQTQVSVLPEGGETPLFRQFFKNWRDPDQTEGLGLAYL

>d1d0na4 d.109.1.1 (A:384-532) Gelsolin {Horse (Equus caballus)}

SSHIAHVERVPFDAATLHTSTAMAAQHGMDDDGTGQKQIWRVEGSNKVPVDPATYGQFYGGDSYIILYNYRHGSRQGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSRVVQGKEPAHLMSLFGGKPMIVYKGGTSREGGQTA

>d1d0na5 d.109.1.1 (A:533-628) Gelsolin {Horse (Equus caballus)}

PASTRLFQVRASSSGATRAVEIIPKAGALNSNDAFVLKTPSAAYLWVGAGASEAEKTGAQELLRVLRAQPVQVAEGSEPDSFWEALGGKATYRTSP

>d1d0na6 d.109.1.1 (A:629-755) Gelsolin {Horse (Equus caballus)}

RLKDKKMDAHPPRLFACSNKIGRFVIEEVPGEFMQEDLATDDVMLLDTWDQVFVWVGKDSQDEEKTEALTSAKRYIDTDPAHRDRRTPITVVKQGFEPPSFVGWFLGWDDSYWSVDPLDRALAELAA

>d1d4xg\_ d.109.1.1 (G:) Gelsolin {Human (Homo sapiens)}

VEHPEFLKAGKEPGLQIWRVEKFDLVPVPTNLYGDFFTGDAYVILKTVQLRNGNLQYDLHYWLGNECSQDESGAAAIFTVQLDDYLNGRAVQHREVQGFESATFLGYFKSGLKYKKGGVASGFK

>d1db0b1 d.109.1.1 (B:412-532) Gelsolin {Human (Homo sapiens)}

MDDDGTGQKQIWRIEGSNKVPVDPATYGQFYGGDSYIILYNYRHGGRQGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSRVVQGKEPAHLMSLFGGKPMIIYKGGTSREGGQTA

>d1db0b3 d.109.1.1 (B:629-742) Gelsolin {Human (Homo sapiens)}

RLKDKKMDAHPPRLFACSNKIGRFVIEEVPGELMQEDLATDDVMLLDTWDQVFVWVGKDSQDEEKTEALTSAKRYIETDPANRDRRTPITVVKQGFEPPSFVGWFLGWDDSYWS

>d1kcqa\_ d.109.1.1 (A:) Gelsolin {Human (Homo sapiens)}

VVQRLFQVKGRRVVRATEVPVSWESFNNGDCFILDLGNNIHQWCGSNSNRYERLKATQVSKGIRDNERSGRARVHVSEEGTEPEAMLQVLGPKPALPAGTEDTA

>d1f7sa\_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Plant (Arabidopsis thaliana), ADF1}

ASGMAVHDDCKLRFLELKAKRTHRFIVYKIEEKQKQVVVEKVGQPIQTYEEFAACLPADECRYAIYDFDFVTAENCQKSKIFFIAWCPDIAKVRSKMIYASSKDRFKRELDGIQVELQATDPTE

>d1cfya\_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Baker's yeast (Saccharomyces cerevisiae)}

VAVADESLTAFNDLKLGKKYKFILFGLNDAKTEIVVKETSTDPSYDAFLEKLPENDCLYAIYDFEYEINGNEGKRSKIVFFTWSPDTAPVRSKMVYASSKDALRRALNGVSTDVQGTDFSEVSYDSVLERVSR

>d1cnua\_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Amoeba (Acanthamoeba castellanii), actophorin}

GIAVSDDCVQKFNELKLGHQHRYVTFKMNASNTEVVVEHVGGPNATYEDFKSQLPERDCRYAIFDYEFQVDGGQRNKITFILWAPDSAPIKSKMMYTSTKDSIKKKLVGIQVEVQATDAAEISEDAVSERAKKD

>d1hqz1\_ d.109.1.2 (1:) Cofilin-like domain of actin-binding protein abp1p {Baker's yeast (Saccharomyces cerevisiae)}

LEPIDYTTHSREIDAEYLKIVRGSDPDTTWLIISPNAKKEYEPESTGSSFHDFLQLFDETKVQYGLARVSPPGSDVEKIIIIGWCPDSAPLKTRASFAANFAAVANNLFKGYHVQVTARDEDDLDENELLMKISNAAGA

>d1ak7\_\_ d.109.1.2 (-) Destrin {Human and pig (Homo sapiens) and (Sus scrofa)}

TMITPSSGNSASGVQVADEVCRIFYDMKVRKCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTITDPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELAPLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLGGSLIVAFEGCPV

>d1pne\_\_ d.110.1.1 (-) Profilin (actin-binding protein) {Cow (Bos taurus)}

AGWNAYIDNLMADGTCQDAAIVGYKDSPSVWAAVPGKTFVNITPAEVGILVGKDRSSFFVNGLTLGGQKCSVIRDSLLQDGEFTMDLRTKSTGGAPTFNITVTMTAKTLVLLMGKEGVHGGMINKKCYEMASHLRRSQY

>d1fil\_\_ d.110.1.1 (-) Profilin (actin-binding protein) {Human (Homo sapiens), isoform I}

AGWNAYIDNLMADGTCQDAAIVGYKDSPSVWAAVPGKTFVNITPAEVGVLVGKDRSSFYVNGLTLGGQKCSVIRDSLLQDGEFSMDLRTKSTGGAPTFNVTVTKTDKTLVLLMGKEGVHGGLINKKCYEMASHLRRSQY

>d1d1ja\_ d.110.1.1 (A:) Profilin (actin-binding protein) {Human (Homo sapiens), isoform II}

AGWQSYVDNLMCDGCCQEAAIVGYCDAKYVWAATAGGVFQSITPIEIDMIVGKDREGFFTNGLTLGAKKCSVIRDSLYVDGDCTMDIRTKSQGGEPTYNVAVGRAGRALVIVMGKEGVHGGTLNKKAYELALYLRRSD

>d1acf\_\_ d.110.1.1 (-) Profilin (actin-binding protein) {Acanthamoeba castellanii}

SWQTYVDTNLVGTGAVTQAAILGLDGNTWATSAGFAVTPAQGTTLAGAFNNADAIRAGGFDLAGVHYVTLRADDRSIYGKKGSSGVITVKTSKAILVGVYNEKIQPGTAANVVEKLADYLIGQGF

>d1f2ka\_ d.110.1.1 (A:) Profilin (actin-binding protein) {Acanthamoeba castellanii}

SWQTYVDTNLVGTGAVTQAAIIGHDGNTWATSAGFAVSPANGAALANAFKDATAIRSNGFELAGTRYVTIRADDRSVYGKKGSAGVITVKTSKAILIGVYNEKIQPGTAANVVEKLADYLIGQGF

>d1ypra\_ d.110.1.1 (A:) Profilin (actin-binding protein) {Baker's yeast (Saccharomyces cerevisiae)}

SWQAYTDNLIGTGKVDKAVIYSRAGDAVWATSGGLSLQPNEIGEIVQGFDNPAGLQSNGLHIQGQKFMLLRADDRSIYGRHDAEGVVCVRTKQTVIIAHYPPTVQAGEATKIVEQLADYLIGVQY

>d1cqa\_\_ d.110.1.1 (-) Profilin (actin-binding protein) {Birch (Betula verrucosa)}

SWQTYVDEHLMCDIDGQGEELAASAIVGHDGSVWAQSSSFPQFKPQEITGIMKDFEEPGHLAPTGLHLGGIKYMVIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEEPVTPGQCNMVVERLGDYLIDQGL

>d3nul\_\_ d.110.1.1 (-) Profilin (actin-binding protein) {Mouse-ear cress (Arabidopsis thaliana)}

SWQSYVDDHLMCDVEGNHLTAAAILGQDGSVWAQSAKFPQLKPQEIDGIKKDFEEPGFLAPTGLFLGGEKYMVIQGEQGAVIRGKKGPGGVTIKKTNQALVFGFYDEPMTGGQCNLVVERLGDYLIESEL

>d1g5ua\_ d.110.1.1 (A:) Profilin (actin-binding protein) {Para rubber tree (Hevea brasiliensis), hevb8}

SWQTYVDDHLMCDIDGHRLTAAAIIGHDGSVWAQSSSFPQFKSDEVAAVMKDFDEPGSLAPTGLHLGGTKYMVIQGEPGAVIRGKKGSGGITVKRTGQALIIGIYDEPLTPGQCNMIVERLGDYLLDQGL

>d1f5ma\_ d.110.2.1 (A:) Hypothetical protein ykl069wp {Baker's yeast (Saccharomyces cerevisiae)}

STGFHHADHVNYSSNLNKEEILEQLLLSYEGLSDGQVNWVCNLSNASSLIWHAYKSLAVDINWAGFYVTQASEENTLILGPFQGKVACQMIQFGKGVCGTAASTKETQIVPDVNKYPGHIACDGETKSEIVVPIISNDGKTLGVIDIDCLDYEGFDHVDKEFLEKLAKLINKSCVF

>d3pyp\_\_ d.110.3.1 (-) Photoactive yellow protein, PYP {Ectothiorhodospira halophila}

MEHVAFGSEDIENTLAKMDDGQLDGLAFGAIQLDGDGNILQYNAAEGDITGRDPKQVIGKNFFKDVAPCTDSPEFYGKFKEGVASGNLNTMFEYTFDYQMTPTKVKVHMKKALSGDSYWVFVKRV

>d1ew0a\_ d.110.3.2 (A:) Histidine kinase FixL heme domain {Rhizobium meliloti}

GSHMLETEDVVRARDAHLRSILDTVPDATVVSATDGTIVSFNAAAVRQFGYAEEEVIGQNLRILMPEPYRHEHDGYLQRYMATGEKRIIGIDRVVSGQRKDGSTFPMKLAVGEMRSGGERFFTGFIRDLT

>d1dp6a\_ d.110.3.2 (A:) Histidine kinase FixL heme domain {Bradyrhizobium japonicum}

DAMIVIDGHGIIQLFSTAAERLFGWSELEAIGQNVNILMPEPDRSRHDSYISRYRTTSDPHIIGIGRIVTGKRRDGTTFPMHLSIGEMQSGGEPYFTGFVRDLTEHQQTQARLQEL

>d1bywa\_ d.110.3.3 (A:) Erg potassium channel, N-terminal domain {Human (Homo sapiens)}

SRKFIIANARVENCAVIYCNDGFCELCGYSRAEVMQRPCTCDFLHGPCTQRRAAAQIAQALLGAEERKVEIAFYRKDGSCFLCLVDVVPVKNEDGAVIMFILNFEVVMEK

>d1g28a\_ d.110.3.4 (A:) Photoreceptor phy3 flavin-binding domain, lov2 {Maidenhair fern (Adiantum capillus-veneris)}

KSFVITDPRLPDNPIIFASDRFLELTEYTREEVLGNNCRFLQGRGTDRKAVQLIRDAVKEQRDVTVQVLNYTKGGRAFWNLFHLQVMRDENGDVQYFIGVQQEM

>d1ifqa\_ d.110.4.1 (A:) Sec22b {Mouse (Mus musculus)}

SVLLTMIARVADGLPLAASMQEDEQSGRDLQQYQSQAKQLFRKLNEQSPTRCTLEAGAMTFHYIIEQGVCYLVLCEAAFPKKLAFAYLEDLHSEFDEQHGKKVPTVSRPYSFIEFDTFIQKTKKLYI

>d1h8ma\_ d.110.4.1 (A:) Synaptobrevin homolog 1 ykt6 {Baker's yeast (Saccharomyces cerevisiae)}

MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSSVGQFMTFFAETVASRTGAGERQSIEEGNYIGHVYARSEGICGVLITDKQYPVRPAYTLLNKILDEYLVAHPKEEWADVTETNDALKMKQLDTYISKYQDPSQADA

>d1cfe\_\_ d.111.1.1 (-) Pathogenesis-related protein 1 (PR1) {Tomato (Lycopersicon esculentum), P14a}

QNSPQDYLAVHNDARAQVGVGPMSWDANLASRAQNYANSRAGDCNLIHSGAGENLAKGGGDFTGRAAVQLWVSERPSYNYATNQCVGGKKCRHYTQVVWRNSVRLGCGRARCNNGWWFISCNYDPVGNWIGQRPY

>d1qnxa\_ d.111.1.1 (A:) Insect allergen 5 (AG5) {Yellow jacket (Vespula vulgaris), Ves v 5}

AEAEFNNYCKIKCLKGGVHTACKYGSLKPNCGNKVVVSYGLTKQEKQDILKEHNDFRQKIARGLETRGNPGPQPPAKNMKNLVWNDELAYVAQVWANQCQYGHDTCRDVAKYQVGQNVALTGSTAAKYDDPVKLVKMWEDEVKDYNPKKKFSGNDFLKTGHYTQMVWANTKEVGCGSIKYIQEKWHKHYLVCNYGPSGNFKNEELYQTK

>d1a6ja\_ d.112.1.1 (A:) Nitrogen regulatory bacterial protein IIa-ntr {Escherichia coli}

LQLSSVLNRECTRSRVHCQSKKRALEIISELAAKQLSLPPQVVFEAILTREKMGSTGIGNGIAIPHGKLEEDTLRAVGVFVQLETPIAFDAIDNQPVDLLFALLVPADQTKTHLHTLSLVAKRLADKTICRRLRAAQSDEELYQIITDTE

>d1a3aa\_ d.112.1.1 (A:) Phosphotransferase IIa-mannitol {Escherichia coli}

LFKLGAENIFLGRKAATKEEAIRFAGEQLVKGGYVEPEYVQAMLDREKLTPTYLGESIAVPHGTVEAKDRVLKTGVVFCQYPEGVRFGEEEDDIARLVIGIAARNNEHIQVITSLTNALDDESVIERLAHTTSVDEVLELLAGRK

>d1hynp\_ d.112.1.2 (P:) Erythrocite membrane Band 3 {Human (Homo sapiens)}

KVYVELQELVMDEKNQELRWMEAARWVQLEENLGENGAWGRPHLSHLTFWSLLELRRVFTKGTVLLDLQETSLAGVANQLLDRFIFEDQIRPQDREELLRALLLKHSHAGELEALGGVKPAVLTRSGDPSQPLLPQHSSLETQLFCEQGDGGTEGHSPSGILEKIPPDSEATLVLVGRADFLEQPVLGFVRLQEAAELEAVELPVPIRFLFVLLGPEAPHIDYTQLGRAAATLMSERVFRIDAYMAQSRGELLHSLEGFLDCSLVLPPTDAPSEQALLSLVPVQRELLRRRYQ

>d1mut\_\_ d.113.1.1 (-) Nucleoside triphosphate pyrophosphorylase (MutT) {Escherichia coli}

MKKLQIAVGIIRNENNEIFITRRAADAHMANKLEFPGGKIEMGETPEQAVVRELQEEVGITPQHFSLFEKLEYEFPDRHITLWFWLVERWEGEPWGKEGQPGEWMSLVGLNADDFPPANEPVIAKLKRL

>d1g0sa\_ d.113.1.1 (A:) ADP-ribose pyrophosphatase {Escherichia coli}

MLKPDNLPVTFGKNDVEIIARETLYRGFFSLDLYRFRHRLFNGQMSHEVRREIFERGHAAVLLPFDPVRDEVVLIEQIRIAAYDTSETPWLLEMVAGMIEEGESVEDVARREAIEEAGLIVKRTKPVLSFLASPGGTSERSSIMVGEVDATTASGIHGLADENEDIRVHVVSREQAYQWVEEGKIDNAASVIALQWLQLHHQALKNEWA

>d1jkna\_ d.113.1.1 (A:) Diadenosine tetraphosphate hydrolase {Narrow-leaved blue lupine (Lupinus angustifolius)}

GPLGSMDSPPEGYRRNVGICLMNNDKKIFAASRLDIPDAWQMPQGGIDEGEDPRNAAIRELREETGVTSAEVIAEVPYWLTYDFPPKVREKLNIQWGSDWKGQAQKWFLFKFTGQDQEINLLGDGSEKPEFGEWSWVTPEQLIDLTVEFKKPVYKEVLSVFAPHL

>d1hx3a\_ d.113.1.2 (A:) Isopentenyl diphosphate isomerase {Escherichia coli}

EHVILLNAQGVPTGTLEKYAAHTADTRLHLAFSSWLFNAKGQLLVTRRALSKKAWPGVWTNSVAGHPQLGESNEDAVIRRCRYELGVEITPPESIYPDFRYRATDPSGIVENEVCPVFAARTTSALQINDDEVMDYQWCDLADVLHGIDATPWAFSPWMVMQATNREARKRLSAFT

>d1hzta\_ d.113.1.2 (A:) Isopentenyl diphosphate isomerase {Escherichia coli}

LHLAFSSWLFNAKGQLLVTRRALSKKAWPGVWTNSVCGHPQLGESNEDAVIRRCRYELGVEITPPESIYPDFRYRATDPSGIVENEVCPVFAARTTSALQINDDEVMDYQWCDLADVLHGIDATPWAFSPWMVMQATNREARKRLSAFTQLKL

>d1ush\_1 d.114.1.1 (363-550) 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain {Escherichia coli}

KIGETNGRLEGDRDKVRFVQTNMGRLILAAQMDRTGADFAVMSGGGIRDSIEAGDISYKNVLKVQPFGNVVVYADMTGKEVIDYLTAVAQMKPDSGAYPQFANVSFVAKDGKLNDLKIKGEPVDPAKTYRMATLNFNATGGDGYPRLDNKPGYVNTGFIDAEVLKAYIQKSSPLDVSVYEPKGEVSWQ

>d1hrua\_ d.115.1.1 (A:) Hypothetical protein YrdC {Escherichia coli}

NNLQRDAIAAAIDVLNEERVIAYPTEAVFGVGCDPDSETAVMRLLELKQRPVDKGLILIAANYEQLKPYIDDTMLTDVQRETIFSRWPGPVTFVFPAPATTPRWLTGRFDSLAVRVTDHPLVVALCQAYGKPLVSTSANLSGLPPCRTVDEVRAQFGAAFPVVPGETGGRLNPSEIRDALTGELFR

>d1g57a\_ d.115.1.2 (A:) 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB {Escherichia coli}

LLSSFGTPFERVENALAALREGRGVMVLDDEDRENEGDMIFPAETMTVEQMALTIRHGSGIVCLCITEDRRKQLDLPMMVENNTSAYGTGFTVTIEAAEGVTTGVSAADRITTVRAAIADGAKPSDLNRPGHVFPLRAQAGGVLTRGGHTEATIDLMTLAGFKPAGVLCELTNDDGTMARAPECIEFANKHNMALVTIEDLVAYRQAHE

>d1dbxa\_ d.116.1.1 (A:) Hypothetical protein HI1434 (YbaK homologue) {Haemophilus influenzae}

TPAIDLLKKQKIPFILHTYDHDPNNQHFGDEAAEKLGIDPNRSFKTLLVAENGDQKKLACFVLATANMLNLKKAAKSIGVKKVEMADKDAAQKSTGYLVGGISPLGQKKRVKTVINSTALEFETIYVSGGKRGLSVEIAPQDLAKVLGAEFTDIVDE

>d1qqqa\_ d.117.1.1 (A:) Thymidylate synthase {Escherichia coli}

MKQYLELMQKVLDEGTQKNDRTGTGTLSIFGHQMRFNLQDGFPLVTTKRCHLRSIIHELLWFLQGDTNIAYLHENNVTIWDEWADENGDLGPVYGKQWRAWPTPDGRHIDQITTVLNQLKNDPDSRRIIVSAWNVGELDKMALAPCHAFFQFYVADGKLSCQLYQRSCDVFLGLPFNIASYALLVHMMAQQCDLEVGDFVWTGGDTHLYSNHMDQTHLQLSREPRPLPKLIIKRKPESIFDYRFEDFEIEGYDSHPGIKAPVAI

>d1tsy\_\_ d.117.1.1 (-) Thymidylate synthase {Lactobacillus casei}

MLEQPYLDLAKKVLDEGHFKPDRTHTGTYSIFGHQMRFDLSKGFPLLTTKKVPFGLIKSELLWFLHGDTNIRFLLQHRNHIWDEWAFEKWVKSDEYHGPDMTDFGHRSQKDPEFAAVYHEEMAKFDDRVLHDDAFAAKYGDLGLVYGSQWRAWHTSKGDTIDQLGDVIEQIKTHPYSRKLIVSAWNPEDVPTMALPPCHTLYQFYVNDGKLSLQLYQRSADIFLGVPFNIASYALLTHLVAHECGLEVGEFIHTFGDAHLYVNHLDQIKEQLSRTPRPAPTLQLNPDKHDIFDFDMKDIKLLNYDPYPAIKAPVAV

>d1bkpa\_ d.117.1.1 (A:) Thymidylate synthase {Bacillus subtilis}

TQFDKQYNSIIKDIINNGISDEEFDVRTKWDSDGTPAHTLSVISKQMRFDNSEVPILTTKKVAWKTAIKELLWIWQLKSNDVNDLNMMGVHIWDQWKQEDGTIGHAYGFQLGKKNRSLNGEKVDQVDYLLHQLKNNPSSRRHITMLWNPDELDAMALTPCVYETQWYVKHGKLHLEVRARSNDMALGNPFNVFQYNVLQRMIAQVTGYELGEYIFNIGDCHVYTRHIDNLKIQMEREQFEAPELWINPEVKDFYDFTIDDFKLINYKHGDKLLFEVAV

>d1tis\_\_ d.117.1.1 (-) Thymidylate synthase {Bacteriophage T4}

MKQYQDLIKDIFENGYETDDRTGTGTIALFGSKLRWDLTKGFPAVTTKKLAWKACIAELIWFLSGSTNVNDLRLIQHDSLIQGKTVWDENYENQAKDLGYHSGELGPIYGKQWRDFGGVDQIIEVIDRIKKLPNDRRQIVSAWNPAELKYMALPPCHMFYQFNVRNGYLDLQWYQRSVDVFLGLPFNIASYATLVHIVAKMCNLIPGDLIFSGGNTHIYMNHVEQCKEILRREPKELCELVISGLPYKFRYLSTKEQLKYVLKLRPKDFVLNNYVSHPPIKGKMAV

>d1f28a\_ d.117.1.1 (A:) Thymidylate synthase {Pneumocystis carinii}

NAEEQQYLNLVQYIINHGEDRPDRTGTGTLSVFAPSPLKFSLRNKTFPLLTTKRVFIRGVIEELLWFIRGETDSLKLREKNIHIWDANGSREYLDSIGLTKRQEGDLGPIYGFQWRHFGAEYIDCKTNYIGQGVDQLANIIQKIRTSPYDRRLILSAWNPADLEKMALPPCHMFCQFYVHIPSNNHRPELSCQLYQRSCDMGLGVPFNIASYALLTCMIAHVCDLDPGDFIHVMGDCHIYKDHIEALQQQLTRSPRPFPTLSLNRSITDIEDFTLDDFNIQNYHPYETIKMKMSI

>d2tsra\_ d.117.1.1 (A:) Thymidylate synthase {Rat (Rattus norvegicus)}

QHGELQYLRQVEHIMRCGFKKEDRTGTGTLSVFGMQARYSLRDEFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSSKGVRIWDANGSRDFLDSLGFSARQEGDLGPVYGFQWRHFGADYKDMDSDYSGQGVDQLQKVIDTIKTNPDDRRIIMCAWNPKDLPLMALPPCHALCQFYVVNGELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLQPGDFVHTLGDAHIYLNHIEPLKIQLQREPRPFPKLRILRKVETIDDFKVEDFQIEGYNPHPTI

>d1hvya\_ d.117.1.1 (A:) Thymidylate synthase {Human (Homo sapiens)}

PPHGELQYLGQIQHILRCGVRKDDRTGTGTLSVFGMQARYSLRDEFPLLTTKRVFWKGVLEELLWFIKGSTNAKELSSKGVKIWDANGSRDFLDSLGFSTREEGDLGPVYGFQWRHFGAEYRDMESDYSGQGVDQLQRVIDTIKTNPDDRRIIMCAWNPRDLPLMALPPCHALCQFYVVNSELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLKPGDFIHTLGDAHIYLNHIEPLKIQLQREPRPFPKLRILRKVEKIDDFKAEDFQIEGYNPHPTIKMEMAV

>d1b5ea\_ d.117.1.1 (A:) dCMP hydroxymethylase {Bacteriophage T4}

MISDSMTVEEIRLHLGLALKEKDFVVDKTGVKTIEIIGASFVADEPFIFGALNDEYIQRELEWYKSKSLFVKDIPGETPKIWQQVASSKGEINSNYGWAIWSEDNYAQYDMCLAELGQNPDSRRGIMIYTRPSMQFDYNKDGMSDFMCTNTVQYLIRDKKINAVVNMRSNDVVFGFRNDYAWQKYVLDKLVSDLNAGDSTRQYKAGSIIWNVGSLHVYSRHFYLVDHWWKTGETHISKKDY

>d1kq4a\_ d.207.1.1 (A:) Thy1 homologue {Thermotoga maritima, TM0449}

HMKIDILDKGFVELVDVMGNDLSAVRAARVSFDMGLKDEERDRHLIEYLMKHGHETPFEHIVFTFHVKAPIFVARQWFRHRIASYNELSGRYSKLSYEFYIPSPERLEGYKTTIPPERVTEKISEIVDKAYRTYLELIESGVPREVARIVLPLNLYTRFFWTVNARSLMNFLNLRADSHAQWEIQQYALAIARIFKEKCPWTFEAFLKYAYKGDIL

>d1lba\_\_ d.118.1.1 (-) Bacteriophage T7 lysozyme (Zn amidase) {Bacteriophage T7}

AKQRESTDAIFVHCSATKPSQNVGVREIRQWHKEQGWLDVGYHFIIKRDGTVEAGRDEMAVGSHAKGYNHNSIGVCLVGGIDDKGKFDANFTPAQMQSLRSLLVTLLAKYEGAVLRAHHEVAPKACPSFDLKRWWEKNELVTSDRG

>d1cyo\_\_ d.120.1.1 (-) Cytochrome b5 {Cow (Bos taurus)}

SKAVKYYTLEEIQKHNNSKSTWLILHYKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTDARELSKTFIIGELHPDDRSKIT

>d1f03a\_ d.120.1.1 (A:) Cytochrome b5 {Cow (Bos taurus)}

AVKYYTLEEIQKHNNSKSTWLILHYKVYDLTKFLEEHPGGEAVLRAQAGGDATANFEAVGHSTDARELSKTFIIGELHPDDR

>d1aqa\_\_ d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}

KYYTLEEIQKHKDSKSTWVILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTDARELSKTYIIGELHPDDRSKIA

>d1axx\_\_ d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}

DKDVKYYTLEEIQKHKDSKSTWVILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTDARELSKTYIIGELHPDDRSKIAKPSETL

>d1euea\_ d.120.1.1 (A:) Cytochrome b5 {Rat (Rattus norvegicus)}

DPAVTYYRLEEVAKRNTAEETWMVIHGRVYDITRFLSEHPGGEEILLEQAGADATESFEDIGHSPDAREMLKQYYIGDVHPNDLKP

>d1icca\_ d.120.1.1 (A:) Cytochrome b5 {Rat (Rattus norvegicus)}

DPAVTYYRLEEVAKRNTSEETWMVIHGRVYDLTRFLSEHPGGEEVLREQAGADATESFEDVGHSPDAREMLKQYYIGDVHPNDLKPK

>d1do9a\_ d.120.1.1 (A:) Cytochrome b5 {Rabbit (Oryctolagus cuniculus)}

DKDVKYYTLEEIKKHNHSKSTWLILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFEDVGHSTDARELSKTFIIGELHPDDRSKLSKPMETL

>d1cxya\_ d.120.1.1 (A:) Cytochrome b558 {Ectothiorhodospira vacuolata}

TLPVFTLEQVAEHHSPDDCWMAIHGKVYDLTPYVPNHPGPAGMMLVWCGQESTEAWETKSYGEPHSSLAARLLQRYLIGTL

>d1ltda2 d.120.1.1 (A:10-97) Flavocytochrome b2, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

KISPAEVAKHNKPDDCWVVINGYVYDLTRFLPNHPGGQDVIKFNAGKDVTAIFEPLHAPNVIDKYIAPEKKLGPLQGSMPPELVCPPY

>d1soxa2 d.120.1.1 (A:3-93) Sulfite oxidase, N-terminal domain {Chicken (Gallus gallus)}

SYPEYTREEVGRHRSPEERVWVTHGTDVFDVTDFVELHPGGPDKILLAAGGALEPFWALYAVHGEPHVLELLQQYKVGELSPDEAPAAPDA

>d1vcc\_\_ d.121.1.1 (-) Vaccinia DNA topoisomerase I, 9 kDa N-terminal fragment {Vaccinia virus, strain WR}

MRALFYKDGKLFTDNNFLNPVSDDNPAYEVLQHVKIPTHLTDVVVYEQTWEEALTRLIFVGSDSKGRRQYFYGKMHV

>d1amw\_\_ d.122.1.1 (-) HSP90 {Baker's yeast (Saccharomyces cerevisiae)}

ASETFEFQAEITQLMSLIINTVYSNKEIFLRELISNASDALDKIRYKSLSDPKQLETEPDLFIRITPKPEQKVLEIRDSGIGMTKAELINNLGTIAKSGTKAFMEALSAGADVSMIGQFGVGFYSLFLVADRVQVISKSNDDEQYIWESNAGGSFTVTLDEVNERIGRGTILRLFLKDDQLEYLEEKRIKEVIKRHSEFVAYPIQLVVTKEVE

>d1byqa\_ d.122.1.1 (A:) HSP90 {Human (Homo sapiens)}

PMEEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIRYETLTDPSKLDSGKELHINLIPNKQDRTLTIVDTGIGMTKADLINNLGTIAKSGTKAFMEALQAGADISMIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGGSFTVRTDTGEPMGRGTKVILHLKEDQTEYLEERRIKEIVKKHSQFIGYPITLFVE

>d1ei1a2 d.122.1.2 (A:2-220) DNA gyrase B {Escherichia coli}

SNSSDSSSIKVLKGLDAVRKRPGMYIGDTDDGTGLHHMVFEVVDNAIDEALAGHCKEIIVTIHADNSVSVQDDGRGIPTGIHPEEGVSAAEVIMTVLHAGGKFDDNSYKVSGGLHGVGVSVVNALSQKLELVIQREGKIHRQIYEHGVPQAPLAVTGETEKTGTMVRFWPSLETFTNVTEFEYEILAKRLRELSFLDSGVSIRLRDKRDGKEDHFHYEG

>d1b63a2 d.122.1.2 (A:-2-216) DNA mismatch repair protein MutL {Escherichia coli}

SHMPIQVLPPQLANQIAAGEVVERPASVVKELVENSLDAGATRIDIDIERGGAKLIRIRDNGCGIKKDELALALARHATSKIASLDDLEAIISLGFRGEALASISSVSRLTLTSRTAEQQEAWQAYAEGRDMNVTVKPAAHPVGTTLEVLDLFYNTPARRKFLRTEKTEFNHIDEIIRRIALARFDVTINLSHNGKIVRQYRAVPEGGQKERRLGAIC

>d1bkna2 d.122.1.2 (A:20-216) DNA mismatch repair protein MutL {Escherichia coli}

VERPASVVKELVENSLDAGATRIDIDIERGGAKLIRIRDNGCGIKKDELALALARHATSKIASLDDLEAIISLGFRGEALASISSVSRLTLTSRTAEQQEAWQAYAEGRDMNVTVKPAAHPVGTTLEVLDLFYNTPARRKFLRTEKTEFNHIDEIIRRIALARFDVTINLSHNGKIVRQYRAVPEGGQKERRLGAIC

>d1h7sa2 d.122.1.2 (A:29-231) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}

GQVVLSLSTAVKELVENSLDAGATNIDLKLKDYGVDLIEVSDNGCGVEEENFEGLTLKHHTSKIQEFADLTQVETFGFRGEALSSLCALSDVTISTCHASAKVGTRLMFDHNGKIIQKTPYPRPRGTTVSVQQLFSTLPVRHKEFQRNIKKEYAKMVQVLHAYCIISAGIRVSCTNQLGQGKRQPVVCTGGSPSIKENIGSVF

>d1bxda\_ d.122.1.3 (A:) Histidine kinase domain of the osmosensor EnvZ {Escherichia coli}

TGQEMPMEMADLNAVLGEVIAAESGYEREIETALYPGSIEVKMHPLSIKRAVANMVVNAARYGNGWIKVSSGTEPNRAWFQVEDDGPGIAPEQRKHLFQPFVRGDSARTISGTGLGLAIVQRIVDNHNGMLELGTSERGGLSIRAWLPVPVTRAQGTTKEG

>d1i58a\_ d.122.1.3 (A:) Histidine kinase CheA {Thermotoga maritima}

GSHMVPISFVFNRFPRMVRDLAKKMNKEVNFIMRGEDTELDRTFVEEIGEPLLHLLRNAIDHGIEPKEERIAKGKPPIGTLILSARHEGNNVVIEVEDDGRGIDKEKIIRKAIEKGLIDESKAATLSDQEILNFLFVPGFSTKEKVSEVSGRGVGMDVVKNVVESLNGSISIESEKDKGTKVTIRLPLT

>d1id0a\_ d.122.1.3 (A:) Histidine kinase PhoQ domain {Escherichia coli}

RELHPVAPLLDNLTSALNKVYQRKGVNISLDISPEISFVGEQNDFVEVMGNVLDNACKYCLEFVEISARQTDEHLYIVVEDDGPGIPLSKREVIFDRGQRVDTLRPGQGVGLAVAREITEQYEGKIVAGESMLGGARMEVIFGRQH

>d1gkza2 d.122.1.4 (A:186-378) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK) {Rat (Rattus norvegicus)}

DFVGIICTRLSPKKIIEKWVDFARRLCEHKYGNAPRVRINGHVAARFPFIPMPLDYILPELLKNAMRATMESHLDTPYNVPDVVITIANNDVDLIIRISDRGGGIAHKDLDRVMDYHFTTAEASTQDPRISPLFGHLDMHSGGQSGPMHGFGFGLPTSRAYAEYLGGSLQLQSLQGIGTDVYLRLRHIDGREE

>d1jm6a2 d.122.1.4 (A:1177-1366) Pyruvate dehydrogenase kinase {Rat (Rattus norvegicus), isozyme 2}

PKHIGSIDPNCSVSDVVKDAYDMAKLLCDKYYMASPDLEIQEVNATNATQPIHMVYVPSHLYHMLFELFKNAMRATVESHESSLTLPPIKIMVALGEEDLSIKMSDRGGGVPLRKIERLFSYMYSTAPTPQPGTGGTPLAGFGYGLPISRLYAKYFQGDLQLFSMEGFGTDAVIYLKALSTDSVERLPVY

>d1ixma\_ d.123.1.1 (A:) Sporulation responce regulatory protein Spo0B {Bacillus subtilis}

SDTALTNELIHLLGHSRHDWMNKLQLIKGNLSLQKYDRVFEMIEEMVIDAKHESKLSNLKTPHLAFDFLTFNWKTHYMTLEYEVLGEIKDLSAYDQKLAKLMRKLFHLFDQAVSRESENHLTVSLQTDHPDRQLILYLDFHGAFADPSAFDDIRQNGYEDVDIMRFEITSHECLIEIGL

>d1bola\_ d.124.1.1 (A:) Ribonuclease Rh {Rhizopus niveus}

SSCSSTALSCSNSANSDTCCSPEYGLVVLNMQWAPGYGPDNAFTLHGLWPDKCSGAYAPSGGCDSNRASSSIASVIKSKDSSLYNSMLTYWPSNQGNNNVFWSHEWSKHGTCVSTYDPDCYDNYEEGEDIVDYFQKAMDLRSQYNVYKAFSSNGITPGGTYTATEMQSAIESYFGAKAKIDCSSGTLSDVALYFYVRGRDTYVITDALSTGSCSGDVEYPTK

>d1bk7a\_ d.124.1.1 (A:) Ribonuclease MC1 {Bitter gourd (Momordica charantia)}

FDSFWFVQQWPPAVCSFQKSGSCPGSGLRTFTIHGLWPQQSGTSLTNCPGSPFDITKISHLQSQLNTLWPNVLRANNQQFWSHEWTKHGTCSESTFNQAAYFKLAVDMRNNYDIIGALRPHAAGPNGRTKSRQAIKGFLKAKFGKFPGLRCRTDPQTKVSYLVQVVACFAQDGSTLIDCTRDTCGANFIF

>d1dixa\_ d.124.1.1 (A:) RNase LE {Tomatoes (Lycopersicon esculentum)}

ASGSKDFDFFYFVQQWPGSYCDTKQSCCYPTTGKPAADFGIHGLWPNNNDGTYPSNCDPNSPYDQSQISDLISSMQQNWPTLACPSGSGSTFWSHEWEKHGTCAESVLTNQHAYFKKALDLKNQIDLLSILQGADIHPDGESYDLVNIRNAIKSAIGYTPWIQCNVDQSGNSQLYQVYICVDGSGSSLIECPIFPGGKCGTSIEFPTF

>d1iqqa\_ d.124.1.1 (A:) S3-RNase {Japanese pear (Pyrus pyrifolia)}

YDYFQFTQQYQLAVCNSNRTLCKDPPDKLFTVHGLWPSNMVGPDPSKCPIKNIRKREKLLEHQLEIIWPNVFDRTKNNLFWDKEWMKHGSCGYPTIDNENHYFETVIKMYISKKQNVSRILSKAKIEPDGKKRALLDIENAIRNGADNKKPKLKCQKKGTTTELVEITLCSDKSGEHFIDCPHPFEPISPHYCPTNNIKY

>d1g2ra\_ d.192.1.1 (A:) Hypothetical cytosolic protein SP0554 {Streptococcus pneumoniae}

RKIPLRKSVVSNEVIDKRDLLRIVKNKEGQVFIDPTGKANGRGAYIKLDNAEALEAKKKKVFNRSFSMEVEESFYDELIAYVDHKVKRRELGLE

>d1c4ka3 d.125.1.1 (A:570-730) Ornithine decarboxylase C-terminal domain {Lactobacillus sp., strain 30a}

APLKQVLPSIYAANEERYNGYTIRELCQELHDFYKNNNTFTYQKRLFLREFFPEQGMLPYEARQEFIRNHNKLVPLNKIEGEIALEGALPYPPGVFCVAPGEKWSETAVKYFTILQDGINNFPGFAPEIQGVYFKQEGDKVVAYGEVYDAEVAKNDDRYNN

>d1g61a\_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Archaeon Methanococcus jannaschii}

MIIRKYFSGIPTIGVLALTTEEITLLPIFLDKDDVNEVSEVLETKCLQTNIGGSSLVGSLSVANKYGLLLPKIVEDEELDRIKNFLKENNLDLNVEIIKSKNTALGNLILTNDKGALISPELKDFKKDIEDSLNVEVEIGTIAELPTVGSNAVVTNKGCLTHPLVEDDELEFLKSLFKVEYIGKGTANKGTTSVGACIIANSKGAVVGGDTTGPELLIIEDALGL

>d1g62a\_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Baker's yeast (Saccharomyces cerevisiae)}

MATRTQFENSNEIGVFSKLTNTYCLVAVGGSENFYSAFEAELGDAIPIVHTTIAGTRIIGRMTAGNRRGLLVPTQTTDQELQHLRNSLPDSVKIQRVEERLSALGNVICCNDYVALVHPDIDRETEELISDVLGVEVFRQTISGNILVGSYCSLSNQGGLVHPQTSVQDQEELSSLLQVPLVAGTVNRGSSVVGAGMVVNDYLAVTGLDTTAPELSVIESIFRL

>d1jdw\_\_ d.126.1.2 (-) L-arginine: glycine amidinotransferase {Human (Homo sapiens)}

CPVSSYNEWDPLEEVIVGRAENACVPPFTIEVKANTYEKYWPFYQKQGGHYFPKDHLKKAVAEIEEMCNILKTEGVTVRRPDPIDWSLKYKTPDFESTGLYSAMPRDILIVVGNEIIEAPMAWRSRFFEYRAYRSIIKDYFHRGAKWTTAPKPTMADELYNQDYPIHSVEDRHKLAAQGKFVTTEFEPCFDAADFIRAGRDIFAQRSQVTNYLGIEWMRRHLAPDYRVHIISFKDPNPMHIDATFNIIGPGIVLSNPDRPCHQIDLFKKAGWTIITPPTPIIPDDHPLWMSSKWLSMNVLMLDEKRVMVDANEVPIQKMFEKLGITTIKVNIRNANSLGGGFHCWTCDVRRRGTLQSYLD

>d1bwda\_ d.126.1.2 (A:) L-arginine: inosamine-phosphate amidinotransferase {Streptomyces griseus}

RSLVSVHNEWDPLEEVIVGTAVGARVPTADRSVFAVEYAGDYESQEQIPSGAYPDRVLKETEEELHVLAAELTKLGVTVRRPGPRDHSALIKTPDWETDGFHDYCPRDGLLSVGQTIIETPMALRSRFLESLAYKDLLLEYFASGSRWLSAPKPRLTDDSYAPQAPAGERLTDEEPVFDAANVLRFGTDLLYLVSDSGNELGAKWLQSAVGDTYTVHPCRKLYASTHVDSTIVPLRPGLVLTNPSRVNDENMPDFLRSWENITCPELVDIGFTGDKPHCSVWIGMNLLVVRPDLAVVDRRQTALIRLLEKHGMNVLPLQLTHSRTLGGGFHCATLDVRRTGALETYQF

>d1h70a\_ d.126.1.3 (A:) Dimethylarginine dimethylaminohydrolase DDAH {Pseudomonas aeruginosa}

FMFKHIIARTPARSLVDGLTSSHLGKPDYAKALEQHNAYIRALQTCDVDITLLPPDERFPDSVFVEDPVLCTSRCAIITRPGAESRRGETEIIEETVQRFYPGKVERIEAPGTVEAGDIMMVGDHFYIGESARTNAEGARQMIAILEKHGLSGSVVRLEKVLHLKTGLAYLEHNNLLAAGEFVSKPEFQDFNIIEIPEEESYAANCIWVNERVIMPAGYPRTREKIARLGYRVIEVDTSEYRKIDGGVSSMSLRF

>d1chma2 d.127.1.1 (A:157-402) Creatinase, catalytic (C-terminal) domain {Pseudomonas putida}

MIKSAEEHVMIRHGARIADIGGAAVVEALGDQVPEYEVALHATQAMVRAIADTFEDVELMDTWTWFQSGINTDGAHNPVTTRKVNKGDILSLNCFPMIAGYYTALERTLFLDHCSDDHLRLWQVNVEVHEAGLKLIKPGARCSDIARELNEIFLKHDVLQYRTFGYGHSFGTLSHYYGREAGLELREDIDTVLEPGMVVSMEPMIMLPEGLPGAGGYREHDILIVNENGAENITKFPYGPEKNIIR

>d1c22a\_ d.127.1.1 (A:) Methionine aminopeptidase {Escherichia coli}

AISIKTPEDIEKMRVAGRLAAEVLEMIEPYVKPGVSTGELDRICNDYIVNEQHAVSACLGYHGYPKSVCISINEVVCHGIPDDAKLLKDGDIVNIDVTVIKDGFHGDTSKMFIVGKPTIMGERLCRITQESLYLALRMVKPGINLREIGAAIQKFVEAEGFSVVREYCGHGIGQGFHEEPQVLHYDSRETNVVLKPGMTFTIEPMVNAGKKEIRTMKDGWTVKTKDRSLSAQYEHTIVVTDNGCEILTLRKDDTIPAIISHD

>d1xgsa2 d.127.1.1 (A:1-194,A:272-295) Methionine aminopeptidase {Archaeon Pyrococcus furiosus}

MDTEKLMKAGEIAKKVREKAIKLARPGMLLLELAESIEKMIMELGGKPAFPVNLSINEIAAHYTPYKGDTTVLKEGDYLKIDVGVHIDGFIADTAVTVRVGMEEDELMEAAKEALNAAISVARAGVEIKELGKAIENEIRKRGFKPIVNLSGHKIERYKLHAGISIPNIYRPHDNYVLKEGDVFAIEPFATIGAXRNGIVAQFEHTIIVEKDSVIVTTE

>d1b6a\_2 d.127.1.1 (110-374,449-478) Methionine aminopeptidase {Human (Homo sapiens)}

KVQTDPPSVPICDLYPNGVFPKGQECEYPPTQDGRTAAWRTTSEEKKALDQASEEIWNDFREAAEAHRQVRKYVMSWIKPGMTMIEICEKLEDCSRKLIKENGLNAGLAFPTGCSLNNCAAHYTPNAGDTTVLQYDDICKIDFGTHISGRIIDCAFTVTFNPKYDTLLKAVKDATNTGIKCAGIDVRLCDVGEAIQEVMESYEVEIDGKTYQVKPIRNLNGHSIGQYRIHAGKTVPIVKGGEATRMEEGEVYAIETFGSTGKGVVXDIKGSYTAQFEHTILLRPTCKEVVSRGDDY

>d1az9\_2 d.127.1.1 (177-440) Aminopeptidase P, C-terminal domain {Escherichia coli}

SPEEIAVLRRAGEITAMAHTRAMEKCRPGMFEYHLEGEIHHEFNRHGARYPSYNTIVGSGENGCILHYTENECEMRDGDLVLIDAGCEYKGYAGDITRTFPVNGKFTQAQREIYDIVLESLETSLRLYRPGTSILEVTGEVVRIMVSGLVKLGILKGDVDELIAQNAHRPFFMHGLSHWLGLDVHDVGVYGQDRSRILEPGMVLTVEPGLYIAPDAEVPEQYRGIGIRIEDDIVITETGNENLTASVVKKPEEIEALMVAARKQ

>d1f52a2 d.128.1.1 (A:101-468) Glutamine synthetase, C-terminal domain {Salmonella typhimurium}

DRDPRSIAKRAEDYLRATGIADTVLFGPEPEFFLFDDIRFGASISGSHVAIDDIEGAWNSSTKYEGGNKGHRPGVKGGYFPVPPVDSAQDIRSEMCLVMEQMGLVVEAHHHEVATAGQNEVATRFNTMTKKADEIQIYKYVVHNVAHRFGKTATFMPKPMFGDNGSGMHCHMSLAKNGTNLFSGDKYAGLSEQALYYIGGVIKHAKAINALANPTTNSYKRLVPGYEAPVMLAYSARNRSASIRIPVVASPKARRIEVRFPDPAANPYLCFAALLMAGLDGIKNKIHPGEPMDKNLYDLPPEEAKEIPQVAGSLEEALNALDLDREFLKAGGVFTDEAIDAYIALRREEDDRVRMTPHPVEFELYYSV

>d1crka2 d.128.1.2 (A:99-380) Creatine kinase, C-terminal domain {Chicken (Gallus gallus), mitochondria}

TMKHHTDLDASKITHGQFDERYVLSSRVRTGRSIRGLSLPPACSRAERREVENVVVTALAGLKGDLSGKYYSLTNMSERDQQQLIDDHFLFDKPVSPLLTCAGMARDWPDARGIWHNNDKTFLVWINEEDHTRVISMEKGGNMKRVFERFCRGLKEVERLIKERGWEFMWNERLGYVLTCPSNLGTGLRAGVHVKLPRLSKDPRFPKILENLRLQKRGTGGVDTAAVADVYDISNLDRMGRSEVELVQIVIDGVNYLVDCEKKLEKGQDIKVPPPLPQFGRK

>d1qh4a2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Chicken (Gallus gallus), brain-type}

TDEHKTDLNADNLQGGDDLDPNYVLSSRVRTGRSIRGFCLPPHCSRGERRAIEKLSVEALGSLGGDLKGKYYALRNMTDAEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKTFLVWINEEDHLRVISMQKGGNMKEVFTRFCTGLTQIETLFKSKNYEFMWNPHLGYILTCPSNLGTGLRAGVHIKLPNLGKHEKFGEVLKRLRLQKRGTGGVDTAAVGGVFDVSNADRLGFSEVELVQMVVDGVKLLIEMEKRLEKGQSIDDLMPAQK

>d1qk1a2 d.128.1.2 (A:103-379) Creatine kinase, C-terminal domain {Human (Homo sapiens), mitochondria}

TTDLDASKIRSGYFDERYVLSSRVRTGRSIRGLSLPPACTRAERREVERVVVDALSGLKGDLAGRYYRLSEMTEAEQQQLIDDHFLFDKPVSPLLTAAGMARDWPDARGIWHNNEKSFLIWVNEEDHTRVISMEKGGNMKRVFERFCRGLKEVERLIQERGWEFMWNERLGYILTCPSNLGTGLRAGVHIKLPLLSKDSRFPKILENLRLQKRGTGGVDTAATGGVFDISNLDRLGKSEVELVQLVIDGVNYLIDCERRLERGQDIRIPTPVIHTKH

>d2crka2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Rabbit (Oryctolagus cuniculus)}

TDKHKTDLNHENLKGGDDLDPHYVLSSRVRTGRSIKGYTLPPHCSRGERRAVEKLSVEALNSLTGEFKGKYYPLKSMTEQEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKSFLVWVNEEDHLRVISMEKGGNMKEVFRRFCVGLQKIEEIFKKAGHPFMWNEHLGYVLTCPSNLGTGLRGGVHVKLAHLSKHPKFEEILTRLRLQKRGTSVFDTAAVGSVFDISNADRLGSSEVEQVQLVVDGVKLMVEMEKKLEKGQSIDDMIPAQK

>d1g0wa2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Cow (Bos taurus), retinal isoform}

TDEHKTDLNPDNLQGGDDLDPNYVLSSRVRTGRSIRGFCLPPHCSRGERRAIEKLAVEALSSLDGDLAGRYYALKSMTEAEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKTFLVWINEEDHLRVISMQKGGNMKEVFTRFCNGLTQIETLFKSKNYEFMWNPHLGYILTCPSNLGTGLRAGVHIKLPHLGKHEKFSEVLKRLRLQKRGTGGVDTAAVGGVFDVSNADRLGFSEVELVQMVVDGVKLLIEMEQRLEQGQAIDDLMPAQK

>d1bg0\_2 d.128.1.2 (96-357) Arginine kinase {Horseshoe crab (Limulus polyphemus)}

TDKHPPKQWGDINTLVGLDPAGQFIISTRVRCGRSLQGYPFNPCLTAEQYKEMEEKVSSTLSSMEDELKGTYYPLTGMSKATQQQLIDDHFLFKEGDRFLQTANACRYWPTGRGIFHNDAKTFLVWVNEEDHLRIISMQKGGDLKTVYKRLVTAVDNIESKLPFSHDDRFGFLTFCPTNLGTTMRASVHIQLPKLAKDRKVLEDIASKFNLQVRGTRGEHTESEGGVYDISNKRRLGLTEYQAVREMQDGILEMIKMEKAAA

>d1cdwa1 d.129.1.1 (A:155-252) TATA-box binding protein (TBP), C-terminal domain {Human (Homo sapiens)}

SGIVPQLQNIVSTVNLGCKLDLKTIALRARNAEYNPKRFAAVIMRIREPRTTALIFSSGKMVCTGAKSEENSRLAARKYARVVQKLGFPAKFLDFKIQ

>d1cdwa2 d.129.1.1 (A:253-333) TATA-box binding protein (TBP), C-terminal domain {Human (Homo sapiens)}

NMVGSCDVKFPIRLEGLVLTHQQFSSYEPELFPGLIYRMIKPRIVLLIFVSGKVVLTGAKVRAEIYEAFENIYPILKGFRK

>d1qnaa1 d.129.1.1 (A:17-115) TATA-box binding protein (TBP), C-terminal domain {Arabidopsis thaliana}

HPSGIVPTLQNIVSTVNLDCKLDLKAIALQARNAEYNPKRFAAVIMRIREPKTTALIFASGKMVCTGAKSEDFSKMAARKYARIVQKLGFPAKFKDFKI

>d1qnaa2 d.129.1.1 (A:116-198) TATA-box binding protein (TBP), C-terminal domain {Arabidopsis thaliana}

QNIVGSCDVKFPIRLEGLAYSHAAFSSYEPELFPGLIYRMKVPKIVLLIFVSGKIVITGAKMRDETYKAFENIYPVLSEFRKI

>d1ytba1 d.129.1.1 (A:61-155) TATA-box binding protein (TBP), C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

SGIVPTLQNIVATVTLGCRLDLKTVALHARNAEYNPKRFAAVIMRIREPKTTALIFASGKMVVTGAKSEDDSKLASRKYARIIQKIGFAAKFTDF

>d1ytba2 d.129.1.1 (A:156-240) TATA-box binding protein (TBP), C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

KIQNIVGSCDVKFPIRLEGLAFSHGTFSSYEPELFPGLIYRMVKPKIVLLIFVSGKIVLTGAKQREEIYQAFEAIYPVLSEFRKM

>d1aisa1 d.129.1.1 (A:1-92) TATA-box binding protein (TBP), C-terminal domain {Archaeon Pyrococcus woesei}

MVDMSKVKLRIENIVASVDLFAQLDLEKVLDLCPNSKYNPEEFPGIICHLDDPKVALLIFSSGKLVVTGAKSVQDIERAVAKLAQKLKSIGV

>d1aisa2 d.129.1.1 (A:93-181) TATA-box binding protein (TBP), C-terminal domain {Archaeon Pyrococcus woesei}

KFKRAPQIDVQNMVFSGDIGREFNLDVVALTLPNCEYEPEQFPGVIYRVKEPKSVILLFSSGKIVCSGAKSEADAWEAVRKLLRELDKY

>d1mpga2 d.129.1.2 (A:1-99) 3-Methyladenine DNA glycosylase II (gene alkA or aidA) {Escherichia coli}

MYTLNWQPPYDWSWMLGFLAARAVSSVETVADSYYARSLAVGEYRGVVTAIPDIARHTLHINLSAGLEPVAAECLAKMSRLFDLQCNPQIVNGALGRLG

>d1ko9a2 d.129.1.2 (A:12-135) 8-oxoguanine glycosylase {Human (Homo sapiens)}

GHRTLASTPALWASIPCPRSELRLDLVLPSGQSFRWREQSPAHWSGVLADQVWTLTQTEEQLHCTVYRGDKSQASRPTPDELEAVRKYFQLDVTLAQLYHHWGSVDSHFQEVAQKFQGVRLLRQ

>d1f46a\_ d.129.4.1 (A:) Cell-division protein ZipA, C-terminal domain {Escherichia coli}

RKEAVIIMNVAAHHGSELNGELLLNSIQQAGFIFGDMNIYHRHLSPDGSGPALFSLANMVKPGTFDPEMKDFTTPGVTIFMQVPSYGDELQLFKLMLQSAQHIADEVGGVVLDDQRRMMTPQKLREYQDIIREVKDANA

>d3pmga4 d.129.2.1 (A:421-561) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

RNFFTRYDYEEVEAEGATKMMKDLEALMFDRSFVGKQFSANDKVYTVEKADNFEYHDPVDGSVSKNQGLRLIFADGSRIIFRLSGTGSAGATIRLYIDSYEKDNAKINQDPQVMLAPLISIALKVSQLQERTGRTAPTVIT

>d1kfia4 d.129.2.1 (A:444-572) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

RNYYSRYDYEQVDSAGANKMMEHLKTKFQYFEQLKQGNKADIYDYVDPVDQSVSKNQGVRFVFGDGSRIIFRLSGTGSVGATIRIYFEQFEQQQIQHETATALANIIKLGLEISDIAQFTGRNEPTVIT

>d1bv1\_\_ d.129.3.1 (-) Major tree pollen allergen {White birch (Betula verrucosa), Bet v 1}

GVFNYETETTSVIPAARLFKAFILDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPEGLPFKYVKDRVDEVDHTNFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKYHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHSDAYN

>d1e09a\_ d.129.3.1 (A:) Major tree pollen allergen {Sweet cherry (Prunus avium), pru av 1}

GVFTYESEFTSEIPPPRLFKAFVLDADNLVPKIAPQAIKHSEILEGDGGPGTIKKITFGEGSQYGYVKHKIDSIDKENYSYSYTLIEGDALGDTLEKISYETKLVASPSGGSIIKSTSHYHTKGNVEIKEEHVKAGKEKASNLFKLIETYLKGHPDAYN

>d1em2a\_ d.129.3.2 (A:) Lipid transport domain of Mln64 {Human (Homo sapiens)}

SFSAQEREYIRQGKEATAVVDQILAQEENWKFEKNNEYGDTVYTIEVPFHGKTFILKTFLPCPAELVYQEVILQPERMVLWNKTVTACQILQRVEDNTLISYDVSAGAAGGVVSPRDFVNVRRIERRRDRYLSSGIATSHSAKPPTHKYVRGENGPGGMIVLKSASNPRVCTFVWILNTDLKGRLPRYLIHQSLAATMFEFAFHLRQRISELGA

>d1fvza\_ d.129.3.4 (A:) Phoshatidylinositol transfer protein, PITP {Rat (Rattus norvegicus)}

VLLKEYRVILPVSVDEYQVGQLYSVAEASKNETGGGEGVEVLVNEPYEKDDGEKGQYTHKIYHLQSKVPTFVRMLAPEGALNIHEKAWNAYPYCRTVITNEYMKEDFLIKIETWHKPDLGTQENVHKLEPEAWKHVEVIYIDIADRSQVLSKDYKAEEDPAKFKSIKTGRGPLGPNWKQELVNQKDCPYMCAYKLVTVKFKWWGLQNKVENFIHKQEKRLFTNFHRQLFCWLDKWVDLTMDDIRRMEEETKRQLDEMRQKDPVKGMTAD

>d1eg9a2 d.129.3.3 (A:155-447) Naphthalene 1,2-dioxygenase alpha subunit, C-domain {Pseudomonas putida}

EAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVFPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTFGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVSSSNWAEFEHASSTWHTELTKTT

>d1mxa\_1 d.130.1.1 (1-102) S-adenosylmethionine synthetase {Escherichia coli}

AKHLFTSESVSEGHPDKIADQISDAVLDAILEQDPKARVACETYVKTGMVLVGGEITTSAWVDIEEITRNTVREIGYVHSDMGFDANSCAVLSAIGKQSPDI

>d1mxa\_2 d.130.1.1 (108-231) S-adenosylmethionine synthetase {Escherichia coli}

RADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHRLVQRQAEVRKNGTLPWLRPDAKSQVTFQYDDGKIVGIDAVVLSTQHSEEIDQKSLQEAVMEEIIKPILPAEWLTSATKFFINPTGRFV

>d1mxa\_3 d.130.1.1 (232-383) S-adenosylmethionine synthetase {Escherichia coli}

IGGPMGDCGLTGRKIIVDTYGGMARHGGGAFSGKDPSKVDRSAAYAARYVAKNIVAAGLADRCEIQVSYAIGVAEPTSIMVETFGTEKVPSEQLTLLVREFFDLRPYGLIQMLDLLHPIYKETAAYGHFGREHFPWEKTDKAQLLRDAAGLK

>d1qm4a1 d.130.1.1 (A:17-116) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}

GAFMFTSESVGEGHPDKICDQISDAVLDAHLKQDPNAKVACETVCKTGMVLLCGEITSMAMIDYQRVVRDTIKHIGYDDSAKGFDFKTCNVLVALEQQSP

>d1qm4a2 d.130.1.1 (A:129-252) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}

EDVGAGDQGLMFGYATDETEECMPLTIVLAHKLNTRMADLRRSGVLPWLRPDSKTQVTVQYVQDNGAVIPVRVHTIVISVQHNEDITLEAMREALKEQVIKAVVPAKYLDEDTIYHLQPSGRFV

>d1qm4a3 d.130.1.1 (A:253-396) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}

IGGPQGDAGVTGRKIIVDTYGGWGAHGGGAFSGKDYTKVDRSAAYAARWVAKSLVKAGLCRRVLVQVSYAIGVAEPLSISIFTYGTSKKTERELLEVVNKNFDLRPGVIVRDLDLKKPIYQKTACYGHFGRSEFPWEVPKKLVF

>d2pola1 d.131.1.1 (A:1-122) DNA polymerase III, beta subunit {Escherichia coli}

MKFTVEREHLLKPLQQVSGPLGGRPTLPILGNLLLQVADGTLSLTGTDLEMEMVARVALVQPHEPGATTVPARKFFDICRGLPEGAEIAVQLEGERMLVRSGRSRFSLSTLPAADFPNLDDW

>d2pola2 d.131.1.1 (A:123-244) DNA polymerase III, beta subunit {Escherichia coli}

QSEVEFTLPQATMKRLIEATQFSMAHQDVRYYLNGMLFETEGEELRTVATDGHRLAVCSMPIGQSLPSHSVIVPRKGVIELMRMLDGGDNPLRVQIGSNNIRAHVGDFIFTSKLVDGRFPDY

>d2pola3 d.131.1.1 (A:245-366) DNA polymerase III, beta subunit {Escherichia coli}

RRVLPKNPDKHLEAGCDLLKQAFARAAILSNEKFRGVRLYVSENQLKITANNPEQEEAEEILDVTYSGAEMEIGFNVSYVLDVLNALKCENVRMMLTDSVSSVQIEDAASQSAAYVVMPMRL

>d1b77a1 d.131.1.2 (A:1-110) gp45 sliding clamp {Bacteriophage RB69}

MKLSKDTIAILKNFASINSGILLSQGKFIMTRAVNGTTYAEANISDEIDFDVALYDLNSFLSILSLVSDDAEISMHTDGNIKIADTRSTVYWPAADKSTIVFPNKPIQFP

>d1b77a2 d.131.1.2 (A:111-228) gp45 sliding clamp {Bacteriophage RB69}

VASVITEIKAEDLQQLLRVSRGLQIDTIAITNKDGKIVINGYNKVEDSGLTRPKYSLTLTDYDGSNNFNFVINMANMKIQPGNYKVMLWGAGDKVAAKFESSQVSYVIAMEADSTHDF

>d1czda1 d.131.1.2 (A:1001-1110) gp45 sliding clamp {Bacteriophage T4}

MKLSKDTTALLKNFATINSGIMLKSGQFIMTRAVNGTTYAEANISDVIDFDVAIYDLNGFLGILSLVNDDAEISQSEDGNIKIADARSTIFWPAADPSTVVAPNKPIPFP

>d1czda2 d.131.1.2 (A:1111-1228) gp45 sliding clamp {Bacteriophage T4}

VASAVTEIKAEDLQQLLRVSRGLQIDTIAITVKEGKIVINGFNKVEDSALTRVKYSLTLGDYDGENTFNFIINMANMKMQPGNYKLLLWAKGKQGAAKFEGEHANYVVALEADSTHDF

>d1dmla1 d.131.1.2 (A:29-169) UL42 {Human herpes virus type 1}

APCQVVLQGAELNGILQAFAPLRTSLLDSLLVMGDRGILIHNTIFGEQVFLPLEHSQFSRYRWRGPTAAFLSLVDQKRSLLSVFRANQYPDLRRVELAITGQAPFRTLVQRIWTTTSDGEAVELASETLMKRELTSFVVLV

>d1dmla2 d.131.1.2 (A:170-319) UL42 {Human herpes virus type 1}

PQGTPDVQLRLTRPQLTKVLNATGADSATPTTFELGVNGKFSVFTTSTCVTFAAREEGVSSSTSTQVQILSNALTKAGQAAANAKTVYGENTHRTFSVVVDDCSMRAVLRRLQVGGGTLKFFLTTPVPSLCVTATGPNAVSAVFLLKPQK

>d1plq\_1 d.131.1.2 (1-126) Prolifirating cell nuclear antigen (PCNA) {Baker's yeast (Saccharomyces cerevisiae)}

MLEAKFEEASLFKRIIDGFKDCVQLVNFQCKEDGIIAQAVDDSRVLLVSLEIGVEAFQEYRCDHPVTLGMDLTSLSKILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIAEYSLKLMDIDADFL

>d1plq\_2 d.131.1.2 (127-258) Prolifirating cell nuclear antigen (PCNA) {Baker's yeast (Saccharomyces cerevisiae)}

KIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSVIIKPFVDMEHPETSIKLEMDQPVDLTFGAKYLLDIIKGSSLSDRVGIRLSSEAPALFQFDLKSGFLQFFLAPKFNDEE

>d1axca1 d.131.1.2 (A:1-126) Prolifirating cell nuclear antigen (PCNA) {Human (Homo sapiens)}

MFEARLVQGSILKKVLEALKDLINEACWDISSSGVNLQSMDSSHVSLVQLTLRSEGFDTYRCDRNLAMGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKLMDLDVEQL

>d1axca2 d.131.1.2 (A:127-255) Prolifirating cell nuclear antigen (PCNA) {Human (Homo sapiens)}

GIPEQEYSCVVKMPSGEFARICRDLSHIGDAVVISCAKDGVKFSASGELGNGNIKLSQTSNVDKEEEAVTIEMNEPVQLTFALRYLNFFTKATPLSSTVTLSMSADVPLVVEYKIADMGHLKYYLAPKI

>d1ge8a1 d.131.1.2 (A:2-117) Prolifirating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}

PFEIVFEGAKEFAQLIDTASKLIDEAAFKVTEDGISMRAMDPSRVVLIDLNLPSSIFSKYEVVEPETIGVNLDHLKKILKRGKAKDTLILKKGEENFLEITIQGTATRTFRVPLID

>d1ge8a2 d.131.1.2 (A:126-247) Prolifirating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}

PELPFTAKVVVLGEVLKDAVKDASLVSDSIKFIARENEFIMKAEGETQEVEIKLTLEDEGLLDIEVQEETKSAYGVSYLSDMVKGLGKADEVTIKFGNEMPMQMEYYIRDEGRLTFLLAPRV

>d1hlra4 d.133.1.1 (A:311-907) Aldehyde oxidoreductase {Desulfovibrio gigas}

MSGPAAAAEDAIEIHPGTPNVYFEQPIVKGEDTGPIFASADVTVEGDFYVGRQPHMPIEPDVAFAYMGDDGKCYIHSKSIGVHLHLYMIAPGVGLEPDQLVLVANPMGGTFGYKFSPTSEALVAVAAMATGRPVHLRYNYQQQQQYTGKRSPWEMNVKFAAKKDGTLLAMESDWLVDHGPYSEFGDLLTLRGAQFIGAGYNIPNIRGLGRTVATNHVWGSAFRGYGAPQSMFASECLMDMLAEKLGMDPLELRYKNAYRPGDTNPTGQEPEVFSLPDMIDQLRPKYQAALEKAQKESTATHKKGVGISIGVYGSGLDGPDASEAWAELNADGTITVHTAWEDHGQGADIGCVGTAHEALRPMGVAPEKIKFTWPNTATTPNSGPSGGSREQVMTGNAIRVACENLLKACEKPGGGYYTYDELKAADKPTKITGNWTASGATHCDAVTGLGKPFVVYMYGVFMAEVTVDVATGQTTVDGMTLMADLGSLCNQLATDGQIYGGLAQGIGLALSEDFEDIKKHATLVGAGFPFIKQIPDKLDIVYVNHPRPDGPFGASGVGELPLTSPHAAIINAIKSATGVRIYRLPAYPEKVLEALKA

>d1dgja4 d.133.1.1 (A:311-906) Aldehyde oxidoreductase {Desulfovibrio desulfuricans}

MSAPEAMAPDAIEIHPGTPNVYYDQLEEKGEDTVPFFNDPANVVAEGSYYTQRQPHLPIEPDVGYGYINEQGQVVIHSKSVAIHLHALMIAPGLGLEFPKDLVLVQNTTGGTFGYKFSPTMEALVGVAVMATGRPCHLRYNYEQQQNYTGKRSPFWTTMRYAADRQGKILAMETDWSVDHGPYSEFGDLLTLRGAQYIGAGYGIANIRGTGRTVATNHCWGAAFRGYGAPESEFPSEVLMDELAEKLGMDPFELRALNCYREGDTTSSGQIPEVMSLPEMFDKMRPYYEESKKRVKERSTAEIKRGVGVALGVYGAGLDGPDTSEAWVELNDDGSVTLGNSWEDHGQGADAGSLGTAHEALRPLGITPENIHLVMNDTSKTPNSGPAGGSRSQVVTGNAIRVACEMLIEGMRKPGGGFFTPAEMKAEGRPMRYDGKWTAPAKDCDAKGQGSPFACYMYGLFLTEVAVEVATGKATVEKMVCVADIGKICNKLVVDGQIYGGLAQGVGLALSEDYEDLKKHSTMGGAGIPSIKMIPDDIEIVYVETPRKDGPFGASGVGEMPLTAPHAAIINGIYNACGARVRHLPARPEKVLEAMP

>d1fo4a5 d.133.1.1 (A:695-1332) Xanthine oxidase, C-terminal domain {Cow (Bos taurus)}

IITIEDAIKNNSFYGSELKIEKGDLKKGFSEADNVVSGELYIGGQDHFYLETHCTIAIPKGEEGEMELFVSTQNAMKTQSFVAKMLGVPVNRILVRVKRMGGGFGGKETRSTLVSVAVALAAYKTGHPVRCMLDRNEDMLITGGRHPFLARYKVGFMKTGTIVALEVDHYSNAGNSRDLSHSIMERALFHMDNCYKIPNIRGTGRLCKTNLSSNTAFRGFGGPQALFIAENWMSEVAVTCGLPAEEVRWKNMYKEGDLTHFNQRLEGFSVPRCWDECLKSSQYYARKSEVDKFNKENCWKKRGLCIIPTKFGISFTVPFLNQAGALIHVYTDGSVLVSHGGTEMGQGLHTKMVQVASKALKIPISKIYISETSTNTVPNSSPTAASVSTDIYGQAVYEACQTILKRLEPFKKKNPDGSWEDWVMAAYQDRVSLSTTGFYRTPNLGYSFETNSGNAFHYFTYGVACSEVEIDCLTGDHKNLRTDIVMDVGSSLNPAIDIGQVEGAFVQGLGLFTLEELHYSPEGSLHTRGPSTYKIPAFGSIPTEFRVSLLRDCPNKKAIYASKAVGEPPLFLGASVFFAIKDAIRAARAQHTNNNTKELFRLDSPATPEKIRNACVDKFTTLCVTGAPGNCKPWSLRV

>d1jrob2 d.133.1.1 (B:124-777) Xanthine dehydrogenase chain B, C-terminal domain {Rhodobacter capsulatus}

PAILTLDQALAADSRFEGGPVIWARGDVETALAGAAHLAEGCFEIGGQEHFYLEGQAALALPAEGGVVIHCSSQHPSEIQHKVAHALGLAFHDVRVEMRRMGGGFGGKESQGNHLAIACAVAARATGRPCKMRYDRDDDMVITGKRHDFRIRYRIGADASGKLLGADFVHLARCGWSADLSLPVCDRAMLHADGSYFVPALRIESHRLRTNTQSNTAFRGFGGPQGALGMERAIEHLARGMGRDPAELRALNFYDPPERGGLSAPPSPPEPIATKKTQTTHYGQEVADCVLGELVTRLQKSANFTTRRAEIAAWNSTNRTLARGIALSPVKFGISFTLTHLNQAGALVQIYTDGSVALNHGGTEMGQGLHAKMVQVAAAVLGIDPVQVRITATDTSKVPNTSATAASSGADMNGMAVKDACETLRGRLAGFVAAREGCAARDVIFDAGQVQASGKSWRFAEIVAAAYMARISLSATGFYATPKLSWDRLRGQGRPFLYFAYGAAITEVVIDRLTGENRILRTDILHDAGASLNPALDIGQIEGAYVQGAGWLTTEELVWDHCGRLMTHAPSTYKIPAFSDRPRIFNVALWDQPNREETIFRSKAVGEPPFLLGISAFLALHDACAACGPHWPDLQAPATPEAVLAAVRRAEGRA

>d1qj2b2 d.133.1.1 (B:147-809) Carbon monoxide (CO) dehydrogenase molybdoprotein {Pseudomonas carboxydovorans}

VDPFKAMEPDAPLLREDIKDKMTGAHGARKHHNHIFRWEIGDKEGTDATFAKAEVVSKDMFTYHRVHPSPLETCQCVASMDKIKGELTLWGTFQAPHVIRTVVSLISGLPEHKIHVIAPDIGGGFGNKVGAYSGYVCAVVASIVLGVPVKWVEDRMENLSTTSFARDYHMTTELAATKDGKILAMRCHVLADHGAFDACADPSKWPAGFMNICTGSYDMPVAHLAVDGVYTNKASGGVAYRXSFRVTEAVYAIERAIETLAQRLEMDSADLRIKNFIQPEQFPYMAPLGWEYDSGNYPLAMKKAMDTVGYHQLRAEQKAKQEAFKRGETREIMGIGISFFTEIVGAGPSKNCDILGVSMFDSAEIRIHPTGSVIARMGTKSQGQGHETTYAQIIATELGIPADDIMIEEGNTDTAPYGLGTYGSRSTPTAGAATAVAARKIKAKAQMIAAHMLEVHEGDLEWDVDRFRVKGLPEKFKTMKELAWASYNSPPPNLEPGLEAVNYYDPPNMTYPFGAYFCIMDIDIDTGVAKTRRFYALDDCGTRINPMIIEGQVHGGLTEAFAVAMGQEIRYDEQGNVLGASFMDFFLPTAVETPKWETDYTVTPSPHHPIGAKGVGESPHVGGVPCFSNAVNDAYAFLNAGHIQMPHDAWRLWKVGEQLGLHV

>d1ffvb2 d.133.1.1 (B:147-803) Carbon monoxide (CO) dehydrogenase molybdoprotein {Hydrogenophaga pseudoflava}

IDALKPDAPVLREDLAGKTSGAHGPREHHNHIFTWGAGDKAATDAVFANAPVTVSQHMYYPRVHPCPLETCGCVASFDPIKGDLTTYITSQAPHVVRTVVSMLSGIPESKVRIVSPDIGGGFGNKVGIYPGYVCAIVASIVLGRPVKWVEDRVENISTTAFARDYHMDGELAATPDGKILGLRVNVVADHGAFDACADPTKFPAGLFHICSGSYDIPRAHCSVKGVYTNKAPGGVAYRCSFRVTEAVYLIERMVDVLAQKLNMDKAEIRAKNFIRKEQFPYTTQFGFEYDSGDYHTALKKVLDAVDYPALRAEQAARRADPNSPTLMGIGLVTFTEVVGAGPSKMCDILGVGMFDSCEIRIHPTGSAIARMGTITQGQGHQTTYAQIIATELGIPSEVIQVEEGDTSTAPYGLGTYGSRSTPVAGAAIALAARKIHAKARKIAAHMLEVNENDLDWEVDRFKVKGDDSKFKTMADIAWQAYHQPPAGLEPGLEAVHYYDPPNFTYPFGIYLCVVDIDRATGETKVRRFYALDDCGTRINPMIIEGQIHGGLTEGYAVAMGQQMPFDAQGNLLGNTLMDYFLPTAVETPHWETDHTVTPSPHHPIGAKGVAESPHVGSIPTFTAAVVDAFAHVGVTHLDMPHTSYRVWKSLKEHNLAL

>d1aop\_3 d.134.1.1 (149-345) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4 {Escherichia coli}

NDMNRNVLCTSNPYESQLHAEAYEWAKKISEHLLPRTRAYAEIWLDQEKVATTDEEPILGQTYLPRKFKTTVVIPPQNDIDLHANDMNFVAIAENGKLVGFNLLVGGGLSIEHGNKKTYARTASEFGYLPLEHTLAVAEAVVTTQRDWGNRTDRKNAKTKYTLERVGVETFKAEVERRAGIKFEPIRPYEFTGRGDR

>d1aop\_4 d.134.1.1 (426-570) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4 {Escherichia coli}

PQRENSMACVSFPTCPLAMAEAERFLPSFIDNIDNLMAKHGVSDEHIVMRVTGCPNGCGRAMLAEVGLVGKAPGRYNLHLGGNRIGTRIPRMYKENITEPEILASLDELIGRWAKEREAGEGFGDFTVRAGIIRPVLDPARDLWD

>d1klqa\_ d.135.1.1 (A:) The spindle assembly checkpoint protein mad2 {Human (Homo sapiens)}

GSITLRGSAEIVAEFFSFGINSILYQRGIYPSETFTRVQKYGLTLLVTTDLELIKYLNNVVEQLKDWLYKCSVQKLVVVISNIESGEVLERWQFDIECDKTAKDDSAPREKSQKAIQDEIRSVIRQITATVTFLPLLEVSCSFDLLIYTDKDLVVPEKWEESGPQFITNSEEVRLRSFTTTIHKVNSMVAYKIPVND

>d1byra\_ d.136.1.1 (A:) Nuclease Nuc {Salmonella typhimurium}

EPSVQVGYSPEGSARVLVLSAIDSAKTSIRMMAYSFTAPDIMKALVAAKKRGVDVKIVIDERGNTGRASIAAMNYIANSGIPLRTDSNFPIQHDKVIIVDNVTVETGSFNFTKAAETKNSENAVVIWNMPKLAESFLEHWQDRWNQGRDYRS

>d1f0ia1 d.136.1.2 (A:6-263) Phospholipase D {Streptomyces sp.}

AATPHLDAVEQTLRQVSPGLEGDVWERTSGNKLDGSAADPSDWLLQTPGCWGDDKCADRVGTKRLLAKMTENIGNATRTVDISTLAPFPNGAFQDAIVAGLKESAAKGNSLKVRILVGAAPVYHMNGIPSKYRDKLTAKLGKAAENITLNVASMTTSKTAFSWNHSKILVVDGQSALTGGINSWKDDYLDTTHPVSDVDLALTGPAAGSAGRYLDTLWTWTCKNKSNIASVWFAASGNAGCMPTMHKDTNPKASPATG

>d1f0ia2 d.136.1.2 (A:264-514) Phospholipase D {Streptomyces sp.}

NVPVIAVGGLGVGIKDVDPKSTFRPDLPTASDTKCVVGLHDNTNADRDYDTVNPEESALRALVASAKGHIEISQQDLNATCPPLPRYDIRLYDALAAKMAAGVKVRIVVSDPANRGAVGSGGYSQIKSLSEISDTLRNRLANITGGQQAAKTAMCSNLQLATFRSSPNGKWADGHPYAQHHKLVSVDSSTFYIGSKNLYPSWLQDFGYIVESPEAAKQLDAKLLDPQWKYSQETATVDYARGICGA

>d1jy1a1 d.136.1.3 (A:145-350) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}

LEDPGEGQDIWDMLDKGNPFQFYLTRVSGVKPKYNSGALHIKDILSPLFGTLVSSAQFNYCFDVDWLVKQYPPEFRKKPILLVHGDKREAKAHLHAQAKPYENISLCQAKLDIAFGTHHTKMMLLLYEEGLRVVIHTSNLIHADWHQKTQGIWLSPLYPRIADGTHKSGESPTHFKANLISYLTAYNAPSLKEWIDVIHKHDLSET

>d1jy1a2 d.136.1.3 (A:351-608) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}

NVYLIGSTPGRFQGSQKDNWGHFRLKKLLKDHASSMPNAESWPVVGQFSSVGSLGADESKWLCSEFKESMLTLGKESKTPGKSSVPLYLIYPSVENVRTSLEGYPAGGSLPYSIQTAEKQNWLHSYFHKWSAETSGRSNAMPHIKTYMRPSPDFSKIAWFLVTSANLSKAAWGALEKNGTQLMIRSYELGVLFLPSALGLDSFKVKQKFFAGSQEPMATFPVPYDLPPELYGSKDRPWIWNIPYVKAPDTHGNMWVPS

>d1ckv\_\_ d.137.1.1 (-) Soluble methane monooxygenase regulatory protein B {Escherichia coli}

MSVNSNAYDAGIMGLKGKDFADQFFADENQVVHESDTVVLVLKKSDEINTFIEEILLTDYKKNVNPTVNVEDRAGYWWIKANGKIEVDCDEISELLGRQFNVYDFLVDVSSTIGRAYTLGNKFTITSELMGLDRKLEDYHA

>d2moba\_ d.137.1.1 (A:) Soluble methane monooxygenase regulatory protein B {Methylosinus trichosporium}

SNAVVLVLMKSDEIDAIIEDIVLKGGKAKNPSIVVEDKAGFWWIKADGAIEIDAAEAGELLGKPFSVYDLLINVSSTVGRAYTLGTKFTITSEL

>d1g10a\_ d.137.1.1 (A:) Toluene-4-monooxygenase catalytic effector protein {Pseudomonas mendocina}

STLADQALHNNNVGPIIRAGDLVEPVIETAEIDNPGKEITVEDRRAYVRIAAEGELILTRKTLEEQLGRPFNMQELEINLASFAGQIQADEDQIRFYFDKTM

>d1hqi\_\_ d.137.1.1 (-) Phenol hydroxylase P2 protein {Pseudomonas sp., CF600}

MSSLVYIAFQDNDNARYVVEAIIQDNPHAVVQHHPAMIRIEAEKRLEIRRETVEENLGRAWDVQEMLVDVITIGGNVDEDDDRFVLEWKN

>d1jjcb6 d.138.1.1 (B:191-399) B3/B4 domain of PheRS, PheT {Thermus thermophilus (Thermus aquaticus)}

LKAEALPLPFALKVEDPEGAPHFTLGYAFGLRVAPSPLWMQRALFAAGMRPINNVVDVTNYVMLERAQPMHAFDLRFVGEGIAVRRAREGERLKTLDGVERTLHPEDLVIAGWRGEESFPLGLAGVMGGAESEVREDTEAIALEVACFDPVSIRKTARRHGLRTEASHRFERGVDPLGQVPAQRRALSLLQALAGARVAEALLEAGSPK

>d1clia2 d.139.1.1 (A:171-345) Aminoimidazole ribonucleotide synthetase (PurM) C-terminal domain {Escherichia coli}

DGSKVSDGDVLIALGSSGPHSNGYSLVRKILEVSGCDPQTTELDGKPLADHLLAPTRIYVKSVLELIEKVDVHAIAHLTGGGFWENIPRVLPDNTQAVIDESSWQWPEVFNWLQTAGNVEHHEMYRTFNCGVGMIIALPAPEVDKALALLNANGENAWKIGIIKASDSEQRVVIE

>d1hw7a\_ d.193.1.1 (A:) Heat shock protein 33, Hsp33 {Escherichia coli}

HDQLHRYLFENFAVRGELVTVSETLQQILENHDYPQPVKNVLAELLVATSLLTATLKFDGDITVQLQGDGPMNLAVINGNNNQQMRGVARVQGEIPENADLKTLVGNGYVVITITPSEGERYQGVVGLEGDTLAACLEDYFMRSEQLPTRLFIRTGDVDGKPAAGGMLLQVMPAQNAQQDDFDHLATLTETIKTEELLTLPANEVLWRLYHEEEVTVYDPQDVEFKCTC

>d1jw3a\_ d.208.1.1 (A:) Hypothetical protein MTH1598 {Archaeon Methanobacterium thermoautotrophicum}

MKGFEFFDVTADAGFWAYGHDLEEVFENAALAMFEVMTDTSLVEAAEERRVEITSEDRVSLLYDWLDELLFIHDTEFILFSKFKVKIDEKDDGLHLTGTAMGEEIKEGHERRDEVKAVTFHMMEILDEDGLIKARVILDL

>d1dl5a2 d.197.1.1 (A:214-317) Protein-L-isoaspartyl O-methyltransferase, C-terminal domain {Thermotoga maritima}

NLLERNRKLLREFPFNREILLVRSHIFVELVDLLTRRLTEIDGTFYYAGPNGVVEFLDDRMRIYGDAPEIENLLTQWESCGYRSFEYLMLHVGYNAFSHISCSI

>d1seia\_ d.140.1.1 (A:) Ribosomal protein S8 {Bacillus stearothermophilus}

VMTDPIADMLTAIRNANMVRHEKLEVPASKIKREIAEILKREGFIRDYEYIEDNKQGILRIFLKYGPNERVITGLKRISKPGLRVYVKAHEVPRVLNGLGIAILSTSQGVLTDKEARQKGTGGEIIAYVI

>d1an7a\_ d.140.1.1 (A:) Ribosomal protein S8 {Thermus thermophilus}

TDPIADMLTRIRNATRVYKESTDVPASRFKEEILRILAREGFIKGYERVDVDGKPYLRVYLKYGPRRQGPDPRPEQVIHHIRRISKPGRRVYVGVKEIPRVRRGLGIAILSTSKGVLTDREARKLGVGGELICEVW

>d1i94h\_ d.140.1.1 (H:) Ribosomal protein S8 {Thermus thermophilus}

MLTDPIADMLTRIRNATRVYKESTEVPASRFKEEILKILAREGFIKGYERVEVDGKPYLRIHLKYGPRRQGPDPRPEQVIKHIRRISRPGRRVYVGVKEIPRVRRGLGIAILSTPKGVLTDREARKLGVGGELICEVW

>d1i6ua\_ d.140.1.1 (A:) Ribosomal protein S8 {Archaeon Methanococcus jannaschii}

SLMDPLANALNHISNCERVGKKVVYIKPASKLIGRVLKVMQDNGYIGEFEFIEDGRAGIFKVELIGKINKCGAIKPRFPVKKFGYEKFEKRYLPARDFGILIVSTTQGVMSHEEAKKRGLGGRLLAYVY

>d1rl6a1 d.141.1.1 (A:7-81) Ribosomal protein L6 {Bacillus stearothermophilus}

PIEIPAGVTVTVNGNTVTVKGPKGELTRTFHPDMTITVEGNVITVTRPSDEKHHRALHGTTRSLLANMVEGVSKG

>d1rl6a2 d.141.1.1 (A:82-170) Ribosomal protein L6 {Bacillus stearothermophilus}

YEKALELVGVGYRASKQGKKLVLSVGYSHPVEIEPEEGLEIEVPSQTKIIVKGADKQRVGELAANIRAVRPPEPYKGKGIRYEGELVRL

>d1jj2e1 d.141.1.1 (E:1-79) Ribosomal protein L6 {Archaeon Haloarcula marismortui}

PRVELEIPEDVDAEQDHLDITVEGDNGSVTRRLWYPDIDVSVDGDTVVIESDEDNAKTMSTIGTFQSHIENMFHGVTEG

>d1jj2e2 d.141.1.1 (E:80-172) Ribosomal protein L6 {Archaeon Haloarcula marismortui}

WEYGMEVFYSHFPMQVNVEGDEVVIENFLGEKAPRRTTIHGDTDVEIDGEELTVSGPDIEAVGQTAADIEQLTRINDKDVRVFQDGVYITRKP

>d1gsa\_2 d.142.1.1 (123-314) Glutathione synthetase {Escherichia coli}

NEKLFTAWFSDLTPETLVTRNKAQLKAFWEKHSDIILKPLDGMGGASIFRVKEGDPNLGVIAETLTEHGTRYCMAQNYLPAIKDGDKRVLVVDGEPVPYCLARIPQGGETRGNLAAGGRGEPRPLTESDWKIARQIGPTLKEKGLIFVGLDIIGDRLTEINVTSPTCIREIEAEFPVSITGMLMDAIEARLQ

>d1iow\_2 d.142.1.1 (97-306) D-ala-D-ala ligase {Escherichia coli, gene ddlB}

KLRSKLLWQGAGLPVAPWVALTRAEFEKGLSDKQLAEISALGLPVIVKPSREGSSVGMSKVVAENALQDALRLAFQHDEEVLIEKWLSGPEFTVAILGEEILPSIRIQPSGTFYDYEAKFLSDETQYFCPAGLEASQEANLQALVLKAWTTLGCKGWGRIDVMLDSDGQFYLLEANTSPGMTSHSLVPMAARQAGMSFSQLVVRILELAD

>d1ehia2 d.142.1.1 (A:135-362) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}

DKALTKELLTVNGIRNTKYIVVDPESANNWSWDKIVAELGNIVFVKAANQGSSVGISRVTNAEEYTEALSDSFQYDYKVLIEEAVNGARELEVGVIGNDQPLVSEIGAHTVPNQGSGDGWYDYNNKFVDNSAVHFQIPAQLSPEVTKEVKQMALDAYKVLNLRGEARMDFLLDENNVPYLGEPNTLPGFTNMSLFKRLWDYSDINNAKLVDMLIDYGFEDFAQNKKLS

>d1e4ea2 d.142.1.1 (A:132-342) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}

DKSLTYIVAKNAGIATPAFWVINKDDRPVAATFTYPVFVKPARSGSSFGVKKVNSADELDYAIESARQYDSKILIEQAVSGCEVGCAVLGNSAALVVGEVDQIRLQYGIFRIHQEVEPEKGSENAVITVPADLSAEERGRIQETVKKIYKTLGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGISLPELIDRLIVLALK

>d1dv1a3 d.142.1.2 (A:115-330) Biotin carboxylase subunit of acetyl-CoA carboxylase {Escherichia coli}

DKVSAIAAMKKAGVPCVPGSDGPLGDDMDKNRAIAKRIGYPVIIKASGGGGGRGMRVVRGDAELAQSISMTRAEAKAAFSNDMVYMEKYLENPRHVEIQVLADGQGNAIYLAERDCSMQRRHQKVVEEAPAPGITPELRRYIGERCAKACVDIGYRGAGTFEFLFENGEFYFIEMNTRIQVEHPVTEMITGVDLIKEQLRIAAGQPLSIKQEEVHV

>d1gsoa3 d.142.1.2 (A:104-327) Glycinamide ribonucleotide synthetase (GAR-syn) {Escherichia coli}

SKAFTKDFLARHKIPTAEYQNFTEVEPALAYLREKGAPIVIKADGLAAGKGVIVAMTLEEAEAAVHDMLAGNAFGDAGHRIVIEEFLDGEEASFIVMVDGEHVLPMATSQDHKRVGDKDTGPNTGGMGAYSPAPVVTDDVHQRTMERIIWPTVKGMAAEGNTYTGFLYAGLMIDKQGNPKVIEFNCRFGDLETQPIMLRMKSDLVELCLAACESKLDEKTSEWD

>d1b6ra3 d.142.1.2 (A:79-276) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

DRLTQKQLFDKLHLPTAPWQLLAERSEWPAVFDRLGELAIVKRRTGGYDGRGQWRLRANETEQLPAECYGECIVEQGINFSGEVSLVGARGFDGSTVFYPLTHNLHQDGILRTSVAFPQANAQQQARAEEMLSAIMQELGYVGVMAMECFVTPQGLLINELAPRVHNSGHWTQNGASISQFELHLRAITDLPLPQPVV

>d1eyza3 d.142.1.2 (A:113-318) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

NREGIRRLAAEELQLPTSTYRFADSESLFREAVADIGYPCIVKPVMSSSGKGQTFIRSAEQLAQAWKYAQQGGRAGAGRVIVEGVVKFDFEITLLTVSAVDGVHFCAPVGHRQEDGDYRESWQPQQMSPLALERAQEIARKVVLALGGYGLFGVELFVCGDEVIFSEVSPRPHDTGMVTLISQDLSEFALHVRAFLGLPVGGIRQY

>d1a9xa5 d.142.1.2 (A:128-402) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

DRRRFDVAMKKIGLETARSGIAHTMEEALAVAADVGFPCIIRPSFTMGGSGGGIAYNREEFEEICARGLDLSPTKELLIDESLIGWKEYEMEVVRDKNDNCIIVCSIENFDAMGIHTGDSITVAPAQTLTDKEYQIMRNASMAVLREIGVETGGSNVQFAVNPKNGRLIVIEMNPRVSRSSALASKATGFPIAKVAAKLAVGYTLDELMNDITGGRTPASFEPSIDYVVTKIPRFNFEKFAGANDRLTTQMKSVGEVMAIGRTQQESLQKALRGL

>d1a9xa6 d.142.1.2 (A:677-935) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

RFQHAVERLKLKQPANATVTAIEMAVEKAKEIGYPLVVRAAMEIVYDEADLRRYFQTAVLLDHFLDDAVEVDVDAICDGEMVLIGGIMEHIEQAGVHSGDSACSLPAYTLSQEIQDVMRQQVQKLAFELQVRGLMNVQFAVKNNEVYLIEVNPRAARTVPFVSKATGVPLAKVAARVMAGKSLAEQGVTKEVIPPYYSVKEVVLPFNKFPGVDPLLGPEMRSTGEVMGVGRTFAEAFAKAQLGS

>d1auva2 d.142.1.3 (A:214-417) Synapsin Ia, C-terminal domain {Cow (Bos taurus)}

NSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLINQTFYPNHKEMLSSTTYPVVVKMGHAHSGMGKVKVDNQHDFQDIASVVALTKTYATTEPFIDAKYDVRIQKIGQNYKAYMRTSVSGNWKTNTGSAMLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIEVVGSSMPLIGDHQDEDKQLIVELVVNKMAQA

>d1jkjb2 d.142.1.4 (B:1-238) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Escherichia coli}

MNLHEYQAKQLFARYGLPAPVGYACTTPREAEEAASKIGAGPWVVKCQVHAGGRGKAGGVKVVNSKEDIRAFAENWLGKRLVTYQTDANGQPVNQILVEAATDIAKELYLGAVVDRSSRRVVFMASTEGGVEIEKVAEETPHLIHKVALDPLTGPMPYQGRELAFKLGLEGKLVQQFTKIFMGLATIFLERDLALIEINPLVITKQGDLICLDGKLGADGNALFRQPDLREMRDQSQE

>d1eucb2 d.142.1.4 (B:0-245) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Pig (Sus scrofa)}

MVNLQEYQSKKLMSDNGVKVQRFFVADTANEALEAAKRLNAKEIVLKAQILAGGRGKGVFSSGLKGGVHLTKDPEVVGQLAKQMIGYNLATKQTPKEGVKVNKVMVAEALDISRETYLAILMDRSCNGPVLVGSPQGGVDIEEVAASNPELIFKEQIDIIEGIKDSQAQRMAENLGFLGPLQNQAADQIKKLYNLFLKIDATQVEVNPFGETPEGQVVCFDAKINFDDNAEFRQKDIFAMDDKSEN

>d1kbla3 d.142.1.5 (A:2-376) Pyruvate phosphate dikinase, N-terminal domain {Clostridium symbiosum}

AKWVYKFEEGNASMRNLLGGKGCNLAEMTILGMPIPQGFTVTTEACTEYYNSGKQITQEIQDQIFEAITWLEELNGKKFGDTEDPLLVSVRSGARASMPGMMDTILNLGLNDVAVEGFAKKTGNPRFAYDSYRRFIQMYSDVVMEVPKSHFEKIIDAMKEEKGVHFDTDLTADDLKELAEKFKAVYKEAMNGEEFPQEPKDQLMGAVKAVFRSWDNPRAIVYRRMNDIPGDWGTAVNVQTMVFGNKGETSGTGVAFTRNPSTGEKGIYGEYLINAQGEDVVAGVRTPQPITQLENDMPDCYKQFMDLAMKLEKHFRDMQDMEFTIEEGKLYFLQTRNGKRTAPAALQIACDLVDEGMITEEEAVVRIEAKSLDQL

>d2hgsa2 d.142.1.6 (A:304-474) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

TKKVQQELSRPGMLEMLLPGQPEAVARLRATFAGLYSLDVGEEGDQAIAEALAAPSRFVLKPQREGGGNNLYGEEMVQALKQLKDSEERASYILMEKIEPEPFENCLLRPGSPARVVQCISELGIFGVYVRQEKTLVMNKHVGHLLRTKAIEHADGGVAAGVAVLDNPYPV

>d2hgsa3 d.142.1.6 (A:3-201) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

TNWGSLLQDKQQLEELARQAVDRALAEGVLLRTSQEPTSSEVVSYAPFTLFPSLVPSALLEQAYAVQMDFNLLVDAVSQNAAFLEQTLSSTIKQDDFTARLFDIHKQVLKEGIAQTVFLGLNRSDYMFQRSADGSPALKQIEINTISASFGGLASRTPAVHRHVLSVLSKTKEAGKILSNNPSKGLALGIAKAWELYGS

>d1a0i\_2 d.142.2.1 (2-240) ATP-dependent DNA ligase, N-terminal domain {Bacteriophage T7}

VNIKTNPFKAVSFVESAIKKALDNAGYLIAEIKYDGVRGNICVDNTANSYWLSRVSKTIPALEHLNGFDVRWKRLLNDDRCFYKDGFMLDGELMVKGVDFNTGSGLLRTKWTDTKNQEFHEELFVEPIRKKDKVPFKLHTGHLHIKLYAILPLHIVESGEDCDVMTLLMQEHVKNMLPLLQEYFPEIEWQAAESYEVYDMVELQQLYEQKRAEGHEGLIVKDPMCIYKRGKKSGWWKMK

>d1fvia2 d.142.2.1 (A:2-189) ATP-dependent DNA ligase, N-terminal domain {Chlorella virus, PBCV-1}

AITKPLLAATLENIEDVQFPCLATPKIAGIRSVKQTQMLSRTFKPIRNSVMNRLLTELLPEGSDGEISIEGATFQDTTSAVMTGHKMYNAKFSYYWFDYVTDDPLKKYIDRVEDMKNYITVHPHILEHAQVKIIPLIPVEINNITELLQYERDVLSKGFEGVMIRKPDGKYKFGRSTLKEGILLKMKQ

>d1b04a\_ d.142.2.2 (A:) Adenylation domain of NAD+-dependent DNA ligase {Bacillus stearothermophilus}

DRQQAERRAAELRELLNRYGYEYYVLDRPSVPDAEYDRLMQELIAIEEQYPELKTSDSPTQRIGGPPLEAFRKVAHRVPMMSLANAFGEGDLRDFDRRVRQEVGEAAYVCELAIDGLAVSVRYEDGYFVQGATRGDGTTGEDITENLKTIRSLPLRLKEPVSLEARGEAFMPKASFLRLNEERKARGEELFANPRNAAAGSLRQLDPKVAASRQLDLFVYGLADAEALGIASHSEALDYLQALGFKVNPERRRCANIDEVIAFVSEWHDKRPQLPYEIDGIVIKVDSFAQQRALGATAKSPRWAIAYKFPAE

>d1dgsa3 d.142.2.2 (A:1-314) Adenylation domain of NAD+-dependent DNA ligase {Thermus filiformis}

MTREEARRRINELRDLIRYHNYRYYVLADPEISDAEYDRLLRELKELEERFPEFKSPDSPTEQVGARPLEPTFRPVRHPTRMYSLDNAFTYEEVLAFEERLEREAEAPSLYTVEHKVDGLSVLYYEEGVWSTGSGDGEVGEEVTQNLLTIPTIPRRLKGVPDRLEVRGEVYMPIEAFLRLNEELEERGEKVFKNPRNAAAGSLRQKDPRVTAKRGLRATFYALGLGLGLEESGLKSQYELLLWLKEKGFPVEHCYEKALGAEGVEEVYRRGLAQRHALPFEADGVVLKLDDLTLWGELGYTARAPRFALAYKFP

>d1ckma2 d.142.2.3 (A:11-238) RNA guanylyltransferase (mRNA capping enzyme), N-terminal domain {Chlorella virus, PBCV-1}

NITTERAVLTLNGLQIKLHKVVGESRDDIVAKMKDLAMDDHKFPRLPGPNPVSIERKDFEKLKQNKYVVSEKTDGIRFMMFFTRVFGFKVCTIIDRAMTVYLLPFKNIPRVLFQGSIFDGELCVDIVEKKFAFVLFDAVVVSGVTVSQMDLASRFFAMKRSLKEFKNVPEDPAILRYKEWIPLEHPTIIKDHLKKANAIYHTDGLIIMSVDEPVIYGRNFNLFKLKPG

>d1a48\_\_ d.143.1.1 (-) SAICAR synthase {Baker's yeast (Saccharomyces cerevisiae)}

SITKTELDGILPLVARGKVRDIYEVDAGTLLFVATDRISAYDVIMENSIPEKGILLTKLSEFWFKFLSNDVRNHLVDIAPGKTIFDYLPAKLSEPKYKTQLEDRSLLVHKHKLIPLEVIVRGYITGSAWKEYVKTGTVHGLKQPQGLKESQEFPEPIFTPSTKAEQGEHDENISPAQAAELVGEDLSRRVAELAVKLYSKCKDYAKEKGIIIADTKFEFGIDEKTNEIILVDEVLTPDSSRFWNGASYKVGESQDSYDKQFLRDWLTANKLNGVNGVKMPQDIVDRTRAKYIEAYETLTGSKWSH

>d1bo1a\_ d.143.1.2 (A:) Phosphatidylinositol phosphate kinase IIbeta, PIPK IIbeta {Human (Homo sapiens)}

KLFRASEPILSVLMWGVNHTINELSNVPVPVMLMPDDFKAYSKIKVDNHLFNKENLPSRFKFKEYCPMVFRNLRERFGIDDQDYQNSVTRSAPINSDSQGRCGTRFLTTYDRRFVIKTVSSEDVAEMHNILKKYHQFIVECHGNTLLPQFLGMYRLTVDGVETYMVVTRNVFSHRLTVHRKYDLKGSTVAREASDKEKAKDLPTFKDNDFLNEGQKLHVGEESKKNFLEKLKRDVEFLAQLKIMDYSLLVGIHDVDRAEQEEMEVEERAEDEECENDGVGGNLLCSYGTPPDSPGNLLSFPRFFGPGEFDPSVDVYAMKSHESSPKKEVYFMAIIDILTPYDTKKKAAHAAKTVKHGAGAEISTVNPEQYSKRFNEFMSNILT

>d1blxa\_ d.144.1.1 (A:) Cyclin-dependent PK (CDK, different isozymes) {Human (Homo sapiens)}

GLCRADQQYECVAEIGEGAYGKVFKARDLKNGGRFVALKRVRVQTGEEGMPLSTIREVAVLRHLETFEHPNVVRLFDVCTVSRTDRETKLTLVFEHVDQDLTTYLDKVPEPGVPTETIKDMMFQLLRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTSVVVTLWYRAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGSSDVDQLGKILDVIGLPGEEDWPRDVALPRQAFHSKSAQPIEKFVTDIDELGKDLLLKCLTFNPAKRISAYSALSHPYFQDLERCKEN

>d1jvpp\_ d.144.1.1 (P:) Cyclin-dependent PK (CDK, different isozymes) {Human (Homo sapiens)}

MENFQKVEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTETEGVPSTAIREISLLKELNHPNIVKLLDVIHTENKLYLVFEFLHQDLKKFMDASALTGIPLPLIKSYLFQLLQGLAFCHSHRVLHRDLKPQNLLINTEGAIKLADFGLARAFGVPVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIFAEMVTRRALFPGDSEIDQLFRIFRTLGTPDEVVWPGVTSMPDYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFFQDVTKPVPHLRL

>d1apme\_ d.144.1.1 (E:) cAMP-dependent PK, catalytic subunit {Mouse (Mus musculus)}

SEQESVKEFLAKAKEDFLKKWETPSQNTAQLDQFDRIKTLGTGSFGRVMLVKHKESGNHYAMKILDKQKVVKLKQIEHTLNEKRILQAVNFPFLVKLEFSFKDNSNLYMVMEYVAGGEMFSHLRRIGRFAEPHARFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDQQGYIQVTDFGFAKRVKGRTWTLCGTPEYLAPEIILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFPSHFSSDLKDLLRNLLQVDLTKRFGNLKNGVNDIKNHKWFATTDWIAIYQRKVEAPFIPKFKGPGDTSNFDDYEEEEIRVSINEKCGKEFTEF

>d1fota\_ d.144.1.1 (A:) cAMP-dependent PK, catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

YSLQDFQILRTLGTGSFGRVHLIRSRHNGRYYAMKVLKKEIVVRLKQVEHTNDERLMLSIVTHPFIIRMWGTFQDAQQIFMIMDYIEGGELFSLLRKSQRFPNPVAKFYAAEVCLALEYLHSKDIIYRDLKPENILLDKNGHIKITDFGFAKYVPDVTYTLCGTPDYIAPEVVSTKPYNKSIDWWSFGILIYEMLAGYTPFYDSNTMKTYEKILNAELRFPPFFNEDVKDLLSRLITRDLSQRLGNLQNGTEDVKNHPWFKEVVWEKLLSRNIETPYEPPIQQGQGDTSQFDKYPEEDINYGVQGEDPYADLFRDF

>d1a06\_\_ d.144.1.1 (-) Calmodulin-dependent protein kinase {Rat (Rattus norvegicus)}

WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAVKYLHDLGIVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPYWDDISDSAKDFIRHLMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKSKWKQAFNATAVVRHM

>d1ia8a\_ d.144.1.1 (A:) Cell cycle checkpoint kinase chk1 {Human (Homo sapiens)}

AVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEAVAVKIVDMKRAVDCPENIKKEICINKMLNHENVVKFYGHRREGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFFHQLMAGVVYLHGIGITHRDIKPENLLLDERDNLKISDFGLATVFRYNNRERLLNKMCGTLPYVAPELLKRREFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKKTYLNPWKKIDSAPLALLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRP

>d1phk\_\_ d.144.1.1 (-) gamma-subunit of glycogen phosphorylase kinase (Phk) {Rabbit (Oryctolagus cuniculus)}

FYENYEPKEILGRGVSSVVRRCIHKPTCKEYAVKIIDVTGGGSFSAEEVQELREATLKEVDILRKVSGHPNIIQLKDTYETNTFFFLVFDLMKKGELFDYLTEKVTLSEKETRKIMRALLEVICALHKLNIVHRDLKPENILLDDDMNIKLTDFGFSCQLDPGEKLREVCGTPSYLAPEIIECSMNDNHPGYGKEVDMWSTGVIMYTLLAGSPPFWHRKQMLMLRMIMSGNYQFGSPEWDDYSDTVKDLVSRFLVVQPQKRYTAEEALAHPFFQQYV

>d1h8fa\_ d.144.1.1 (A:) Glycogen synthase kinase-3 beta (Gsk3b) {Human (Homo sapiens)}

SKVTTVVATPGQGPDRPQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKKVLQGKAFKNRELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYLNLVLDYVPETVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHRDIKPQNLLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLLGQPIFPGDSGVDQLVEIIKVLGTPTREQIREMNPNYTEFAFPQIKAHPWTKVFRPRTPPEAIALCSRLLEYTPTARLTPLEACAHSFFDELRDPNVKLPNGRDTPALFNFTTQELSSNPPLATILIPPHARIQA

>d1tkia\_ d.144.1.1 (A:) Titin, kinase domain {Human (Homo sapiens)}

KELYEKYMIAEDLGRGEFGIVHRCVETSSKKTYMAKFVKVKGTDQVLVKKEISILNIARHRNILHLHESFESMEELVMIFEFISGLDIFERINTSAFELNEREIVSYVHQVCEALQFLHSHNIGHFDIRPENIIYQTRRSSTIKIIEFGQARQLKPGDNFRLLFTAPEYYAPEVHQHDVVSTATDMWSLGTLVYVLLSGINPFLAETNQQIIENIMNAEYTFDEEAFKEISIEAMDFVDRLLVKERKSRMTASEALQHPWLKQKIERVSTKVIRTLKHRRYYHTLIKKDLNMVVSAARISCGGAIRSQKGVSVAKVKVASI

>d1koba\_ d.144.1.1 (A:) Twitchin, kinase domain {California sea hare (Aplysia californica), twk43}

INDYDKFYEDIWKKYVPQPVEVKQGSVYDYYDILEELGSGAFGVVHRCVEKATGRVFVAKFINTPYPLDKYTVKNEISIMNQLHHPKLINLHDAFEDKYEMVLILEFLSGGELFDRIAAEDYKMSEAEVINYMRQACEGLKHMHEHSIVHLDIKPENIMCETKKASSVKIIDFGLATKLNPDEIVKVTTATAEFAAPEIVDREPVGFYTDMWAIGVLGYVLLSGLSPFAGEDDLETLQNVKRCDWEFDEDAFSSVSPEAKDFIKNLLQKEPRKRLTVHDALEHPWLKGDHSNLTSRIPSSRYNKIRQKIKEKYADWPAPQPAIGRIANFSSLRKHRPQEYQIYDSYFDRKEAV

>d1koa\_2 d.144.1.1 (5915-6264) Twitchin, kinase domain {Caenorhabditis elegans, pjk4}

YDNYVFDIWKQYYPQPVEIKHDHVLDHYDIHEELGTGAFGVVHRVTERATGNNFAAKFVMTPHESDKETVRKEIQTMSVLRHPTLVNLHDAFEDDNEMVMIYEFMSGGELFEKVADEHNKMSEDEAVEYMRQVCKGLCHMHENNYVHLDLKPENIMFTTKRSNELKLIDFGLTAHLDPKQSVKVTTGTAEFAAPEVAEGKPVGYYTDMWSVGVLSYILLSGLSPFGGENDDETLRNVKSCDWNMDDSAFSGISEDGKDFIRKLLLADPNTRMTIHQALEHPWLTPGNAPGRDSQIPSSRYTKIRDSIKTKYDAWPEPLPPLGRISNYSSLRKHRPQEYSIRDAFWDRSEA

>d1p38\_\_ d.144.1.1 (-) MAP kinase p38 {Mouse (Mus musculus)}

ERPTFYRQELNKTIWEVPERYQNLSPVGSGAYGSVCAAFDTKTGHRVAVKKLSRPFQSIIHAKRTYRELRLLKHMKHENVIGLLDVFTPARSLEEFNDVYLVTHLMGADLNNIVKCQKLTDDHVQFLIYQILRGLKYIHSADIIHRDLKPSNLAVNEDCELKILDFGLARHTDDEMTGYVATRWYRAPEIMLNWMHYNQTVDIWSVGCIMAELLTGRTLFPGTDHIDQLKLILRLVGTPGAELLKKISSESARNYIQSLAQMPKMNFANVFIGANPLAVDLLEKMLVLDSDKRITAAQALAHAYFAQYHDPDDEPVADPYDQSFESRDLLIDEWKSLTYDEVISFVPPPLD

>d1cm8a\_ d.144.1.1 (A:) MAP kinase p38-gamma {Human (Homo sapiens)}

RSGFYRQEVTKTAWEVRAVYRDLQPVGSGAYGAVCSAVDGRTGAKVAIKKLYRPFQSELFAKRAYRELRLLKHMRHENVIGLLDVFTPDETLDDFTDFYLVMPFMGTDLGKLMKHEKLGEDRIQFLVYQMLKGLRYIHAAGIIHRDLKPGNLAVNEDCELKILDFGLARQADSEMTGYVVTRWYRAPEVILNWMRYTQTVDIWSVGCIMAEMITGKTLFKGSDHLDQLKEIMKVTGTPPAEFVQRLQSDEAKNYMKGLPELEKKDFASILTNASPLAVNLLEKMLVLDAEQRVTAGEALAHPYFESLHDTEDEPQVQKYDDSFDDVDRTLDEWKRVTYKEVLSFKP

>d1pme\_\_ d.144.1.1 (-) MAP kinase Erk2 {Human (Homo sapiens)}

GQVFDVGPRYTNLSYIGEGAYGMVCSAYDNVNKVRVAIKKISPFEHQTYCQRTLREIKILLRFRHENIIGINDIIRAPTIEQMKDVYLVTHLMGADLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLLNTTCDLKICDFGLARVADPDHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINLKARNYLLSLPHKNKVPWNRLFPNADSKALDLLDKMLTFNPHKRIEVEQALAHPYLEQYYDPSDEPIAEAPFKFDMELDDLPKEKLKELIFEETARFQPGYRS

>d1jnk\_\_ d.144.1.1 (-) c-jun N-terminal kinase (jnk3s) {Human (Homo sapiens)}

DNQFYSVEVGDSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDRNVAIKKLSRPFQNQTHAKRAYRELVLMKCVNHKNIISLLNVFTPQKTLEEFQDVYLVMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKSDCTLKILDFGLARTAGTSFMMTPYVVTRYYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYIDQWNKVIEQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHNKLKASQARDLLSKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKELIYKEVMN

>d1ckia\_ d.144.1.1 (A:) Casein kinase-1, CK1 {Rat (Rattus norvegicus)}

MELRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVKTKHPQLHIESKIYKMMQGGVGIPTIRWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLLADQMISRIEYIHSKNFIHRDVKPDNFLMGLGKKGNLVYIIDFGLAKKYRDARTHQHIPYRENKNLTGTARYASINTHLGIEQSRRDDLESLGYVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFATYLNFCRSLRFDDKPDYSYLRQLFRNLFHRQGFSYDYVFDWNMLKFGASR

>d1csn\_\_ d.144.1.1 (-) Casein kinase-1, CK1 {Fission yeast (Schizosaccharomyces pombe)}

NVVGVHYKVGRRIGEGSFGVIFEGTNLLNNQQVAIKFEPRRSDAPQLRDEYRTYKLLAGCTGIPNVYYFGQEGLHNVLVIDLLGPSLEDLLDLCGRKFSVKTVAMAAKQMLARVQSIHEKSLVYRDIKPDNFLIGRPNSKNANMIYVVDFGMVKFYRDPVTKQHIPYREKKNLSGTARYMSINTHLGREQSRRDDLEALGHVFMYFLRGSLPWQGLKAATNKQKYERIGEKKQSTPLRELCAGFPEEFYKYMHYARNLAFDATPDYDYLQGLFSKVLERLNTTEDENFDWNLL

>d1a6o\_\_ d.144.1.1 (-) Protein kinase CK2, alpha subunit {Maize (Zea mays)}

SKARVYADVNVLRPKEYWDYEALTVQWGEQDDYEVVRKVGRGKYSEVFEGINVNNNEKCIIKILKPVKKKKIKREIKILQNLCGGPNIVKLLDIVRDQHSKTPSLIFEYVNNTDFKVLYPTLTDYDIRYYIYELLKALDYCHSQGIMHRDVKPHNVMIDHELRKLRLIDWGLAEFYHPGKEYNVRVASRYFKGPELLVDLQDYDYSLDMWSLGCMFAGMIFRKEPFFYGHDNHDQLVKIAKVLGTDGLNVYLNKYRIELDPQLEALVGRHSRKPWLKFMNADNQHLVSPEAIDFLDKLLRYDHQERLTALEAMTHPYFQQVRAAENS

>d1b6cb\_ d.144.1.1 (B:) Type I TGF-beta receptor R4 {Human (Homo sapiens)}

TTLKDLIYDMTTSGSGSGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSSREERSWFREAEIYQTVMLRHENILGFIAADNKDNGTWTQLWLVSDYHEHGSLFDYLNRYTVTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAVRHDSATDTIDIAPNHRVGTKRYMAPEVLDDSINMKHFESFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMRECWYANGAARLTALRIKKTLSQLSQQEG

>d1f3mc\_ d.144.1.1 (C:) pak1 {Human (Homo sapiens)}

SDEEILEKLRSIVSVGDPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIRQMNLQQQPKKELIINEILVMRENKNPNIVNYLDSYLVGDELWVVMEYLAGGSLTDVVTETCMDEGQIAAVCRECLQALEFLHSNQVIHRDIKSDNILLGMDGSVKLTDFGFCAQITPEQSKRSTMVGTPYWMAPEVVTRKAYGPKVDIWSLGIMAIEMIEGEPPYLNENPLRALYLIATNGTPELQNPEKLSAIFRDFLNRCLDMDVEKRGSAKELLQHQFLKIAKPLSSLTPLIAAAKEATK

>d1howa\_ d.144.1.1 (A:) Sky1p {Baker's yeast (Saccharomyces cerevisiae)}

FHPAFKGEPYKDARYILVRKLGWGHFSTVWLAKDMVNNTHVAMKIVRGDKVYTEAAEDEIKLLQRVNDADNTKEDSMGANHILKLLDHFNHKGPNGVHVVMVFEVLGENLLALIKKYEHRGIPLIYVKQISKQLLLGLDYMHRRCGIIHTDIKPENVLMEIVDSPENLIQIKIADLGNACWYDEHYTNSIQTREYRSPEVLLGAPWGCGADIWSTACLIFELITGDFLFEPDEGHSYTKDDDHIAQIIELLGELPSYLLRNGKYTRTFFNSRGLLRNISKLKFWPLEDVLTEKYKFSKDEAKEISDFLSPMLQLDPRKRADAGGLVNHPWLKDTLGMEEIRVPDRELYGSGSDIPGWFEEVR

>d1qcfa3 d.144.1.2 (A:249-531) Haemopoetic cell kinase Hck {Human (Homo sapiens)}

KPQKPWEKDAWEIPRESLKLEKKLGAGQFGEVWMATYNKHTKVAVKTMKPGSMSVEAFLAEANVMKTLQHDKLVKLHAVVTKEPIYIITEFMAKGSLLDFLKSDEGSKQPLPKLIDFSAQIAEGMAFIEQRNYIHRDLRAANILVSASLVCKIADFGLARVIEDNEYTAREGAKFPIKWTAPEAINFGSFTIKSDVWSFGILLMEIVTYGRIPYPGMSNPEVIRALERGYRMPRPENCPEELYNIMMRCWKNRPEERPTFEYIQSVLDDFYTATESQYEEIP

>d1qpca\_ d.144.1.2 (A:) Lymphocyte kinase (lck) {Human (Homo sapiens)}

KPWWEDEWEVPRETLKLVERLGAGQFGEVWMGYYNGHTKVAVKSLKQGSMSPDAFLAEANLMKQLQHQRLVRLYAVVTQEPIYIITEYMENGSLVDFLKTPSGIKLTINKLLDMAAQIAEGMAFIEERNYIHRDLRAANILVSDTLSCKIADFGLARLIEDNEYTAREGAKFPIKWTAPEAINYGTFTIKSDVWSFGILLTEIVTHGRIPYPGMTNPEVIQNLERGYRMVRPDNCPEELYQLMRLCWKERPEDRPTFDYLRSVLEDFFTATE

>d1fmk\_3 d.144.1.2 (249-533) c-src tyrosine kinase {Human (Homo sapiens)}

KPQTQGLAKDAWEIPRESLRLEVKLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAVVSEEPIYIVTEYMSKGSLLDFLKGETGKYLRLPQLVDMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGLARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWSFGILLTELTTKGRVPYPGMVNREVLDQVERGYRMPCPPECPESLHDLMCQCWRKEPEERPTFEYLQAFLEDYFTSTEPQYQPGENL

>d1fgka\_ d.144.1.2 (A:) Fibroblast growth factor receptor 1 {Human (Homo sapiens)}

ELPEDPRWELPRDRLVLGKPLGEGAFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYSYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNGRLPVKWMAPEALFDRIYTHQSDVWSFGVLLWEIFTLGGSPYPGVPVEELFKLLKEGHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTS

>d1vr2a\_ d.144.1.2 (A:) Vascular endothelial growth factor receptor 2 (kdr) {Human (Homo sapiens)}

LPYDASKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTVAVKMLKEGATHSEHRALMSELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKVAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHLGNLLQANA

>d1ir3a\_ d.144.1.2 (A:) Insulin receptor {Human (Homo sapiens)}

SSVFVPDEWEVSREKITLLRELGQGSFGMVYEGNARDIIKGEAETRVAVKTVNESASLRERIEFLNEASVMKGFTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNPGRPPPTLQEMIQMAAEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPVRWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDNCPERVTDLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSFFHSEENK

>d1k3aa\_ d.144.1.2 (A:) Insulin-like growth factor 1 receptor {Human (Homo sapiens)}

VPDEWEVAREKITMSRELGQGSFGMVYEGVAKGVVKDEPETRVAIKTVNEAASMRERIEFLNEASVMKEFNCHHVVRLLGVVSQGQPTLVIMELMTRGDLKSYLRSLRPEMENNPVLAPPSLSKMIQMAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGGKGLLPVRWMSPESLKDGVFTTYSDVWSFGVVLWEIATLAEQPYQGLSNEQVLRFVMEGGLLDKPDNCPDMLLELMRMCWQYNPKMRPSFLEIISSIKEEMEPGFREVSFYYSEENK

>d1byga\_ d.144.1.2 (A:) C-terminal src kinase (csk) {Human (Homo sapiens)}

GWALNMKELKLLQTIGKGEFGDVMLGDYRGNKVAVKCIKNDATAQAFLAEASVMTQLRHSNLVQLLGVIVEEKGGLYIVTEYMAKGSLVDYLRSRGRSVLGGDCLLKFSLDVCEAMEYLEGNNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALREKKFSTKSDVWSFGILLWEIYSFGRVPYPRIPLKDVVPRVEKGYKMDAPDGCPPAVYEVMKNCWHLDAAMRPSFLQLREQLEHIKTHEL

>d1iepa\_ d.144.1.2 (A:) Abelsone tyrosine kinase (abl) {Mouse (Mus musculus)}

MDPSSPNYDKWEMERTDITMKHKLGGGQYGEVYEGVWKKYSLTVAVKTLKEDTMEVEEFLKEAAVMKEIKHPNLVQLLGVCTREPPFYIITEFMTYGNLLDYLRECNRQEVSAVVLLYMATQISSAMEYLEKKNFIHRDLAARNCLVGENHLVKVADFGLSRLMTGDTYTAHAGAKFPIKWTAPESLAYNKFSIKSDVWAFGVLLWEIATYGMSPYPGIDLSQVYELLEKDYRMERPEGCPEKVYELMRACWQWNPSDRPSFAEIHQAFETMFQ

>d1jpaa\_ d.144.1.2 (A:) ephb2 receptor tyrosine kinase {Mouse (Mus musculus)}

KIFIDPFTFEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPGKREIFVAIKTLKSGYTEKQRRDFLSEASIMGQFDHPNVIHLEGVVTKSTPVMIITEFMENGSLDSFLRQNDGQFTVIQLVGMLRGIAAGMKYLADMNYVHRDLAARNILVNSNLVCKVSDFGLSRFLEDDTSDPTYTSALGGKIPIRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYWDMTNQDVINAIEQDYRLPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMIRNPNSLKA

>d1fvra\_ d.144.1.2 (A:) Tie2 kinase {Human (Homo sapiens)}

PTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVLCKLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIESLNYSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKFTYAGIDCSAE

>d1cjaa\_ d.144.1.3 (A:) Actin-fragmin kinase, catalytic domain {Slime mold (Physarum polycephalum)}

AGALWEIEKELFTKLPAPSSAINSHLQPAKPKVPQKKPSKWDPPAEFKVDLSTAVSYNDIGDINWKNLQQFKGIERSEKGTEGLFFVETESGVFIVKRSTNIESETFCSLLCMRLGLHAPKVRVVSSNSEEGTNMLECLAAIDKSFRVITTLANQANILLMELVRGITLNKLTTTSAPEVLTKSTMQQLGSLMALDVIVNNSDRLPIAWTNEGNLDNIMLSERGATVVPIDSKIIPLDASHPHGERVRELLRTLIAHPGHESSQFHSIRDIITLYTGYDVGTEGSISMQEGFLATVRECASFDLDAFERELLSWQESLQKCHNLSISPQAIPFILRMLRIFH

>d1ia9a\_ d.144.1.5 (A:) Trp Ca-channel kinase domain {Mouse (Mus musculus)}

YYYSAVERNNLMRLSQSIPFVPVPPRGEPVTVYRLEESSPSILNNSMSSWSQLGLCAKIEFLSKEEMGGGLRRAVKVLCTWSEHDILKSGHLYIIKSFLPEVINTWSSIYKEDTVLHLCLREIQQQRAAQKLTFAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEFRKYNNNNGDEIIPTNTLEEIMLAFSHWTYEYTRGELLVLDLQGVGENLTDPSVIKAEEKRSCDMVFGPANLGEDAIKNFRAKHHCNSCCRKLKLPDLKRNDYT

>d1e8xa4 d.144.1.4 (A:726-1092) Phoshoinositide 3-kinase (PI3K), catalytic domain {Pig (Sus scrofa)}

TAMLHDFTQQVQVIDMLQKVTIDIKSLSAEKYDVSSQVISQLKQKLENLQNLNLPQSFRVPYDPGLKAGALVIEKCKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLRQDMLILQILRIMESIWETESLDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFLGINKERVPFVLTPDFLFVMGTSGKKTSLHFQKFQDVCVKAYLALRHHTNLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHLVL

>d1j7la\_ d.144.1.6 (A:) Type IIIa 3',5"-aminoglycoside phosphotransferase {Enterococcus faecalis}

AKMRISPELKKLIEKYRCVKDTEGMSPAKVYKLVGENENLYLKMTDSRYKGTTYDVEREKDMMLWLEGKLPVPKVLHFERHDGWSNLLMSEADGVLCSEEYEDEQSPEKIIELYAECIRLFHSIDISDCPYTNSLDSRLAELDYLLNNDLADVDCENWEEDTPFKDPRELYDFLKTEKPEEELVFSHGDLGDSNIFVKDGKVSGFIDLGRSGRADKWYDIAFCVRSIREDIGEEQYVELFFDLLGIKPDWEKIKYYILLDELF

>d1e8ga2 d.145.1.1 (A:6-273) Vanillyl-alcohol oxidase {Fungus (Penicillium simplicissimum)}

EFRPLTLPPKLSLSDFNEFIQDIIRIVGSENVEVISSKDQIVDGSYMKPTHTHDPTHVMDQDYFLASAIVAPRNVADVQSIVGLANKFSFPLWPISIGRNSGYGGAAPRVSGSVVLDMGKNMNRVLEVNVEGAYCVVEPGVTYHDLHNYLEANNLRDKLWLDVPDLGGGSVLGNAVERGVGYTPYGDHWMMHSGMEVVLANGELLRTGMGALPDPKRPETMGLKPEDQPWSKIAHLFPYGFGPYIDGLFSQSNMGIVTKIGIWLMPNP

>d1diqa2 d.145.1.1 (A:7-242) Flavoprotein subunit of p-cresol methylhydroxylase {Pseudomonas putida}

AVLPKGVTQGEFNKAVQKFRALLGDDNVLVESDQLVPYNKIMMPVENAAHAPSAAVTATTVEQVQGVVKICNEHKIPIWTISTGRNFGYGSAAPVQRGQVILDLKKMNKIIKIDPEMCYALVEPGVTFGQMYDYIQENNLPVMLSFSAPSAIAGPVGNTMDRGVGYTPYGEHFMMQCGMEVVLANGDVYRTGMGGVPGSNTWQIFKWGYGPTLDGMFTQANYGICTKMGFWLMPKP

>d1f0xa2 d.145.1.1 (A:9-273) D-lactate dehydrogenase {Escherichia coli}

NKAFLNELARLVGSSHLLTDPAKTARYRKGFRSGQGDALAVVFPGSLLELWRVLKACVTADKIILMQAANTGLTEGSTPNGNDYDRDVVIISTLRLDKLHVLGKGEQVLAYPGTTLYSLEKALKPLGREPHSVIGSSCIGASVIGGICNNSGGSLVQRGPAYTEMSLFARINEDGKLTLVNHLGIDLGETPEQILSKLDDDRIKDDDVRHDGRHAHDYDYVHRVRDIEADTPARYNADPDRLFESSGCAGKLAVFAVRLDTFEAE

>d1i19a2 d.145.1.1 (A:57-273) Cholesterol oxidase {Brevibacterium sterolicum}

VAPLPTPPNFPNDIALFQQAYQNWSKEIMLDATWVCSPKTPQDVVRLANWAHEHDYKIRPRGAMHGWTPLTVEKGANVEKVILADTMTHLNGITVNTGGPVATVTAGAGASIEAIVTELQKHDLGWANLPAPGVLSIGGALAVNAHGAALPAVGQTTLPGHTYGSLSNLVTELTAVVWNGTTYALETYQRNDPRITPLLTNLGRCFLTSVTMQAGPN

>d1uxy\_1 d.145.1.2 (3-200) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Escherichia coli}

HSLKPWNTFGIDHNAQHIVCAEDEQQLLNAWQYATAEGQPVLILGEGSNVLFLEDYRGTVIINRIKGIEIHDEPDAWYLHVGAGENWHRLVKYTLQEGMPGLENLALIPGCVGSSPIQNIGAYGVELQRVCAYVDSVELATGKQVRLTAKECRFGYRDSIFKHEYQDRFAIVAVGLRLPKEWQPVLTYGDLTRLDPTT

>d1hska1 d.145.1.2 (A:15-208) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Staphylococcus aureus}

NKDIYQALQQLIPNEKIKVDEPLKRYTYTKTGGNADFYITPTKNEEVQAVVKYAYQNEIPVTYLGNGSNIIIREGGIRGIVISLLSLDHIEVSDDAIIAGSGAAIIDVSRVARDYALTGLEFACGIPGSIGGAVYMNAGAYGGEVKDCIDYALCVNEQGSLIKLTTKELELDYRNSIIQKEHLVVLEAAFTLAP

>d1qj2c2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal domain {Pseudomonas carboxydovorans}

MIPGSFDYHRPKSIADAVALLTKLGEDARPLAGGHSLIPIMKTRLATPEHLVDLRDIGDLVGIREEGTDVVIGAMTTQHALIGSDFLAAKLPIIRETSLLIADPQIRYMGTIGGNAANGDPGNDMPALMQCLGAAYELTGPEGARIVAARDYYQGAYFTAIEPGELLTAIRIPVPPT

>d1ffvc2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal domain {Hydrogenophaga pseudoflava}

MIPPRFEYHAPKSVGEAVALLGQLGSDAKLLAGGHSLLPMMKLRFAQPEHLIDINRIPELRGIREEGSTVVIGAMTVENDLISSPIVQARLPLLAEAAKLIADPQVRNRGTIGGDIAHGDPGNDHPALSIAVEAHFVLEGPNGRRTVPADGFFLGTYMTLLEENEVMVEIRVPAFAQ

>d1fiqb2 d.145.1.3 (B:224-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}

PKQLRFEGERVTWIQASTLKELLDLKAQHPEAKLVVGNTEIGIEMKFKNQLFPMIICPAWIPELNAVEHGPEGISFGAACALSSVEKTLLEAVAKLPTQKTEVFRGVLEQLRWFAGKQVKSVASLGGNIITASPISDLNPVFMASGTKLTIVSRGTRRTVPMDHTFFPSYRKTLLGPEEILLSIEIPYSRE

>d1fo4a6 d.145.1.3 (A:192-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}

SPSLFNPEEFMPLDPTQEPIFPPELLRLKDVPPKQLRFEGERVTWIQASTLKELLDLKAQHPEAKLVVGNTEIGIEMKFKNQLFPMIICPAWIPELNAVEHGPEGISFGAACALSSVEKTLLEAVAKLPTQKTEVFRGVLEQLRWFAGKQVKSVASLGGNIITASPISDLNPVFMASGTKLTIVSRGTRRTVPMDHTFFPSYRKTLLGPEEILLSIEIPYSRE

>d1jroa4 d.145.1.3 (A:179-345) Xanthine dehydrogenase chain A, domain 3 {Rhodobacter capsulatus}

PAFLPETSDALADWYLAHPEATLIAGGTDVSLWVTKALRDLPEVAFLSHCKDLAQIRETPDGYGIGAGVTIAALRAFAEGPHPALAGLLRRFASEQVRQVATIGGNIANGSPIGDGPPALIAMGASLTLRRGQERRRMPLEDFFLEYRKQDRRPGEFVESVTLPKSA

>d1uxy\_2 d.146.1.1 (201-342) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Escherichia coli}

VTPQQVFNAVCHMRTTKLPDPKVNGNAGAFFKNPVVSAETAKALLSQFPTAPNYPQADGSVKLAAGWLIDQCQLKGMQIGGAAVHRQQALVLINEDNAKSEDVVQLAHHVRQKVGEKFNVWLEPEVRFIGASGEVSAVETIS

>d1hska2 d.146.1.1 (A:209-317) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Staphylococcus aureus}

GKMTEIQAKMDDLTERRESKQPLEYPSCGSVFQRPPGHFAGKLIQDSNLQGHRIGGVEVSTKHAGFMVNVDNGTATDYENLIHYVQKTVKEKFGIELNREVRIIGEHPK

>d1qlma\_ d.147.1.1 (A:) Methenyltetrahydromethanopterin cyclohydrolase {Archaeon Methanopyrus kandleri}

MVSVNENALPLVERMIERAELLNVEVQELENGTTVIDCGVEAAGGFEAGLLFSEVCMGGLATVELTEFEHDGLCLPAVQVTTDHPAVSTLAAQKAGWQVQVGDYFAMGSGPARALALKPKETYEEIDYEDDADVAILCLESSELPDEDVAEHVADECGVDPENLYLLVAPTASIVGSVQVSARVVETGLYKLLEVLEYDVTRVKYATGTAPIAPVADDDGEAMGRTNDCILYGGTVYLYVEGDDELPEVVEELPSEASEDYGKPFMKIFEEADYDFYKIDPGVFAPARVVVNDLSTGKTYTAGEINVDVLKESFSL

>d1c4za\_ d.148.1.1 (A:) Ubiquitin-protein ligase E3a, Hect catalytic domain (E6ap) {Human (Homo sapiens)}

NPYLRLKVRRDHIIDDALVRLEMIAMENPADLKKQLYVEFEGEQGVDEGGVSKEFFQLVVEEIFNPDIGMFTYDESTKLFWFNPSSFETEGQFTLIGIVLGLAIYNNCILDVHFPMVVYRKLMGKKGTFRDLGDSHPVLYQSLKDLLEYEGNVEDDMMITFQISQTDLFGNPMMYDLKENGDKIPITNENRKEFVNLYSDYILNKSVEKQFKAFRRGFHMVTNESPLKYLFRPEEIELLICGSRNLDFQALEETTEYDGGYTRDSVLIREFWEIVHSFTDEQKRLFLQFTTGTDRAPVGGLGKLKMIIAKNGPDTERLPTSHTCFNVLLLPEYSSKEKLKERLLKAITYA

>d2ahja\_ d.149.1.1 (A:) Nitrile hydratase alpha chain {Rhodococcus erythropolis}

IDHTTENAAPAQAPVSDRAWALFRALDGKGLVPDGYVEGWKKTFEEDFSPRRGAELVARAWTDPEFRQLLLTDGTAAVAQYGYLGPQGEYIVAVEDTPTLKNVIVCSLASCTAWPILGLPPTWYKSFEYRARVVREPRKVLSEMGTEIASDIEIRVYDTTAETRYMVLPQRPAGTEGWSQEQLQEIVTKDCLIGVAIPQV

>d1f7la\_ d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS {Bacillus subtilis}

GIYGIGLDITELKRIASMAGRQKRFAERILTRSELDQYYELSEKRKNEFLAGRFAAKEAFSKAFGTGIGRQLSFQDIEIRKDQNGKPYIICTKLSPAAVHVSITHTKEYAAAQVVIER

>d1ftha\_ d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS {Streptococcus pneumoniae}

MIVGHGIDIEELASIESAVTRHEGFAKRVLTALEMERFTSLKGRRQIEYLAGRWSAKEAFSKAMGTGISKLGFQDLEVLNNERGAPYFSQAPFSGKIWLSISHTDQFVTASVILEEN

>d1qr0a1 d.150.1.1 (A:1-101) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

MKIYGIYMDRPLSQEENERFMTFISPEKREKCRRFYHKEDAHRTLLGDVLVRSVISRQYQLDKSDIRFSTQEYGKPCIPDLPDAHFNISHSGRWVIGAFDS

>d1qr0a2 d.150.1.1 (A:102-228) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

QPIGIDIEKTKPISLEIAKRFFSKTEYSDLLAKDKDEQTDYFYHLWSMKESFIKQEGKGLSLPLDSFSVRLHQDGQVSIELPDSHSPCYIKTYEVDPGYKMAVCAAHPDFPEDITMVSYEELLRAAA

>d1ako\_\_ d.151.1.1 (-) DNA-repair enzyme exonuclease III {Escherichia coli}

MKFVSFNINGLRARPHQLEAIVEKHQPDVIGLQETKVHDDMFPLEEVAKLGYNVFYHGQKGHYGVALLTKETPIAVRRGFPGDDEEAQRRIIMAEIPSLLGNVTVINGYFPQGESRDHPIKFPAKAQFYQNLQNYLETELKRDNPVLIMGDMNISPTDLDIGIGEENRKRWLRTGKCSFLPEEREWMDRLMSWGLVDTFRHANPQTADRFSWFDYRSKGFDDNRGLRIDLLLASQPLAECCVETGIDYEIRSMEKPSDHAPVWATFRR

>d1hd7a\_ d.151.1.1 (A:) DNA repair endonuclease Hap1 {Human (Homo sapiens)}

LYEDPPDQKTSPSGKPATLKICSWNVDGLRAWIKKKGLDWVKEEAPDILCLQETKCSENKLPAELQELPGLSHQYWSAPSDKEGYSGVGLLSRQCPLKVSYGIGDEEHDQEGRVIVAEFDSFVLVTAYVPNAGRGLVRLEYRQRWDEAFRKFLKGLASRKPLVLCGDLNVAHEEIDLRNPKGNKKNAGFTPQERQGFGELLQAVPLADSFRHLYPNTPYAYTFWTYMMNARSKNVGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPITLYLAL

>d2dnja\_ d.151.1.1 (A:) Deoxyribonuclease I {Cow (Bos taurus)}

LKIAAFNIRTFGETKMSNATLASYIVRIVRRYDIVLIQEVRDSHLVAVGKLLDYLNQDDPNTYHYVVSEPLGRNSYKERYLFLFRPNKVSVLDTYQYDDGCESCGNDSFSREPAVVKFSSHSTKVKEFAIVALHSAPSDAVAEINSLYDVYLDVQQKWHLNDVMLMGDFNADCSYVTSSQWSSIRLRTSSTFQWLIPDSADTTATSTNCAYDRIVVAGSLLQSSVVPGSAAPFDFQAAYGLSNEMALAISDHYPVEVTLT

>d1i9za\_ d.151.1.2 (A:) Synaptojanin, IPP5C domain {Yeast (Schizosaccharomyces pombe)}

YDPIHEYVNHELRKRENEFSEHKNVKIFVASYNLNGCSATTKLENWLFPENTPLADIYVVGFQEIVQLTPQQVISADPAKRREWESCVKRLLNGKCTSGPGYVQLRSGQLVGTALMIFCKESCLPSIKNVEGTVKKTGLGGVSGNKGAVAIRFDYEDTGLCFITSHLAAGYTNYDERDHDYRTIASGLRFRRGRSIFNHDYVVWFGDFNYRISLTYEEVVPCIAQGKLSYLFEYDQLNKQMLTGKVFPFFSELPITFPPTYKFDIGTDIYDTSDKHRVPAWTDRILYRGELVPHSYQSVPLYYSDHRPIYATYEANIVKVDREKKKILFEELYNQRKQEVRDASQ

>d1aora2 d.152.1.1 (A:1-210) Aldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

MYGNWGRFIRVNLSTGDIKVEEYDEELAKKWLGSRGLAIYLLLKEMDPTVDPLSPENKLIIAAGPLTGTSAPTGGRYNVVTKSPLTGFITMANSGGYFGAELKFAGYDAIVVEGKAEKPVYIYIKDEHIEIRDASHIWGKKVSETEATIRKEVGSEKVKIASIGPAGENLVKFAAIMNDGHRAAGRGGVGAVMGSKNLKAIAVEGSKTVP

>d1b25a2 d.152.1.1 (A:1-210) Formaldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

MYGWWGRILRVNLTTGEVKVQEYPEEVAKKFIGGRGLAAWILWNEARGVEPLSPENKLIFAAGPFNGLPTPSGGKLVVAAKSPLTGGYGDGNLGTMASVHLRRAGYDALVVEGKAKKPVYIYIEDDNVSILSAEGLWGKTTFETERELKEIHGKNVGVLTIGPAGENLVKYAVVISQEGRAAGRPGMGAVMGSKKLKAVVIRGTKEIPVA

>d1gdoa\_ d.153.1.1 (A:) Glucosamine 6-phosphate synthase, N-terminal domain {Escherichia coli}

CGIVGAIAQRDVAEILLEGLRRLEYRGYDSAGLAVVDAEGHMTRLRRLGKVQMLAQAAEEHPLHGGTGIAHTRWATHGEPSEVNAHPHVSEHIVVVHNGIIENHEPLREELKARGYTFVSETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVIMDSRHPDTLLAARSGSPLVIGLGMGENFIASDQLALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRQDIESNL

>d1gph12 d.153.1.1 (1:1-234) Glutamine PRPP amidotransferase, N-terminal domain {Bacillus subtilis}

CGVFGIWGHEEAPQITYYGLHSLQHRGQEGAGIVATDGEKLTAHKGQGLITEVFQNGELSKVKGKGAIGHVRYATAGGGGYENVQPLLFRSQNNGSLALAHNGNLVNATQLKQQLENQGSIFQTSSDTEVLAHLIKRSGHFTLKDQIKNSLSMLKGAYAFLIMTETEMIVALDPNGLRPLSIGMMGDAYVVASETCAFDVVGATYLREVEPGEMLIINDEGMKSERFSMNINRS

>d1ecfa2 d.153.1.1 (A:1-249) Glutamine PRPP amidotransferase, N-terminal domain {Escherichia coli}

CGIVGIAGVMPVNQSIYDALTVLQHRGQDAAGIITIDANNCFRLRKANGLVSDVFEARHMQRLQGNMGIGHVRYPTAGSSSASEAQPFYVNSPYGITLAHNGNLTNAHELRKKLFEEKRRHINTTSDSEILLNIFASELDNFRHYPLEADNIFAAIAATNRLIRGAYACVAMIIGHGMVAFRDPNGIRPLVLGKRDIDENRTEYMVASESVALDTLGFDFLRDVAPGEAIYITEEGQLFTRQCADNPVS

>d1ct9a2 d.153.1.1 (A:1-192) Asparagine synthetase B, N-terminal domain {Escherichia coli}

ASIFGVFDIKTDAVELRKKALELSRLMRHRGPDWSGIYASDNAILAHERLSIVDVNAGAQPLYNQQKTHVLAVNGEIYNHQALRAEYGDRYQFQTGSDCEVILALYQEKGPEFLDDLQGMFAFALYDSEKDAYLIGRDHLGIIPLYMGYDEHGQLYVASEMKALVPVCRTIKEFPAGSYLWSQDGEIRSYYH

>d1jgta2 d.153.1.1 (A:4-209) beta-Lactam synthetase {Streptomyces clavuligerus}

PVLPAAFGFLASARTGGGRAPGPVFATRGSHTDIDTPQGERSLAATLVHAPSVAPDRAVARSLTGAPTTAVLAGEIYNRDELLSVLPAGPAPEGDAELVLRLLERYDLHAFRLVNGRFATVVRTGDRVLLATDHAGSVPLYTCVAPGEVRASTEAKALAAHRDPKGFPLADARRVAGLTGVYQVPAGAVMDIDLGSGTAVTHRTWT

>d1ea0a3 d.153.1.1 (A:1-422) Alpha subunit of glutamate synthase, N-terminal domain {Azospirillum brasilense}

CGVGFIAAIDGKPRRSVVEKGIEALKAVWHRGAVDADGKTGDGAGIHVAVPQKFFKDHVKVIGHRAPDNKLAVGQVFLPRISLDAQEACRCIVETEILAFGYYIYGWRQVPINVDIIGEKANATRPEIEQIIVGNNKGVSDEQFELDLYIIRRRIEKAVKGEQINDFYICSLSARSIIYKGMFLAEQLTTFYPDLLDERFESDFAIYHQRYSTNTFPTWPLAQPFRMLAHNGEINTVKGNVNWMKAHETRMEHPAFGTHMQDLKPVIGVGLSDSGSLDTVFEVMVRAGRTAPMVKMMLVPQALTSSQTTPDNHKALIQYCNSVMEPWDGPAALAMTDGRWVVGGMDRNGLRPMRYTITTDGLIIGGSETGMVKIDETQVIEKGRLGPGEMIAVDLQSGKLYRDRELKDHLATLKPWDKWVQN

>g1gk9.1 d.153.1.2 (A:,B:) Penicillin acylase {Escherichia coli}

QSSSEIKIVRDEYGMPHIYANDTWHLFYGYGYVVAQDRLFQMEMARRSTQGTVAEVLGKDFVKFDKDIRRNYWPDAIRAQIAALSPEDMSILQGYADGMNAWIDKVNTNPETLLPKQFNTFGFTPKRWEPFDVAMIFVGTMANRFSDSTSEIDNLALLTALKDKYGVSQGMAVFNQLKWLVNPSAPTTIAVQESNYPLKFNQQNSQTAXSNMWVIGKSKAQDAKAIMVNGPQFGWYAPAYTYGIGLHGAGYDVTGNTPFAYPGLVFGHNGVISWGSTAGFGDDVDIFAERLSAEKPGYYLHNGKWVKMLSREETITVKNGQAETFTVWRTVHGNILQTDQTTQTAYAKSRAWDGKEVASLLAWTHQMKAKNWQEWTQQAAKQALTINWYYADVNGNIGYVHTGAYPDRQSGHDPRLPVPGTGKWDWKGLLPFEMNPKVYNPQSGYIANWNNSPQKDYPASDLFAFLWGGADRVTEIDRLLEQKPRLTADQAWDVIRQTSRQDLNLRLFLPTLQAATSGLTQSDPRRQLVETLTRWDGINLLNDDGKTWQQPGSAILNVWLTSMLKRTVVAAVPMPFDKWYSASGYETTQDGPTGSLNISVGAKILYEAVQGDKSPIPQAVDLFAGKPQQEVVLAALEDTWETLSKRYGNNVSNWKTPAMALTFRANNFFGVPQAAAEETRHQAEYQNRGTENDMIVFSPTTSDRPVLAWDVVAPGQSGFIAPDGTVDKHYEDQLKMYENFGRKSLWLTKQDVEAHKESQEVLHVQR

>g1cp9.1 d.153.1.2 (A:,B:) Penicillin acylase {Providencia rettgeri}

ESTQIKIERDNYGVPHIYANDTYSLFYGYGYAVAQDRLFQMEMAKRSTQGTVSEVFGKDYISFDKEIRNNYWPDSIHKQINQLPSQEQDILRGYADGMNAWIKQINTKPDDLMPKQFIDYDFLPSQWTSFDVAMIMVGTLANRFSDMNSEIDNLALLTALKDKYGEQLGVEFFNQINWLNNPNAPTTISSEEFTYSDXSNVWLVGKTKASGAKAILLNGPQFGWFNPAYTYGIGLHGAGFNIVGNTPFAYPAILFGHNGHVSWGSTAGFGDGVDIFAEQVSPEDPNSYLHQGQWKKMLSRQETLNVKGEQPITFEIYRTVHGNVVKRDKTTHTAYSKARAWDGKELTSLMAWVKQGQAQNWQQWLDQAQNQALTINWYYADKDGNIGYVHTGHYPDRQINHDPRLPVSGTGEWDWKGIQPFANNPKVYNPKSGYIANWNNSPAKNYPASDLFAFLWGSADRVKEIDNRIEAYDKLTADDMWAILQQTSRVDLNHRLFTPFLTQATQGLPSNDNSVKLVSMLQQWDGINQLSSDGKHYIHPGSAILDIWLKEMLKATLGQTVPAPFDKWYLASGYETTQEGPTGSLNISTGAKLLYESLLEDKSPISQSIDLFSGQPQNDVIRKTLNTTYQKMIEKYGDNPANWQTPATALTFRENNFFGIPQALPQENFHQNEYHNRGTENDLIVFTEEGVSAWDVVAPGQSGFISPQGKPSPHYQDQLSLYQQFGKKPLWLNSEDVAPYIESTETLIIER

>g1fm2.1 d.153.1.2 (A:,B:) Cephalosporin acylase {Brevundimonas diminuta}

QAPIAAYKPRSNEILWDGYGVPHIYGVDAPSAFYGYGWAQARSHGDNILRLYGEARGKGAEYWGPDYEQTTVWLLTNGVPERAQQWYAQQSPDFRANLDAFAAGINAYAQQNPDDISPEVRQVLPVSGADVVAHAHRLMNFLYVASPGRTLGXSNSWAVAPGKTANGNALLLQNPHLSWTTDYFTYYEAHLVTPDFEIYGATQIGLPVIRFAFNQRMGITNTVNGMVGATNYRLTLQDGGYLYDGQVRPFERRQASYRLRQADGSTVDKPLEIRSSVHGPVFERADGTAVAVRVAGLDRPGMLEQYFDMITAHSFDDYEAAMARMQVPTFNIVYADREGTINYSFNGVAPKRAEGDIAFWQGNVPGDSSRYLWTETHPLDDLPRVTNPPGGFVQNSNDPPWTPTWPVTYCPANHPSYLAPQTPHSLRAQQSVRLMSENDDLTLERFMALQFSHRAVMADRTLPDLIPAALIDPDPEVQAAARLLAAWDRDFTSDSRAALLFEEWARLFAGQNFAGQAAFATPWSLDKPVSTPYGVRDPKAAVDQLRTAIANTKRKYGAIDRPFGDASRMILNDVNVPGAAGYGNLGSFRVFTWSDPDENGIRTPVHGETWVAMIEFSTPVRAYGLMSYGNSRQPGTTHYSDQIERVSRADFRELLLRREQVEAAVQERTPFNF

>d2pvaa\_ d.153.1.3 (A:) Penicillin V acylase {Bacillus sphaericus}

CSSLSIRTTDDKSLFARTMDFTMEPDSKVIIVPRNYGIRLLEKENVVINNSYAFVGMGSTDITSPVLYDGVNEKTYADEPKKGTGLMGAMLYYATFATYADEPKKGTTGINPVYVISQVLGNCVTVDDVIEKLTSYTLLNEANIILGFAPPLHYTFTDASGESIVIEPDKTGITIHRKTIGVMTNSPGYEWHQTNLRAYIGVTPNPPQDIMMGDLDLTPFGQGAGGLGLPGDFTPSARFLRVAYWKKYTEKAKNETEGVTNLFHILSSVNIPKGVVLTNEGKTDYTIYTSAMCAQSKNYYFKLYDNSRISAVSLMAENLNSQDLITFEWDRKQDIKQLNQVN

>d1pma1\_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Archaeon Thermoplasma acidophilum}

TTTVGITLKDAVIMATERRVTMENFIMHKNGKKLFQIDTYTGMTIAGLVGDAQVLVRYMKAELELYRLQRRVNMPIEAVATLLSNMLNQVKYMPYMVQLLVGGIDTAPHVFSIDAAGGSVEDIYASTGSGSPFVYGVLESQYSEKMTVDEGVDLVIRAISAAKQRDSASGGMIDVAVITRKDGYVQLPTDQIESRIRKLGLIL

>d1ryp1\_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

QFNPYGDNGGTILGIAGEDFAVLAGDTRNITDYSINSRYEPKVFDCGDNIVMSANGFAADGDALVKRFKNSVKWYHFDHNDKKLSINSAARNIQHLLYGKRFFPYYVHTIIAGLDEDGKGAVYSFDPVGSYEREQCRAGGAAASLIMPFLDNQVNFKNQYEPGTNGKVKKPLKYLSVEEVIKLVRDSFTSATERHIQVGDGLEILIVTKDGVRKEFYELKRD

>d1ryp2\_ d.153.1.4 (2:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TQQPIVTGTSVISMKYDNGVIIAADNLGSYGSLLRFNGVERLIPVGDNTVVGISGDISDMQHIERLLKDLVTENAYDNPLADAEEALEPSYIFEYLATVMYQRRSKMNPLWNAIIVAGVQSNGDQFLRYVNLLGVTYSSPTLATGFGAHMANPLLRKVVDRESDIPKTTVQVAEEAIVNAMRVLYYRDARSSRNFSLAIIDKNTGLTFKKNLQVENMKWDFAKDIKGYGTQKI

>d1ryph\_ d.153.1.4 (H:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

LKKGEVSLGASIMAVTFKDGVILGADSRTTTGAYIANRVTDKLTRVHDKIWCCRSGSAADTQAIADIVQYHLELYTSQYGTPSTETAASVFKELCYENKDNLTAGIIVAGYDDKNKGEVYTIPLGGSVHKLPYAIAGSGSTFIYGYCDKNFRENMSKEETVDFIKHSLSQAIKWDGSSGGVIRMVVLTAAGVERLIFYPDEYEQL

>d1rypi\_ d.153.1.4 (I:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTIVGVKFNNGVVIAADTRSTQGPIVADKNCAKLHRISPKIWCAGAGTAADTEAVTQLIGSNIELHSLYTSREPRVVSALQMLKQHLFKYQGHIGAYLIVAGVDPTGSHLFSIHAHGSTDVGYYLSLGSGSLAAMAVLESHWKQDLTKEEAIKLASDAIQAGIWNDLGSGSNVDVCVMEIGKDAEYLRNYLTPNVREEKQKSYKFPRGTTAVLKESIVNICD

>d1rypj\_ d.153.1.4 (J:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

SDPSSINGGIVVAMTGKDCVAIACDLRLGSQSLGVSNKFEKIFHYGHVFLGITGLATDVTTLNEMFRYKTNLYKLKEERAIEPETFTQLVSSSLYERRFGPYFVGPVVAGINSKSGKPFIAGFDLIGCIDEAKDFIVSGTASDQLFGMCESLYEPNLEPEDLFETISQALLNAADRDALSGWGAVVYIIKKDEVVKRYLKMRQD

>d1rypk\_ d.153.1.4 (K:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MDIILGIRVQDSVILASSKAVTRGISVLKDSDDKTRQLSPHTLMSFAGEAGDTVQFAEYIQANIQLYSIREDYELSPQAVSSFVRQELAKSIRSRRPYQVNVLIGGYDKKKNKPELYQIDYLGTKVELPYGAHGYSGFYTFSLLDHHYRPDMTTEEGLDLLKLCVQELEKRMPMDFKGVIVKIVDKDGIRQVDDFQAQ

>d1rypl\_ d.153.1.4 (L:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTTLAFRFQGGIIVAVDSRATAGNWVASQTVKRVIEINPFLLGTMAGGAADCQFWETWLGSQCRLHELREKERISVAAASKILSNLVYQYKGAGLSMGTMICGYTRKEGPTIYYVDSDGTRLKGDIFCVGSGQTFAYGVLDSNYKWDLSVEDALYLGKRSILAAAHRDAYSGGSVNLYHVTEDGWIYHGNHDVGELFWKVKEEEGSFNNVIG

>d1pmaa\_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Archaeon Thermoplasma acidophilum}

TVFSPDGRLFQVEYAREAVKKGSTALGMKFANGVLLISDKKVRSRLIEQNSIEKIQLIDDYVAAVTSGLVADARVLVDFARISAQQEKVTYGSLVNIENLVKRVADQMQQYTQYGGVRPYGVSLIFAGIDQIGPRLFDCDPAGTINEYKATAIGSGKDAVVSFLEREYKENLPEKEAVTLGIKALKSSLEEGEELKAPEIASITVGNKYRIYDQEEVKKFL

>d1rypa\_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

AGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVPDKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFRYKYGYDMPCDVLAKRMANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDPAGYYVGYKATATGPKQQEITTNLENHFKKSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVGVATKDKFFTLSAENIEERLVAIAEQD

>d1rypb\_ d.153.1.4 (B:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MTDRYSFSLTTFSPSGKLGQIDYALTAVKQGVTSLGIKATNGVVIATEKKSSSPLAMSETLSKVSLLTPDIGAVYSGMGPDYRVLVDKSRKVAHTSYKRIYGEYPPTKLLVSEVAKIMQEATQSGGVRPFGVSLLIAGHDEFNGFSLYQVDPSGSYFPWKATAIGKGSVAAKTFLEKRWNDELELEDAIHIALLTLKESVEGEFNGDTIELAIIGDENPDLLGYTGIPTDKGPRFRKLTSQEINDRLEAL

>d1rypc\_ d.153.1.4 (C:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GSRRYDSRTTIFSPEGRLYQVEYALESISHAGTAIGIMASDGIVLAAERKVTSTLLEQDTSTEKLYKLNDKIAVAVAGLTADAEILINTARIHAQNYLKTYNEDIPVEILVRRLSDIKQGYTQHGGLRPFGVSFIYAGYDDRYGYQLYTSNPSGNYTGWKAISVGANTSAAQTLLQMDYKDDMKVDDAIELALKTLSKTTDSSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILVKTGIT

>d1rypd\_ d.153.1.4 (D:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GYDRALSIFSPDGHIFQVEYALEAVKRGTCAVGVKGKNCVVLGCERRSTLKLQDTRITPSKVSKIDSHVVLSFSGLNADSRILIEKARVEAQSHRLTLEDPVTVEYLTRYVAGVQQRYTQSGGVRPFGVSTLIAGFDPRDDEPKLYQTEPSGIYSSWSAQTIGRNSKTVREFLEKNYDRKEPPATVEECVKLTVRSLLEVVQTGAKNIEITVVKPDSDIVALSSEEINQYVTQIEQEKQEQ

>d1rype\_ d.153.1.4 (E:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

DRGVSTFSPEGRLFQVEYSLEAIKLGSTAIGIATKEGVVLGVEKRATSPLLESDSIEKIVEIDRHIGCAMSGLTADARSMIEHARTAAVTHNLYYDEDINVESLTQSVCDLALRFGEGASGEERLMSRPFGVALLIAGHDADDGYQLFHAEPSGTFYRYNAKAIGSGSEGAQAELLNEWHSSLTLKEAELLVLKILKQVMEEKLDENNAQLSCITKQDGFKIYDNEKTAELIKELKEKEAAE

>d1rypf\_ d.153.1.4 (F:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

FRNNYDGDTVTFSPTGRLFQVEYALEAIKQGSVTVGLRSNTHAVLVALKRNADELSSYQKKIIKCDEHMGLSLAGLAPDARVLSNYLRQQCNYSSLVFNRKLAVERAGHLLCDKAQKNTQSYGGRPYGVGLLIIGYDKSGAHLLEFQPSGNVTELYGTAIGARSQGAKTYLERTLDTFIKIDGNPDELIKAGVEAISQSLRDESLTVDNLSIAIVGKDTPFTIYDGEAVAKYI

>d1rypg\_ d.153.1.4 (G:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GTGYDLSNSVFSPDGRNFQVEYAVKAVENGTTSIGIKCNDGVVFAVEKLITSKLLVPQKNVKIQVVDRHIGCVYSGLIPDGRHLVNRGREEAASFKKLYKTPIPIPAFADRLGQYVQAHTLYNSVRPFGVSTIFGGVDKNGAHLYMLEPSGSYWGYKGAATGKGRQSAKAELEKLVDHHPEGLSAREAVKQAAKIIYLAHEDNKEKDFELEISWCSLSETNGLHKFVKGDLLQEAIDFAQKEIN

>d1ht1a\_ d.153.1.4 (A:) HslV (ClpQ) protease {Escherichia coli}

TTIVSVRRNGHVVIAGDGQATLGNTVMKGNVKKVRRLYNDKVIAGFAGGTADAFTLFELFERKLEMHQGHLVKAAVELAKDWRTDRMLRKLEALLAVADETASLIITGNGDVVQPENDLIAIGSGGPYAQAAARALLENTELSAREIAEKALDIAGDICIYTNHFHTIEELSYK

>d1jjwa\_ d.153.1.4 (A:) HslV (ClpQ) protease {Haemophilus influenzae}

TTIVSVRRNGQVVVGGDGQVSLGNTVMKGNARKVRRLYNGKVLAGFAGGTADAFTLFELFERKLEMHQGHLLKSAVELAKDWRTDRALRKLEAMLIVADEKESLIITGIGDVVQPEEDQILAIGSGGNYALSAARALVENTELSAHEIVEKSLRIAGDICVFTNTNFTIEELP

>g1apy.1 d.153.1.5 (A:,B:) Glycosylasparaginase (aspartylglucosaminidase, AGA) {Human (Homo sapiens)}

SPLPLVVNTWPFKNATEAAWRALASGGSALDAVESGCAMCEREQCDGSVGFGGSPDELGETTLDAMIMDGTTMDVGAVGDLRRIKNAIGVARKVLEHTTHTLLVGESATTFAQSMGFINEDLSTSASQALHSDWLARNCQPNYWRNVIPDPSKYCGPYKPPXTIGMVVIHKTGHIAAGTSTNGIKFKIHGRVGDSPIPGAGAYADDTAGAAAATGNGDILMRFLPSYQAVEYMRRGEDPTIACQKVISRIQKHFPEFFGAVICANVTGSYGAACNKLSTFTQFSFMVYNSEKNQPTEEKVDCI

>g2gac.1 d.153.1.5 (A:,B:) Glycosylasparaginase (aspartylglucosaminidase, AGA) {Flavobacterium meningosepticum}

NKPIVLSTWNFGLHANVEAWKVLSKGGKALDAVEKGVRLVEDDPTERSVGYGGRPDRDGRVTLDACIMDENYNIGSVACMEHIKNPISVARAVMEKTPHVMLVGDGALEFALSQGFKKENLLTAESEKEWKEWLKTXCIGMIALDAQGNLSGACTTSGMAYKMHGRVGDSPIIGAGLFVDNEIGAATATGHGEEVIRTVGTHLVVELMNQGRTPQQACKEAVERIVKIVNRRGKNLKDIQVGFIALNKKGEYGAYCIQDGFNFAVHDQKGNRLETP

>d1b65a\_ d.154.1.1 (A:) L-aminopeptidase D-Ala-esterase/amidase {Ochrobactrum anthropi}

KPRARDLGLPFTGVTGPYNAITDVDGVGVGFQTIIENEPRPGRKRPARSGVTAILPHMQSETPVPVYAGVHRFNGNGEMTGTHWIEDGGYFLGPVVITNTHGIGMAHHATVRWMVDRYASTYQTDDFLWIMPVVAETYDGALNDINGFPVTEADVRKALDNVASGPVQEGNCGGGTGMITYGFKGGTGTASRVVEFGGRSFTIGALVQANHGQRDWLTIAGVPVGQHMRDGTPQSQLQERGSIIVVLATDLPLMPHQLKRLARRASIGIGRNGTPGGNNSGDIFIAFSTANQRPMQHRSAPFLDVEMVNDEPLDTVYLAAVDSVEEAVVNAMIAAEDMGGTPFDRLLVQAIDHERLRAVLRQYGRLA

>g1pya.1 d.155.1.1 (A:,B:) Histidine decarboxylase {Lactobacillus sp., strain 30a}

SELDAKLNKLGVDRIAISPYKQWTRGYMEPGNIGNGYVTGLKVDAGVRDKSDDDVLDGIVSYDRAETKNAYIGQINMTTASXFTGVQGRVIGYDILRSPEVDKAKPLFTETQWDGSELPIYDAKPLQDALVEYFGTEQDRRHYPAPGSFIVCANKGVTAERPKNDADMKPGQGYGVWSAIAISFAKDPTKDSSMFVEDAGVWETPNEDELLEYLEGRRKAMAKSIAECGQDAHASFESSWIGFAYTMMEPGQIGNAITVAPYVSLPIDSIPGGSILTPDKDMEIMENLTMPEWLEKMGYKSLSANNALKY

>d1jl0a\_ d.156.1.1 (A:) S-adenosylmethionine decarboxylase {Human (Homo sapiens)}

HFFEGTEKLLEVWFSRQQPDANQGSGDLRTIPRSEWDILLKDVQCSIISVTKTDKQEAYVLSESSMFVSKRRFILKTCGTTLLLKALVPLLKLARDYSGFDSIQSFFYSRKNFMKPSHQGYPHRNFQEEIEFLNAIFPNGAGYCMGRMNSDCWYLYTLDFPESRVISQPDQTLEILMSELDPAVMDQFYMKDGVTAKDVTRESGIRDLIPGSVIDATMFNPCGYSMNGMKSDGTYWTIAITPEPEFSYVSFETNLSQTSYDDLIRKVVEVFKPGKFVTTLFVNQSSKCRTVLASPQKIEGFKRLDCQSAMFNDYNFVFTSFAKKQ

>d2bc2a\_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacillus cereus}

TVIKNETGTISISQLNKNVWVHTELGSFNGEAVPSNGLVLNTSKGLVLVDSSWDDKLTKELIEMVEKKFQKRVTDVIITHAHADRIGGIKTLKERGIKAHSTALTAELAKKNGYEEPLGDLQTVTNLKFGNMKVETFYPGKGHTEDNIVVWLPQYNILVGGALVKSTSAKDLGNVADAYVNEWSTSIENVLKRYRNINAVVPGHGEVGDKGLLLHTLDLLK

>d1a7ta\_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacteroides fragilis}

SVKISDDISITQLSDKVYTYVSLAEIEGWGMVPSNGMIVINNHQAALLDTPINDAQTEMLVNWVTDSLHAKVTTFIPNHWHGDCIGGLGYLQRKGVQSYANQMTIDLAKEKGLPVPEHGFTDSLTVSLDGMPLQCYYLGGGHATDNIVVWLPTENILFGGCMLKDNQTTSIGNISDADVTAWPKTLDKVKAKFPSARYVVPGHGNYGGTELIEHTKQIVNQYIESTS

>d1smla\_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Xanthomonas maltophilia}

EVPLPQLRAYTVDASWLQPMAPLQIADHTWQIGTEDLTALLVQTPDGAVLLDGGMPQMASHLLDNMKARGVTPRDLRLILLSHAHADHAGPVAELKRRTGAKVAANAESAVLLARGGSDDLHFGDGITYPPANADRIVMDGEVITVGGIVFTAHFMAGHTPGSTAWTWTDTRNGKPVRIAYADSLSAPGYQLQGNPRYPHLIEDYRRSFATVRALPCDVLLTPHPGASNWDYAAGARAGAKALTCKAYADAAEQKFDGQLAKETAG

>d1jjea\_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Pseudomonas aeruginosa, IMP-1}

SLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYASELTNELLKKDGKVQATNSFSGVNYWLVKNKIEVFYPGPGHTPDNVVVWLPERKILFGGCFIKPYGLGNLGDANIEAWPKSAKLLKSKYGKAKLVVPSHSEVGDASLLKLTLEQAVKGLNESKK

>d1qh5a\_ d.157.1.2 (A:) Glyoxalase II (hydroxyacylglutathione hydrolase) {Human (Homo sapiens)}

MKVEVLPALTDNYMYLVIDDETKEAAIVDPVQPQKVVDAARKHGVKLTTVLTTHHHWDHAGGNEKLVKLESGLKVYGGDDRIGALTHKITHLSTLQVGSLNVKCLATPCHTSGHICYFVSKPGGSEPPAVFTGDTLFVAGCGKFYEGTADEMCKALLEVLGRLPPDTRVYCGHEYTINNLKFARHVEPGNAAIREKLAWAKEKYSIGEPTVPSTLAEEFTYNPFMRVREKTVQQHAGETDPVTTMRAVRREKDQFKMPRD

>d1e5da2 d.157.1.3 (A:2-250) Rubredoxin oxygen:oxidoreductase (ROO), N-terminal domain {Desulfovibrio gigas}

QATKIIDGFHLVGAIDWNSRDFHGYTLSPMGTTYNAYLVEDEKTTLFDTVKAEYKGELLCGIASVIDPKKIDYLVIQHLELDHAGALPALIEACQPEKIFTSSLGQKAMESHFHYKDWPVQVVKHGETLSLGKRTVTFYETRMLHWPDSMVSWFADEKVLISNDIFGQNIAASERFSDQIPVHTLERAMREYYANIVNPYAPQTLKAIETLVGAGVAPEFICPDHGVIFRGADQCTFAVQKYVEYAEQK

>d1a6q\_\_ d.158.1.1 (-) Protein serine/threonine phosphatase 2C {Human (Homo sapiens)}

GAFLDKPKMEKHNAQGQGNGLRYGLSSMQGWRVEMEDAHTAVIGLPSGLESWSFFAVYDGHAGSQVAKYCCEHLLDHITNNQDFKGSAGAPSVENVKNGIRTGFLEIDEHMRVMSEKKHGADRSGSTAVGVLISPQHTYFINCGDSRGLLCRNRKVHFFTQDHKPSNPLEKERIQNAGGSVMIQRVNGSLAVSRALGDFDYKCVHGKGPTEQLVSPEPEVHDIERSEEDDQFIILACDGIWDVMGNEELCDFVRSRLEVTDDLEKVCNEVVDTCLYKGSRDNMSVILICFPNAPKVSPEAVKKEAELDKYLECRVEEIIKKQGEGVPDLVHVMRTLASENIPSLPPGGELASKRNVIEAVYNRLNPY

>d4kbpa2 d.159.1.1 (A:121-432) Plant purple acid phosphatase, catalytic domain {Kidney bean (Phaseolus vulgaris)}

QTGLDVPYTFGLIGDLGQSFDSNTTLSHYELSPKKGQTVLFVGDLSYADRYPNHDNVRWDTWGRFTERSVAYQPWIWTAGNHEIEFAPEINETEPFKPFSYRYHVPYEASQSTSPFWYSIKRASAHIIVLSSYSAYGRGTPQYTWLKKELRKVKRSETPWLIVLMHSPLYNSYNHHFMEGEAMRTKFEAWFVKYKVDVVFAGHVHAYERSERVSNIAYKITDGLCTPVKDQSAPVYITIGDAGNYGVIDSNMIQPQPEYSAFREASFGHGMFDIKNRTHAHFSWNRNQDGVAVEADSVWFFNRHWYPVDDST

>d1qhwa\_ d.159.1.1 (A:) Mammalian purple acid phosphatase {Rat (Rattus norvegicus)}

STLRFVAVGDWGGVPNAPFHTAREMANAKEIARTVQIMGADFIMSLGDNFYFTGVHDANDKRFQETFEDVFSDRALRNIPWYVLAGNHDHLGNVSAQIAYSKISKRWNFPSPYYRLRFKVPRSNITVAIFMLDTVMLCGNSDDFVSQQPEMPRDLGVARTQLSWLKKQLAAAKEDYVLVAGHYPIWSIAEHGPTRCLVKNLRPLLAAYGVTAYLCGHDHNLQYLQDENGVGYVLSGAGNFMDPSVRHQRKVPNGYLRFHYGSEDSLGGFTYVEIGSKEMSITYVEASGKSLFKTSLPRRP

>d1utea\_ d.159.1.1 (A:) Mammalian purple acid phosphatase {Pig (Sus scrofa)}

PTPILRFVAVGDWGGVPNAPFHTAREMANAKAIATTVKTLGADFILSLGDNFYFTGVHDAKDKRFQETFEDVFSDPSLRNVPWHVLAGNHDHLGNVSAQIAYSKISKRWNFPSPYYRLRFKIPRSNVSVAIFMLDTVTLCGNSDDFVSQQPERPRNLALARTQLAWIKKQLAAAKEDYVLVAGHYPVWSIAEHGPTHCLVKQLLPLLTTHKVTAYLCGHDHNLQYLQDENGLGFVLSGAGNFMDPSKKHLRKVPNGYLRFHFGAENSLGGFAYVEITPKEMSVTYIEASGKSLFKTKLPRRA

>d1ii7a\_ d.159.1.4 (A:) Mre11 {Archaeon Pyrococcus furiosus}

MKFAHLADIHLGYEQFHKPQREEEFAEAFKNALEIAVQENVDFILIAGDLFHSSRPSPGTLKKAIALLQIPKEHSIPVFAIEGNHDRTQRGPSVLNLLEDFGLVYVIGMRKEKVENEYLTSERLGNGEYLVKGVYKDLEIHGMKYMSSAWFEANKEILKRLFRPTDNAILMLHQGVREVSEARGEDYFEIGLGDLPEGYLYYALGHIHKRYETSYSGSPVVYPGSLERWDFGDYEVRYEWDGIKFKERYGVNKGFYIVEDFKPRFVEIKVRPFIDVKIKGSEEEIRKAIKRLIPLIPKNAYVRLNIGWRKPFDLTEIKELLNVEYLKIDTWRI

>d1ush\_2 d.159.1.2 (26-362) 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain {Escherichia coli}

YEQDKTYKITVLHTNDHHGHFWRNEYGEYGLAAQKTLVDGIRKEVAAEGGSVLLLSGGDINTGVPESDLQDAEPDFRGMNLVGYDAMAIGNHEFDNPLTVLRQQEKWAKFPLLSANIYQKSTGERLFKPWALFKRQDLKIAVIGLTTDDTAKIGNPEYFTDIEFRKPADEAKLVIQELQQTEKPDIIIAATHMGHYDNGEHGSNAPGDVEMARALPAGSLAMIVGGHSQDPVCMAAENKKQVDYVPGTPCKPDQQNGIWIVQAHEWGKYVGRADFEFRNGEMKMVNYQLIPVNLKKKVTWEDGKSERVLYTPEIAENQQMISLLSPFQNKGKAQLEV

>d1jk7a\_ d.159.1.3 (A:) Protein phosphatase-1 (PP-1) {Human (Homo sapiens)}

KLNIDSIIQRLLEVRGSKPGKNVQLQENEIRGLCLKSREIFLSQPILLELEAPLKICGDIHGQYYDLLRLFEYGGFPPESNYLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNHECASINRIYGFYDECKRRYNIKLWKTFTDCFNCLPIAAIVDEKIFCCHGGLSPDLQSMEQIRRIMRPTDVPDQGLLCDLLWSDPDKDVLGWGENDRGVSFTFGAEVVAKFLHKHDLDLICRAHQVVEDGYEFFAKRQLVTLFSAPNYCGEFDNAGAMMSVDETLMCSFQILKPA

>d1tcoa\_ d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Cow (Bos taurus)}

VPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEETVALRIITEGASILRQEKNLLDIDAPVTVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLLRGNHECRHLTEYFTFKQECKIKYSERVYDACMDAFDCLPLAALMNQQFLCVHGGLSPEINTLDDIRKLDRFKEPPAYGPMCDILWSDPLEDFGNEKTQEHFTHNTVRGCSYFYSYPAVCEFLQHNNLLSILRAHEAQDAGYRMYRKSQTTGFPSLITIFSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPHPYWLPNFMDVFTWSLPFVGEKVTEMLVNVLNIC

>d1auia\_ d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Human (Homo sapiens)}

TDRVVKAVPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALRIITEGASILRQEKNLLDIDAPVTVCGDIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLLRGNHECRHLTEYFTFKQECKIKYSERVYDACMDAFDCLPLAALMNQQFLCVHGGLSPEINTLDDIRKLDRFKEPPAYGPMCDILWSDPLEDFGNEKTQEHFTHNTVRGCSYFYSYPAVCEFLQHNNLLSILRAHEAQDAGYRMYRKSQTTGFPSLITIFSAPNYLDVYNNKAAVLKYENNVMNIRQFNCSPHPYWLPNFMDVFTWSLPFVGEKVTEMLVNVLNICSDDELGSEEDGFDGATAAARKEVIRNKIRAIGKMARVFSVLREESESVLTLKGLTPTGMLPSGVLSGGKQTLQSATVEAIEADEAIKGFSPQHKITSFEEAKGLDRINERMPPR

>d1g5ba\_ d.159.1.3 (A:) lambda ser/thr protein phosphatase {Bacteriophage lambda}

MRYYEKIDGSKYRNIWVVGDLHGCYTNLMNKLDTIGFDNKKDLLISVGDLVDRGAENVECLELITFPWFRAVRGNHEQMMIDGLSERGNVNHWLLNGGGWFFNLDYDKEILAKALAHKADELPLIIELVSKDKKYVICHADYPFDEYEFGKPVDHQQVIWNRERISNSQNGIVKEIKGADTFIFGHTPAVKPLKFANQMYIDTGAVFCGNLTLIQVQGA

>d1emsa2 d.160.1.1 (A:10-280) NIT-FHIT fusion protein, N-terminal domain {Nematode (Caenorhabditis elegans)}

MATGRHFIAVCQMTSDNDLEKNFQAAKNMIERAGEKKCEMVFLPECFDFIGLNKNEQIDLAMATDCEYMEKYRELARKHNIWLSLGGLHHKDPSDAAHPWNTHLIIDSDGVTRAEYNKLHLFDLEIPGKVRLMESEFSKAGTEMIPPVDTPIGRLGLSICYDVRFPELSLWNRKRGAQLLSFPSAFTLNTGLAHWETLLRARAIENQCYVVAAAQTGAHNPKRQSYGHSMVVDPWGAVVAQCSERVDMCFAEIDLSYVDTLREMQPVFSHR

>d1f89a\_ d.160.1.1 (A:) hypothetical protein yl85 {Baker's yeast (Saccharomyces cerevisiae)}

SASKILSQKIKVALVQLSGSSPDKMANLQRAATFIERAMKEQPDTKLVVLPECFNSPYSTDQFRKYSEVINPKEPSTSVQFLSNLANKFKIILVGGTIPELDPKTDKIYNTSIIFNEDGKLIDKHRKVHLFDVDIPNGISFHESETLSPGEKSTTIDTKYGKFGVGICYDMRFPELAMLSARKGAFAMIYPSAFNTVTGPLHWHLLARSRAVDNQVYVMLCSPARNLQSSYHAYGHSIVVDPRGKIVAEAGEGEEIIYAELDPEVIESFRQAVPLTKQRRF

>d1erza\_ d.160.1.2 (A:) N-carbamoyl-D-aminoacid amidohydrolase {Agrobacterium sp.}

TRQMILAVGQQGPIARAETREQVVVRLLDMLTKAASRGANFIVFPELALTTFFPRWHFTDEAELDSFYETEMPGPVVRPLFEKAAELGIGFNLGYAELVVEGGVKRRFNTSILVDKSGKIVGKYRKIHLPGHKEYEAYRPFQHLEKRYFEPGDLGFPVYDVDAAKMGMFICNDRRWPEAWRVMGLRGAEIICGGYNTPTHNPPVPQHDHLTSFHHLLSMQAGSYQNGAWSAAAGKVGMEENCMLLGHSCIVAPTGEIVALTTTLEDEVITAAVDLDRCRELREHIFNFKQHRQPQHYGLIAEL

>d1hq0a\_ d.194.1.1 (A:) Type 1 cytotoxic necrotizing factor, catalytic domain {Escherichia coli}

SIESTSKSNFQKLSRGNIDVLKGRGSISSTRQRAIYPYFEAANADEQQPLFFYIKKDRFDNHGYDQYFYDNTVGPNGIPTLNTYTGEIPSDSSSLGSTYWKKYNLTNETSIIRVSNSARGANGIKIALEEVQEGKPVIITSGNLSGCTTIVARKEGYIYKVHTGTTKSLAGFTSTTGVKKAVEVLELLTKEPIPRVEGIMSNDFLVDYLSENFEDSLITYSSSEKKPDSQITIIRDNVSVFPYFLDNIPEHGFGTSATVLVRVDGNVVVRSLSESYSLNADASEISVLKVFSKKF

>d1qdla\_ d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase subunit, TrpE {Archaeon Sulfolobus solfataricus}

AMEVHPISEFASPFEVFKCIERDFKVAGLLESIGGPQYKARYSVIAWSTNGYLKIHDDPVNILNGYLKDLKLADIPGLFKGGMIGYISYDAVRFWEKIRDLKPAAEDWPYAEFFTPDNIIIYDHNEGKVYVNADLSSVGGCGDIGEFKVSFYDESLNKNSYERIVSESLEYIRSGYIFQVVLSRFYRYIFSGDPLRIYYNLRRINPSPYMFYLKFDEKYLIGSSPELLFRVQDNIVETYPIAGTRPRGADQEEDLKLELELMNSEKDKAEHLMLVDLARNDLGKVCVPGTVKVPELMYVEKYSHVQHIVSKVIGTLKKKYNALNVLSATFPAGTVSGAPKPMAMNIIETLEEYKRGPYAGAVGFISADGNAEFAIAIRTAFLNKELLRIHAGAGIVYDSNPESEYFETEHKLKALKTAIGVR

>d1i1qa\_ d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase subunit, TrpE {Salmonella typhimurium}

KPTLELLTCDAAYRENPTALFHQVCGDRPATLLLESADIDSKDDLKSLLLVDSALRITALGDTVTIQALSDNGASLLPLLDTALPAGVENDVLPAGRVLRFPPVSPLLDENARLCSLSVFDAFRLLQGVVNIPTQEREAMFFGGLFAYDLVAGFEALPHLEAGNNCPDYCFYLAETLMVIDHQKKSTRIQASLFTASDREKQRLNARLAYLSQQLTQPAPPLPVTPVPDMRCECNQSDDAFGAVVRQLQKAIRAGEIFQVVPSRRFSLPCPSPLAAYYVLKKSNPSPYMFFMQDNDFTLFGASPESSLKYDAASRQIEIYPIAGTRPRGRRADGTLDRDLDSRIELDMRTDHKELSEHLMLVDLARNDLARICTPGSRYVADLTKVDRYSYVMHLVSRVVGELRHDLDALHAYRACMNMGTLSGAPKVRAMQLIADAEGQRRGSYGGAVGYFTAHGDLDTCIVIRSALVENGIATVQAGAGIVLDSVPQSEADETRNKARAVLRAIATAHHA

>d1i7qa\_ d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase subunit, TrpE {Serratia marcescens}

TKPQLTLLKVQASYRGDPTTLFHQLCGARPATLLLESAEINDKQNLQSLLVIDSALRITALGHTVSVQALTANGPALLPLLDEALPPEVRNQARPNGRELTFPAIDAVQDEDARLRSLSVFDALRTILTLVDSPADEREAVMLGGLFAYDLVAGFENLPALRQDQRCPDFCFYLAETLLVLDHQRGSARLQASVFSEQASEAQRLQHRLEQLQAELQQPPQPIPHQKLENMQLSCNQSDEEYGAVVSELQEAIRQGEIFQVVPSRRFSLPCPAPLGPYQTLKDNNPSPYMFFMQDDDFTLFGASPESALKYDAGNRQIEIYPIAGTRPRGRRADGSLDLDLDSRIELEMRTDHKELAEHLMLVDLARNDLARICQAGSRYVADLTKVDRYSFVMHLVSRVVGTLRADLDVLHAYQACMNMGTLSGAPKVRAMQLIAALRSTRRGSYGGRVGYFTAVRNLDTCIVIRSAYVEDGHRTVQAGAGVVQDSIPEREADETRNKARAVLRAIATAHHAKEVF

>d1k0ga\_ d.161.1.1 (A:) P-aminobenzoate synthase component I {Escherichia coli}

MKTLSPAVITLLWRQDAAEFYFSRLSHLPWAMLLHSGYADHPYSRFDIVVAEPICTLTTFGKETVVSESEKRTTTTDDPLQVLQQVLDRADIRPTHNEDLPFQGGALGLFGYDLGRRFESLPEIAEQDIVLPDMAVGIYDWALIVDHQRHTVSLLSHNDVNARRAWLESQQFSPQEDFTLTSDWQSNMTREQYGEKFRQVQEYLHSGDCYQVNLAQRFHATYSGDEWQAFLQLNQANRAPFSAFLRLEQGAILSLSPERFILCDNSEIQTRPIKGTLPRLPDPQEDSKQAVKLANSAKDRAENLMIVDLMRNDIGRVAVAGSVKVPELFVVEPFPAVHHLVSTITAQLPEQLHASDLLRAAFPGGSITGAPKVRAMEIIDELEPQRRNAWCGSIGYLSFCGNMDTSITIRTLTAINGQIFCSAGGGIVADSQEEAEYQETFDKVNRILKQLEK

>d1mlda2 d.162.1.1 (A:145-313) Malate dehydrogenase {Pig (Sus scrofa)}

VTTLDIVRANAFVAELKGLDPARVSVPVIGGHAGKTIIPLISQCTPKVDFPQDQLSTLTGRIQEAGTEVVKAKAGAGSATLSMAYAGARFVFSLVDAMNGKEGVVECSFVKSQETDCPYFSTPLLLGKKGIEKNLGIGKISPFEEKMIAEAIPELKASIKKGEEFVKNM

>d5mdha2 d.162.1.1 (A:155-333) Malate dehydrogenase {Pig (Sus scrofa)}

TRLDHNRAKAQIALKLGVTSDDVKNVIIWGNHSSTQYPDVNHAKVKLQAKEVGVYEAVKDDSWLKGEFITTVQQRGAAVIKARKLSSAMSAAKAICDHVRDIWFGTPEGEFVSMGIISDGNSYGVPDDLLYSFPVTIKDKTWKIVEGLPINDFSREKMDLTAKELAEEKETAFEFLSSA

>d7mdha2 d.162.1.1 (A:198-385) Malate dehydrogenase {Sorghum (Sorghum vulgare), chloroplast}

TRLDENRAKCQLALKAGVFYDKVSNVTIWGNHSTTQVPDFLNAKIDGRPVKEVIKRTKWLEEEFTITVQKRGGALIQKWGRSSAASTAVSIADAIKSLVTPTPEGDWFSTGVYTTGNPYGIAEDIVFSMPCRSKGDGDYELATDVSNDDFLWERIKKSEAELLAEKKCVAHLTGEGNAYCDVPEDTML

>d1civa2 d.162.1.1 (A:194-385) Malate dehydrogenase {Flaveria bidentis, chloroplast}

TRLDENRAKCQLALKAGVFYDKVSNVTIWGNHSTTQVPDFLNAKIHGIPVTEVIRDRKWLEDEFTNMVQTRGGVLIKKWGRSSAASTAVSIVDAIRSLVTPTPEGDWFSTGVYTNGNPYGIAEDIVFSMPCRSKGDGDYEFVKDVIFDDYLSKKIKKSEDELLAEKKCVAHLTGEGIAVCDLPEDTMLPGEM

>d2cmd\_2 d.162.1.1 (146-312) Malate dehydrogenase {Escherichia coli}

VTTLDIIRSNTFVAELKGKQPGEVEVPVIGGHSGVTILPLLSQVPGVSFTEQEVADLTKRIQNAGTEVVEAKAGGGSATLSMGQAAARFGLSLVRALQGEQGVVECAYVEGDGQYARFFSQPLLLGKNGVEERKSIGTLSAFEQNALEGMLDTLKKDIALGQEFVNK

>d1bdma2 d.162.1.1 (A:155-332) Malate dehydrogenase {Thermus flavus}

TRLDHNRAKAQLAKKTGTGVDRIRRMTVWGNHSSIMFPDLFHAEVDGRPALELVDMEWYEKVFIPTVAQRGAAIIQARGASSAASAANAAIEHIRDWALGTPEGDWVSMAVPSQGEYGIPEGIVYSFPVTAKDGAYRVVEGLEINEFARKRMEITAQELLDEMEQVKALGLI

>d2hlpa2 d.162.1.1 (A:163-330) Malate dehydrogenase {Archaeon Haloarcula marismortui}

FGGRLDSARFRYVLSEEFDAPVQNVEGTILGEHGDAQVPVFSKVRVDGTDPEFSGDEKEQLLGDLQESAMDVIERKGATEWGPARGVAHMVEAILHDTGRVLPASVKLEGEFGHEDTAFGVPVRLGSNGVEEIVEWDLDDYEQDLMADAAEKLSDQYDKIS

>d1b8pa2 d.162.1.1 (A:159-329) Malate dehydrogenase {Aquaspirillum arcticum}

LRLDHNRALSQIAAKTGKPVSSIEKLFVWGNHSPTMYADYRYAQIDGASVKDMINDDAWNRDTFLPTVGKRGAAIIDARGVSSAASAANAAIDHIHDWVLGTAGKWTTMGIPSDGSYGIPEGVIFGFPVTTENGEYKIVQGLSIDAFSQERINVTLNELLEEQNGVQHLLG

>d1guya2 d.162.1.1 (A:144-306) Malate dehydrogenase {Chloroflexus aurantiacus}

AGVLDAARYRTFIAMEAGVSVEDVQAMLMGGHGDEMVPLPRFSTISGIPVSEFIAPDRLAQIVERTRKGGGEIVNLLKTGSAYYAPAAATAQMVEAVLKDKKRVMPVAAYLTGQYGLNDIYFGVPVILGAGGVEKILELPLNEEEMALLNASAKAVRATLDTL

>d1gv0a2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium tepidum}

AGVLDSARFRSFIAMELGVSMQDVTACVLGGHGDAMVPVVKYTTVAGIPVADLISAERIAELVERTRTGGAEIVNHLKQGSAFYSPATSVVEMVESIVLDRKRVLTCAVSLDGQYGIDGTFVGVPVKLGKNGVEHIYEIKLDQSDLDLLQKSAKIVDENCKML

>d1guza2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium vibrioforme}

AGVLDAARFRSFIAMELGVSMQDINACVLGGHGDAMVPVVKYTTVAGIPISDLLPAETIDKLVERTRNGGAEIVEHLKQGSAFYAPASSVVEMVESIVLDRKRVLPCAVGLEGQYGIDKTFVGVPVKLGRNGVEQIYEINLDQADLDLLQKSAKIVDENCKML

>d1hyha2 d.162.1.1 (A:167-329) L-2-hydroxyisocapronate dehydrogenase, L-HICDH {Lactobacillus confusus}

GTLLDTARMQRAVGEAFDLDPRSVSGYNLGEHGNSQFVAWSTVRVMGQPIVTLADAGDIDLAAIEEEARKGGFTVLNGKGYTSYGVATSAIRIAKAVMADAHAELVVSNRRDDMGMYLSYPAIIGRDGVLAETTLDLTTDEQEKLLQSRDYIQQRFDEIVDTL

>d9ldta2 d.162.1.1 (A:163-331) Lactate dehydrogenase {Pig (Sus scrofa)}

SGCNLDSARFRYLMGERLGVHPLSCHGWILGEHGDSSVPVWSGVNVAGVSLKNLHPELGTDADKEHWKAVHKEVVDSAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGLYGIKENVFLSVPCILGQNGISDVVKVTLTPEEEAHLKKSADTLWGIQKELQF

>d1i0za2 d.162.1.1 (A:161-332) Lactate dehydrogenase {Human (Homo sapiens), heart isoform (H chain)}

SGCNLDSARFRYLMAEKLGIHPSSCHGWILGEHGDSSVAVWSGVNVAGVSLQELNPEMGTDNDSENWKEVHKMVVESAYEVIKLKGYTNWAIGLSVADLIESMLKNLSRIHPVSTMVKGMYGIENEVFLSLPCILNARGLTSVINQKLKDDEVAQLKKSADTLWDIQKDLKD

>d1i10a2 d.162.1.1 (A:160-331) Lactate dehydrogenase {Human (Homo sapiens), muscle isoform (M chain)}

SGCNLDSARFRYLMGERLGVHPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDKEQWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLRRVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEEEARLKKSADTLWGIQKELQF

>d2ldx\_2 d.162.1.1 (160-331) Lactate dehydrogenase {Mouse (Mus musculus)}

SGCNLDSARFRYLIGEKLGVNPTSCHGWVLGEHGDSSVPIWSGVNVAGVTLKSLNPAIGTDKNKQHWKNVHKQVVEGGYEVLDMKGYTSWAIGLSVTDLARSILKNLKRVHPVTTLVKGFHGIKEEVFLSIPCVLGESGITDFVKVNMTAEEEGLLKKSADTLWNMQKNLEL

>d1ldm\_2 d.162.1.1 (161-329) Lactate dehydrogenase {Dogfish (Squalus acanthias)}

SGCNLDSARFRYLMGERLGVHSCSCHGWVIGEHGDSVPSVWSGMNVASIKLHPLDGTNKDKQDWKKLHKDVVDSAYEVIKLKGYTSWAIGLSVADLAETIMKNLCRVHPVSTMVKDFYGIKDNVFLSLPCVLNDHGISNIVKMKLKPNEEQQLQKSATTLWDIQKDLKF

>d1ceqa2 d.162.1.1 (A:164-329) Lactate dehydrogenase {Malaria parasite (Plasmodium falciparum)}

GGVLDTSRLKYYISQKLNVCPRDVNAHIVGAHGNKMVLLKRYITVGGIPLQEFINNKLISDAELEAIFDRTVNTALEIVNLHASPYVAPAAAIIEMAESYLKDLKKVLICSTLLEGQYGHSDIFGGTPVVLGANGVEQVIELQLNSEEKAKFDEAIAETKRMKALA

>d1ldna2 d.162.1.1 (A:163-330) Lactate dehydrogenase {Bacillus stearothermophilus}

TILDTARFRFLLGEYFSVAPQNVHAYIIGEHGDTELPVWSQAYIGVMPIRKLVESKGEEAQKDLERIFVNVRDAAYQIIEKKGATYYGIAMGLARVTRAILHNENAILTVSAYLDGLYGERDVYIGVPAVINRNGIREVIEIELNDDEKNRFHHSAATLKSVLARAFT

>d1llc\_2 d.162.1.1 (165-334) Lactate dehydrogenase {Lactobacillus casei}

TSLDTARFRQSIAEMVNVDARSVHAYIMGEHGDTEFPVWSHANIGGVTIAEWVKAHPEIKEDKLVKMFEDVRDAAYEIIKLKGATFYGIATALARISKAILNDENAVLPLSVYMDGQYGINDLYIGTPAVINRNGIQNILEIPLTDHEEESMQKSASQLKKVLTDAFAKNDI

>d1ez4a2 d.162.1.1 (A:163-334) Lactate dehydrogenase {Lactobacillus pentosus}

TSLDSSRLRVALGKQFNVDPRSVDAYIMGEHGDSEFAAYSTATIGTRPVRDVAKEQGVSDDDLAKLEDGVRNKAYDIINLKGATFYGIGTALMRISKAILRDENAVLPVGAYMDGQYGLNDIYIGTPAIIGGTGLKQIIESPLSADELKKMQDSAATLKKVLNDGLAELEN

>d1llda2 d.162.1.1 (A:150-319) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}

TNLDSARLRFLIAQQTGVNVKNVHAYIAGEHGDSEVPLWESATIGGVPMSDWTPLPGHDPLDADKREEIHQEVKNAAYKIINGKGATNYAIGMSGVDIIEAVLHDTNRILPVSSMLKDFHGISDICMSVPTLLNRQGVNNTINTPVSDKELAALKRSAETLKETAAQFGF

>d1a5z\_2 d.162.1.1 (164-333) Lactate dehydrogenase {Thermotoga maritima}

GTVLDTARLRTLIAQHCGFSPRSVHVYVIGEHGDSEVPVWSGAMIGGIPLQNMCQVCQKCDSKILENFAEKTKRAAYEIIERKGATHYAIALAVADIVESIFFDEKRVLTLSVYLEDYLGVKDLCISVPVTLGKHGVERILELNLNEEELEAFRKSASILKNAINEITAEEN

>d1hyea2 d.162.1.1 (A:146-313) MJ0490, lactate/malate dehydrogenase {Archaeon Methanococcus jannaschii}

LGTHLDSLRFKVAIAKFFGVHIDEVRTRIIGEHGDSMVPLLSATSIGGIPIQKFERFKELPIDEIIEDVKTKGEQIIRLKGGSEFGPAAAILNVVRCIVNNEKRLLTLSAYVDGEFDGIRDVCIGVPVKIGRDGIEEVVSIELDKDEIIAFRKSAEIIKKYCEEVKNL

>d1aiha\_ d.163.1.1 (A:) Integrase {Bacteriophage HP1}

ETELAFLYERDIYRLLAECDNSRNPDLGLIVRICLATGARWSEAETLTQSQVMPYKITFTNTKSKKNRTVPISDELFDMLPKKRGRLFNDAYESFENAVLRAEIELPKGQLTHVLRHTFASHFMMNGGNILVLKEILGHSTIEMTMRYAHFAPSHLESAVKFNPLSNPAQ

>d1ae9a\_ d.163.1.1 (A:) Integrase (Int) {Bacteriophage lambda}

RSRLTADEYLKIYQAAESSPCWLRLAMELAVVTGQRVGDLCEMKWSDIVDGYLYVEQSKTGVKIAIPTALHIDALGISMKETLDKCKEILGGETIIASTRREPLSSGTVSRYFMRARKASGLSFEGDPPTFHELRSLSARLYEKQISDKFAQHLLGHKSDTMASQFRDDRGREWDKIEI

>d1f44a2 d.163.1.1 (A:130-343) Cre recombinase {Bacteriophage P1}

RAKQALAFERTDFDQVRSLMENSDRCQDIRNLAFLGIAYNTLLRIAEIARIRVKDISRTDGGRMLIHIGRTKTLVSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLFCRVRKNGVAAPSATSQLSTRALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGGWTNVNIVMNFIRNLDSETGAMVRLLEDGD

>d5crxb2 d.163.1.1 (B:130-314) Cre recombinase {Bacteriophage P1}

RAKQALAFERTDFDQVRSLMENSDRCQDIRNLAFLGIAYNTLLRIAEIARIRVKDISRTDGGRMLIHIGRTKTLVSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLFCRVRKNGVAAPSATSQLSTRALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGG

>d1a0p\_2 d.163.1.1 (111-292) Recombinase XerD {Escherichia coli}

KDLSEAQVERLLQAPLIDQPLELRDKAMLEVLYATGLRVSELVGLTMSDISLRQGVVRVIGKGNKERLVPLGEEAVYWLETYLEHGRPWLLNGVSIDVLFPSQRAQQMTRQTFWHRIKHYAVLAGIDSEKLSPHVLRHAFATHLLNHGADLRVVQMLLGHSDLSTTQIYTHVATERLRQLHQ

>d1floa2 d.163.1.1 (A:135-423) Flp recombinase {Baker's yeast (Saccharomyces cerevisiae)}

KGNSHSKKMLKALLSEGESIWEITEKILNSFEYTSRFTKTKTLYQFLFLATFINCGRFSDIKNVDPKSFKLVQNKYLGVIIQCLVTETKTSVSRHIYFFSARGRIDPLVYLDEFLRNSEPVLKRVNRTGNSSSNKQEYQLLKDNLVRSYNKALKKNAPYSIFAIKNGPKSHIGRHLMTSFLSMKGLTELTNVVGNWSDKRASAVARTTYTHQITAIPDHYFALVSRYYAYDPISKEMIALKDETNPIEEWQHIEQLKGSAEGSIRYPAWNGIISQEVLDYLSSYINRRI

>d1a31a1 d.163.1.2 (A:431-626,A:720-765) Eukaryotic DNA topoisomerase I, catalytic core {Human (Homo sapiens)}

PSSRIKGEKDWQKYETARRLKKCVDKIRNQYREDWKSKEMKVRQRAVALYFIDKLALRAGNEKEEGETADTVGCCSLRVEHINLHPELDGQEYVVEFDFLGKDSIRYYNKVPVEKRVFKNLQLFMENKQPEDDLFDRLNTGILNKHLQDLMEGLTAKVFRTYNASITLQQQLKELTAPDENIPAKILSYNRANRAVXKLNYLDPRITVAWCKKWGVPIEKIYNKTQREKFAWAIDMADEDYEF

>d1a41\_\_ d.163.1.2 (-) Eukaryotic DNA topoisomerase I, catalytic core {Vaccinia virus}

NAKRDRIFVRVYNVMKRINCFINKNIKKSSTDSNYQLAVFMLMETMFFIRFGKMKYLKENETVGLLTLKNKHIEISPDEIVIKFVGKDKVSHEFVVHKSNRLYKPLLKLTDDSSPEEFLFNKLSERKVYECIKQFGIRIKDLRTYGVNYTFLYNFWTNVKSISPLPSPKKLIALTIKQTAEVVGHTPSISKRAYMATTILEMVKDKNFLDVVSKTTFDEFLSIVVDHVKS

>d1mhda\_ d.164.1.1 (A:) SMAD MH1 domain {Human (Homo sapiens)}

PIVKRLLGWKKGEQNGQEEKWCEKAVKSLVKKLKKTGQLDELEKAITTQNVNTKCITIPRSLDGRLQVSHRKGLPHVIYCRLWRWPDLHSHHELRAMELCEFAFNMKKDEVCVNPYHYQRVET

>d1hufa\_ d.195.1.1 (A:) YopH tyrosine phosphatase N-terminal domain {Yersinia pestis}

LSLSDLHRQVSRLVQQESGDCTGKLRGNVAANKETTFQGLTIASGARESEKVFAQTVLSHVANVVLTQEDTAKLLQSTVKHNLNNYDLRSVGNGNSVLVSLRSDQMTLQDAKVLLEAALRQES

>d1mrj\_\_ d.165.1.1 (-) alpha-Trichosanthin {Mongolian snake gourd (Trichosanthes kirilowii maxim)}

DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETISVAIDVTNVYIMGYRAGDTSYFFNEASATEAAKYVFKDAMRKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTLFYYNANSAASALMVLIQSTSEAARYKFIEQQIGKRVDKTFLPSLAIISLENSWSALSKQIQIASTNNGQFESPVVLINAQNQRVTITNVDAGVVTSNIALLLNRNNMA

>d1bryy\_ d.165.1.1 (Y:) Bryodin {Red briony (Bryonia dioica)}

DVSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYTLLHLTNYADETISVAVDVTNVYIMGYLAGDVSYFFNEASATEAAKFVFKDAKKKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTLYYYTASSAASALLVLIQSTAESARYKFIEQQIGKRVDKTFLPSLATISLENNWSALSKQIQIASTNNGQFESPVVLIDGNNQRVSITNASARVVTSNIALLLNRNNIA

>d1mrg\_\_ d.165.1.1 (-) alpha-Momorcharin (momordin) {Bitter gourd (Momordica charantia)}

DVSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNRDGKTITVAVDVTNIYIMGYLADTTSYFFNEPAAELASQYVFRDARRKITLPYSGDYERLQIAAGKPREKIPIGLPALDSAISTLLHYDSTAAAGALLVLIQTTAEAARFKYIEQQIQERAYRDEVPSLATISLENSWSGLSKQIQLAQGNNGIFRTPIVLVDNKGNRVQITNVTSKVVTSNIQLLLNTRNI

>d1cf5a\_ d.165.1.1 (A:) Beta-momorcharin {Bitter gourd (Momordica charantia)}

DVNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETISVAIDVTNVYVVAYRTRDVSYFFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIRENIDLGLPALSSAITTLFYYNAQSAPSALLVLIQTTAEAARFKYIERHVAKYVATNFKPNLAIISLENQWSALSKQIFLAQNQGGKFRNPVDLIKPTGQRFQVTNVDSDVVKGNIKLLLNSRASTADEN

>d1ce7a\_ d.165.1.1 (A:) Mistletoe lectin I A-chain {European mistletoe (Viscum album)}

YERGDLDVTAQTTGAGYFSFITLLRDYVSSGSFSNAIPLLSQSGGGGEAGRFVLVELTNSGGDGITVAIDVTNLYVVAYQAGSQSYFLSGPGGRHGFTGTTRSSLPFNGSYPDLEQYGGQRKQIPLGIDQLIQSVTALKFPGSTRTGARSILILIQMISEAARFNPILWRARQYINSGASFLPDVYMLELETSWGQQSTQVQHSTDGVFNNPIALADPGGGVTLTNVRDVIASLAIMLFVC

>d1abra\_ d.165.1.1 (A:) Abrin A-chain {Abrus precatorius}

EDRPIKFSTEGATSQSYKQFIEALRERLRGGLIHDIPVLPDPTTLQERNRYITVELSNSDTESIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASDYLFTGTDQHSLPFYGTYGDLERWAHQSRQQIPLGLQALTHGISFFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRVRVSIQTGTAFQPDAAMISLENNWDNLSRGVQESVQDTFPNQVTLTNIRNEPVIVDSLSHPTVAVLALMLFVCNPPN

>d1apa\_\_ d.165.1.1 (-) Pokeweed antiviral protein alpha {Pokeweed (Phytolacca americana)}

INTITFDVGNATINKYATFMKSIHNQAKDPTLKCYGIPMLPNTNLTPKYLLVTLQDSSLKTITLMLKRNNLYVMGYADTYNGKCRYHIFKDISNTTERNDVMTTLCPNPSSRVGKNINYDSSYPALEKKVGRPRSQVQLGIQILNSGIGKIYGVDSFTEKTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAFYPNAKVLNLEESWGKISTAIHNAKNGALTSPLELKNANGSKWIVLRVDDIEPDVGLLKYVNGTCQAT

>d1d6aa\_ d.165.1.1 (A:) Pokeweed antiviral protein alpha {Pokeweed (Phytolacca americana)}

VNTIIYNVGSTTISKYATFLNDLRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKKTITLMLRRNNLYVMGYSDPFETNKCRYHIFNDISGTERQDVETTLCPNANSRVSKNINFDSRYPTLESKAGVKSRSQVQLGIQILDSNIGKISGVMSFTEKTEAEFLLVAIQMVSEAARFKYIENQVKTNFNRAFNPNPKVLNLQETWGKISTAIHDAKNGVLPKPLELVDASGAKWIVLRVDEIKPDVALLNYVGGSCQTT

>d1qi7a\_ d.165.1.1 (A:) Saporin So6 {Common soapwort (Saponaria officinalis)}

VTSITLDLVNPTAGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGPPSKEKFLRINFQSSRGTVSLGLKRDNLYVVAYLAMDNTNVNRAYYFKSEITSAELTALFPEATTANQKALEYTEDYQSIEKNAQITQGDKSRKELGLGIDLLLTFMEAVNKKARVVKNEARFLLIAIQMTAEVARFRYIQNLVTKNFPNKFDSDNKVIQFEVSWRKISTAIYGDAKNGVFNKDYDFGFGKVRQVKDLQMGLLMYLGKPK

>d1ift\_\_ d.165.1.1 (-) Ricin A-chain {Castor bean (Ricinus communis)}

YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPP

>d1hwma\_ d.165.1.1 (A:) Ebulin A-chain {Sambucus ebulus}

IDYPSVSFNLAGAKSTTYRDFLKNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLVRLTNYNGDTVTSAVDVTNLYLVAFSANGNSYFFKDATELQKSNLFLGTTQHTLSFTGNYDNLETAAGTRRESIELGPNPLDGAITSLWYDGGVARSLLVLIQMVPEAARFRYIEQEVRRSLQQLTSFTPNALMLSMENNWSSMSLEVQLSGDNVSPFSGTVQLQNYDHTPRLVDNFEELYKITGIAILLFRCVA

>d1dm0a\_ d.165.1.2 (A:) Shiga toxin, A-chain {Shigella dysenteriae}

KEFTLDFSTAKTYVDSLNVIRSAIGTPLQTISSGGTSLLMIDSGTGDNLFAVDVRGIDPEEGRFNNLRLIVERNNLYVTGFVNRTNNVFYRFADFSHVTFPGTTAVTLSGDSSYTTLQRVAGISRTGMQINRHSLTTSYLDLMSHSGTSLTQSVARAMLRFVTVTAEALRFRQIQRGFRTTLDDLSGRSYVMTAEDVDLTLNWGRLSSVLPDYHGQDSVRVGRISFGSINAILGSVALILNCHHHASRVARMASDEFPSMCPADGRVRGITHNKILWDSSTLGAILM

>g1lts.1 d.166.1.1 (A:,C:) Heat-labile toxin, A-chain {Escherichia coli, type IB}

RLYRADSRPPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSLRSAHLAGQSILSGYSTYYIYVIATAPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRNLNIAPAEDGYRLAGFPPDHQAWREEPWIHHAPQGCGXGDTCNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRI

>g1tii.1 d.166.1.1 (A:,C:) Heat-labile toxin, A-chain {Escherichia coli, type IIB}

NDYFRADSRTPDEVRRSGGLIPRGQDEAYERGTPININLYDHARGTATGNTRYNDGYVSTTTTLRQAHLLGQNMLGGYNEYYIYVVAAAPNLFDVNGVLGRYSPYPSENEYAALGGIPLSQIIGWYRVSFGAIEGGMHRNRDYRRDLFRGLSAAPNEDGYRIAGFPDGFPAWEEVPWREFAPNSCLPXTTCASLTNKLSQHDLADFKKYIKRKFTLMTLLSINN

>d1f0la2 d.166.1.1 (A:1-187) Diphtheria toxin, N-terminal domain {Corynebacterium diphtheriae}

GADDVVDSSKSFVMENFSSYHGTKPGYVDSIQKGIQKPKSGTQGNYDDDWKGFYSTDNKYDAAGYSVDNENPLSGKAGGVVKVTYPGLTKVLALKVDNAETIKKELGLSLTEPLMEQVGTEEFIKRFGDGASRVVLSLPFAEGSSSVEYINNWEQAKALSVELEINFETRGKRGQDAMYEYMAQACA

>d1ikpa2 d.166.1.1 (A:395-606) Exotoxin A, C-terminal domain {Pseudomonas aeruginosa}

PTGAEFLGDGGDVSFSTRGTQNWTVERLLQAHRQLEERGYVFVGYHGTFLEAAQSIVFGGVRARSQDLDAIWRGFYIAGDPALAYGYAQDQEPDARGRIRNGALLRVYVPRSSLPGFYRTSLTLAAPEAAGEVERLIGHPLPLRLDAITGPEEEGGRLETILGWPLAERTVVIPSAIPTDPRNVGGDLDPSSIPDKEQAISALPDYASQPGK

>d1prta\_ d.166.1.1 (A:) Pertussis toxin, S1 subunit {Bordetella pertussis}

DPPATVYRYDSRPPEDVFQNGFTAWGNNDNVLEHLTGRSCQVGSSNSAFVSTSSSRRYTEVYLEHRMQEAVEAERAGRGTGHFIGYIYEVRADNNFYGAASSYFEYVDTYGDNAGRILAGALATYQSEYLAHRRIPPENIRRVTRVYHNGITGETTTTEYSNARYVSQQTRANPNPYTSRRSVASIVGTLVRMAPVVGACMARQAESSEAMAAWSERAGEAMVLVYYESIAYSF

>g1xtc.1 d.166.1.1 (A:,C:) Cholera toxin {Vibrio cholerae}

NDDKLYRADSRPPDEIKQSGGLMPRGQSEYFDRGTQMNINLYDHARGTQTGFVRHDDGYVSTSISLRSAHLVGQTILSGHSTYYLYVLATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHFGVLDEQLHRNRGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPPGCGNAPRXSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL

>d1qs1a1 d.166.1.1 (A:60-264) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}

TDKVEDFKEDKEKAKEWGKEKEKEWKLTATEKGKMNNFLDNKNDIKTNYKEITFSMAGSFEDEIKDLKEIDKMFDKTNLSNSIITYKNVEPTTIGFNKSLTEGNTINSDAMAQFKEQFLDRDIKFDSYLDTHLTAQQVSSKERVILKVTVPSGKGSTTPTKAGVILNNSEYKMLIDNGYMVHVDKVSKVVKKGVECLQIEGTLKK

>d1qs1a2 d.166.1.1 (A:265-461) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}

SLDFKNDINAEAHSWGMKNYEEWAKDLTDSQREALDGYARQDYKEINNYLRNQGGSGNEKLDAQIKNISDALGKKPIPENITVYRWCGMPEFGYQISDPLPSLKDFEEQFLNTIKEDKGYMSTSLSSERLAAFGSRKIILRLQVPKGSTGAYLSAIGGFASEKEILLDKDSKYHIDKVTEVIIKGVKRYVVDATLLT

>d1g24a\_ d.166.1.1 (A:) Exoenzyme c3 {Clostridium botulinum}

AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNLIKQVELLDKSFNKMKTPENIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAKAKFLNKDRLEYGYISTSLMNVSQFAGRPIITKFKVAKGSKAGYIDPISAFAGQLEMLLPRHSTYHIDDMRLSSDGKQIIITATMMGTAINPK

>d1j7na3 d.166.1.1 (A:264-550) Anthrax toxin lethal factor, middle domain {Bacillus anthracis}

MLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKLQIPIEPKKDDIIHSLSQEEKELLKRIQIDSSDFLSTEEKEFLKKLQIDIRDSLSEEEKELLNRIQVDSSNPLSEKEKEFLKKLKLDIQPYDINQRLQDTGGLIDSPSINLDVRKQYKRDIQNIDALLHQSIGSTLYNKIYLYENMNINNLTATLGADLVDSTDNTKINRGIFNEFKKNFKYSISSNYMIVDINERPALDNERLKWRIQLSPDTRAGYLENGKLILQRNIGLEIKDVQIIKQSEKEYIRIDAKVV

>d1a26\_2 d.166.1.2 (797-1012) Poly(ADP-ribose) polymerase, C-terminal domain {Chicken (Gallus gallus)}

LRTDIKVVDKDSEEAKIIKQYVKNTHAATHNAYDLKVVEIFRIEREGESQRYKPFKQLHNRQLLWHGSRTTNFAGILSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHTSQADPIGLILLGEVALGNMYELKNASHITKLPKGKHSVKGLGKTAPDPTATTTLDGVEVPLGNGISTGINDTCLLYNEYIVYDVAQVNLKYLLKLKFNYKTS

>d1g2aa\_ d.167.1.1 (A:) Peptide deformylase {Escherichia coli}

SVLQVLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSENRDERLVLINPELLEKSGETGIEEGCLSIPEQRALVPRAEKVKIRALDRDGKPFELEADGLLAICIQHEMDHLVGKLFMDYLSPLKQQRIRQKVEKLDRL

>d2def\_\_ d.167.1.1 (-) Peptide deformylase {Escherichia coli}

VLQVLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSENRDERLVLINPELLEKSGETGIEEGCLSIPEQRALVPRAEKVKIRALDRDGKPFELEADGLLAICIQHEMDHLVGKLFMDYLS

>d1jbia\_ d.209.1.1 (A:) Cochlin {Human (Homo sapiens)}

TAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVYGNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVTLE

>d1chua3 d.168.1.1 (A:238-353) L-aspartate oxidase {Escherichia coli}

LEFNQFHPTALYHPQARNFLLTEALRGEGAYLKRPDGTRFMPDFDERGELAPRDIVARAIDHEMKRLGADCMFLDISHKPADFIRQHFPMIYEKLLGLGIDLTQEPVPIVPAAHYT

>d1fuma3 d.168.1.1 (A:226-357) Fumarate reductase flavoprotein subunit {Escherichia coli}

MEFVQYHPTGLPGSGILMTEGCRGEGGILVNKNGYRYLQDYGMGPETPLGEPKNKYMELGPRDKVSQAFWHEWRKGNTISTPRGDVVYLDLRHLGEKKLHERLPFICELAKAYVGVDPVKEPIPVRPTAHYT

>d1qlaa3 d.168.1.1 (A:251-371) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}

MEAVQFHPTPLFPSGILLTEGCRGDGGILRDVDGHRFMPDYEPEKKELASRDVVSRRMIEHIRKGKGVQSPYGQHLWLDISILGRKHIETNLRDVQEICEYFAGIDPAEKWAPVLPMQHYS

>d1e39a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

QYIQAAPTLSVKGGVMVTEAVRGNGAILVNREGKRFVNEITTRDKASAAILAQTGKSAYLIFDDSVRKSLSKIDKYIGLGVAPTADSLVKLGKMEGIDGKALTETVARYNSLVSSGKDTDFERPNLPRALNEGNYYAIEVTPGVHH

>d1qo8a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

HPTVGKDSRILISETVRGVGAVMVNKDGNRFISELTTRDKASDAILKQPGQFAWIIFDNQLYKKAKMVRGYDHLEMLYKGDTVEQLAKSTGMKVADLAKTVSDYNGYVASGKDTAFGRADMPLNMTQSPYYAVKVAPGIHHTMGGV

>d1d4ca3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella putrefaciens}

YIQAHPTYSPAGGVMITEAVRGNGAIVVNREGNRFMNEITTRDKASAAILQQKGESAYLVFDDSIRKSLKAIEGYVHLNIVKEGKTIEELAKQIDVPAAELAKTVTAYNGFVKSGKDAQFERPDLPRELVVAPFYALEIAPAVHHT

>d1jnra3 d.168.1.1 (A:257-401) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

FEHRFIPFRFKDGYGPVGAWFLFFKCKAKNAYGEEYIKTRAAELEKYKPYGAAQPIPTPLRNHQVMLEIMDGNQPIYMHTEEALAELAGGDKKKLKHIYEEAFEDFLDMTVSQALLWACQNIDPQEQPSEAAPAEPYIMGSHSGE

>d1lit\_\_ d.169.1.1 (-) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}

CPEGTNAYRSYCYYFNEDRETWVDADLYCQNMNSGNLVSVLTQAEGAFVASLIKESGTDDFNVWIGLHDPKKNRRWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKWKDVPCEDKFSFVCKFKN

>d1qdda\_ d.169.1.1 (A:) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}

QEAQTELPQARISCPEGTNAYRSYCYYFNEDRETWVDADLYCQNMNSGNLVSVLTQAEGAFVASLIKESGTDDFNVWIGLHDPKKNRAWHWSSGSLVSYKSWGIGAPSSVNPGYCVSLTSSTGFQKWKDVPCEDKFSFVCKFKN

>d1b6e\_\_ d.169.1.1 (-) CD94 {Human (Homo sapiens)}

CSCQEKWVGYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSSSQQFYWIGLSYSEEHTAWLWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQLI

>d1e87a\_ d.169.1.1 (A:) CD69 {Human (Homo sapiens)}

SSCSEDWVGYQRKCYFISTVKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWVGLKKEPGHPWKWSNGKEFNNWFNVTGSDKCVFLKNTEVSSMECEKNLYWICNKPYK

>d1hq8a\_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Mouse (Mus musculus)}

GYCGPCPNNWICHRNNCYQFFNEEKTWNQSQASCLSQNSSLLKIYSKEEQDFLKLVKSYHWMGLVQIPANGSWQWEDGSSLSYNQLTLVEIPKGSCAVYGSSFKAYTEDCANLNTYICMKRAV

>d1hyra\_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Human (Homo sapiens)}

ESYCGPCPKNWICYKNNCYQFFDESKNWYESQASCMSQNASLLKVYSKEDQDLLKLVKSYHWMGLVHIPTNGSWQWEDGSILSPNLLTIIEMQKGDCALYASSFKGYIENCSTPNTYICMQRTV

>d1egia\_ d.169.1.1 (A:) Macrophage mannose receptor, CRD4 {Human (Homo sapiens)}

CPEDWGASSRTSLCFKLYAKGKHEKKTWFESRDFCRALGGDLASINNKEEQQTIWRLITASGSYHKLFWLGLTYGSPSEGFTWSDGSPVSYENWAYGEPNNYQNVEYCGELKGDPTMSWNDINCEHLNNWICQIQ

>d1bj3a\_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis)}

DCPSGWSSYEGHCYKPFKLYKTWDDAERFCTEQAKGGHLVSIESAGEADFVAQLVTENIQNTKSYVWIGLRVQGKEKQCSSEWSDGSSVSYENWIEAESKTCLGLEKETGFRKWVNIYCGQQNPFVCEA

>d1ixxa\_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis)}

DCLSGWSSYEGHCYKAFEKYKTWEDAERVCTEQAKGAHLVSIESSGEADFVAQLVTQNMKRLDFYIWIGLRVQGKVKQCNSEWSDGSSVSYENWIEAESKTCLGLEKETDFRKWVNIYCGQQNPFVCEA

>d1ixxb\_ d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis)}

DCPSDWSSYEGHCYKPFSEPKNWADAENFCTQQHAGGHLVSFQSSEEADFVVKLAFQTFGHSIFWMGLSNVWNQCNWQWSNAAMLRYKAWAEESYCVYFKSTNNKWRSRACRMMAQFVCEFQA

>d1c3aa\_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis), flavocetin-A}

DFDCIPGWSAYDRYCYQAFSKPKNWEDAESFCEEGVKTSHLVSIESSGEGDFVAQLVAEKIKTSFQYVWIGLRIQNKEQQCRSEWSDASSVNYENLVKQFSKKCYALKKGTELRTWFNVYCGTENPEVCKYTPEC

>d1c3ab\_ d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis), flavocetin-A}

GFCCPLGWSSYDEHCYQVFQQKMNWEDAEKFCTQQHKGSHLVSFHSSEEVDFVTSKTFPILKYDFVWIGLSNVWNECTKEWSDGTKLDYKAWSGGSDCIVSKTTDNQWLSMDCSSKYYVVCKFQA

>d1fvua\_ d.169.1.1 (A:) Snake coagglutinin {Snake (Bothrops jararaca), botrocetin}

DCPSGWSSYEGNCYKFFQQKMNWADAERFCSEQAKGGHLVSIKIYSKEKDFVGDLVTKNIQSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEKDLGFVLWINLYCAQKNPFVCKSPPP

>d1fvub\_ d.169.1.1 (B:) Snake coagglutinin {Snake (Bothrops jararaca), botrocetin}

DCPPDWSSYEGHCYRFFKEWMHWDDAEEFCTEQQTGAHLVSFQSKEEADFVRSLTSEMLKGDVVWIGLSDVWNKCRFEWTDGMEFDYDDYYLIAEYECVASKPTNNKWWIIPCTRFKNFVCEFQA

>d1ioda\_ d.169.1.1 (A:) Snake coagglutinin {Sharp-nosed viper (Deinagkistrodon acutus)}

DCSSGWSSYEGHCYKVFKQSKTWADAESFCTKQVNGGHLVSIESSGEADFVGQLIAQKIKSAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEESKKCLGVHIETGFHKWENFYCEQQDPFVCEA

>d1iodb\_ d.169.1.1 (B:) Snake coagglutinin {Sharp-nosed viper (Deinagkistrodon acutus)}

DCPSDWSSYEGHCYKPFNEPKNWADAENFCTQQHTGSHLVSFQSTEEADFVVKLAFQTFDYGIFWMGLSKIWNQCNWQWSNAAMLKYTDWAEESYCVYFKSTNNKWRSITCRMIANFVCEFQA

>d1jwia\_ d.169.1.1 (A:) Snake coagglutinin {Puff adder (Bitis arientans), bitiscetin}

CLPDWSSYKGHCYKVFKKVGTWEDAEKFCVENSGHLASIDSKEEADFVTKLASQTLTKFVYDAWIGLRDESKTQQCSPQWTDGSSVVYENVDEPTKCFGLDVHTEYRTWTDLPCGEKNPFICKS

>d1jwib\_ d.169.1.1 (B:) Snake coagglutinin {Puff adder (Bitis arientans), bitiscetin}

GCLPDWSSYKGHCYKVFKVEKTWADAEKFCKELVNGGHLMSVNSREEGEFISKLALEKMRIVLVWIGLSHFWRICPLRWTDGARLDYRALSDEPICFVAESFHNKWIQWTCNRKKSFVCKYRV

>d2afpa\_ d.169.1.1 (A:) Type II antifreeze protein {Sea raven (Hemitripterus americanus)}

QRAGPNCPAGWQPLGDRCIYYETTAMTWALAETNCMKLGGHLASIHSQEEHSFIQTLNAGVVWIGGSACLQAGAWTWSDGTPMNFRSWCSTKPDDVLAACCMQMTAAADQCWDDLPCPASHKSVCAMTF

>d1h8ua\_ d.169.1.1 (A:) Eosinophil major basic protein {Human (Homo sapiens)}

RYLLVRSLQTFSQAWFTCRRCYRGNLVSIHNFNINYRIQCSVSALNQGQVWIGGRITGSGRCRRFQWVDGSRWNFAYWAAHQPWSRGGHCVALCTRGGYWRRAHCLRRLPFICSY

>d1qo3c\_ d.169.1.1 (C:) NK cell receptor ly49a {Mouse (Mus musculus)}

STVLDSLQHTGRGDKVYWFCYGMKCYYFVMDRKTWSGCKQTCQSSSLSLLKIDDEDELKFLQLVVPSDSCWVGLSYDNKKKDWAWIDNRPSKLALNTRKYNIRDGGCMLLSKTRLDNGNCDQVFICICGKRLD

>d1qo3d\_ d.169.1.1 (D:) NK cell receptor ly49a {Mouse (Mus musculus)}

DKVYWFCYGMKCYYFVMDRKTWSGCKQTCQSSSLSLLKIDDEDELKFLQLVVPSDSCWVGLSYDNKKKDWAWIDNRPSKLALNTRKYNIRDGGCMLLSKTRLDNGNCDQVFICICGKRLDK

>d1dv8a\_ d.169.1.1 (A:) H1 subunit of the asialoglycoprotein receptor {Human (Homo sapiens)}

CPVNWVEHERSCYWFSRSGKAWADADNYCRLEDAHLVVVTSWEEQKFVQHHIGPVNTWMGLHDQNGPWKWVDGTDYETGFKNWRPEQPDDWYGHGLGGGEDCAHFTDDGRWNDDVCQRPYRWVCETEL

>d1k9ia\_ d.169.1.1 (A:) DC-SIGN (dendritic cell-specific ICAM-3 grabbing nonintegrin) {Human (Homo sapiens)}

PCPWEWTFFQGNCYFMSNSQRNWHDSITACKEVGAQLVVIKSAEEQNFLQLQSSRSNRFTWMGLSDLNQEGTWQWVDGSPLLPSFKQYWNRGEPNNVGEEDCAEFSGNGWNDDKCNLAKFWICKKSAA

>d1k9ja\_ d.169.1.1 (A:) DC-SIGNR (DC-SIGN related receptor) {Human (Homo sapiens)}

CRHCPKDWTFFQGNCYFMSNSQRNWHDSVTACQEVRAQLVVIKTAEEQNFLQLQTSRSNRFSWMGLSDLNQEGTWQWVDGSPLSPSFQRYWNSGEPNNSGNEDCAEFSGSGWNDNRCDVDNYWICKKPAA

>d1g1sa1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}

WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVLPYYSSYYWIGIRKNNKTWTWVGTKKALTNEAENWADNEPNNKRNNEDCVEIYIKSPSAPGKWNDEHCLKKKHALCY

>d1g1ta1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}

WSYNTSTEAMTYDEASAYCQQRYTHLVAIQNKEEIEYLNSILSYSPSYYWIGIRKVNNVWVWVGTQKPLTEEAKNWAPGEPNNRQKDEDCVEIYIKREKDVGMWNDERCSKKKLALCY

>d1hup\_1 d.169.1.1 (112-228) Mannose-binding protein A, lectin domain {Human (Homo sapiens)}

KQVGNKFFLTNGEIMTFEKVKALCVKFQASVATPRNAAENGAIQNLIKEEAFLGITDEKTEGQFVDLTGNRLTYTNWNEGEPNNAGSDEDCVLLLKNGQWNDVPCSTSHLAVCEFPI

>d1fifa1 d.169.1.1 (A:105-226) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}

KKSGKKFFVTNHERMPFSKVKALCSELRGTVAIPRNAEENKAIQEVAKTSAFLGITDEVTEGQFMYVTGGRLTYSNWKKDQPDDWYGHGLGGGEDCVHIVDNGLWNDDSCQRPYTAVCEFPA

>d1rdl1\_ d.169.1.1 (1:) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}

KYFMSSVRRMPLNRAKALCSELQGTVATPRNAEENRAIQNVAKDVAFLGITDQRTENVFEDLTGNRVRYTNWNEGEPNNVGSGENCVVLLTNGKWNDVPCSDSFLVVCEFS

>d2msba\_ d.169.1.1 (A:) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}

KKFFVTNHERMPFSKVKALCSELRGTVAIPRNAEENKAIQEVAKTSAFLGITDEVTEGQFMYVTGGRLTYSNWKKDEPNDHGSGEDCVTIVDNGLWNDISCQASHTAVCEFP

>d1b08a1 d.169.1.1 (A:235-355) Surfactant protein, lectin domain {Human (Homo sapiens), SP-D}

PNGQSVGEKIFKTAGFVKPFTEAQLLCTQAGGQLASPRSAAENAALQQLVVAKNEAAFLSMTDSKTEGKFTYPTGESLVYSNWAPGEPNDDGGSEDCVEIFTNGKWNDRACGEKRLVVCEF

>d1byfa\_ d.169.1.1 (A:) Lectin TC14 {Tunicate (Polyandrocarpa misakiensis)}

DYEILFSDETMNYADAGTYCQSRGMALVSSAMRDSTMVKAILAFTEVKGHDYWVGADNLQDGAYNFLWNDGVSLPTDSDLWSPNEPSNPQSWQLCVQIWSKYNLLDDVGCGGARRVICEKELD

>d1tn3\_\_ d.169.1.1 (-) Tetranectin {Human (Homo sapiens)}

ALQTVCLKGTKVHMKCFLAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYLRQSVGNEAEIWLGLNDMAAEGTWVDMTGARIAYKNWETEITAQPDGGKTENCAVLSGAANGKWFDKRCRDQLPYICQFGIV

>d1prtb2 d.169.1.2 (B:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain {Bordetella pertussis}

GIVIPPQEQITQHGSPYGRCANKTRALTVAELRGSGDLQEYLRHVTRGWSIFALYDGTYLGGEYGGVIKDGTPGGAFDLKTTFCIM

>d1prtc2 d.169.1.2 (C:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain {Bordetella pertussis}

GIVIPPKALFTQQGGAYGRCPNGTRALTVAELRGNAELQTYLRQITPGWSIYGLYDGTYLGQAYGGIIKDAPPGAGFIYRETFCIT

>d1prea1 d.169.1.2 (A:2-84) Proaerolysin, N-terminal domain {Aeromonas hydrophila}

EPVYPDQLRLFSLGQGVCGDKYRPVNREEAQSVKSNIVGMMGQWQISGLANGWVIMGPGYNGEIKPGTASNTWCYPTNPVTGE

>d1f00i3 d.169.1.3 (I:842-939) Intimin {Escherichia coli}

LIVPNMSKRVTYNDAVNTCKNFGGKLPSSQNELENVFKAWGAANKYEYYKSSQTIISWVQQTAQDAKSGVASTYDLVKQNPLNNIKASESNAYATCVK

>d1cwva5 d.169.1.3 (A:887-986) Invasin {Yersinia pseudotuberculosis}

NRWIYDGGRSLVSSLEASRQCQGSDMSAVLESSRATNGTRAPDGTLWGEWGSLTAYSSDWQSGEYWVKKTSTDFETMNMDTGALQPGPAYLAFPLCALSI

>d1tsg\_\_ d.169.1.4 (-) TSG-6, Link module {Human (Homo sapiens)}

GVYHREARSGKYKLTYAEAKAVCEFEGGHLATYKQLEAARKIGFHVCAAGWMAKGRVGYPIVKPGPNCGFGKTGIIDYGIRLNRSERWDAYCYNPHAK

>d1bnla\_ d.169.1.5 (A:) Endostatin {Human (Homo sapiens)}

HSHRDFQPVLHLVALNAPLSGGMRGIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRADRAAVPIVNLKDELLFPSWEALFSGSEGPLKPGARIFSFDGKDVLRHPTWPQKSVWHGSDPNGRRLTESYCETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENSF

>d1koe\_\_ d.169.1.5 (-) Endostatin {Mouse (Mus musculus)}

QPVLHLVALNTPLSGGMRGIRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSIVRRADRGSVPIVNLKDEVLSPSWDSLFSGSQGQLQPGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLMESYCETWRTETTGATGQASSLLSGRLLEQKAASCHNSYIVLCIENSF

>d1dy2a\_ d.169.1.5 (A:) Endostatin domain of collagen alpha1(xv) {Mouse (Mus musculus)}

RPVLHLVALNTPVAGDIRADFQCFQQARAAGLLSTFRAFLSSHLQDLSTVVRKAERFGLPIVNLKGQVLFNNWDSIFSGDGGQFNTHIPIYSFDGRDVMTDPSWPQKVVWHGSNPHGVRLVDKYCEAWRTTDMAVTGFASPLSTGKILDQKAYSCANRLIVLCIENSF

>d1by2\_\_ d.170.1.1 (-) M2BP {Human (Homo sapiens)}

AVNDGDMRLADGGATNQGRVEIFYRGQWGTVCDNLWDLTDASVVCRALGFENATQALGRAAFGQGSGPIMLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVCTNETRSTHTL

>d1mwpa\_ d.170.2.1 (A:) N-terminal domain of the amyloid precursor protein {Human (Homo sapiens)}

LLAEPQIAMFCGRLNMHMNVQNGKWDSDPSGTKTCIDTKEGILQYCQEVYPELQITNVVEANQPVTIQNWCKRGRKQCKTHPHFVIPYRCLVGEFV

>d1fid\_\_ d.171.1.1 (-) Fibrinogen C-terminal domains {Human (Homo sapiens), gamma}

QIHDITGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWTVFQKRLDGSVDFKKNWIQYKEGFGHLSPTGTTEFWLGNEKIHLISTQSAIPYALRVELEDWNGRTSTADYAMFKVGPEADKYRLTYAYFAGGDAGDAFDGFDFGDDPSDKFFTSHNGMQFSTWDNDNDKFEGNCAEQDGSGWWMNKCHAGHLNGVYYQGGTYSKASTPNGYDNGIIWATWKTRWYSMKKTTMKIIPFNRLTIGEGQQHHL

>d1fzcb1 d.171.1.1 (B:200-458) Fibrinogen C-terminal domains {Human (Homo sapiens), beta}

SCNIPVVSGKECEEIIRKGGETSEMYLIQPDSSVKPYRVYCDMNTENGGWTVIQNRQDGSVDFGRKWDPYKQGFGNVATNTDGKNYCGLPGEYWLGNDKISQLTRMGPTELLIEMEDWKGDKVKAHYGGFTVQNEANKYQISVNKYRGTAGNALMDGASQLMGENRTMTIHNGMFFSTYDRDNDGWLTSDPRKQCSKEDGGGWWYNRCHAANPNGRYYWGGQYTWDMAKHGTDDGVVWMNWKGSWYSMRKMSMKIRPFF

>d1fzda\_ d.171.1.1 (A:) Fibrinogen C-terminal domains {Human (Homo sapiens), fibrinogen-420, alpha-E}

GGWLLIQQRMDGSLNFNRTWQDYKRGFGSLNDEGEGEFWLGNDYLHLLTQRGSVLRVELEDWAGNEAYAEYHFRVGSEAEGYALQVSSYEGTAGDALIEGSVEEGAEYTSHNNMQFSTFDRDADQWEENCAEVYGGGWWYNNCQAANLNGIYYPGGSYDPRNNSPYEIENGVVWVSFRGADYSLRAVRMKIRPLVTQ

>d1jfec1 d.171.1.1 (C:142-393) Fibrinogen C-terminal domains {Chicken (Gallus gallus), gamma}

TAEIQETTGRDCQDIANKGARKSGLYFIKPQKAKQSFLVYCEIDTYGNGWTVLQRRLDGSEDFRRNWVQYKEGFGHLSPDDTTEFWLGNEKIHLITTQSTLPYALRIELEDWSGKKGTADYAVFKVGTEEDKYRLTYAYFIGGEAGDAFDGFNFGDDPSDKSYTYHNGMRFSTFDNDNDNFEGNCAEQDGSGWWMNRCHAGHLNGPYYIGGVYSRDTGTNSYDNGIIWATWRDRWYSMKKTTMKIIPFNRLS

>d1jfeb1 d.171.1.1 (B:200-464) Fibrinogen C-terminal domains {Chicken (Gallus gallus), beta}

SPCVASCNIPVVSGRECEDIYRKGGETSEMYIIQPDPFTTPYRVYCDMETDNGGWTLIQNRQDGSVNFGRAWDEYKRGFGNIAKSGGKKYCDTPGEYWLGNDKISQLTKIGPTKVLIEMEDWNGDKVSALYGGFTIHNEGNKYQLSVSNYKGNAGNALMEGASQLYGENRTMTIHNGMYFSTYDRDNDGWLTTDPRKQCSKEDGGGWWYNRCHAANPNGRYYWGGTYSWDMAKHGTDDGIVWMNWKGSWYSMKKMSMKIKPYFPD

>d1jc9a\_ d.171.1.1 (A:) Tachylectin 5a {Japanese horseshoe crab (Tachypleus tridentatus)}

DPTDCADILLNGYRSSGGYRIWPKSWMTVGTLNVYCDMETDGGGWTVIQRRGNYGNPSDYFYKPWKNYKLGFGNIEKDFWLGNDRIFALTNQRNYMIRFDLKDKENDTRYAIYQDFWIENEDYLYCLHIGNYSGDAGNSFGRHNGHNFSTIDKDHDTHETHCAQTYKGGWWYDRCHESNLNGLYLNGEHNSYADGIEWRAWKGYHYSLPQVEMKIRPVEF

>d1g9mg\_ d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type 1}

EVVLVNVTENFNMWKNDMVEQMHEDIISLWDQSLKPCVKLTPLCVGAGSCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNNKTFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEVVIRSVNFTDNAKTIIVQLNTSVEINCTGAGHCNISRAKWNNTLKQIASKLREQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTWFNSTWSTEGSNNTEGSDTITLPCRIKQIINMWQKVGKAMYAPPISGQIRCSSNITGLLLTRDGGNSNNESEIFRPGGGDMRDNWRSELYKYKVVKIE

>d1g9ng\_ d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type 1}

LENVTENFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVGAGSCNTSVITQACPKVSFEPIPIHYCAPAGFAILKCNDKKFNGTGPCTNVSTVQCTHGIRPVVSTQLLLNGSLAEEEIVIRSENFTNNAKTIIVQLNESVVINCTGAGHCNLSKTQWENTLEQIAIKLKEQFGNNKTIIFNPSSGGDPEIVTHSFNCGGEFFYCNSTQLFTWNDTRKLNNTGRNITLPCRIKQIINMWQEVGKAMYAPPIRGQIRCSSNITGLLLTRDGGKDTNGTEIFRPGGGDMRDNWRSELYKYKVVKIE

>d1msk\_\_ d.173.1.1 (-) Methionine synthase (activation domain) {Escherichia coli}

TPPVTLEAARDNDFAFDWQAYTPPVAHRLGVQEVEASIETLRNYIDWTPFFMTWSLAGKYPRILEDEVVGVEAQRLFKDANDMLDKLSAEKTLNPRGVVGLFPANRVGDDIEIYRDETRTHVINVSHHLRQQTEKTGFANYCLADFVAPKLSGKADYIGAFAVTGGLEEDALADAFEAQHDDYNKIMVKALADRLAEAFAEYLHERVRKVYWGYAPNENLSNEELIRENYQGIRPAPGYPACPEHTEKATIWELLEVEKHTGMKLTESFAMWPGASVSGWYFSHPDSKYYAVAQIQRDQVEDYARRKGMSVTEVERWLAPNLGYDAD

>d1jwka\_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Mouse (Mus musculus)}

QYVRIKNWGSGEILHDTLHHKATSCDFTCKSKSCLGSIMNPKSLTRGPRDKPTPLEELLPHAIEFINQYYGSFKEAKIEEHLARLEAVTKEIETTGTYQLTLDELIFATKMAWRNAPRCIGRIQWSNLQVFDARNCSTAQEMFQHICRHILYATNNGNIRSAITVFPQRSDGKHDFRLWNSQLIRYAGYQMPDGTIRGDAATLEFTQLCIDLGWKPRYGRFDVLPLVLQADGQDPEVFEIPPDLVLEVTMEHPKYEWFQELGLKWYALPAVANMLLEVGGLEFPACPFNGWYMGTEIGVRDFCDTQRYNILEEVGRRMGLETHTLASLWKDRAVTEINVAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRARGGCPADWIALVPPVSGSITPVFHQEMLNYVLSPFYYYQIEPWKTHIWQN

>d1nos\_\_ d.174.1.1 (-) Nitric oxide (NO) synthase oxygenase domain {Mouse (Mus musculus)}

NPKSLTRGPRDKPTPLEELLPHAIEFINQYYGSFKEAKIEEHLARLEAVTKEIETTGTYQLTLDELIFATKMAWRNAPRCIGRIQWSNLQVFDARNCSTAQEMFQHICRHILYATNNGNIRSAITVFPQRSDGKHDFRLWNSQLIRYAGYQMPDGTIRGDAATLEFTQLCIDLGWKPRYGRFDVLPLVLQADGQDPEVFEIPPDLVLEVTMEHPKYEWFQELGLKWYALPAVANMLLEVGGLEFPACPFNGWYMGTEIGVRDFCDTQRYNILEEVGRRMGLETHTLASLWKDRAVTEINVAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRARGGCPADWIWLVPPVSGSITPVFHQEMLNYVLSPFYYYQIEPWKTHIWQNEHHHH

>d3nosa\_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Human (Homo sapiens)}

KFPRVKNWEVGSITYDTLSAQAQQDGPCTPRRCLGSLVFPRKLQGRPSPGPPAPEQLLSQARDFINQYYSSIKRSGSQAHEQRLQEVEAEVAATGTYQLRESELVFGAKQAWRNAPRCVGRIQWGKLQVFDARDCRSAQEMFTYICNHIKYATNRGNLRSAITVFPQRCPGRGDFRIWNSQLVRYAGYRQQDGSVRGDPANVEITELCIQHGWTPGNGRFDVLPLLLQAPDEPPELFLLPPELVLEVPLEHPTLEWFAALGLRWYALPAVSNMLLEIGGLEFPAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMDLDTRTTSSLWKDKAAVEINVAVLHSYQLAKVTIVDHHAATASFMKHLENEQKARGGCPADWAWIVPPISGSLTPVFHQEMVNYFLSPAFRYQPDPW

>d4nosa\_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Human (Homo sapiens)}

RHVRIKNWGSGMTFQDTLHHKAKGILTCRSKSCLGSIMTPKSLTRGPRDKPTPPDELLPQAIEFVNQYYGSFKEAKIEEHLARVEAVTKEIETTGTYQLTGDELIFATKQAWRNAPRCIGRIQWSNLQVFDARSCSTAREMFEHICRHVRYSTNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGSIRGDPANVEFTQLCIDLGWKPKYGRFDVVPLVLQANGRDPELFEIPPDLVLEVAMEHPKYEWFRELELKWYALPAVANMLLEVGGLEFPGCPFNGWYMGTEIGVRDFCDVQRYNILEEVGRRMGLETHKLASLWKDQAVVEINIAVIHSFQKQNVTIMDHHSAAESFMKYMQNEYRSRGGCPADWIWLVPPMSGSITPVFHQEMLNYVLSPFYYYQVEAWKTHVWQD

>d1d0ca\_ d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Cow (Bos taurus)}

GPKFPRVKNWELGSITYDTLCAQSQQDGPCTPRRCLGSLVLPRKLQTRPSPGPPPAEQLLSQARDFINQYYSSIKRSGSQAHEERLQEVEAEVASTGTYHLRESELVFGAKQAWRNAPRCVGRIQWGKLQVFDARDCSSAQEMFTYICNHIKYATNRGNLRSAITVFPQRAPGRGDFRIWNSQLVRYAGYRQQDGSVRGDPANVEITELCIQHGWTPGNGRFDVLPLLLQAPDEAPELFVLPPELVLEVPLEHPTLEWFAALGLRWYALPAVSNMLLEIGGLEFSAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMDLDTRTTSSLWKDKAAVEINLAVLHSFQLAKVTIVDHHAATVSFMKHLDNEQKARGGCPADWAWIVPPISGSLTPVFHQEMVNYILSPAFRYQPDPW

>d1k25a3 d.175.1.1 (A:67-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}

QITRTVPAKRGTIYDRNGVPIAEDATSYNVYAVIDKKYKSATGKILYVEDAQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGSKGNGITYANMMAIKKELETAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRVGNIVPGTELVSQQTVDGKDVYT

>d1qmea3 d.175.1.1 (A:71-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}

TVPAKRGTIYDRNGVPIAEDATSYNVYAVIDENYKSATGKILYVEKTQFNKVAEVFHKYLDMEESYVREQLSQPNLKQVSFGAKGNGITYANMMSIKKELEAAEVKGIDFTTSPNRSYPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVYT

>d1soxa3 d.176.1.1 (A:94-343) Sulfite oxidase, middle catalytic domain {Chicken (Gallus gallus)}

QDPFAGDPPRHPGLRVNSQKPFNAEPPAELLAERFLTPNELFFTRNHLPVPAVEPSSYRLRVDGPGGGTLSLSLAELRSRFPKHEVTATLQCAGNRRSEMSRVRPVKGLPWDIGAISTARWGGARLRDVLLHAGFPEELQGEWHVCFEGLDADPGGAPYGASIPYGRALSPAADVLLAYEMNGTELPRDHGFPVRVVVPGVVGARSVKWLRRVAVSPDESPSHWQQNDYKGFSPCVDWDTVDYRTAPAIQ

>d1hyoa2 d.177.1.1 (A:119-416) Fumarylacetoacetate hydrolase, FAH, C-terminal domain {Mouse (Mus musculus)}

ATIGDYTDFYSSRQHATNVGIMFRGKENALLPNWLHLPVGYHGRASSIVVSGTPIRRPMGQMRPDNSKPPVYGACRLLDMELEMAFFVGPGNRFGEPIPISKAHEHIFGMVLMNDWSARDIQQWEYVPLGPFLGKSFGTTISPWVVPMDALMPFVVPNPKQDPKPLPYLCHSQPYTFDINLSVSLKGEGMSQAATICRSNFKHMYWTMLQQLTHHSVNGCNLRPGDLLASGTISGSDPESFGSMLELSWKGTKAIDVGQGQTRTFLLDGDEVIITGHCQGDGYRVGFGQCAGKVLPAL

>d1i7oa1 d.177.1.1 (A:1-213) 4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase HpcE {Escherichia coli}

MKGTIFAVALNHRSQLDAWQEAFQQSPYKAPPKTAVWFIKPRNTVIGCGEPIPFPQGEKVLSGATVALIVGKTATKVREEDAAEYIAGYALANDVSLPEESFYRPAIKAKCRDGFCPIGETVALSNVDNLTIYTEINGRPADHWNTADLQRNAAQLLSALSEFATLNPGDAILLGTPQARVEIQPGDRVRVLAEGFPPLENPVVDEREVTTRK

>d1i7oa2 d.177.1.1 (A:214-429) 4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase HpcE {Escherichia coli}

SFPTLPHPHGTLFALGLNYADHASELEFKPPEEPLVFLKAPNTLTGDNQTSVRPNNIEYMHYEAELVVVIGKQARNVSEADAMDYVAGYTVCNDYAIRDYLENYYRPNLRVKSRDGLTPMLSTIVPKEAIPDPHNLTLRTFVNGELRQQGTTADLIFSVPFLIAYLSEFMTLNPGDMIATGTPKGLSDVVPGDEVVVEVEGVGRLVNRIVSEETAK

>d1toh\_\_ d.178.1.1 (-) Tyrosine hydroxylase {Rat (Rattus norvegicus)}

KVPWFPRKVSELDKCHHLVTKFDPDLDLDHPGFSDQVYRQRRKLIAEIAFQYKHGEPIPHVEYTAEEIATWKEVYVTLKGLYATHACREHLEGFQLLERYCGYREDSIPQLEDVSRFLKERTGFQLRPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMLADRTFAQFSQDIGLASLGASDEEIEKLSTVYWFTVEFGLCKQNGELKAYGAGLLSSYGELLHSLSEEPEVRAFDPDTAAVQPYQDQTYQPVYFVSESFNDAKDKLRNYASRIQRPFSVKFDPYTLAIDVLDSPHTIQRSLEGVQDELHTLAHALSAIS

>d3pah\_\_ d.178.1.1 (-) Phenylalanine hydroxylase {Human (Homo sapiens)}

TVPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYMEEEKKTWGTVFKTLKSLYKTHACYEYNHIFPLLEKYCGFHEDNIPQLEDVSQFLQTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIGLASLGAPDEYIEKLATIYWFTVEFGLCKQGDSIKAYGAGLLSSFGELQYCLSEKPKLLPLELEKTAIQNYTVTEFQPLYYVAESFNDAKEKVRNFAATIPRPFSVRYDPYTQRIEVL

>d1phza2 d.178.1.1 (A:116-427) Phenylalanine hydroxylase {Rat (Rattus norvegicus)}

NTVPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYTEEEKQTWGTVFRTLKALYKTHACYEHNHIFPLLEKYCGFREDNIPQLEDVSQFLQTCTGFRLRPVAGLLSSRDFLGGLAFRVFHCTQYIRHGSKPMYTPEPDICHELLGHVPLFSDRSFAQFSQEIGLASLGAPDEYIEKLATIYWFTVEFGLCKEGDSIKAYGAGLLSSFGELQYCLSDKPKLLPLELEKTACQEYSVTEFQPLYYVAESFSDAKEKVRTFAATIPRPFSVRYDPYTQRVEVLDNT

>d1dqaa4 d.179.1.1 (A:462-586,A:704-870) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

LSDAEIIQLVNAKHIPAYKLETLIETHERGVSIRRQLLSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRGCRAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNAHAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALAAGHLVKSHMIHN

>d1hw8a2 d.179.1.1 (A:441-586,A:704-861) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

EPRPNEECLQILGNAEKGAKFLSDAEIIQLVNAKHIPAYKLETLIETHERGVSIRRQLLSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRGCRAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNAHAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALAAGH

>d1hw8c2 d.179.1.1 (C:488-586,C:704-860) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

HERGVSIRRQLLSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRGCRAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNAHAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALAAG

>d1qaxa2 d.179.1.1 (A:4-110,A:221-428) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLLANAGALPMDIANGMIENVIGTFELPYAVASNFQINGRDVLVPLVVEEPSIVAAASYMAKLARANGGFTTSSSAPXRLARAQVRITPQQLETAEFSGEAVIEGILDAYAFAAVDPYRAATHNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGSLTTWEKDNNGHLVGTLEMPMPVGLVGGATKTHPLAQLSLRILGVKTAQALAEIAVAVGLAQNLGAMRALATEGIQRGHMALHARNIAVVAGARGDEVDWVARQLVEYHDVRADRAVALLKQKRGQ

>d1qaxb2 d.179.1.1 (B:504-610,B:721-875) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLLANAGALPMDIANGMIENVIGTFELPYAVASNFQINGRDVLVPLVVEEPSIVAAASYMAKLARANGGFTTSSSAPXRLARAQVRITPQQLETAEFSGEAVIEGILDAYAFAAVDPYRAATHNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGSLTTWEKDNNGHLVGTLEMPMPVGLVGGATKTHPLAQLSLRILGVKTAQALAEIAVAVGLAQNLGAMRALATE

>d1k92a2 d.210.1.1 (A:189-444) Argininosuccinate synthetase, C-terminal domain {Escherichia coli}

AYSTDSNMLGATHEAKDLEYLNSSVKIVNPIMGVKFWDESVKIPAEEVTVRFEQGHPVALNGKTFSDDVEMMLEANRIGGRHGLGMSDQIENRIIEAKSRGIYEAPGMALLHIAYERLLTGIHNEDTIEQYHAHGRQLGRLLYQGRWFDSQALMLRDSLQRWVASQITGEVTLELRRGNDYSILNTVSENLTYKPERLTMEKGDSVFSPDDRIGQLTMRNLDITDTREKLFGYAKTGLLSSSAASGVPQVENLENK

>d16vpa\_ d.180.1.1 (A:) Conserved core of transcriptional regulatory protein vp16 {Herpes simplex virus type 1}

SRMPSPPMPVPPAALFNRLLDDLGFSAGPALCTMLDTWNEDLFSALPTNADLYRECKFLSTLPSDVVEWGDAYVPERTQIDIRAHGDVAFPTLPATRDGLGLYYEALSRFFHAELRAREESYRTVLANFCSALYRYLRASVRQLHRQAHMRGRDRDLGEMLRATIADRYYRETARLARVLFLHLYLFLTREILWAAYAEQMMRPDLFDCLCCDLESWRQLAGLFQPFMFVNGALTVRGVPIEARRLRELNHIREHLNLPLVRSAATEEPGAPLTTPPTLHGNQARASGYFMVLIRAKLDSYSSFTTSPSEAVMREHAYSRAPTKNNYGSTIEGLLDLPDDDAPEEAGLAAPRLSFL

>d1bdfa2 d.181.1.1 (A:53-178) RNA polymerase alpha subunit {Escherichia coli}

GCAVTEVEIDGVLHEYSTKEGVQEDILEILLNLKGLAVRVQGKDEVILTLNKSGIGPVTAADITHDGDVEIVKPQHVICHLTDENASISMRIKVQRGRGYVPASTRIHSEEDERPIGRLLVDACYS

>d1i6va2 d.181.1.1 (A:50-172) RNA polymerase alpha subunit {Thermus aquaticus}

GTAVTSVYIEDVLHEFSTIPGVKEDVVEIILNLKELVVRFLDPKMASTTLILRAEGPKEVRAVDFTPSADVEIMNPDLHIATLEEGGKLYMEVRVDRGVGYVPAERHGIKDRINAIPVDAIFS

>d1i50c2 d.181.1.1 (C:42-172) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

PTLAIDSVEVETNTTVLADEFIAHRLGLIPLQSMDIEQLEYSRDCFCEDHCDKCSVVLTLQAFGESESTTNVYSKDLVIVSNLMGRNIGHPIIQDKEGNGVLICKLRKGQELKLTCVAKKGIAKEHAKWGP

>d1el6a\_ d.182.1.1 (A:) Baseplate structural protein gp11 {Bacteriophage T4}

SRLADFLGFRPKTGDIDVMNRQSVGSVTISQLAKGFYEPNIESAINDVHNFSIKDVGTIITNKTGVSPEGVSQTDYWAFSGTVTDDSLPPGSPITVLVFGLPVSATTGMTAIEFVAKVRVALQEAIASFTAINSYKDHPTDGSKLEVTYLDNQKHVLSTYSTYGITISQEIISESKPGYGTWNLLGAQTVTLDNQQTPTVFYHFERTA

>d1fh6a\_ d.183.1.1 (A:) Major capsid protein gp5 {Bacteriophage HK97}

SLGSDADSAGSLIQPMQIPGIIMPGLRRLTIRDLLAQGRTSSNALEYVREEVFTNNADVVAEKALKPESDITFSKQTANVKTIAHWVQASRQVMDDAPMLQSYINNRLMYGLALKEEGQLLNGDGTGDNLEGLNKVATAYDTSLNATGDTRADIIAHAIYQVTESEFSASGIVLNPRDWHNIALLKDNEGRYIFGGPQAFTSNIMWGLPVVPTKAQAAGTFTVGGFDMASQVWDRMDATVEVSREDRDNFVKNMLTILCEERLALAHYRPTAIIKGTFSS

>d1fn9a\_ d.196.1.1 (A:) Outer capsid protein sigma 3 {Reovirus}

MEVCLPNGHQVVDLINNAFEGRVSIYSAQEGWDKTISAQPDMMVCGGAVVCMHCLGVVGSLQRKLKHLPHHRCNQQIRHQDYVDVQFADRVTAHWKRGMLSFVAQMHEMMNDVSPDDLDRVRTEGGSLVELNWLQVDPNSMFRSIHSSWTDPLQVVDDLDTKLDQYWTALNLMIDSSDLIPNFMMRDPSHAFNGVKLGGDARQTQFSRTFDSRSSLEWGVMVYDYSELEHDPSKGRAYRKELVTPARDFGHFGLSHYSRATTPILGKMPAVFSGMLTGNCKMYPFIKGTAKLKTVRKLVEAVNHAWGVEKIRYALGPGGMTGWYNRTMQQAPIVLTPAALTMFPDTIKFGDLNYPVMIGDPMILG

>d1qgwa\_ d.184.1.1 (A:) Phycoerythrin 545 alpha-subunits {Cryptophyte (Rhodomonas sp.), cs24}

AMDKSAKAPQITIFDHRGCSRAPKESTGGKAGGQDDEMMVKVASTKVTVSESDAAKKLQEFITFEKGIDGPFTSKN

>d1qgwb\_ d.184.1.1 (B:) Phycoerythrin 545 alpha-subunits {Cryptophyte (Rhodomonas sp.), cs24}

AMDKSAKAPVITIFDHRGCSRAPKEYTGAKAGGKDDEMMVKAQSVKIEVSTGTAEGVLATSLAKMTK

>d1jyoe\_ d.184.1.2 (E:) Virulence effector SptP domain {Salmonella typhimurium}

DKAYVAPEKFSSKVLTWLGKMPLFKNTEVVQKHTENIRVQDQKILQTFLHALTEKYGETAVNDALLMSRINMNKPLTQRLAVQITECVKAADEGFINLIKSK

>g1hle.1 e.1.1.1 (A:,B:) Elastase inhibitor {Horse (Equus caballus)}

MEQLSTANTHFAVDLFRALNESDPTGNIFISPLSISSALAMIFLGTRGNTAAQVSKALYFDTVEDIHSRFQSLNADINKPGAPYILKLANRLYGEKTYNFLADFLASTQKMYGAELASVDFQQAPEDARKEINEWVKGQTEGKIPELLVKGMVDNMTKLVLVNAIYFKGNWQQKFMKEATRDAPFRLNKKDTKTVKMMYQKKKFPYNYIEDLKCRVLELPYQGKELSMIILLPDDIEDESTGLEKIEKQLTLDKLREWTKPENLYLAEVNVHLPRFKLEESYDLTSHLARLGVQDLFNRGKADLSGMSGARDLFVSKIIHKSFVDLNEEGTEAAAATAGTILLAXEENFNADHPFIFFIRHNPSANILFLGRFSSP

>d1ovaa\_ e.1.1.1 (A:) Ovalbumin {Hen (Gallus gallus)}

GSIGAASMEFCFDVFKELKVHHANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRFDKLPGFGDSIEAQCGTSVNVHSSLRDILNQITKPNDVYSFSLASRLYAEERYPILPEYLQCVKELYRGGLEPINFQTAADQARELINSWVESQTNGIIRNVLQPSSVDSQTAMVLVNAIVFKGLWEKAFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPFASGTMSMLVLLPDEVSGLEQLESIINFEKLTEWTSSNVMEERKIKVYLPRMKMEEKYNLTSVLMAMGITDVFSSSANLSGISSAESLKISQAVHAAHAEINEAGREVVGSAEAGVDAASVSEEFRADHPFLFCIKHIATNAVLFFGRCVSP

>g1as4.1 e.1.1.1 (A:,B:) Antichymotrypsin, alpha-1 {Human (Homo sapiens)}

GLASANVDFAFSLYKQLVLKAPDKNVIFSPLSISTALAFLSLGAHNTTLTEILKGLKFNLTETSEAEIHQSFQHLLRTLNQSSDELQLSMGNAMFVKEQLSLLDRFTEDAKRLYGSEAFATDFQDSAAAKKLINDYVKNGTRGKITDLIKDLDSQTMMVLVNYIFFKAKWEMPFDPQDTHQSRFYLSKKKWVMVPMMSLHHLTIPYFRDEELSCTVVELKYTGNASALFILPDQDKMEEVEAMLLPETLKRWRDSLEFREIGELYLPKFSISRDYNLNDILLQLGIEEAFTSKADLSGITGARNLAVSQVVHKAVLDVFEEGTEASRATAVKITLLXGTIVRFNRPFLMIIVPTDTQNIFFMSKVTNPKQ

>d1qlpa\_ e.1.1.1 (A:) Antitrypsin, alpha-1 {Human (Homo sapiens)}

FNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK

>d1atta\_ e.1.1.1 (A:) Antithrombin {Cow (Bos taurus)}

VEDVCTAKPRDIPVNPMCIYRATEGQGSEQKIPGATNRRVWELSKANSHFATAFYQHLADSKNNNDNIFLSPLSISTAFAMTKLGACNNTLTQLMEVFKFDTISEKTSDQIHFFFAKLNCRLYRKANKSSELVSANRLFGDKSITFNETYQDISEVVYGAKLQPLDFKGNAEQSRLTINQWISNKTEGRITDVIPPQAINEFTVLVLVNTIYFKGLWKSKFSPENTRKELFYKADGESCSVLMMYQESKFRYRRVAESTQVLELPFKGDDITMVLILPKLEKTLAKVEQELTPDMLQEWLDELTETLLVVHMPRFRIEDSFSVKEQLQDMGLEDLFSPEKSRLPGIVAEGRSDLYVSDAFHKAFLEVNEEGSEAAASTVISIAGRSLRVTFKANRPFLVLIREVALNTIIFMGRVANPCVD

>d1e05i\_ e.1.1.1 (I:) Antithrombin {Human (Homo sapiens)}

SPVDICTAKPRDIPMNPMCIYRSPEKKATEDEGSEQKIPEATNRRVWELSKANSRFATTFYQHLADSKNDNDNIFLSPLSISTAFAMTKLGACNDTLQQLMEVFKFDTISEKTSDQIHFFFAKLNCRLYRKANKSSKLVSANRLFGDKSLTFNETYQDISELVYGAKLQPLDFKENAEQSRAAINKWVSNKTEGRITDVIPSEAINELTVLVLVNTIYFKGLWKSKFSPENTRKELFYKADGESCSASMMYQEGKFRYRRVAEGTQVLELPFKGDDITMVLILPKPEKSLAKVEKELTPEVLQEWLDELEEMMLVVHMPRFRIEDGFSLKEQLQDMGLVDLFSPEKSKLPGIVAEGRDDLYVSDAFHKAFLEVNEEGSEAAASTAVVIAGRSLNPNRVTFKANRPFLVFIREVPLNTIIFMGRVANPCV

>d1a7ca\_ e.1.1.1 (A:) Plasminogen activator inhibitor-1 {Human (Homo sapiens)}

HHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMLQLTTGGETQQQIQAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFPDSSTHRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVKIEVNESGTVESSSTAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP

>d1by7a\_ e.1.1.1 (A:) Plasminogen activator inhibitor-2 {Human (Homo sapiens)}

EDLCVANTLFALNLFKHLAKASPTQNLFLSPWSISSTMAMVYMGSRGSTEDQMAKVLQFNEVGAAADKIHSSFRSLSSAINASTGNYLLESVNKLFGEKSASFREEYIRLCQKYYSSEPQAVDFLECAEEARKKINSWVKTQTKGKIPNLLPEGSVDGDTRMVLVNAVYFKGKWKTPFEKKLNGLYPFRVNSAQRTPVQMMYLREKLNIGYIEDLKAQILELPYAGDVSMFLLLPDEIADVSTGLELLESEITYDKLNKWTSKDKMAEDEVEVYIPQFKLEEHYELRSILRSMGMEDAFNKGRANFSGMSERNDLFLSEVFHQAMVDVNEEGTEAAAGTGGVMTGRTGHGGPQFVADHPFLFLIMHKITNCILFFGRFSSP

>g1jjo.1 e.1.1.1 (A:,C:,E:) Neuroserpin {Mouse (Mus musculus)}

TITEWSVNMYNHLRGTGEDENILFSPLSIALAMGMMELGAXENQYVMKLANSLFVQNGFHVNEEFLQMLKMYFNAEVNHVDFSQNVAVANSINKWVENYTNSLLKDLVSPEDFDGVTNLALINAVYFKGNWKSQFRPENTRTFSFTKDDESEVQIPMMYQQGEFYYGEFSDGSNEAGGIYQVLEIPYEGDEISMMLALSRQEVPLATLEPLLKAQLIEEWANSVKKQKVEVYLPRFTVEQEIDLKDILKALGVTEIFIKDANLTAMSDKKELFLSKAVHKSCIEVNEEGSEAAAASGMIAISXYPQVIVDHPFLYLIRNRKSGIILFMGRVMNPHH

>d1sek\_\_ e.1.1.1 (-) Serpin K {Tobacco hawkmoth (Manduca sexta)}

GETDLQKILRESNDQFTAQMFSEVVKANPGQNVVLSAFSVLPPLGQLALASVGESHDELLRALALPNDNVTKDVFADLNRGVRAVKGVDLKMASKIYVAKGLELNDDFAAVSRDVFGSEVQNVDFVKSVEAAGAINKWVEDQTNNRIKNLVDPDALDETTRSVLVNAIYFKGSWKDKFNKERTMDRDFHVSKDKTIKVPTMIGKKDVRYADVPELDAKMIEMSYEGDQASMIIILPNQVDGITALEQKLKDPKALSRAEERLYNTEVEIYLPKFKIETTTDLKEVLSNMNIKKLFTPGAARLENLLKTKESLYVDAAIQKAFIEVNEEGAEAAAANAFKITTYSFHFVPKVEINKPFFFSLKYNRNSMFSGVCVQP

>d1k9oi\_ e.1.1.1 (I:) Alaserpin (serpin 1) {Tobacco hornworm (Manduca sexta)}

GETDLQKILRESNDQFTAQMFSEVVKANPGQNVVLSAFSVLPPLGQLALASVGESHDELLRALALPNDNVTKDVFADLNRGVRAVKGVDLKMASKIYVAKGLELNDDFAAVSRDVFGSEVQNVDFVKSVEAAGAINKWVEDQTNNRIKNLVDPDALDETTRSVLVNAIYFKGSWKDKFVKERTMDRDFHVSKDKTIKVPTMIGKKDVRYADVPELDAKMIEMSYEGDQASMIIILPNQVDGITALEQKLKDPKALSRAEERLYNTEVEITLPKFKIETTTDLKEVLSNMNIKKLFTPGAARLENLLKTKESLTVDAAIQKAFIEVNEEGAEAAAANAFGIVPKSLILYPEVHIDRPFYFELKIDGIPMFNGKVIEP

>g1f0c.1 e.1.1.1 (A:,B:) Viral serpin crmA (cytokine response modifier protein) {Cowpox virus}

MDIFREIASSMKGENVFISPPSISSVLTILYYGANGSTAEQLSKYVEKEADKNKDDISFKSMNKVYGRYSAVFKDSFLRKIGDNFQTVDFTDCRTVDAINKCVDIFTEGKINPLLDEPLSPDTCLLAISAVYFKAKWLMPFEKEFTSDYPFYVSPTEMVDVSMMSMYGEAFNHASVKESFGNFSIIELPYVGDTSMVVILPDNIDGLESIEQNLTDTNFKKWCDSMDAMFIDVHIPKFKVTGSYNLVDALVKLGLTEVFGSTGDYSNMCNSDVSVDAMIHKTYIDVNEEYTEAAAATCALVADCAXSTVTNEFCADHPFIYVIRHVDGKILFVGRYCSPTTN

>d1imva\_ e.1.1.1 (A:) Rigment epithelium-derived factor, PEDF {Human (Homo sapiens)}

TGALVEEEDPFFKVPVNKLAAAVSNFGYDLYRVRSSMSPTTNVLLSPLSVATALSALSLGADERTESIIHRALYYDLISSPDIHGTYKELLDTVTAPQKNLKSASRIVFEKKLRIKSSFVAPLEKSYGTRPRVLTGNPRLDLQEINNWVQAQMKGKLARSTKEIPDEISILLLGVAHFKGQWVTKFDSRKTSLEDFYLDEERTVRVPMMSDPKAVLRYGLDSDLSCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTSEFIHDIDRELKTVQAVLTVPKLKLSYEGEVTKSLQEMKLQSLFDSPDFSKITGKPIKLTQVEHRAGFEWNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDTDTGALLFIGKILDPRGP

>d1ecra\_ e.2.1.1 (A:) Replication terminator protein (Tus) {Escherichia coli}

DLVDRLNTTFRQMEQELAIFAAHLEQHKLLVARVFSLPEVKKEDEHNPLNRIEVKQHLGNDAQSLALRHFRHLFIQQQSENRSSKAAVRLPGVLCYQVDNLSQAALVSHIQHINKLKTTFEHIVTVESELPTAARFEWVHRHLPGLITLNAYRTLTVLHDPATLRFGWANKHIIKNLHRDEVLAQLEKSLKSPRSVAPWTREEWQRKLEREYQDIAALPQNAKLKIKRPVKVQPIARVWYKGDQKQVQHACPTPLIALINRDNGAGVPDVGELLNYDADNVQHRYKPQAQPLRLIIPRLHLYVAD

>d1es5a\_ e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., K15}

KPTIAAVGGYAMNNGTGTTLYTKAADTRRSTGSTTKIMTAKVVLAQSNLNLDAKVTIQKAYSDYVVANNASQAHLIVGDKVTVRQLLYGLMLPSGCDAAYALADKYGSGSTRAARVKSFIGKMNTAATNLGLHNTHFDSFDGIGNGANYSTPRDLTKIASSAMKNSTFRTVVKTKAYTAKTVTKTGSIRTMDTWKNTNGLLSSYSGAIGVKTGAGPEAKYCLVFAATRGGKTVIGTVLASTSIPARESDATKIMNYGFAL

>d1hvba\_ e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., R61}

DLPAPDDTGLQAVLHTALSQGAPGAMVRVDDNGTIHQLSEGVADRATGRAITTTDRFRVGSVTKSFSAVVLLQLVDEGKLDLDASVNTYLPGLLPDDRITVRQVMSHRSGLYDYTNDMFAQTVPGFESVRNKVFSYQDLITLSLKHGVTNAPGAAYSYSNTNFVVAGMLIEKLTGHSVATEYQNRIFTPLNLTDTFYVHPDTVIPGTHANGYLTPDEAGGALVDSTEQTVSWAQSAGAVISSTQDLDTFFSALMSGQLMSAAQLAQMQQWTTVNSTQGYGLGLRRRDLSCGISVYGHTGTVQGYYTYAFASKDGKRSVTALANTSNNVNVLNTMARTLESAFCGKP

>d1ci9a\_ e.3.1.1 (A:) Esterase EstB {Burkholderia gladioli}

AASLAARLDAVFDQALRERRLVGAVAIVARHGEILYRRAQGLADREAGRPMREDTLFRLASVTKPIVALAVLRLVARGELALDAPVTRWLPEFRPRLADGSEPLVTIHHLLTHTSGLGYWLLEGAGSVYDRLGISDGIDLRDFDLDENLRRLASAPLSFAPGSGWQYSLALDVLGAVVERATGQPLAAAVDALVAQPLGMRDCGFVSAEPERFAVPYHDGQPEPVRMRDGIEVPLPEGHGAAVRFAPSRVFEPGAYPSGGAGMYGSADDVLRALEAIRANPGFLPETLADAARRDQAGVGAETRGPGWGFGYLSAVLDDPAAAGTPQHAGTLQWGGVYGHSWFVDRALGLSVLLLTNTAYEGMSGPLTIALRDAVYA

>d1btl\_\_ e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TEM-1}

HPETLVKVKDAEDQLGARVGYIELDLNSGKILESFRPEERFPMMSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVEYSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTTMPVAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPLLRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIAEIGASLIKHW

>d1bza\_\_ e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TOHO-1}

SVQQQLEALEKSSGGRLGVALINTADNSQILYRADERFAMCSTSKVMAAAAVLKQSESDKHLLNQRVEIKKSDLVNYNPIAEKHVNGTMTLAELGAAALQYSDNTAMNKLIAHLGGPDKVTAFARSLGDETFRLDRTAPTLNTAIPGDPRDTTTPLAMAQTLKNLTLGKALAETQRAQLVTWLKGNTTGSASIRAGLPKSWVVGDKTGSGDYGTTNDIAVIWPENHAPLVLVTYFTQPEQKAERRRDILAAAAKIVT

>d1g56a\_ e.3.1.1 (A:) beta-Lactamase, class A {Klebsiella pneumoniae, SHV-1}

SPQPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERFPMMSTFKVVLCGAVLARVDAGDEQLERKIHYRQQDLVDYSPVSEKHLADGMTVGELCAAAITMSDNSAANLLLATVGGPAGLTAFLRQIGDNVTRLDRWETELNEALPGDARDTTTPASMAATLRKLLTSQRLSARSQRQLLQWMVDDRVAGPLIRSVLPAGWFIADKTGAGERGARGIVALLGPNNKAERIVVIYLRDTPASMAERNQQIAGIGAALIEHWQR

>d1g6aa\_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PSE-4 carbenicillinase}

SKFQQVEQDVKAIEVSLSARIGVSVLDTQNGEYWDYNGNQRFPLTSTFKTIACAKLLYDAEQGKVNPNSTVEIKKADLVTYSPVIEKQVGQAITLDDACFATMTTSDNTAANIILSAVGGPKGVTDFLRQIGDKETRLDRIEPDLNEGKLGDLRDTTTPKAIASTLNKFLFGSALSEMNQKKLESWMVNNQVTGNLLRSVLPAGWNIADKSGAGGFGARSITAVVWSEHQAPIIVSIYLAQTQASMEERNDAIVKIGHSIFDVYTS

>d1alq\_\_ e.3.1.1 (-) beta-Lactamase, class A {Staphylococcus aureus}

SEPIVLVIFTNKDNKSDKPNDKLISETAKSVMKEFAAGSKNAAKELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYNKLNKKVHINKDDIVAYSPILEKYVGKDITLKALIEASMTYSDNTANNKIIKEIGGIKKVKQRLKELGDKVTNPVRYEIELNYYSPKSKKDTSTPAAFGKTLNKLIANGKLSKENKKFLLDLMLNNKSGDTLIKDGVPKDYKVADKSGQAITYASRNDVAFVYPK

>d1ghpa\_ e.3.1.1 (A:) beta-Lactamase, class A {Staphylococcus aureus}

KELNDLEKKYNAHIGVYALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYNKLNKKVHINKDDIVAYSPILEKYVGKDITLKALIEASMTYSDNTANNKIIKEIGGIKKVKQRLKELGDKVTNPVRYDIELQYYSPKSKKDTSTPAAFGKTLNKLIANGKLSKENKKFLLDLMLNNKSGDTLIKDGVPKDYKVADKSGQAITYASRNDVAFVYPKGQSEPIVLVIFTNKDNKSDKPNDKLISETAKSVMKEF

>d4blma\_ e.3.1.1 (A:) beta-Lactamase, class A {Bacillus licheniformis}

DDFAKLEEQFDAKLGIFALDTGTNRTVAYRPDERFAFASTIKALTVGVLLQQKSIEDLNQRITYTRDDLVNYNPITEKHVDTGMTLKELADASLRYSDNAAQNLILKQIGGPESLKKELRKIGDEVTNPERFEPELNEVNPGETQDTSTARALVTSLRAFALEDKLPSEKRELLIDWMKRNTTGDALIRAGVPDGWEVADKTGAASYGTRNDIAIIWPPKGDPVVLAVLSSRDKKDAKYDDKLIAEATKVVMKALN

>d1buea\_ e.3.1.1 (A:) beta-Lactamase, class A {Enterobacter cloacae, NMC-A carbapenemase}

NTKGIDEIKNLETDFNGRIGVYALDTGSGKSFSYRANERFPLCSSFKGFLAAAVLKGSQDNRLNLNQIVNYNTRSLEFHSPITTKYKDNGMSLGDMAAAALQYSDNGATNIILERYIGGPEGMTKFMRSIGDEDFRLDRWELDLNTAIPGDERDTSTPAAVAKSLKTLALGNILSEHEKETYQTWLKGNTTGAARIRASVPSDWVVGDKTGSCGAYGTANDYAVVWPKNRAPLIISVYTTKNEKEAKHEDKVIAEASRIAIDNLK

>d1bsg\_\_ e.3.1.1 (-) beta-Lactamase, class A {Streptomyces albus G}

SDAERRLAGLERASGARLGVYAYDTGSGRTVAYRADELFPMCSVFKTLSSAAVLRDLDRNGEFLSRRILYTQDDVEQADGAPETGKPQNLANGMTVEELCEVSITASDNCAANLMLRELGGPAAVTRFVRSLGDRVTRLDRWEPELNSAEPGRVTDTTSPRAITRTYGRLVLGDALNPRDRRLLTSWLLANTTSGDRFRAGLPDDWTLGDKTGAGRYGTNNDAGVTWPPGRAPIVLTVLTAKTEQDAARDDGLVADAARVLAETLG

>d1mfoa\_ e.3.1.1 (A:) beta-Lactamase, class A {Mycobacterium fortuitum}

APIDDQLAELERRDNVLIGLYAANLQSGRRITHRPDEMFAMCSTFKGYVAARVLQMAEHGEISLDNRVFVDADALVPNSPVTEARAGAEMTLAELCQAALQRSDNTAANLLLKTIGGPAAVTAFARSVGDERTRLDRWEVELNSAIPGDPRDTSTPAALAVGYRAILAGDALSPPQRGLLEDWMRANQTSSMRAGLPEGWTTADKTGSGDYGSTNDAGIAFGPDGQRLLLVMMTRSQAHDPKAENLRPLIGELTALVLPSLL

>d1e25a\_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PER-1}

SPLLKEQIESIVIGKKATVGVAVWGPDDLEPLLINPFEKFPMQSVFKLHLAMLVLHQVDQGKLDLNQTVIVNRAKVLQNTWAPIMKAYQGDEFSVPVQQLLQYSVSHSDNVACDLLFELVGGPAALHDYIQSMGIKETAVVANEAQMHADDQVQYQNWTSMKGAAEILKKFEQKTQLSETSQALLWKWMVETTTGPERLKGLLPAGTVVAHKTGTSQIKAGKTAATNDLGIILLPDGRPLLVAVFVKDSAESSRTNEAIIAQVAQTAYQFELKKLSAL

>d1dy6a\_ e.3.1.1 (A:) beta-Lactamase, class A {Serratia marcescens, Sme-1}

NKSDAAAKQIKKLEEDFDGRIGVFAIDTGSGNTFGYRSDERFPLCSSFKGFLAAAVLERVQQKKLDINQKVKYESRDLEYHSPITTKYKGSGMTLGDMASAALQYSDNGATNIIMERFLGGPEGMTKFMRSIGDNEFRLDRWELELNTAIPGDKRDTSTPKAVANSLNKLALGNVLNAKVKAIYQNWLKGNTTGDARIRASVPADWVVGDKTGSCGAYGTANDYAVIWPKNRAPLIVSIYTTRKSKDDKHSDKTIAEASRIAIQAID

>d1fr1a\_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Citrobacter freundii}

AAKTEQQIADIVNRTITPLMQEQAIPGMAVAIIYQGKPYYFTWGKADIANNRPVTQQTLFELGSVSKTFNGVLGGDAIARGEIKLSDPVTQYWPELTGKQWQGISLLHLATYTAGGLPLQVPDDVTDKAALLRFYQNWQPQWAPGAKRLYANSSIGLFGALAVKPSGMSYEEAMSKRVLHPLKLAHTWITVPQSEQKDYAWGYREGKPVHVSPGQLDAEAYGVKSSVIDMTRWVQANMDASQVQEKTLQQGIELAQSRYWRIGDMYQGLGWEMLNWPVKADSIISGSDSKVALAALPAVEVNPPAPAVKASWVHKTGSTGGFGSYVAFVPEKNLGIVMLANKSYPNPVRVEAAWRILEKLQ

>d1ga0a\_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Enterobacter cloacae, P99, cephalosporinase}

PVSEKQLAEVVANTVTPLMKAQSVPGMAVAVIYQGKPHYYTFGKADIAANKPVTPQTLFELGSISKTFTGVLGGDAIARGEISLDDPVTRYWPQLTGKQWQGIRMLDLATYTAGGLPLQVPDEVTDNASLLRFYQNWQPQWKPGTTRLYANASIGLFGALAVKPSGMPYEQAMTTRVLKPLKLDHTWINVPKAEEAHYAWGYRDGKAVRAVRVSPGMLDAQAYGVKTNVQDMANWVMANMAPENVADASLKQGIALAQSRYWRIGSMYQGLGWEMLNWPVEANTVVEGSDSKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIVMLANTSYPNPARVEAAYHILEALQ

>d1i5qa\_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Escherichia coli, cephalosporinase}

APQQINDIVHRTITPLIEQQKIPGMAVAVIYQGKPYYFTWGYADIAKKQPVTQQTLFELGSVSKTFTGVLGGDAIARGEIKLSDPTTKYWPELTAKQWNGITLLHLATYTAGGLPLQVPDEVKSSSDLLRFYQNWQPAWAPGTQRLYAASSIGLFGALAVKPSGLSFEQAMQTRVFQPLKLNHTWINVPPAEEKNYAWGYREGKAVHVSPGALDAEAYGVKSTIEDMARWVQSNLKPLDINEKTLQQGIQLAQSRYWQTGDMYQGLGWEMLDWPVNPDSIINGSDNKIALAARPVKAITPPTPAVRASWVHKTGATGGFGSYVAFIPEKELGIVMLANKNYPNPARVDAAWQILNALQ

>d1k55a\_ e.3.1.1 (A:) Class D beta-lactamase {Pseudomonas aeruginosa, OXA-10}

SITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFWLEGQLRISAVNQVEFLESLYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNMDIDNESKLPLRKSIPTKIMESEGIIG

>d1k25a4 e.3.1.1 (A:264-631) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain {Streptococcus pneumoniae}

TLSSPLQSFMETQMDAFLEKVKGKYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSELKIADATTRDWDVNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRFKFGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVSKEAASTTRNHMILVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVGSTNYIFSAVTMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKNLDKVT

>d1qmea4 e.3.1.1 (A:264-620) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain {Streptococcus pneumoniae}

TISSPLQSFMETQMDAFQEKVKGKYMTATLVSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGSTMKVMMLAAAIDNNTFPGGEVFNSSELKIADATIRDWDVNEGLTGGRMMTFSQGFAHSSNVGMTLLEQKMGDATWLDYLNRFKFGVPTRFGLTDEYAGQLPADNIVNIAQSSFGQGISVTQTQMIRAFTAIANDGVMLEPKFISAIYDPNDQTARKSQKEIVGNPVSKDAASLTRTNMVLVGTDPVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIADEKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSGIQLGEFANPILERASAMKDSLNL

>d1hd8a2 e.3.1.1 (A:3-262) Penicillin-binding protein 5, N-terminal domain {Escherichia coli}

LNIKTMIPGVPQIDAESYILIDYNSGKVLAEQNADVRRDPASLTKMMTSYVIGQAMKAGKFKETDLVTIGNDAWATGNPVFKGSSLMFLKPGMQVPVSQLIRDINLQSGNDACVAMADFAAGSQDAFVGLMNSYVNALGLKNTHFQTVHGLDADGQYSSARDMALIGQALIRDVPNEYSIYKEKEFTFNGIRQLNRNGLLWDNSLNVDGIKTGHTDKAGYNLVASATEGQMRLISAVMGGRTFKGREAESKKLLTWGFRF

>d1ei5a3 e.3.1.1 (A:3-335) D-aminopeptidase, N-terminal domain {Ochrobactrum anthropi}

KFDTSALEAFVRHIPQNYKGPGGVVAVVKDGEVVLQHAWGFADLRTRTPMTLDTRMPICSVSKQFTCAVLLDAVGEPELLDDALEAYLDKFEDERPAVRDLCNNQSGLRDYWALSVLCGADPEGVFLPAQAQSLLRRLKTTHFEPGSHYSYCNGNFRILADLIEAHTGRTLVDILSERIFAPAGMKRAELISDTALFDECTGYEGDTVRGFLPATNRIQWMGDAGICASLNDMIAWEQFIDATRDDESGLYRRLSGPQTFKDGVAAPYGFGLNLHETGGKRLTGHGGALRGWRCQRWHCADERLSTIAMFNFEGGASEVAFKLMNIALGVSSS

>d1lbea\_ e.4.1.1 (A:) ADP ribosyl cyclase {Sea hare (Aplysia californica)}

IVPTRELENVFLGRCKDYEITRYLDILPRVRSDCSALWKDFFKAFSFKNPCDLDLGSYKDFFTSAQQQLPKNKVMFWSGVYDEAHDYANTGRKYITLEDTLPGYMLNSLVWCGQRANPGFNEKVCPDFKTCPVQARESFWGMASSSYAHSAEGEVTYMVDGSNPKVPAYRPDSFFGKYELPNLTNKVTRVKVIVLHRLGEKIIEKCGAGSLLDLEKLVKAKHFAFDCVENPRAVLFLLCSDNPNARECRL

>d4blca\_ e.5.1.1 (A:) Catalase I {Cow (Bos taurus)}

NRDPASDQMKHWKEQRAAQKPDVLTTGGGNPVGDKLNSLTVGPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITRYSKAKVFEHIGKRTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDLVGNNTPIFFIRDALLFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLFSDRGIPDGHRHMDGYGSHTFKLVNADGEAVYCKFHYKTDQGIKNLSVEDAARLAHEDPDYGLRDLFNAIATGNYPSWTLYIQVMTFSEAEIFPFNPFDLTKVWPHGDYPLIPVGKLVLNRNPVNYFAEVEQLAFDPSNMPPGIEPSPDKMLQGRLFAYPDTHRHRLGPNYLQIPVNCPYRARVANYQRDGPMCMMDNQGGAPNYYPNSFSAPEHQPSALEHRTHFSGDVQRFNSANDDNVTQVRTFYLKVLNEEQRKRLCENIAGHLKDAQLFIQKKAVKNFSDVHPEYGSRIQALLDKYNE

>d1dgfa\_ e.5.1.1 (A:) Catalase I {Human (Homo sapiens)}

RDPASDQMQHWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVFTDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDLVGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSWTFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRNPVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHRLGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSFGAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNEEQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALLDKYN

>d1a4ea\_ e.5.1.1 (A:) Catalase I {Baker's yeast (Saccharomyces cerevisiae)}

DVREDRVVTNSTGNPINEPFVTQRIGEHGPLLLQDYNLIDSLAHFNRENIPQRNPHAHGSGAFGYFEVTDDITDICGSAMFSKIGKRTKCLTRFSTVGGDKGSADTVRDPRGFATKFYTEEGNLDWVYNNTPVFFIRDPSKFPHFIHTQKRNPQTNLRDADMFWDFLTTPENQVAIHQVMILFSDRGTPANYRSMHGYSGHTYKWSNKNGDWHYVQVHIKTDQGIKNLTIEEATKIAGSNPDYCQQDLFEAIQNGNYPSWTVYIQTMTERDAKKLPFSVFDLTKVWPQGQFPLRRVGKIVLNENPLNFFAQVEQAAFAPSTTVPYQEASADPVLQARLFSYADAHRYRLGPNFHQIPVNCPYASKFFNPAIRDGPMNVNGNFGSEPTYLANDKSYTYIQQDRPIQQHQEVWNGPAIPYHWATSPGDVDFVQARNLYRVLGKQPGQQKNLAYNIGIHVEGACPQIQQRVYDMFARVDKGLSEAIKKVAE

>d1e93a\_ e.5.1.1 (A:) Catalase I {Proteus mirabilis}

KKLTTAAGAPVVDNNNVITAGPRGPMLLQDVWFLEKLAHFDREVIPERRMHAKGSGAFGTFTVTHDITKYTRAKIFSEVGKKTEMFARFSTVAGERGAADAERDIRGFALKFYTEEGNWDMVGNNTPVFYLRDPLKFPDLNHIVKRDPRTNMRNMAYKWDFFSHLPESLHQLTIDMSDRGLPLSYRFVHGFGSHTYSFINKDNERFWVKFHFRCQQGIKNLMDDEAEALVGKDRESSQRDLFEAIKRGDYPRWKLQIQIMPEKEASTVPYNPFDLTKVWPHADYPLMDVGYFELNRNPDNYFSDVEQAAFSPANIVPGISFSPDKMLQGRLFSYGDAHRYRLGVNHHQIPVNAPKCPFHNYHRDGAMRVDGNSGNGITYEPNSGGVFQEQPDFKEPPLSIEGAADHWNHREDEDYFSQPRALYELLSDDEHQRMFARIAGELSQASKETQQRQIDLFTKVHPEYGAGVEKAIKVLE

>d1hbza\_ e.5.1.1 (A:) Catalase I {Micrococcus lysodeikticus}

TTPHATGSTRQNGAPAVSDRQSLTVGSEGPIVLHDTHLLETHQHFNRMNIPERRPHAKGSGAFGEFEVTEDVSKYTKALVFQPGTKTETLLRFSTVAGELGSPDTWRDVRGFALRFYTEEGNYDLVGNNTPIFFLRDPMKFTHFIRSQKRLPDSGLRDATMQWDFWTNNPESAHQVTYLMGPRGLPRTWREMNGYGSHTYLWVNAQGEKHWVKYHFISQQGVHNLSNDEATKIAGENADFHRQDLFESIAKGDHPKWDLYIQAIPYEEGKTYRFNPFDLTKTISQKDYPRIKVGTLTLNRNPKNHFAQIESAAFSPSNTVPGIGLSPDRMLLGRAFAYHDAQLYRVGAHVNQLPVNRPKNAVHNYAFEGQMWYDHTGDRSTYVPNSNGDSWSDETGPVDDGWEADGTLTREAQALRADDDDFGQAGTLVREVFSDQERDDFVETVAGALKGVRQDVQARAFEYWKNVDATIGQRIEDEVKRHEGDGIPGVEAGGEARI

>d1cf9a2 e.5.1.1 (A:27-597) Catalase II {Escherichia coli, HPII}

DSLAPEDGSHRPAAEPTPPGAQPTAPGSLKAPDTRNEKLNSLEDVRKGSENYALTTNQGVRIADDQNSLRAGSRGPTLLEDFILREKITHFDHERIPERIVHARGSAAHGYFQPYKSLSDITKADFLSDPNKITPVFVRFSTCQGGAGSADTVRDIRGFATKFYTEEGIFDLVGNNTPIFFIQDAHKFPDFVHAVKPEPHWAIPQGQSAHDTFWDYVSLQPETLHNVMWAMSDRGIPRSYRTMEGFGIHTFRLINAEGKATFVRFHWKPLAGKASLVWDEAQKLTGRDPDFHRRELWEAIEAGDFPEYELGFQLIPEEDEFKFDFDLLDPTKLIPEELVPVQRVGKMVLNRNPDNFFAENEQAAFHPGHIVPGLDFTNDPLLQGRLFSYTDTQISRLGGPNFHEIPINRPTCPYHNFQRDGMHRMGIDTNPANYEPNSINDNWPRETPPGPKRGGFESYQERVEGNKVRERSPSFGEYYSHPRLFWLSQTPFEQRHIVDGFSFELSKVVRPYIRERVVDQLAHIDLTLAQAVAKNLGIELTDDQLNITPPPDVNGLKKDPSLSLYAIPDGD

>d1buca2 e.6.1.1 (A:1-232) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}

MDFNLTDIQQDFLKLAHDFGEKKLAPTVTERDHKGIYDKELIDELLSLGITGAYFEEKYGGSGDDGGDVLSYILAVEELAKYDAGVAITLSATVSLCANPIWQFGTEAQKEKFLVPLVEGTKLGAFGLTEPNAGTDASGQQTIATKNDDGTYTLNGSKIFITNGGAADIYIVFAMTDKSKGNHGITAFILEDGTPGFTYGKKEDKMGIHTSQTMELVFQDVKVPAENMLGEE

>d1jqia2 e.6.1.1 (A:4-234) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus)}

VYQSVELPETHQMLRQTCRDFAEKELVPIAAQLDKEHLFPTSQVKKMGELGLLAMDVPEELSGAGLDYLAYSIALEEISRGCASTGVIMSVNNSLYLGPILKFGSSQQKQQWITPFTNGDKIGCFALSEPGNGSDAGAASTTAREEGDSWVLNGTKAWITNSWEASATVVFASTDRSRQNKGISAFLVPMPTPGLTLGKKEDKLGIRASSTANLIFEDCRIPKENLLGEPG

>d3mdda2 e.6.1.1 (A:11-241) Medium chain acyl-CoA dehydrogenase {Pig (Sus scrofa)}

GFSFELTEQQKEFQATARKFAREEIIPVAAEYDRTGEYPVPLLKRAWELGLMNTHIPESFGGLGLGIIDSCLITEELAYGCTGVQTAIEANTLGQVPLIIGGNYQQQKKYLGRMTEEPLMCAYCVTEPGAGSDVAGIKTKAEKKGDEYIINGQKMWITNGGKANWYFLLARSDPDPKAPASKAFTGFIVEADTPGVQIGRKEINMGQRCSDTRGIVFEDVRVPKENVLTGE

>d1egda2 e.6.1.1 (A:10-241) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens)}

LGFSFEFTEQQKEFQATARKFAREEIIPVAAEYDKTGEYPVPLIRRAWELGLMNTHIPENCGGLGLGTFDACLISEELAYGCTGVQTAIEGNSLGQMPIIIAGNDQQKKKYLGRMTEEPLMCAYCVTEPGAGSDVAGIKTKAEKKGDEYIINGQKMWITNGGKANWYFLLARSDPDPKAPANKAFTGFIVEADTPGIQIGRKELNMGQRCSDTRGIVFEDVKVPKENVLIGD

>d1ivha2 e.6.1.1 (A:6-241) Isovaleryl-coa dehydrogenase {Human (Homo sapiens)}

VDDAINGLSEEQRQLRQTMAKFLQEHLAPKAQEIDRSNEFKNLREFWKQLGNLGVLGITAPVQYGGSGLGYLEHVLVMEEISRASGAVGLSYGAHSNLCINQLVRNGNEAQKEKYLPKLISGEYIGALAMSEPNAGSDVVSMKLKAEKKGNHYILNGNKFWITNGPDADVLIVYAKTDLAAVPASRGITAFIVEKGMPGFSTSKKLDKLGMRGSNTCELIFEDCKIPAANILGHEN

>d1frpa\_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Pig (Sus scrofa)}

NIVTLTRFVMEQGRKARGTGEMTQLLNSLCTAVKAISTAVRKAGIAHLYGIAGATNVTGDQVKKLDVLSNDLVINVLKSSFATCVLVTEEDKNAIIVEPEKRGKYVVCFDPLDGSSNIDCLVSIGTIFGIYRKNSTDEPSEKDALQPGRNLVAAGYALYGSATMLVLAMVNGVNCFMLDPAIGEFILVDRNVKIKKKGSIYSINEGYAKEFDPAITEYIQRKKFPPDNSAPYGARYVGSMVADVHRTLVYGGIFMYPANKKSPKGKLRLLYECNPMAYVMEKAGGLATTGKEAVLDIVPTDIHQRAPIILGSPEDVTELLEIYQKHA

>d1ftaa\_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Human (Homo sapiens)}

DVVTLTRFVMEEGRKARGTGELTQLLNSLCTAVKAISSAVRKAGIAHLYGIAGSTNVTGDQVKKLDVLSNDLVMNMLKSSFATCVLVSEEDKHAIIVEPEKRGKYVVCFDPLDGSSNIDCLVSVGTIFGIYRKKSTDEPSEKDALQPGRNLVAAGYALYGSATMLVLAMDCGVNCFMLDPAIGEFILVDKDVKIKKKGKIYSLNEAYAKDFDPAVTEYIQRKKFPPDNSAPYGARYVGSMVADVHRTLVYGGIFLYPANKKSPNGKLRLLYECNPMAYVMEKAGGMATTGKEAVLDVIPTDIHQRAPIILGSPDDVLEFLKVYEKHS

>d1bk4a\_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Rabbit (Oryctolagus cuniculus)}

FDTDISTMTRFVMEEGRKAGGTGEMTQLLNSLCTAVKAISTAVRKAGIAHLYGIAGSTNVTGDQVKKLDVLSNDLVMNMLKSSFATCVLVSEEDKNAIIVEPEKRGKYVVCFDPLDGSSNIDCLVSIGTIFGIYRKKSTDEPSTKDALQPGRNLVAAGYALYGSATMLVLAGGSGVNSFMLDPAIGEFILVDKNVKIKKKGNIYSLNEGYAKDFDPAVTEYIQKKKFPPDNSSPYGARYVGSMVADVHRTLVYGGIFLYPANKKSPDGKLRLLYECNPMAFIMEKAGGMATTGKEAILDIVPTDIHQRAPVILGSPDDVQEFLEIYKKHAVK

>d1spia\_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Spinach (Spinacia oleracea)}

AATQTKARTRSKYEIETLTGWLLKQPMAGVIDAELTIVLSSISLACKQIASLVQRAGISNLTGIQGAVNIQGEDQKKLDVVSNEVFSSCLRSSGRTGIIASEEEDVPVAVEESYSGNYIVVFDPLDGSSNIDAAVSTGSIFGIYSPNDECIVDSDHDDESQLSAEEQRCVVNVCQPGDNLLAAGYCMYSSSVIFVLTIGKGVYAFTLDPMYGEFVLTSEKIQIPKAGKIYSFNEGNYKMWPDKLKKYMDDLKEPGESQKPYSSRYIGSLVGDFHRTLLYGGIYGYPRDAKSKNGKLRLLYECAPMSFIVEQAGGKGSDGHQRILDIQPTEIHQRVPLYIGSVEEVEKLEKYLA

>d1dcua\_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Garden pea (Pisum sativum)}

KRSGYEIITLTSWLLQQEQKGIIDAELTIVLSSISMACKQIASLVQRANISNLTGTQGAVNIQGEDQKKLDVISNEVFSNCLRSSGRTGIIASEEEDVPVAVEESYSGNYIVVFDPLDGSSNLDAAVSTGSIFGIYSPNDECLPDFGDDSDDNTLGTEEQRCIVNVCQPGSNLLAAGYCMYSSSVIFVLTIGKGVFVFTLDPLYGEFVLTQENLQIPKSGKIYSFNEGNYKLWDENLKKYIDDLKEPGPSGKPYSARYIGSLVGDFHRTLLYGGIYGYPRDKKSKNGKLRLLYECAPMSFIVEQAGGKGSDGHQRVLDIQPTEIHQRVPLYIGSTEEVEKVEKYLA

>d2hhma\_ e.7.1.1 (A:) Inositol monophosphatase {Human (Homo sapiens)}

WQECMDYAVTLARQAGEVVCEAIKNEMNVMLKSSPVDLVTATDQKVEKMLISSIKEKYPSHSFIGEESVAAGEKSILTDNPTWIIDPIDGTTNFVHRFPFVAVSIGFAVNKKIEFGVVYSCVEGKMYTARKGKGAFCNGQKLQVSQQEDITKSLLVTELGSSRTPETVRMVLSNMEKLFCIPVHGIRSVGTAAVNMCLVATGGADAYYEMGIHCWDVAGAGIIVTEAGGVLMDVTGGPFDLMSRRVIAANNRILAERIAKEIQVIPLQRDDE

>d1g0ha\_ e.7.1.1 (A:) Archaeal inositol monophosphatase/fructose-1,6-bisphosphatase {Archaeon Methanococcus jannaschii, MJ0109}

MKWDEIGKNIAKEIEKEILPYFGRKDKSYVVGTSPSGDETEIFDKISEDIALKYLKSLNVNIVSEELGVIDNSSEWTVVIDPIDGSFNFINGIPFFAFCFGVFKNNEPYYGLTYEFLTKSFYEAYKGKGAYLNGRKIKVKDFNPNNIVISYYPSKKIDLEKLRNKVKRVRIFGAFGLEMCYVAKGTLDAVFDVRPKVRAVDIASSYIICKEAGALITDENGDELKFDLNATDRLNIIVANSKEMLDIILDLL

>d1inp\_\_ e.7.1.1 (-) Inositol polyphosphate 1-phosphatase {Cow (Bos taurus), brain}

MSDILQELLRVSEKAANIARACRQQETLFQLLIEEKKEGEKNKKFAVDFKTLADVLVQEVIKENMENKFPGLGKKIFGEESNELTNDLGEKIIMRLGPTEEETVALLSKVLNGNKLASEALAKVVHQDVFFSDPALDSVEINIPQDILGIWVDPIDSTYQYIKGSADITPNQGIFPSGLQCVTVLIGVYDIQTGVPLMGVINQPFVSQDLHTRRWKGQCYWGLSYLGTNIHSLLPPVSTRSNSEAQSQGTQNPSSEGSCRFSVVISTSEKETIKGALSHVCGERIFRAAGAGYKSLCVILGLADIYIFSEDTTFKWDSCAAHAILRAMGGGMVDLKECLERNPDTGLDLPQLVYHVGNEGAAGVDQWANKGGLIAYRSEKQLETFLSRLLQHLAPVATHT

>d1ka1a\_ e.7.1.1 (A:) 3';5'-adenosine bisphosphatase, PAP phosphatase {Baker's yeast (Saccharomyces cerevisiae)}

ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIIINAIKSNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDVRQIIDFGNYEGGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLSSYGAQDLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGHSSHDEQTAIKNKLNISKSLHLDSQAKYCLLALGLADVYLRLPIKLSYQEKIWDHAAGNVIVHEAGGIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSR

>d1jp4a\_ e.7.1.1 (A:) PIPase {Rat (Rattus norvegicus)}

HNVLMRLVASAYSIAQKAGTIVRCVIAEGDLGIVQKTSATDLQTKADRMVQMSICSSLSRKFPKLTIIGEEDLPPGEVDQELIEDGQSEEILKQPCPSQYSAIKEEDLVVWVDPVDGTKEYTEGLLDNVTVLIGIAYEGKAIAGIINQPYYNYQAGPDAVLGRTIWGVLGLGAFGFQLKEAPAGKHIITTTRSHSNKLVTDCIAAMNPDNVLRVGGAGNKIIQLIEGKASAYVFASPGCKKWDTCAPEVILHAVGGKLTDIHGNPLQYDKEVKHMNSAGVLAALRNYEYYASRVPESVKSALIP

>d1kfsa2 e.8.1.1 (A:519-928) DNA polymerase I (Klenow fragment) {Escherichia coli}

HKGPLNVFENIEMPLVPVLSRIERNGVKIDPKVLHNHSEELTLRLAELEKKAHEIAGEEFNLSSTKQLQTILFEKQGIKPLKKTPGGAPSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYTDKLPLMINPKTGRVHTSYHQAVTATGRLSSTDPNLQNIPVRNEEGRRIRQAFIAPEDYVIVSADYSQIELRIMAHLSRDKGLLTAFAEGKDIHRATAAEVFGLPLETVTSEQRRSAKAINFGLIYGMSAFGLARQLNIPRKEAQKYMDLYFERYPGVLEYMERTRAQAKEQGYVETLDGRRLYLPDIKSSNGARRAAAERAAINAPMQGTAADIIKRAMIAVDAWLQAEQPRVRMIMQVHDELVFEVHKDDVDAVAKQIHQLMENCTRLDVPLLVEVGSGENWDQAH

>d1qtma2 e.8.1.1 (A:423-831) DNA polymerase I (Klenow fragment) {Thermus aquaticus}

EERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRALSLEVAEEIARLEAEVFRLAGHPFNLNSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATATGRLSSSDPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYSQIELRVLAHLSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFGVLYGMSAHRLSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGRRRYVPDLEARVKSVREAAERMAFNMPVQGTAADLMKLAMVKLFPRLEEMGARMLLQVHDELVLEAPKERAEAVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAK

>d1xwl\_2 e.8.1.1 (469-876) DNA polymerase I (Klenow fragment) {Bacillus stearothermophilus, newly identified strain as yet unnamed}

EQDRLLVELEQPLSSILAEMEFAGVKVDTKRLEQMGKELAEQLGTVEQRIYELAGQEFNINSPKQLGVILFEKLQLPVLKKTKTGYSTSADVLEKLAPYHEIVENILHYRQLGKLQSTYIEGLLKVVRPDTKKVHTIFNQALTQTGRLSSTEPNLQNIPIRLEEGRKIRQAFVPSESDWLIFAADYSQIELRVLAHIAEDDNLMEAFRRDLDIHTKTAMDIFQVSEDEVTPNMRRQAKAVNFGIVYGISDYGLAQNLNISRKEAAEFIERYFESFPGVKRYMENIVQEAKQKGYVTTLLHRRRYLPDITSRNFNVRSFAERMAMNTPIQGSAADIIKKAMIDLNARLKEERLQAHLLLQVHDELILEAPKEEMERLCRLVPEVMEQAVTLRVPLKVDYHYGSTWYDAK

>d1t7pa2 e.8.1.1 (A:211-704) T7 phage DNA polymerase {Bacteriophage T7}

LEAVDIEHRAAWLLAKQERNGFPFDTKAIEELYVELAARRSELLRKLTETFGSWYQPKGGTEMFCHPRTGKPLPKYPRIKTPKVGGIFKKPKNKAQREGREPCELDTREYVAGAPYTPVEHVVFNPSSRDHIQKKLQEAGWVPTKYTDKGAPVVDDEVLEGVRVDDPEKQAAIDLIKEYLMIQKRIGQSAEGDKAWLRYVAEDGKIHGSVNPNGAVTGRATHAFPNLAQIPGVRSPYGEQCRAAFGAEHHLDGITGKPWVQAGIDASGLELRCLAHFMARFDNGEYAHEILNGDIHTKNQIAAELPTRDNAKTFIYGFLYGAGDEKIGQIVGAGKERGKELKKKFLENTPAIAALRESIQQTLVESSQWVAGEQQVKWKRRWIKGLDGRKVHVRSPHAALNTLLQSAGALICKLWIIKTEEMLVEKGLKHGWDGDFAYMAWVHDEIQVGCRTEEIAQVVIETAQEAMRWVGDHWNFRCLLDTEGKMGPNWAICH

>d1ih7a2 e.8.1.1 (A:376-903) T4-like DNA polymerase {Bacteriophage RB69}

QNKVIPQGRSHPVQPYPGAFVKEPIPNRYKYVMSFDLTSLYPSIIRQVNISPETIAGTFKVAPLHDYINAVAERPSDVYSCSPNGMMYYKDRDGVVPTEITKVFNQRKEHKGYMLAAQRNGEIIKEALHNPNLSVDEPLDVDYRFDFSDEIKEKIKKLSAKSLNEMLFRAQRTEVAGMTAQINRKLLINSLYGALGNVWFRYYDLRNATAITTFGQMALQWIERKVNEYLNEVCGTEGEAFVLYGDTDSIYVSADKIIDKVGESKFRDTNHWVDFLDKFARERMEPAIDRGFREMCEYMNNKQHLMFMDREAIAGPPLGSKGIGGFWTGKKRYALNVWDMEGTRYAEPKLKIMGLETQKSSTPKAVQKALKECIRRMLQEGEESLQEYFKEFEKEFRQLNYISIASVSSANNIAKYDVGGFPGPKCPFHIRGILTYNRAIKGNIDAPQVVEGEKVYVLPLREGNPFGDKCIAWPSGTEITDLIKDDVLHWMDYTVLLEKTFIKPLEGFTSAAKLDYEKKASLFDMFDF

>d1tgoa2 e.8.1.1 (A:348-773) T4-like DNA polymerase {Archaeon Thermococcus gorgonarius}

STGNLVEWFLLRKAYERNELAPNKPDERELARRRESYAGGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSLLGDLLEERQKVKKKMKATIDPIEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYADTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKIRPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQKTRQVGLGAWLKPKT

>d1qhta2 e.8.1.1 (A:348-750) T4-like DNA polymerase {Archaeon Thermococcus sp., 9on-7}

STGNLVEWFLLRKAYKRNELAPNKPDERELARRRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPEVGHKFCKDFPGFIPSLLGDLLEERQKIKRKMKATVDPLEKKLLDYRQRAIKILANSFYGYYGYAKARWYCKECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKKAKEFLKYINPKLPGLLELEYEGFYVRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLRDYKATGPHVAVAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPADEFDPTKHRYDAEYYIENQVLPAVERILKAFGY

>d1d5aa2 e.8.1.1 (A:348-756) T4-like DNA polymerase {Archaeon Desulfurococcus tok}

STGNLVEWFLLRKAYERNDVAPNKPDERELARRTESYAGGYVKEPEKGLWENIVYLDYKSLYPSIIITHNVSPDTLNREGCREYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQKVKKKMKATVDPIERKLLDYRQRAIKILANSYYGYYAYANARWYCRECAESVTAWGRQYIETTMREIEEKFGFKVLYADTDGFFATIPGADAETVKNKAKEFLNYINPRLPGLLELEYEGFYRRGFFVTKKKYAVIDEEDKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSRHEVPPEKLVIYEAGPHVAAAATVISYIVLKGPGRVGDRAIPFDEFDPAKHRYDAEYYIENQVLPAVERILRAFGYRKEDLR

>d1gcxa2 e.8.1.1 (A:348-758) T4-like DNA polymerase {Archaeon Pyrococcus kodakaraensis}

STGNLVEWFLLRKAYERNELAPNKPDEKELARRRQSYEGGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQKIKKKMKATIDPIERKLLDYRQRAIKILANSYYGYYGYARARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYSDTDGFFATIPGADAETVKKKAMEFLKYINAKLPGALELEYEGFYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQARVLEALLKDGDVEKAVRIVKEVTEKLSKYEVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPFDEFDPTKHKYDAEYYIENQVLPAVERILRAFGYRKEDLRYQ

>d1jx4a\_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus, DNA polymerase IV}

MIVLFVDFDYFYAQVEEVLNPSLKGKPVVVCVFSGRFEDSGAVATANYEARKFGVKAGIPIVEAKKILPNAVYLPMRKEVYQQVSSRIMNLLREYSEKIEIASIDEAYLDISDKVRDYREAYNLGLEIKNKILEKEKITVTVGISKNKVFAKIAADMAKPNGIKVIDDEEVKRLIRELDIADVPGIGNITAEKLKKLGINKLVDTLSIEFDKLKGMIGEAKAKYLISLARDEYNEPIRTRVRKSIGRIVTMKRNSRNLEEIKPYLFRAIEESYYKLDKRIPKAIHVVAVTEDLDIVSRGRTFPHGISKETAYSESVKLLQKILEEDERKIRRIGVRFSKFI

>d1im4a\_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}

HHHHHIVIFVDFDYFFAQVEEVLNPQYKGKPLVVCVYSGRTKTSGAVATANYEARKLGVKAGMPIIKAMQIAPSAIYVPMRKPIYEAFSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGNFENGIELARKIKQEILEKEKITVTVGVAPNKILAKIIADKSKPNGLGVIRPTEVQDFLNELDIDEIPGIGSVLARRLNELGIQKLRD

>d1k1sa\_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}

MIVIFVDFDYFFAQVEEVLNPQYKGKPLVVSVYSGRTKTSGAVATANYEARKLGVKAGMPIIKAMQIAPSAIYVPMRKPIYEAFSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGNFENGIELARKIKQEILEKEKITVTVGVAPNKILAKIIADKSKPNGLGVIRPTEVQDFLNELDIDEIPGIGSVLARRLNELGIQKLRDILSKNYNELEKITGKAKALYLLKLAQNKYSEPVENKSKIPHGRYLTLPYNTRDVKVILPYLKKAINEAYNKVNGIPMRITVIAIMEDLDILSKGKKFKHGISIDNAYKVAEDLLRELLVRDKRRNVRRIGVKLDNIIIN

>d1jiha\_ e.8.1.5 (A:) DNA polymerase eta {Baker's yeast (Saccharomyces cerevisiae)}

MSKFTWKELIQLGSPSKAYESSLACIAHIDMNAFFAQVEQMRCGLSKEDPVVCVQWNSIIAVSYAARKYGISRMDTIQEALKKCSNLIPIHTAVFKKGEDFWQYHDGCGSWVQDPAKQISVEDHKVSLEPYRRESRKALKIFKSACDLVERASIDEVFLDLGRICFNMLMFDNEYELTGDLKLKDALSNIREAFIGGNYDINSHLPLIPEKIKSLKFEGDVFNPEGRDLITDWDDVILALGSQVCKGIRDSIKDILGYTTSCGLSSTKNVCKLASNYKKPDAQTIVKNDCLLDFLDCGKFEITSFWTLGGVLGKELIDVLDLPHENSIKHIRETWPDNAGQLKEFLDAKVKQSDYDRSTSNIDPLKTADLAEKLFKLSRGRYGLPLSSRPVVKSMMSNKNLRGKSCNSIVDCISWLEVFCAELTSRIQDLEQEYNKIVIPRTVSISLKTKSYEVYRKSGPVAYKGINFQSHELLKVGIKFVTDLDIKGKNKSYYPLTKLSMTITNFDII

>d1mml\_\_ e.8.1.2 (-) MMLV reverse transcriptase {Moloney murine leukemia virus}

TWLSDFPQAWAETGGMGLAVRQAPLIIPLKATSTPVSIKQYPMSQEARLGIKPHIQRLLDQGILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNKRVEDIHPTVPNPYNLLSGLPPSHQWYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLLAATSELDCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLK

>d1c9ra2 e.8.1.2 (A:1-429) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PISPIETVPVKLAPGMDGPKVKQWPLTAEAIAALVAICTAMEAEGKISKIGPENPYNTPVFAIKKAAAAAAAALVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSIANATPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFKKQNPDIVIYQYIDDLYVGSDLEIGQHATKIAELRQHLLAWGLTTPDKKHAAEPPFLWMGYELHPDAWTVAPAALAAAASAAVNDIQKLVGKLNWASQIYPGIAVRALSAAAAGTKAAAEAAAATAAAALALAAAREALAAPVHGVYYDPSKDLIAEIQAQGQGQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWWTEYWQATWIPEWEFVNTPPLVKLWYQL

>d1c9rb1 e.8.1.2 (B:) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PISPIETVPVKLAPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEAALGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFKAQNPDIVIYQYIDDLYVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWAAAAAAAAAAAAATVNDIQKLVGKLNWAAQIYPGIAAAALSAALAGTKALTAAAPLTAAAALELAANRAAAAAAAAGVYYDPSKDLIAEIQKQGQGQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWWTEYWQATWIPEWEFVNTPPLVALWYALE

>d1har\_\_ e.8.1.2 (-) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PISPIETVPVKLKPGMDGPKVAQWPLTAAKIAALVAICTEMEKEGKISKIGPENPYNTPVFAIKKKDSTKWAKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILAPFKAANPDIVIYQYMDDLYVGSDLAIGAHRTKIEELRQHLLRWGLTT

>d1vrta2 e.8.1.2 (A:4-429) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PIETVPVKLKPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKKDSTKWRKLVDFRELNKRTQDFWEVQLGIPHPAGLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRKQNPDIVIYQYMDDLYVGSDLEIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWTVQPIVLPEKDSWTVNDIQKLVGKLNWASQIYPGIKVRQLCKLLRGTKALTEVIPLTEEAELELAENREILKEPVHGVYYDPSKDLIAEIQKQGQGQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWWTEYWQATWIPEWEFVNTPPLVKLWYQL

>d1ceza\_ e.8.1.3 (A:) T7 RNA polymerase {Bacteriophage T7}

IAKNDFSDIELAAIPFNTLADHYGERLAREQLALEHESYEMGEARFRKMFERQLKAGEVADNAAAKPLITTLLPKMIARINDWFEEVKAKRGKRPTAFQFLQEIKPEAVAYITIKTTLACLTSADNTTVQAVASAIGRAIEDEARFGRIRDLEAKHFKKNVEEQLNKRVGHVYKKAFMQVVEADMLSKGLLGGEAWSSWHKEDSIHVGVRCIEMLIESTGMVSLHRQNAGVVGQDSETIELAPEYAEAIATRAGALAGISPMFQPCVVPPKPWTGITGGGYWANGRRPLALVRTHSKKALMRYEDVYMPEVYKAINIAQNTAWKINKKVLAVANVITKWKHCPVEDIPAIEREELPMKPEDIDMNPEALTAWKRAAAAVYRKDKARKSRRISLEFMLEQANKFANHKAIWFPYNMDWRGRVYAVSMFNPQGNDMTKGLLTLAKGKPIGKEGYYWLKIHGANCAGVDKVPFPERIKFIEENHENIMACAKSPLENTWWAEQDSPFCFLAFCFEYAGVQHHGLSYNCSLPLAFDGSCSGIQHFSAMLRDEVGGRAVNLLPSETVQDIYGIVAKKVNEILQADAINGTDNEVVTVTDENTGEISEKVKLGTKALAGQWLAYGVTRSVTKRSVMTLAYGSKEFGFRQQVLEDTIQPAIDSGKGLMFTQPNQAAGYMAKLIWESVSVTVVAAVEAMNWLKSAAKLLAAEVKDKKTGEILRKRCAVHWVTPDGFPVWQEYKKPIQTRLNLMFLGQFRLQPTINTNKDSEIDAHKQESGIAPNFVHSQDGSHLRKTVVWAHEKYGIESFALIHDSFGTIPADAANLFKAVRETMVDTYESCDVLADFYDQFADQLHESQLDKMPALPAKGNLNLRDILESDFAFA

>d1rdr\_\_ e.8.1.4 (-) Viral RNA-dependent RNA-polymerase {Poliovirus type 1, strain Mahoney}

VGYPIINAPSKTKLEPSAFHYVFEGVKEPAVLTKNDPRLKTDFEEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMSLDINTEQMCLEDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGCDPDLFWSKIPVLMEEKLFAFDYTGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGGMPSGCSGTSIFNSMINNLIIRTLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWENVTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLCLLAWHNGEEEYNKFLAKIRSVPIGRALLLPEYSTLYRRWLDSF

>d1c2pa\_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Hepatitis C virus}

HHSYTWTGALITPCAAEESKLPINALSNSLLRHHNMVYATTSRSAGLRQKKVTFDRLQVLDDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHIHSVWKDLLEDTVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDVVSTLPQVVMGSSYGFQYSPGQRVEFLVNTWKSKKNPMGFSYDTRCFDSTVTENDIRVEESIYQCCDLAPEARQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTSCGNTLTCYLKASAACRAAKLQDCTMLVNGDDLVVICESAGVQEDAASLRAFTEAMTRYSAPPGDPPQPEYDLELITSCSSNVSVAHDASGKRVYYLTRDPTTPLARAAWETARHTPVNSWLGNIIMYAPTLWARMILMTHFFSILLAQEQLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPGEINRVASCLRKLGVPPLRVWRHRARSVRARLLSQGGRAATCGKYLFNWAVKTKLKLTPIPAASQLDLSGWFVAGYSGGDIYHS

>d1khva\_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Rabbit hemorrhagic disease virus}

FCGEPIDYRGITAHRLVGAEPRPPVSGTRYAKVPGVPDEYKTGYRPANLGRSDPDSDKSLMNIAVKNLQVYQQEPKLDKVDEFIERAAADVLGYLRFLTKGERQANLNFKAAFNTLDLSTSCGPFVPGKKIDHVKDGVMDQVLAKHLYKCWSVANSGKALHHIYACGLKDELRPLDKVKEGKKRLLWGCDVGVAVCAAAVFHNICYKLKMVARFGPIAVGVDMTSRDVDVIINNLTSKASDFLCLDYSKWDSTMSPCVVRLAIDILADCCEQTELTKSVVLTLKSHPMTILDAMIVQTKRGLPSGMPFTSVINSICHWLLWSAAVYKSCAEIGLHCSNLYEDAPFYTYGDDGVYAMTPMMVSLLPAIIENLRDYGLSPTAADKTEFIDVCPLNKISFLKRTFELTDIGWVSKLDKSSILRQLEWSKTTSRHMVIEETYDLAKEERGVQLEELQVAAAAHGQEFFNFVCRELERQQAYTQFSVYSYDAARKILADRKR

>d1hhsa\_ e.8.1.6 (A:) dsRNA phage RNA-dependent RNA-polymerase {Bacteriophage PHI-6}

PRRAPAFPLSDIKAQMLFANNIKAQQASKRSFKEGAIETYEGLLSVDPRFLSFKNELSRYLTDHFPANVDEYGRVYGNGVRTNFFGMRHMNGFPMIPATWPLASNLKKRADADLADGPVSERDNLLFRAAVRLMFSDLEPVPLKIRKGSSTCIPYFSNDMGTKIEIAERALEKAEEAGNLMLQGKFDDAYQLHQMGGAYYVVYRAQSTDAITLDPKTGKFVSKDRMVADFEYAVTGGEQGSLFAASKDASRLKEQYGIDVPDGFFCERRRTAMGGPFALNAPIMAVAQPVRNKIYSKYAYTFHHTTRLNKEEKVKEWSLCVATDVSDHDTFWPGWLRDLICDELLNMGYAPWWVKLFETSLKLPVYVGAPAPEQGHTLLGDPSNPDLEVGLSSGQGATDLMGTLLMSITYLVMQLDHTAPHLNSRIKDMPSACRFLDSYWQGHEEIRQISKSDDAMLGWTKGRALVGGHRLFEMLKEGKVNPSPYMKISYEHGGAFLGDILLYDSRREPGSAIFVGNINSMLNNQFSPEYGVQSGVRDRSKRKRPFPGLAWASMKDTYGACPIYSDVLEAIERCWWNAFGESYRAYREDMLKRDTLELSRYVASMARQAGLAELTPIDLEVLADPNKLQYKWTEADVSANIHEVLMHGVSVEKTERFLRSVMPR

>d1i50a\_ e.29.1.1 (A:) RBP1 {Baker's yeast (Saccharomyces cerevisiae)}

VGQQYSSAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMDETQTRAKIGGLNDPRLGSIDRNLKCQTCQEGMNECPGHFGHIDLAKPVFHVGFIAKIKKVCECVCMHCGKLLLDEHNELMRQALAIKDSKKRFAAIWTLCKTKMVCETDVPSEDDPTQLVSRGGCGNTQPTIRKDGLKLVGSWKKDRATGDADEPELRVLSTEEILNIFKHISVKDFTSLGFNEVFSRPEWMILTCLPVPPPPVRPSISFNESQRGEDDLTFKLADILKANISLETLEHNGAPHHAIEEAESLLQFHVATYMDNDIAGQPQALQKSGRPVKSIRARLKGKEGRIRGNLMGKRVDFSARTVISGDPNLELDQVGVPKSIAKTLTYPEVVTPYNIDRLTQLVRNGPNEHPGAKYVIRDSGDRIDLRYSKRAGDIQLQYGWKVERHIMDNDPVLFNRQPSLHKMSMMAHRVKVIPYSTFRLNLSVTSPYNADFDGDEMNLHVPQSEETRAELSQLCAVPLQIVSPQSNKPCMGIVQDTLCGIRKLTLRDTFIELDQVLNMLYWVPDWDGVIPTPAIIKPKPLWSGKQILSVAIPNGIHLQRFDEGTTLLSPKDNGMLIIDGQIIFGVVEKKTVGSSNGGLIHVVTREKGPQVCAKLFGNIQKVVNFWLLHNGFSTGIGDTIADGPTMREITETIAEAKKKVLDVTKEAQANLLTAKHGMTLRESFEDNVVRFLNEARDKAGRLAEVNLKDLNNVKQMVMAGSKGSFINIAQMSACVGQQSVEGKRIAFGFVDRTLPHFSKDDYSPESKGFVENSYLRGLTPQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDNTTRNSLGNVIQFIYGEDGMDAAHIEKQSLDTIGGSDAAFEKRYRVDLLNTDHTLDPSLLESGSEILGDLKLQVLLDEEYKQLVKDRKFLREVFVDGEANWPLPVNIRRIIQNAQQTFHIDHTKPSDLTIKDIVLGVKDLQENLLVLRGKNEIIQNAQRDAVTLFCCLLRSRLATRRVLQEYRLTKQAFDWVLSNIEAQFLRSVVHPGEMVGVLAAQSIGEPATQMTLNTFHFAGVASKKVTSGVPRLKEILNVAKNMKTPSLTVYLEPGHAADQEQAKLIRSAIEHTTLKSVTIASEIYYDPDPRSTVIPEDEEIIQLHFSLLDEEAEQSFDQQSPWLLRLELDRAAMNDKDLTMGQVGERIKQTFKNDLFVIWSEDNDEKLIIRCRVVRPKSLDAETEAEEDHMLKKIENTMLENITLRGVENIERVVMMKYDRKVPSPTGEYVKEPEWVLETDGVNLSEVMTVPGIDPTRIYTNSFIDIMEVLGIEAGRAALYKEVYNVIASDGSYVNYRHMALLVDVMTTQGGLTSVTRHGFNRSNTGALMRCSFEETVEILFEAGASAELDDCRGVSENVILGQMAPIGTGAFDVMIDEESL

>d1i6vc\_ e.29.1.1 (C:) RNA-polymerase beta {Thermus aquaticus}

KIKRFGRIREVIPLPPLTEIQVESYKKALQADVPPEKRENVGIQAAFKETFPIEEGDKGKGGLVLDFLEYRIGDPPFSQDECREKDLTYQAPLYARLQLIHKDTGLIKEDEVFLGHLPLMTEDGSFIINGADRVIVSQIHRSPGVYFTPDPARPGRYIASIIPLPKRGPWIDLEVEASGVVTMKVNKRKFPLVLLLRVLGYDQETLVRELSAYGDLVQGLLDEAVLAMRPEEAMVRLFTLLRPGDPPKKDKALAYLFGLLADPKRYDLGEAGRYKAEEKLGVGLSGRTLVRFEDGEFKDEVFLPTLRYLFALTAGVPGHEVDDIDHLGNRRIRTVGELMADQFRVGLARLARGVRERMVMGSPDTLTPAKLVNSRPLEAALREFFSRSQLSQFKDETNPLSSLRHKRRISALGPGGLTRERAGFDVRDVHRTHYGRICPVETPEGANIGLITSLAAYARVDALGFIRTPYRRVKNGVVTEEVVYMTASEEDRYTIAQANTPLEGDRIATDRVVARRRGEPVIVAPEEVEFMDVSPKQVFSLNTNLIPFLEHDDANRALMGSNMQTQAVPLIRAQAPVVMTGLEERVVRDSLAALYAEEDGEVVKVDGTRIAVRYEDGRLVHPLRRYARSNQGTAFDQRPRVRVGQRVKKGDLLADGPASEEGFLALGQNVLVAIMPFDGYNFEDAIVISEELLKRDFYTSIHIERYEIEARDTKLGPERITRDIPHLSEAALRDLDEEGIVRIGAEVKPGDILVGRTSFKGEQEPSPEERLLRSIFGEKARDVKDTSLRVPPGEGGIVVGRLRLRRGDPGVELKPGVREVVRVFVAQKRKLQVGDKLANRHGNKGVVAKILPVEDMPHLPDGTPVDVILNPLGVPSRMNLGQILETHLGLAGYFLGQRYISPVFDGATEPEIKELLAEAFNLYFGKRQGEGFGVDKREKEVLARAEKLGLVSPGKSPEEQLKELFDLGKVVLYDGRTGEPFEGPIVVGQMFIMKLYHMVEDKMHARSTGPYSLITQQPLGGKAQFGGQRFGEMEVWALEAYGAAHTLQEMLTIKSDDIEGRNAAYQAIIKGEDVPEPSVPESFRVLVKELQALALDVQTLDEKDNPVDVFEGL

>d1i50b\_ e.29.1.2 (B:) RBP2 {Baker's yeast (Saccharomyces cerevisiae)}

FEDESAPITAEDSWAVISAFFREKGLVSQQLDSFNQFVDYTLQDIICEDSTLILEQLAQHTTESDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLRNLTYSSGLFVDVKKRTYEAIDVPGRELKYELIAEESEDDSESGKVFIGRLPIMLRSKNCYLSEATESDLYKLKECPFDMGGYFIINGSEKVLIAQERSAGNIVQVFKKAAPSPISHVAEIRSALEKGSRFISTLQVKLYGREGSSARTIKATLPYIKQDIPIVIIFRALGIIPDGEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRETALDFIGRRGTALGIKKEKRIQYAKDILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCALDRKDQDDRDHFGKKRLDLAGPLLAQLFKTLFKKLTKDIFRYMQRTVEEAHDFNMKLAINAKTITSGLKYALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEPLEDYVPHQSPDATRVFVNGVWHGVHRNPARLMETLRTLRRKGDINPEVSMIRDIREKELKIFTDAGRVYRPLFIVEDDESLGHKELKVRKGHIAKLMATEYQDIEGGFEDVEEYTWSSLLNEGLVEYIDAEEEESILIAMQPEDLEPAEANEENDLDVDPAKRIRVSHHATTFTHCEIHPSMILGVAASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMANILYYPQKPLGTTRAMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQEKKYGMSITETFEKPQRTNTLRMKHGTYDKLDDDGLIAPGVRVSGEDVIIGKTTPISPDEEELGQRTAYHSKRDASTPLRSTENGIVDQVLVTTNQDGLKFVKVRVRTTKIPQIGDKFASRHGQKGTIGITYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDASPFTDITVEGISKLLREHGYQSRGFEVMYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLTRQPVEGRSRDGGLRFGEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMTVIAKLNHNQFECKGCDNKIDIYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF

>d1i6vd\_ e.29.1.2 (D:) RNA-polymerase beta-prime {Thermus aquaticus}

KEVRKVRIALASPEKIRSWSYGEVEKPETINYRTLKPERDGLFDERIFGPIKDYECACGKYKRQRFEAKVCERCAVEVTRSIVRRYRMAHIELATPAAHIWFVKDVPSKIATLLDLSATELEQVLYFNKYIVLDPKAAVLDAVPVEKRQLLTDXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIDARMGAEAIQELLKELDLEKLERELLEEMKHPSRARRAKARKRLEVVRAFLDSGNRPEWMILEAVPVLPPDLRPMVQVDGGRFATSDLNDLYRRLINRNNRLKKLLAQGAPEIIIRNEKRMLQEAVDAVIDNGRRGSPVTNPGSERPLRSLTDILSGKQGRFRQNLLGKRVDYSGRSVIVVGPQLKLHQCGLPKRMALELFKPFLLKKMEEKAFAPNVKAARRMLERQRDIKDEVWDALEEVIHGKVVLLNRAPTLHRLGIQAFQPVLVEGQSIQLHPLVCEAFNADFDGDQMAVHVPLSSFAQAEARIQMLSAHNLLSPASGEPLAKPSRDIILGLYYITQVRKEKKGAGMAFATPEEALAAYERGEVALNAPIVVAGRETSVGRLKFVFANPDEALLAVAHGLLDLQDTVTTRYLGRRLETSPGRILFARIVGEAVGDEKVAQELIQMDVPQEKNSLKDLVYQAFLRLGMEKTARLLDALKYYGFTLSTTSGITIGIDDAVIPEEKQRYLEEADRKLRQIEQAYEMGFLTDRERYDQVIQLWTETTEKVTQAVFNNFEENYPFNPLYVMAQSGARGNPQQIRQLCGMRGLMQKPSGETFEVPVRSSFREGLTVLEYFISSHGARKGGADTALRTADSGYLTRKLVDVAHEIVVREADCGTTNYISVPLFQMDEVTRTLRLRKRSDIESGLYGRVLAREVEALGRRLEEGRYLSLEDVHFLIKAAEAGEVREVPVRSPLTCQTRYGVCQKCYGYDLSMARPVSIGEAVGVVAAESIGEPGTQLTMRTFHTGGVAVGTDITQGLPRVIELFEARRPKAKAVISEIDGVVRIEEGEDRLSVFVESEGFSKEYKLPKDARLLVKDGDYVEAGQPLTRGAIDPHQLLEAKGPEAVERYLVDEIQKVYRAQGVKLHDKHIEIVVRQMLKYVEVTDPGDSRLLEGQVLEKWDVEALNERLIAEGKVPVAWKPLLMGVTKSALSTKSWLSAASFQNTTHVLTEAAIAGKKDELIGLKENVILGRLIPAGTGSDFVRFTQVVDQRTLKAIE

>d1bpya2 e.9.1.1 (A:92-335) DNA polymerase beta, catalytic (31 kD) fragment {Human (Homo sapiens)}

DTSSSINFLTRVSGIGPSAARKFVDEGIKTLEDLRKNEDKLNHHQRIGLKYFGDFEKRIPREEMLQMQDIVLNEVKKVDSEYIATVCGSFRRGAESSGDMDVLLTHPSFTSESTKQPKLLHQVVEQLQKVHFITDTLSKGETKFMGVCQLPSKNDEKEYPHRRIDIRLIPKDQYYCGVLYFTGSDIFNKNMRAHALEKGFTINEYTIRPLGVTGVAGEPLPVDSEKDIFDYIQWKYREPKDRSE

>d1jn3a\_ e.9.1.1 (A:) DNA polymerase beta, catalytic (31 kD) fragment {Rat (Rattus norvegicus)}

DDTSSSINFLTRVTGIGPSAARKLVDEGIKTLEDLRKNEDKLNHHQRIGLKYFEDFEKRIPREEMLQMQDIVLNEVKKLDPEYIATVCGSFRRGAESSGDMDVLLTHPNFTSESSKQPKLLHRVVEQLQKVRFITDTLSKGETKFMGVCQLPSENDENEYPHRRIDIRLIPKDQYYCGVLYFTGSDIFNKNLRAHALEKGFTINEYTIRPLGVTGVAGEPLPVDSEQDIFDYIQWRYREPKDRSE

>d1jmsa2 e.9.1.1 (A:243-510) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}

DERYKSFKLFTSVFGVGLKTAEKWFRMGFRTLSKIQSDKSLRFTQMQKAGFLYYEDLVSCVNRPEAEAVSMLVKEAVVTFLPDALVTMTGGFRRGKMTGHDVDFLITSPEATEDEEQQLLHKVTDFWKQQGLLLYCDILESTFEKFKQPSRKVDALDHFQKCFLILKLDHGRVHSEKSGQQEGKGWKAIRVDLVMCPYDRRAFALLGWTGSRQFERDLRRYATHERKMMLDNHALYDRTKRVFLEAESEEEIFAHLGLDYIEPWERNA

>d1jaja\_ e.9.1.1 (A:) DNA polymerase X {African swine fever virus}

MLTLIQGKKIVNHLRSRLAFEYNGQLIKILSKNIVAVGSLRREEKMLNDVDLLIIVPEKKLLKHVLPNIRIKGLSFSVKVCGERKCVLFIEWEKKTYQLDLFTALAEEKPYAIFHFTGPVSYLIRIRAALKKKNYKLNQYGLFKNQTLVPLKITTEKELIKELGFTYRIPKKRL

>d1fa0a2 e.9.1.2 (A:3-351) Poly(A) polymerase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

SQKVFGITGPVSTVGATAAENKLNDSLIQELKKEGSFETEQETANRVQVLKILQELAQRFVYEVSKKKNMSDGMARDAGGKIFTYGSYRLGVHGPGSDIDTLVVVPKHVTREDFFTVFDSLLRERKELDEIAPVPDAFVPIIKIKFSGISIDLICARLDQPQVPLSLTLSDKNLLRNLDEKDLRALNGTRVTDEILELVPKPNVFRIALRAIKLWAQRRAVYANIFGFPGGVAWAMLVARICQLYPNACSAVILNRFFIILSEWNWPQPVILKPIEDGPLQVRVWNPKIYAQDRSHRMPVITPAYPSMCATHNITESTKKVILQEFVRGVQITNDIFSNKKSWANLFEK

>d1f5aa2 e.9.1.2 (A:20-364) Poly(A) polymerase, catalytic domain {Cow (Bos taurus)}

YGITSPISLAAPKETDCLLTQKLVETLKPFGVFEEEEELQRRILILGKLNNLVKEWIREISESKNLPQSVIENVGGKIFTFGSYRLGVHTKGADIDALCVAPRHVDRSDFFTSFYDKLKLQEEVKDLRAVEEAFVPVIKLCFDGIEIDILFARLALQTIPEDLDLRDDSLLKNLDIRCIRSLNGCRVTDEILHLVPNIDNFRLTLRAIKLWAKRHNIYSNILGFLGGVSWAMLVARTCQLYPNAIASTLVHKFFLVFSKWEWPNPVLLKQPEECNLNLPVWDPRVNPSDRYHLMPIITPAYPQQNSTYNVSVSTRMVMVEEFKQGLAITDEILLSKAEWSKLFEA

>d1knya\_ e.9.1.3 (A:) Kanamycin nucleotidyltransferase (KNTase) {Staphylococcus aureus}

MNGPIIMTREERMKIVHEIKERILDKYGDDVKAIGVYGSLGRQTDGPYSDIEMMCVMSTEEAEFSHEWTTGEWKVEVNFYSEEILLDYASQVESDWPLTHGQFFSILPIYDSGGYLEKVYQTAKSVEAQTFHDAICALIVEELFEYAGKWRNIRVQGPTTFLPSLTVQVAMAGAMLIGLHHRICYTTSASVLTEAVKQSDLPSGYDHLCQFVMSGQLSDSEKLLESLENFWNGIQEWTERHGYIVDVSKRIPF

>d1k8ta\_ e.9.1.4 (A:) Adenylylcyclase toxin (the edema factor) {Bacillus anthracis}

DRIDVLKGEKALKASGLVPEHADAFKKIARELNTYILFRPVNKLATNLIKSGVATKGLNVHGKSSDWGPVAGYIPFDQDLSKKHGQQLAVEKGNLENKKSITEHEGEIGKIPLKLDHLRIEELKENGIILKGKKEIDNGKKYYLLESNNQVYEFRISDENNEVQYKTKEGKITVLGEKFNWRNIEVMAKNVEGVLKPLTADYDLFALAPSLTEIKKQIPQKEWDKVVNTPNSLEKQKGVTNLLIKYGIERKPDSTKGTLSNWQKQMLDRLNEAVKYTGYTGGDVVNHGTEQDNEEFPEKDNEIFIINPEGEFILTKNWEMTGRFIEKNITGKDYLYYFNRSYNKIAPGNKAYIEWTDPITKAKINTIPTSAEFIKNLSSIRRSSNVGVYKDSGDKDEFAKKESVKKIAGYLSDYYNSANHIFSQEKKRKISIFRGIQAYNEIENVLKSKQIAPEYKNYFQYLKERITNQVQLLLTHQKSNIEFKLLYKQLNFTENETDNFEVFQKIIDE

>d1cy9a\_ e.10.1.1 (A:) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}

FVPEEFWEVDASTTTPSGEALALQVTHQNDKPFRPVNKEQTQAAVSLLEKARYSVLEREDKPTTSKPGAPFITSTLQQAASTRLGFGVKKTMMMAQRLYEAGYITYMRTDSTNLSQDAVNMVRGYISDNFGKKYLPESPNQYASKENSQEAHEAIRPSDVNVMAESLKDMEADAQKLYQLIWRQFVACQMTPAKYDSTTLTVGAGDFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKGDALTLVELTPAQHFTKP

>d1ecl\_\_ e.10.1.1 (-) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}

GKALVIVESPAKAKTINKYLGSDYVVKSSVGHIRDLTSGSAAKKSADSTSTKTAKKPKKPDERGALVNRMGVDPWHNWEAHYEVLPGKEKVVSELKQLAEKADHIYLATDLDREGEAIAWHLREVIGGDDARYSRVVFNEITKNAIRQAFNKPGELNIDRVNAQQARRFMDRVVGYMVSPLLWKKIARGLSAGRVQSVAVRLVVEREREIKAFVPEEFWEVDASTTTPSGEALALQVTHQNDKPFRPVNKEQTQAAVSLLEKARYSVLEREDKPTTSKPGAPFITSTLQQAASTRLGFGVKKTMMMAQRLYEAGYITYMRTDSTNLSQDAVNMVRGYISDNFGKKYLPESPNQYASKGNSQEAHEAIRPSDVNVMAESLKDMEADAQKLYQLIWRQFVACQMTPAKYDSTTLTVGAGDFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKGDALTLVELTPAQHFTKPPARFSEASLVKELEKRGIGRPSTYASIISTIQDRGYVRVENRRFYAEKMGEIVTDRLEENFRELMNYDFTAQMENSLDQVANHEAEWKAVLDHFFSDFTQQLDKAEKDPEEGGMRPN

>d1i7da\_ e.10.1.1 (A:) DNA topoisomerase III {Escherichia coli}

MRLFIAEKPSLARAIADVLPKPHRKGDGFIECGNGQVVTWCIGHLLEQAQPDAYDSRYARWNLADLPIVPEKWQLQPRPSVTKQLNVIKRFLHEASEIVHAGDPDREGQLLVDEVLDYLQLAPEKRQQVQRCLINDLNPQAVERAIDRLRSNSEFVPLCVSALARARADWLYGINMTRAYTILGRNAGYQGVLSVGRVQTPVLGLVVRRDEEIENFVAKDFFEVKAHIVTPADERFTAIWQPSEACEPYQDEEGRLLHRPLAEHVVNRISGQPAIVTSYNDKRESESAPLPFSLSALQIEAAKRFGLSAQNVLDICQKLYETHKLITFPRSDCRYLPEEHFAGRHAVMNAISVHAPDLLPQPVVDPDIRNRCWDDKKVDAHHAIIPTARSSAINLTENEAKVYNLIARQYLMQFCPDAVFRKCVIELDIAKGKFVAKARFLAEAGWRTLLGSKERDEENDGTPLPVVAKGDELLCEKGEVVERQTQPPRHFTDATLLSAMTGIARFVQDKDLKKILRATDGLGTEATRAGIIELLFKRGFLTKKGRYIHSTDAGKALFHSLPEMATRPDMTAHWESVLTQISEKQCRYQDFMQPLVGTLYQLIDQAKRTPVRQFRGIVAP

>d1gkub3 e.10.1.1 (B:499-1054) Topoisomerase "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

QEFDLIKPALFIVESPTKARQISRFFGKPSVKVLDGAVVYEIPMQKYVLMVTASIGHVVDLITNRGFHGVLVNGRFVPVYASIKRCRDCGYQFTEDRESCPKCGSENVDNSRSRIEALRKLAHDAEFVIVGTDPDTEGEKIAWDLKNLLSGCGAVKRAEFHEVTRRAILEALESLRDVDENLVKAQVVRRIEDRWIGFVLSQKLWERFNNRNLSAGRAQTLVLGWIIDRFQESRERRKIAIVRDFDLVLEHDEEEFDLTIKLVEEREELRTPLPPYTTETMLSDANRILKFSVKQTMQIAQELFENGLITYHRTDSTRVSDVGQRIAKEYLGDDFVGREWGESGAHECIRPTRPLTRDDVQRLIQEGVLVVEGLRWEHFALYDLIFRRFMASQCRPFKVVVKKYSIEFDGKTAEEERIVRAEGRAYELYRAVWVKNELPTGTFRVKAEVKSVPKVLPFTQSEIIQMMKERGIGRPSTYATIVDRLFMRNYVVEKYGRMIPTKLGIDVFRFLVRRYAKFVSEDRTRDLESRMDAIERGELDYLKALEDMYAEIKSID

>d1bjt\_\_ e.11.1.1 (-) DNA topoisomerase II, C-terminal fragment (residues 410-1202) {Baker's yeast (Saccharomyces cerevisiae)}

RKSRITNYPKLEDANKAGTKEGYKCTLVLTEGDSALSLAVAGLAVVGRDYYGCYPLRGKMLNVREASADQILKNAEIQAIKKIMGLQHRKKYEDTKSLRYGHLMIMTDQDHDGSHIKGLIINFLESSFLGLLDIQGFLLEFITPIIKVSITKPTKNTIAFYNMPDYEKWREEESHKFTWKQKYYKGLGTSLAQEVREYFSNLDRHLKIFHSLQGNDKDYIDLAFSKKKADDRKEWLRQYEPGTVLDPTLKEIPISDFINKELILFSLADNIRSIPNVLDGFKPGQRKVLYGCFKKNLKSELKVAQLAPYVSECTAYHHGEQSLAQTIIGLAQNFVGSNNIYLLLPNGAFGTRATGGKDAAAARYIYTELNKLTRKIFHPADDPLYKYIQEDEKTVEPEWYLPILPMILVNGAEGIGTGWSTYIPPFNPLEIIKNIRHLMNDEELEQMHPWFRGWTGTIEEIEPLRYRMYGRIEQIGDNVLEITELPARTWTSTIKEYLLLGLSGNDKIKPWIKDMEEQHDDNIKFIITLSPEEMAKTRKIGFYERFKLISPISLMNMVAFDPHGKIKKYNSVNEILSEFYYVRLEYYQKRKDHMSERLQWEVEKYSFQVKFIKMIIEKELTVTNKPRNAIIQELENLGFPRFNKEGKPYYGSPNDEIAEQINDVKGATSDEEDEESSHEDTENVINGPEELYGTYEYLLGMRIWSLTKERYQKLLKQKQEKETELENLLKLSAKDIWNTDLKAFEVGYQEFLQRDAEARG

>d1ab4\_\_ e.11.1.1 (-) DNA Gyrase A {Escherichia coli}

VGRALPDVRDGLKPVHRRVLYAMNVLGNDWNKAYKKSARVVGDVIGKYHPHGDSAVYDTIVRMAQPFSLRYMLVDGQGNFGSIDGDSAAAMRYTEIRLAKIAHELMADLEKETVDFVDNYDGTEKIPDVMPTKIPNLLVNGSSGIAVGMATNIPPHNLTEVINGCLAYIDDEDISIEGLMEHIPGPDFPTAAIINGRRGIEEAYRTGRGKVYIRARAEVEVETIIVHEIPYQVNKARLIEKIAELVKEKRVEGISALRDESDKDGMRIVIEGEVVLNNLYSQTQLQVSFGINMVALHHGQPKIMNLKDIIAAFVRHRREVVTRRTIFELRKARDRAHILEALAVALANIDPIIELIRHAPTPAEAKTALVANPWQLGNVAAMLEDAARPEWLEPEFGVRDGLYYLTEQQAQAILDLRLQKLTGLEHEKLLDEYKELLDQIAELLRILGSADRLMEVIREELELVREQFGDKRRTEIT

>d1d3ya\_ e.12.1.1 (A:) DNA topoisomerase IV, alpha subunit {Archaeon Methanococcus jannaschii}

QAKIFAQTTKMLEFAKQLLETDDFSTLREAYYVSKNWGEARFDDQQASNNVIEDLEAALGVLREHLGFIPEEDGSSVVGPLKIIEETPEGELVVDCTKLGTGAYNIPNDVTKLNLETDADFILAIETSGMFARLNAERFWDKHNCILVSLKGVPARATRRFIKRLHEEHDLPVLVFTDGDPYGYLNIYRTLKVGSGKAIHLADKLSIPAARLIGVTPQDIIDYDLPTHPLKEQDIKRIKDGLKNDDFVRSFPEWQKALKQMLDMGVRAEQQSLAKYGLKYVVNTYLPEKIKDESTWLP

>d1dd9a\_ e.13.1.1 (A:) DNA primase DnaG catalytic core {Escherichia coli}

TLYQLMDGLNTFYQQSLQQPVATSARQYLEKRGLSHEVIARFAIGFAPPGWDNVLKRFGGNPENRQSLIDAGMLVTNDQGRSYDRFRERVMFPIRDKRGRVIGFGGRVLGNDTPKYLNSPETDIFHKGRQLYGLYEAQQDNAEPNRLLVVEGYMDVVALAQYGINYAVASLGTSTTADHIQLLFRATNNVICCYDGDRAGRDAAWRALETALPYMTDGRQLRFMFLPDGEDPDTLVRKEGKEAFEARMEQAMPLSAFLFNSLMPQVDLSTPDGRARLSTLALPLISQVPGETLRIYLRQELGNKLGILDDSQLE

>d1ee8a\_ e.14.1.1 (A:) DNA repair protein MutM (Fpg) {Thermus thermophilus}

PELPEVETTRRRLRPLVLGQTLRQVVHRDPARYRNTALAEGRRILEVDRRGKFLLFALEGGVELVAHLGMTGGFRLEPTPHTRAALVLEGRTLYFHDPRRFGRLFGVRRGDYREIPLLLRLGPEPLSEAFAFPGFFRGLKESARPLKALLLDQRLAAGVGNIYADEALFRARLSPFRPARSLTEEEARRLYRALREVLAEAVELGGSTLSDQSYRQPDGLPGGFQTRHAVYGREGLPCPACGRPVERRVVAGRGTHFCPTCQGEGP

>d1i3ja\_ e.30.1.1 (A:) DNA-binding domain of intron endonuclease I-TevI {Bacteriophage T4}

KFCKCGVRIQTSAYTCSKCRNRSGENNSFFNHKHSDITKSKISEKMKGKKPSNIKKISCDGVIFDCAADAARHFKISSGLVTYRVKSDKWNWFYIN

>d1a31a2 e.15.1.1 (A:215-430) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment {Human (Homo sapiens)}

IKWKFLEHKGPVFAPPYEPLPENVKFYYDGKVMKLSPKAEEVATFFAKMLDHEYTTKEIFRKNFFKDWRKEMTNEEKNIITNLSKCDFTQMSQYFKAQTEARKQMSKEEKLKIKEENEKLLKEYGFCIMDNHKERIANFKIEPPGLFRGRGNHPKMGMLKRRIMPEDIIINCSKDAKVPSPPPGHKWKEVRHDNKVTWLVSWTENIQGSIKYIMLN

>d1ois\_\_ e.15.1.1 (-) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment {Baker's yeast (Saccharomyces cerevisiae)}

DTIKWVTLKHNGVIFPPPYQPLPSHIKLYYDGKPVDLPPQAEEVAGFFAALLESDHAKNPVFQKNFFNDFLQVLKESGGPLNGIEIKEFSRCDFTKMFDYFQLQKEQKKQLTSQEKKQIRLEREKFEEDYKFCELDGRREQVGNFKVEPPDLFRGRGAHPKTGKLKRRVNPEDIVLNLSKDAPVPPAPEGHKWGEIRHDNTVQWLAMWRENIFNSFKYVRLAA

>d1g71a\_ e.16.1.1 (A:) DNA primase {Archaeon Pyrococcus furiosus}

MLMREVTKEERSEFYSKEWSAKKIPKFIVDTLESREFGFDHNGEGPSDRKNQYSDIRDLEDYIRATSPYAVYSSVAFYENPREMEGWRGAELVFDIDAKDLPLKRCNHEPGTVCPICLEDAKELAKDTLIILREELGFENIHVVYSGRGYHIRILDEWALQLDSKSRERILAFISASEIENVEEFRRFLLEKRGWFVLKHGYPRVFRLRLGYFILRVNVPHLLSIGIRRNIAKKILDHKEEIYEGFVRKAILASFPEGVGIESMAKLFALSTRFSKAYFDGRVTVDIKRILRLPSTLHSKVGLIATYVGTKEREVMKFNPFRHAVPKFRKKEVREAYKLWRESL

>d1jeya\_ e.31.1.1 (A:) Ku70 subunit {Human (Homo sapiens)}

GRDSLIFLVDASKAMFESQSEDELTPFDMSIQCIQSVYISKIISSDRDLLAVVFYGTEKDKNSVNFKNIYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDYSLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDSAKASRARTKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDEDLRVHFEESSKLEDLLRKVRAKETRKRALSRLKLKLNKDIVISVGIYNLVQKALKPPPIKLYRETNEPVKTKTRTFNTSTGGLLLPSDTKRSQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHYLRPSLFVYPEESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQKIQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRSDSFENPVLQQHFRNLEALALDLMEPEQAVDLTLPKVEAMNKRLGSLVDEFKELVYPPDY

>d1jeyb\_ e.31.1.2 (B:) Ku80 subunit {Human (Homo sapiens)}

NKAAVVLCMDVGFTMSNSIPGIESPFEQAKKVITMFVQRQVFAENKDEIALVLFGTDGTDNPLSGGDQYQNITVHRHLMLPDFDLLEDIESKIQPGSQQADFLDALIVSMDVIQHETIGKKFEKRHIEIFTDLSSRFSKSQLDIIIHSLKKCDISLQFFLPFSLGKEDGSGDRGDGPFRLGGHGPSFPLKGITEQQKEGLEIVKMVMISLEGEDGLDEIYSFSESLRKLCVFKKIERHSIHWPCRLTIGSNLSIRIAAYKSILQERVKKTWTVVDAKTLKKEDIQKETVYCLNDDDETEVLKEDIIQGFRYGSDIVPFSKVDEEQMKYKSEGKCFSVLGFCKSSQVQRRFFMGNQVLKVFAARDDEAAAVALSSLIHALDDLDMVAIVRYAYDKRANPQVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQLNAVDALIDSMSLAKKDEKTDTLEDLFPTTKIPNPRFQRLFQCLLHRALHPREPLPPIQQHIWNMLNPPAEVTTKSQIPLSKIKTLFPLIEAKKK

>d1daaa\_ e.17.1.1 (A:) D-amino acid aminotransferase {Bacillus sp., strain YM-1}

GYTLWNDQIVKDEEVKIDKEDRGYQFGDGVYEVVKVYNGEMFTVNEHIDRLYASAEKIRITIPYTKDKFHQLLHELVEKNELNTGHIYFQVTRGTSPRAHQFPENTVKPVIIGYTKENPRPLENLEKGVKATFVEDIRWLRCDIKSLNLLGAVLAKQEAHEKGCYEAILHRNNTVTEGSSSNVFGIKDGILYTHPANNMILKGITRDVVIACANEINMPVKEIPFTTHEALKMDELFVTSTTSEITPVIEIDGKLIRDGKVGEWTRKLQKQFETKIP

>d1i1ka\_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Escherichia coli}

KADYIWFNGEMVRWEDAKVHVMSHALHYGTSVFEGIRCYDSHKGPVVFRHREHMQRLHDSAKIYRFPVSQSIDELMEACRDVIRKNNLTSAYIRPLIFVGDVGMGVNPPAGYSTDVIIAAFPWGAYLGAEALEQGIDAMVSSWNRAAPNTIPTAAKAGGNYLSSLLVGSEARRHGYQEGIALDVNGYISEGAGENLFEVKDGVLFTPPFTSSALPGITRDAIIKLAKELGIEVREQVLSRESLYLADEVFMSGTAAEITPVRSVDGIQVGEGRCGPVTKRIQQAFFGLFTGETEDKWGWLDQVNQ

>d1ekfa\_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Human (Homo sapiens), mitochondrial}

ASSSFKAADLQLEMTQKPHKKPGPGEPLVFGKTFTDHMLMVEWNDKGWGQPRIQPFQNLTLHPASSSLHYSLQLFEGMKAFKGKDQQVRLFRPWLNMDRMLRSAMRLCLPSFDKLELLECIRRLIEVDKDWVPDAAGTSLYVRPVLIGNEPSLGVSQPRRALLFVILCPVGAYFPGGSVTPVSLLADPAFIRAWVGGVGNYKLGGNYGPTVLVQQEALKRGCEQVLWLYGPDHQLTEVGTMNIFVYWTHEDGVLELVTPPLNGVILPGVVRQSLLDMAQTWGEFRVVERTITMKQLLRALEEGRVREVFGSGTACQVCPVHRILYKDRNLHIPTMENGPELILRFQKELKEIQYGIRAHEWMFPV

>d1et0a\_ e.17.1.1 (A:) Aminodeoxychorismate lyase {Escherichia coli}

MFLINGHKQESLAVSDRATQFGDGCFTTARVIDGKVSLLSAHIQRLQDACQRLMISCDFWPQLEQEMKTLAAEQQNGVLKVVISRGSGGRGYSTLNSGPATRILSVTAYPAHYDRLRNEGITLALSPVRLGRNPHLAGIKHLNRLEQVLIRSHLEQTNADEALVLDSEGWVTECCAANLFWRKGNVVYTPRLDQAGVNGIMRQFCIRLLAQSSYQLVEVQASLEESLQADEMVICNALMPVMPVCACGDVSFSSATLYEYLAPLCE

>d2frvb\_ e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit {Desulfovibrio gigas}

NKIVVDPITRIEGHLRIEVEVEGGKIKNAWSMSTLFRGLEMILKGRDPRDAQHFTQRACGVCTYVHALASVRAVDNCVGVKIPENATLMRNLTMGAQYMHDHLVHFYHLHALDWVNVANALNADPAKAARLANDLSPKKTTTESLKAVQAKVKALVESGQLGIFTNAYFLGGHPAYVLPAEVDLIATAHYLEALRVQVKAARAMAIFGAKNPHTQFTVVGGCTNYDSLRPERIAEFRKLYKEVREFIEQVYITDLLAVAGFYKNWAGIGKTSNFLTCGEFPTDEYDLNSRYTPQGVIWGNDLSKVDDFNPDLIEEHVKYSWYEGAGAHHPYKGVTKPKWTEFHGEDRYSWMKAPRYKGEAFEVGPLASVLVAYAKKHEPTVKAVDLVLKTLGVGPEALFSTLGRTAARGIQCLTAAQEVEVWLDKLEANVKAGKDDLYTDWQYPTESQGVGFVNAPRGMLSHWIVQRGGKIENFQLVVPSTWNLGPRCAEGKLSAVEQALIGTPIADPKRPVEILRTVHSYDPCIACGVH

>d1h2rl\_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio vulgaris}

SSYSGPIVVDPVTRIEGHLRIEVEVENGKVKNAYSSSTLFRGLEIILKGRDPRDAQHFTQRTCGVCTYTHALASTRCVDNAVGVHIPKNATYIRNLVLGAQYLHDHIVHFYHLHALDFVDVTAALKADPAKAAKVASSISPRKTTAADLKAVQDKLKTFVETGQLGPFTNAYFLGGHPAYYLDPETNLIATAHYLEALRLQVKAARAMAVFGAKNPHTQFTVVGGVTCYDALTPQRIAEFEALWKETKAFVDEVYIPDLLVVAAAYKDWTQYGGTDNFITFGEFPKDEYDLNSRFFKPGVVFKRDFKNIKPFDKMQIEEHVRHSWYEGAEARHPWKGQTQPKYTDLHGDDRYSWMKAPRYMGEPMETGPLAQVLIAYSQGHPKVKAVTDAVLAKLGVGPEALFSTLGRTAARGIETAVIAEYVGVMLQEYKDNIAKGDNVICAPWEMPKQAEGVGFVNAPRGGLSHWIRIEDGKIGNFQLVVPSTWTLGPRCDKNNVSPVEASLIGTPVADAKRPVEILRTVHSFDPCIACGVH

>d1frfl\_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio fructosovorans}

TPQSTFTGPIVVDPITRIEGHLRIMVEVENGKVKDAWSSSQLFRGLEIILKGRDPRDAQHFTQRACGVCTYVHALASSRCVDDAVKVSIPANARMMRNLVMASQYLHDHLVHFYHLHALDWVDVTAALKADPNKAAKLAASIDTARTGNSEKALKAVQDKLKAFVESGQLGIFTNAYFLGGHKAYYLPPEVNLIATAHYLEALHMQVKAASAMAILGGKNPHTQFTVVGGCSNYQGLTKDPLANYLALSKEVCQFVNECYIPDLLAVAGFYKDWGGIGGTSNYLAFGEFATDDSSPEKHLATSQFPSGVITGRDLGKVDNVDLGAIYEDVKYSWYAPGGDGKHPYDGVTDPKYTKLDDKDHYSWMKAPRYKGKAMEVGPLARTFIAYAKGQPDFKKVVDMVLGKLSVPATALHSTLGRTAARGIETAIVCANMEKWIKEMADSGAKDNTLCAKWEMPEESKGVGLADAPRGSLSHWIRIKGKKIDNFQLVVPSTWNLGPRGPQGDKSPVEEALIGTPIADPKRPVEILRTVHAFDPCIACGVH

>d1cc1l\_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfomicrobium baculatum}

VKISIDPLTRVEGHLKIEVEVKDGKVVDAKCSGGMFRGFEQILRGRDPRDSSQIVQRICGVCPTAHCTASVMAQDDAFGVKVTTNGRITRNLIFGANYLQSHILHFYHLAALDYVKGPDVSPFVPRYANADLLTDRIKDGAKADATNTYGLNQYLKALEIRRICHEMVAMFGGRMPHVQGMVVGGATEIPTADKVAEYAARFKEVQKFVIEEYLPLIYTLGSVYTDLFETGIGWKNVIAFGVFPEDDDYKTFLLKPGVYIDGKDEEFDSKLVKEYVGHSFFDHSAPGGLHYSVGETNPNPDKPGAYSFVKAPRYKDKPCEVGPLARMWVQNPELSPVGQKLLKELYGIEAKKFRDLGDKAFSIMGRHVLRAEETWLTAVAVEKWLKQVQPGAETYVKSEIPDAAEGTGFTEAPRGALLHYLKIKDKKIENYQIVSATLWNANPRDDMGQRGPIEEALIGVPVPDIKNPVNVGRLVRSYDPXLGCAVH

>d1e3db\_ e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit {Desulfovibrio desulfuricans}

TPRSNYTGPIVVDPLTRIEGHLRIEVEVEGGVIKEARSCATLFRGIETILKGRDPRDAQHFTQRTCGVCTYTHALASTRCLEDAINKPIPANATYIRNLVLGNQFMHDHLVHFYHLHALDFVDVTSALLADPAKAAKLANSISPRKATTEEFAAVQAKLKTFVASGQLGPFTNAYFLGGHEGYYMDPEANLVCTAHYLQALRAQVEVAKGMAVFGAKNPHTQFTVAGGVTCYEALTPERIKQFRELYVKARAFIEEVYIPDLLLVASYYKDWGKIGGTNNFMAFGEFPAPGGERDLNSRWYKPGVIYDRKVGSVQPFDPSKIEEHVRHSWYEGKARAPFEGETNPHFTFMGDTDKYSWNKAPRYDGHAVETGPLAQMLVAYGHNHKTIKPTIDAVLGKLNLGPEALFSTLGRTAARGIQTLVIAQQMENWLNEYENNIVKDKQIVEDYAVPTSARGVGFADVSRGGLSHWMTIEDGKIDNFQLVVPTTWNLGPRDDKGVPSAAEAALVGTPVADPKRPVEILRTIHSFDPCIACSTH

>d2frva\_ e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio gigas}

KKRPSVVYLHNAECTGCSESVLRTVDPYVDELILDVISMDYHETLMAGAGHAVEEALHEAIKGDFVCVIEGGIPMGDGGYWGKVGGRNMYDICAEVAPKAKAVIAIGTCATYGGVQAAKPNPTGTVGVNEALGKLGVKAINIAGCPPNPMNFVGTVVHLLTKGMPELDKQGRPVMFFGETVHDNCPRLKHFEAGEFATSFGSPEAKKGYCLYELGCKGPDTYNNCPKQLFNQVNWPVQAGHPCIACSEPNFWDLYSPFYSA

>d1h2rs\_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfovibrio vulgaris}

LMGPRRPSVVYLHNAECTGCSESVLRAFEPYIDTLILDTLSLDYHETIMAAAGDAAEAALEQAVNSPHGFIAVVEGGIPTAANGIYGKVANHTMLDICSRILPKAQAVIAYGTCATFGGVQAAKPNPTGAKGVNDALKHLGVKAINIAGCPPNPYNLVGTIVYYLKNKAAPELDSLNRPTMFFGQTVHEQCPRLPHFDAGEFAPSFESEEARKGWCLYELGCKGPVTMNNCPKIKFNQTNWPVDAGHPCIGCSEPDFWDAMTPFYQN

>d1frfs\_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfovibrio fructosovorans}

KHRPSVVWLHNAECTGCTEAAIRTIKPYIDALILDTISLDYQETIMAAAGETSEAALHEALEGKDGYYLVVEGGLPTIDGGQWGMVAGHPMIETCKKAAAKAKGIICIGTCSPYGGVQKAKPNPSQAKGVSEALGVKTINIPGCPPNPINFVGAVVHVLTKGIPDLDENGRPKLFYGELVHDNCPRLPHFEASEFAPSFDSEEAKKGFCLYELGCKGPVTYNNCPKVLFNQVNWPVQAGHPCLGCSEPDFWDTMTPFYEQG

>d1cc1s\_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfomicrobium baculatum}

KKAPVIWVQGQGCTGCSVSLLNAVHPRIKEILLDVISLEFHPTVMASEGEMALAHMYEIAEKFNGNFFLLVEGAIPTAKEGRYCIVGETLDAKAHHHEVTMMELIRDLAPKSLATVAVGTCSAYGGIPAAEGNVTGSKSVRDFFADEKIEKLLVNVPGCPPHPDWMVGTLVAAWSHVLNPTEHPLPELDDDGRPLLFFGDNIHENCPYLDKYDNSEFAETFTKPGCKAELGCKGPSTYADCAKRRWNNGINWCVENAVCIGCVEPDFPDGKSPFYVAE

>d1e3da\_ e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio desulfuricans}

SRPSVVYLHAAECTGCSEALLRTYQPFIDTLILDTISLDYHETIMAAAGEAAEEALQAAVNGPDGFICLVEGAIPTGMDNKYGYIAGHTMYDICKNILPKAKAVVSIGTCACYGGIQAAKPNPTAAKGINDCYADLGVKAINVPGCPPNPLNMVGTLVAFLKGQKIELDEVGRPVMFFGQSVHDLCERRKHFDAGEFAPSFNSEEARKGWCLYDVGCKGPETYNNCPKVLFNETNWPVAAGHPCIGCSEPNFWDDMTPFYQN

>d1dg4a\_ e.20.1.1 (A:) DnaK {Escherichia coli}

LSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSAKDKNSGKEQKITIKASSGL

>d1dkza\_ e.20.1.1 (A:) DnaK {Escherichia coli}

VLLLDVTPLSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVSIHVLQGERKRAADNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSAKDKNSGKEQKITIKASSGLNEDEIQKMVRDAEANAEADRKFEELVQTRNQGDHLLHSTRKQVEEAGDKLPADDKTAIESALTALETALKGEDKAAIEAKMQELAQVSQKLMEIAQ

>d2bpr\_\_ e.20.1.1 (-) DnaK {Escherichia coli}

SIEGRVKDVLLLDVTPLSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSAKDKNSGKEQKITIKASSGLNEDEIQKMVRDAEANAEADRKFEELVQTRNQGDHLLHSTRKQVEEA

>d1ckra\_ e.20.1.1 (A:) DnaK {Rat (Rattus norvegicus)}

SENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNTTIPTKQTQTFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITITNDKGRLSKEDIERMVQEAEKYKAEDEKQRDKVSSKNSLE

>d1dqsa\_ e.22.1.1 (A:) Dehydroquinate synthase, DHQS {Aspergillus nidulans}

PTKISILGRESIIADFGLWRNYVAKDLISDCSSTTYVLVTDTNIGSIYTPSFEEAFRKRAAEITPSPRLLIYNRPPGEVSKSRQTKADIEDWMLSQNPPCGRDTVVIALGGGVIGDLTGFVASTYMRGVRYVQVPTTLLAMVDSSIGGKTAIDTPLGKNLIGAIWQPTKIYIDLEFLETLPVREFINGMAEVIKTAAISSEEEFTALEENAETILKAVRREVTPGEHRFEGTEEILKARILASARHKAYVVSADEREGGLRNLLNWGHSIGHAIEAILTPQILHGECVAIGMVKEAELARHLGILKGVAVSRIVKCLAAYGLPTSLKDARIRKLTAGKHCSVDQLMFNMALDKKNDGPKKKIVLLSAIGTPYETRASVVANEDIRVVL

>d1jq5a\_ e.22.1.2 (A:) Glycerol dehydrogenase {Bacillus stearothermophilus}

AAERVFISPAKYVQGKNVITKIANYLEGIGNKTVVIADEIVWKIAGHTIVNELKKGNIAAEEVVFSGEASRNEVERIANIARKAEAAIVIGVGGGKTLDTAKAVADELDAYIVIVPTAASTDAPTSALSVIYSDDGVFESYRFYKKNPDLVLVDTKIIANAPPRLLASGIADALATWVEARSVIKSGGKTMAGGIPTIAAEAIAEKCEQTLFKYGKLAYESVKAKVVTPALEAVVEANTLLSGLGFESGGLAAAHAIHNGFTALEGEIHHLTHGEKVAFGTLVQLALEEHSQQEIERYIELYLCLDLPVTLEDIKLKDASREDILKVAKAATAEGETIHNAFNVTADDVADAIFAADQYAKAYKEK

>d1kq3a\_ e.22.1.2 (A:) Glycerol dehydrogenase {Thermotoga maritima, TM0423}

HMITTTIFPGRYVQGAGAINILEEELSRFGERAFVVIDDFVDKNVLGENFFSSFTKVRVNKQIFGGECSDEEIERLSGLVEEETDVVVGIGGGKTLDTAKAVAYKLKKPVVIVPTIASTDAPCSALSVIYTPNGEFKRYLFLPRNPDVVLVDTEIVAKAPARFLVAGMGDALATWFEAESCKQKYAPNMTGRLGSMTAYALARLCYETLLEYGVLAKRSVEEKSVTPALEKIVEANTLLSGLGFESGGLAAAHAIHNGLTVLENTHKYLHGEKVAIGVLASLFLTDKPRKMIEEVYSFCEEVGLPTTLAEIGLDGVSDEDLMKVAEKACDKNETIHNEPQPVTSKDVFFALKAADRYGRMRKNL

>d1lci\_\_ e.23.1.1 (-) Luciferase {Firefly (Photinus pyralis)}

AKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVNITYAEYFEMSVRLAEAMKRYGLNTNHRIVVCSENSLQFFMPVLGALFIGVAVAPANDIYNERELLNSMNISQPTVVFVSKKGLQKILNVQKKLPIIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYDFVPESFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFSHARDPIFGNQIIPDTAILSVVPFHHGFGMFTTLGYLICGFRVVLMYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPGAVGKVVPFFEAKVVDLDTGKTLGVNQRGELCVRGPMIMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELPAAVVVLEHGKTMTEKEIVDYVASQVTTAKKLRGGVVFVDEVPKGLTGKLDARKIREILIKAKK

>d1amua\_ e.23.1.1 (A:) Phenylalanine activating domain of gramicidin synthetase 1 {Bacillus brevis}

GTHEEEQYLFAVNNTKAEYPRDKTIHQLFEEQVSKRPNNVAIVCENEQLTYHELNVKANQLARIFIEKGIGKDTLVGIMMEKSIDLFIGILAVLKAGGAYVPIDIEYPKERIQYILDDSQARMLLTQKHLVHLIHNIQFNGQVEIFEEDTIKIREGTNLHVPSKSTDLAYVIYTSGTTGNPKGTMLEHKGISNLKVFFENSLNVTEKDRIGQFASISFDASVWEMFMALLTGASLYIILKDTINDFVKFEQYINQKEITVITLPPTYVVHLDPERILSIQTLITAGSATSPSLVNKWKEKVTYINAYGPTETTICATTWVATKETIGHSVPIGAPIQNTQIYIVDENLQLKSVGEAGELCIGGEGLARGYWKRPELTSQKFVDNPFVPGEKLYKTGDQARWLSDGNIEYLGRIDNQVKIRGHRVELEEVESILLKHMYISETAVSVHKDHQEQPYLCAYFVSEKHIPLEQLRQFSSEELPTYMIPSYFIQLDKMPLTSNGKIDRKQLPEPDLTF

>d1ad2\_\_ e.24.1.1 (-) Ribosomal protein L1 {Thermus thermophilus}

KRYRALLEKVDPNKIYTIDEAAHLVKELATAKFDETVEVHAKLGIDPRRSDQNVRGTVSLPHGLGKQVRVLAIAKGEKIKEAEEAGADYVGGEEIIQKILDGWMDFDAVVATPDVMGAVGSKLGRILGPRGLLPNPKAGTVGFNIGEIIREIKAGRIEFRNDKTGAIHAPVGKACFPPEKLADNIRAFIRALEAHKPEGAKGTFLRSVYVTTTMGPSVRINPHS

>d1cjsa\_ e.24.1.1 (A:) Ribosomal protein L1 {Archaeon Methanococcus jannaschii}

MDREALLQAVKEARELAKPRNFTQSFEFIATLKEIDMRKPENRIKTEVVLPHGRGKEAKIAVIGTGDLAKQAEELGLTVIRKEEIEELGKNKRKLRKIAKAHDFFIAQADLMPLIGRYMGVILGPRGKMPKPVPANANIKPLVERLKKTVVINTRDKPYFQVLVGNEKMTDEQIVDNIEAVLNVVAKKYEKGLYHIKDAYVKLTMGPAVKVKK

>d1dwua\_ e.24.1.1 (A:) Ribosomal protein L1 {Archaeon Methanococcus thermolithotrophicus}

MDRENILKAVKEARSLAKPRNFTQSLDLIINLKELDLSRPENRLKEQVVLPNGRGKEPKIAVIAKGDLAAQAEEMGLTVIRQDELEELGKNKKMAKKIANEHDFFIAQADMMPLVGKTLGPVLGPRGKMPQPVPANANLTPLVERLKKTVLINTRDKPLFHVLVGNEKMSDEELAENIEAILNTVSRKYEKGLYHVKSAYTKLTMGPPAQIEK

>d1dn1a\_ e.25.1.1 (A:) Neuronal Sec1, NSec1 {Rat (Rattus norvegicus)}

IGLKAVVGEKIMHDVIKKVKKKGEWKVLVVDQLSMRMLSSCCKMTDIMTEGITIVEDINKRREPLPSLEAVYLITPSEKSVHSLISDFKDPPTAKYRAAHVFFTDSCPDALFNELVKSRAAKVIKTLTEINIAFLPYESQVYSLDSADSFQSFYSPHKAQMKNPILERLAEQIATLCATLKEYPAVRYRGEYKDNALLAQLIQDKLDAYKADDPTMGEGPDKARSQLLILDRGFDPSSPVLHELTFQAMSYDLLPIENDVYKYETSGIGEARVKEVLLDEDDDLWIALRHKHIAEVSQEVTRSLKDFSSSKRMNTGEKTTMRDLSQMLKKMPQYQKELSKYSTHLHLAEDCMKHYQGTVDKLCRVEQDLAMGTDAEGEKIKDPMRAIVPILLDANVSTYDKIRIILLYIFLKNGITEENLNKLIQHAQIPPEDSEIITNMAHLGVPIVTDSTLRRRSKPERKERISEQTYQLSRWTPIIKDIMEDTIEDKLDTKHYPYISTRSSASFSTTAVSARYGHWHKNKAPGEYRSGPRLIIFILGGVSLNEMRCAYEVTQANGKWEVLIGSTHILTPQKLLDTLKKLNKTDEEI

>d1epua\_ e.25.1.1 (A:) Neuronal Sec1, NSec1 {Longfin inshore squid (Loligo pealei)}

ALKTAVHEKIMNDVVLAVKKNAEWKVLIVDQLSMRMVSACCKMHEIMSEGITLVEDINRRREPLPLLEAVYLITPTEESVKCLMADFQNPDNPQYRGAHIFFTEACPEELFKELCKSTTARFIKTLKEINIAFLPYESQIFSLDSPDTFQVYYNPSRAQGGIPNKERCAEQIATLCATLGEYPSVRYRSDFDENASFAQLVQQKLDAYRADDPTMGEGPQKDRSQLLILDRGFDPISPLLHELTFQAMAYDLLPIENDVYKYVNTGGNEVPEKEVLLDEKDDLWVEMRHQHIAVVSQNVTKKLKQFADEKRMGTAADKAGIKDLSQMLKKMPQYQKELSKYSTHLHLAEDCMKQYQQHVDKLCKVEQDLAMGTDADGEKIRDHMRNIVPILLDQKISAYDKIRIILLYIIHKGGISEENLAKLVQHAHIPAEEKWIINDMQNLGVPIIQDGGRRKIPQPYHTHNRKERQADHTYQMSRWTPYMKDIMEAAVEDKLDTRHYPFLNGGGPRPSCQQPVSVRYGHWHKDKGQASYKSGPRLIIFVVGGISYSEMRSAYEVTQTAKNNWEVILGSTHILTPEGLLRDLRKISNP

>d1e2ua\_ e.26.1.1 (A:) Hybrid cluster protein (prismane protein) {Desulfovibrio vulgaris}

MFCFQCQETAKNTGCTVKGMCGKPEETANLQDLLIFVLRGIAIYGEKLKELGQPDRSNDDFVLQGLFATITNANWDDARFEAMISEGLARRDKLRNAFLAVYKAKNGKDFSEPLPEAATWTGDSTAFAEKAKSVGILATENEDVRSLRELLIIGLKGVAAYAEHAAVLGFRKTEIDEFMLEALASTTKDLSVDEMVALVMKAGGMAVTTMALLDEANTTTYGNPEITQVNIGVGKNPGILISGHDLKDMAELLKQTEGTGVDVYTHGEMLPANYYPAFKKYPHFVGNYGGSWWQQNPEFESFNGPILLTTNCLVPLKKENTYLDRLYTTGVVGYEGAKHIADRPAGGAKDFSALIAQAKKCPPPVEIETGSIVGGFAHHQVLALADKVVEAVKSGAIKRFVVMAGCDGRQKSRSYYTEVAENLPKDTVILTAGCAKYRYNKLNLGDIGGIPRVLDAGQCNDSYSLAVIALKLKEVFGLDDINDLPVSYDIAWYEQKAVAVLLALLFLGVKGIRLGPTLPAFLSPNVAKVLVENFNIKPIGTVQDDIAAMMAGK

>d1jjya\_ e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase {Carboxydothermus hydrogenoformans}

QNLKSTDRAVQQMLDKAKREGIQTVWDRYEAMKPQCGFGETGLCCRHCLQGPCRINPFGDEPKVGICGATAEVIVARGLDRSIAAGAAGHSGHAKHLAHTLKKAVQGKAASYMIKDRTKLHSIAKRLGIPTEGQKDEDIALEVAKAALADFHEKDTPVLWVTTVLPPSRVKVLSAHGLIPAGIDHEIAEIMHRTSMGCDADAQNLLLGGLRCSLADLAGCYMGTDLADILFGTPAPVVTESNLGVLKADAVNVAVHGHNPVLSDIIVSVSKEMENEARAAGATGINVVGICCTGNEVLMRHGIPACTHSVSQEMAMITGALDAMILDYQCIQPSVATIAECTGTTVITTMEMSKITGATHVNFAEEAAVENAKQILRLAIDTFKRRKGKPVEIPNIKTKVVAGFSTEAIINALSKLNANDPLKPLIDNVVNGNIRGVCLFAGCNNVKVPQDQNFTTIARKLLKQNVLVVATGCGAGALMRHGFMDPANVDELCGDGLKAVLTAIGEANGLGGPLPPVLHMGSCVDNSRSVALVAALANRLGVDMDRLPVVASAAQAMHEKAVAIGTWAVTIGLPTHIGVFPPITGSLPVTQILTSSVKDITGGYFIVELDPQVAADKLLAAINERRAGLGLPR

>d1jqka\_ e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase {Rhodospirillum rubrum}

ETAWHRYEKQQPQCGFGSAGLCCRICLKGPCRIDPFGEGPKYGVCGADRDTIVARHLVRMIAAGTAAHSEHGRHIALAMQHISQGELHDYSIRDEAKLYAIAKTLGVATEGRGLLAIVGDLAAITLGDFQNQDYDKPCAWLAASLTPRRVKRLGDLGLLPHNIDASVAQTMSRTHVGCDADPTNLILGGLRVAMADLDGSMLATELSDALFGTPQPVVSAANLGVMKRGAVNIAVNGHNPMLSDIICDVAADLRDEAIAAGAAEGINIIGICCTGHEVMMRHGVPLATNYLSQELPILTGALEAMVVDVQCIMPSLPRIAECFHTQIITTDKHNKISGATHVPFDEHKAVETAKTIIRMAIAAFGRRDPNRVAIPAFKQKSIVGFSAEAVVAALAKVNADDPLKPLVDNVVNGNIQGIVLFVGCNTTKVQQDSAYVDLAKSLAKRNVLVLATGCAAGAFAKAGLMTSEATTQYAGEGLKGVLSAIGTAAGLGGPLPLVMHMGSCVDNSRAVALATALANKLGVDLSDLPLVASAPECMSEKALAIGSWAVTIGLPTHVGSVPPVIGSQIVTKLVTETAKDLVGGYFIVDTDPKSAGDKLYAAIQERRAGL

>d1h5wa\_ e.27.1.1 (A:) Upper collar protein gp10 (connector protein) {Bacteriophage PHI29}

RQKRNRWFIHYLNYLQSLAYQLFEWENLPPTINPSFLEKSIHQFGYVGFYKDPVISYIACNGALSGQRDVYNQATVFRAASPVYQKEFKLYNYRDMKEEDMGVVIYNNDMAFPTTPTLELFAAELAELKEIISVNQNAQKTPVLIRANDNNQLSLKQVYNQYEGNAPVIFAHEALDSDSIEVFKTDAPYVVDKLNAQKNAVWNEMMTFLGIKNANLEKKERMVTDEVSSNDEQIESSGTVFLKSREEACEKINELYGLNVKVKFRYDI

>d1io1a\_ e.32.1.1 (A:) F41 fragment of flagellin {Salmonella typhimurium}

NIKGLTQASRNANDGISIAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLDSIQAEITQRLNEIDRVSGQTQFNGVKVLAQDNTLTIQVGANDGETIDIDLKQINSQTLGLDTLNVQQKYKVSDTAATVTGYADTTIALDNSTFKASATGLGGTDQKIDGDLKFDDTTGKYYAKVTVTGGTGKDGYYEVSVDKTNGEVTLAGGATSPLTGGLPATATEDVKNVQVANADLTEAKAALTAAGVTGTASVVKMSYTDNNGKTIDGGLAVKVGDDYYSATQNKDGSISINTTKYTADDGTSKTALNKLGGADGKTEVVSIGGKTYAASKAEGHNFKAQPDLAEAAATTTENPLQKIDAALAQVDTLRSDLAAVQNRFNSAITNLGNTVNNLTSAR

>d1htya\_ e.33.1.1 (A:) Golgi alpha-mannosidase II {Fruit fly (Drosophila melanogaster)}

CQDVVQDVPNVDVQMLELYDRMSFKDIDGGVWKQGWNIKYDPLKYNAHHKLKVFVVPHSHNDPGWIQTFEEYYQHDTKHILSNALRHLHDNPEMKFIWAEISYFARFYHDLGENKKLQMKSIVKNGQLEFVTGGWVMPDEANSHWRNVLLQLTEGQTWLKQFMNVTPTASWAIDPFGHSPTMPYILQKSGFKNMLIQRTHYSVKKELAQQRQLEFLWRQIWDNKGDTALFTHMMPFYSYDIPHTCGPDPKVCCQFDFKRMGSFGLSCPWKVPPRTISDQNVAARSDLLVDQWKKKAELYRTNVLLIPLGDDFRFKQNTEWDVQRVNYERLFEHINSQAHFNVQAQFGTLQEYFDAVHQAERAGQAEFPTLSGDFFTYADRSDNYWSGYYTSRPYHKRMDRVLMHYVRAAEMLSAWHSWDGMARIEERLEQARRELSLFQHHDGITGTAKTHVVVDYEQRMQEALKACQMVMQQSVYRLLTKPSIYSPDFSFSYFTLDDSRWPGSGVEDSRTTIILGEDILPSKHVVMHNTLPHWREQLVDFYVSSPFVSVTDLANNPVEAQVSPVWSWHHDTLTKTIHPQGSTTKYRIIFKARVPPMGLATYVLTISDSKPEHTSYASNLLLRKNPTSLPLGQYPEDVKFGDPREISLRVGNGPTLAFSEQGLLKSIQLTQDSPHVPVHFKFLKYGVRSHGDRSGAYLFLPNGPASPVELGQPVVLVTKGKLESSVSVGLPSVVHQTIMRGGAPEIRNLVDIGSLDNTEIVMRLETHIDSGDIFYTDLNGLQFIKRRRLDKLPLQANYYPIPSGMFIEDANTRLTLLTGQPLGGSSLASGELEIMQDRRLASDDERGLGQGVLDNKPVLHIYRLVLEKVNNCVRPSKLHPAGYLTSAAHKASQSLLDPLDKFIFAENEWIGAQGQFGGDHPSAREDLDVSVMRRLTKSSAKTQRVGYVLHRTNLMQCGTPEEHTQKLDVCHLLPNVARCERTTLTFLQNLEHLDGMVAPEVCPMETAAYVSSHS

>d1knza\_ e.34.1.1 (A:) NSP3 homodimer {Simian 11 rotavirus}

TQQMAVSIINSSFEAAVVAATSALENMGIEYDYQDIYSRVKNKFDFVMDDSGVKNNPIGKAITIDQALNNKFGSAIRNRNWLADTSRPAKLDEDVNKLRMMLSSKGIDQKMRVLNACFSVKRIPGKSSSIIKCTKLMRDKLERGEVEVDDSFVDEKM

>g1jmu.1 e.35.1.1 (A:,B:) Membrane penetration protein mu1 {Reovirus}

TINVTGDGNVFKPSAETSSTAVPSLSLSPGMLNXPGGVPWIAIGDETSVTSPGALRRMTSKDIPETAIINTDNSSGAVPSESALVPYNDEPLVVVTEHAIANFTKAEMALEFNREFLDKLRVLSVSPKYSDLLTYVDCYVGVSARQALNNFQKQVPVITPTRQTMYVDSIQAALKALEKWEIDLRVAQTLLPTNVPIGEVSCPMQSVVKLLDDQLPDDSLIRRYPKEAAVALAKRNGGIQWMDVSEGTVMNEAVNAVAASALAPSASAPPLEEKSKLTEQAMDLVTAAEPEIIASLVPVPAPVFAIPPKPADYNVRTLKIDEATWLRMIPKTMGTLFQIQVTDNTGTNWHFNLRGGTRVVNLDQIAPMRFVLDLGGKSYKETSWDPNGKKVGFIVFQSKIPFELWTAASQIGQATVVNYVQLYAEDSSFTAQSIIATTSLAYNYEPEQLNKTDPEMNYYLLATFIDSAAITPTNMTQPDVWDALLTMSPLSAGEVTVKGAVVSEVVPAELIGSYTPESLNASLPNDAARCMIDRASKIAEAIKIDDDAGPDEYSPNSVPIQGQLAISQLETGYGVRIFNPKGILSKIASRAMQAFIGDPSTIITQAAPVLSDKNNWIALAQGVKTSLRTKSLSAGVKTAVSKLSSSESIQNWTQGFLDKVSTHFPAP

>d2btva\_ e.28.1.1 (A:) BTV inner layer core protein vp3 {Bluetongue virus, strain 1}

VDFTVPDVQQILDDIKALAAEQVYKIVKVPSTSFRHIVTQSRDRVLRVDTYYEEMSQVGDVITEDEPEKFYSTIIKKVRFIRGKGSFILHDIPARDHRGMEVAEPEVLGVEFKNVLPVLTAEHRAMIQNALDGSIIENGNVATRDVDVFIGACSEPIYRIYNRLQGYIEAVQLQELRNSIGWLERLGQRKRITYSQEVLTDFRRQDMIWVLALQLPVNPQVVWDVPRSSIANLIMNIATCLPTGEYIAPNPRISSITLTQRITTTGPFAILTGSTPTAQQLNDVRKIYLALMFPGQIILDLKIDPGERMDPAVRMVAGVVGHLLFTAGGRFTNLTQNMARQLDIALNDYLLYMYNTRVQVNYGPTGEPLDFQIGRNQYDCNVFRADFATGTGYNGWATIDVEYRDPAPYVHAQRYIRYCGIDSRELINPTTYGIGMTYHCYNEMLRMLVAAGKDSEAAYFRSMLPFHMVRFARINQIINEDLHSVFSLPDDMFNALLPDLIAGAHQNADPVVLDVSWISLWFAFNRSFEPTHRNEMLEIAPLIESVYASELSVMKVDMRHLSLMQRRFPDVLIQARPSHFWKAVLNDSPEAVKAVMNLSHSHNFINIRDMMRWVLLPSLQPSLKLVLEEEAWAAANDFEDLMLTDQVYMHRDMLPEPRLDDIERFRQEGFYYTNMLEAPPEIDRVVQYTYEIARLQANMGQFRAALRRIMDDDDWVRFGGVLRTVRVKFFDARPPDDILQGLPFSYDTNEKGGLSYATIKYATETTIFYLIYNVEFSNTPDSLVLINPTYTMTKVFINKRIVERVRVGQILAVLNRRFVAYKGKMRIMDITQSLKMGTKLAAPTV

>d1cola\_ f.1.1.1 (A:) Colicin A {Escherichia coli}

AKDERELLEKTSELIAGMGDKIGEHLGDKYKAIAKDIADNIKNFQGKTIRSFDDAMASLNKITANPAMKINKADRDALVNAWKHVDAQDMANKLGNLSKAFKVADVVMKVEKVREKSIEGYETGNWGPLMLEVESWVLSGIASSVALGIFSATLGAYALSLGVPAIAVGIAGILLAAVVGALIDDKFADALNNEIIR

>d1a87\_\_ f.1.1.1 (-) Colicin N {Escherichia coli}

SAKVGEITITPDNSKPGRYISSNPEYSLLAKLIDAESIKGTEVYTFHTRKGQYVKVTVPDSNIDKMRVDYVNWKGPKYNNKLVKRFVSQFLLFRKEEKEKNEKEALLKASELVSGMGDKLGEYLGVKYKNVAKEVANDIKNFHGRNIRSYNEAMASLNKVLANPKMKVNKSDKDAIVNAWKQVNAKDMANKIGNLGKAFKVADLAIKVEKIREKSIEGYNTGNWGPLLLEVESWIIGGVVAGVAISLFGAVLSFLPISGLAVTALGVIGIMTISYLSSFIDANRVSNINNIISSVIR

>d1cii\_1 f.1.1.1 (451-624) Colicin Ia {Escherichia coli}

DAINFTTEFLKSVSEKYGAKAEQLAREMAGQAKGKKIRNVEEALKTYEKYRADINKKINAKDRAAIAAALESVKLSDISSNLNRFSRGLGYAGKFTSLADWITEFGKAVRTENWRPLFVKTETIIAGNAATALVALVFSILTGSALGIIGYGLLMAVTGALIDESLVEKANKFW

>d1f0la3 f.1.2.1 (A:201-380) Diphtheria toxin, middle domain {Corynebacterium diphtheriae}

CINLDWDVIRDKTKTKIESLKEHGPIKNKMSESPNKTVSEEKAKQYLEEFHQTALEHPELSELKTVTGTNPVFAGANYAAWAVNVAQVIDSETADNLEKTTAALSILPGIGSVMGIADGAVHHNTEEIVAQSIALSSLMVAQAIPLVGELVDIGFAAYNFVESIINLFQVVHNSYNRPAY

>d1dlc\_3 f.1.3.1 (61-289) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}

TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSEDPWKAFMEQVEALMDQKIADYAKNKALAELQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR

>d1ji6a3 f.1.3.1 (A:64-290) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis, CRY3bb1}

DAVGTGISVVGQILGVVGVPFAGALTSFYQSFLNTIWPSDADPWKAFMAQVEVLIDKKIEEYAKSKALAELQGLQNNFEDYVNALNSWKKTPLSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDVAEFYHRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFYDIR

>d1ciy\_3 f.1.3.1 (33-255) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis, CRYIA (A)}

YTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTLTVLDIVALFSNYDSRRY

>d1i5pa3 f.1.3.1 (A:1-263) delta-Endotoxin (insectocide), N-terminal domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

MNNVLNSGRTTICDAYNVVAHDPFSFEHKSLDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLLKKVGSLIGKRILSELWGIIFPSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELIGLQANIREFNQQVDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLSFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHDMLEFRTYMFLNVFEYVSIWSLFK

>d1g5ma\_ f.1.4.1 (A:) Bcl-2 {Human (Homo sapiens)}

HAGRTGYDNREIVMKYIHYKLSQRGYEWDAGDDVEENRTEAPEGTESEVVHLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGRFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRHLHTWIQDNGGWDAFVELYGPSMR

>d1bxla\_ f.1.4.1 (A:) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSMAMSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERLEHHHHHH

>d1lxl\_\_ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSMAMSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYGNNAAAESRKGQERLEHHHHHH

>d1maz\_\_ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLNDHLEPWIQENGGWDTFVELYG

>d2bida\_ f.1.4.1 (A:) Proapoptotic molecule Bid {Human (Homo sapiens)}

GSMDCEVNNGSSLRDECITNLLVFGFLQSCSDNSFRRELDALGHELPVLAPQWEGYDELQTDGNRSSHSRLGRIEADSESQEDIIRNIARHLAQVGDSMDRSIPPGLVNGLALQLRNTSRSEEDRNRDLATALEQLLQAYPRDMEKEKTMLVLALLLAKKVASHTPSLLRDVFHTTVNFINQNLRTYVRSLARNGMD

>d1ddba\_ f.1.4.1 (A:) Proapoptotic molecule Bid {Mouse (Mus musculus)}

MDSEVSNGSGLGAKHITDLLVFGFLQSSGCTRQELEVLGRELPVQAYWEADLEDELQTDGSQASRSFNQGRIEPDSESQEEIIHNIARHLAQIGDEMDHNIQPTLVRQLAAQFMNGSLSEEDKRNCLAKALDEVKTAFPRDMENDKAMLIMTMLLAKKVASHAPSLLRDVFHTTVNFINQNLFSYVRNLVRNEMD

>d1f16a\_ f.1.4.1 (A:) Proapoptotic molecule Bax {Human (Homo sapiens)}

MDGSGEQPRGGGPTSSEQIMKTGALLLQGFIQDRAGRMGGEAPELALDPVPQDASTKKLSECLKRIGDELDSNMELQRMIAAVDTDSPREVFFRVAADMFSDGNFNWGRVVALFYFASKLVLKALCTKVPELIRTIMGWTLDFLRERLLGWIQDQGGWDGLLSYFGTPTWQTVTIFVAGVLTASLTIWKKMG

>d1ikpa3 f.1.5.1 (A:252-394) Exotoxin A, middle domain {Pseudomonas aeruginosa}

EGGSLAALTAHQACHLPLETFTRHRQPRGAEQLEQCGYPVQRLVALYLAARLSWNQVDQVIRNALASPGSGGDLGEAIREQPEQARLALTLAAAESERFVRQGTGNDEAGAANADVVSLTCPVAAGECAGPADSGDALLERNY

>d1c3wa\_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGEQNPIYWARYADWLFTTPLLLLDLALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYRFVWWAISTAAMLYILYVLFFGFSMRPEVASTFKVLRNVTVVLWSAYPVVWLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGLILLRSRAIFG

>d1c8sa\_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGYGLTMVPFGGEQNPIYWARYADWLFTTPLLLLNLALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYRFVWWAISTAAMLYILYVLFNVTVVLWSAYPVVWLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGLI

>d1e12a\_ f.2.1.1 (A:) Halorhodopsin {Halobacterium salinarum}

RENALLSSSLWVNVALAGIAILVFVYMGRTIRPGRPRLIWGATLMIPLVSISSYLGLLSGLTVGMIEMPAGHALAGEMVRSQWGRYLTWALSTPMILLALGLLADVDLGSLFTVIAADIGMCVTGLAAAMTTSALLFRWAFYAISCAFFVVVLSALVTDWAASASSAGTAEIFDTLRVLTVVLWLGYPIVWAVGVEGLALVQSVGATSWAYSVLDVFAKYVFAFILLRWVANNERTVAV

>d1h68a\_ f.2.1.1 (A:) Sensory rhodopsin II {Natronobacterium pharaonis}

VGLTTLFWLGAIGMLVGTLAFAWAGRDAGSGERRYYVTLVGISGIAAVAYVVMALGVGWVPVAERTVFAPRYIDWILTTPLIVYFLGLLAGLDSREFGIVITLNTVVMLAGFAGAMVPGIERYALFGMGAVAFLGLVYYLVGPMTESASQRSSGIKSLYVRLRNLTVILWAIYPFIWLLGPPGVALLTPTVDVALIVYLDLVTKVGFGFIALDAAATL

>d1hzxa\_ f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}

MNGTEGPNFYVPFSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLLIMLGFPINFLTLYVTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYTPHEETNNESFVIYMFVVHFIIPLIVIFFCYGQLVFTVKEAAAQQQESATTQKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRNCMVTTLCCGKNPLGDDEASTTVSKTETSQVAPA

>d1jfpa\_ f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}

LAAYMFLLIMLGFPINFLTLYVTVQHKKLRTPLNYILLNLAVADLFMVFGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYTPHEETNNESFVIYMFVVHFIIPLIVIFFCYGQLVFTVKEAAAQQQESATTQKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAVYNPVIYIMMNKQFRNCMVTTLCCGKNPLGDDEASTTVSKTETSQVAPA

>d1dxrh2 f.2.1.2 (H:1-36) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

MYHGALAQHLDIAQLVWYAQWLVIWTVVLLYLRRED

>d1dxrl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

ALLSFERKYRVRGGTLIGGDLFDFWVGPYFVGFFGVSAIFFIFLGVSLIGYAASQGPTWDPFAISINPPDLKYGLGAAPLLEGGFWQAITVCALGAFISWMLREVEISRKLGIGWHVPLAFCVPIFMFCVLQVFRPLLLGSWGHAFPYGILSHLDWVNNFGYQYLNWFYNPGHMSSVSFLFVNAMALGLHGGLILSVANPGDGDKVKTAEHENQYFRDVVGYSIGALSIHRLGLFLASNIFLTGAFGTIASGPFWTRGWPEWWGWWLDIPFWS

>d1dxrm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

ADYQTIYTQIQARGPHITVSGEWGDNDRVGKPFYSYWLGKIGDAQIGPIYLGASGIAAFAFGSTAILIILFNMAAEVHFDPLQFFRQFFWLGLYPPKAQYGMGIPPLHDGGWWLMAGLFMTLSLGSWWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVPFGIWPHIDWLTAFSIRYGNFYYCPWHGFSIGFAYGCGLLFAAHGATILAVARFGGDREIEQITDRGTAVERAALFWRWTIGFNATIESVHRWGWFFSLMVMVSASVGILLTGTFVDNWYLWCVKHGAAPDYPAYLPATPDPASLPGAPK

>d1qovh2 f.2.1.2 (H:11-35) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

DLASLAIYSFWIFLAGLIYYLQTEN

>d1qovl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

ALLSFERKYRVPGGTLVGGNLFDFWVGPFYVGFFGVATFFFAALGIILIAWSAVLQGTWNPQLISVYPPALEYGLGGAPLAKGGLWQIITICATGAFVSWALREVEICRKLGIGYHIPFAFAFAILAYLTLVLFRPVMMGAWGYAFPYGIWTHLDWVSNTGYTYGNFHYNPAHMIAISFFFTNALALALHGALVLSAANPEKGKEMRTPDHEDTFFRDLVGYSIGTLGIHRLGLLLSLSAVFFSALCMIITGTIWFDQWVDWWQWWVKLPWWANIPGGING

>d1qovm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

AEYQNIFSQVQVRGPADLGMTEDVNLANRSGVGPFSTLLGWFGNAQLGPIYLGSLGVLSLFSGLMWFFTIGIWFWYQAGWNPAVFLRDLFFFSLEPPAPEYGLSFAAPLKEGGLWLIASFFMFVAVWSWWGRTYLRAQALGMGKHTAWAFLSAIWLWMVLGFIRPILMGSWSEAVPYGIFSHLDWTNNFSLVHGNLFYNPFHGLSIAFLYGSALLFAMHGATILAVSRFGGERELEQIADRGTAAERAALFWRWTMGFNWTMEGIHRWAIWMAVLVTLTGGIGILLSGTVVDNWYVWGQNHG

>d2rcrh2 f.2.1.2 (H:1-35) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

MVGVTAFGNFDLASLAIYSFWIFLAGLIYYLQTEN

>d1eysh2 f.2.1.2 (H:7-43) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

HYIDAAQITIWAFWLFFFGLIIYLRREDKREGYPLDS

>d1eysl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

AMLSFEKKYRVRGGTLIGGDLFDFWVGPFYVGFFGVVGFCFTLLGVLLIVWGATIGPTGPTSDLQTYNLWRISIAPPDLSYGLRMAPLTEGGLWQIITICAAGAFISWALREVEICRKLGIGFHVPFAFSFAIGAYLVLVFVRPLLMGAWGHGFPYGILSHLDWVSNVGYQFLHFHYNPAHMLAISFFFTNCLALSMHGSLILSVTNPQRGEPVKTSEHENTFFRDIVGYSIGALAIHRLGLFLALSAAFWSAVCILISGPFWTRGWPEWWNWWLELPLW

>d1eysm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

PEYQNIFTAVQVRAPAYPGVPLPKGNLPRIGRPIFSYWLGKIGDAQIGPIYLGLTGTLSIFFGLVAISIIGFNMLASVHWDVFQFLKHFFWLGLEPPPPQYGLRIPPLSEGGWWLIAGLFLTLSILLWWVRTYKRAEALGMSQHLSWAFAAAIFFYLVLGFIRPVMMGSWAKAVPFGIFPHLDWTAAFSIRYGNLYYNPFHMLSIAFLYGSALLFAMHGATILSVSRFGGDREIDQITHRGTAAEGAALFWRWTMGFNATMESIHRWAWWCAVLTVITAGIGILLSGTVVDNWYLWAVKHGMAPAYPEVVTAVNPYET

>d1ocra1 f.2.1.3 (A:) Cytochrome c oxidase {Cow (Bos taurus)}

MFINRWLFSTNHKDIGTLYLLFGAWAGMVGTALSLLIRAELGQPGTLLGDDQIYNVVVTAHAFVMIFFMVMPIMIGGFGNWLVPLMIGAPDMAFPRMNNMSFWLLPPSFLLLLASSMVEAGAGTGWTVYPPLAGNLAHAGASVDLTIFSLHLAGVSSILGAINFITTIINMKPPAMSQYQTPLFVWSVMITAVLLLLSLPVLAAGITMLLTDRNLNTTFFDPAGGGDPILYQHLFWFFGHPEVYILILPGFGMISHIVTYYSGKKEPFGYMGMVWAMMSIGFLGFIVWAHHMFTVGMDVDTRAYFTSATMIIAIPTGVKVFSWLATLHGGNIKWSPAMMWALGFIFLFTVGGLTGIVLANSSLDIVLHDTYYVVAHFHYVLSMGAVFAIMGGFVHWFPLFSGYTLNDTWAKIHFAIMFVGVNMTFFPQHFLGLSGMPRRYSDYPDAYTMWNTISSMGSFISLTAVMLMVFIIWEAFASKREVLTVDLTTTNLEWLNGCPPPYHTFEEPTYVNLK

>d1ocrb2 f.2.1.3 (B:1-90) Cytochrome c oxidase {Cow (Bos taurus)}

MAYPMQLGFQDATSPIMEELLHFHDHTLMIVFLISSLVLYIISLMLTTKLTHTSTMDAQEVETIWTILPAIILILIALPSLRILYMMDEI

>d1ocrc1 f.2.1.3 (C:) Cytochrome c oxidase {Cow (Bos taurus)}

MTHQTHAYHMVNPSPWPLTGALSALLMTSGLTMWFHFNSMTLLMIGLTTNMLTMYQWWRDVIRESTFQGHHTPAVQKGLRYGMILFIISEVLFFTGFFWAFYHSSLAPTPELGGCWPPTGIHPLNPLEVPLLNTSVLLASGVSITWAHHSLMEGDRKHMLQALFITITLGVYFTLLQASEYYEAPFTISDGVYGSTFFVATGFHGLHVIIGSTFLIVCFFRQLKFHFTSNHHFGFEAGAWYWHFVDVVWLFLYVSIYWWGS

>d1ocrd1 f.2.1.3 (D:) Cytochrome c oxidase {Cow (Bos taurus)}

SVVKSEDYALPSYVDRRDYPLPDVAHVKNLSASQKALKEKEKASWSSLSIDEKVELYRLKFKESFAEMNRSTNEWKTVVGAAMFFIGFTALLLIWEKHYVYGPIPHTFEEEWVAKQTKRMLDMKVAPIQGFSAKWDYDKNEWKK

>d1ocrg1 f.2.1.3 (G:) Cytochrome c oxidase {Cow (Bos taurus)}

ASAAKGDHGGTGARTWRFLTFGLALPSVALCTLNSWLHSGHRERPAFIPYHHLRIRTKPFSWGDGNHTFFHNPRVNPLPTGYEK

>d1ocri1 f.2.1.3 (I:) Cytochrome c oxidase {Cow (Bos taurus)}

STALAKPQMRGLLARRLRFHIVGAFMVSLGFATFYKFAVAEKRKKAYADFYRNYDSMKDFEEMRKAGIFQSAK

>d1ocrj1 f.2.1.3 (J:) Cytochrome c oxidase {Cow (Bos taurus)}

FENRVAEKQKLFQEDNGLPVHLKGGATDNILYRVTMTLCLGGTLYSLYCLGWASFPHK

>d1ocrk1 f.2.1.3 (K:) Cytochrome c oxidase {Cow (Bos taurus)}

APDFHDKYGNAVLASGATFCVAVWVYMATQIGIEWNPSPVGRVTPKEWR

>d1ocrl1 f.2.1.3 (L:) Cytochrome c oxidase {Cow (Bos taurus)}

SHYEEGPGKNIPFSVENKWRLLAMMTLFFGSGFAAPFFIVRHQLLKK

>d1ocrm1 f.2.1.3 (M:) Cytochrome c oxidase {Cow (Bos taurus)}

ITAKPAKTPTSPKEQAIGLSVTFLSFLLPAGWVLYHLDNYKKS

>d1ar1a1 f.2.1.3 (A:) Cytochrome c oxidase {Paracoccus denitrificans}

GFFTRWFMSTNHKDIGILYLFTAGIVGLISVCFTVYMRMELQHPGVQYMCLEGARLIADASAECTPNGHLWNVMITYHGVLMMFFVVIPALFGGFGNYFMPLHIGAPDMAFPRLNNLSYWMYVCGVALGVASLLAPGGNDQMGSGVGWVLYPPLSTTEAGYSMDLAIFAVHVSGASSILGAINIITTFLNMRAPGMTLFKVPLFAWSVFITAWLILLSLPVLAGAITMLLMDRNFGTQFFDPAGGGDPVLYQHILWFFGHPEVYIIILPGFGIISHVISTFAKKPIFGYLPMVLAMAAIGILGFVVWAHHMYTAGMSLTQQAYFMLATMTIAVPTGIKVFSWIATMWGGSIEFKTPMLWAFGFLFLFTVGGVTGVVLSQAPLDRVYHDTYYVVAHFHYVMSLGAVFGIFAGVYYWIGKMSGRQYPEWAGQLHFWMMFIGSNLIFFPQHFLGRQGMPRRYIDYPVEFAYWNNISSIGAYISFASFLFFIGIVFYTLFAGKRVNVPNYWNEHADTLEWTLPSPPPEHTFET

>d1ar1b2 f.2.1.3 (B:1-107) Cytochrome c oxidase {Paracoccus denitrificans}

QDVLGDLPVIGKPVNGGMNFQPASSPLAHDQQWLDHFVLYIITAVTIFVCLLLLICIVRFNRRANPVPARFTHNTPIEVIWTLVPVLILVAIGAFSLPILFRSQEMP

>d1qlec1 f.2.1.3 (C:) Cytochrome c oxidase {Paracoccus denitrificans}

AHVKNHDYQILPPSIWPFFGAIGAFVMLTGAVAWMKGITFFGLPVEGPWMFLIGLVGVLYVMFGWWADVVNEGETGEHTPVVRIGLQYGFILFIMSEVMFFVAWFWAFIKNALYPMGPDSPIKDGVWPPEGIVTFDPWHLPLINTLILLLSGVAVTWAHHAFVLEGDRKTTINGLIVAVILGVCFTGLQAYEYSHAAFGLADTVYAGAFYMATGFHGAHVIIGTIFLFVCLIRLLKGQMTQKQHVGFEAAAWYWHFVDVVWLFLFVVIYIWGR

>d1qled1 f.2.1.3 (D:) Cytochrome c oxidase {Paracoccus denitrificans}

TDHKHGEMDIRHQQATFAGFIKGATWVSILSIAVLVFLALANS

>d1ehka1 f.2.1.3 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AYPEKKATLYFLVLGFLALIVGSLFGPFQALNYGNVDAYPLLKRLLPFVQSYYQGLTLHGVLNAIVFTQLFAQAIMVYLPARELNMRPNMGLMWLSWWMAFIGLVVAALPLLANEATVLYTFYPPLKGHWAFYLGASVFVLSTWVSIYIVLDLWRRWKAANPGKVTPLVTYMAVVFWLMWFLASLGLVLEAVLFLLPWSFGLVEGVDPLVARTLFWWTGHPIVYFWLLPAYAIIYTILPKQAGGKLVSDPMARLAFLLFLLLSTPVGFHHQFADPGIDPTWKMIHSVLTLFVAVPSLMTAFTVAASLEFAGRLRGGRGLFGWIRALPWDNPAFVAPVLGLLGFIPGGAGGIVNASFTLDYVVHNTAWVPGHFHLQVASLVTLTAMGSLYWLLPNLTGKPISDAQRRLGLAVVWLWFLGMMIMAVGLHWAGLLNVPRRAYIAQVPDAYPHAAVPMVFNVLAGIVLLVALLLFIYGLFSVLLSRERKPELAEAPLPFAEVISGPEDRRLVLAMDRIGFWFAVAAILVVLAYGPTLVQLFGHLNPVPGWRLW

>d1ehkb2 f.2.1.3 (B:3-40) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

DEHKAHKAILAYEKGWLAFSLAMLFVFIALIAYTLATH

>d1ehkc1 f.2.1.3 (C:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

EEKPKGALAVILVLTLTILVFWLGVYAVFFARG

>d1ffta1 f.2.1.3 (A:) Ubiquinol oxidase {Escherichia coli}

VDHKRLGIMYIIVAIVMLLRGFADAIMMRSQQALASAGEAGFLPPHHYDQIFTAHGVIMIFFVAMPFVIGLMNLVVPLQIGARDVAFPFLNNLSFWFTVVGVILVNVSLGVGEFAQTGWLAYPPLSGIEYSPGVGVDYWIWSLQLSGIGTTLTGINFFVTILKMRAPGMTMFKMPVFTWASLCANVLIIASFPILTVTVALLTLDRYLGTHFFTNDMGGNMMMYINLIWAWGHPEVYILILPVFGVFSEIAATFSRKRLFGYTSLVWATVCITVLSFIVWLHHFFTMGAGANVNAFFGITTMIIAIPTGVKIFNWLFTMYQGRIVFHSAMLWTIGFIVTFSVGGMTGVLLAVPGADFVLHNSLFLIAHFHNVIIGGVVFGCFAGMTYWWPKAFGFKLNETWGKRAFWFWIIGFFVAFMPLYALGFMGMTRRLSQQIDPQFHTMLMIAASGAVLIALGILCLVIQMYVSIRDRDQNRDLTGDPWGGRTLEWATSSPPPFYNF

>d1fftb2 f.2.1.3 (B:27-117) Ubiquinol oxidase {Escherichia coli}

SALLDPKGQIGLEQRSLILTAFGLMLIVVIPAILMAVGFAWKYRASNKDAKYSPNWSHSNKVEAVVWTVPILIIIFLAVLTWKTTHALEPS

>d1fftc1 f.2.1.3 (C:) Ubiquinol oxidase {Escherichia coli}

HDAGGTKIFGFWIYLMSDCILFSILFATYAVLVNGTAGGPTGKDIFELPFVLVETFLLLFSSITYGMAAIAMYKNNKSQVISWLALTWLFGAGFIGMEIYEFHHLIVNGMGPDRSGFLSAFFALVGTHGLHVTSGLIWMAVLMVQIARRGLTSTNRTRIMCLSLFWHFLDVVWICVFTVVYLMGA

>d1c0va\_ f.2.1.4 (A:) Subunit C {Escherichia coli}

MENLNMDLLYMAAAVMMGLAAIGAAIGIGILGGKFLEGAARQPDLIPLLRTQFFIVMGLVDAIPMIAVGLGLYVMFAVA

>d1c17m\_ f.2.1.4 (M:) Subunit A {Escherichia coli}

HGKSKLIAPLALTIFVWVFLMNLMDLLPIDLLPYIAEHVLGLPALRVVPSADVNVTLSMALGVFILILFYSIKMKGIGGFTKELTLQPFNHWAFIPVNLILEGVSLLSKPVSLGLRLFGNMYAGELIFILIAGLLPWWSQWILNVPWAIFHILIITLQAFIFMVLTIVYLS

>d1h6ia\_ f.2.1.5 (A:) Aquaporin-1 {Human (Homo sapiens)}

LFWRAVVAEFLATTLFVFISIGSALGFKYPVGNNQTAVQDNVKVSLAFGLSIATLAQSVGHISGAHLNPAVTLGLLLSCQISIFRALMYIIAQCVGAIVATAILSGITSSLTGNSLGRNDLADGVNSGQGLGIEIIGTLQLVLCVLATTDRRRRDLGGSAPLAIGLSVALGHLLAIDYTGCGINPARSFGSAVITHNFSNHWIFWVGPFIGGALAVLIYDFILAP

>d1fx8a\_ f.2.1.5 (A:) Glycerol uptake facilitator protein GlpF {Escherichia coli}

TLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAHLNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAILMGLILALTDDGNGVPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHL

>d1kpka\_ f.2.1.13 (A:) Clc chloride channel {Escherichia coli}

QAARLRRRQLIRQLLERDKTPLAILFMAAVVGTLVGLAAVAFDKGVAWLQNQRMGALVHTADNYPLLLTVAFLCSAVLAMFGYFLVRKYAPEAGGSGIPEIEGALEDQRPVRWWRVLPVKFFGGLGTLGGGMVLGREGPTVQIGGNIGRMVLDIFRLKGDEARHTLLATGAAAGLAAAFNAPLAGILFIIEEMRPQFRYTLISIKAVFIGVIMSTIMYRIFNHEVALIDVGKLSDAPLNTLWLYLILGIIFGIFGPIFNKWVLGMQDLLHRVHGGNITKWVLMGGAIGGLCGLLGFVAPATSGGGFNLIPIATAGNFSMGMLVFIFVARVITTLLCFSSGAPGGIFAPMLALGTVLGTAFGMVAVELFPQYHLEAGTFAIAGMGALLAASIRAPLTGIILVLEMTDNYQLILPMIITGLGATLLAQFTGGKPLYSAILARTLAKQEAEQL

>d1kpla\_ f.2.1.13 (A:) Clc chloride channel {Salmonella typhimurium}

TPLAILFMAAVVGTLTGLVGVAFEKAVSWVQNMRIGALVQVADHAFLLWPLAFILSALLAMVGYFLVRKFAPEAGGSGIPEIEGALEELRPVRWWRVLPVKFIGGMGTLGAGMVLGREGPTVQIGGNLGRMVLDVFRMRSAEARHTLLATGAAAGLSAAFNAPLAGILFIIEEMRPQFRYNLISIKAVFTGVIMSSIVFRIFNGEAPIIEVGKLSDAPVNTLWLYLILGIIFGVVGPVFNSLVLRTQDMFQRFHGGEIKKWVLMGGAIGGLCGILGLIEPAAAGGGFNLIPIAAAGNFSVGLLLFIFITRVVTTLLCFSSGAPGGIFAPMLALGTLLGTAFGMAAAVLFPQYHLEAGTFAIAGMGALMAASVRAPLTGIVLVLEMTDNYQLILPMIITCLGATLLAQFLGGKPLYSTILARTLAKQDAEQ

>d1f6ga\_ f.2.1.11 (A:) Potassium chanel protein {Streptomyces lividans}

MPPMLSGLLARLVKLLLGRHGSALHWAAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLITYPAALWWSVETATTVGYGDLYPVTLWGRCVAVVVMVAGITSFGLVTAALATWFVGREQERRGHFVRHSEKAAEEAYTRTTRALHERFDRLERMLDDNRR

>d1jq2a\_ f.2.1.11 (A:) Potassium chanel protein {Streptomyces lividans}

LWGRCVAVVVMVAGITSFGLVTAALATWFVGREQ

>d1k4cc\_ f.2.1.11 (C:) Potassium chanel protein {Streptomyces lividans}

SALHWRAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLITYPRALWWSVETATTVGYGDLYPVTLWGRCVAVVVMVAGITSFGLVTAALATWFVGREQERRGH

>d1g4yb\_ f.2.1.11 (B:) Small conductance potassium channel {Rat (Rattus norvegicus)}

DTQLTKRVKNAAANVLRETWLIYKNTKLVKKIDHAKVRKHQRKFLQAIHQLRSVKMEQRKLNDQANTLVDLAKTQLEHHHHH

>d1kkda\_ f.2.1.11 (A:) Small conductance potassium channel {Rat (Rattus norvegicus)}

RKLELTKAEKHVHNFMMDTQLTKRVKNAAANVLRETWLIYKNTKLVKKIDHAKVRKHQRKFLQAIHQLRSVKMEQRKLNDQANTLVDLAKTQ

>d1msla\_ f.2.1.11 (A:) Gated mechanosensitive channel {Mycobacterium tuberculosis}

ARGNIVDLAVAVVIGTAFTALVTKFTDSIITPLINRIGVNAQSDVGILRIGIGGGQTIDLNVLLSAAINFFLIAFAVYFLVVLPYNTLRKKGEVEQPGDTQVVLLTEIR

>d1be3c1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

MTNIRKSHPLMKIVNNAFIDLPAPSNISSWWNFGSLLGICLILQILTGLFLAMHYTSDTTTAFSSVTHICRDVNYGWIIRYMHANGASMFFICLYMHVGRGLYYGSYTFLETWNIGVILLLTVMATAFMGYVLPWGQMSFWGATVITNLLSAIPYIGTNLVEWIWGGFSVDKATLTRFFAFHFILPFIIMAIAMVHLLFLHETGSNNPTGISSDVDKIPFHPYYTIKDILGALLLILALMLLVLFAPDLLGDPDNYTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALAFSILILALIPLLHTSKQRSMMFRPLSQCLFWALVADLLTLTWIGGQPVEHPYITIGQLASVLYFLLILVLMPTAGTIENKLLKW

>d1be3e2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

SHTDIKVPDFSDYRRPEVLDSTKSSKESSEARKGFSYLVTATTTVGVAYAAKNVVSQFVSSMSASADVL

>d1be3f1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

AVSASSRWLEGIRKWYYNAAGFNKLGLMRDDTIHENDDVKEAIRRLPENLYDDRVFRIKRALDLSMRQQILPKEQWTKYEEDKSYLEPYLKEVIRERKEREEWAKK

>d1be3g1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRRTRACILRVAPPFVAFYLVYTWGTQEFEKSKRKNPAAYENDR

>d1be3k1 f.2.1.8 (K:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

RNWVPTAQLWGAVGAVGLVSAT

>d1qcrg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRRTRACILRVAPPFVAFYLVYTWGTQEFEKSK

>d1qcrh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

TTVREQCEQLEKCVKARERLELCDERVSSRSQTEEDCTEELLDFLHARDHCVAHKLFNSL

>d1qcrk1 f.2.1.8 (K:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

MLTRFLGPRYRQLARNWVPTAQLWGAVGAVGLVSATDSRLILDWV

>d1bccc1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

APNIRKSHPLLKMINNSLIDLPAPSNISAWWNFGSLLAVCLMTQILTGLLLAMHYTADTSLAFSSVAHTCRNVQYGWLIRNLHANGASFFFICIFLHIGRGLYYGSYLYKETWNTGVILLLTLMATAFVGYVLPWGQMSFWGATVITNLFSAIPYIGHTLVEWAWGGFSVDNPTLTRFFALHFLLPFAIAGITIIHLTFLHESGSNNPLGISSDSDKIPFHPYYSFKDILGLTLMLTPFLTLALFSPNLLGDPENFTPANPLVTPPHIKPEWYFLFAYAILRSIPNKLGGVLALAASVLILFLIPFLHKSKQRTMTFRPLSQTLFWLLVANLLILTWIGSQPVEHPFIIIGQMASLSYFTILLILFPTIGTLENKMLNY

>d1bccd3 f.2.1.8 (D:196-241) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

PEHDHRKRMGLKMLLMMGLLVPLVYYMKRHKWSVLKSRKLAYRPPK

>d1bcce2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

SHTDIKVPNFSDYRRPPDDYSTKSSRESDPSRKGFSYLVTAVTTLGVAYAAKNVVTQFVSSMSASADVL

>d1bccf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

SRWLEGIRKWYYNAAGFNKYGLMRDDTIYENDDVKEAIRRLPENLYDDRMFRIKRALDLNMRQQILPKEQWTKYEEDVPYLEPYLKEVIRERKEREEWDK

>d1bccg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

RQFGHLTRVRHLITYSLSPFEQRPFPHYFSKGVPNVWRRLRACILRVAPPFLAFYLLYTWGTQEFEKSKRKNPAAYVN

>d1bcch1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

LVDPLTTVREQCEQLEKCVKARERLELCDERVSSRSQTEEDCTEELFDFLHARDHCVAHKLFNSLK

>d1bccj1 f.2.1.8 (J:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

TLTARLYSLLFRRTSTFALTIVVGALLFERAFDQGADAIYEHINEGKLWKHIKHKYENK

>d1ezvc1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

MAFRKSNVYLSLVNSYIIDSPQPSSINYWWNMGSLLGLCLVIQIVTGIFMAMHYSSNIELAFSSVEHIMRDVHNGYILRYLHANGASFFFMVMFMHMAKGLYYGSYRSPRVTLWNVGVIIFTLTIATAFLGYCCVYGQMSHWGATVITNLFSAIPFVGNDIVSWLWGGFSVSNPTIQRFFALHYLVPFIIAAMVIMHLMALHIHGSSNPLGITGNLDRIPMHSYFIFKDLVTVFLFMLILALFVFYSPNTLGHPDNYIPGNPLVTPASIVPEWYLLPFYAILRSIPDKLLGVITMFAAILVLLVLPFTDRSVVRGNTFKVLSKFFFFIFVFNFVLLGQIGACHVEVPYVLMGQIATFIYFAYFLIIVPVISTIENVLFYIGRVNK

>d1ezvd2 f.2.1.8 (D:261-306) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

PEHDERKRLGLKTVIILSSLYLLSIWVKKFKWAGIKTRKFVFNPPK

>d1ezve2 f.2.1.8 (E:31-86) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

KSTYRTPNFDDVLKENNDADKGRSYAYFMVGAMGLLSSAGAKSTVETFISSMTATA

>d1ezvf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

QSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRRLPEDESYARAYRIIRAHQTELTHHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIEVSK

>d1ezvg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

GPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGIFHNAVFNSFRRFKSQFLYVLIPAGIYWYWWKNGNEYNEFLYSKAGREELERVNV

>d1ezvh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

VTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQQPGYADLEHKEDCVEEFFHLQHYLDTATAPRLFDKLK

>d1ezvi1 f.2.1.8 (I:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

SSLYKTFFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAA

>d1fumc\_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {Escherichia coli}

TTKRKPYVRPMTSTWWKKLPFYRFYMLREGTAVPAVWFSIELIFGLFALKNGPEAWAGFVDFLQNPVIVIINLITLAAALLHTKTWFELAPKAANIIVKDEKMGPEPIIKSLWAVTVVATIVILFVALYW

>d1fumd\_ f.2.1.9 (D:) Fumarate reductase respiratory complex transmembrane subunits {Escherichia coli}

INPNPKRSDEPVFWGLFGAGGMWSAIIAPVMILLVGILLPLGLFPGDALSYERVLAFAQSFIGRVFLFLMIVLPLWCGLHRMHHAMHDLKIHVPAGKWVFYGLAAILTVVTLIGVVTI

>d1qlac\_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {Wolinella succinogenes}

MTNESILESYSGVTPERKKSRMPAKLDWWQSATGLFLGLFMIGHMFFVSTILLGDNVMLWVTKKFELDFIFEGGKPIVVSFLAAFVFAVFIAHAFLAMRKFPINYRQYLTFKTHKDLMRHGDTTLWWIQAMTGFAMFFLGSVHLYIMMTQPQTIGPVSSSFRMVSEWMWPLYLVLLFAVELHGSVGLYRLAVKWGWFDGETPDKTRANLKKLKTLMSAFLIVLGLLTFGAYVKKGLEQTDPNIDYKYFDYKRTH

>d1jb0a\_ f.2.1.12 (A:) Photosystem I {Synechococcus elongatus}

RVVVDNDPVPTSFEKWAKPGHFDRTLARGPQTTTWIWNLHALAHDFDTHTSDLEDISRKIFSAHFGHLAVVFIWLSGMYFHGAKFSNYEAWLADPTGIKPSAQVVWPIVGQGILNGDVGGGFHGIQITSGLFQLWRASGITNEFQLYCTAIGGLVMAGLMLFAGWFHYHKRAPKLEWFQNVESMLNHHLAGLLGLGSLAWAGHQIHVSLPINKLLDAGVAAKDIPLPHEFILNPSLMAELYPKVDWGFFSGVIPFFTFNWAAYSDFLTFNGGLNPVTGGLWLSDTAHHHLAIAVLFIIAGHMYRTNWGIGHSLKEILEAHKGPFTGAGHKGLYEVLTTSWHAQLAINLAMMGSLSIIVAQHMYAMPPYPYLATDYPTQLSLFTHHMWIGGFLVVGGAAHGAIFMVRDYDPAMNQNNVLDRVLRHRDAIISHLNWVCIFLGFHSFGLYVHNDTMRAFGRPQDMFSDTGIQLQPVFAQWVQNLHTLAPGGTAPNAAATASVAFGGDVVAVGGKVAMMPIVLGTADFMVHHIHAFTIHVTVLILLKGVLFARSSRLIPDKANLGFRFPCDGPGRGGTCQVSGWDHVFLGLFWMYNCISVVIFHFSWKMQSDVWGTVAPDGTVSHITGGNFAQSAITINGWLRDFLWAQASQVIGSYGSALSAYGLLFLGAHFIWAFSLMFLFSGRGYWQELIESIVWAHNKLKVAPAIQPRALSIIQGRAVGVAHYLLGGIATTWAFFLARIISVG

>d1jb0b\_ f.2.1.12 (B:) Photosystem I {Synechococcus elongatus}

ATKFPKFSQDLAQDPTTRRIWYAIAMAHDFESHDGMTEENLYQKIFASHFGHLAIIFLWVSGSLFHVAWQGNFEQWVQDPVNTRPIAHAIWDPQFGKAAVDAFTQAGASNPVDIAYSGVYHWWYTIGMRTNGDLYQGAIFLLILASLALFAGWLHLQPKFRPSLSWFKNAESRLNHHLAGLFGVSSLAWAGHLIHVAIPESRGQHVGWDNFLSTMPHPAGLAPFFTGNWGVYAQNPDTASHVFGTAQGAGTAILTFLGGFHPQTESLWLTDMAHHHLAIAVLFIVAGHMYRTQFGIGHSIKEMMDAKDFFGTKVEGPFNMPHQGIYETYNNSLHFQLGWHLACLGVITSLVAQHMYSLPPYAFIAQDHTTMAALYTHHQYIAGFLMVGAFAHGAIFLVRDYDPAQNKGNVLDRVLQHKEAIISHLSWVSLFLGFHTLGLYVHNDVVVAFGTPEKQILIEPVFAQFIQAAHGKLLYGFDTLLSNPDSIASTAWPNYGNVWLPGWLDAINSGTNSLFLTIGPGDFLVHHAIALGLHTTTLILVKGALDARGSKLMPDKKDFGYAFPCDGPGRGGTCDISAWDAFYLAMFWMLNTIGWVTFYWHWKHLGVWEGNVAQFNESSTYLMGWLRDYLWLNSSQLINGYNPFGTNNLSVWAWMFLFGHLVWATGFMFLISWRGYWQELIETLVWAHERTPLANLVRWKDKPVALSIVQARLVGLAHFSVGYILTYAAFLIASTAAKF

>d1jb0f\_ f.2.1.12 (F:) Photosystem I {Synechococcus elongatus}

DVAGLVPCKDSPAFQKRAAAAVNTTADPASGQKRFERYSQALCGEDGLPHLVVDGRLSRAGDFLIPSVLFLYIAGWIGWVGRAYLIAVRNSGEANEKEIIIDVPLAIKCMLTGFAWPLAALKELASGELTAKDNEITVSPR

>d1jb0i\_ f.2.1.12 (I:) Photosystem I {Synechococcus elongatus}

MMGSYAASFLPWIFIPVVCWLMPTVVMGLLFLYIEGEA

>d1jb0j\_ f.2.1.12 (J:) Photosystem I {Synechococcus elongatus}

MKHFLTYLSTAPVLAAIWMTITAGILIEFNRFYPDLLFHPL

>d1jb0k\_ f.2.1.12 (K:) Photosystem I {Synechococcus elongatus}

ILCNLFAIALGRYAIQSRGKGPGLPIALPALFEGFGLPELLATTSFGHLLAAGVVSGL

>d1jb0l\_ f.2.1.12 (L:) Photosystem I {Synechococcus elongatus}

LVKPYNGDPFVGHLSTPISDSGLVKTFIGNLPAYRQGLSPILRGLEVGMAHGYFLIGPWVKLGPLRDSDVANLGGLISGIALILVATACLAAYGLVSFQKGGSSSDPLKTSEGWSQFTAGFFVGAMGSAFVAFFLLENFLVVDGIMTGLFN

>d1jb0m\_ f.2.1.12 (M:) Photosystem I {Synechococcus elongatus}

MALTDTQVYVALVIALLPAVLAFRLSTELYK

>d1jb0x\_ f.2.1.12 (X:) Photosystem I {Synechococcus elongatus}

PTYAFRTFWAVLLLAINFLVAAYYFAAAA

>d1eula\_ f.2.1.10 (A:) Calcium ATPase {Rabbit (Oryctolagus cuniculus)}

MEAAHSKSTEECLAYFGVSETTGLTPDQVKRHLEKYGHNELPAEEGKSLWELVIEQFEDLLVRILLLAACISFVLAWFEEGEETITAFVEPFVILLILIANAIVGVWQERNAENAIEALKEYEPEMGKVYRADRKSVQRIKARDIVPGDIVEVAVGDKVPADIRILSIKSTTLRVDQSILTGESVSVIKHTEPVPDPRAVNQDKKNMLFSGTNIAAGKALGIVATTGVSTEIGKIRDQMAATEQDKTPLQQKLDEFGEQLSKVISLICVAVWLINIGHFNDPVHGGSWIRGAIYYFKIAVALAVAAIPEGLPAVITTCLALGTRRMAKKNAIVRSLPSVETLGCTSVICSDKTGTLTTNQMSVCKMFIIDKVDGDFCSLNEFSITGSTYAPEGEVLKNDKPIRSGQFDGLVELATICALCNDSSLDFNETKGVYEKVGEATETALTTLVEKMNVFNTEVRNLSKVERANACNSVIRQLMKKEFTLEFSRDRKSMSVYCSPAKSSRAAVGNKMFVKGAPEGVIDRCNYVRVGTTRVPMTGPVKEKILSVIKEWGTGRDTLRCLALATRDTPPKREEMVLDDSSRFMEYETDLTFVGVVGMLDPPRKEVMGSIQLCRDAGIRVIMITGDNKGTAIAICRRIGIFGENEEVADRAYTGREFDDLPLAEQREACRRACCFARVEPSHKSKIVEYLQSYDEITAMTGDGVNDAPALKKAEIGIAMGSGTAVAKTASEMVLADDNFSTIVAAVEEGRAIYNNMKQFIRYLISSNVGEVVCIFLTAALGLPEALIPVQLLWVNLVTDGLPATALGFNPPDLDIMDRPPRSPKEPLISGWLFFRYMAIGGYVGAATVGAAAWWFMYAEDGPGVTYHQLTHFMQCTEDHPHFEGLDCEIFEAPEPMTMALSVLVTIEMCNALNSLSENQSLMRMPPWVNIWLLGSICLSMSLHFLILYVDPLPMIFKLKALDLTQWLMVLKISLPVIGLDEILKFIARNYLEG

>d1kzua\_ f.3.1.1 (A:) Light-harvesting complex subunits {Purple bacterium (Rhodopseudomonas acidophila)}

MNQGKIWTVVNPAIGIPALLGSVTVIAILVHLAILSHTTWFPAYWQGGV

>d1kzub\_ f.3.1.1 (B:) Light-harvesting complex subunits {Purple bacterium (Rhodopseudomonas acidophila)}

ATLTAEQSEELHKYVIDGTRVFLGLALVAHFLAFSATPWLH

>d1lgha\_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodospirillum molischianum}

SNPKDDYKIWLVINPSTWLPVIWIVATVVAIAVHAAVLAAPGFNWIALGAAKSAAK

>d1lghb\_ f.3.1.1 (B:) Light-harvesting complex subunits {Rhodospirillum molischianum}

RSLSGLTEEEAIAVHDQFKTTFSAFIILAAVAHVLVWVWKPWF

>d1jo5a\_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodobacter sphaeroides}

ADKSDLGYTGLTDEQAQELHSVYMSGLWLFSAVAIVAHLAVYIWRPWF

>d1ijda\_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodopseudomonas acidophila}

MNQGKIWTVVPPAFGLPLMLGAVAITALLVHAAVLTHTTWYAAFLQ

>d1ijdb\_ f.3.1.1 (B:) Light-harvesting complex subunits {Rhodopseudomonas acidophila}

AEVLTSEQAEELHKHVIDGTRVFLVIAAIAHFLAFTLTPW

>d1g90a\_ f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}

APKDNTWYTGAKLGFSQYHDTGFINNNGPTHENQLGAGAFGGYQVNPYVGFEMGYDFLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVFRADTKSNVYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQFTNNIGDAHTIGTRPDNGMLSLGVSYRFGQGEAA

>d1qjpa\_ f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}

APKDNTWYTGAKLGWSQYHDTGLINNNGPTHENKLGAGAFGGYQVNPYVGFEMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVWRADTYSNVYGKNHDTGVSPVFAGGVEYAITPEIATRLEYQWTNNIGDAHTIGTRPDNGMLSLGVSYRFG

>d1qj8a\_ f.4.1.1 (A:) Outer membrane protein X (OMPX) {Escherichia coli}

ATSTVTGGYAQSDAQGQMNKMGGFNLKYRYEEDNSPLGVIGSFTYTEKSRTASSGDYNKNQYYGITAGPAYRINDWASIYGVVGVGYGKFQTTEYPTYKNDTSDYGFSYGAGLQFNPMENVALDFSYEQSRIRSVDVGTWIAGVGYRF

>d1i78a\_ f.4.4.1 (A:) Outer membrane protease OMPT {Escherichia coli}

STETLSFTPDNINADISLGTLSGKTKERVYLAEEGGRKVSQLDWKFNNAAIIKGAINWDLMPQISIGAAGWTTLGSRGGNMVDQDWMDSSNPGTWTDEARHPDTQLNYANEFDLNIKGWLLNEPNYRLGLMAGYQESRYSFTARGGSYIYSSEEGFRDDIGSFPNGERAIGYKQRFKMPYIGLTGSYRYEDFELGGTFKYSGWVESSDNDEHYDPKGRITYRSKVKDQNYYSVAVNAGYYVTPNAKVYVEGAWNRVTNKKGNTSLYDHNNNTSDYSKNGAGIENYNFITTAGLKYTF

>g1qd6.1 f.4.2.1 (A:,C:) Outer membrane phospholipase A (OMPLA) {Escherichia coli}

AVRGSIIANMLQEXFTLYPYDTNYLIYTQTSDLNKEAIASYDWAENARKDEVKFQLSLAFPLWRGILGPNSVLGASYTQKSWWQLSNSEESSPFRETNYEPQLFLGFATDYRFAGWTLRDVEMGYNHDSNGRSDPTSRSWNRLYTRLMAENGNWLVEVKPWYVVGNTDDNPDITKYMGYYQLKIGYHLGDAVLSAKGQYNWNTGYGGAELGLSYPITKHVRLYTQVYSGYGESLIDYNFNQTRVGVGVMLNDLF

>d1hxxa\_ f.4.3.1 (A:) Porin {Escherichia coli, different sequences}

AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQWEYNFQGNNSEGADAQTGNKTRLAFAGLKYADVGSFDYGRNYGVVFDALGYTDMLPEFGGDTAYSDDFFVGRVGGVATYRNSNFFGLVDGLNFAVQYLGKNERDTARRSNGDGVGGSISYEYEGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWATGLKYDANNIYLAANYGETRNATPITNKFTNTSGFANKTQDVLLVAQYQFDFGLRPSIAYTKSKAKDVEGIGDVDLVNYFEVGATYYFNKNMSTYVDYIINQIDSDNKLGVGSDDTVAVGIVYQF

>d1pho\_\_ f.4.3.1 (-) Porin {Escherichia coli, different sequences}

AEIYNKDGNKLDVYGKVKAMHYMSDNASKDGDQSYIRFGFKGETQINDQLTGYGRWEAEFAGNKAESDTAQQKTRLAFAGLKYKDLGSFDYGRNLGALYDVEAWTDMFPEFGGDSSAQTDNFMTKRASGLATYRNTDFFGVIDGLNLTLQYQGKNENRDVKKQNGDGFGTSLTYDFGGSDFAISGAYTNSDRTNEQNLQSRGTGKRAEAWATGLKYDANNIYLATFYSETRKMTPITGGFANKTQNFEAVAQYQFDFGLRPSLGYVLSKGKDIEGIGDEDLVNYIDVGATYYFNKNMSAFVDYKINQLDSDNKLNINNDDIVAVGMTYQF

>d2por\_\_ f.4.3.1 (-) Porin {Rhodobacter capsulatus}

EVKLSGDARMGVMYNGDDWNFSSRSRVLFTMSGTTDSGLEFGASFKAHESVGAETGEDGTVFLSGAFGKIEMGDALGASEALFGDLYEVGYTDLDDRGGNDIPYLTGDERLTAEDNPVLLYTYSAGAFSVAASMSDGKVGETSEDDAQEMAVAAAYTFGNYTVGLGYEKIDSPDTALMADMEQLELAAIAKFGATNVKAYYADGELDRDFARAVFDLTPVAAAATAVDHKAYGLSVDSTFGATTVGGYVQVLDIDTIDDVTYYGLGASYDLGGGASIVGGIADNDLPNSDMVADLGVKFKF

>d3prn\_\_ f.4.3.1 (-) Porin {Rhodopseudomonas blastica, strain DSM2131}

MISLNGYGRFGLQYVEDRGVGLEDTIISSRLRINIVGTTETDQGVTFGAKLRMQWDDGDAFAGTAGNAAQFWTSYNGVTVSVGNVDTAFDSVALTYDSEMGYEWSSFGDAQSSFFAYNSKYDASGALDNYNGIAVTYSISGVNLYLSYVDPDQTVDSSLVTEEFGIAADWSNDMISLAAAYTTDAGGIVDNDIAFVGAAYKFNDAGTVGLNWYDNGLSTAGDQVTLYGNYAFGATTVRAYVSDIDRAGADTAYGIGADYQFAEGVKVSGSVQSGFANETVADVGVRFDF

>d1osma\_ f.4.3.1 (A:) Porin {Klebsiella pneumoniae}

AEIYNKDGNKLDLYGKIDGLHYFSDDKDVDGDQTYMRLGVKGETQINDQLTGYGQWEYNVQANNTESSSDQAWTRLAFAGLKFGDAGSFDYGRNYGVVYDVTSWTDVLPEFGGDTYGSDNFLQSRANGVATYRNSDFFGLVDGLNFALQYQGKNGSVSGEGATNNGRGALKQNGDGFGTSVTYDIFDGISAGFAYANSKRTDDQNQLLLGEGDHAETYTGGLKYDANNIYLATQYTQTYNATRAGSLGFANKAQNFEVAAQYQFDFGLRPSVAYLQSKGKDLNGYGDQDILKYVDVGATYYFNKNMSTYVDYKINLLDDNSFTRSAGISTDDVVALGLVYQF

>d1e54a\_ f.4.3.1 (A:) Porin {Comamonas acidovorans}

ESSVTLFGIVDTNVAYVNKDAAGDSRYGLGTSGASTSRLGLRGTEDLGGGLKAGFWLEGEIFGDDGNASGFNFKRRSTVSLSGNFGEVRLGRDLVPTSQKLTSYDLFSATGIGPFMGFRNWAAGQGADDNGIRANNLISYYTPNFGGFNAGFGYAFDEKQTIGTADSVGRYIGGYVAYDNGPLSASLGLAQQKTAVGGLATDRDEITLGASYNFGVAKLSGLLQQTKFKRDIGGDIKTNSYMLGASAPVGGVGEVKLQYALYDQKAIDSKAHQITLGYVHNLSKRTALYGNLAFLKNKDASTLGLQAKGVYAGGVQAGESQTGVQVGIRHAF

>d1af6a\_ f.4.3.2 (A:) Maltoporin (also LamB protein) {Escherichia coli}

VDFHGYARSGIGWTGSGGEQQCFQTTGAQSKYRLGNECETYAELKLGQEVWKEGDKSFYFDTNVAYSVAQQNDWEATDPAFREANVQGKNLIEWLPGSTIWAGKRFYQRHDVHMIDFYYWDISGPGAGLENIDVGFGKLSLAATRSSEAGGSSSFASNNIYDYTNETANDVFDVRLAQMEINPGGTLELGVDYGRANLRDNYRLVDGASKDGWLFTAEHTQSVLKGFNKFVVQYATDSMTSQGKGLSQGSGVAFDNEKFAYNINNNGHMLRILDHGAISMGDNWDMMYVGMYQDINWDNDNGTKWWTVGIRPMYKWTPIMSTVMEIGYDNVESQRTGDKNNQYKITLAQQWQAGDSIWSRPAIRVFATYAKWDEKWGYDYTGNADNNANFGKAVPADFNGGSFGRGDSDEWTFGAQMEIWW

>d2mpra\_ f.4.3.2 (A:) Maltoporin (also LamB protein) {Salmonella typhimurium}

VDFHGYARSGIGWTGSGGEQQCFQATGAQSKYRLGNECETYAELKLGQEVWKEGDKSFYFDTNVAYSVNQQNDWESTDPAFREANVQGKNLIEWLPGSTIWAGKRFYQRHDVHMIDFYYWDISGPGAGIENIDLGFGKLSLAATRSTEAGGSYTFSSQNIYDEVKDTANDVFDVRLAGLQTNPDGVLELGVDYGRANTTDGYKLADGASKDGWMFTAEHTQSMLKGYNKFVVQYATDAMTTQGKGQARGSDGSSSFTEKINYANKVINNNGNMWRILDHGAISLGDKWDLMYVGMYQNIDWDNNLGTEWWTVGVRPMYKWTPIMSTLLEVGYDNVKSQQTGDRNNQYKITLAQQWQAGDSIWSRPAIRIFATYAKWDEKWGYIKDGDNISRYAAATNSGISTNSRGDSDEWTFGAQMEIWW

>d1a0tp\_ f.4.3.2 (P:) Sucrose-specific porin {Enterobacterium (Salmonella typhimurium)}

SGFEFHGYARSGVIMNDSGASTKSGAYITPAGETGGAIGRLGNQADTYVEMNLEHKQTLDNGATTRFKVMVADGQTSYNDWTASTSDLNVRQAFVELGNLPTFAGPFKGSTLWAGKRFDRDNFDIHWIDSDVVFLAGTGGGIYDVKWNDGLRSNFSLYGRNFGDIDDSSNSVQNYILTMNHFAGPLQMMVSGLRAKDNDERKDSNGNLAKGDAANTGVHALLGLHNDSFYGLRDGSSKTALLYGHGLGAEVKGIGSDGALRPGADTWRIASYGTTPLSENWSVAPAMLAQRSKDRYADGDSYQWATFNLRLIQAINQNFALAYEGSYQYMDLKPEGYNDRQAVNGSFYKLTFAPTFKVGSIGDFFSRPEIRFYTSWMDWSKKLNNYASDDALGSDGFNSGGEWSFGVQMETWF

>d1by5a\_ f.4.3.3 (A:) Ferric hydroxamate uptake receptor FhuA {Escherichia coli}

QESAWGPAATIAARQSATGTKTDTPIQKVPQSISVVTAEEMALHQPKSVKEALSYTPGVSVGTRGASNTYDHLIIRGFAAEGQSQNNYLNGLKLQGNFYNDAVIDPYMLERAEIMRGPVSVLYGKSSPGGLLNMVSKRPTTEPLKEVQFKAGTDSLFQTGFDFSDSLDDDGVYSYRLTGLARSANAQQKGSEEQRYAIAPAFTWRPDDKTNFTFLSYFQNEPETGYYGWLPKEGTVEPLPNGKRLPTDFNEGAKNNTYSRNEKMVGYSFDHEFNDTFTVRQNLRFAENKTSQNSVYGYGVCSDPANAYSKQCAALAPADKGHYLARKYVVDDEKLQNFSVDTQLQSKFATGDIDHTLLTGVDFMRMRNDINAWFGYDDSVPLLNLYNPVNTDFDFNAKDPANSGPYRILNKQKQTGVYVQDQAQWDKVLVTLGGRYDWADQESLNRVAGTTDKRDDKQFTWRGGVNYLFDNGVTPYFSYSESFEPSSQVGKDGNIFAPSKGKQYEVGVKYVPEDRPIVVTGAVYNLTKTNNLMADPEGSFFSVEGGEIRARGVEIEAKRPLSASVNVVGSYTYTDAEYTTDTTYKGNTPAQVPKHMASLWADYTFFDGPLSGLTLGTGGRYTGSSYGDPANSFKVGSYTVVDALVRYDLARVGMAGSNVALHVNNLFDREYVASCFNTYGCFWGAERQVVATATFRF

>d1fepa\_ f.4.3.3 (A:) Ferric enterobactin receptor FepA {Escherichia coli}

DDTIVVTAAEQNLQAPGVSTITADEIRKNPVARDVSKIIRTMPGVNLTGNSTSGQRGNNRQIDIRGMGPENTLILIDGKPVSSRNSVRQGWRGERDTRGDTSWVPPEMIERIEVLRGPAAARYGNGAAGGVVNIITKKGSGEWHGSWDAYFNAPEHKEEGATKRTNFSLTGPLGDEFSFRLYGNLDKTQADAWDINQGHQSARAGTYATTLPAGREGVINKDINGVVRWDFAPLQSLELEAGYSRQGNLYAGDTQNTNSDSYTRSKYGDETNRLYRQNYALTWNGGWDNGVTTSNWVQYEHTRNSRIPEGLAGGTEGKFNEKATQDFVDIDLDDVMLHSEVNLPIDFLVNQTLTLGTEWNQQRMKDLSSNTQALTGTNTGGAIDGVSTTDRSPYSKAEIFSLFAENNMELTDSTIVTPGLRFDHHSIVGNNWSPALNISQGLGDDFTLKMGIARAYKAPSLYQTNPNYILYSKGQGCYASAGGCYLQGNDDLKAETSINKEIGLEFKRDGWLAGVTWFRNDYRNKIEAGYVAVGQNAVGTDLYQWDNVPKAVVEGLEGSLNVPVSETVMWTNNITYMLKSENKTTGDRLSIIPEYTLNSTLSWQAREDLSMQTTFTWYGKQQPKKYNYKGQPAVGPETKEISPYSIVGLSATWDVTKNVSLTGGVDNLFDKRLWRAGNAQTTGDLAGANYIAGAGAYTYNEPGRTWYMSVNTHF

>d1ek9a\_ f.5.1.1 (A:) Integral outer membrane protein TolC, efflux pump component {Escherichia coli}

ENLMQVYQQARLSNPELRKSAADRDAAFEKINEARSPLLPQLGLGADYTYSNGYRDANGINSNATSASLQLTQSIFDMSKWRALTLQEKAAGIQDVTYQTDQQTLILNTATAYFNVLNAIDVLSYTQAQKEAIYRQLDQTTQRFNVGLVAITDVQNARAQYDTVLANELTARNNLDNAVEQLRQITGNYYPELAALNVENFKTDKPQPVNALLKEAEKRNLSLLQARLSQDLAREQIRQAQDGHLPTLDLTASTGISDTSYSGSKTRGAAGTQYDDSNMGQNKVGLSFSLPIYQGGMVNSQVKQAQYNFVGASEQLESAHRSVVQTVRSSFNNINASISSINAYKQAVVSAQSSLDAMEAGYSVGTRTIVDVLDATTTLYNAKQELANARYNYLINQLNIKSALGTLNEQDLLALNNALSKPVSTNPE

>d7ahla\_ f.6.1.1 (A:) Alpha-hemolysin {Staphylococcus aureus}

ADSDINIKTGTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFIDDKNHNKKLLVIRTKGTIAGQYRVYSEEGANKSGLAWPSAFKVQLQLPDNEVAQISDYYPRNSIDTKEYMSTLTYGFNGNVTGDDTGKIGGLIGANVSIGHTLKYVQPDFKTILESPTDKKVGWKVIFNNMVNQNWGPYDRDSWNPVYGNQLFMKTRNGSMKAADNFLDPNKASSLLSSGFSPDFATVITMDRKASKQQTNIDVIYERVRDDYQLHWTSTNWKGTNTKDKWTDRSSERYKIDWEKEEMTN

>d1pvl\_\_ f.6.1.1 (-) Leucocidin K component LukF-PV {Staphylococcus aureus}

AQHITPVSEKKVDDKITLYKTTATSDSDKLKISQILTFNFIKDKSYDKDTLILKAAGNIYSGYTKPNPKDTISSQFYWGSKYNISINSDSNDSVNVVDYAPKNQNEEFQVQQTVGYSYGGDINISNGLSGGGNGSKSFSETINYKQESYRTSLDKRTNFKKIGWDVEAHKIMNNGWGPYGRDSYHSTYGNEMFLGSRQSNLNAGQNFLEYHKMPVLSRGNFNPEFIGVLSRKQNAAKKSKITVTYQREMDRYTNFWNQLHWIGNNYKDENRATHTSIYEVDWENHTVKLIDTQSKEKNPMS

>d3lkfa\_ f.6.1.1 (A:) Leukocidin F (HlgB) {Staphylococcus aureus}

EGKITPVSVKKVDDKVTLYKTTATADSDKFKISQILTFNFIKDKSYDKDTLVLKATGNINSGFVKPNPNDYDFSKLYWGAKYNVSISSQSNDSVNVVDYAPKNQNEEFQVQNTLGYTFGGDISISNGLSGGLNGNTAFSETINYKQESYRTTLSRNTNYKNVGWGVEAHKIMNNGWGPYGRDSFHPTYGNELFLAGRQSSAYAGQNFIAQHQMPLLSRSNFNPEFLSVLSHRQDGAKKSKITVTYQREMDLYQIRWNGFYWAGANYKNFKTRTFKSTYEIDWENHKVKLLDTKETENNK

>d1prea2 f.8.1.1 (A:85-470) (Pro)aerolysin, pore-forming lobe {Aeromonas hydrophila}

IPTLSALDIPDGDEVDVQWRLVHDSANFIKPTSYLAHYLGYAWVGGNHSQYVGEDMDVTRDGDGWVIRGNNDGGCDGYRCGDKTAIKVSNFAYNLDPDSFKHGDVTQSDRQLVKTVVGWAVNDSDTPQSGYDVTLRYDTATNWSKTNTYGLSEKVTTKNKFKWPLVGETELSIEIAANQSWASQNGGSTTTSLSQSVRPTVPARSKIPVKIELYKADISYPYEFKADVSYDLTLSGFLRWGGNAWYTHPDNRPNWNHTFVIGPYKDKASSIRYQWDKRYIPGEVKWWDWNWTIQQNGLSTMQNNLARVLRPVRAGITGDFSAESQFAGNIEIGAPVPLAADSKVRRARSVDGAGQGLRLEIPLDAQELSGLGFNNVSLSVTPAANQ

>d1pfo\_\_ f.9.1.1 (-) Perfringolysin {Clostridium perfringens}

DITDKNQSIDSGISSLSYNRNEVLASNGDKIESFVPKEGKKAGNKFIVVERQKRSLTTSPVDISIIDSVNDRTYPGALQLADKALVENRPTILMVKRKPININIDLPGLKGENSIKVDDPTYGKVSGAIDELVSKWNEKYSSTHTLPARTQYSESMVYSKSQISSALNVNAKVLENSLGVDFNAVANNEKKVMILAYKQIFYTVSADLPKNPSDLFDDSVTFNDLKQKGVSNEAPPLMVSNVAYGRTIYVKLETTSSSKDVQAAFKALIKNTDIKNSQQYKDIYENSSFTAVVLGGDAQEHNKVVTKDFDEIRKVIKDNATFSTKNPAYPISYTSVFLKDNSVAAVHNKTDYIETTSTEYSKGKINLDHSGAYVAQFEVAWDEVSYDKEGNEVLTHKTWDGNYQDKTAHYSTVIPLEANARNIRIKARECTGLAWEWWRDVISEYDVPLTNNINVSIWGTTLYPGSSITYN

>d1svb\_2 f.10.1.1 (1-302) Envelope glycoprotein, central and dimerisation domains {Tick-borne encephalitis virus}

SRCTHLENRDFVTGTQGTTRVTLVLELGGCVTITAEGKPSMDVWLDAIYQENPAKTREYCLHAKLSDTKVAARCPTMGPATLAEEHQGGTVCKRDQSDRGWGNHCGLFGKGSIVACVKAACEAKKKATGHVYDANKIVYTVKVEPHTGDYVAANETHSGRKTASFTISSEKTILTMGEYGDVSLLCRVASGVDLAQTVILELDKTVEHLPTAWQVHRDWFNDLALPWKHEGAQNWNNAERLVEFGAPHAVKMDVYNLGDQTGVLLKALAGVPVAHIEGTKYHLKSGHVTCEVGLEKLKMKGL

>d1g5ga1 f.12.1.1 (A:33-66,A:224-454) Head and neck region of the ectodomain of NDV fusion glycoprotein {Newcastle disease virus}

DGRPLAAAGIVVTGDKAVNIYTSSQTGSIIIKLLXQITSPALTQLTIQALYNLAGGNMDYLLTKLGVGNNQLSSLISSGLITGNPILYDSQTQLLGIQVTLPSVGNLNNMRATYLETLSVSTTKGFASALVPKVVTQVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIYSCLSGNTSACMYSKTEGALTTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLIDRQSCNILSLDGITLRLSGEFDATYQKNISIQDSQ

>d1acc\_\_ f.11.1.1 (-) Anthrax protective antigen {Anthrax bacillus (Bacillus anthracis)}

SSSQGLLGYYFSDLNFQAPMVVTSSTTGDLSIPSSELENIPSENQYFQSAIWSGFIKVKKSDEYTFATSADNHVTMWVDDQEVINKASNSNKIRLEKGRLYQIKIQYQRENPTEKGLDFKLYWTDSQNKKEVISSDNLQLPELKQKSSNSRKKRSTSAGPTVPDRDNDGIPDSLEVEGYTVDVKNKRTFLSPWISNIHEKKGLTKYKSSPEKWSTASDPYSDFEKVTGRIDKNVSPEARHPLVAAYPIVHVDMENIILSKNEDQSTQNTDSETRTISKNTSTSRTHTSEVHGNAEVHASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVLGKNQTLATIKAKENQLSQILAPNNYYPSKNLAPIALNAQDDFSSTPITMNYNQFLELEKTKQLRLDTDQVYGNIATYNFENGRVRVDTGSNWSEVLPQIQETTARIIFNGKDLNLVERRIAAVNPSDPLETTKPDMTLKEALKIAFGFNEPNGNLQYQGKDITEFDFNFDQQTSQNIKNQLAELNATNIYTVLDKIKLNAKMNILIRDKRFHYDRNNIAVGADESVVKEAHREVINSSTEGLLLNIDKDIRKILSGYIVEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPLYISNPNYKVNVYAVTKENTIINPSENGDTSTNGIKKILIFSKKGYEIG

>g1cph.1 g.1.1.1 (B:,A:) Insulin {Cow (Bos taurus)}

FVNQHLCGSHLVEALYLVCGERGFFYTPKAXGIVEQCCASVCSLYQLENYCN

>g1pid.1 g.1.1.1 (B:,A:) Insulin {Cow (Bos taurus)}

FVNQHLCGSHLVEALYLVCGERGFFXGIVEQCCASVCSLYQLENYCN

>d1efea\_ g.1.1.1 (A:) Insulin {Human (Homo sapiens)}

FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRYPGDVKRGIVEQCCTSICSLYQLENYCN

>g1a7f.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}

FVNQHLCGSHLVEALELVCGERGGFYTPKXGIVEQCCTSICSLYQLENYCN

>g1g7a.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}

FVNQHLCGSHLVEALYLVCGERGFFYTPKTXGIVEQCCTSICSLYQLENYCN

>g1hui.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}

EVNQHLCGSELVEALELVCGERGFFYEPKXGIVEQCCTSICSLYQLENYCN

>g1qj0.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}

VNQYLCGSHLVEALYLVCGERGFFYTPKXGIVEQCCTSICSLYQLENYCN

>g1sjt.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}

FVNQHLCGSDLVEALYLVCGERGFFYTDKXGIVEQCCTSICSLYQLENYCN

>g1vks.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}

FVNQHLCGSDLVEALYLVCGERGFFYTKPTXGIVEQCCTSICSLYQLENYCN

>d1zeia\_ g.1.1.1 (A:) Insulin {Pig (Sus scrofa)}

FVNQHLCGSHLVEALYLVCGERGFFYTDKAAKGIVEQCCTSICSLYQLENYCN

>g1dei.1 g.1.1.1 (B:,A:) Insulin {Pig (Sus scrofa)}

FVNQHLCGSHLVEALYLVCGERGXGIVEQCCTSICSLYQLENYCN

>g1sdb.1 g.1.1.1 (B:,A:) Insulin {Pig (Sus scrofa)}

NQHLCGSHLVEALYLVCGERGFFXGIVEQCCTSICSLYQLENYCN

>g6rlx.1 g.1.1.1 (B:,A:) Relaxin {Human (Homo sapiens)}

SWMEEVIKLCGRELVRAQIAICGMSTWXELYSALANKCCHVGCTKRSLARFC

>d1b9ga\_ g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}

GPETLCGAELVDALQFVCGDRGFYFNKPGIVDECCFRSCDLRRLEMYCAPLKPAKSA

>d1igl\_\_ g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}

AYRPSETLCGGELVDTLQFVCGDRGFYFSRPASRVSRRSRGIVEECCFRSCDLALLETYCATPAKSE

>d1imxa\_ g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}

ETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEMYCAPL

>d2gf1\_\_ g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}

GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEMYCAPLKPAKSA

>d3lria\_ g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}

MFPAMPLSSLFVNGPRTLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRACQTGIVDECCFRSCDLRRLEMYCAPLKPAKSA

>g1bom.1 g.1.1.1 (B:,A:) Bombyxin-II {Silkworm (Bombyx mori)}

EQPQAVHTYCGRHLARTLADLCWEAGVDXGIVDECCLRPCSVDVLLSYC

>d1ehs\_\_ g.2.1.1 (-) Heat-stable enterotoxin B {Escherichia coli}

STQSNKKDLCEHYRQIAKESCKKGFLGVRDGTAGACFGAQIMVAAKGC

>d1vib\_\_ g.2.2.1 (-) Neurotoxin B-IV {Milky ribbon worm (Cerebratulus lacteus)}

ASATWGAAYPACENNCRKKYDLCIRCQGKWAGKRGKCAAHCIIQKNNCKGKCKKE

>d1wgta3 g.3.1.1 (A:87-129) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

IKCGSQAGGKLCPNNLCCSQWGYCGLGSEFCGEGCQNGACSTD

>d2cwga2 g.3.1.1 (A:53-86) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

ATCTNNQCCSQYGYCGFGAEYCGAGCQGGPCRAD

>d9wgaa1 g.3.1.1 (A:1-52) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

ERCGEQGSNMECPNNLCCSQYGYCGMGGDYCGKGCQNGACWTSKRCGSQAGG

>d9wgaa2 g.3.1.1 (A:53-86) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

ATCPNNHCCSQYGHCGFGAEYCGAGCQGGPCRAD

>d9wgaa3 g.3.1.1 (A:87-129) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

IKCGSQSGGKLCPNNLCCSQWGFCGLGSEFCGGGCQSGACSTD

>d9wgaa4 g.3.1.1 (A:130-171) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

KPCGKDAGGRVCTNNYCCSKWGSCGIGPGYCGAGCQSGGCDA

>d1ehda1 g.3.1.1 (A:1-45) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

ERCGSQGGGATCPGLRCCSIWGWCGDSEPYCGRTCENKCWSGERS

>d1ehda2 g.3.1.1 (A:46-89) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

DHRCGAAVGNPPCGQDRCCSVHGWCGGGNDYCSGGKCQYRCSSS

>d1en2a1 g.3.1.1 (A:1-45) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

ERCGSQGGGGTCPALWCCSIWGWCGDSEPYCGRTCENKCWSGERS

>d1en2a2 g.3.1.1 (A:46-86) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

DHRCGAAVGNPPCGQDRCCSVHGWCGGGNDYCSGSKCQYRC

>d1hev\_\_ g.3.1.1 (-) Hevein {Hevea brasiliensis}

EQCGRQAGGKLCPNNLCCSQWGWCGSTDEYCSPDHNCQSNCKD

>d1mmc\_\_ g.3.1.2 (-) Antimicrobial peptide 2, AC-AMP2 {Tassel (Amaranthus caudatus)}

VGECVRGRCPSGMCCSQFGYCGKGPKYCGR

>d1f2si\_ g.3.2.1 (I:) Trypsin inhibitor {Bitter gourd (Momordica charantia), linn. Cucurbitaceae, seed}

RICPRIWMECKRDSDCMAECICVMGHCG

>d1mcti\_ g.3.2.1 (I:) Trypsin inhibitor {Bitter gourd (Momordica charantia), linn. Cucurbitaceae, seed}

RICPRIWMECTRDSDCMAKCICVAGHCG

>d2stai\_ g.3.2.1 (I:) Trypsin inhibitor {Squash (Cucurbita maxima)}

RVCPRILMECKKDSDCLAECVCLEHGYCG

>d1ha9a\_ g.3.2.1 (A:) Trypsin inhibitor {Spiny bitter cucumber (Momordica cochinchinensis), MCOTI-II}

SGSDGGVCPKILKKCRRDSDCPGACICRGNGYCG

>d2btci\_ g.3.2.1 (I:) Trypsin inhibitor {Vegetable marrow (Cucurbita pepo)}

RVCPKILMECKKDSDCLAECICLEHGYCG

>d2let\_\_ g.3.2.1 (-) Trypsin inhibitor {Jumping cucumber (Ecballium elaterium)}

GCPRLLMRCKQDSDCLAGCVCGPNGFCG

>d4cpai\_ g.3.2.1 (I:) Carboxypeptidase A inhibitor {Potato}

ZHADPICNKPCKTHDDCSGAWFCQACWNSARTCGPYV

>d1clvi\_ g.3.2.1 (I:) alpha-amylase inhibitor (AAI) {Prince's feather (Amaranthus hypochondriacus)}

CIPKWNRCGPKMDGVPCCEPYTCTSDYYGNCS

>d1kal\_\_ g.3.3.1 (-) Kalata B1 {African plant (Oldenlandia affinis dc)}

SWPVCTRNGLPVCGETCVGGTCNTPGCTC

>d1df6a\_ g.3.3.2 (A:) Cycloviolacin O1 {Plant (Viola odorata)}

SCVYIPCTVTALLGCSCSNRVCYNGIPCAE

>d1bh4\_\_ g.3.3.3 (-) Circulin A {Chassalia parviflora}

CGESCVWIPCISAALGCSCKNKVCYRNGIP

>d1c4ea\_ g.3.4.1 (A:) Gurmarin, a sweet taste-suppressing polypeptide {Gymnema sylvestre}

EQCVKKDELCIPYYLDCCEPLECKKVNWWDHKCIG

>d1dkca\_ g.3.4.2 (A:) Antifungal peptide PAFP-S {Pokeweed (Phytolacca americana)}

AGCIKNGGRCNASAGPPYCCSSYCFQIAGQSYGVCKNR

>d1hyka\_ g.3.5.1 (A:) Agouti-related protein {Synthetic, based on Homo sapiens sequence}

CVRLHESCLGQQVPCCDPCATCYCRFFNAFCYCRKLGTAMNPCSRT

>d1omc\_\_ g.3.6.1 (-) Conotoxin {Sea snail (Conus geographus), G IVa}

CKSPGSSCSPTSYNCCRSCNPYTKRCY

>d1ag7\_\_ g.3.6.1 (-) Conotoxin {Synthetic, based on Conus geographus, GS}

ACSGRGSRCPPQCCMGLRCGRGNPQKCIGAHEDV

>d1cnna\_ g.3.6.1 (A:) Conotoxin {Sea snail (Conus magus), M VIIc}

CKGKGAPCRKTMYDCCSGSCGRRGKC

>d1omg\_\_ g.3.6.1 (-) Conotoxin {Sea snail (Conus magus), M VIIa}

CKGKGAKCSRLMYDCCTGSCRSGKC

>d1mvj\_\_ g.3.6.1 (-) Conotoxin {Conus striatus, S VIb}

CKLKGQSCRKTSYDCCSGSCGRSGKC

>d1fyga\_ g.3.6.1 (A:) Conotoxin {Conus striatus, SO3}

CKAAGKPCSRIAYNCCTGSCRSGKC

>d1kcp\_\_ g.3.6.1 (-) Conotoxin {Conus purpurascens, kappa-pVIIa}

CRIPNQKCFQHLDDCCSRKCNRFNKCV

>d1eyoa\_ g.3.6.1 (A:) Conotoxin {Conus tulipa, T VIIa}

SCSGRDSRCPPVCCMGLMCSRGKCVSIYGE

>d1g1za\_ g.3.6.1 (A:) Conotoxin {Conus ermineus, E VIa}

DDCIKPYGFCSLPILKNGLCCSGACVGVCADL

>d1f3ka\_ g.3.6.1 (A:) Conotoxin {Conus textile, Tx VII}

CKQADEPCDVFSLDCCTGICLGVCMW

>d1agg\_\_ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}

EDNCIAEDYGKCTWGGTKCCRGRPCRCSMIGTNCECTPRLIMEGLSFA

>d1oav\_\_ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}

KKKCIAKDYGRCKWGGTPCCRGRGCICSIMGTNCECKPRLIMEGLGLA

>d1omb\_\_ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}

CIAEDYGKCTWGGTKCCRGRPCRCSMIGTNCECTP

>d1eit\_\_ g.3.6.2 (-) mu-Agatoxin-I {Funnel web spider (Agelenopsis aperta)}

ECVPENGHCRDWYDECCEGFYCSCRQPPKCICRNNN

>d1kqha\_ g.3.6.2 (A:) ACTX-HI:OB4219 {Funnel-web spider (Hadronyche infensa)}

KCLAEAADCSPWSGDSCCKPYLCSCIFFYPCSCRPKGW

>d1axh\_\_ g.3.6.2 (-) Atracotoxin-hvI (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}

SPTCIPSGQPCPYNENCCSQSCTFKENENGNTVKRCD

>d1hvwa\_ g.3.6.2 (A:) Atracotoxin-hvI (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}

CIPSGQPCPYNENCCSQSCTGGRCD

>d1vtx\_\_ g.3.6.2 (-) Atracotoxin-hvI (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}

CAKKRNWCGKTEDCCCPMKCVYAWYNEQGSCQSTISALWKKC

>d1dl0a\_ g.3.6.2 (A:) J-atracotoxin-hv1c {Australian funnel-web spider (Hadronyche versuta)}

AICTGADRPCAACCPCCPGTSCKAESNGVSYCRKDEP

>d1g9pa\_ g.3.6.2 (A:) Atracotoxin-hv2a {Funnel-web spider (Hadronyche versuta)}

LLACLFGNGRCSSNRDCCELTPVCKRGSCVSSGPGLVGGILGGIL

>d1qdp\_\_ g.3.6.2 (-) Robustoxin {Funnel-web spider (Atrax robustus)}

CAKKRNWCGKNEDCCCPMKCIYAWYNQQGSCQTTITGLFKKC

>d1qk6a\_ g.3.6.2 (A:) Huwentoxin-I {Chinese bird spider (Selenocosmia huwena)}

ACKGVFDACTPGKNECCPNRVCSDKHKWCKWKL

>d1i25a\_ g.3.6.2 (A:) Huwentoxin-II {Chinese bird spider (Selenocosmia huwena)}

LFECSFSCEIEKEGDKPCKKKKCKGGWKCKFNMCVKV

>d1qk7a\_ g.3.6.2 (A:) Lectin SHL-I {Chinese bird spider (Selenocosmia huwena)}

GCLGDKCDYNNGCCSGYVCSRTWKWCVLAGPW

>d1d1ha\_ g.3.6.2 (A:) Hanatoxin 1 {Tarantula (Grammostola spatulata)}

ECRYLFGGCKTTSDCCKHLGCKFRDKYCAWDFTFS

>d1emxa\_ g.3.6.2 (A:) Heteropdatoxin 2, hptx2 {Spider (Heteropodidae venatoria)}

DDCGKLFSGCDTNADCCEGYVCRLWCKLDW

>d1c6wa\_ g.3.6.2 (A:) Maurocalcin {Scorpio maurus}

GDCLPHLKLCKENKDCCSKKCKRRGTNIEKRCR

>d1i26a\_ g.3.6.3 (A:) PTU-1 {Assassin bug (Peirates turpis)}

AEKDCIAPGAPCFGTDKPCCNPRAWCSSYANKCL

>d1jzaa\_ g.3.7.1 (A:) Scorpion toxin {Centruroides sculpturatus ewing, variant 2}

KEGYLVNKSTGCKYGCLKLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSCS

>d2sn3\_\_ g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing, variant 3}

KEGYLVKKSDGCKYGCLKLGENEGCDTECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC

>d1b3ca\_ g.3.7.1 (A:) Scorpion toxin {Centruroides sculpturatus ewing, beta}

KDGYLVEKTGCKKTCYKLGENDFCNRECKWKHIGGSYGYCYGFGCYCEGLPDSTQTWPLPNKTC

>d1vnb\_\_ g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing, variant 1}

KEGYLVKKSDGCKYDCFWLGKNEHCNTECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC

>d1nrb\_\_ g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing, variant V}

KKDGYPVDSGNCKYECLKDDYCNDLCLERKADKGYCYWGKVSCYCYGLPDNSPTKTSGKCNPA

>d1aho\_\_ g.3.7.1 (-) Scorpion toxin {Scorpion (Androctonus australis hector), Toxin II}

VKDGYIVDDVNCTYFCGRNAYCNEECTKLKGESGYCQWASPYGNACYCYKLPDHVRTKGPGRCH

>d1cn2\_\_ g.3.7.1 (-) Scorpion toxin {Mexican scorpion (Centruroides noxius hoffmann), toxin II}

KEGYLVDKNTGCKYECLKLGDNDYCLRECKQQYGKGAGGYCYAFACWCTHLYEQAIVWPLPNKRCS

>d1bcg\_\_ g.3.7.1 (-) Scorpion toxin {Scorpion (Buthotus judaicus), BJXTR-IT}

MKKNGYPLDRNGKTTECSGVNAIAPHYCNSECTKVYYAESGYCCWGACYCFGLEDDKPIGPMKDITKKYCDVQI

>d1snb\_\_ g.3.7.1 (-) Scorpion toxin {Scorpion (Buthus martensii), toxin m8}

GRDAYIADSENCTYFCGSNPYCNDVCTENGAKSGYCQWAGRYGNACYCIDLPASERIKEGGRCG

>d1djta\_ g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus martensii), toxin m1}

VRDAYIAKPHNCVYECARNEYCNDLCTKNGAKSGYCQWVGKYGNGCWCIELPDNVPIRVPGKCH

>d1sn4a\_ g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus martensii), toxin m4}

VRDAYIAKPENCVYHCAGNEGCNKLCTDNGAESGYCQWGGRYGNACWCIKLPDDVPIRVPGKCH

>d1dq7a\_ g.3.7.1 (A:) Scorpion toxin {Indian red scorpion (Buthus tamulus), neurotoxin}

GEDGYIADGDNCTYICTFNNYCHALCTDKKGDSGACDWWVPYGVVCWCEDLPTPVPIRGSGKCR

>d1b7da\_ g.3.7.1 (A:) Scorpion toxin {Scorpion (Tityus serrulatus)}

KEGYLMDHEGCKLSCFIRPSGYCGRECGIKKGSSGYCAWPACYCYGLPNWVKVWDRATNKC

>d1i6fa\_ g.3.7.1 (A:) Scorpion toxin {Bark scorpion (Centruroides sculpturatus), cse-v5}

KDGYPVDSKGCKLSCVANNYCDNQCKMKKASGGHCYAMSCYCEGLPENAKVSDSATNICG

>d1lqq\_\_ g.3.7.1 (-) alpha toxin {Leiurus quinquestriatus quinquestriatus, LQQIII}

VRDAYIAKNYNCVYECFRDSYCNDLCTKNGASSGYCQWAGKYGNACWCYALPDNVPIRVPGKCH

>d1lqi\_\_ g.3.7.1 (-) alpha toxin {Scorpion (Leiurus quinquestriatus hebraeus)}

MVRDAYIAKNYNCVYECFRDAYCNELCTKNGASSGYCQWAGKYGNACWCYALPDNVPIRVPGKCR

>d1bmr\_\_ g.3.7.1 (-) LQH III alpha-like toxin, LQH {Hebraei scorpion (Leiurus quinquestriatus hebraeus)}

VRDGYIAQPENCVYHCFPGSSGCDTLCKEKGGTSGHCGFKVGHGLACWCNALPDNVGIIVEGEKCHS

>d1big\_\_ g.3.7.2 (-) Bmtx1 {Buthus martensii}

EFTDVKCTGSKQCWPVCKQMFGKPNGKCMNGKCRCYS

>d1bkt\_\_ g.3.7.2 (-) Bmktx {Buthus martensii}

VGINVKCKHSGQCLKPCKDAGMRFGKCINGKCDCTPK

>d2bmt\_\_ g.3.7.2 (-) Bmtx2 {Buthus martensii}

EFTNVSCSASSQCWPVCKKLFGTYRGKCMNSKCRCYS

>d1du9a\_ g.3.7.2 (A:) Bmp02 neurotoxin {Chinese scorpion (Buthus martensii)}

VGCEECPMHCKGKNAKPTCDDGVCNCNV

>d1hp2a\_ g.3.7.2 (A:) alpha-KTX, K+-channel blocker {Brazilian scorpion (Tityus serrulatus), Tstx-k alpha}

VFINAKCRGSPECLPKCKEAIGKAAGKCMNGKCKCYP

>d1jlza\_ g.3.7.2 (A:) alpha-KTX, K+-channel blocker {Scorpion (Tityus cambridgei)}

ACGSCRKKCKGSGKCINGRCKCY

>d1mtx\_\_ g.3.7.2 (-) Margatoxin {Scorpion (Centruroides margaritatus)}

TIINVKCTSPKQCLPPCKAQFGQSAGAKCMNGKCKCYPH

>d1sxm\_\_ g.3.7.2 (-) Noxiustoxin {Scorpion (Centruroides noxius hoffmann)}

TIINVKCTSPKQCSKPCKELYGSSAGAKCMNGKCKCYNN

>d1txm\_\_ g.3.7.2 (-) Maurotoxin {Scorpion (Scorpio maurus)}

VSCTGSKDCYAPCRKQTGCPNAKCINKSCKCYGC

>d1cmr\_\_ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}

CTTSKECWSVCQRLHNTSKGWCDHRGCICES

>d2crd\_\_ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}

EFTNVSCTTSKECWSVCQRLHNTSRGKCMNKKCRCYS

>d1scy\_\_ g.3.7.2 (-) Scyllatoxin {Scorpion (Leiurus quinquestriatus hebraeus)}

AFCNLRMCQLSCRSLGLLGKCIGDKCECVKH

>d1agt\_\_ g.3.7.2 (-) Agitoxin {Scorpion (Leiurus quinquestriatus hebraeus)}

GVPINVSCTGSPQCIKPCKDAGMRFGKCMNRKCHCTPK

>d1chl\_\_ g.3.7.2 (-) Chlorootoxin {Scorpion (Leiurus quinquestriatus), venom}

MCMPCFTTDHQMARKCDDCCGGKGRGKCYGPQCLCR

>d1c55a\_ g.3.7.2 (A:) Butantoxin {Brazilian scorpion (Tityus serrulatus)}

WCSTCLDLACGASRECYDPCFKAFGRAHGKCMNNKCRCYT

>d1tsk\_\_ g.3.7.2 (-) Toxin ts kappa {Scorpion (Tityus serrulatus)}

VVIGQRCYRSPDCYSACKKLVGKATGKCTNGRCDC

>d1sis\_\_ g.3.7.2 (-) Toxin I5a {Scorpion (Buthus eupeus)}

MCMPCFTTDPNMAKKCRDCCGGNGKCFGPQCLCNR

>d1pnh\_\_ g.3.7.2 (-) Toxin analog {Scorpion (Androctonus mauretanicus mauretanicus)}

TVCNLRRCQLSCRSLGLLGKCIGVKCECVKH

>d1acw\_\_ g.3.7.2 (-) Toxin analog P01 {Scorpion (Androctonus mauretanicus mauretanicus)}

VSCEDCPEHCSTQKAQAKCDNDKCVCEPI

>d1sco\_\_ g.3.7.2 (-) OSK1 TOXIN {Central asian scorpion (Orthochirus scrobiculosus)}

GVIINVKCKISRQCLEPCKKAGMRFGKCMNGKCHCTPK

>d2ktx\_\_ g.3.7.2 (-) Kaliotoxin (KTX) {Scorpion (Androctonus mauretanicus mauretanicus)}

GVEINVKCSGSPQCLKPCKDAGMRFGKCMNRKCHCTPK

>d1lir\_\_ g.3.7.2 (-) LQ2 toxin {Scorpion (Leiurus quinquestriatus hebraeus)}

EFTQESCTASNQCWSICKRLHNTNRGKCMNKKCRCYS

>d1c49a\_ g.3.7.2 (A:) Pandinus toxin {Emperor scorpion (Pandinus imperator), PITX-Kb}

TISCTNEKQCYPHCKKETGYPNAKCMNRKCKCFGR

>d1qkya\_ g.3.7.2 (A:) PI7 {Scorpion (Pandinus imperator)}

DEAIRCTGTKDCYIPCRYITGCFNSRCINKSCKCYGCT

>d1fjna\_ g.3.7.3 (A:) Defensin MGD-1 {Mediterranean mussel (Mytilus galloprovincialis)}

GFGCPNNYQCHRHCKSIPGRCGGYCGGWHRLRCTCYRCG

>d1i2ua\_ g.3.7.4 (A:) Heliomicin {Tobacco budworm (Heliothis virescens)}

DKLIGSCVWGAVNYTSDCNGECKRRGYKGGHCGSFANVNCWCET

>d1myn\_\_ g.3.7.4 (-) Drosomycin {Fruit fly (Drosophila melanogaster)}

DCLSGRYKGPCAVWDNETCRRVCKEEGRSSGHCSPSLKCWCEGC

>d1ica\_\_ g.3.7.4 (-) Defensin A {Flesh fly (Phormia terranovae), larva}

ATCDLLSGTGINHSACAAHCLLRGNRGGYCNGKGVCVCRN

>d1gpt\_\_ g.3.7.5 (-) gamma-Thionin {Barley (Hordeum vulgare)}

RICRRRSAGFKGPCVSNKNCAQVCMQEGWGGGNCDGPLRRCKCMRRC

>d1gps\_\_ g.3.7.5 (-) gamma-Thionin {Wheat (Triticum turgidum)}

KICRRRSAGFKGPCMSNKNCAQVCQQEGWGGGNCDGPFRRCKCIRQC

>d1ayj\_\_ g.3.7.5 (-) Antifungal protein 1 (RS-AFP1) {Radish (Raphanus sativus)}

EKLCERPSGTWSGVCGNNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC

>d1bk8\_\_ g.3.7.5 (-) Antimicrobial protein 1 (AH-AMP1) {Horse chestnut (Aesculus hippocastanum)}

LCNERPSQTWSGNCGNTAHCDKQCQDWEKASHGACHKRENHWKCFCYFNC

>d1jkza\_ g.3.7.5 (A:) Defensin 1 (PSD1) {Pea (Pisum sativum)}

KTCEHLADTYRGVCFTNASCDDHCKNKAHLISGTCHNWKCFCTQNC

>d1brz\_\_ g.3.7.5 (-) Brazzein {J'oublie (Pentadiplandra brazzeana)}

EDKCKKVYENYPVSKCQLANQCNYDCKLDKHARSGECFYDEKRNLQCICDYCEY

>d2cbh\_\_ g.3.8.1 (-) Cellobiohydrolase I {Trichoderma reesei, ct-cbh I}

TQSHYGQCGGIGYSGPTVCASGTTCQVLNPYYSQCL

>d1boea\_ g.3.9.1 (A:) Insulin-like growth factor-binding protein-5 (IGFBP-5) {Human (Homo sapiens)}

ALAEGQSCGVYTERCAQGLRCLPRQDEEKPLHALLHGRGVCLNEKS

>d1igra3 g.3.9.1 (A:150-299) Cys-rich domain of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

DLCPGTMEEKPMCEKTTINNEYNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGSCSAPDNDTACVACRHYYYAGVCVPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFIRNGSQSMYCIPCEGPCP

>d1lpba1 g.3.10.1 (A:6-44) (Pro)colipase {Pig (Sus scrofa)}

GIIINLDEGELCLNSAQCKSNCCQHDTILSLSRCALKAR

>d1lpba2 g.3.10.1 (A:45-90) (Pro)colipase {Pig (Sus scrofa)}

ENSECSAFTLYGVYYKCPCERGLTCEGDKSLVGSITNTNFGICHNV

>d1pco\_1 g.3.10.1 (1-44) (Pro)colipase {Pig (Sus scrofa)}

VPDPRGIIINLDEGELCLNSAQCKSNCCQHDTILSLSRCALKAR

>d1imt\_1 g.3.10.1 (1-36) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}

AVITGACERDLQCGKGTCCAVSLWIKSVRVCTPVGT

>d1imt\_2 g.3.10.1 (37-80) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}

SGEDCHPASHKIPFSGQRMHHTCPCAPNLACVQTSPKKFKCLSK

>d1edmb\_ g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}

VDGDQCESNPCLNGGSCKDDINSYECWCPFGFEGKNCEL

>d1rfnb\_ g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}

MTCNIKNGRCEQFCKNSADNKVVCSCTEGYRLAENQKSCEPAVPFPCGRVSVSQTSK

>d1pfxl1 g.3.11.1 (L:47-86) Factor IX (IXa) {Pig (Sus scrofa)}

DGDQCEPNPCLNGGLCKXDINSYECWCQVGFEGKNCELDA

>d1pfxl2 g.3.11.1 (L:87-146) Factor IX (IXa) {Pig (Sus scrofa)}

TCNIKNGRCKQFCKTGADSKVLCSCTTGYRLAPDQKSCKPAVPFPCGRVSVSHSPTTLTR

>d1danl1 g.3.11.1 (L:49-86) Coagulation factor VIIa {Human (Homo sapiens)}

QCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKD

>d1danl2 g.3.11.1 (L:87-142) Coagulation factor VIIa {Human (Homo sapiens)}

DQLICVNENGGCEQYCSDHTGTKRSCRCHEGYSLLADGVSCTPTVEYPCGKIPILE

>d1dval1 g.3.11.1 (L:42-86) Coagulation factor VIIa {Human (Homo sapiens)}

ISYSDGDQCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKD

>d1f7ea\_ g.3.11.1 (A:) Coagulation factor VIIa {Human (Homo sapiens)}

SDGDQCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKDDGSA

>d1g1sa2 g.3.11.1 (A:119-158) E-selectin, EGF-domain {Human (Homo sapiens)}

TASCQDMSCSKQGECLETIGNYTCSCYPGFYGPECEYVRD

>d1g1ta2 g.3.11.1 (A:119-157) E-selectin, EGF-domain {Human (Homo sapiens)}

TAACTNTSCSGHGECVETINNYTCKCDPGFSGLKCEQIV

>d1fjsl\_ g.3.11.1 (L:) Factor X, N-terminal module {Human (Homo sapiens)}

KLCSLDNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGPYPCGKQTLE

>d1xkba1 g.3.11.1 (A:48-86) Factor X, N-terminal module {Human (Homo sapiens)}

DQCETSPCQNQGKCKDGLGEYTCTCLEGFEGKNCELFTR

>d1apo\_\_ g.3.11.1 (-) Factor X, N-terminal module {Cow (Bos taurus)}

KDGDQCEGHPCLNQGHCKDGIGDYTCTCAEGFEGKNCEFSTR

>d1kigl\_ g.3.11.1 (L:) Factor X, N-terminal module {Cow (Bos taurus)}

CSLDNGGCDQFCREERSEVRCSCAHGYVLGDDSKSCVSTERFPCGKFTQGR

>d1autl1 g.3.11.1 (L:49-96) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}

QCLVLPLEHPCASLCCGHGTCIDGIGSFSCDCRSGWEGRFCQREVSFL

>d1autl2 g.3.11.1 (L:97-146) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}

NCSLDNGGCTHYCLEEVGWRRCSCAPGYKLGDDLLQCHPAVKFPCGRPWK

>d1eqga2 g.3.11.1 (A:33-73) Prostaglandin H2 synthase-1, EGF-like module {Sheep (Ovis aries)}

VNPCCYYPCQHQGICVRFGLDRYQCDCTRTGYSGPNCTIPE

>d1cvua2 g.3.11.1 (A:33-73) Prostaglandin H2 synthase-1, EGF-like module {Mouse (Mus musculus)}

ANPCCSNPCQNRGECMSTGFDQYKCDCTRTGFYGENCTTPE

>d1a3p\_\_ g.3.11.1 (-) Epidermal growth factor, EGF {Mouse (Mus musculus)}

PGXPSSYDGYCLNGGVXMHIESLDSYTCNCVIGYSGDRCQTRDLR

>d3egf\_\_ g.3.11.1 (-) Epidermal growth factor, EGF {Mouse (Mus musculus)}

NSYPGCPSSYDGYCLNGGVCMHIESLDSYTCNCVIGYSGDRCQTRDLRWWELR

>d1jl9a\_ g.3.11.1 (A:) Epidermal growth factor, EGF {Human (Homo sapiens)}

CPLSHDGYCLHDGVCMYIEALDKYACNCVVGYIGERCQYRDL

>d3tgf\_\_ g.3.11.1 (-) Transforming growth factor alpha {Human (Homo sapiens)}

VVSHFNDCPDSHTQFCFHGTCRFLVQEDKPACVCHSGYVGARCEHADLLA

>d1xdtr\_ g.3.11.1 (R:) Heparin-binding epidermal growth factor, HBEGF {Human (Homo sapiens)}

PCLRKYKDFCIHGECKYVKELRAPSCICHPGYHGERCHGLS

>d1urk\_1 g.3.11.1 (6-49) Plasminogen activator (urokinase-type) {Human (Homo sapiens)}

QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKT

>d1hae\_\_ g.3.11.1 (-) Heregulin-alpha, EGF-like domain {Human (Homo sapiens)}

SHLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTENVPMKVQNQEKAEELY

>d1adx\_\_ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}

QMFCNQTACPADCDPNTQASCECPEGYILDDGFICTDIDE

>d1dx5i1 g.3.11.1 (I:345-387) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}

VEPVDPCFRANCEYQCQPLDQTSYLCVCAEGFAPIPHEPHRCQ

>d1dx5i2 g.3.11.1 (I:388-422) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}

MFCNQTACPADCDPNTQASCECPEGYILDDGFICT

>d1dx5i3 g.3.11.1 (I:423-462) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}

DIDECENGGFCSGVCHNLPGTFECICGPDSALAGQIGTDC

>d1zaq\_\_ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}

EPVDPCFRANCEYQCQPLNQTSYLCVCAEGFAPIPHEPHRCQMF

>d1emo\_1 g.3.11.1 (2124-2166) Fibrillin-1 fragment (residues 2124-2205) {Human (Homo sapiens)}

SAVDMDECKEPDVCKHGQCINTDGSYRCECPFGYILAGNECVD

>d1emo\_2 g.3.11.1 (2167-2205) Fibrillin-1 fragment (residues 2124-2205) {Human (Homo sapiens)}

TDECSVGNPCGNGTCKNVIGGFECTCEEGFEPGPMMTCE

>d1apq\_\_ g.3.11.1 (-) Complement protease C1R {Human (Homo sapiens)}

AVDLDECASRSKSGEEDPQPQCQHLCHNYVGGYFCSCRPGYELQEDRHSCQAE

>d1tpg\_1 g.3.11.1 (51-91) Plasminogen activator (tissue-type), t-PA {Human (Homo sapiens)}

CSEPRCFNGGTCQQALYFSDFVCQCPEGFAGKSCEIDTRAT

>d1hz8a1 g.3.11.1 (A:1-41) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}

GTNECLDNNGGCSHVCNDLKIGYECLCPDGFQLVAQRRCED

>d1hz8a2 g.3.11.1 (A:42-82) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}

IDECQDPDTCSQLCVNLEGGYKCQCEEGFQLDPHTKACKAV

>d1ijqa2 g.3.11.1 (A:643-692) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}

VNWCERTTLSNGGCQYLCLPAPQINPHSPKFTCACPDGMLLARDMRSCLT

>d1jv2b4 g.3.11.6 (B:532-562) Integrin beta EGF-like domains {Human (Homo sapiens)}

KGEMCSGHGQCSCGDCLCDSDWTGYYCNCTT

>d1jv2b5 g.3.11.6 (B:563-605) Integrin beta EGF-like domains {Human (Homo sapiens)}

RTDTCMSSNGLLCSGRGKCECGSCVCIQPGSYGDTCEKCPTCP

>d1gl4a2 g.3.11.5 (A:359-398) EGF-like domain of nidogen-1 {Mouse (Mus musculus)}

TCANNRHQCSVHAECRDYATGFCCRCVANYTGNGRQCVAE

>d1h4ua2 g.3.11.5 (A:367-398) EGF-like domain of nidogen-1 {Mouse (Mus musculus)}

CSVHAECRDYATGFCCRCVANYTGNGRQCVAE

>d1klo\_1 g.3.11.2 (11-65) Laminin gamma1 chain {Mouse (Mus musculus)}

CPCPGGSSCAIVPKTKEVVCTHCPTGTAGKRCELCDDGYFGDPLGSNGPVRLCRP

>d1klo\_2 g.3.11.2 (66-121) Laminin gamma1 chain {Mouse (Mus musculus)}

CQCNDNIDPNAVGNCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKA

>d1klo\_3 g.3.11.2 (122-172) Laminin gamma1 chain {Mouse (Mus musculus)}

CACNPYGTVQQQSSCNPVTGQCQCLPHVSGRDCGTCDPGYYNLQSGQGCER

>d1nuba2 g.3.11.3 (A:53-77) Domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}

APCQNHHCKHGKVCELDENNTPMCV

>d1b9wa1 g.3.11.4 (A:1-45) Merozoite surface protein 1 (MSP-1) {Plasmodium cynomolgi}

MSSEHRCIDTNVPENAACYRYLDGTEEWRCLLYFKEDAGKCVPAP

>d1b9wa2 g.3.11.4 (A:46-89) Merozoite surface protein 1 (MSP-1) {Plasmodium cynomolgi}

NMTCKDKNGGCAPEAECKMNDKNEIVCKCTKEGSEPLFEGVFCS

>d1ceja1 g.3.11.4 (A:1-45) Merozoite surface protein 1 (MSP-1) {Plasmodium falciparum}

NISQHQCVKKQCPQNSGCFRHLDEREECKCLLNYKQEGDKCVENP

>d1ceja2 g.3.11.4 (A:46-96) Merozoite surface protein 1 (MSP-1) {Plasmodium falciparum}

NPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN

>d2bi6h1 g.3.12.1 (H:8-31) Bromelain inhibitor VI (cysteine protease inhibitor) {Pineapple (Ananas comosus)}

TDTYSDCPGFCKTCKAEFGKYICL

>g2bi6.2 g.3.12.1 (L:,H:1-7,H:32-41) Bromelain inhibitor VI (cysteine protease inhibitor) {Pineapple (Ananas comosus)}

TACSECVCPLRXEEYKCYCXDLISPNDCVK

>d1pi2\_\_ g.3.13.1 (-) Bowman-Birk inhibitor, BBI {Soybean (Glycine max), PI-II}

YSKPCCDLCMCTRSMPPQCSCEDRINSCHSDCKSCMCTRSQPGQCRCLDTNDFCYKPCKSR

>d1d6ri\_ g.3.13.1 (I:) Bowman-Birk inhibitor, BBI {Soybean (Glycine max)}

KPCCDQCACTKSNPPQCRCSDMRLNSCHSACKSCICALSYPAQCFCVDITDFCYEPCK

>d2bbi\_\_ g.3.13.1 (-) Bowman-Birk inhibitor, BBI {Soybean (Glycine max)}

DDESSKPCCDQCACTKSNPPQCRCSDMRLNSCHSACKSCICALSYPAQCFCVDITDFCYEPCKPSEDDKEN

>d1pbia\_ g.3.13.1 (A:) Bowman-Birk inhibitor, BBI {Winter pea (Pisum sativum)}

KSACCDTCLCTKSNPPTCRCVDVGETCHSACLSCICAYSNPPKCQCFDTQKFCYKQCHNSELEEVIKN

>d1df9c\_ g.3.13.1 (C:) Bowman-Birk inhibitor, BBI {Mung bean (Vigna radiata)}

SHDEPSESSEPCCDSCDCTKSIPPQCHCANIRLNSCHSACKSCICTRSMPGKCRCLDTDDFCYKPCESMDKD

>d1c2aa1 g.3.13.1 (A:4-64) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}

KRPWKCCDEAVCTRSIPPICTCMDEVFECPKTCKSCGPSMGDPSRRICQDQYVGDPGPICR

>d1c2aa2 g.3.13.1 (A:65-123) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}

PWECCDKAICTRSNPPTCRCVDEVKKCAPTCKTCLPSRSRPSRRVCIDSYFGPVPPRCT

>d1tabi\_ g.3.13.1 (I:) Bowman-Birk inhibitor, BBI {Adzuki bean (Phaseolus angularis)}

SESSKPCCDQCSCTKSMPPKCRCSDIRLNSCHSACKSCACTYSIPAKCFCTDINDFCYEPCK

>d1flei\_ g.3.14.1 (I:) Elafin, elastase-specific inhibitor {Human (Homo sapiens)}

TKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ

>d2rel\_\_ g.3.14.1 (-) Elafin, elastase-specific inhibitor {Human (Homo sapiens)}

AQEPVKGPVSTKPGSCPIILIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ

>d1bx7\_\_ g.3.15.1 (-) Hirustasin {Medicinal leech (Hirudo medicinalis)}

GNTCGGETCSAAQVCLKGKCVCNEVHCRIRCKYGLKKDENGCEYPCSCAKA

>d1ejab\_ g.3.15.1 (B:) Bdellastasin {Medicinal leech (Hirudo medicinalis)}

TTPCGPVTCSGAQMCEVDKCVCSDLHCKVKCEHGFKKDDNGCEYACICADAPQ

>d1skz\_1 g.3.15.1 (7-58) Factor Xa inhibitor antistasin {Mexican leech (Haementeria officinalis)}

GCEEAGCPEGSACNIITDRCTCSGVRCRVHCPHGFQRSRYGCEFCKCRLEPM

>d1skz\_2 g.3.15.1 (59-110) Factor Xa inhibitor antistasin {Mexican leech (Haementeria officinalis)}

KATCDISECPEGMMCSRLTNKCDCKIDINCRKTCPNGLKRDKLGCEYCECRP

>d1hic\_\_ g.3.15.2 (-) Hirudin {Leech (Hirudo medicinalis)}

VVYTDCTESGQNLCLCEGSNVCGQGNKCILGSDGEKNQCVTGEGTPKPQSH

>d1hrti\_ g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}

VVYTDCTESGQNLCLCEGSNVCGQGNKCILGSDGEKNQCVTGEGTPKPQSHNDGDFEEIPEEYLQ

>d4htci\_ g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}

ITYTDCTESGQNLCLCEGSNVCGKGNKCILGSNGKGNQCVTGEGTPKPESHNNGDFEEIPEEYLQ

>d1dec\_\_ g.3.15.2 (-) Decorsin {North american leech (Macrobdella decora)}

APRLPQCQGDDQEKCLCNKDECPPGQCRFPRGDADPYCE

>d1e0fi\_ g.3.15.2 (I:) Haemadin {Indian leech (Haemadipsa sylvestris)}

IRFGMGKVPCPDGEVGYTCDCGEKICLYGQSCNDGQCSGDPKPSSEFEEFEIDEEEK

>d1qgma\_ g.3.16.1 (A:) N-terminal domain of granulin-1 {Carp (Cyprinus carpio)}

VIHCDAATICPDGTTCSLSPYGVWYCSPFS

>d1g26a\_ g.3.16.1 (A:) N-terminal domain of granulin-1 {Human (Homo sapiens)}

VVHCDMEVICPDGYTCCRLPSGAWGCCPFTQ

>d1fwoa\_ g.3.16.1 (A:) Oryzain beta chain {Rice (Oryza sativa)}

DHVCDDNFSCPAGSTCSSAFGFRNLSLVWGCSPVE

>d1hy9a\_ g.3.17.1 (A:) Satiety factor CART (cocaine and amphetamine regulated transcript) {Human (Homo sapiens)}

YGQVPMCDAGEQCAVRKGARIGKLCDCPRGTSCNSFLLKCL

>d1gl1i\_ g.4.1.1 (I:) Protease inhibitor PMP-C {Migratory locust (Locusta migratoria)}

ISCEPGKTFKDKCNTCRCGADGKSAACTLKACPN

>d1gl0i\_ g.4.1.1 (I:) Protease inhibitor PMP-D2V {Migratory locust (Locusta migratoria)}

KCTPGQVKQQDCNTCTCTPTGVWGCTLMGCQP

>d1kgma\_ g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}

EVTCEPGTTFKDKCNTCRCGSDGKSAACTLKACPQ

>d1kioa\_ g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}

EVTCEPGTTFKDKCNTCRCGSDGKSAACTRMACPQ

>d1kj0a\_ g.4.1.1 (A:) Protease inhibitor SGTI {Desert locust (Schistocerca gregaria)}

EQECTPGQTKKQDCNTCNCTPTGVWACTRKGCPPH

>d1mkna\_ g.5.1.1 (A:) Midkine, a heparin-binding growth factor, N-terminal domain {Synthetic}

KKKDKVKKGGPGSECAEWAWGPCTPSSKDCGVGFREGTCGAQTQRIRCRVPCNWKKEFG

>d1mkca\_ g.5.1.2 (A:) Midkine, a heparin-binding growth factor, C-terminal domain {Synthetic}

CKYKFENWGACDGGTGTKVRQGTLKKARYNAQCQETIRVTKPC

>d2bbg\_\_ g.6.1.1 (-) Amb V allergen {Giant ragweed (Ambrosia trifida), pollen}

DDGLCYEGTNCGKVGKYCCSPIGKYCVCYDSKAICNKNCT

>d3ebx\_\_ g.7.1.1 (-) Erabutoxin B (also neurotoxin B) {Sea snake (Laticauda semifasciata)}

RICFNHQSSQPQTTKTCSPGESSCYHKQWSDFRGTIIERGCGCPTVKPGIKLSCCESEVCNN

>d1tgxa\_ g.7.1.1 (A:) gamma-Cardiotoxin {Snake (Naja nigricollis)}

LKCNQLIPPFWKTCPKGKNLCYKMTMRAAPMVPVKRGCIDVCPKSSLLIKYMCCNTDKCN

>d1fas\_\_ g.7.1.1 (-) Fasciculin {Green mamba (Dendroaspis angusticeps)}

TMCYSHTTTSRAILTNCGENSCYRKSRRHPPKMVLGRGCGCPPGDDYLEVKCCTSPDKCNY

>d1qm7a\_ g.7.1.1 (A:) Fasciculin {Green mamba (Dendroaspis angusticeps)}

TMCYSHTTTSRAILTNCPGETNCYKKSRRHPPKMVLGRGCGCPTVAPGIKLNCCTTDKCNY

>d1ntn\_\_ g.7.1.1 (-) Neurotoxin I {Snake (Naja naja oxiana)}

ITCYKTPIITSETCAPGQNLCYTKTWCDAWCGSRGKVIELGCAATCPTVESYQDIKCCSTDNCNPHPKQKRP

>d1cdta\_ g.7.1.1 (A:) Cardiotoxin V4II (Toxin III) {Naja mossambica mossambica}

LKCNKLIPIAYKTCPEGKNLCYKMMLASKKMVPVKRGCINVCPKNSALVKYVCCSTDRCN

>d1kxia\_ g.7.1.1 (A:) Cardiotoxin V {Taiwan cobra (Naja naja atra)}

LKCHNTQLPFIYKTCPEGKNLCFKATLKKFPLKFPVKRGCADNCPKNSALLKYVCCSTDKCN

>d2ctx\_\_ g.7.1.1 (-) alpha-Cobratoxin {Cobra (Naja naja siamensis)}

IRCFITPDITSKDCPNGHVCYTKTWCDAFCSIRGKRVDLGCAATCPTVKTGVDIQCCSTDNCNPFPTRKRP

>d1lsi\_\_ g.7.1.1 (-) Long neurotoxin 1 (component LSIII) {Sea snake (Laticauda semifasciata)}

RECYLNPHDTQTCPSGQEICYVKSWCNAWCSSRGKVLEFGCAATCPSVNTGTEIKCCSADKCNTYP

>d1tfs\_\_ g.7.1.1 (-) FS2 toxin {Black mamba (Dendroaspis polylepis polylepis)}

RICYSHKASLPRATKTCVENTCYKMFIRTHREYISERGCGCPTAMWPYQTECCKGDRCNK

>d1hc9a\_ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), Alpha-bungarotoxin}

IVCHTTATSPISAVTCPPGENLCYRKMWCDVFCSSRGKVVELGCAATCPSKKPYEEVTCCSTDKCNPHPKQRPG

>d2abxa\_ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), Alpha-bungarotoxin}

IVCHTTATIPSSAVTCPPGENLCYRKMWCDAFCSSRGKVVELGCAATCPSKKPYEEVTCCSTDKCNHPPKRQPG

>d1kbaa\_ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), kappa-bungarotoxin}

RTCLISPSSTPQTCPNGQDICFLKAQCDKFCSIRGPVIEQGCVATCPQFRSNYRSLLCCTTDNCNH

>d1f94a\_ g.7.1.1 (A:) Bucandin {Malayan krait (Bungarus candidus)}

MECYRCGVSGCHLKITCSAEETFCYKWLNKISNERWLGCAKTCTEIDTWNVYNKCCTTNLCNT

>d2cdx\_\_ g.7.1.1 (-) Cardiotoxin CTXI {Taiwan cobra (Naja naja atra)}

LKCNKLIPIASKTCPAGKNLCYKMFMMSDLTIPVKRGCIDVCPKNSLLVKYVCCNTDRCN

>d1chvs\_ g.7.1.1 (S:) Cardiotoxin II {Taiwan cobra (Naja naja atra)}

LKCNKLVPLFYKTCPAGKNLCYKMFMVSNKMVPVKRGCIDVCPKSSLLVKYVCCNTDRCN

>d1cb9a\_ g.7.1.1 (A:) Cardiotoxin II {Central asian cobra (Naja naja oxiana)}

LKCKKLVPLFSKTCPAGKNLCYKMFMVAAPHVPVKRGCIDVCPKSSLLVKYVCCNTDKCN

>d1i02a\_ g.7.1.1 (A:) Cardiotoxin III {Taiwan cobra (Naja naja atra)}

LKCNKLVPLFYKTCPAGKNLCYKMFMVATPKVPVKRGCIDVCPKSSLLVKYVCCNTDRCN

>d1kbs\_\_ g.7.1.1 (-) Cardiotoxin IV {Taiwan cobra (Naja naja atra)}

RKCNKLVPLFYKTCPAGKNLCYKMFMVSNLTVPVKRGCIDVCPKNSALVKYVCCNTDRCN

>d1cod\_\_ g.7.1.1 (-) Cobrotoxin II (ct2) {Taiwan cobra (Naja naja atra)}

LECHNQQSSQTPTTTGCSGGETNCYKKRWRDHRGYRTERGCGCPSVKNGIEINCCTTDRCNN

>d1g6ma\_ g.7.1.1 (A:) Cobrotoxin II (ct2) {Monocled cobra (Naja kaouthia)}

LECHNQQSSQTPTTTGCSGGENNCYKKEWRDNRGYRTERGCGCPSVKKGIGINCCTTDRCNN

>d1nea\_\_ g.7.1.1 (-) alpha-Toxin {Snake (Naja nigricollis)}

LECHNQQSSQPPTTKTCPGETNCYKKVWRDHRGTIIERGCGCPTVKPGIKLNCCTTDKCNN

>d1ntx\_\_ g.7.1.1 (-) alpha-Toxin {Black mamba (Dendroaspis polylepis polylepis)}

RICYNHQSTTRATTKSCEENSCYKKYWRDHRGTIIERGCGCPKVKPGVGIHCCQSDKCNY

>d1nor\_\_ g.7.1.1 (-) Neurotoxin II (Nt2) {Central asian cobra (Naja naja oxiana)}

LECHNQQSSQPPTTKTCSGETNCYKKWWSDHRGTIIERGCGCPKVKPGVNLNCCRTDRCNN

>d1txb\_\_ g.7.1.1 (-) Toxin B (long neurotoxin) {King cobra (Ophiophagus hannah)}

TKCYVTPDATSQTCPDGQDICYTKTWCDGFCSSRGKRIDLGCAATCPKVKPGVDIKCCSTDNCNPFPTWKRKH

>d1jgka\_ g.7.1.1 (A:) Candoxin {Malayan krait (Bungarus candidus)}

MKCKICNFDTCRAGELKVCASGEKYCFKESWREARGTRIERGCAATCPKGSVYGLYVLCCTTDDCN

>d1drs\_\_ g.7.1.2 (-) Dendroaspin {Dendroaspis jamesoni kaimosae}

RICYNHLGTKPPTTETCQEDSCYKNIWTFDNIIRRGCGCFTPRGDMPGPYCCESDKCNL

>d1erh\_\_ g.7.1.3 (-) CD59 {Human (Homo sapiens)}

LQCYNCPNPTADCKTAVNCSSDFDACLITKAGLQVYNKCWKFEHCNFNDVTTRLRENELTYYCCKKDLCN

>d1btea\_ g.7.1.3 (A:) Type II activin receptor {Mouse (Mus musculus)}

ETQECLFFNANWERDRTNQTGVEPCYGDKDKRRHCFATWKNISGSIEIVKQGCWLDDINCYDRTDCIEKKDSPEVYFCCCEGNMCNEKFSYFPEME

>d1es7b\_ g.7.1.3 (B:) BMP receptor Ia ectodomain {Human (Homo sapiens)}

TLPFLKCYCSGHCPDDAINNTCITNGHCFAIIEEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRRTIECCRTNLCNQYLQPTLPP

>d1ktzb\_ g.7.1.3 (B:) TGF-beta type II receptor extracellular domain {Human (Homo sapiens)}

PQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAASPKCIMKEKKKPGETFFMCSCSSDECNDNIIFSEEY

>d1brbi\_ g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}

AGEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTA

>d1ejmb\_ g.8.1.1 (B:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}

RPDFCLEPPYTGPCRLRIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA

>d1faki\_ g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}

APDFCLEPPYDGPCRALHLRYFYNAKAGLCQTFYYGGCLAKRNNFESAEDCMRTC

>d1g6xa\_ g.8.1.1 (A:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}

RPDFCLEPPYAGACRARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA

>d3bthi\_ g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}

DFCLEPPYTGPCHARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA

>d5pti\_\_ g.8.1.1 (-) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}

RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGA

>d1ktha\_ g.8.1.1 (A:) Collagen type VI (domain C5 from alpha 3 chain) {Human (Homo sapiens)}

ETDICKLPKDEGTCRDFILKWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCAPV

>d1adz\_\_ g.8.1.1 (-) Tissue factor pathway inhibitor {Human (Homo sapiens)}

DYKDDDDKLKPDFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICEDGPNGF

>d1irha\_ g.8.1.1 (A:) Tissue factor pathway inhibitor {Human (Homo sapiens)}

EFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGCGGNENNFTSKQECLRACKKG

>d1tfxc\_ g.8.1.1 (C:) Tissue factor pathway inhibitor {Human (Homo sapiens)}

KPDFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICEDG

>d1aapa\_ g.8.1.1 (A:) Alzheimer's amyloid B-protein precursor, APPI {Human (Homo sapiens)}

VREVCSEQAETGPCRAMISRWYFDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCG

>d1bik\_1 g.8.1.1 (25-78) Bikunin from inter-alpha-inhibitor complex {Human (Homo sapiens)}

SCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRT

>d1bik\_2 g.8.1.1 (79-134) Bikunin from inter-alpha-inhibitor complex {Human (Homo sapiens)}

VAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQGNGNKFYSEKECREYCGV

>d1dtx\_\_ g.8.1.1 (-) alpha-Dendrotoxin {Green mamba (Dendroaspis angusticeps)}

EPRRKLCILHRNPGRCYDKIPAFYYNQKKKQCERFDWSGCGGNSNRFKTIEECRRTCIG

>d1bunb\_ g.8.1.1 (B:) beta2-bungarotoxin, neurotoxin chain {Many-banded krait (elapid) (Bungarus multicinctus)}

RKRHPDCDKPPDTKICQTVVRAFYYKPSAKRCVQFRYGGCNGNGNHFKSDHLCRCECLEYR

>d1shp\_\_ g.8.1.1 (-) Trypsin inhibitor {Sea anemone (Stichodactyla helianthus)}

SICSEPKKVGRCKGYFPRFYFDSETGKCTPFIYGGCGGNGNNFETLHQCRAICRA

>d1dtk\_\_ g.8.1.1 (-) Dendrotoxin K {Black mamba (Dendroaspis polylepis polylepis)}

AAKYCKLPLRIGPCKRKIPSFYYKWKAKQCLPFDYSGCGGNANRFKTIEECRRTCVG

>d1den\_\_ g.8.1.1 (-) Dendrotoxin I {African elapid snake (Dendroaspis polylepis polylepis)}

QPLRKLCILHRNPGRCYQKIPAFYYNQKKKQCEGFTWSGCGGNSNRFKTIEECRRTCIRK

>d1bf0\_\_ g.8.1.1 (-) Calcicludine (cac) {Green mamba (Dendroaspis angusticeps)}

WQPPWYCKEPVRIGSCKKQFSSFYFKWTAKKCLPFLFSGCGGNANRFQTIGECRKKCLGK

>d1tocr1 g.8.1.2 (R:1A-56) Ornithodorin {Soft tick (Ornithodoros moubata)}

SLNVLCNNPHTADCNNDAQVDRYFREGTTCLMSPACTSEGYASQHECQQACFVGGED

>d1tocr2 g.8.1.2 (R:57-119) Ornithodorin {Soft tick (Ornithodoros moubata)}

HSSEMHSSCLGDPPTSCAEGTDITYYDSDSKTCKVLAASCPSGENTFESEVECQVACGAPIEG

>d1d0da\_ g.8.1.2 (A:) Anticoagulant protein, factor Xa inhibitor {Soft tick (Ornithodoros moubata)}

YNRLCIKPRDWIDECDSNEGGERAYFRNGKGGCDSFWICPEDHTGADYYSSYRDCFNACI

>d1dfna\_ g.9.1.1 (A:) Defensin HNP-3 {Human (Homo sapiens)}

DCYCRIPACIAGERRYGTCIYQGRLWAFCC

>d1ijva\_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD1}

DHYNCVSSGGQCLYSACPIFTKIQGTCYRGKAKCCK

>d1e4qa\_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}

PVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKP

>d1fd3a\_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}

GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKP

>d1e4ta\_ g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD5}

NSKRACYREGGECLQRCIGLFHKIGTCNFRFKCCKFQ

>d1e4ra\_ g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD6}

NEPVSCIRNGGICQYRCIGLRHKIGTCGSPFKCCK

>d1bnb\_\_ g.9.1.1 (-) Beta-defensin, BD {Cow (Bos taurus), BD12}

APLSCGRNGGVCIPIRCPVPMRQIGTCFGRPVKCCRSW

>d1ewsa\_ g.9.1.1 (A:) Alpha-defensin rk-1 {Rabbit (Oryctolagus cuniculus)}

MPCSCKKYCDPWEVIDGSCGLFNSKYICCREK

>d1b8wa\_ g.9.1.1 (A:) Defensin-like peptide, DLP {Duckbilled platypus (Ornithorhynchus anatinus), DLP-1}

FVQHRPRDCESINGVCRHKDTVNCREIFLADCYNDGQKCCRK

>d1d6ba\_ g.9.1.1 (A:) Defensin-like peptide, DLP {Duckbilled platypus (Ornithorhynchus anatinus), DLP-2}

IMFFEMQACWSHSGVCRDKSERNCKPMAWTYCENRNQKCCEY

>d2bds\_\_ g.9.1.1 (-) BDs-I defensin {Sea anemone (Anemonia sulcata)}

AAPCFCSGKPGRGDLWILRGTCPGGYGYTSNCYKWPNICCYPH

>d1sh1\_\_ g.9.1.1 (-) Sea anemone neurotoxin-1 {Sea anemone (Stichodactyla helianthus)}

AACKCDDEGPDIRTAPLTGTVDLGSCNAGWEKCASYYTIIADCCRKKK

>d1atx\_\_ g.9.1.1 (-) Sea anemone toxin IA {Sea anemone (Anemonia sulcata)}

GAACLCKSDGPNTRGNSMSGTIWVFGCPSGWNNCEGRAIIGYCCKQ

>d1ahl\_\_ g.9.1.1 (-) Anthopleurin-A {Giant green sea anemone (Anthopleura xanthogrammica)}

GVSCLCDSDGPSVRGNTLSGTLWLYPSGCPSGWHNCKAHGPTIGWCCKQ

>d1apf\_\_ g.9.1.1 (-) Anthopleurin-B {Giant green sea anemone (Anthopleura xanthogrammica)}

GVPCLCDSDGPRPRGNTLSGILWFYPSGCPSGWHNCKAHGPNIGWCCKK

>d1bhta1 g.10.1.1 (A:35-126) Hepatocyte growth factor {Human (Homo sapiens)}

RRNTIHEFKKSAKTTLIKIDPALKIKTKKVNTADQCANRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYIR

>d1gmnb1 g.10.1.1 (B:42-125) Hepatocyte growth factor {Human (Homo sapiens)}

FKKSAKTTLIKIDPALKIKTKKVNTADQCADRCTRNKGLPFTCKAFVFDKARKQCLWFPFNSMSSGVKKEFGHEFDLYENKDYI

>d1i8na\_ g.10.1.2 (A:) Anti-platelet protein {Leech (Haementeria officinalis)}

ETITAGNEDCWSKRPGWKLPDNLLTKTEFTSVDECRKMCEESAVEPSCYILQINTETNECYRNNEGDVTWSSLQYDQPNVVQWHLHACS

>d1ans\_\_ g.11.1.1 (-) Neurotoxin III (ATX III) {Sea anemone (Anemonia sulcata)}

RSCCPCYWGGCPWGQNCYPEGCSGPKV

>d1ajj\_\_ g.12.1.1 (-) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

PCSAFEFHCLSGECIHSSWRCDGGPDCKDKSDEENCA

>d1cr8a\_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

PGGCHTDEFQCRLDGLCIPLRWRCDGDTDCMDSSDEKSCEGV

>d1d2la\_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

GSPPQCQPGEFACANSRCIQERWKCDGDNDCLDNSDEAPALCHQH

>d1f5ya1 g.12.1.1 (A:1-44) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

GSAVGDRCERNEFQCQDGKCISYKWVCDGSAECQDGSDESQETC

>d1f5ya2 g.12.1.1 (A:45-85) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

LSVTCKSGDFSCGGRVNRCIPQFWRCDGQVDCDNGSDEQGC

>d1f8za\_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

ATCRPDEFQCSDGNCIHGSRQCDREYDCKDMSDEVGCVN

>d1j8ea\_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

GSHSCSSTQFKCNSGRCIPEHWTCDGDNDCGDYSDETHANCTNQ

>d1ldl\_\_ g.12.1.1 (-) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

AVGDRCERNEFQCQDGKCISYKWVCDGSAECQDGSDESQETCLSVT

>d1k7ba\_ g.12.1.1 (A:) soluble Tva ectodomain, sTva47 {Quail (Coturnix coturnix)}

SCPPGQFRCSEPPGAHGECYPQDWLCDGHPDCDDGRDEWGCG

>d1ejga\_ g.13.1.1 (A:) Crambin {Abyssinian cabbage (Crambe abyssinica)}

TTCCPSIVARSNFNVCRLPGTPEALCATYTGCIIIPGATCPGDYAN

>d1bhp\_\_ g.13.1.1 (-) beta-Purothionin {Wheat (Triticum aestivum)}

KSCCKSTLGRNCYNLCRARGAQKLCANVCRCKLTSGLSCPKDFPK

>d2plh\_\_ g.13.1.1 (-) alpha-1-Purothionin {Wheat (Triticum aestivum)}

KSCCRSTLGRNCYNLCRARGAQKLCAGVCRCKISSGLSCPKGFPK

>d1ed0a\_ g.13.1.1 (A:) Viscotoxin a3 {European mistletoe (Viscum album)}

KSCCPNTTGRNIYNACRLTGAPRPTCAKLSGCKIISGSTCPSDYPK

>d1i5ka\_ g.14.1.1 (A:) Plasminogen kringles {Human (Homo sapiens)}

ECMHGSGENYDGKISKTMSGLECQAWDSQSPHAHGYIPSKFPNKNLKKNYCRNPDRDLRPWCFTTDPNKRWEYCDIPRC

>d1krn\_\_ g.14.1.1 (-) Plasminogen kringles {Human (Homo sapiens)}

DCYHGDGQSYRGTSSTTTTGKKCQSWSSMTPHRHQKTPENYPNAGLTMNYCRNPDADKGPWCFTTDPSVRWEYCNLKKC

>d1pmla\_ g.14.1.1 (A:) Plasminogen kringles {Human (Homo sapiens)}

SDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCST

>d1ceaa\_ g.14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}

ECKTGNGKNYRGTMSKTKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDPQGPWCYTTDPEKRYDYCDILEC

>d5hpga\_ g.14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}

DCMFGNGKGYRGKRVTTVTGTPCQDWAAQEPHRHSIFTPETNPRAGLEKNYCRNPDGDVGGPWCYTTNPRKLYDYCDVPQCAAP

>d2pf1\_1 g.14.1.1 (66-156) Prothrombin kringle domain {Cow (Bos taurus)}

CAEGVGMNYRGNVSVTRSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSITGPWCYTTSPTLRREECSVPVCGQDRVTVEVIPR

>d2pf2\_1 g.14.1.1 (66-146) Prothrombin kringle domain {Cow (Bos taurus)}

CAEGVGMNYRGNVSVTRSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSITGPWCYTTSPTLRREECSVPVCGQ

>d1a0ha1 g.14.1.1 (A:164-270) Meizothrombin kringle domain {Cow (Bos taurus)}

SPLLETCVPDRGREYRGRLAVTTHGSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVADQPGDFEYCDLNYCEEPVDGDLGDRLGEDPDPDAAIEG

>d2hppp\_ g.14.1.1 (P:) Meizothrombin kringle domain {Cow (Bos taurus)}

CVPDRGREYRGRLAVTTSGSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVADQPGDFEYCNLNYC

>d2hpqp\_ g.14.1.1 (P:) Meizothrombin kringle domain {Human (Homo sapiens)}

CVPDRGQQYQGRLAVTTHGLPCLAWASAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVWCYVAGKPGDFGYCDLNYC

>d1kdu\_\_ g.14.1.1 (-) Urokinase-type plasminogen activator kringle domain {Human (Homo sapiens)}

TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRRPWCYVQVGLKPLVQECMVHDCAD

>d3kiv\_\_ g.14.1.1 (-) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-10/M66 variant}

QCYHGNGQSYRGTFSTTVTGRTCQSWSSMTPHRHQRTPENYPNDGLTMNYCRNPDADTGPWCFTTDPSIRWEYCNLTRC

>d1i71a\_ g.14.1.1 (A:) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-7 variant}

DCYHGDGQSYRGSFSTTVTGRTCQSWSSMTPHWHQRTTEYYPNGGLTRNYCRNPDAEIRPWCYTMDPSVRWEYCNLTQCPVME

>d1bhta2 g.14.1.1 (A:127-210) NK1 fragment of hepatocyte growth factor {Human (Homo sapiens)}

NCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGEEGGPWCFTSNPEVRYEVCDIPQCSEVE

>d1pdc\_\_ g.14.1.2 (-) PDC-109, collagen-binding type II domain {Cow (Bos taurus)}

DYAKCVFPFIYGGKKYETCTKIGSMWMSWCSLSPNYDKDRAWKYC

>d1e88a1 g.14.1.2 (A:42-101) Fibronectin {Human (Homo sapiens)}

AVTQTYGGNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQKYSFCTDHT

>d1e88a2 g.14.1.2 (A:102-160) Fibronectin {Human (Homo sapiens)}

VLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRRDNMKWCGTTQNYDADQKFGFCPMA

>d1ck7a3 g.14.1.2 (A:217-277) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

EGQVVRVKYGNADGEYCKFPFLFNGKEYNSCTDTGRSDGFLWCSTTYNFEKDGKYGFCPHE

>d1ck7a4 g.14.1.2 (A:278-335) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

ALFTMGGNAEGQPCKFPFRFQGTSYDSCTTEGRTDGYRWCGTTEDYDRDKKYGFCPET

>d1ck7a5 g.14.1.2 (A:336-393) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

AMSTVGGNSEGAPCVFPFTFLGNKYESCTSAGRSDGKMWCATTANYDDDRKWGFCPDQ

>d1j7ma\_ g.14.1.2 (A:) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

SWMSTVGGNSGGAPCVFPFTFLGNKYESCTSAGRSDGKMWCATTANYDDDRKWGFCPDQG

>d1ks0a\_ g.14.1.2 (A:) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

RIPVKYGNADGEYCKFPFLFNGKEYNSCTDTGRSDGFLWCSTTYNFEKDGKYGFCPHEA

>d1sgpi\_ g.15.1.1 (I:) Ovomucoid III domain {Turkey (Meleagris gallopavo)}

VDCSEYPKPACTAEYRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC

>d3ovo\_\_ g.15.1.1 (-) Ovomucoid III domain {Japanese quail (Coturnix coturnix japonica)}

LAAVSVDCSEYPKPACPKDYRPVCGSDNKTYSNKCNFCNAVVESNGTLTLNHFGKC

>d2ovo\_\_ g.15.1.1 (-) Ovomucoid III domain {Silver pheasant (Lophura nycthemera)}

LAAVSVDCSEYPKPACTMEYRPLCGSDNKTYGNKCNFCNAVVESNGTLTLSHFGKC

>d1hpt\_\_ g.15.1.1 (-) Secretory trypsin inhibitor {Human (Homo sapiens)}

DSLGREAKCYNELNGCTYEYRPVCGTDGDTYPNECVLCFENRKRQTSILIQKSGPC

>d1tgsi\_ g.15.1.1 (I:) Secretory trypsin inhibitor {Pig (Sus scrofa)}

TSPQREATCTSEVSGCPKIYNPVCGTDGITYSNECVLCSENKKRQTPVLIQKSGPC

>d1tbrr1 g.15.1.1 (R:1-51) Rhodniin {Bug (Rhodnius prolixus)}

EGGEPCACPHALHRVCGSDGETYSNPCTLNCAKFNGKPELVKVHDGPCEPD

>d1tbrr2 g.15.1.1 (R:52-103) Rhodniin {Bug (Rhodnius prolixus)}

EDEDVCQECDGDEYKPVCGSDDITYDNNCRLECASISSSPGVELKHEGPCRT

>d1nuba3 g.15.1.1 (A:78-135) Domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}

CQDPTSCPAPIGEFEKVCSNDNKTFDSSCHFFATKCTLEGTKKGHKLHLDYIGPCKYI

>d2bus\_\_ g.15.1.1 (-) Seminal plasma inhibitor IIa {Cow (Bos taurus)}

EGAQVDCAEFKDPKVYCTRESNPHCGSNGETYGNKCAFCKAVMKSGGKINLKHRGKC

>d1pce\_\_ g.15.1.1 (-) PEC-60 peptide {Pig (Sus scrofa)}

EKQVFSRMPICEHMTESPDCSRIYDPVCGTDGVTYESECKLCLARIENKQDIQIVKDGEC

>d1an1i\_ g.15.1.1 (I:) Leech derived tryptase inhibitor (LDTI-C) {Medicinal leech (Hirudo medicinalis)}

KVCACPKILKPVCGSDGRTYANSCIARCNGVSIKSEGSCP

>d1ldtl\_ g.15.1.1 (L:) Leech derived tryptase inhibitor (LDTI-C) {Medicinal leech (Hirudo medicinalis)}

KKVCACPKILKPVCGSDGRTYANSCIARCNGVSIKSEGSCPTGILN

>d4sgbi\_ g.15.1.2 (I:) Plant chymotrypsin inhibitor {Potato tuber (Solanum tuberosum)}

PICTNCCAGYKGCNYYSANGAFICEGQSDPKKPKACPLNCDPHIAYSKCPR

>d1ce3a\_ g.15.1.2 (A:) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}

MKACTLNCDPRIAYGVCPRSEEKKNDRICTNCCAGTKGCKYFSDDGTFVCEGES

>d1fyba1 g.15.1.2 (A:1-55) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}

DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACTLNCDPRIAYGVCPRSEE

>d1tih\_\_ g.15.1.2 (-) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}

DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDPRIAYGICPLA

>g1qh2.1 g.15.1.2 (B:,A:) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}

RICTNCCAGKKGCKYFSDDGTFICEGESXKACTLNCDPRIAYGVCPR

>d2pspa1 g.16.1.1 (A:1-53) Pancreatic spasmolytic polypeptide {Pig (Sus scrofa)}

EKPAACRCSRQDPKNRVNCGFPGITSDQCFTSGCCFDSQVPGVPWCFKPLPAQ

>d2pspa2 g.16.1.1 (A:54-106) Pancreatic spasmolytic polypeptide {Pig (Sus scrofa)}

ESEECVMQVSARKNCGYPGISPEDCAARNCCFSDTIPEVPWCFFPMSVEDCHY

>d1hi7a\_ g.16.1.1 (A:) PNR-2/PS2, TFF1 {Human (Homo sapiens)}

EAQTETCTVAPRERQNCGFPGVTPSQCANKGCCFDDTVRGVPWCFYPNTIDVPPEEECEF

>d1e9ta\_ g.16.1.1 (A:) Intestinal trefoil factor {Human (Homo sapiens)}

EEYVGLSANQCAVPAKDRVDCGYPHVTPKECNNRGCCFDSRIPGVPWCFKPLQEAECTF

>d1pdga\_ g.17.1.1 (A:) Platelet-derived growth factor BB {Human (Homo sapiens)}

EPAMIAECKTRTEVFEISRRLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQCRPTQVQLRPVQVRKIEIVRKKPIFKKATVTLEDHLACKCETVAA

>d1fltv\_ g.17.1.1 (V:) Vascular endothelial growth factor, VEGF {Human (Homo sapiens)}

EVVKFMDVYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEESNITMQIMRIKPHQGQHIGEMSFLQHNKCECRPK

>d1fzva\_ g.17.1.1 (A:) Placenta growth factor-1, PLGF-1 {Human (Homo sapiens)}

SSEVEVVPFQEVWGRSYCRALERLVDVVSEYPSEVEHMFSPSCVSLLRCTGCCGDENLHCVPVETANVTMQLLKIRSGDRPSYVELTFSQHVRCECRPLR

>d1ktza\_ g.17.1.2 (A:) TGF-beta3 {Human (Homo sapiens)}

ENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS

>d1tgj\_\_ g.17.1.2 (-) TGF-beta3 {Human (Homo sapiens)}

ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCKCS

>d2tgi\_\_ g.17.1.2 (-) TGF-beta2 {Human (Homo sapiens)}

ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASASPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVKSCKCS

>d1klaa\_ g.17.1.2 (A:) TGF-beta1 {Human (Homo sapiens)}

ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS

>d1bmp\_\_ g.17.1.2 (-) Bone morphogenetic protein-7 (BMP-7) {Human (Homo sapiens)}

QACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGCH

>d1es7a\_ g.17.1.2 (A:) Bone morphogenetic protein-2 (BMP-2) {Human (Homo sapiens)}

KSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLVNSVNSKIPKACCVPTELSAISMLYLDENEKVVLKNYQDMVVEGCGCR

>d1agqa\_ g.17.1.2 (A:) Glial cell-derived neurotrophic factor, GDNF {Rat (Rattus norvegicus)}

NRGCVLTAIHLNVTDLGLGYETKEELIFRYCSGSCEAAETMYDKILKNLSRSRRLTSDKVGQACCRPVAFDDDLSFLDDSLVYHILRKHSAKRCGCI

>d1bnda\_ g.17.1.3 (A:) Brain-derived neurotrophic factor/neurotrophin 3 heterodimer, BDNF/NT3 {Human (Homo sapiens)}

GQLSVCDSISEWVTAADKKTAVDMSGGTVTVLEKVPVSKGQLKQYFYETKCNPMGYTKEGCRGIDKRHWNSQCRTTQSYVRALTMDSKKRIGWRFIRIDTSCVCTLTIK

>d1bndb\_ g.17.1.3 (B:) Brain-derived neurotrophic factor/neurotrophin 3 heterodimer, BDNF/NT3 {Human (Homo sapiens)}

RGEVSVCDSESLWVTDKSSAIDIRGHQVTVLGEIKTQNSPVKQYFYETRCKEARPVKNGCRGIDDKHWNSQCKTSQTYVRALTSENNKLVGWRWIRIDTSCVCALSRK

>d1b8mb\_ g.17.1.3 (B:) Neurotrophin 4 {Human (Homo sapiens)}

GELAVCDAVSGWVTDRRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRRHWVSECKAKQSYVRALTADAQGRVGWRWIRIDTACVCTLLSRTGRA

>d1hcfa\_ g.17.1.3 (A:) Neurotrophin 4 {Human (Homo sapiens)}

GVSETAPASRRGELAVCDAVSGWVTDRRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRRHWVSECKAKQSYVRALTADAQGRVGWRWIRIDTACVCTLLSRT

>d1bet\_\_ g.17.1.3 (-) beta-Nerve growth factor {Mouse (Mus musculus)}

GEFSVCDSVSVWVGDKTTATDIKGKEVTVLAEVNINNSVFRQYFFETKCRASNPVESGCRGIDSKHWNSYCTTTHTFVKALTTDEKQAAWRFIRIDTACVCVLSRKA

>d1wwwv\_ g.17.1.3 (V:) beta-Nerve growth factor {Human (Homo sapiens)}

SSHPIFHRGEFSVCDSVSVWVGDKTTATDIKGKEVMVLGEVNINNSVFKQYFFETKCRDPNPVDSGCRGIDSKHWNSYCTTTHTFVKALTMDGKQAAWRFIRIDTACVCVLSRK

>d1hcna\_ g.17.1.4 (A:) Glycoprotein hormones alpha chain (Gonadotropin A, Follitropin alpha) {Human (Homo sapiens)}

QDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCYY

>d1hcnb\_ g.17.1.4 (B:) Gonadotropin B chain {Human (Homo sapiens)}

KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDVRFESIRLPGCPRGVNPVVSYAVALSCQCALCRRSTTDCGGPKDHPLTCD

>d1fl7b\_ g.17.1.4 (B:) Follicle stimulating hormone, follitropin, beta chain {Human (Homo sapiens)}

CELTNITIAIEKEECRFCISINTAWCAGYCYTRDLVYKDPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTYPVATQCHCGKCDSDSTDCTVRGLGPSYCSFGEM

>d1jpya\_ g.17.1.6 (A:) Interleukin 17F, IL-17F {Human (Homo sapiens)}

HTFFQKPESCPPVPGGSMKLDIGIINENQRVSMSRNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRNLGCINAQGKEDISMNSVPIQQETLVVRRKHQGCSVSFQLEKVLVTVGCTCVTPV

>d1aoca\_ g.17.1.5 (A:) Coagulogen {Japanese horseshoe crab (Tachypleus tridentatus)}

ADTNAPICLCDEPGVLGRTQIVTTEIKDKIEKAVEAVAQESGVSGRGFSIFSHHPVFRECGKYECRTVRPEHSRCYNFPPFTHFKSECPVSTRDCEPVFGYTVAGEFRVIVQAPRAGFRQCVWQHKCRFGSNSCGYNGRCTQQRSVVRLVTYNLEKDGFLCESFRTCCGCPCRSF

>d1hcc\_\_ g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}

EGLPCKSPPEISHGVVAHMSDSYQYGEEVTYKCFEGFGIDGPAIAKCLGEKWSHPPSCI

>d1hfi\_\_ g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}

EKIPCSQPPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMGKWSSPPQCE

>d1g40a1 g.18.1.1 (A:1-64) Complement control protein {Vaccinia virus}

CCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFNQCIK

>d1g40a2 g.18.1.1 (A:65-126) Complement control protein {Vaccinia virus}

RRCPSPRDIDNGQLDIGGVDFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICES

>d1g40a3 g.18.1.1 (A:127-184) Complement control protein {Vaccinia virus}

VKCQSPPSISNGRHNGYEDFYTDGSVVTYSCNSGYSLIGNSGVLCSGGEWSDPPTCQI

>d1g40a4 g.18.1.1 (A:185-243) Complement control protein {Vaccinia virus}

VKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKCV

>d1ckla1 g.18.1.1 (A:1-62) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}

CEEPPTFEAMELIGKPKPYYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACYR

>d1ckla2 g.18.1.1 (A:63-126) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}

ETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELKGSVAIWSGKPPICEKV

>d1c1za5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}

SCKLPVKKATVVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFKEHSSLAFWKTDASDVKPC

>d1quba1 g.18.1.1 (A:1-62) beta2-glycoprotein I {Human (Homo sapiens)}

GRTCPKPDDLPFSTVVPLKTFYEPGEEITYSCKPGYVSRGGMRKFICPLTGLWPINTLKCTP

>d1quba2 g.18.1.1 (A:63-120) beta2-glycoprotein I {Human (Homo sapiens)}

RVCPFAGILENGAVRYTTFEYPNTISFSCNTGFYLNGADSAKCTEEGKWSPELPVCAP

>d1quba3 g.18.1.1 (A:121-183) beta2-glycoprotein I {Human (Homo sapiens)}

IICPPPSIPTFATLRVYKPSAGNNSLYRDTAVFECLPQHAMFGNDTITCTTHGNWTKLPECRE

>d1quba4 g.18.1.1 (A:184-243) beta2-glycoprotein I {Human (Homo sapiens)}

VKCPFPSRPDNGFVNYPAKPTLYYKDKATFGCHDGYSLDGPEEIECTKLGNWSAMPSCKA

>d1quba5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}

SCKVPVKKATVVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFKEHTDASDVKPC

>d1ghqb1 g.18.1.1 (B:1-66) Complement receptor 2, cr2 {Human (Homo sapiens)}

AISCGSPPPILNGRISYYSTPIAVGTVIRYSCSGTFRLIGEKSLLCITKDKVDGTWDKPAPKCEYF

>d1ghqb2 g.18.1.1 (B:67-129) Complement receptor 2, cr2 {Human (Homo sapiens)}

NKYSSCPEPIVPGGYKIRGSTPYRHGDSVTFACKTNFSMNGNKSVWCQANNMWGPTRLPTCVS

>d1elva2 g.18.1.1 (A:342-409) Complement C1S protease domain {Human (Homo sapiens)}

LDCGIPESIENGKVEDPESTLFGSVIRYTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGPELPKCVPV

>d1bgk\_\_ g.19.1.1 (-) Sea anemone toxin k {Sea anemone (Bunodosoma granulifera), BGK}

VCRDWFKETACRHAKSLGNCRTSQKYRANCAKTCELC

>d1c2ua\_ g.19.1.1 (A:) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}

RSXIDTIPKSRCTAFQCKHSAKYRLSFCRKTCGTX

>d1roo\_\_ g.19.1.1 (-) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}

RSCIDTIPKSRCTAFQCKHSMKYRLSFCRKTCGTC

>d2ech\_\_ g.20.1.1 (-) Echistatin {Echis carinatus}

ECESGPCCRNCKFLKEGTICKRARGDDMDDYCNGKTCDCPRNPHKGPAT

>d1fvl\_\_ g.20.1.1 (-) Flavoridin {Snake (Trimeresurus flavoviridis)}

GEECDCGSPSNPCCDAATCKLRPGAQCADGLCCDQCRFKKKRTICRIARGDFPDDRCTGLSNDCPRWNDL

>d1kst\_\_ g.20.1.1 (-) Kistrin {Agkistrodon rhodostoma}

GKECDCSSPENPCCDAATCKLRPGAQCGEGLCCEQCKFSRAGKICRIPRGDMPDDRCTGQSADCPRYH

>d1mdal\_ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}

VDPRAKWQPQDNDIQACDYWRHCSIAGNICDCSAGSLTSCPPGTLVASGSWVGSCYNPPDPNKYITAYRDCCGYNVSGRCACLNTEGELPVYNKDANDIIWCFGGEDGMTYHCSISPVSGA

>d2bbkl\_ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}

TDPRAKWVPQDNDIQACDYWRHCSIDGNICDCSGGSLTNCPPGTKLATASWVASCYNPTDGQSYLIAYRDCCGYNVSGRCPCLNTEGELPVYRPEFANDIIWCFGAEDDAMTYHCTISPIVGKAS

>d1atb\_\_ g.22.1.1 (-) Ascaris trypsin inhibitor, ATI {Pig roundworm (Ascaris Lumbricoides), variant suum}

EAEKCTKPNEQWTKCGGCEGTCAQKIVPCTRECKPPRCECIASAGFVRDAQGNCIKFEDCPK

>d1eaic\_ g.22.1.1 (C:) Ascaris elastase inhibitor {Pig roundworm (Ascaris suum)}

GQESCGPNEVWTECTGCEMKCGPDENTPCPLMCRRPSCECSPGRGMRRTNDGKCIPASQCP

>d1coua\_ g.22.1.1 (A:) Anticoagulant protein {Dog hookworm (Ancylostoma caninum)}

KATMQCGENEKYDSCGSKECDKKCKYDGVEEEDDEEPNVPCLVRVCHQDCVCEEGFYRNKDDKCVSAEDCELDNMDFIYPGTRNP

>d1ccva\_ g.22.1.1 (A:) Chymotrypsin inhibitor AMCI {Honeybee (Apis mellifera)}

EECGPNEVFNTCGSACAPTCAQPKTRICTMQCRIGCQCQEGFLRNGEGACVLPENC

>d1hx2a\_ g.22.1.2 (A:) BSTI {Fire-bellied toad (Bombina bombina)}

NFVCPPGQTFQTCASSCPKTCETRNKLVLCDKKCNQRCGCISGTVLKSKDSSECVHPSKC

>d1apj\_\_ g.23.1.1 (-) Fibrillin {Human (Homo sapiens)}

SAQDLRMSYCYAKFEGGKCSSPKSRNHSKQECCCALKGEGWGDPCELCPTEPDEAFRQICPYGSGIIVGPDDSA

>d1exta1 g.24.1.1 (A:13-71) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}

SVCPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL

>d1exta2 g.24.1.1 (A:72-115) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}

SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCF

>d1exta3 g.24.1.1 (A:116-172) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}

NCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN

>d1ncfa3 g.24.1.1 (A:116-150) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}

NCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENEC

>d1ncfb3 g.24.1.1 (B:116-155) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}

NCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSN

>d1d0gr1 g.24.1.1 (R:21-61) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}

SSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCL

>d1d0gr3 g.24.1.1 (R:102-128) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}

KCRTGCPRGMVKVGDCTPWSDIECVHK

>d1d4va1 g.24.1.1 (A:69-114) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}

PQQKRSSPSEGLCPPGHHISEDGRDCISCKYGQDYSTHWNDLLFCL

>d1d4va2 g.24.1.1 (A:115-154) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}

RCTRCDSGEVELSPCTTTRNTVCQCEEGTFREEDSPEMCR

>d1d4va3 g.24.1.1 (A:155-185) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}

KCRTGCPRGMVKVGDCTPWSDIECVHKESGD

>d1du3a3 g.24.1.1 (A:102-123) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}

KCRTGCPRGMVKVGDCTPWSDI

>d1jmab1 g.24.1.1 (B:4-59) Cellular receptor HveA {Human (Homo sapiens)}

CKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQ

>d1jmab2 g.24.1.1 (B:60-105) Cellular receptor HveA {Human (Homo sapiens)}

MCDPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYAT

>d1vgh\_\_ g.25.1.1 (-) Heparin-binding domain from vascular endothelial growth factor {Human (Homo sapiens)}

ARQENPCGPCSERRKHLFVQDPQTCKCSCKNTDSRCKARQLELNERTCRCDKPRR

>d1afp\_\_ g.26.1.1 (-) Antifungal protein (AGAFP) {Mold (Aspergillus giganteus)}

ATYNGKCYKKDNICKYKAQSGKTAICKCYVKKCPRDGAKCEFDSYKGKCYC

>d1e88a3 g.27.1.1 (A:1-41) Fibronectin {Human (Homo sapiens)}

YGHCVTDSGVVYSVGMQWLKTQGNKQMLCTCLGNGVSCQET

>d1fbr\_1 g.27.1.1 (1-46) Fibronectin {Human (Homo sapiens)}

AEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGRITCTSR

>d1fbr\_2 g.27.1.1 (47-93) Fibronectin {Human (Homo sapiens)}

NRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRGEWKCERHTS

>d1qgba1 g.27.1.1 (A:17-60) Fibronectin {Human (Homo sapiens)}

SKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESKP

>d1qgba2 g.27.1.1 (A:61-109) Fibronectin {Human (Homo sapiens)}

EAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANR

>d1tpg\_2 g.27.1.1 (1-50) Tissue-type plasminogen activator, t-PA {Human (Homo sapiens)}

SYQVICRDEKTQMIYQQHQSWLRPVLRSNRVEYCWCNSGRAQCHSVPVKS

>d1icfi\_ g.28.1.1 (I:) MHC class II associated p41 invariant chain fragment {Human (Homo sapiens)}

LTKCQEEVSHIPAVHPGSFRPKCDENGNYLPLQCYGSIGYCWCVFPNGTEVPNTRSRGHHNCSES

>d1e8ra\_ g.29.1.1 (A:) Endo-1;4-beta-xylanase A CBDX {Pseudomonas fluorescens, subsp. cellulosa}

MGNQQCNWYGTLYPLCVTTTNGWGWEDQRSCIARSTCAAQPAPFGIVGSG

>d1e8qa\_ g.55.1.1 (A:) Cellulose docking domain, dockering {Piromyces equi}

ASCWAQSQGYNCCNNPSSTKVEYTDASGQWGVQNGQWCGIDYSYGQ

>d1dtdb\_ g.30.1.1 (B:) Carboxypeptidase inhibitor {Medicinal leech (Hirudo medicinalis)}

DESFLCYQPDQVCCFICRGAAPLPSEGECNPHPTAPWCREGAVEWVPYSTGQCRTTCIPYV

>d1hdla\_ g.57.1.1 (A:) Serine proteinase inhibitor lekti, domain one {Human (Homo sapiens)}

KNEDQEMCHEFQAFMKNGKLFCPQDKKFFQSLDGIMFINKCATCKMILEKEAKSQ

>d1dqca\_ g.31.1.1 (A:) Tachycitin {Horseshoe crab (Tachypleus tridentatus)}

YLAFRCGRYSPCLDDGPNVNLYSCCSFYNCHKCLARLENCPKGLHYNAYLKVCDWPSKAGCTSVNKECHLWKT

>d1ha8a\_ g.58.1.1 (A:) Pheromone ER-23 {Euplotes raikovi}

GECEQCFSDGGDCTTCFNNGTGPCANCLAGYPAGCSNSDCTAFLSQCYGGC

>d1danl3 g.32.1.1 (L:1-48) Coagulation factor VIIa {Human (Homo sapiens)}

ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGD

>d2pf1\_2 g.32.1.1 (36-65) Prothrombin {Cow (Bos taurus)}

SATDAFWAKYTACESARNPREKLNECLEGN

>d2pf2\_2 g.32.1.1 (1-65) Prothrombin {Cow (Bos taurus)}

ANKGFLEEVRKGNLREECLEEPCSREEAFEALESLSATDAFWAKYTACESARNPREKLNECLEGN

>d1cfi\_\_ g.32.1.1 (-) Coagulation factor IX (IXa) {Human (Homo sapiens)}

YNSGKLEEFVQGNLERECMEEKCSFEEAREVFENTERTTEFWKQYVD

>d1pfxl3 g.32.1.1 (L:1-46) Coagulation factor IX (IXa) {Pig (Sus scrofa)}

YNSGKLEEFVRGNLERECIEEKCSFEEAREVFENTEKTNEFWKQYV

>d1iodg\_ g.32.1.1 (G:) Coagulation factor X {Cow (Bos taurus)}

ANSFLEEVKQGNLERECLEEACSLEEAREVFEDAEQTDEFWSKY

>d1d6ga\_ g.33.1.1 (A:) Cholecystokinin A receptor, N-domain {Human (Homo sapiens)}

MDVVDSLLVNGSNITPPCELGLENETLFCLDQPRPSKEWQPAQVILL

>d1vpu\_\_ g.34.1.1 (-) HIV-1 VPU cytoplasmic domain {Human immunodeficiency virus type 1}

LQIDRLIDRITERAEDSGNESEGDQEELSALVERGHLAPWDVDDL

>d1isua\_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Rhodocyclus tenuis}

GTNAAMRKAFNYQDTAKNGKKCSGCAQFVPGASPTAAGGCKVIPGDNQIAPGGYCDAFIVKK

>d1b0ya\_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochromatium vinosum, (formerly Chromatium vinosum)}

SAPANAVAADNATAIALKYNQDATKSERVAAARPGLPPEEQQCANCQFMQADAAGATDEWKGCQLFPGKLINVNGWCASWTLKAG

>d1js2a\_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochromatium vinosum, (formerly Chromatium vinosum)}

MEFMSAPANAVAADDATAIALKYNQDATKSERVAAARPGLPPEEQHCANCQFMQADAAGATDEWKGCQLFPGKLINVNGWSASWTLKAG

>d3hipa\_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Chromatium purpuratum}

VPANAVTESDPAAVALKYHRDAASSERVAAARPGLPPEEQHCENCQFMNPDSAAADWKGCQLFPGKLINLSGWCASWTLRAG

>d2hipa\_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Ectothiorhodospira halophila}

EPRAEDGHAHDYVNEAADASGHPRYQEGQLCENCAFWGEAVQDGWGRCTHPDFDEVLVKAEGWCSVYAPAS

>d1hpi\_\_ g.35.1.1 (-) HIPIP (high potential iron protein) {Ectothiorhodospira vacuolata}

MERLSEDDPAAQALEYRHDASSVQHPAYEEGQTCLNCLLYTDASAQDWGPCSVFPGKLVSANGWCTAWVAR

>d1eyta\_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Thermochromatium tepidum}

AAPANAVTADDPTAIALKYNQDATKSERVAAARPGLPPEEQHCANCQFMQANVGEGDWKGCQLFPGKLINVNGWCASWTLKAG

>d1dj7a\_ g.36.1.1 (A:) Ferredoxin thioredoxin reductase (FTR), catalytic beta chain {Synechocystis sp.}

NNKTLAAMKNFAEQYAKRTDTYFCSDLSVTAVVIEGLARHKEELGSPLCPCRHYEDKEAEVKNTFWNCPCVPMRERKECHCMLFLTPDNDFAGDAQDIPMETLEEVKAS

>d1a1ga1 g.37.1.1 (A:103-131) ZIF268 {Mouse (Mus musculus)}

RPYACPVESCDRRFSDSSNLTRHIRIHTG

>d1a1ha1 g.37.1.1 (A:103-131) ZIF268 {Mouse (Mus musculus)}

RPYACPVESCDRRFSQSGSLTRHIRIHTG

>d1a1ia1 g.37.1.1 (A:103-131) ZIF268 {Mouse (Mus musculus)}

RPYACPVESCDRRFSRSADLTRHIRIHTG

>d1a1ia2 g.37.1.1 (A:132-159) ZIF268 {Mouse (Mus musculus)}

QKPFQCRICMRNFSRSDHLTTHIRTHTG

>d1a1ia3 g.37.1.1 (A:160-187) ZIF268 {Mouse (Mus musculus)}

EKPFACDICGRKFARSDERKRHTKIHLR

>d1aaya1 g.37.1.1 (A:103-131) ZIF268 {Mouse (Mus musculus)}

RPYACPVESCDRRFSRSDELTRHIRIHTG

>d1f2ig1 g.37.1.1 (G:1093-1131) ZIF268 {Mouse (Mus musculus)}

NLLNYVVPKMRPYACPVESCDRRFSRSDELTRHIRIHTG

>d1rmd\_1 g.37.1.1 (87-116) V(D)J recombination activating protein 1 (RAG1), dimerization domain {Mouse (Mus musculus)}

LMVKCPAQDCNEEVSLEKYNHHVSSHKESK

>d2drpa1 g.37.1.1 (A:103-139) Tramtrack protein (two zinc-finger peptide) {Drosophila melanogaster}

FTKEGEHTYRCKVCSRVYTHISNFCRHYVTSHKRNVK

>d2drpa2 g.37.1.1 (A:140-165) Tramtrack protein (two zinc-finger peptide) {Drosophila melanogaster}

VYPCPFCFKEFTRKDNMTAHVKIIHK

>d1paa\_\_ g.37.1.1 (-) ADR1 {Synthetic, based on Saccharomyces cerevisiae sequence}

KAYACGLCNRAFTRRDLLIRHAQKIHSGNL

>d2adr\_1 g.37.1.1 (102-130) ADR1 {Synthetic, based on Saccharomyces cerevisiae sequence}

RSFVCEVCTRAFARQEHLKRHYRSHTNEK

>d2adr\_2 g.37.1.1 (131-161) ADR1 {Synthetic, based on Saccharomyces cerevisiae sequence}

PYPCGLCNRAFTRRDLLIRHAQKIHSGNLGE

>d1znf\_\_ g.37.1.1 (-) XFIN, third domain {Xenopus laevis}

YKCGLCERSFVEKSALSRHQRVHKN

>d5znf\_\_ g.37.1.1 (-) ZFY {Human (Homo sapiens)}

KTYQCQYCEYRSADSSNLKTHIKTKHSKEK

>d7znf\_\_ g.37.1.1 (-) ZFY {Human (Homo sapiens)}

KTYQCQYCEKRFADSSNLKTHIKTKHSKEK

>d1ncs\_\_ g.37.1.1 (-) SWI5 zinc-finger domains {Baker's yeast (Saccharomyces cerevisiae)}

TLPRGSIDKYVKEMPDKTFECLFPGCTKTFKRRYNIRSHIQTHLEDR

>d1zfd\_\_ g.37.1.1 (-) SWI5 zinc-finger domains {Baker's yeast (Saccharomyces cerevisiae)}

DRPYSCDHPGCDKAFVRNHDLIRHKKSHQEKA

>d2glia1 g.37.1.1 (A:103-134) Five-finger GLI1 {Human (Homo sapiens)}

ETDCRWDGCSQEFDSQEQLVHHINSEHIHGER

>d2glia2 g.37.1.1 (A:135-167) Five-finger GLI1 {Human (Homo sapiens)}

KEFVCHWGGCSRELRPFKAQYMLVVHMRRHTGE

>d2glia3 g.37.1.1 (A:168-197) Five-finger GLI1 {Human (Homo sapiens)}

KPHKCTFEGCRKSYSRLENLKTHLRSHTGE

>d2glia4 g.37.1.1 (A:198-228) Five-finger GLI1 {Human (Homo sapiens)}

KPYMCEHEGCSKAFSNASDRAKHQNRTHSNE

>d2glia5 g.37.1.1 (A:229-257) Five-finger GLI1 {Human (Homo sapiens)}

KPYVCKLPGCTKRYTDPSSLRKHVKTVHG

>d1bbo\_1 g.37.1.1 (1-28) Enhancer binding protein {Human (Homo sapiens)}

KYICEECGIRXKKPSMLKKHIRTHTDVR

>d1bbo\_2 g.37.1.1 (29-57) Enhancer binding protein {Human (Homo sapiens)}

PYHCTYCNFSFKTKGNLTKHMKSKAHSKK

>d4znf\_\_ g.37.1.1 (-) Enhancer binding protein {Human (Homo sapiens)}

RPYHCSYCNFSFKTKGNLTKHMKSKAHSKK

>d1sp1\_\_ g.37.1.1 (-) Transcription factor sp1 {Human (Homo sapiens)}

KKFACPECPKRFMRSDHLSKHIKTHQNKK

>d1sp2\_\_ g.37.1.1 (-) Transcription factor sp1 {Human (Homo sapiens)}

RPFMCTWSYCGKRFTRSDELQRHKRTHTGEK

>d1bhi\_\_ g.37.1.1 (-) Transactivation domain of cre-bp1/atf-2 {Human (Homo sapiens)}

MSDDKPFLCTAPGCGQRFTNEDHLAVHKHKHEMTLKFG

>d1ubdc1 g.37.1.1 (C:295-322) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}

TIACPHKGCTKMFRDNSAMRKHLHTHGP

>d1ubdc2 g.37.1.1 (C:323-350) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}

RVHVCAECGKAFVESSKLKRHQLVHTGE

>d1ubdc3 g.37.1.1 (C:351-380) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}

KPFQCTFEGCGKRFSLDFNLRTHVRIHTGD

>d1ubdc4 g.37.1.1 (C:381-408) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}

RPYVCPFDGCNKKFAQSTNLKSHILTHA

>d1tf3a1 g.37.1.1 (A:1-40) Transcription factor IIIA, TFIIIA {Xenopus laevis}

MKRYICSFADCGAAYNKNWKLQAHLSKHTGE

>d1tf3a2 g.37.1.1 (A:41-70) Transcription factor IIIA, TFIIIA {Xenopus laevis}

KPFPCKEEGCEKGFTSLHHLTRHSLTHTGE

>d1tf3a3 g.37.1.1 (A:71-101) Transcription factor IIIA, TFIIIA {Xenopus laevis}

KNFTCDSDGCDLRFTTKANMKKHFNRFHNIK

>d1tf6a1 g.37.1.1 (A:10-40) Transcription factor IIIA, TFIIIA {Xenopus laevis}

YKRYICSFADCGAAYNKNWKLQAHLCKHTGE

>d1tf6a4 g.37.1.1 (A:101-131) Transcription factor IIIA, TFIIIA {Xenopus laevis}

KICVYVCHFENCGKAFKKHNQLKVHQFSHTQ

>d1tf6a5 g.37.1.1 (A:132-160) Transcription factor IIIA, TFIIIA {Xenopus laevis}

QLPYECPHEGCDKRFSLPSRLKRHEKVHA

>d1tf6a6 g.37.1.1 (A:161-188) Transcription factor IIIA, TFIIIA {Xenopus laevis}

GYPCKKDDSCSFVGKTWTLYLKHVAECH

>d1yuja\_ g.37.1.1 (A:) GAGA factor {Drosophila melanogaster}

PKAKRAKHPPGTEKPRSRSQSEQPATCPICYAVIRQSRNLRRHLELRHFAKPGV

>d1fu9a\_ g.37.1.2 (A:) U-shaped transcription factor, different fingers {Fruit fly (Drosophila melanogaster)}

GSAAEVMKKYCSTCDISFNYVKTYLAHKQFYCKNKP

>d1fv5a\_ g.37.1.2 (A:) U-shaped transcription factor, different fingers {Fruit fly (Drosophila melanogaster)}

GSLLKPARFMCLPCGIAFSSPSTLEAHQAYYCSHRI

>d1aw6\_\_ g.38.1.1 (-) Gal4 {Baker's yeast (Saccharomyces cerevisiae)}

MKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPK

>d1d66a1 g.38.1.1 (A:8-48) Gal4 {Baker's yeast (Saccharomyces cerevisiae)}

EQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPKTKRSP

>d1pyia1 g.38.1.1 (A:30-71) PPR1 {Baker's yeast (Saccharomyces cerevisiae)}

SRTACKRCRLKKIKCDQEFPSCKRCAKLEVPCVSLDPATGKD

>d1zmec1 g.38.1.1 (C:31-66) PUT3 {Baker's yeast (Saccharomyces cerevisiae)}

SVACLSCRKRHIKCPGGNPCQKCVTSNAICEYLEPS

>d1hwtc1 g.38.1.1 (C:59-97) Hap1 (Cyp1) {Baker's yeast (Saccharomyces cerevisiae)}

RIPLSCTICRKRKVKCDKLRPHCQQCTKTGVAHLCHYME

>d2hapc1 g.38.1.1 (C:55-97) Hap1 (Cyp1) {Baker's yeast (Saccharomyces cerevisiae)}

RKRNRIPLRCTICRKRKVKCDKLRPHCQQCTKTGVAHLCHYME

>d1cld\_\_ g.38.1.1 (-) CD2-Lac9 {Milk yeast (Kluyveromyces lactis)}

QACDACRKKKWKCSKTVPTCTNCLKYNLDCVYS

>d2alca\_ g.38.1.1 (A:) Ethanol regulon transcriptional activator ALCR DNA-binding domain {Aspergillus nidulans and Emericella nidulans}

GSMADTRRRQNHSCDPCRKGKRRCDAPENRNEANENGWVSCSNCKRWNKDCTFNWLSSQRSKNSS

>d3gata\_ g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}

KRAGTVCSNCQTSTTTLWRRSPMGDPVCNACGLYYKLHQVNRPLTMRKDGIQTRNRKVSSKGKKRR

>d7gata\_ g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}

MKNGEQNGPTTCTNCFTQTTPVWRRNPEGQPLCNACGLFLKLHGVVRPLSLKTDVIKKRNRNSANS

>d1gnf\_\_ g.39.1.1 (-) Erythroid transcription factor GATA-1 {Mouse (Mus musculus)}

GSEARECVNCGATATPLWRRDRTGHYLCNACGLYHKMNGQNRPLIR

>d1dszb\_ g.39.1.2 (B:) Retinoid X receptor (RXR-alpha) DNA-binding domain {Human (Homo sapiens)}

GSFTKHICAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRYQKCLAMGMKREAVQEERQR

>d2nlla\_ g.39.1.2 (A:) Retinoid X receptor (RXR-alpha) DNA-binding domain {Human (Homo sapiens)}

CAICGDRSSGKHYGVYSCEGCKGFFKRTVRKDLTYTCRDNKDCLIDKRQRNRCQYCRYQKCLAMGM

>d2nllb\_ g.39.1.2 (B:) Thyroid hormone receptor (TR-beta) DNA-binding domain {Human (Homo sapiens)}

DELCVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLHPSYSCKYEGKCVIDKVTRNQCQECRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRRREELEK

>d1cita\_ g.39.1.2 (A:) Orphan nuclear receptor NGFI-B {Rat (Rattus norvegicus)}

GRCAVCGDNASCQHYGVRTCEGCKGFFKRTVQKSAKYICLANKDCPVDKRRRNRCQFCRFQKCLAVGMVKEVVRTDSLKGRRGRLPSKP

>d1hcqa\_ g.39.1.2 (A:) Estrogen receptor DNA-binding domain {Human and chicken (Homo sapiens) and (Gallus gallus)}

MKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVGMMK

>d1glua\_ g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain {Rat (Rattus norvegicus)}

MKPARPCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRYRKCLQAGMNLEARKTKK

>d1lata\_ g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain {Rat (Rattus norvegicus)}

RPCLVCSDEASGCHYGVLTCEGCKAFFKRAVEGQHNYLCKYEGKCIIDKIRRKNCPACRYRKCLQAGMNLE

>d2gda\_\_ g.39.1.2 (-) Glucocorticoid receptor DNA-binding domain {Rat (Rattus norvegicus)}

LCLVCSDEASGCHYGVLTCGSCKVFFKRAVEGQHNYLCAGRNDCIIDKIRRKNCPACRYRKCLQAGMNLEAR

>d1dsza\_ g.39.1.2 (A:) Retinoic acid receptor DNA-binding domain {Human (Homo sapiens)}

PCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCFEVGMSKESVRND

>d1hra\_\_ g.39.1.2 (-) Retinoic acid receptor DNA-binding domain {Human (Homo sapiens)}

PPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRRSIQKNMIYTCHRDKNCVINKVTRNRCQYCRLQKCFEVGMSKESVRN

>d1a6ya\_ g.39.1.2 (A:) Orphan nuclear receptor reverb {Human (Homo sapiens)}

LLCKVCGDVASGFHYGVHACEGCKGFFRRSIQQNIQYKRCLKNENCSIVRINRNRCQQCRFKKCLSVGMSRDAVRFGR

>d1b8ta1 g.39.1.3 (A:1-35) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

MPNWGGGKKCGVCQKAVYFAEEVQCEGSSFHKSCF

>d1b8ta2 g.39.1.3 (A:36-100) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

LCMVCKKNLDSTTVAVHGDEIYCKSCYGKKYGPKGKGKGMGAGTLSTDKGESLGIKYEEGQSHRP

>d1b8ta3 g.39.1.3 (A:101-143) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

TNPNASRMAQKVGGSDGCPRCGQAVYAAEKVIGAGKSWHKSCF

>d1b8ta4 g.39.1.3 (A:144-192) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

RCAKCGKSLESTTLADKDGEIYCKGCYAKNFGPKGFGFGQGAGALIHSQ

>d1ctl\_1 g.39.1.3 (1-35) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

MAQKVGGSDGCPRCGQAVYAAEKVIGAGKSWHKSC

>d1a7i\_1 g.39.1.3 (8-35) Cysteine-rich (intestinal) protein, CRP, CRIP {Japanese quail (Coturnix coturnix japonica), CRP2}

NKCGACGRTVYHAEEVQCDGRSFHRCCF

>d1a7i\_2 g.39.1.3 (36-67) Cysteine-rich (intestinal) protein, CRP, CRIP {Japanese quail (Coturnix coturnix japonica), CRP2}

LCMVCRKNLDSTTVAIHDAEVYCKSCYGKKYG

>d1ibia1 g.39.1.3 (A:117-144) Cysteine-rich (intestinal) protein, CRP, CRIP {Japanese quail (Coturnix coturnix japonica), CRP2}

AEKCSRCGDSVYAAEKVIGAGKPWHKNC

>d1ibia2 g.39.1.3 (A:145-175) Cysteine-rich (intestinal) protein, CRP, CRIP {Japanese quail (Coturnix coturnix japonica), CRP2}

FRCAKCGKSLESTTLTEKEGEIYCKGCYAKN

>d1iml\_1 g.39.1.3 (1-28) Cysteine-rich (intestinal) protein, CRP, CRIP {Rat (Rattus rattus)}

PKCPKCDKEVYFAERVTSLGKDWHRPCL

>d1iml\_2 g.39.1.3 (29-76) Cysteine-rich (intestinal) protein, CRP, CRIP {Rat (Rattus rattus)}

KCEKCGKTLTSGGHAEHEGKPYCNHPCYSAMFGPKGFGRGGAESHTFK

>d1g47a1 g.39.1.3 (A:1-35) Pinch (particularly interesting new Cys-His) protein {Human (Homo sapiens)}

MANALASATCERCKGGFAPAEKIVNSNGELYHEQC

>d1g47a2 g.39.1.3 (A:36-70) Pinch (particularly interesting new Cys-His) protein {Human (Homo sapiens)}

FVCAQCFQQFPEGLFYEFEGRKYCEHDFQMLFAPC

>d1zfo\_\_ g.39.1.4 (-) LASP-1 {Pig (Sus scrofa)}

MNPNCARCGKIVYPTEKVNCLDKFWHKACF

>d1d4ua2 g.39.1.5 (A:1-36) DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain {Human (Homo sapiens)}

MEFDYVICEECGKEFMDSYLMDHFDLPTCDDCRDAD

>d1xpa\_2 g.39.1.5 (98-133) DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain {Human (Homo sapiens)}

MEFDYVICEECGKEFMDSYLMNHFDLPTCDNCRDAD

>d1jj2t\_ g.39.1.6 (T:) Ribosomal protein L24e {Archaeon Haloarcula marismortui}

RECDYCGTDIEPGTGTMFVHKDGATTHFCSSKCENNADLGREARNLEWTDTAR

>d1fjgn\_ g.39.1.7 (N:) Ribosomal protein S14 {Thermus thermophilus}

ARKALIEKAKRTPKFKVRAYTRCVRCGRARSVYRFFGLCRICLRELAHKGQLPGVRKASW

>d1aaf\_\_ g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}

MQRGNFRNQRKIIKCFNCGKEGHIAKNCRAPRKRGCWKCGKEGHQMKDCTERQAN

>d1eska\_ g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}

NVKCFNCGKEGHTARNCRAPRKKGCWKCGKEGHQMKDCTERQ

>d1f6ua\_ g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}

MQKGNFRNQRKTVKCFNCGKEGHIAKNCRAPRKKGCWKCGKEGHQMKDCTERQAN

>d1nc8\_\_ g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 2}

AQQRKVIRCWNCGKEGHSARQCRAPRRQG

>d1cl4a\_ g.40.1.1 (A:) Nucleocapsid protein from mason-pfizer monkey virus (MPMV) {Mason-pfizer monkey virus}

VPGLCPRCKRGKHWANECKSKTDNQGNPIPPH

>d1a6bb\_ g.40.1.1 (B:) Zinc finger protein ncp10 {Moloney murine leukemia virus}

GERRRSQLDRDQCAYCKEKGHWAKDCPKKPRGPRGPRPQT

>d1dsqa\_ g.40.1.1 (A:) Nucleic acid binding protein p14 {Mouse mammary tumor virus}

KGPVCFSCGKTGHIKRDCKEE

>d1dsva\_ g.40.1.1 (A:) Nucleic acid binding protein p14 {Mouse mammary tumor virus}

PPGLCPRCKKGYHWKSECKSKFDKDGNPLPP

>d1f4la3 g.41.1.1 (A:141-175) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}

VKGTCPKCKSPDQYGDNCEVCGATYSPTELIEPKS

>d1mea\_\_ g.41.1.1 (-) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}

GSDRFVKGTCPKCKSPDQYGDNCEVCGA

>d1zin\_2 g.41.2.1 (126-160) Microbial and mitochondrial ADK, insert "zinc finger" domain {Bacillus stearothermophilus}

GRRICRNCGATYHLIFHPPAKPGVCDKCGGELYQR

>d1e4ya2 g.41.2.1 (A:122-156) Microbial and mitochondrial ADK, insert "zinc finger" domain {Escherichia coli}

GRRVHAPSGRVYHVKFNPPKVEGKDDVTGEELTTR

>d2ak3a2 g.41.2.1 (A:125-161) Microbial and mitochondrial ADK, insert "zinc finger" domain {Cow (Bos taurus), mitochondrial izozyme-3}

ARWIHPGSGRVYNIEFNPPKTMGIDDLTGEPLVQRED

>d1ak2\_2 g.41.2.1 (147-176) Microbial and mitochondrial ADK, insert "zinc finger" domain {Cow (Bos taurus), mitochondrial izozyme-2}

PQSGRSYHEEFNPPKEPMKDDITGEPLIRR

>d1aky\_2 g.41.2.1 (131-168) Microbial and mitochondrial ADK, insert "zinc finger" domain {Baker's yeast (Saccharomyces cerevisiae)}

GRLIHPASGRSYHKIFNPPKEDMKDDVTGEALVQRSDD

>d1zaka2 g.41.2.1 (A:128-158) Microbial and mitochondrial ADK, insert "zinc finger" domain {Maize (Zea mays)}

GRRLDPVTGKIYHLKYSPPENEEIASRLTQR

>d1tfi\_\_ g.41.3.1 (-) Transcriptional factor SII, C-terminal domain {Human (Homo sapiens)}

KTGGTQTDLFTCGKCKKKNCTYTQVQTRSADEPMTTFVVCNECGNRWKFC

>d1pft\_\_ g.41.3.1 (-) Transcription inititiation factor TFIIB, N-terminal domain {Archaeon Pyrococcus furiosus}

MVNKQKVCPACESAELIYDPERGEIVCAKCGYVIEENIIDMGPEWRAFDA

>d1dl6a\_ g.41.3.1 (A:) Transcription inititiation factor TFIIB, N-terminal domain {Human (Homo sapiens)}

ASTSRLDALPRVTCPNHPDAILVEDYRAGDMICPECGLVVGDRVIDVGSEWRTFSNDK

>d1d0qa\_ g.41.3.2 (A:) Zinc-binding domain of DNA primase {Bacillus stearothermophilus}

GHRIPEETIEAIRRGVDIVDVIGEYVQLKRQGRNYFGLCPFHGEKTPSFSVSPEKQIFHCFGCGAGGNAFTFLMDIEGIPFVEAAKRLAAKAGVDLSVYELD

>d1yua\_1 g.41.3.3 (1-65) Prokariotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}

MNGEVAPPKEDPVPLPELPCEKSDAYFVLRDGAAGVFLAANTFPKSRETRAPLVEELYRFRDRLP

>d1yua\_2 g.41.3.3 (66-122) Prokariotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}

EKLRYLADAPQQDPEGNKTMVRFSRKTKQQYVSSEKDGKATGWSAFYVDGKWVEGKK

>d1qf8a\_ g.41.4.1 (A:) Casein kinase II beta subunit {Human (Homo sapiens)}

VSWISWFCGLRGNEFFCEVDEDYIQDKFNLTGLNEQVPHYRQALDMILDLEPDEELEDNPNQSDLIEQAAEMLYGLIHARYILTNRGIAQMLEKYQQGDFGYCPRVYCENQPMLPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHHTDGAYFGTGFPHMLFMVHPEYRPKRP

>d1rb9\_\_ g.41.5.1 (-) Rubredoxin {Desulfovibrio vulgaris}

MKKYVCTVCGYEYDPAEGDPDNGVKPGTSFDDLPADWVCPVCGAPKSEFEAA

>d2rdva\_ g.41.5.1 (A:) Rubredoxin {Desulfovibrio vulgaris}

MKKYVCTVCGYEYDPAEGDPDNGVKPGTAFEDVPADWVCPICGAPKSEFEPA

>d1rdg\_\_ g.41.5.1 (-) Rubredoxin {Desulfovibrio gigas}

MDIYVCTVCGYEYDPAKGDPDSGIKPGTKFEDLPDDWACPVCGASKDAFEKQ

>d6rxn\_\_ g.41.5.1 (-) Rubredoxin {Desulfovibrio desulfuricans, strain 27774}

MQKYVCNVCGYEYDPAEHDNVPFDQLPDDWCCPVCGVSKDQFSPA

>d1iro\_\_ g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}

MKKYTCTVCGYIYNPEDGDPDNGVNPGTDFKDIPDDWVCPLCGVGKDQFEEVE

>d5rxn\_\_ g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}

MKKYTCTVCGYIYDPEDGDPDDGVNPGTDFKDIPDDWVCPLCGVGKDEFEEVEE

>d1brfa\_ g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}

AKWVCKICGYIYDEDAGDPDNGISPGTKFEELPDDWVCPICGAPKSEFEKLED

>d1qcva\_ g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}

AKWVLKITGYIYDEDAGDPDNGISPGTKFEELPDDWVAPITGAPKSEFEKLED

>d1dx8a\_ g.41.5.1 (A:) Rubredoxin {Guillardia theta}

MEIDEGKYECEACGYIYEPEKGDKFAGIPPGTPFVDLSDSFMCPACRSPKNQFKSIKKVIAGFAENQKYG

>d1h7va\_ g.41.5.1 (A:) Rubredoxin {Guillardia theta}

MEIDEGKYECEACGYIYEPEKGDKFAGIPPGTPFVDLSDSFMCPACRSPKNQFKSIKKVI

>d1dvba2 g.41.5.1 (A:148-191) Rubrerythrin, C-terminal domain {Desulfovibrio vulgaris}

FLREQATKWRCRNCGYVHEGTGAPELCPACAHPKAHFELLGINW

>d1dxga\_ g.41.5.2 (A:) Desulforedoxin {Desulfovibrio gigas}

ANEGDVYKCELCGQVVKVLEEGGGTLVCCGEDMVKQ

>d1dfx\_2 g.41.5.2 (1-36) Desulfoferrodoxin N-terminal domain {Desulfovibrio desulfuricans}

PKHLEVYKCTHCGNIVEVLHGGGAELVCCGEPMKHM

>d1ocrf\_ g.41.5.3 (F:) Cytochrome c oxidase Subunit F {Cow (Bos taurus)}

ASGGGVPTDEEQATGLEREVMLAARKGQDPYNILAPKATSGTKEDPNLVPSITNKRIVGCICEEDNSTVIWFWLHKGEAQRCPSCGTHYKLVPHQLAH

>d1gh9a\_ g.41.6.1 (A:) Hypothetical protein MTH1184 {Archaeon Methanobacterium thermoautotrophicum}

MYIIFRCDCGRALYSREGAKTRKCVCGRTVNVKDRRIFGRADDFEEASELVRKLQEEKYGSCHFTNPSKRE

>d1d09b2 g.41.7.1 (B:101-153) Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain {Escherichia coli}

ERIDNVLVCPNSNCISHAEPVSSSFAVRKRANDIALKCKYCEKEFSHNVVLAN

>d2atcb2 g.41.7.1 (B:101-152) Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain {Escherichia coli}

ERNIDVLVCPDSNCISHAEPVSSSFAVRRADDIALKCKYCEKEFSHNVVLAN

>d1ffkw\_ g.41.8.1 (W:) Ribosomal protein L37ae {Archaeon Haloarcula marismortui}

PTGRFGPRYGLKIRVRVRDVEIKHKKKYKCPVCGFPKLKRASTSIWVCGHCGYKIAGGAYTPETVAGKAVMKA

>d1jj2y\_ g.41.8.1 (Y:) Ribosomal protein L37ae {Archaeon Haloarcula marismortui}

RTGRFGPRYGLKIRVRVADVEIKHKKKHKCPVCGFKKLKRAGTGIWMCGHCGYKIAGGCYQPETVAGKAVMKA

>d1jj2z\_ g.41.8.2 (Z:) Ribosomal protein L37e {Archaeon Haloarcula marismortui}

TGAGTPSQGKKNTTTHTKCRRCGEKSYHTKKKVCSSCGFGKSAKRRDYEWQSKAGE

>d1jj22\_ g.41.8.3 (2:) Ribosomal protein L44e {Archaeon Haloarcula marismortui}

MQMPRRFNTYCPHCNEHQEHEVEKVRSGRQTGMKWIDRQRERNSGIGNDGKFSKVPGGDKPTKKTDLKYRCGECGKAHLREGWRAGRLEFQE

>d1qyp\_\_ g.41.9.1 (-) RBP9 subunit of RNA polymerase II {Archaeon Thermococcus celer}

GSHMEQDLKTLPTTKITCPKCGNDTAYWWEMQTRAGDEPSTIFYKCTKCGHTWRSYE

>d1i50i1 g.41.9.1 (I:1-49) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}

MTTFRFCRDCNNMLYPREDKENNRLLFECRTCSYVEEAGSPLVYRHELI

>d1i50i2 g.41.9.1 (I:50-122) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}

TNIGETAGVVQDIGSDPTLPRSDRECPKCHSRENVFFQSQQRRKDTSMVLFFVCLSCSHIFTSDQKNKRTQFS

>d1i50l\_ g.41.9.2 (L:) RBP12 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}

ATLKYICAECSSKLSLSRTDAVRCKDCGHRILLKARTKRLVQFEAR

>d1dfea\_ g.42.1.1 (A:) Ribosomal protein L36 {Thermus thermophilus}

MKVRASVKRICDKCKVIRRHGRVYVICENPKHKQRQG

>d1fre\_\_ g.43.1.1 (-) Nuclear factor XNF7 {African clawed frog (Xenopus laevis)}

EKCSEHDERLKLYCKDDGTLSCVICRDSLKHASHNFLPI

>d1fbva4 g.44.1.1 (A:356-434) CBL {Human (Homo sapiens)}

TPQDHIKVTQEQYELYCEMGSTFQLCKICAENDKDVKIEPCGHLMCTSCLTSWQESEGQGCPFCRCEIKGTEPIVVDPF

>d1rmd\_2 g.44.1.1 (1-86) V(D)J recombination activating protein 1 (RAG1), dimerization domain {Mouse (Mus musculus)}

NCSKIHLSTKLLAVDFPAHFVKSISCQICEHILADPVETSCKHLFCRICILRCLKVMGSYCPSCRYPCFPTDLESPVKSFLNILNS

>d1chc\_\_ g.44.1.1 (-) Immediate early protein, IEEHV {Equine herpes virus type 1}

MATVAERCPICLEDPSNYSMALPCLHAFCYVCITRWIRQNPTCPLCKVPVESVVHTIESDSEFGDQLI

>d1bor\_\_ g.44.1.1 (-) Acute promyelocytic leukaemia proto-onkoprotein PML {Human (Homo sapiens)}

EEEFQFLRCQQCQAEAKCPKLLPCLHTLCSGCLEASGMQCPICQAPWPLGADTPAL

>d1g25a\_ g.44.1.1 (A:) TFIIH Mat1 subunit {Human (Homo sapiens)}

MDDQGCPRCKTTKYRNPSLKLMVNVCGHTLCESCVDLLFVRGAGNCPECGTPLRKSNFRVQLFED

>d1e4ua\_ g.44.1.1 (A:) Not-4 N-terminal RING finger domain {Human (Homo sapiens)}

MSRSPDAKEDPVECPLCMEPLEIDDINFFPCTCGYQICRFCWHRIRTDENGLCPACRKPYPEDPAVYKPLSQEELQRI

>d1jm7a\_ g.44.1.1 (A:) brca1 RING domain {Human (Homo sapiens)}

MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQESTRFSQLVEELLKIICAFQLDTGLEYAN

>d1jm7b\_ g.44.1.1 (B:) bard1 RING domain {Human (Homo sapiens)}

MEPDGRGAWAHSRAALDRLEKLLRCSRCTNILREPVCLGGCEHIFCSNCVSDCIGTGCPVCYTPAWIQDLKINRQLDSMIQLCSKLRNLLHDNELSD

>d1dcqa2 g.45.1.1 (A:247-368) Pyk2-associated protein beta ARF-GAP domain {Mouse (Mus musculus)}

LTKEIISEVQRMTGNDVCCDCGAPDPTWLSTNLGILTCIECSGIHRELGVHYSRMQSLTLDVLGTSELLLAKNIGNAGFNEIMECCLPSEDPVKPNPGSDMIARKDYITAKYMERRYARKKH

>d1mhu\_\_ g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}

KSCCSCCPVGCAKCAQGCICKGASDKCSCCA

>d2mhu\_\_ g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}

MDPNCSCAAGDSCTCAGSCKCKECKCTSCK

>d2mrb\_\_ g.46.1.1 (-) Metallothionein {Rabbit (Oryctolagus cuniculus)}

MDPNCSCAAAGDSCTCANSCTCKACKCTSCK

>d1mrt\_\_ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}

KSCCSCCPVGCAKCSQGCICKEASDKCSCCA

>d2mrt\_\_ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}

MDPNCSCATDGSCSCAGSCKCKQCKCTSCK

>d4mt2\_\_ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}

MDPNCSCATDGSCSCAGSCKCKQCKCTSCKKSCCSCCPVGCAKCSQGCICKEASDKCSCCA

>d1dfsa\_ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}

KSCCSCCPVGCSKCAQGCVCKGAADKCTCCA

>d1dfta\_ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}

MDPNCSCSTGGSCTCTSSCACKNCKCTSCK

>d1ji9a\_ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}

KSCCSCCPAGCEKCAKDCVCKGEEGAKAEAEKCSCCQ

>d1dmc\_\_ g.46.1.1 (-) Metallothionein {Crab (Callinectes sapidus), alpha and beta domains}

SPCQKCTSGCKCATKEECSKTCTKPCSCCPK

>d1dme\_\_ g.46.1.1 (-) Metallothionein {Crab (Callinectes sapidus), alpha and beta domains}

PGPCCNDKCVCQEGGCKAGCQCTSCRCS

>d1fmya\_ g.46.1.1 (A:) Metallothionein {Baker's yeast (Saccharomyces cerevisiae)}

QNEGHECQCQCGSCKNNEQCQKSCSCPTGCNSDDKCPCGN

>d1qjka\_ g.46.1.1 (A:) Metallothionein {Purple sea urchin (Strongylocentrotus purpuratus)}

PDVKCVCCTEGKECACFGQDCCVTGECCKDGTCCGI

>d1qjla\_ g.46.1.1 (A:) Metallothionein {Purple sea urchin (Strongylocentrotus purpuratus)}

ICTNAACKCANGCKCGSGCSCTEGNCAC

>d1jjda\_ g.46.1.1 (A:) Cyanobacterial metallothionein SmtA {Synechococcus sp., PCC 7942}

TLVKCACEPCLCNVDPSKAIDRNGLYYCSEACADGHTGGSKGCGHTGCNCHG

>d1co4a\_ g.47.1.1 (A:) Zinc domain conserved in yeast copper-regulated transcription factors {Synthetic}

MVVINGVKYACDSCIKSHKAAQCEHNDRPLKILKPRGRPPTT

>d1adn\_\_ g.48.1.1 (-) Ada DNA repair protein, N-terminal domain (N-Ada 10) {Escherichia coli}

MKKATCLTDDQRWQSVLARDPNADGEFVFAVRTTGIFCRPSCRARHALRENVSFYANASEALAAGFRPCKRCQPDKANPRQHRLDKITHACR

>d1ptq\_\_ g.49.1.1 (-) Protein kinase C-delta (PKCdelta) {Mouse (Mus musculus)}

HRFKVYNYMSPTFCDHCGSLLWGLVKQGLKCEDCGMNVHHKCREKVANLC

>d1faq\_\_ g.49.1.1 (-) RAF-1 {Human (Homo sapiens)}

LTTHNFARKTFLKLAFCDICQKFLLNGFRCQTCGYKFHEHCSTKVPTMCVDW

>d1tbo\_\_ g.49.1.1 (-) Protein kinase c-gamma {Rat (Rattus rattus)}

QTDDPRNKHKFRLHSYSSPTFCDHCGSLLYGLVHQGMKCSCCEMNVHRRCVRSVPSLCGVDHTERR

>d1kbea\_ g.49.1.1 (A:) Kinase suppressor of Ras, Ksr {Mouse (Mus musculus)}

GSVTHRFSTKSWLSQVCNVCQKSMIFGVKCKHCRLKCHNKCTKEAPACR

>d1e53a\_ g.49.1.2 (A:) TFIIH p44 subunit cysteine-rich domain {Human (Homo sapiens)}

LDAFQEIPLEEYNGERFCYGCQGELKDQHVYVCAVCQNVFCVDCDVFVHDSLHCCPGCI

>d1vfya\_ g.50.1.1 (A:) vps27p protein {Baker's yeast (Saccharomyces cerevisiae)}

DWIDSDACMICSKKFSLLNRKHHCRSCGGVFCQEHSSNSIPLPDLGIYEPVRVCDSCFEDYEFIVTD

>d1joca1 g.50.1.1 (A:1348-1411) Eea1 {Human (Homo sapiens)}

KWAEDNEVQNCMACGKGFSVTVRRHHCRQCGNIFCAECSAKNALTPSSKKPVRVCDACFNDLQG

>d1dvpa2 g.50.1.1 (A:149-220) Hrs {Fruit fly (Drosophila melanogaster)}

MFTADTAPNWADGRVCHRCRVEFTFTNRKHHCRNCGQVFCGQCTAKQCPLPKYGIEKEVRVCDGCFAALQRG

>d1zbdb\_ g.50.1.1 (B:) Effector domain of rabphilin-3a {Rat (Rattus norvegicus)}

EELTDEEKEIINRVIARAEKMETMEQERIGRLVDRLETMRKNVAGDGVNRCILCGEQLGMLGSASVVCEDCKKNVCTKCGVETSNNRPHPVWLCKICLEQREVWKRSGAWFFKGFPKQVLPQPM

>d1f62a\_ g.50.1.2 (A:) Williams-Beuren syndrome transcription factor, WSTF {Human (Homo sapiens)}

ARCKVCRKKGEDDKLILCDECNKAFHLFCLRPALYEVPDGEWQCPACQPAT

>d1fp0a1 g.50.1.2 (A:19-88) Nuclear corepressor KAP-1 (TIF-1beta) {Human (Homo sapiens)}

GTLDDSATICRVCQKPGDLVMCNQCEFCFHLDCHLPALQDVPGEEWSCSLCHVLPDLKEEDVDLQACKLN

>d1adt\_2 g.51.1.1 (266-385) First Zn-domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}

TGCALWLHRCAEIEGELKCLHGSIMINKEHVIEMDVTSENGQRALKEQSSKAKIVKNRWGRNVVQISNTDARCCVHDAACPANQFSGKSCGMFFSEGAKAQVAFKQIKAFMQALYPNAQT

>d1adt\_3 g.51.1.1 (386-529) Second Zn-domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}

GHGHLLMPLRCECNSKPGHAPFLGRQLPKLTPFALSNAEDLDADLISDKSVLASVHHPALIVFQCCNPVYRNSRAQGGGPNCDFKISAPDLLNALVMVRSLWSENFTELPRMVVPQFKWSTKHQYRNVSLPVAHSDARQNPFDF

>d1qbha\_ g.52.1.1 (A:) 2MIHB/C-IAP-1 {Human (Homo sapiens)}

GSHMQTHAARMRTFMYWPSSVPVQPEQLASAGFYYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWFPRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTS

>d1f9xa\_ g.52.1.1 (A:) BIR domains of XIAP {Human (Homo sapiens)}

MSDAVSSDRNFPNSTNLPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTT

>d1g73c\_ g.52.1.1 (C:) BIR domains of XIAP {Human (Homo sapiens)}

LPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYLLEQKGQEYINNIHL

>d1g73d\_ g.52.1.1 (D:) BIR domains of XIAP {Human (Homo sapiens)}

LPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTTE

>d1i3oe\_ g.52.1.1 (E:) BIR domains of XIAP {Human (Homo sapiens)}

FALDRPSETHADYLLRTGQVVDISDTIYPRNPAMYSEEARLKSFQNWPDYAHLTPRELASAGLYYTGIGDQVQCFACGGKLKNWEPGDRAWSEHRRHFPNCFFVLGRNLNI

>d1jd5a\_ g.52.1.1 (A:) BIR2 domain of DIAP1 {Fruit fly (Drosophila melanogaster)}

GNYFPQYPEYAIETARLRTFEAWPRNLKQKPHQLAEAGFFYTGVGDRVRCFSCGGGLMDWNDNDEPWEQHALWLSQCRFVKLMKGQLYIDTVAAKPVLAEEKEES

>d1e31a\_ g.52.1.1 (A:) Anti-apoptotic protein survivin {Human (Homo sapiens)}

TLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFFCFKELEGWEPDDDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRRAIEQLAA

>d1f81a\_ g.53.1.1 (A:) CREB-binding transcriptional adaptor protein CBP {Mouse (Mus musculus)}

SPQESRRLSIQRCIQSLVHACQCRNANCSLPSCQKMKRVVQHTKGCKRKTNGGCPVCKQLIALCCYHAKHCQENKCPVPFCLNIKHK

>d1hc7a3 g.56.1.1 (A:404-477) C-terminal domain of ProRS {Thermus thermophilus}

TRKVDTYEAFKEAVQEGFALAFHCGDKACERLIQEETTATTRCVPFEAEPEEGFCVRCGRPSAYGKRVVFAKAY

>d1exka\_ g.54.1.1 (A:) Cysteine-rich domain of the chaperone protein DnaJ. {Escherichia coli}

GVTKEIRIPTLEECDVCHGSGAKPGTQPQTCPTCHGSGQVQMRQGFFAVQQTCPHCQGRGTLIKDPCNKCHGHGRVERS