

>d1dlwa_a.1.1.1 (A:) Truncated hemoglobin {Ciliate (Paramecium caudatum)}

SLFEQLGGQAAVQAVTAQFYANIQADATVATFFNGIDMPNQTNKTAFLCAALGGPNAWTGRNLKEVHANMGVSNAQFTTIGHRLSALTGAGV
AAALVEQTVAVAETVRGDVVTV

>d1dlya_a.1.1.1 (A:) Truncated hemoglobin {Green alga (Chlamydomonas eugametos)}

SLFAKLGGEAEEAVDKFYNKIVADPTVSTYFSNTDMKVQRSKQFAFLAYALGGASEWKGKDMRTAHKDLVPHLSDVHFQAVARHLSDTLTELGV
PEDITDAMAVVASTRTEVLNMPQQ

>d1idra_a.1.1.1 (A:) Truncated hemoglobin {Mycobacterium tuberculosis}

GLLSRLRKREPISIYDKIGGHEAIEVVVEDFYVRVLADDQLSAFFSGTNMSRLKGKQVEFFAAALGGPEPYTGAPMKQVHQGRGITMHHSVLVAGHL
ADALTAAGVPSETITEILGVIAPLAUDVTS

>d1scta_a.1.1.2 (A:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}

VDAAVAKVCGSEA IKANLRRSGVLSADIEATGLMLMSNLFTPDTKTYFTRLGDVQKGKANSKLRGHAITLTYALNNFVDSLDDPSRLKCVVEKFA
VNHNKRKISGDAFGAIVEPMKETLKARMGNYSDDVAGAWAALVGVVQAAL

>d1sctb_a.1.1.2 (B:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}

KVAELANAVVSNADQKDLLRMSWGVLSDMEGTGLMLMANLFKTPSAKGKFARLGDSAGKDN SKLRGHSITLMYALQNFVDALDDVERLKC
VEKFAVNHNRIQISADEFGEIVGPLRQTLKARMGNYSDDVAGAWAALVGVVQAAL

>d3sdha_a.1.1.2 (A:) Hemoglobin I {Ark clam (Scapharca inaequivalvis)}

SVYDAAAQLTADVKKDLRDSWKVIGSDKKGNGVALMTTFADNQETIGYFKRLGNVSQGMANDKLRGHSITLMYALQNFIDQLDNPDDLCVVEK
FAVNHNTRKISAAEFGKINGPIKKVLASKNFGDKYANAWAKLVAVVQAAL

>d1b0b__a.1.1.2 (-) Hemoglobin I {Clam (Lucina pectinata)}

SLSAAQKD NVKSSWAKASA AAWGTAGPEFFMALFDAHDDVF AKFSGLFS GAAKGTVKNTPEMA QAQSFKGLVSNWVDNLDNAGALEGQCKTFA
ANHKARGISAGQLEAFKVLAGFMKS YGGDEGA WTAVAGALMG MIRPD M

>d1h97a_a.1.1.2 (A:) Trematode hemoglobin/myoglobin {Paramphistomum epiclitum}

TLTKHEQDILLKELGPHVDTPAHIVETGLGAYHALFTAHPQYISHFSRLEGHTIENVMQSEGIKHYARTLTEAIVHMLKEISNDAEVKKIAAQYGKDHTS
RKVTKDEFMSGEPIFTKYFQNLVKDAEGKA AVEKFLKHVFPMMAAEI

>d1vrea_a.1.1.2 (A:) Glycera globin {Marine bloodworm (Glycera dibranchiata)}

GLSAAQRQV VASTWKDIAGSDNGAGVGK CFTKFLSAH DMAAVFGF SGASDPGVADLGAKV LAQIGV AVSHLGDEGKMVAEMKAVGVRHKGY
GNKHIKA EYFEPLGASLLS SAMEHRIGGKMNAAKDAWAAAYADISG ALISGLQS

>d2hbg__a.1.1.2 (-) Glycera globin {Marine bloodworm (Glycera dibranchiata)}

GLSAAQRQVIAATWKDIAGADNGAGVGK CLIKFLSAHPQMAAVFGF SGASDPGV AALGAKV LAQIGV AVSHLGDEGKMVAQM KAVGVRHKGY
GNKHIKA QYFEPLGASLLS SAMEHRIGGKMNAAKDAWAAAYADISG ALISGLQS

>d1a6m__a.1.1.2 (-) Myoglobin {Sperm whale (Physeter catodon)}

VLSEGEWQLVLHVWAKVEADVAGHGQDILRLFKSHPETLEKFDKFHLKTEAEMKASEDLKKHGNTVLTALGAILKKGHHEAELKPLAQSHATKHK
IPIKYLEFISEAIIHV LHSRHPGDFGADAQGAMNKALELFRKDIAAKYKELGY

>d1mba__a.1.1.2 (-) Myoglobin {Sea hare (Aplysia limacina)}

SLSAAEADLAGKSWAPFANKNANGLDFLVALFEKFPDSANFFADFKGSVADI KASPKL RDVSSRIFTRLNEVNNAANAGKMSAMLSQFAKEHV
GFGVGSAQFENVRSMPGFVASVAPPAGADA AAWTKLFG LIIDALK AAGA

>d1mbs__a.1.1.2 (-) Myoglobin {Common seal (Phoca vitulina)}

GLSDGEWQLVNVWGKVETDLAGHGQEVLIRLFKSHPETLEKFDKFHLKSEDEM KASEDLKKHGNTVLTALGGILKKGHHEAELKPLAQSHATK
KIPIKYLEFISEAIIHV LHSKHPAEFGADAQGAMK KALELFRNDIAAKYKELGFHG

>d1mwca_a.1.1.2 (A:) Myoglobin {Pig (Sus scrofa)}

GLSDGEWQLVNVWGKV EADVAGHGQEV LIRLFKGHPETLEKFDKFHLKSEDEM KASEDLKKHGNTVLTALGGILKKGHHEAELTPLAQSHATK
HKIPVKYLEFISEAIIQVLQSKH PGDFGADAQGAMSKALELFRNDMAAKYKELGFQG

>d1dwta_a.1.1.2 (A:) Myoglobin {Horse (Equus caballus)}

GLSDGEWQQV LNVWGKV EADIA GHGQEV LIRLF GHPETLEKFDKFHLKTEAEMKASEDLKKHGNTVLTALGGILKKGHHEAELKPLAQSHATK

KIPIKYLEFISDAIIHVLSHKHPGDFGADAQGAMTKALELFRNDIAAKYKELGFQ
>d2mm1_a.1.1.2 (-) Myoglobin {Human (Homo sapiens)}

GLSDGEWQLVNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDRFKHLKSEDEMKAESDLKKHGATVLALGGILKKKGHHEAEIKPLAQSHATKH
KIPVKYLEFISEAIIQVLQSKHPGDFGADAQGAMNKALELFRKDMASNYKELGFQG
>d1emy_a.1.1.2 (-) Myoglobin {Asian elephant (Elephas maximus)}

GLSDGEWEVLKTWGKVEADIPGHGETVFVRLFTGHPETLEKFDFKHLKTEGEMKASEDLKKQGVTVITALGGILKKKGHHEAEIQPLAQSHATKH
KIPIKYLEFISDAIIHVLSQSKHPAEGFADAQGAMKKAELFRNDIAAKYKELGFQG
>d1lht_a.1.1.2 (-) Myoglobin {Loggerhead sea turtle (Caretta caretta)}

GLSDDEWNHVLGIWAKVEPDLSAHGQEVIIRLFQLHPETQERFAFKNLTTIDALKSSEEVKHGTTLTALGRILKQNNHEQELKPLAESHTAKH
PVKYLEFICEIIVKVIAEKHPDSFGADSQAAMKKAELFRNDMASKYKEFGFQG
>d1myt_a.1.1.2 (-) Myoglobin {Yellowfin tuna (Thunnus albacares)}

ADFDAVLKCWGPVEADYTTMGLVLTRLFKEHPETQKLFPKFAGIAQADIAGNAISAHGATVLKKLGEELLAKGSAAILKPLANSHTAKH
KLISEVLVVKMVHEKAGLDAGGQTALRNVMGIIADLEANYKELGFSG
>d1eco_a.1.1.2 (-) Erythrocrorin {Midge (Chironomus thummi), fraction III}

LSADQISTVQASFDFDKVKGDPVGILYAVFKADPSIMAKFTQFAGKDLESIKGTAPFETHANRIVGFFSKIIGELPNIEADVNTFVASHKPRGVTHDQLNNF
RAGFVSYMKAHTDFAGAEAAWGATLDTFFGMIFSKM
>d2gdm_a.1.1.2 (-) Leghemoglobin {Yellow lupin (Lupinus luteus)}

GALTESQAALVKSSWEENANIPKHTHRFILVLEIAPAAKDLFSFLKGTEVPQNNPELOAHAGKVFKLVYEAAIQLEVTGVVVTDATLKNLGSVHVS
KGVAADHFVVKEAILTIKEVVVGAKWSEELNSAWTIAYDELAIVKEMDDAA
>d1fsla_a.1.1.2 (A:) Leghemoglobin {Soybean (Glycine max), isoform A}

VAFTEKQDALVSSSEAFAKANIPQYSVVFYTSILEKAPAAKDLFSFLANGVDPTNPQLTGHAEKLFLALVRDSAGQLKASGTVVADAALGSVHAQKAVTD
PQFVVVKEALLTIKAAVGDKWSDELSRAWEVAYDELAAAIKKA
>d1d8ua_a.1.1.2 (A:) Non-symbiotic plant hemoglobin {Rice (Oryza sativa)}

ALVEDNNNAVASFSEEQEALVLKSWAILKKDSANIALRFFLKIFEVAPSASQMFSFLRNSDVPLEKNPKLKTHAMSVFVMTCEAAAQLRKAGKVTVRD
TTLKRLGATHLKYGVGDAHFEVVKFALLDTIKEEVPAWMSPAMKSAWSEAYDHLVAAIKQEMKPAE
>d1i3da_a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (Homo sapiens)}

GHFTEEDKATITSLWGKVNVEDAGGETLGRLLVVPWTQRFFDSFGNLSSASAIMGNPKVKAHGKKVLTSLGDAIKHLDLKGTFQAQLSELHCDKLH
VDPENFKLLGNVLTVLAIHFGKEFTPEVQASWQKMTAVASALSSRYH
>d1irda_a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (Homo sapiens)}

VLSPADKTNVKAAGWKVGAHAGEYGAEEALERMFLSFPTTKTYFPHFDLSHGSAQVKHGKKVADALTNAVAVHVDMPNALSALSDLHAKLDRV
PVNFKLLSHCLLTVLAAHLPAPFTPAVHASLDKFLASVSTVLTSKYR
>d1jeba_a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (Homo sapiens), zeta isoform}

SLTKTERTIIVSMWAKISTQADTIGTETLERFLSHPQTKTYFPHFDLHPGSAQLRAHGSKVAAVGDAVKSIDDIGGALKSELHAYILRVDPVNFKLL
SHCLLVTLAARFPADFTAEEAAWDKFLSVSSVLT SKYR
>d1ibe_a.1.1.2 (A:) Hemoglobin, alpha-chain {Horse (Equus caballus)}

VLSAADKTNVKAAGWKVGGHAGEYGAEEALERMFGLFPPTKTYFPHFDLSHGSAQVKAHGKKVGDALTAVGHLDLPGALSDLSNLHAKLDRV
VNFKLLSHCLLSTLAVHLPNDFTPAVHASLDKFLSSVSTVLT SKYR
>d1hds_a.1.1.2 (A:) Hemoglobin, alpha-chain {Deer (Odocoileus virginianus)}

VLSAANKSNVKAAGWKVGGNAPAYGAQALQRMFLSFPTTKTYFPHFDLSHGSAQQKAHGQKVANALTKAQGHLNDLPGTLSNLSNLHAKLDRV
PVNFKLLSHCLLTVLASHLPTNFTPAPVHANLNKFLANDSTVLT SKYR
>d1g08a_a.1.1.2 (A:) Hemoglobin, alpha-chain {Cow (Bos taurus)}

VLSAADKGNVKAAGWKVGGHAAEYGAEEALERMFLSFPTTKTYFPHFDLSHGSAQVKHGAKVAAALTKAVEHLDLPGALSELSDLHAKLDRV
VNFKLLSHCLLTVLASHLPSDFTPAVHASLDKFLANVSTVLT SKYR
>d1qpwa_a.1.1.2 (A:) Hemoglobin, alpha-chain {Pig (Sus scrofa)}

VLSAADKANVKAAWGKVGGQAGAHGAEALERMFLGFPTTKTYFPHFNLSHGSDQVKAHGQKVADALTKAVGHLDLPGALSALSDLHAHKLRVD
PVNFKLLSHCLLVTAAHHPDDNPSVHASLDKFLANVSTVLTSKYR
>d1fhja_a.1.1.2 (A:) Hemoglobin, alpha-chain {Maned wolf (*Chrysocyon brachyurus*)}
VLSPADKTNIKSTWDKIGGHAGDYGGEALDRTFQSFTKTYFPHFDLSPGSAQVKAHGKKVADALTTAVAHLDLPGALSALSDLHAYKLRVPVN
FKLLSHCLLVTLACHHPTEFTPASLDKFTAVSTVLTSKYR
>d1hbra_a.1.1.2 (A:) Hemoglobin, alpha-chain {Chicken (*Gallus gallus*)}
MLTAEDKKLIQQAWekaASHQEFGAEALTRMFTTYPQTCKTYFPHFDLSPGSDQVRGHGKVLGALGNAVKNVDNLSQLAMAELSNLHAYNLRVD
PVNFKLLSQCIQVVLAVHMGKDYTPEVHAADFCKFLSAVSAVLAEKYR
>d1a4fa_a.1.1.2 (A:) Hemoglobin, alpha-chain {Bar-headed goose (*Anser indicus*)}
VLSAADKTNVKGVFSKISGHAEYGAETLERMFTAYPQTCKTYFPHFDLQHGSAQIKAHGKKVVAALVEAVNHIDDIAGALKSDLHAQKLRVPVN
KFLGCFLVVVIAHPSALTAEVHASLDKFLCAVGTVLTAKYR
>d1outa_a.1.1.2 (A:) Hemoglobin, alpha-chain {Trout (*Oncorhynchus mykiss*)}
SLTAKDKSVVKAFWGKISGKADVVGAEALGRMLTAYPQTCKTYFSHWADLSPGSGPVKKHGGIIMGAIGKAVGLMDDLGGMSALSDLHAFKLRVD
PGNFKILSHNIVLTLAIHFPSDFTPEVHIAVDKFLAAVSAALADKYR
>d1cg5a_a.1.1.2 (A:) Hemoglobin, alpha-chain {Cartilaginous fish akaei (*Dasyatis akajei*)}
VLSSQNKKAAEELGNLIKANAEEAWGADALARLFELHPQTCKTYFSKFSGFEACNEQVKKHGKRVMNALADATHHLDNLHLHEDLARKHGENLLVDP
HNFLHFADCIVVTLAVNLQAFTPVTHCAVDKFLELVAYELSSCYR
>d1t1na_a.1.1.2 (A:) Hemoglobin, alpha-chain {Fish (*Trematomus newnesi*)}
SLSDKDKAAVRALWSKIGKSSDAIGNDALSRMIVVYPQTCKYFSHWPDVTPGSPNIKAHGKKVMGGIALAVSKIDLKTGLMELSEQHAYKLRVDPS
NFKILNHCIILVISTMFPEAKVSLDKFLSGVALALAERYR
>d1spga_a.1.1.2 (A:) Hemoglobin, alpha-chain {Teleost fish (*Leiostomus xanthurus*)}
SLSATDKARVKALWDKIEGKSAELGAEALGRMLVSFPQTCKYFSEWQGQDLGPQTPQVRNHGAVIMAAGKAVKSIDNLVGGSQLSELHAFKLRVP
ANFKILAHNIIILVISMYFPGDFTEVHLSVDKFLACLALASEKYR
>d1gcva_a.1.1.2 (A:) Hemoglobin, alpha-chain {Houndshark (*Mustelus griseus*)}
AFTACEKQTIGKIAQVLAKSPEAYGAECLARLFVTHPGSKSYFEYKDYSAGAKVQVHGGKVIRAVVKAEEHVDDLHSLETLALTHGKLLVDPQNF
PMLSECIIVTLATHLTFSPDTHCAVDKLLSAICQELSSRYR
>d1irdb_a.1.1.2 (B:) Hemoglobin, beta-chain {Human (*Homo sapiens*)}
VHLTPEEKSAVTALWGKVNDEVGGEALGRLLVYPWTQRFFESFGDLSFTDAVMGNPKVKAHGKKVLGAFSDGLAHLNDLKGTFATLSELHCDKL
HVDPENFRLLGNVLVCVLAHHFGKEFTPVQAAYQKVVAGVANALAHKYH
>d1a9we_a.1.1.2 (E:) Hemoglobin, beta-chain {Human (*Homo sapiens*), embryonic gower II}
VHFTAAEKAAVTSLSKMNVVEAGGEALGRLLVYPWTQRFFDSFGNLSSPSAILGNPKVKAHGKKVLTSGDAIKNMDNLKPAFAKLSELHCDKLH
VDPENFKLLGNVMVIIILATHFGKEFTPVEVQAAWQKLVSAVIALAHKY
>d1ibeb_a.1.1.2 (B:) Hemoglobin, beta-chain {Horse (*Equus caballus*)}
VQLSGEEKAAVLALWDKVNEEVGGEALGRLLVYPWTQRFFESFGDLSNPGAVMGNPKVKAHGKKVLHSFEGVHLDNLKGTFAAALSELHCDK
LHVDPENFRLLGNVLVVLARHFGKDFTEPLQASYQKVVAGVANALAHKYH
>d1hdsb_a.1.1.2 (B:) Hemoglobin, beta-chain {Deer (*Odocoileus virginianus*)}
MLTAEEKAATGFWGKVDVDVVAQALGRLLVYPWTQRFFQHFGNLSSAGAVMNNPKVKAHGKRVLDAFTQGLKHLDLKGFAQLSGLHCN
KLHVNPNQFRLLGNVLALVARNFGQFTPNVQALFQKVVAGVANALAHKYH
>d1g08b_a.1.1.2 (B:) Hemoglobin, beta-chain {Cow (*Bos taurus*)}
MLTAEEKAATFWGKVDEVGGEALGRLLVYPWTQRFFESFGDLSFTADAVMNNPKVKAHGKKVLDSFSNGMKHLDLKGTFAAALSELHCDKL
HVDPENFKLLGNVLVVLARHFGKEFTPVLQADFQKVVAGVANALAHRYH
>d1qpwb_a.1.1.2 (B:) Hemoglobin, beta-chain {Pig (*Sus scrofa*)}
VHLSAEEKEAVLGLWGKVNDEVGGEALGRLLVYPWTQRFFESFGDLSNADAVMGNPKVKAHGKKVLQSFSDGLKHLDNLKGTFAKLSELHCDQ
LHVDPENFRLLGNVIVVVLARRLGHDNPDVQAAFKVVAGVANALAHKYH

>d1fhjb_a.1.1.2 (B:) Hemoglobin, beta-chain {Maned wolf (*Chrysocyon brachyurus*)}
VHLTAEKSLVGLWGKVNVDEVGEALGRLLIVYPWTQRFDSFGDLSTPDAVMSNAVKAHGKKVLNSFSDGLKNLDNLKGTFAKLSELHCDKLH
VPENFKLLGNVLVCVLAHHFGKEFTPQVQAAYQKVAGVANALAHKYH
>d1jebb_a.1.1.2 (B:) Hemoglobin, beta-chain {Mouse (*Mus musculus*)}
VHLTDAEKAASVGLWGKVNADEVGGEALGRLLVVYPWTQRFDSFGDLSSASAIMGNAVKAHGKKVITAFNDGLNHLDLSKGTFASLSELHCDKL
HVDPENFRLGNMIVIVLGHHLGKDFTPAAQAAFKVVAAGVAAALAH
>d1hbrb_a.1.1.2 (B:) Hemoglobin, beta-chain {Chicken (*Gallus gallus*)}
VHWTAEEKQLITGLWGKVNVACGAEARLLIVYPWTQRFASFGNLSSPTAILGNPMVRAHGKKVLTSGDAVKNLDNIKNTFSQLSELHCDKLH
VPENFRLLGDIILIVLAHFSKDFTPECQAAWQKLVRVVAHALARK
>d1a4fb_a.1.1.2 (B:) Hemoglobin, beta-chain {Bar-headed goose (*Anser indicus*)}
VHWSAEEKQLITGLWGKVNVADCGAEALARLLIVYPWTQRFSSFGNLSSPTAILGNPMVRAHGKKVLTSGDAVKNLDNIKNTFAQLSELHCDKLH
VPENFRLLGDIILIVLAHFAKEFTPDCQAAWQKLVRVVAHALARKYH
>d1outb_a.1.1.2 (B:) Hemoglobin, beta-chain {Trout (*Oncorhynchus mykiss*)}
VEWTDAEKSTISAVWGKVNIIDEIGPLALARVLIVYPWTQRYFGSGNVSTPAIMGNPKVAAHGKVVCGALDKAVKNMGNILATYKSLSETHANKL
FVDPDNFRVLADVTIVIAAKFGASFTPEIQATWQKFMKVVAAMGSRYF
>d1pbxb_a.1.1.2 (B:) Hemoglobin, beta-chain {Antarctic fish (*Pagothenia bernacchii*)}
VEWTDKERSIISDFSHMDYDDIGPKALSRCCLIVYPWTQRFSGFGNLYNAEAIIGNANVAAHGIKVLHGLDRGVKNMDNIAATYADLSTLHSEKLHV
DPDNFKLLSDCITIVLAAKMGHAFTAETQGAFQKFLAVVVSALGKQYH
>d1cg5b_a.1.1.2 (B:) Hemoglobin, beta-chain {Cartilaginous fish akaei (*Dasyatis akajei*)}
VKLSEDQEYIKGVVWKDVHKQJTAKALERVFVVPWTTRLFSKLQGLFSANDIVQQHADKVQRALGEAIDLKVEINFQNLGKHQEIGVDTQ
NFKLLGQTFMVELALHYKKTFRPKEHAAAYKFFRLVAEALSSNYH
>d1t1nb_a.1.1.2 (B:) Hemoglobin, beta-chain {Fish (*Trematomus newnesi*)}
VEWTDKERSIISDFSHMDYDDIGPKALSRCCLIVYPWTQRYFGFGNLYNAEGIMSANVAAHGIKVLHGLDRGMKNMDNIADAYTDLSTLHSEKL
HVDPDNFKLLSDCITIVLAAKMGHAFTAETQGAFQKFLAVVVSALGKQYH
>d1spgb_a.1.1.2 (B:) Hemoglobin, beta-chain {Teleost fish (*Leiostomus xanthurus*)}
VDWDTDAERAIAKALWGKIDVGEIGPQALSRLLIVYPWTQRFKGFGNISTNAAILGNAKVAEHGKTVMGGLDRAVQNMNDNIKNVYKQLSIKHSEKI
HVDPDNFRLGEIITMCVGAKFGPSAFTPEIHEAWQKFLAVVVSALGRQYH
>d1gcvb_a.1.1.2 (B:) Hemoglobin, beta-chain {Houndshark (*Mustelus griseus*)}
VHWTQEERDEISKTFQGTDMKTVVTQALDRMFKVYPWTQRFQKRTDFRSSIHAGIVVGALQDAVKHMDDVTLFKDSLKHADDLHVDPGSFH
LTDCCIIVELAYLRKDCFTPHIQGIWDKFFEVVIDAIISKQYH
>d1ch4a_a.1.1.2 (A:) Chimeric hemoglobin beta-alpha {Synthetic, based on *Homo sapiens* sequence}
VHLTPEEKSAVTALWGKVNVDEVGEALGRLLVVPWTQRFESFGDLSTPDAVMGNPKVAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKL
RVDPVNFKLLSHCLLVTAAHLPAEFTPAVHASLDKVLASVSTVLTSKYR
>d1it2a_a.1.1.2 (A:) Hagfish hemoglobin {Inshore hagfish (*Eptatretus burgeri*)}
PIIDQGPLTLDGDKAINKIWPKIYKEYEQYSLNILLRFLKCFPQAQASFPEKFSTKKSNEQDPEVKHQAVVIFNKVNEIINSMDNQEEIISLKDLSQ
KHKTVFVDSIWFKELSSIFVSTIDGGAEEFEKLFISIICILLRSAY
>d2lhb_a.1.1.2 (-) Lamprey globin {Sea lamprey (*Petromyzon marinus*)}
PIVDTGSVAPLSAAEKTIRSAWAPVYSTYETSGVDILVKFFTSTPAAQEFFPKFKGLTTADELKSADVRWHAERIINAVDDAVASMDDEKMSMCLR
NLSGKHAKSFQVDPEYFKVLAASIADTVAAAGDAGFEKLMSMICILLRSAY
>d1ash_a.1.1.2 (-) Ascaris hemoglobin, domain 1 {Pig roundworm (*Ascaris suum*)}
ANKTRELCKMSLEHAKVDTSENARQDGIDLYKHMFENYPPPLRKYFKSREYTAEDVQNDPFFAKQGQKILLACHVLCATYDDRETFNAYTRELLDRH
ARDHVHMPPEVWTDFWLFEYLGKTTLDEPTKQAWHEIGREFAKEINK
>d1itha_a.1.1.2 (A:) Hemoglobin {Innkeeper worm (*Urechis caupo*)}
GLTAAQIKAIQDHWFNLNIKGCLQAAAISIFFKYLTAYPEGLAFFHKFSSVPLYGLRSNPAYKAQTLTVINYLDKVVDALGGNAGALMAKVPSHDAMG

ITPKHFGQLLKLVGGVFQEESADPTTVAAWGDAAGVLVAAMK
>d1hlb_a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (Caudina (Molpadia) arenicola)}
GGTLAIQAQGDLTLAQKKIVRKTWHQLMRNKTFSVTDFIRIFAYDPSAQNKFPQMAGMSASQLRSSRQM QAHAIRVSSIMSEYVEELSDILPELL
ATLARTHDLNKVGADHYNLFAKVLMEALQAEGLSDFNEKTRDAWAKAFSVVQAVLLVKHG
>d1hlm_a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (Caudina (Molpadia) arenicola)}
GATQSFSQSGDLTPAEKDILRSTWDQLMTHRTGFADVIFIRIFHDPTAQRKFPQMAGLSPAELRTSRQM HAHAIRVSALMTTYIDEMDTEVLPEL
LATLTRTHDKNHVGKKNYDLFGKVLMEAIAKAEGLGVGFTKQVHDAWAKTFAIVQGVLLTKHAS
>d1vhba_a.1.1.2 (A:) Bacterial dimeric hemoglobin {Vitreoscilla stercoraria}
LDQQTNIKATVPVLKEHGVTTTFYKNLFAKHPEVRPLFDMGRQESLEQPKA LAMTVLAAQNIENLPAILPAVKKIAVHCQAGVAAAHPIVGQ
ELLGAIKEVLGDAATDDILDAWGKAYGVIADVFIQVEADLYAQAV
>d1cqxa1_a.1.1.2 (A:1-150) Flavohemoglobin, N-terminal domain {Alcaligenes eutrophus}
MLTQKTKDIVKATAPVLAEHGYDIICKFYQRMFEAHPELKVNFM AHQEQQQQALARAVVAYAENIEDPNSLMAVLKNIANKHASLGVKPEQY
PIVGEHLLAAIKEVLGNAATDDIISAWAQAYGNLADVLMGM ESELYERSAEQPGG
>d1ew6a_a.1.1.2 (A:) Dehaloperoxidase {Marine worm (Amphitrite ornata)}
GFKQDIATRGDLRTYAQDIFLAFLNKYPDERRYFKNYVGKSDQELKSMAKFGDHTEKVFNLMMEVADRATDCVPLASDANTLVQMKQHSSLTTGN
FEKLFWALVEYMRASGQSFDQSWSDRFGKKNLVSALSSAGMK
>d1phna_a.1.1.3 (A:) Phycocyanin {Red alga (Cyanidium caldarium)}
MKTPITEAIAAADNQGRFLSNTELQAVNGRYQRAA SLEAARS LTSNAERLINGAAQAVYSKFPYTSQMPGPQYASSAVGKAKCARDIGYYLRMV
CLVGGTGPMDYLIAGLEEINRTFDLSPSWYVEALNYIKANHGLSGQAANEANTYIDYAINALS
>d1phnb_a.1.1.3 (B:) Phycocyanin {Red alga (Cyanidium caldarium)}
MLDAFAKVVVAQADARGEFLSNTQLDALSKMVSEGNKR LDVVNRITSNASAIVTAARALFSEQPQLIQPGGNAYTNRRMAACLRDMEII
IAGDSSILDDRCLNGLRETYQALGVP GAS VAVGIEKMKD AIAI ANDPSGTTGDCS ALMAEVGTYFDRAATAVQ
>d1f99a_a.1.1.3 (A:) Phycocyanin {Red alga (Polysiphonia urceolata)}
MKTPLTEAIAAADSQGRFLSNTQIDALLAIVSEGNKRLDV
VNRITSNASAIVTAARALFAEQPQLISP
GGNAYTSRRMAACLRDMEI
LVGGTGPMDYLVAGLEEINRTFELSPSWYEALKYIKNNHGLSGDV
VANEANTYIDYAINLS
>d1f99b_a.1.1.3 (B:) Phycocyanin {Red alga (Polysiphonia urceolata)}
MLDAFAKVVVAQADARGEFLSNTQIDALLAIVSEGNKRLDV
VNRITSNASAIVTAARALFAEQPQLISP
GGNAYTSRRMAACLRDMEI
IAGDASVLD
FDRCLNGLRETYQALGTPGAS VAVI
QKMKD AALALVNDTTGTPAGDCASL
VAEIATYFDRAAAA
>d1cpca_a.1.1.3 (A:) Phycocyanin {Cyanobacterium (Fremyella diplosiphon)}
MKTPLTEAIAAADSQGRFLSSTEIQTAFGRFRQASLA
AAKALTEKASSLASGAANAVYSKFPY
TTSQNGPNFASTQTGKDKCVRDIGYYLRMV
LVGGTGPLDDYLIGGIAEINRTFDLSPSWY
VEALKYIKANHGLSGDP
AVEANSYIDYAINLS
>d1pcb_a.1.1.3 (B:) Phycocyanin {Cyanobacterium (Fremyella diplosiphon)}
MLDAFAKVVVSQADARGEYLSGSQIDAL
SALVADGNKRM
DVNRITGNS
TIVANAARSLFAEQPQLIAP
GGNAYTSRRMAACLRDMEI
FAGDASVLD
FDRCLNGLKETYLALGTPGSS
VAVG VQ
KMKD AALAIAGDTNG
ITRGDCASL
MAEVASYFDA
ASAVA
>d1i7ya_a.1.1.3 (A:) Phycocyanin {Synechococcus vulgaris}
MKTPITEAIAAADTQGRFLSNTELQAVDGRFK
RAV ASMEA
ARALTNN
AQS
LIDG
AAQAVY
QKF
PYTTM
MQGSQY
ASTPEG
KAKCARDIGYYLR
MIT
YCLVAGGTGP
MDYLIAGL
SEINST
FDLSP
SWYEALKY
IKANHGL
GDA
VEANAY
IDYAIN
LS
>d1i7yb_a.1.1.3 (B:) Phycocyanin {Synechococcus vulgaris}
MLDAFAKVVVAQADARGEFL
TNAQFD
ALSNLV
KEGNK
RLDAVN
RITS
NASTIV
ANAAR
ALFAEQ
PQLIQ
PGGNAY
TNRR
MAACLR
DMEI
ILRY
VTYAI
LAGDSSVLD
FDRCLNGL
RETYQAL
GTPGSS
VAVI
QKMKD
AALAI
ANDPNG
ITPGDC
SALM
SEIAGY
FDRA
AAA
VA
>d1gh0a_a.1.1.3 (A:) Phycocyanin {Spirulina platensis}
MKTPLTEAVS
ADSQGRFL
SSTEI
QVAF
GRFRQ
AKGLE
AAKAL
TSKAD
SLS
GAAQ
AVY
QKF
PYTT
MQGP
NYA
ADQR
GKDK
CARDIG
YYLR
MVT
YCL
IAGGT
GPMDY
LIAG
IDE
INRT
FEL
SPSW
YEALKY
IKANH
GLSGD
AAVE
ANSY
LDY
AIN
LS
>d1gh0b_a.1.1.3 (B:) Phycocyanin {Spirulina platensis}

MFDAFTKVVSQADTRGEMLSTAQIDALSQMVAESNKRLDVNRITSNASTIVSNAARSLFAEQPQLIAPGGNAYTSRRMAACLRDMEIILRYVTYAV
FAGDASVLEDRCLNGLRETYALGTPGSSAVVGVKMKEAALAIVNPDAGITPGDCSALASEIAGYFDRAAAAVS
>d1alla_a.1.1.3 (A:) Allophycocyanin {Spirulina platensis}
SIVTKSIVNADAEARYLSPGEELDRIKSFVTSGERRVIAETMTGARERIIKQAGDQLFGKRPDVSPGGNAYADMATCLRDLDDYRLITYGIVAGDV
TPIEEIGVGVREMYKSLGTPIEAIAEGVRAMKSATLSGADAAEAGSYFDYLIGAMS
>d1allb_a.1.1.3 (B:) Allophycocyanin {Spirulina platensis}
MQDAITSVINSSDVQGKYLDASAIQKLKAYFATGELRVRAATTISANAANIVKEAVAKSLLYSDVTRPGGNMYTTRYYACIRLDYLYRATYAMLAG
DPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTAGLVGGAGKEMGIYFDYICSGLS
>d1b33a_a.1.1.3 (A:) Allophycocyanin {Cyanobacterium (Mastigocladus laminosus)}
SIVTKSIVNADAEARYLSPGEELDRIKSFVSSGEKRLRIAQILTDNRERIVKQAGDQLFQKRPDVSPGGNAYQEMTATCLRDLDDYRLITYGIVAGDV
TPIEEIGVGVREMYKSLGTPIDAVAAGVSAMKNVASSILSAEDAAEAGAYFDYVAGALA
>d1b33b_a.1.1.3 (B:) Allophycocyanin {Cyanobacterium (Mastigocladus laminosus)}
MQDAITAVINSSDVQGKYLDATAALEKLKSFSTGELRVRAATTIAANAAAIVKEAVAKSLLYSDITRPGGNMYTTRYYACIRLDYLYRATYAMLAGD
PSILDERVLNGLKETYNSLGVPISATVQAIQAMKEVTASLVPDAGKEMGVYFDYICSGLS
>d1liaa_a.1.1.3 (A:) Phycoerythrin {Red alga (Polysiphonia urceolata)}
MKSVITTTISAADAAGRYPSTSLSQVQGNIQRRAARLEAAEKLGSNHEAVVKEAGDACFSKYGYNKNPGEAGENQEKINKCYRDIDHYMRLINYTL
VVGGTGPLDEWGIAGAREVYRTLNPLSAAYIAAFVTRDRLCIPRDMQAQAGVEFTALDYLINSLS
>d1liab_a.1.1.3 (B:) Phycoerythrin {Red alga (Polysiphonia urceolata)}
MLDAFSRVVVNSDSKAAYVGSSDLQALKTFINDGNKRLDAVNIVSNSSCIVSDAISGMICENPGLITPGGNCYTNRMAACLRDGEIILRYVSYALLA
GDASVLEDRCLNGLKETYIALGVPTNSTRAVSIMKAAAVCFISNTASQRKVEVIEGDCSALASEVASYCDRVVAAVS
>d1b8da_a.1.1.3 (A:) Phycoerythrin {Red alga (Griffithsia monilis)}
MKSVITTTISAADAAGRFPSSSDLESIQGNIQRRAARLEAAQKLSGNHEAVVKEAGDACFKSYLKNGEAGDSPEKINKCYRDIDHYMRLINYSLV
VGGTGPVDEWGIAGSREVYRALNLPSAYIAAFFTRDRLCVPRDMSSQAGVEFTSALDYVINSLC
>d1b8db_a.1.1.3 (B:) Phycoerythrin {Red alga (Griffithsia monilis)}
MLDAFSRVVTSDAKAAYVGGSDLQSLKFINDGNKRLDAVNIVSNASCIVSDAVSGMICENPGLIAPGGNCYTNRMAACLRDGEIILRYVSYALL
AGDSSVLDRCNLGLKETYIALGVPTASSRAVSIMKATATAFITNTASGRKVEVAGDCQALQAEAASYFDKVGSID
>d1eyxa_a.1.1.3 (A:) Phycoerythrin {Red algae (Gracilaria chilensis)}
MKSVITTVISAADSAGRFPSSSDLESVQGNIQRASARLEAAEKLASNHEAVVKEAGDACFGKYGYLKNPGEAGENQEKINKCYRDIDHYMRLVNYSLV
IGGTGPLDEWGIAGAREVYRTLNPLTSAYIAAFTRDRLCGPRDMAQAGVEYSTALDYIINSLS
>d1eyxb_a.1.1.3 (B:) Phycoerythrin {Red algae (Gracilaria chilensis)}
MLDAFSRVISNADAKAAYVGGSDLQALRTFISDGKRLDAVNIVSNSSCIVSDAISGMICENPGLITPGGNCYTNRMAACLRDGEIILRYISYALLAG
DSSVLEDRCLNGLKETYIALGVPTNSTRAVSIMKAAVGAFISNTASQRKGEVIEGDCSALAAEIASYCDRISAAVS
>d1qgwc_a.1.1.3 (C:) Phycoerythrin {Cryptophite (Rhodomonas sp.), cs24}
DAFSRVVTNADSKAAYVGGADLQALKFISEGNKRLDSVNSIVSNASCIVSDAVSGMICENPGLISPSGNCYTNRMAACLRDGEIILRYVSYALLSGD
ASVLEDRCLNGLKETYSSLGVPANSNARAVSIMKACAVAFVNNTASQKKLSTPQGDCSGLASEVGGYFDKVTAIS
>d1fumb1_a.1.2.1 (B:106-243) Fumarate reductase iron-sulfur protein, C-terminal domain {Escherichia coli}
MTHFIESLEAIKPVIIGNSRTADQGTNIQTPAQMAKYHQFSGCINCGLCYAACPQFGLNPEFIGPAITLAHRYNEDSRDHGKKERMAQLNSQNGV
WSCTFVGYCSEVCPKHVDPAAAIQQGKVESSKDFLIATLKPR
>d1qlab1_a.1.2.1 (B:107-239) Fumarate reductase iron-sulfur protein, C-terminal domain {Wolinella succinogenes}
TGNWFNGMSQRVESWIHQKEHDISKLEERIEPEVAQEVFELDRCIEGCCIAACGKIMREDFVGAAGLNRVRFMIDPHDERTDEDYYELIGDD
DGVFGCMTLLACHDVCVPNPLQSKIYLRRKMVSVN
>d1h7wa1_a.1.2.2 (A:2-183) Dihydropyrimidine dehydrogenase, N-terminal domain {Pig (Sus scrofa)}
APVLSKDVADIESILALNPRTQSHAALHSTLAKKLDKKHWKRNPDKNCFHCEKLENNFDDIKHTTLGERGALREAMRCLKCADAPCQKSCPTHLDIKS
FITISNKNYYGAAKMIFSDNPGLTCGMVCPTSDLCVGGCNLYATEEGSINIGGLQQFASEVFKAMNIPQIRNPCLPSQEKM

>d1grj_1 a.2.1.1 (2-79) GreA transcript cleavage protein, N-terminal domain {Escherichia coli}
QAIPMTLRAEKLREELDFLKSRRPEIIAAIAEAREHDLKENAEYHAAREQQGFCEGRIKIDIEAKLSNAQVIDVTK

>d1jj2u_a.2.2.1 (U:) Ribosomal protein L29 (L29p) {Archaeon Haloarcula marismortui}
TVLHVQEIRDMDTPAEREAELDDLKTELLNARAVQAAGGAPENPGRIKELRKAIARIKTIQGEEGD

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

>d1hdj_a.2.3.1 (-) HSP40 {Human (Homo sapiens)}
MGKDYYQTGLARGASDEEIKRAYRRQALRYHPDKNKEPGAEKFKEIAEAYDVLSDPRKREIFDRYGEGLKGSGC

>d1xbl_a.2.3.1 (-) DnaJ chaperone, N-terminal (J) domain {Escherichia coli}
AKQDYYEILGVSKTAEEEREIRKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEAYEVLTDSQKRAAYDQYGHAAFEQ

>d1faf_a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Murine polyomavirus}
MDRVLRSRADKERLLELLKLPRQLWGDFGRMQQAYQQSLLHPDKGGSHALMQELNSLWGTFKTEVYNLRMNLGGTGFQ

>d1gh6a_a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Simian virus 40, Sv40}
SHMREESLQLMDLLGLERSAWGNIPLMRKAYLKKCEFHPDKGGDEEKMKKMNTLYKKMEDGVKYAHQPDFGGFWDATEIPTYGTDEWEQWW
NAFNEENLFCSEEMPSSDEAT

>d1du2a_a.2.4.1 (A:) Theta subunit of DNA polymerase III {Escherichia coli}
MLKNLAKLDQTEMVKVNDLAAAGVAFKERYNMPVIAEAVEREQPEHLRSWFRERLIAHRLASVNSRLPYEPKLK

>d1fxkc_a.2.5.1 (C:) Prefoldin alpha subunit {Archaeon Methanobacterium thermoautotrophicum}
AALAEIVAQLNIYQSQVELIQQQMEAVRATISELEILEKTLSDIQGKDGSETLVPVGAGSFIAELKDTSEIMSVGAGVAIKKNFEDAMESIKSQKNEL
ESTLQKMGGENLRAITDIMMKLSPQAELLAAVA

>d1fxka_a.2.5.1 (A:) Prefoldin beta subunit {Archaeon Methanobacterium thermoautotrophicum}
QNVQHQLAQFQQLQQQAQAIKVQKQTVEQMNETQKALEELSRAADDAEVYKSSGNILIRVAKDELTEELQEKTETLQLREKTIERQEERVMKKLQE
MQVNIQEAMK

>d1cxzb_a.2.6.1 (B:) Effector domain of the protein kinase pkn/prk1 {Human (Homo sapiens)}
WSLLEQLGLAGADLAAPGVQQQLELERERLRRERKELKLKEGAENLRRATTDLGRSLGPVELLRGSSRRLLLLHQQLQELHAHV

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

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

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

>d1e52a_a.2.9.1 (A:) C-terminal, UvrC-binding domain of UvrB {Escherichia coli}
LEPDNVPMMDMSPKALQQKIHELEGLMMQHAQNLEFEEAAQIRDQLHQLRELFIAAS

>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}
QDLDEARAMEAKRKAEEHISSSHGDVDYAQASAEALAKIAQLRVIELTKK

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

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

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

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

>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}
VIQLKRYEFPLPYKVDALEPYISKDIIDVHYNGHHKGYVNGANSLLDRLEKLIKGDLPQQYDLQGILRGLTFNINGHKLHAIYWNNA

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

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

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

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

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

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

>d1dava_a.139.1.1 (A:) Cellulosome endoglucanase SS {Clostridium thermocellum}
MSTKLYGDVNDDGKVNSTDAVALKRYVLRSGISINTDNADLNEDGRVNSTDLGILKRYILKEIDTLPYKNG

>d1h9ea_a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}
PEFLEDPSVLTCKDKLKSELVANNVTLPAGEQRKDYYVQLYLQHLTARNRPLPLAGT

>d1h9fa_a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}
RQEDKDDLVTELTNE CDDLQLVKYGVNPPIVGTTRKLYEKLLKLREQGTESRSS

>d1jeia_a.140.1.1 (A:) Inner nuclear membrane protein emerin {Human (Homo sapiens)}
DNYADLSDELTLLRRYNIPHGPVGSTRRLYEKKIFEYETQRRLSPSSS

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

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

>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}
IHPNFVGDKSKEFSRLGKEEMMAEMLQRGFNEYNESDTKTQLIASFKQLRKSLK

>d1c75a_a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Bacillus pasteurii}
VDAEAVVQQKCISCHGGDLTGASAPAIDKAGANYSEEIILDIILNGQGGMPGGIAKGAEAEAVAAWLAEEKK

>d1ctj_a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Monoraphidium braunii}
EADLALGKAVFDGNCAACHAGGGNNVIPDHTLQKAAIEQFLDGGFNIEAVYQIENGKGAMPWAUDGRLDEDEIAGVAAYVYDQAAGNKW

>d1c53_a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Desulfovibrio vulgaris, different strains}
ADGAALYKSCVGCHGADGSKQAMGVGVHAVKGQKADEFKKLGYADGSYGGKEKAVMTNLVKRYSDEEMKAMADYMSKL

>d2dvh__ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Desulfovibrio desulfuricans}
ADGAALYKSCIGCHGADGSKAAMGSAKPVKGQGAEELYKKMKGYADGSYGERKAMMTNAVKKASDEELKALADYMSKL

>d1cyi__ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Chlamydomonas reinhardtii}
ADLALGAQVFNGNCAACHMGGRNSVMPEKTLKAALEQYLDDGFVKEIIYQVENGKAMPWAADRLEEEIQAVAEVFKQATDAAWK

>d1c6s__ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Cyanobacterium (Synechococcus elongatus)}
ADLANGAKVFSGNCAACHMGGGNVVMANKTLKKEALEQFGMYSEDAIYQVQHGNAMPAGFRLTDEQIJDVAAYVLDQAAKGWAG

>d1f1fa__ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Arthospira maxima}
DVAAGASVFSANCAACHMGGRNIVANKTLSKDLAKYLKGFDDEAVAAYQVTNGKNAMPGFNRSLPLQIEDVAAYVVDQAEKGW

>d1c6ra__ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Green alga (Scenedesmus obliquus)}
ADLALGKQTFAECAACHAGGNNSVIPDHTLRKAAMEQFLQGGFNLEAITYQVENGKAMPWAWSGTLDDEIAAVAAAYVYDQASGDKW

>d1gdva__ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Red alga (Porphyra yezoensis)}
ADLDNGEKVFSANCAACHAGGNNAIMPDKTLKDVLEANSMTIDAITYQVQNGKNAMPAGFGLVDEDIEDAANYVLSQSEKGW

>d1c52__ a.3.1.1 (-) Cytochrome c552 {Thermus thermophilus}
QADGAKIYAQCAGCHQQNGQGIPGAFPPLAGHVAEILAKEGGREYLVLQGLQQIEVKGMKYNGVMSSFAQLKDEEIAAVLNHIATAWGDAKK
VKGFPFTAEEVKKLRAKKTLPQQVLAERKKLGLK

>d1cnoa__ a.3.1.1 (A:) Cytochrome c552 {Pseudomonas nautica}
AGDIEAGKAKAAVCAACHGQNGISQVPIYPNLAGQKEQYLVAAALKYKAGQRQGGQAPVMQGQATALSDADIANLAAYYASNPAAC

>d1qj3a__ a.3.1.1 (A:) Cytochrome c552 {Paracoccus denitrificans}
ADPAAGEKVFGCKACKLDGNDGVPHLNGVVGRVTAGVDFNYSDPMKAHGGDWTPPEALQEFLNPKA VVKGTKMAFAGLPKIEDRANLIA
YLEGQQ

>d1ayg__ a.3.1.1 (-) Cytochrome c552 {Hydrogenobacter thermophilus}
NEQLAKQKGMACHDLKAKKVGPAYADVAKYAGRKDAVDYLAGKIKGGSGVWGSVPMPQQVTDAAKQLAQWILSIK

>d1a56__ a.3.1.1 (-) Cytochrome c552 {Nitrosomonas europaea}
DADLAKNNCIACHQVETKVVGPALKDIAAKYADKDDAATYLAGKIKGGSGVWGSVPMPQQVTDAAKQLAQWILSIK

>d1e29a__ a.3.1.1 (A:) Photosystem II associated cytochrome c549 {Synechocystis sp., pcc 6803}
VELTESTRTIPLDEAGGTTLTARQFTNGQKIFVDTCTQCHLQGKTKTNNNVSLGLADLAGEPRRDNVLALVEFLKNPKSYDGEDDYSELHPNISRDPD
IYPEMRNYTEDDIFDVAGYTLIAPKLDERWGQTIF

>d1f1ca__ a.3.1.1 (A:) Photosystem II associated cytochrome c549 {Arthospira maxima}
LTEELRTFPINAQGDTAVSLKIEKKQQVFNAAACQCHALGVTRTNPDVNL SPEALALATPPRDNIAALVDYIKNPTTYDGFVEISELHPSLKSSDIFPK
MRNISEDDLYNVAGYILLOPKVRGEQWV

>d1ycc__ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}
TEFKAGSAKKGATLFKTRCLQCHTVEKGPHKVGPNLHGIFGRHSQAEQSYTDANIKNVLWDENNMSYLTNPKKYIPGTMAGFFGLKEKDR
NDLITYLKKACE

>d1yeb__ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}
TEFKAGSAKKGATLFKTRCLQCHTIEEGGPNKVGPNLHGIFGRHSQVKGYSYTDANIKNVKWDEDSMSEYLTNPKKYIPGTMAGFFGLKEKDR
NDLITYLKKACE

>d1ytc__ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}
AKESTGFKPGSAKKGATLFKTRCLQCHTIEEGGPNKVGPNLHGIFGRHSQVKGYSYTDANIKNVKWDEDSMSEYLTNPKKYIPGTMAGFFGLKE
KDRNDLITYMTKAAC

>d1wejf__ a.3.1.1 (F:) Mitochondrial cytochrome c {Horse (Equus caballus)}
GDVEKGKKIFVQKCAQCHTVEKGKHKTPNLHGLFGRKTGQAPGFTYTDANKNGITWKEETLMYELENPKKYIPGTMIFAGIKKTEREDLIAYL
KKATNE

>d1ccr__ a.3.1.1 (-) Mitochondrial cytochrome c {Rice embryos (Oryza sativa)}
ASFSEAPPGNPKAGEKIFTKCAQCHTVDKGAGHKQGPNLNGLFGRQSGTPGYSYSTADKNMAVIWEENTLYDYLNPKKYIPGTMVFPLKPP

QERADLISYLKEATS

>d5cytr_a.3.1.1 (R:) Mitochondrial cytochrome c {Tuna (*Thunnus alalunga* and *Thunnus thynnus*)}

GDVAKGKKTFVQKCAQCHTVENGKHKVGPNLWGLFGRKTGQAEGSYTDANKSKGIVWNNDTLMYEYLENPKKYIPGTKMIFAGIKKKGERQDLV
AYLKSATS

>d1qn2a_a.3.1.1 (A:) Cytochrome ch {Methylobacterium extorquens}

EGDAAAGEKAFAPCKACHNFEKNGVGPTLKGVVGAKAGEGADGYAFSDALKSGLTWDQADLKQWLADPKKVPGTKMVFPGISDPKKVDDIAY
LTKT

>d3c2c__ a.3.1.1 (-) Cytochrome c2 {Rhodospirillum rubrum}

EGDAAGEKVSKKCLACHTFDQGGANKVGPNLFGVFENTAAHKDNYAYSESYTEMKAKGLTWEANLAAYVKNPKAFVLEKSGDPKAKSMTFKLT
TKDEIENVIAYLKTLK

>d1c2ra_a.3.1.1 (A:) Cytochrome c2 {Rhodobacter capsulatus}

GDAAKGEKEFNKCTCHSIIAPDGTEIVGAKTGPNLYGVVGRTAGTYPEFKYKDSIVALGASGF AWTEEDIATVKDPAFLKEKDDKKAKTGMAF
KLAKGGEDVAAYLASVVK

>d1cxc_a.3.1.1 (-) Cytochrome c2 {Rhodobacter sphaeroides}

QEGDPPEAGAKAFNQCQTCHIVDDSGTTIAGRANKTGPNLGYVVRTAGTQADFKGYGEGMKEAGAKGLAWDEEHFVQYVQDPTKFLKEYTGDA
KAKGKMTFKLKKEADAHNIIWAYLQQVAVRP

>d1co6a_a.3.1.1 (A:) Cytochrome c2 {Rhodopseudomonas viridis}

QDAASGEQVFQCLVCHSIGPGAKNKVGVLNGLFGRHSGTIEGFAYSDANKNSGITWTEEVFREYIRDPAKIPGTMIFAGVKDEQKVSDLIAYIK
QFNADGSKK

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

EDAKAGEAVFKQCMTCRADKNMVGPAAGVGRKAGTAAGFTYSPLNHNSGEAGLVWTADNIVPYLADPNAFLKKLTEKGKADQAVGVTKM
TFKLANEFOORKDVVAYLATLK

>d1hraa a.3.1.1 (A:) Cytochrome c2 {Rhodopila globiformis}

SAPP GDP VEG KHL FHT IC TDI KGANKV GPS LYGV VGR HSG IE PG NY SEAN IK SGIV WTP DVLF KYIE HPQ KIV PGT KM GY PG QP DPQ KRAD II A
YI ETI K

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

NEGDAAKGEKEFKNCKACHMIQAPDGTIDKGGTKGPNLGYGVVGRKIASEEGFKYGEGLAEKNPDLTWTEANLIEYVTDPKPLVKKMTDDKGAKT
KMTFKMGKNOADVVAELAODDPDXXXXXXXXXXXXXXX

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

DGDAAKGEKEFNKCKACHMIQAPDGTDIIGGGKTGPNLGYVGRKIASEEGFKYEGEILEVAEKNPDLTWTEADLIEYVTDPKPWLVKMTDDKGAKT
KMTTEKMGKNGOADVVAELAONSRDA

>d1idla_a 3.1.1 (A:) Cytochrome c2 {Rhodospirillum centenum}

GDPAKGEAVFKKCMACHRVGPDAKNLVGPALTGVIDRQAGTAPGFNYSAINHAAGEAGLHWTPENIIAYLPDPNAFLRKFLADAGHAEQAKGSTK
MVEKLBRDEOEFRKDVAWYKQESP

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

GGGARSGDDVVAKYCNACHGTGLIAPRKVGDSAAWKTRADAKGLDGILAOISLGLNAMPRKGTCACGSDDELKAAGKMSGI

>d1kx2a_23.1.1 (A:) Mono-heme c-type cytochrome ScyA {Shewanella putrefaciens}

ADLQDAEAIYNKACTVCHSMGVAGARKSHNTADWERPLAKGVDNLVSKVTGLNAMPRGGMCTDCTDEDYKAJIEEMSKAK

>d1ccb -> 3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}

ODGEALEKSKPAAACHSVDTKMVGALKEVAKNAGVEGAADTLAIHKNGSOGVWGRIPMRPNPVTEEEAKILAEWVLSK

>d1cor...>3.1.1() Cytochrome c551 {Pseudomonas stutzeri}

EDGAEALEKSKRCAACHSIDAKLVGRAEKVEAALKYACODGAADUAGH

>d1dyw_a3.1.1(A): Cytochrome c551 [Pseudomonas aeruginosa]

EDREVI LA KNKGCMACHAIDTKMVGRAVKRVA AKYAGOAGAEAYLAQRIK

>d451c__ a.3.1.1 (-) Cytochrome c551 {Pseudomonas aeruginosa}
EDPEVLFKNKCVACHAIDTKMVGPAYKDVAAKFAGQAGAEELAQRIKNGSQGVWGPPIPMPNAVSDEAQTLAKWVLSQK

>d2mtac_ a.3.1.1 (C:) Cytochrome c551 {Paracoccus denitrificans}
APQFFNIIDGSPLNFDDAMEEGRDTEAVKHFLTGENVYNEDPEILPEAEELYAGMCGCHGHYAEGKIGPGLNDAYWTYPGNETDVLFLSTLYGGA
TGQMGPMWGSITLDEMILRTMAWVRHLYTGDPKDASWLTDEQKAGFTPQF

>d1gks__ a.3.1.1 (-) Cytochrome c551 {Ectothiorhodospira halophila}
DGESIYINGTAPTCSSCHDRGVAGAPELNAPEDWADRPSSVDELVESTLAGKGAMPAYDGRADREDLVKAIEYMLSTL

>d05c1__ a.3.1.1 (-) Cytochrome c555 {Chlorobium thiosulfatophilum}
YDAAAGKATYDASCAMCHKTGMMGAPKVGDKAAWAPHIAKGGMNVMVANSIKGYKGTMMPAKGGNPKLTDAQVGNAVAYMVGQSK

>d1dw0a_ a.3.1.1 (A:) SHP, an oxygen binding cytochrome c {Rhodobacter sphaeroides}
GDTSPAQLIAGYEEAAGAPADAERGRALFLSTQTGGKPDTSPCTTCHGADVTRAGQRTGKEIAPLAPSATPDRFTDSARVEKWLRNCNSVIGRDC
TPGEKADLLAWLAAQ

>d1e8ea_ a.3.1.1 (A:) Cytochrome c" {Methylophilus methylotrophus, strain w3a1}
DVTNAEKLVKYTNIAHSANPMYEAPSITDGKIFFNRKFKTPSGKEAACASCHTNNPANVGKNITGKEIPPLAPRVNTKRFTDIDKVEDEFTKHCNDI
LGADCSPSEKANFIAYLLTEKPTK

>d1diqc_ a.3.1.1 (C:) p-Cresol methylhydroxylase, cytochrome c subunit {Pseudomonas putida}
SQWGSGKNLYDKVCGHCHKPEVGVPVLEGRGLPEAYIKDIVRNGFRAMPAFPASYVDES LTQVAEYLSSLPA

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

>d1h9xa1 a.3.1.2 (A:42-133) N-terminal (heme c) domain of cytochrome cd1-nitrite reductase {Paracoccus pantotrophus}
APEGV SALS DAQYNEANKIYFERCAGCHGVLKGATGKALTPDLTRDLGF DYLQSFI TGSPAGMPNWGTSGELSAEQV DLMANYL
LLDPAA

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

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

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

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

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

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

>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)}
SDLELHPPSYPWSHRGPLSSLHTSIRRGFQVYKQVCSSCHSM DYVAYRHLVGVCYTEDEAKA LEEVEVQDGP NedGEMFM RPGKLSDYFPKPYP
NPEAARAANNGALPPDSLIVRARHGGEDYVFSLLTG YCEPPTGVSVREGLYFNPYFPGQAIGMAPPIYNDVLEFDDGTPATMSQVAKDVCTFLRW

AAE

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

MTAAEHGLAHAPAYAWSHNGPFETFDHASIRRGYQVYREVCAACHSLDRVWRTLGVHSHTNEEVNMAEEFEYDDEPDEQGNPKRPGKLSDYIP
GPYPNEQAARAANQGALPPDSLIVKARHGGCDYIFSLLTGYPDEPPAGVALPPGSNYNPYFPGGSIAMARVLFDDMVVEYEDGTPATTSQMAKDVT
TFLNWCAE

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

AGDAEAGQKGKVAVCGACHGVGDGNSPAPNFPKLAGQQERYLLQLQDIKAGSTPGAPEGVGRKVLEMTGMILDPLSDQDLEDIAAYFSSQKGSV

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

GYADPALAKQGEKLFRGGKLDQGMPACTGCHAPNGVGNL��AGFPKLGQHAAYTAKQLDFREGNRTNDGDTMIMRGVAALKSNKDI
EALSSYI
QGLH

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

EPTAEMITNNCAGCHGTHGNSGPASPQIAQMIDPMVFVEVMEGFKSGEIASTIMGRIAKGYSTADFEKMAGYFKQQTYQP

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

AKQSFDTALADTGAKLHDKYCEKCHVEGGKPLADEEDYHILAGQWTPLQYAMSDFREERRPMEKKMASKLRELLKAEGDAGLDALFAFYASQQ

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

DALHDQASALFKPIPEQVTELRGQPSEQKRELGKKLFFDPRLSRSHVLCNTCHNVGTGGADNVPTSGHGQWKGPRNSPTVFNAVNAQFW
DGRAKDLGEQAKGPIQNSVEMHSTPQLVEQTLSIPEYVDAFRKAFPKAGKPVSFDNMALAI
EAYEATLV

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

TPDSPFDLYLGDDKALDAQKKGLKAFMDSGCSACHNGINLGGQAYFPFGLVKKPDASVPSGDKGRAVTKTQSDEYV
FRAAPLRNVALTAPYFH
SGQVWELKDAVAMGNAQLKQ LAPDVENIAVFLHSLSGKQPRVEYPLL
PASTETTPRPAE

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

ANEPIQPIKAVTPENADMAELGKMLFDPRLSKSGFISCNSCHNL
SMGGTDNITTSIGHKWQQGPINAPTVLNSSMNLAQFW
DGRAKDLGEQAKGPIQNSVEMHSTPQLVEQTLSIPEYV
DAFRKAFPKAGKPVSFDNMALAI
EAYEATLV

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

TPGSKFDWKLEGDKNALNQDELEGYNLFKGSGCVQCHNGPAVGSSYQKMGVFKPYETKNPAAGRMDVTGNEADRN
VFVPTLRNIELTYPYFH
DGGAA
TLEQAVETMGRQLNREFNKDEVSKIVAFKL
LTGDQPDFKLPILPPSNN
DTPRSQPYE

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

VTGEEVLQNACAA
CHVQHEDGRWERIDA
ARKTPEGWD
MTVTRMMRNHGVALE
PEERAA
VRLHS
LSDTRGL
SLAETE
ERRYL
EREP

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

VAWDEGP
DTSMT
TCGRCHSY
ARVAL
QRRT
PEDW
KHLVNF
HLGQF
PTLEY
QALARD
RDWW
GIAQAE
IIPFLARTY
PLGEA

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

EQG
QPSL
LNQ
NCK
CMG
CHI
PI
GE
NDT
YSR
ISH
QR
KT
PEG
WLM
SIAR
MQV
MH
GLQ
IS
DD
RR
TLV
KYL
AD
KQ
GL
SET
DG
VRY
AMERR

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

LNT
V
EQF
DT
QL
SET
C
GR
CH
SG
AR
VAL
Q
RR
PA
KE
WE
HL
NF
H
LG
Q
W
P
S
LEY
QA
Q
A
R
D
R
D
W
L
P
I
A
L
Q
Q
V
P
D
L
A
K
R
Y
PL

>d1enh_ a.4.1.1 (-) Engrailed Homeodomain {*Drosophila melanogaster*}

RP
RTAF
S
SE
QL
A
R
L
K
R
E
F
N
E
N
R
Y
L
T
E
R
R
Q
Q
L
S
E
L
G
L
N
E
A
Q
I
K
I
W
F
Q
N
K
R
A
K
K
S

>d2hdda_ a.4.1.1 (A:) Engrailed Homeodomain {*Drosophila melanogaster*}

RTAF
S
SE
QL
A
R
L
K
R
E
F
N
E
N
R
Y
L
T
E
R
R
Q
Q
L
S
E
L
G
L
N
E
A
Q
I
K
I
W
F
Q
N
K
R
A
K
K
S

>d1akha_ a.4.1.1 (A:) Mating type protein A1 Homeodomain {Baker's yeast (*Saccharomyces cerevisiae*)}

ISP
Q
A
R
A
F
L
E
E
V
F
R
R
K
Q
S
L
N
S
K
E
K
E
E
V
A
K
C
G
I
T
P
L
Q
V
R
W
F
I
N
K
R
M
R
S
K

>d1f43a_ a.4.1.1 (A:) Mating type protein A1 Homeodomain {Baker's yeast (*Saccharomyces cerevisiae*)}

K
K
E
K
S
P
K
G
K
S
I
S
P
Q
A
R
A
F
L
E
E
V
F
R
R
K
Q
S
L
N
S
K
E
K
E
E
V
A
K
C
G
I
T
P
L
Q
V
R
W
F
I
N
K
R
M
R
S
K

>d1akhb_a.4.1.1 (B:) mat alpha2 Homeodomain {Baker's yeast (*Saccharomyces cerevisiae*)}
TKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSIQIKNWVSNRRKEKTITIAPELADLLSGEPL

>d1aplc_a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast (*Saccharomyces cerevisiae*)}
YRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSIQIKNWVSNRRKEKT

>d1mnmc_a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast (*Saccharomyces cerevisiae*)}
GLVFNVVTQDMINKSTKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTSLSIQIKNWVSNRRKEKT

>d1lfb_a.4.1.1 (-) Transcription factor LFB1 {Rat (*Rattus rattus*)}
RFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAGLGSNLVTEVRVYNWFANRRKEAFRHK

>d2lfb_a.4.1.1 (-) Transcription factor LFB1 {Rat (*Rattus rattus*)}
MARIDPTKKGRNRFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAGLGSNLVTEVRVYNWFANRRKEAFRHKLAMD
TYKLN

>d1e3oc1_a.4.1.1 (C:104-160) Oct-1 POU Homeodomain {Human (*Homo sapiens*)}
KRTSIETNIRVALEKSFMENQKPTSEEDITLIAEQLNMEKEVIRVWFSNRRQKEKRIN

>d1hf0a1_a.4.1.1 (A:102-159) Oct-1 POU Homeodomain {Human (*Homo sapiens*)}
RKKRTSIETNIRVALEKSFLENQKPTSEEITMIADQLNMEKEVIRVWFCNRRQKEKRIN

>d1au7a1_a.4.1.1 (A:103-160) Pit-1 POU homeodomain {Rat (*Rattus norvegicus*)}
KRRTTISIAAKDALERHFGEHSKPSSQEIMRMAEELNLEKEVVVRWFNCNRRQREKRVK

>d1ftt_a.4.1.1 (-) Thyroid transcription factor 1 homeodomain {Rat (*Rattus norvegicus*)}
MRRKRRVLFSQAQVYELERRFKQQKYLAPEREHLASMIHLPTQVKIWFQNHRYKMKRQAKDAAQQ

>d1hdp_a.4.1.1 (-) Oct-2 POU Homeodomain {Human (*Homo sapiens*)}
RRKKRTSIETNVRALEKSFLANQKPTSEEILLIAEQLHMEKEVIRVWFCNRRQKEKRINPCS

>d1ocp_a.4.1.1 (-) Oct-3 POU Homeodomain {Mouse (*Mus musculus*)}
METLVQARKRKRTSIENRVWSLETMFCKPKPSLQQITHIANQLGLEKDVRVWFNCNRRQKGKRS

>d1b72a_a.4.1.1 (A:) Homeobox protein hox-b1 {Human (*Homo sapiens*)}
ARTFDWMVKRNPPKTAKVSEPLGSPGLRTNFTRQLTEKEFHFNKYLSARRVEIAATLENETQVKIWFQNRRMKQKKRERE

>d1b72b_a.4.1.1 (B:) pbx1 {Human (*Homo sapiens*)}
RKRRNFNKQATEILNEYFYSHLSNPYPSEEAKELAKCGITVSQVSNWFGNKRIRYKKNIGKFQEEANIYAA

>d1du6a_a.4.1.1 (A:) pbx1 {Mouse (*Mus musculus*)}
SSGHIEGRHMNKQATEILNEYFYSHLSNPYPSEEAKELAKCGITVSQVSNWFGNKRIRYKKN

>d1bw5_a.4.1.1 (-) Insulin gene enhancer protein isl-1 {Rat (*Rattus norvegicus*)}
MKTTRVRTVLNEKQLHTLRTCYAANPRPDALMKEQLVEMTGLSPRVRVWFQNKRCKDKRSIMMK

>d1ig7a_a.4.1.1 (A:) Msx-1 homeodomain {Mouse (*Mus musculus*)}
RKPRTPTTAQLLALERKFRQKQYLSIAERAESLTSLETQVKIWFQNRRAKAKRL

>d1ahdp_a.4.1.1 (P:) Antennapedia Homeodomain {Drosophila melanogaster}
MRKGRGRQTYTRYQTLLEKEFHFNRYLTRRRRIEIAHALSLTERQKIWFQNRRMKWKENKTGEPEG

>d1san_a.4.1.1 (-) Antennapedia Homeodomain {Drosophila melanogaster}
MTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQKIWFQNRRMKWKENKTGEPEG

>d9anta_a.4.1.1 (A:) Antennapedia Homeodomain {Drosophila melanogaster}
RQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQKIWFQNRRMKWKENKTGEPEG

>d1b8ia_a.4.1.1 (A:) Ultrabithorax (ubx) homeodomain {Drosophila melanogaster}
FYPWMAIAGTNGLRRGRQTYTRYQTLLEKEFHTNHYLTRRRRIEAMAHALSLTERQKIWFQNRRMKLKKEI

>d1b8ib_a.4.1.1 (B:) Extradenticle (exd) homeodomain {Drosophila melanogaster}
RRNFSKQASEILNEYFYSHLSNPYPSEEAKELARKCGITVSQVSNWFGNKRIRYKKN

>d1jgga_a.4.1.1 (A:) Even-skipped homeodomain {Fruit fly (*Drosophila melanogaster*)}

RYRTAFTRDQLGRLEKEFYKENYVSRRRCELAAQLNLPESTIKVWFQNRRMKDKRQ
>d1ftz__ a.4.1.1 (-) Fushi Tarazu protein {Fruit fly (*Drosophila melanogaster*)}
MDSKRTRQTTRYTLEKEFHFNRYITRRRIDIANALSLSERQIKIWFQNRRMKSKKDRTLDSSPEH
>d1nk3p_ a.4.1.1 (P:) VND/NK-2 protein {Fruit fly (*Drosophila melanogaster*)}
KKRKRRLVLFKAQTYELERRFRQQRYLSAPEREHLASLIRLPTQVKIWFQNHRYKTKRAQNE
>d1vnd__ a.4.1.1 (-) VND/NK-2 protein {Fruit fly (*Drosophila melanogaster*)}
ASDGLPNKRKRRVLFTKAQTYELERRFRQQRYLSAPEREHLASLIRLPTQVKIWFQNHRYKTKRAQNEKGEGHP
>d1fjla_ a.4.1.1 (A:) Paired protein {Fruit fly (*Drosophila melanogaster*)}
KQRRSRTTFASQLDELEAFERTQYPDIYTREELAQRTNLTEARIQVWFQNRRARLRKQHTSVS
>d1fjl_ a.4.1.1 (B:) Paired protein {Fruit fly (*Drosophila melanogaster*)}
QRSSRTTFASQLDELEAFERTQYPDIYTREELAQRTNLTEARIQVWFQNRRARLRK
>d1hcra_ a.4.1.2 (A:) HIN recombinase (DNA-binding domain) {Synthetic}
GRPRAINKHEQEIQISRLLEKGHPRQQQLAIIFGIVGSTLYRFPASSIKKRMN
>d1ijwc_ a.4.1.2 (C:) HIN recombinase (DNA-binding domain) {Synthetic}
GRPRAINKHEQEIQISRLLEKGHPRQQQLAIIFGIVGSTLYRFPASSI
>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}
PRGSALSDTERAQLDVMKLLNVSLHEMSRKISRSRHCIRVYLKDPSYGTS
>d2ezl__ a.4.1.2 (-) Ibeta subdomain of the mu end DNA-binding domain of phage mu transposase {Bacteriophage mu}
MIARPTLEAHDYDREALWSKWDNASDSQRLAEKWLPAVQADEMILNQGISTKTAFATVAGHYQVSASTLRDKYYQVQKFAKPDWAAALVDGR
GASRRN
>d2ezh__ a.4.1.2 (-) Transposase {Bacteriophage mu}
SEFDEDAWQFLIADYLRLPEKPAFRKYERLELAAREHGWSIPSRTAFRRQLDEAMVVACREG
>d2ezi__ a.4.1.2 (-) Transposase {Bacteriophage mu}
MNVHKSEFDEDAWQFLIADYLRLPEKPAFRKYERLELAAREHGWSIPSRTAFRRQLDEAMVVACREGEHALM
>d1h88c1 a.4.1.3 (C:39-88) c-Myb, DNA-binding domain {Mouse (*Mus musculus*)}
GKTRWTREEDEKLKKLVEQNGTDDWKVIANLPNRTDVQCQHRWQKVLPN
>d1h88c2 a.4.1.3 (C:89-143) c-Myb, DNA-binding domain {Mouse (*Mus musculus*)}
ELIKGPWTKEEDQRVILQKYGPKRWSVIAKHLKGRIGKQCRERWHNHLNPEVK
>d1idz__ a.4.1.3 (-) c-Myb, DNA-binding domain {Mouse (*Mus musculus*)}
MEVKKTSWTEEDRILYQAHKRLGNRWAEIAKLLPGRTDNAIKHNWNSTMRRKV
>d1a5j_1 a.4.1.3 (1-55) b-Myb DNA binding domain {Chicken (*Gallus gallus*)}
GIPDLVKGPWTKEEDQKVIELVKKYGTQWTIAKHLKGRIGKQCRERWHNHLNP
>d1a5j_2 a.4.1.3 (56-110) b-Myb DNA binding domain {Chicken (*Gallus gallus*)}
EVKKSSWTEEDRIIFEAHKVLGNRWAEIAKLLPGRTDNAVKHNWNSTIKRKVDT
>d1h8ac1 a.4.1.3 (C:87-143) v-Myb {Avian myeloblastosis virus}
NPELNKGWPWTKEEDQRVIEHVQKYGPKRWSDIAKHLKGRIGKQCRERWHNHLNPEVK
>d1h8ac2 a.4.1.3 (C:144-191) v-Myb {Avian myeloblastosis virus}
KTSWTEEDRILYQAHKRLGNRWAEIAKLLPGRTDNAVKHNWNSTMRR
>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*)}
RKRQAWLWEEDKNLRSVRYGEGNWSKILLHYKFNNRTSVMLKDRWRTMKKL

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

GVNQLGGVFVNGRPLPDVVRQIRVELAHQGVRPCDISRQLRVSHGCVSKILGRYYETGSIKPG

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

VIGGSKPKVATPKVVEKIAEYKRQNPTMFAWEIRDRLAERVCNDTVPSSINRIIRTK

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

SHSGVNQLGGVFVNGRPLPDSTRQRIVELAHS GARPCDISRILQVSNGCVSKILGRYYATGSIRPRAI

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

GGSKPRVATPEVVSKIAQYKQECPSIFAWEIRDRLSEGVCTNDNIPSVSSINRVLRLASEKQQ

>d1pdnc_ a.4.1.5 (C:) Paired protein (prd) {Fruit fly (Drosophila melanogaster)}

QGRVNQLGGVFINGRPLPNNIRLKIVEMAADGIRPCVISRQLRVS HGCVSKILNRYQETGSIRPGVIGGSKPRIATPEIENRIEEYKRSSPGMFWEIRE
KLIREGVCDRSTAPSVAISRLV

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

KASFTDEEDEFILDVVRKNPTRRTHTLYDEISHYVPNHTGNSIRHRFRVYLSKRLEYVYEVDFGKLVRRDDGNLIKT KVLPPSI

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

RKFKSADEDYTLAIAVKQFYRDLQIDPDTGRSLITDEDPTAIARRNMTMDPNHVGSEPNFAAYRTQSRRGPIAREFFKHFAEHAAHTENAWR
DRFRKFLLAYGIDDYISYYAEKAQNREPEPMKNLTNRPKRPGVPTPGNYNS

>d1bw6a_ a.4.1.7 (A:) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}

MGPKRRQLTFREKSRIIQVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASE

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

MGPKRRQLTFREKSRIIQVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKVGVASTCR

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

TKNKLSPYDKLEGGLIAWFQQIRAAGLPVKGIILKEKALRIAEEGMDDFTASNGWLDRFRRRS

>d1g2ha_ a.4.1.10 (A:) Transcriptional regulator TyrR, C-terminal domain {Haemophilus influenzae}

SAVISLDEFENKTLDIIGFYEAQVLKLFYAEYPSTRKLAQRLGVSVTAIANKLKQYIGK

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

DAITIHSILDWIEDNLESPLSLEKVSERSGYSKWHLQRMFKKETGHSLGQYIRS

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

RKMTEIAQKLKESNEPILYLAERYGFESQQTTRFKNYFDVPPHKYRMTNMQGESRFLHPL

>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}

SRLDKSKVINSALLELLNEVGIEGLTRKLAQKLGVEQPTLYWHVKNKRALLDALAVEILARHHDYS

>d2tct_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}

ARLNRESVIDAALELLNETGIDGLTRKLAQKLGIEQPTLYWHVKNKRALLDALAVEILARHHDYS

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

NLKDKILGVAKELFKNGYNATTGEIVKLESESSKGKGNLYHFKTKENLNFLEILNIEESKWQEYWKEQIKA

>d1sfe_1 a.4.2.1 (93-176) Ada DNA repair protein {Escherichia coli}

GTAFFQQVWQALRTIPCGETVSYQLANAIGKPKAVRAVASACAANKLAIVIPCHRVVRGDGSLSGYRWGVSRKAQLLRREAEN

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

ESFTRQVLWKLKVVFGEVISYQQLAALAGNPKAARAVGGAMRGNPVPLIPCHRVCSSGAVGNYSGGLAVKEWLLAHEGHRL

>d1mgt a.4.2.1 (A:89-169) O6-alkylguanine-DNA alkyltransferase {Archaeon Pyrococcus kodakaraensis}

VTPEKKVYEWLTKNVKRGSVITYGDLAKALNTSPRAVGGAMKRNPYPIVVPCHRVAHDGIGYYSSGIEEKKFLLEIEGV

>d1c20a_a.4.3.1 (A:) DNA-binding domain from the dead ringer protein {Fruit fly (*Drosophila melanogaster*)}
GWSFEEQFKQVRQLYEINDDPKRKEFLDDLFSFMQKRGTPINRPLIMAKSVLDLYELYNLVIARGGLVDVINKKLWQEIIKGLHLPPSITSAAFLRTQY
MKYLYPYCEKKNLSTPAELQAAIDGNR

>d1ig6a_a.4.3.2 (A:) MRF-2 DNA-binding domain {Human (*Homo sapiens*)}
RADEQAFLVALYKYMKERKTPIERIPYLGFQINLWTMFQAAQKLGGYETITARRQWKHIYDELGGNPGSTSAATCTRRHYERLILPYERFIKGEEKDPL
PPIKPRK

>d1bia_1 a.4.5.1 (1-63) Biotin repressor, N-terminal domain {Escherichia coli}
MKDNTVPLKLIALLANGEFHSGEQLGETLGMSRAINKHIQTLRDWGVDFVPGKGYSLPEP

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

>d1ao_y_a.4.5.3 (-) Arginine repressor (ArgR), N-terminal DNA-binding domain {Escherichia coli}
MRSSAKQEEVKAFKALLKEKFSSQGEIVAAALQEQQFDNIINQSKVSRLMTKFGAVRTRNAKMEMVYCLPAELGVPTT

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

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

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

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

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

>d1smta_a.4.5.5 (A:) SmtB repressor {Cyanobacteria (*Synechococcus*), pcc7942}
ELQAIAPVAQSLAEFFAVLADPNRLRLSLLARSELCVGDLAQAIQVSEAVSHQLRSRLNRLVSYRKQGRHVYYQLQDHIVALYQNALDHLQEC

>d1jgsa_a.4.5.28 (A:) Multiple antibiotic resistance repressor, MarR {Escherichia coli}
LFNEIIPLGRLIHMVNQKKDRLLNEYLSPLDITAQFKVLCISRCAACITPVELKKVLSVLGALTRMLDRLVCKGWVERLPNPNDKRGVLVKLTGGAA
ICEQCHQLVGQDLHQELTKNLTADEVATLEYLLKKVLP

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

>d1fzpb_a.4.5.28 (B:) Pleiotropic regulator of virulence genes, SarA {Staphylococcus aureus}
AITKINDCFELLSMVTYADKLKSLIKKEFSISFEFAVLTYISENKEKEYYLKDIINHLNYKQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIE
SLLSRVNKRIT

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

>d1bm9a_a.4.5.7 (A:) Replication terminator protein (RTP) {Bacillus subtilis}
EEKRSSTGFLVKQRAFLKLYMITMTEQERLYGLKLEVLSEFKEIGFKPNHTEVYRSLHELLDDGILKQIKVKKEGAKLQEVVLYQFKDYEAALKYKKQLK
VELDRCKKLIKEKALSDNF

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

>d1bjaa_a.4.5.9 (A:) Transcription factor MotA, activation domain {Bacteriophage T4}
SKVTYIIKASNDVLNEKTATILITIAKKDFITAAEVREVHPDLGNAVNSNIGVLIKKGLVEKSGDGLIITGEAQDIISNAATLYAQENAPELLK

>d1repcl_a.4.5.10 (C:15-143) RepE54 {Escherichia coli, mini-F plasmid}

SPRIVQSNDLTEAAYSLSRDQKRMILYLFVDQIRKSDGTLQEHDGICEIHAKYAEIFGLTSAEASKDIRQALKSFAGKEVVFYRPEEDAGDEKGYESFPW
FIKPAHSPSRGLYSVHINPYLIPFFIGLQ

>d1repC2 a.4.5.10 (C:144-246) RepE54 {Escherichia coli, mini-F plasmid}

NRFTQFRLSETKEITNPYAMRLYESLCQYRKPDGSGIVSLKIDWIIERYQLPQSYQRMPDFRRFLQVCNEINSRTPMRLSYIEKKGRQTTHIVFSRDIT

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

LGLEKRDREILEVLILRGFGGPVGLATLALSEDPGTLEEVHEPYLIRQGLLKRTPRGRVPTELAYRHLGYPPPV

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

EGLDEFDRKILKTIIEIYRGGPVGLNALAASLGVEADTLSEVYEPYLLQAGFLARTPRGRIVTEKAYKHLKYEV

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

ISEEVILGPLHEKLFLLAIVRSLKISHTPYITFGDAEESYKIVCEEYGERPRVHSQWLWSYLNDLREKGIVETRQNKRGEVGRRTLISIGTEPLDTLEAVIT
KLIKEELR

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

VPKRVYWEMLATNLTDKKEYVRTRRALILEILIKAGSLKIEQIQDNLKKLGDEVITIENDIKGLINTGIFIEIKGRFYQLKDHLQVIPNRGVTKQLV

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

IRTFGWVQNPQKFENLKRVVQVFDRNSKVHNEVKNIKIPTLVKESKIQKELVAIMNQHDLITYKELVGTGTSIRSEAPCDAIQATIADQGNKKGYIDN
WSSDGFLRWHALGFIEYINKSDSFVTDVGLAYSKSAD

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

GSAIEKEILIEAISYYPPAIRITLLEDGQHLTKFDLGKNLGSGESGFTSLPEGILLDTLANAMPDKGEIRNNWEGSSDKYARMIGGWLDKLGKQGK
KEFIPIITLGKPDNKEFISHAFKITGEGLVLRRAKGSTKFTR

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

VPKRVYWEMLATNLTDKKEYVRTRRALILEILIKAGSLKIEQIQDNLKKLGDEVITIENDIKGLINTGIFIEIKGRFYQLKDHLQVIPNRGLKPDLV

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

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

QTEDSACLSAMVLTNTLVYPAVLNAAIDLNLFEIIAKATPPGAFMSPSEIAKLPASTQHSDLPNRLRMLLLASYSVLTSTRTIEDGGAERVYGLSM
VGKYLVPDES

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

RKPSEIFKAQALLYKHIYAFIDSMSLKWALEMNIPNIIQNHGPISLSNLVSILQVPSSKIGNVRRLMRYLAHNGFFEITKEESEYALTVASELLVRGSD

>d1hsta_a.4.5.13 (A:) Histone H5, globular domain {Chicken (Gallus gallus)}

SHPTYSEMAIAAIRAEKSRGGSSRSQSIQYIHKSHYKVGHNAIDLQIKLSIRRLAAGVLKQTKGVGASGSFRLAK

>d1ghc__ a.4.5.13 (-) Histone H1, globular domain {Chicken (Gallus gallus)}

MAGPSVTELITKAVSASKERKGLSLAALKKALAAGGYDVEKNNSRIKGLKSLVSKGLVQTKGTGASGSFRLSK

>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)}

MLVKPPSYIALITMAIQNAPEKKITLNGIYQFIMDRPFYRENKQGWQNSIRHNLSLNECFVKVPRDDKKPGKGSYWTLDPSYNMFENGSL

>d2hdca_a.4.5.14 (A:) Genesis {Rat (Rattus norvegicus)}

VKPPPSYIALITMAILQSPQKKLTLGICFISNRFPPYREKPAWQNSIRHNLSLNDCFVKIPREPGNPGKGNWTLDPSYNMFENGSL

>d1kq8a_a.4.5.14 (A:) HFH-1 (HNF-3 forkhead homolog-1) {Rat (Rattus norvegicus)}

YIALITMAIRDSAGGRRTLAEINEYLMGKFPFRGSYTGWRNSVRHNLSLNDCFVKVLRDPSPRGKDNWMLNP

>d2bby__ a.4.5.15 (-) DNA-binding domain from rap30 {Human (Homo sapiens)}

RARADKQHVLDMLFSAFEKHQQYNLKLDVITKQPVVYLKEILKEIGVQNVKGIIHKNTWELKPEYRHYQ

>d1i27a_a.4.5.30 (A:) C-terminal domain of the rap74 subunit of TFIIF {Human (Homo sapiens)}

GPLGSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTCKTGLSSEQTVNLAQILKRLNPERKMINDKMHFLKE
>d1dpua_a.4.5.16 (A:) C-terminal domain of RPA32 {Human (Homo sapiens)}
ANGLTVAQNQVNLNIKACPRPEGLNFQDLKNQLKHMSVSSIKQAVDFLSNEGHYISTVDDDHFKSTD
>d1fsha_a.4.5.31 (A:) Segment polarity protein Dishevelled-1 {Mouse (Mus musculus)}
EAPLTVKSDMSAIVRVMQLPDSGLEIRDRMWLKITIANAVIGADVVDWLYTHVEGFKERREARYASSMLKHGFLRHTV
>d1cf7a_a.4.5.17 (A:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}
SRHEKSLGLLTTKFVSLLQEAKDGVLDLKAADTLAVRQKRRIYDITNVLEGILIEKKSKNSIQWK
>d1cf7b_a.4.5.17 (B:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}
GKGLRHFSMKVCEVKQRKGTTSYNEVADELVSEFTNSNNHLAADSAYDQKNIRR
>d1d8ja_a.4.5.18 (A:) The central core domain of TFIIE beta {Human (Homo sapiens)}
ALSGSSGYKFGVLAKIVNYMKTRHQRGDTPLTDEILD
>d1qbja_a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1 {Human (Homo sapiens)}
SIYQDQEQRILKFLEELGEGKATTAHDL
>d1qgpa_a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1 {Human (Homo sapiens)}
LSSHQFQELSIYQDQEQRILKFLEELGEGKATTAHDL
>d1j75a_a.4.5.19 (A:) Dlm-1 {Mouse (Mus musculus)}
NLEQKILQVLSDDGGPVKIGQLVKKCQVPKTLNQVLYRLKKEDRVSSPEPATWSIG
>d1dp7p_a.4.5.20 (P:) MHC class II transcription factor RFX1 {Human (Homo sapiens)}
TVQWL
>d1flia_a.4.5.21 (A:) Fli-1 {Human (Homo sapiens)}
PGSGQIQLWQFLLELLSDSANASCITWEGTN
>d1k78b_a.4.5.21 (B:) ETS-1 transcription factor, residues 331-440 {Mouse (Mus musculus)}
IQLWQFLLELLTDKSCQSISWTGDGWEFKLSDPDEVARRWGKRKNPKMNYEKL
>d2stta_a.4.5.21 (A:) ETS-1 transcription factor, residues 331-440 {Human (Homo sapiens)}
VIPAAALAGYTGS
>d1puee_a.4.5.21 (E:) Transcription factor PU.1, residues 171-259 {Mouse (Mus musculus)}
KIRLYQFLLD
>d1awca_a.4.5.21 (A:) GA binding protein (GABP) alpha {Mouse (Mus musculus)}
IQLWQFLLELLTDK
>d1bc8c_a.4.5.21 (C:) Serum responce factor accessory protein 1a, SAP-1 {Human (Homo sapiens)}
MDSAITLWQFL
>d1hbhg_a.4.5.21 (G:) Serum responce factor accessory protein 1a, SAP-1 {Human (Homo sapiens)}
DSA
>d1dux_c_a.4.5.21 (C:) Elk-1 {Human (Homo sapiens)}
VTLWQFL
>d1hks_a.4.5.22 (-) Heat-shock transcription factor {Drosophila melanogaster}
GSGVPAFLAKLW
>d1fbqa_a.4.5.22 (A:) Heat-shock transcription factor {Milk yeast (*Kluyveromyces lactis*)}
PAFVNKLW
>d1fbqa_a.4.5.22 (A:) Heat-shock transcription factor {Milk yeast (*Kluyveromyces lactis*)}

>d2hts__ a.4.5.22 (-) Heat-shock transcription factor {Milk yeast (*Kluyveromyces lactis*)}
ARPAFVNKLWSMVNDKSNEKFIHWSTSGESIVVPNRERFVQEVLPKYFKHSNFAFVQLNMGYWHKVQDVSGNSDRWEFENERHA

>d1if1a_ a.4.5.23 (A:) Interferon regulatory factor 1 (IRF-1) {Mouse (*Mus musculus*)}
RMRPWLEMQINSNQIPGLIWINKEEMIFQIPWKAAKGWDINKDACLFRSWAIHTGRYKAGEKEPDPKTWKANFRCAMNSLPDIEVKDQSR
NKGSSAVRVYRM

>d2irfg_ a.4.5.23 (G:) Interferon regulatory factor-2, IRF-2 {Mouse (*Mus musculus*)}
RMRMRPWLEEQINSNTIPGLKWLNEKKIFQIPWMHAARHGWDVEKDAPLFRNWIHTGHQPGIDKPDPKTWKANFRCAMNSLPDIEEVK
RSIKKGNNAFRVYRMLP

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

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

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

>d1b6a_1 a.4.5.25 (375-448) Methionine aminopeptidase, insert domain {Human (*Homo sapiens*)}
HDDMECSHYMKNFVGHPRLPRTKHLLNVINENFGTLAFCRRWLDLGEVKYLMALKNLCDLGIVDPYPPLC

>d1g4da_ a.4.5.26 (A:) mu transposase, DNA-binding domain {Bacteriophage mu}
KSIWCSPQEIMAADGMPGSVAGVHYRANVQGWTKRKKEGVGGKAVEYDVMMSMPTKEREQVIAHGLST

>d1tns__ a.4.5.26 (-) mu transposase, DNA-binding domain {Bacteriophage mu}
MELWVSPKELANLPGLPKTSAGVIYVAKKQGWQRTRAGVKGGKAIEYNANSLPVEAKAALLRQGEIETSLGYFE

>d1opc__ a.4.6.1 (-) OmpR {Escherichia coli}
VIAFGKFKLNLTREMFRDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNLARGREYSAMERSIDVQISRLRRMVEEDPAHPRYIQTWGLGYVFV
PD

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

>d1qqia_ a.4.6.1 (A:) PhoB {Escherichia coli}
MAVEEVIEMQGLSLDPTSHRVMAGEEPELEMGPTEFKLLHFFMTHPERVYSREQLLNHVWGTNVYVEDRTVDVHIRRLRKALEPGGHDRMVQTV
RGTGYRFSTRF

>d1fsea_ a.4.6.2 (A:) Germination protein GerE {Bacillus subtilis}
SKPLLTKREREVFELLVQDKTTKEIASLFISEKTVRNHISNAMQKLGVKGRSQAVERLLRMGELEL

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

>d1fc3a_ a.4.6.3 (A:) SpoOA {Bacillus stearothermophilus}
NPKKNLDASITSIHEIGVPAHIKYLYLREAIAMVYHDIELLSITKVLYPDIACKYNTTASRVERAIRHAEVAWSRGNLESISLFGYTVSVSKAKPTNSE
FIAMVADKLRLEHK

>d1fox__ a.4.7.1 (-) Ribosomal protein L11, C-terminal domain {Bacillus stearothermophilus}
MTFITKTPPAVLLKKAAGIESGSGEPRNKVATIKRDVKREIAELKMPDLNAASIAAMRMIEGTARSMGIVVED

>d1qa6a_ a.4.7.1 (A:) Ribosomal protein L11, C-terminal domain {Bacillus stearothermophilus}
KTPPAVLLKKAAGIESGSGEPRNKVATIKRDVKREIAELKMPDLNAASIAAMRMIEGTARSMGI

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

>d1fjgr_ a.4.8.1 (R:) Ribosomal protein S18 {Thermus thermophilus}
PSRKAKVKATLGEFDLDRYRNVEVLKRLFSETGKILPRTTGLSGKEQRILAKTIKRARILGLPFTEKLVRK

>d1g1xc_a.4.8.1 (C:) Ribosomal protein S18 {Thermus thermophilus}
DLRDYRNVEVLKRFLSETGKILPRTTGLSGKEQRILAKTIKRARILGLLPFT
>d1i94r_a.4.8.1 (R:) Ribosomal protein S18 {Thermus thermophilus}
KPKKEAQRPSRKAKVKATLGEFDLRDYNVEVLKRFLSETGKILPRTTGLSGKEQRILAKTIKRARILGLLPFTKLVRK
>d1e3ha1_a.4.9.1 (A:263-345) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 {Streptomyces antibioticus}
YQDDVLEALSAAVRPPELSAALTIAGKQDREAELDRVKA
LAEEKLLPEFEGREKEISAAYRALTKSLVR
ERVIAEKKRIDGRGV
>d1k6ya1_a.4.10.1 (A:1-46) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 1}
FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLK
GEAMHGQVD
>d1wjba_a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 1}
FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLK
GEAMHGQVD
>d1e0ea_a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 2}
FLEKIEPAQEEHEKYHSNWKELSHKFGIPNLVARQIVNSCAQCQQK
>d1ef4a_a.4.11.1 (A:) RNA polymerase subunit RPB10 {Archaeon Methanobacterium thermoautotrophicum}
MIPVRCCLSCGKPV
SAYFNEYQRRVADGEDPKDV
LDDLGKRYCCRMLISHVETW
>d1i50j_a.4.11.1 (J:) RNA polymerase subunit RPB10 {Baker's yeast (Saccharomyces cerevisiae)}
MIVPVRCFCGKVVGDKWESYLNL
LQEDELDEGTALSRLGLKRYCCRMLTHVDIEKFLRYNP
>d1cuk_1_a.5.1.1 (156-203) DNA helicase RuvA subunit, C-terminal domain {Escherichia coli}
TDDAEQEAVARLVALGYKPQEASRMVSKIARP
DASSETLIREALRAAL
>d1bvsa1_a.5.1.1 (A:148-203) DNA helicase RuvA subunit, C-terminal domain {Mycobacterium leprae}
NAVRGSV
VEALVGLGFAAKQAAEATDQVL
DGELGKDGA
VATSSALRAAL
SLLGKTR
>d1f4ia_a.5.2.1 (A:) C-terminal UBA domain of the hhr23a DNA repair protein {Human (Homo sapiens)}
QEKEA
IERLKALGFEESLV
IQAYFACE
KENLN
AANFL
LSQNF
DDE
>d1efub3_a.5.2.2 (B:1-54) Elongation factor Ts (EF-Ts), N-terminal domain {Escherichia coli}
AEITASLV
KELRERTGAGMM
DCKK
ALTEANG
DIELAI
ENMRKSG
AIKA
AKKAG
>d1aipc1_a.5.2.2 (C:2-53) Elongation factor Ts (EF-Ts), N-terminal domain {Thermus thermophilus}
SQMELIK
KLREATGAG
MMDV
KRAEDAG
WDEEKAV
QLLR
ERGAM
KA
AKK
ADR
>d1go5a_a.5.2.3 (A:) FG-binding, C-terminal domain of TAP {Human (Homo sapiens)}
PAPTP
SSSPV
PTLSPE
QQEML
QAFST
QSGMN
LEWSQ
KCLQ
DN
WDY
TRSA
QAF
THL
KAK
GEI
PEV
AFMK
>d1aua_1_a.5.3.1 (4-96) N-terminal domain of phosphatidylinositol transfer protein sec14p {Baker's yeast (Saccharomyces cerevisiae)}
QQEKF
LESYP
QNCP
PDAL
PGTP
GNL
DSA
QE
KAL
AEL
RKL
LED
AGF
IER
LDD
STL
LR
R
KFD
V
QLA
KE
MF
ENCE
K
WR
KD
Y
G
T
D
T
I
L
QDFH
>d1enwa_a.5.4.1 (A:) Elongation factor TFIIS domain 2 {Baker's yeast (Saccharomyces cerevisiae)}
GSHMP
RNSKNDG
VDTAI
YHH
KLD
QVL
KALY
D
V
LA
KE
EH
PP
QS
IL
HT
AK
AI
E
SEM
NK
VNN
CDT
NE
A
AY
K
ARY
RI
Y
SV
N
V
ISK
NN
P
DL
KH
KI
ANG
DIT
PE
FLAT
CD
AK
DL
AP
>d1fjgm_a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}
ARIAG
VEIPRN
KRV
D
VAL
TYI
YGIG
KAR
AKE
ALE
KTG
IN
PAT
RV
K
DL
TE
EV
V
RL
REY
VENT
W
K
LEG
EL
R
A
E
V
A
A
NI
K
R
L
M
D
I
G
C
Y
R
G
L
R
P
V
R
G
R
H
R
R
>d1i94m_a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}
ARIAG
VEIPRN
KRV
D
VAL
TYI
YGIG
KAR
AKE
ALE
KTG
IN
PAT
RV
K
DL
TE
EV
V
RL
REY
VENT
W
K
LEG
EL
R
A
E
V
A
A
NI
K
R
L
M
D
I
G
C
Y
R
G
L
R
H
R
>d1eija_a.5.6.1 (A:) Hypothetical protein MTH1615 {Archaeon Methanobacterium thermoautotrophicum}
MRQQLEM
QKKQIM
MQILT
PEARS
RLAN
LRL
TRPDF
VEQ
IEL
QLI
LAQM
GRV
RSK
IT
D
EQL
K
ELL
K
RV
AGKK
>d1jjcb1_a.6.1.1 (B:1-38,B:152-190) Domains B1 and B5 of PheRS-beta, PheT {Thermus thermophilus (Thermus aquaticus)}
MRVP
FSWL
KAYV
PELES
PEV
LEER
LAGL
GFET
DRI
ERV
XEE
VV
LD
EV
TP
NRP
DAL
GLL
GARD
LHAL
GYAL
VEPEAA

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

PPEAIPFRPEYANRLLGTSYPEAEQIAILKRLGCRVEGEGPTYRVTPSHRLDLRLEEDLVEEVARIQGYETIPL

>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}

ESYYSIGEVSKLANVSINKALRYYDKIDLKPAYVDPDTSYRYYDSQLIHLDLICKSLKYIGTPLEEMKKAQDLEMEELFAFYTEQERQIREKLDLFSALEQTISLVKKRMKRQMEYPA

>d1jbga_ a.6.1.3 (A:) Multidrug transporter activator MtaN {Bacillus subtilis}

KYQVKQVAEISGVSIRTLHHYDNIELLNPALTDAGYRLYSADLERLQQILFFKEIGFRLDEIKEMLDHPNFDRKAALQSQKEILMKKKQRMDEMIQTDRTLLS

>d2spca_ a.7.1.1 (A:) Spectrin {Fruit fly (Drosophila sp.)}

QNLDLQLYMRDCELAESWMSAREFLNADDANAGGNVEALIKKHEDFDAINGHEQKIAALQTVADQLIAQNHYASNLVDEKRKQVLERWRHLKEGLIEKRSRLGD

>d1aj3__ a.7.1.1 (-) Spectrin {Chicken (Gallus gallus)}

HQFFRDMDDDESWIKEKKLLVSSEDYGRDLTVQNLRKHKRLEAELAAHEPAIQGVLDGKKLSDDNTIGKEEIQQRLAQFVDHWKELKQLAAARGQ

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

MVHQFFRDMDDDESWIKEKKLLVSSEDYGRDLTVQNLRKHKRLEAELAAHEPAIQSVLDGKKLSDDNTIGKEEIQQRLAQFVDHWKELKQLAAARGQRLEESLEYQ

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

QFVANVEEEAWINEKMTLVASEDYGDTLAAIQGLKKHEAFETDFTVHKDRVNDVCANGEDLIKKNNHHVENITAKMKGKGVSDLEKAAQRKAKLDENSA

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

SSAVNQENERLMEEYERLASLEWIRRTIPWLENRTPEKTMQMAMQKKLEDFRDYRRKHKPPKVQEKCQLEINFNTLQTKLISRNPAPMPSEGKMWSDIAGAWQRLEQAEKGYEEWLLNEIRRL

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

HANERLRRQFAAQANAIGPWIQNKMEEIARSSIQTGALEDQMNQLKQYEHHNIINYKNNIDKLEGDHQLIQEALVFDNKHTNYTMEHIRVGWELLTTIARTINEVETQJLTRD

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

GSSNEIRRRLERLEHIAEKFRQKASTHETWAYGKEQILQKDYESASLTEVRAALLRKHEAFESDLAAHQRVEQIAIAQELNELDYHDADVNVNDRCQKICDQWDRLGTLTQKRREALERMEKLL

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

ETIDQLHLEFAKRAAPFNWMEGAMEDLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSIMAIQNEVEKVIQSYNIRISSSNPYSTVTMDELRTKWDKVQLVPIRDQSLQEELARQHAN

>d1e2aa_ a.7.2.1 (A:) Enzyme Ila from lactose specific PTS, Ila-lac {Lactococcus lactis}

MNREEMTLLGFEIVAYAGDARSKLEALKAAENGDFAKADSLVVEAGSCIAEAHSSQTGMLAREASGEELPVSVTMMHGQDHLMTTILLKDVIIHHLELYKR

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

DESRVENPDERVVIQHNWHELRLFMWDYVGIVRTTKRLERALRRITMLQQIDEYYAHFRVSNNLRLNLVQVAELIVRCAMMRKESRGLHFTLDYPELLTHSGPSILSP

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

DGGENWAKIRDEMGLAMEEGCGIYRPELMQKTIDKLAELQERFKVRVITDTSSVFNTDLYTIELGHGLNVAECMAHSAMARKESRGAHQRLEGCTERDDVNFLKHTLAFRADGTRLEYSDVKITLPP

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

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

>d1fewa_a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}
SLSSEALMRRAVSLVTDSLTSRQTYALIEAITETKAVYTLTSLYRQYTSLLGKMNSEEDEVWQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEM
AAEAAYQTGADQASITARNHIQLVKLQVEEVHQLSRKAETKLAEAQIEELQKQTQEEGEERAESSEQEAYLRED

>d1g73a_a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}
AVPIAQKSEPHSLSEALMRRAVSLVTDSLTSRQTYALIEAITETKAVYTLTSLYRQYTSLLGKMNSEEDEVWQVIIGARAEMTSKHQEYLKLETT
WMTAVGLSEMAAAYQTGADQASITARNHIQLVKLQVEEVHQLSRKAETKLAEAQ

>d1hx1b_a.7.7.1 (B:) BAG-family molecular chaperon regulator-1, BAG1 {Human (Homo sapiens)}
GNSPQEEVKKLKHEKSVEKIADQLEELNKELTGICQQGFLPKDLQAEALCKLDRRKATIEQFMKILEEIDTLIPNFKDSRLKRKGLVKVQAFLAE
CDTVEQNQCQE

>d1i6za_a.7.7.1 (A:) BAG-family molecular chaperon regulator-1, BAG1 {Mouse (Mus musculus)}
GSPEFMLIGEKSNPPEEVELKKLKDLEVAEKIANHLQELNKELESGIQQQGFLAKELQAEALCKLDRRKATIEQFMKILEEIDTMVLPEQFKDSRLKRKN
LVKKVQVFLAECDTVEQYICQETERLQSTNLALAE

>d1qsda_a.7.5.1 (A:) beta-Tubulin binding post-chaperonin cofactor Rbl2p {Baker's yeast (Saccharomyces cerevisiae)}
TQLDIKVALKRRLTKEEGYYQQELKDQEAHVAKLKEDKSVDPYDLKKQEEVLDDTKRLLPTLYEKIREFKEDLEQFLKTYQGTEDVSDARSAITSQAQELLD
S

>d1fgt_a.7.6.1 (T:) Ribosomal protein S20 {Thermus thermophilus}
RNLSALKRHRQSLKRRRLRNKAKKSAIKTLSKAVQLAQEGKAEEALKIMRKAESLIDKAAGSTLHKNAARRKSRLMRKVRQLLEAGAPLIGGGLS
A

>d1bdc_a.8.1.1 (-) Immunoglobulin-binding protein A modules {Staphylococcus aureus}
TADNKFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSQSANLLAEAKKLNDQAPKA

>d1deeg_a.8.1.1 (G:) Immunoglobulin-binding protein A modules {Staphylococcus aureus}
DQQSAFYEILNMPNLNEAQRNGFIQSLKDDPSQSTNVLGAEAKLNESQAPK

>d1edj_a.8.1.1 (-) Immunoglobulin-binding protein A modules {Staphylococcus aureus}
AQHDEAQQNAFYQVLNMPNLNADQRNGFIQSLKDDPSQSANVLGEAQKLNDQAPK

>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}
VDNKFNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSQSANLLAEAKKLNDQAPK

>d1gab_a.8.1.2 (-) PAB {Peptostreptococcus magnus}
TIDQWLLNAKEDAIAELKKAGITSDFYNAINKAKTVEEVNALNEILKAHA

>d1gjta_a.8.1.2 (A:) IgG binding protein G {Streptococcus sp., group G}
MKAIFVLANAQHDEAVDANSLEAKVLANRELDKYGVSDYYKNLINNAKTVEGVKALIDEILAALP

>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}
YASLEEQQNNDALSPAIRRLAEHNLDASAIGTGVGGRLTREDVEKHLAKA

>d1bbi_a.9.1.1 (-) E3-binding domain of dihydrolipoamide succinyltransferase {Escherichia coli}

LSPAIRRLAEHNLDSAIKGTGVGGRLTREDVEKHL
>d2erl__ a.10.1.1 (-) ER-1 {Euplotes raikovi}
DACEQAAICVESACESLCTEGEDRTGCMYIYNSCNPYV
>d1erd__ a.10.1.1 (-) ER-2 {Euplotes raikovi}
DPMTCEQAMASCEHTMCYCGPPLYMTCIGITDPECGLP
>d1erp__ a.10.1.1 (-) ER-10 {Euplotes raikovi}
DLCEQSALQCNEQGCHNFCSPEDKPGCLGMVNPELCP
>d1ery__ a.10.1.1 (-) ER-11 {Euplotes raikovi}
DECANAAAQCSITLCNLYCGPLIEICELTVMQNCEPPFS
>d1hd6a_ a.10.1.1 (A:) ER-22 {Euplotes raikovi}
DICDIAIAQCSLTLCQDCENTPICELVKGSCPPPWS
>d1aca__ a.11.1.1 (-) Acyl-CoA binding protein {Cow (Bos taurus)}
SQAEDFDKAEEVKHLKTPADEEMLFIYSHYKQATVDINTERPGMLDFKGAKWDAWNELKTSKEDAMKAYIDKVEELKKYGI
>d1hbka_ a.11.1.1 (A:) Acyl-CoA binding protein {Plasmodium falciparum}
HMAQQVFEECVSFINGLPTINNLPNELKLDLYKYYKQSTIGNCNIKEPSAHKYIDRKYYEAWKSVENLNREDAQKKRYDIVSEIFPYWQD
>d1ef1a1 a.11.2.1 (A:88-198) Moezin {Human (Homo sapiens)}
DVSEELIQDITQRLLFLQVKEGILNDDIYCPPETAVLLASYAVQSKYGFNKEVHKSGYLAGDKLLPQRVLEQHKLTKEQWEERIQNWHEEHRGMLRED
EDAVLEYLKIAQDL
>d1gc7a1 a.11.2.1 (A:88-198) Radixin {Mouse (Mus musculus)}
DVSEELIQEITQRLFFLQVKKEAILNDEIYCPPETAVLLASYAVQAKYGDYNKEIHKGYLANDRLLPQRVLEQHKLTKEQWEERIQNWHEEHRGMLRED
SMMEYLKIAQDL
>d1gg3a1 a.11.2.1 (A:82-187) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
PDPAQLTEDITRYYLCLQLRQDIVAGRLPCSFATALLGTYIQSELGVDPELHGVDYVSDFKLAPNQTKEEAKVMELHKSRSMTPAQADLEFLENA
KKLSMY
>d1h4ra1 a.11.2.1 (A:104-214) Merlin {Human (Homo sapiens)}
NAEEELVQEITQHLLFLQVKKQILDEKIYCPPEASVLLASYAVQAKYGDYDPSVHKGFLAQEELPKRVINLYQMTPEMWEEIRATAWYAEHRGRARD
EAEMEYLKIAQDL
>d1kdx_ a.12.1.1 (A:) Kix domain of CBP (creb binding protein) {Mouse (Mus musculus)}
GVRKGWHEHTQDLRSHLVHKLVQAIFFPTPDPAALKDRRMENLVAYAKVVEGDMYESANSRDEYYHLLAEKIYKIQKELEE
>d1ire__ a.13.1.1 (-) alpha-2-Macroglobulin receptor associated protein (RAP) domain 1 {Human (Homo sapiens)}
GEEFRMEKLNQLWEKAQRLHLLPPVRLAELHADLKIQERDELAWKLLKLDGLDEDGEKEARLIRNLNVILAKYGLDGKKDAR
>d1qqva_ a.14.1.1 (A:) Thermostable subdomain from chicken villin headpiece {Chicken (Gallus gallus)}
PTKLETFPLDVNTAAEDLPRGVDPDSRKENHLSDEFKAVFGMTRSAFANLPLWKQQNLKEKGLF
>d1vii__ a.14.1.1 (-) Thermostable subdomain from chicken villin headpiece {Chicken (Gallus gallus)}
MLSDEDFKAVFGMTRSAFANLPLWKQQNLKEKGLF
>d1tbaa_ a.15.1.1 (A:) TAF(II)230 TBP-binding fragment {Fruit fly (Drosophila melanogaster)}
EGSIGNGLDTGILFGNIDSEGRLLQDDGEGRRGTGFDALRENIGSLSKLGLDSMLLEVIDLKEA
>d1ail__ a.16.1.1 (-) N-terminal, RNA-binding domain of nonstructural protein NS1 {Influenza A virus}
MDSNTVSSFQVDCFLWHRKQVVQELGDAPFLDRLRRDQKSLRGGSTLGLNIEATHVGKQIVEKILK
>d1a32__ a.16.1.2 (-) Ribosomal protein S15 {Bacillus stearothermophilus}
LTQERKREIIEQFKVHENDTGSPEVQIALTEQINNLNEHLRVHKKDHHSRRGLLMVGKRRRLAYLRNKDVARYREIVEKGL
>d1dk1a_ a.16.1.2 (A:) Ribosomal protein S15 {Thermus thermophilus}
PITKEEKQKVQMEEFARFPGDTGSTEVQVALTLRINRLSEHLKVHKKDHHSRRGLMMVGQRRRLRYLQREDPERYRMLIEKLG
>d1g1xb_ a.16.1.2 (B:) Ribosomal protein S15 {Thermus thermophilus}

PITKEEKQKVIQEFARFPGDTGSTEVQVALLTRINRLSEHLKVHKKDHSHRGLLMMVGQRRRLRYLQREDPERYREIVEKGLRG
>d1d2da_ a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS) second repeated element {Chinese hamster (*Cricetulus griseus*)}
MVYDKIAAQGEVVRKLKAEKAPAKVTEAVECLLSLKAEYKEKTGKEYVPGLEHHH
>d1fyja_ a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS) second repeated element {Human (*Homo sapiens*)}
DSLVLYNRVAVQGDVVRELKAKKAPKEDVAAVKQLLSLKAEYKEKTGQEYKPGNPP
>d2hp8_ a.17.1.1 (-) p8-MTCP1 {Human (*Homo sapiens*)}
MPQKDPCKQKQACEIQKCLQANSYMESKCQAVIQELRKCCAQYPKGRSVVCSGFEKEEEENLTKSASK
>d1jxa_ a.141.1.1 (A:) Secreted Frizzled-related protein 3 (SFRP-3;fzb) {Mouse (*Mus musculus*)}
AACCEPVRIPLCKSLPWEMTKMPNHLHSTQANAILAMEQFEGLLGTHCSPDLLFLCAMYAPICTIDFQHEPIPKCSVCERARQGCEPILIKYRHSW
PESLACDELVPYDRGVCISPEAIVTAD
>d1jya_ a.141.1.1 (A:) Frizzled 8 (FZ8) {Mouse (*Mus musculus*)}
ELACQEITVPLCKGIGYEYTYMPNQFNHDTQDEAGLEVHQFWPLVEIQCSPDLKFFLCMYTPICLEDYKKPLPPCRSVCKERAKAGCAPLMRQYGFA
WPDRMRCDRLPEQGNPDTCMDYER
>d2end_ a.18.1.1 (-) T4 endonuclease V {Bacteriophage T4 (*Escherichia coli*)}
TRINLTLSQELADQHLMAYRELPRVFGAVRKHVANGKRVRDFKISPTFILGAGHVTFFYDKLEFLRKQRQIELIAECLKRGFNIKDTTVQDISDIPQEFRG
DYIPHEASIAISQARLDEKIAQRPTWYKYYGKAIYA
>d2lisa_ a.19.1.1 (A:) Lysin {Red abalone (*Haliotis rufescens*)}
HYVEPKFLNKAFFEVALKVQIIAGFDRLGVKWLRLVHGRTLSTVQKKALYFVNRRYMQTHWANYMLWINKKIDALGRTPVVGDYTRLGAEIGRRVDMVFFYNFL
YFYDFLKDKNMIPKYLPMEEINRMRPADPVVKYM
>d3lyna_ a.19.1.1 (A:) Lysin {Green abalone (*Haliotis fulgens*)}
INKAYEVMTKIQIISGFDRQLTAWLRLVHGRRLTNNQKTLFFVNRRYMQTHWQNYMLWVKRKIKALGRPAAVGDYTRLGAEIGRRVDMVFFYNFL
SGRKMIIPPSSAYMAKLNALRPADPVVK
>d1gaka_ a.19.1.1 (A:) SP18 {Abalone (*Haliotis fulgens*)}
FDDVVVSQRQEWSYVQRGMVNFLDEEMHKLVKRFRDMRWNLPGFVFLLKKVNRRMRYCMDYARYSKKILQLKHLPVNKTLKMGRFVGYR
NYGVIRELYADVFRDVQGFRGPKMTAAMRKYSSKDPGTFCCKNE
>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*)}
PSPIIKFPGDVAPKTDKELAVQYLNTFYGCPKESCNLFVLKDTLKKMQKFFGLPQTGDLQNTIETMRKPRCGNPDV
>d1slm_1 a.20.1.2 (16-80) Stromelysin-1 (MMP-3) {Human (*Homo sapiens*), fibroblast}
LVQKYLENYYDLKKDVQFVRRKDSGPVVKKIREMQKFLGLEVTGKLDSDTLEVMRKPRCGVPDV
>d1aab_ a.21.1.1 (-) HMG1, domains A and B {Rat (*Rattus norvegicus*)}
GKGDPKKPRGKMSYYAFFVQTSREEHKKHPDASVNFSKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTYIPPKGE
>d1ckta_ a.21.1.1 (A:) HMG1, domains A and B {Rat (*Rattus norvegicus*)}
KPRGKMSYYAFFVQTCREEHKKHPDASVNFSKCSERWKTMSAKEKGKFEDMAKADKARYEREMKTY
>d1hme_ a.21.1.1 (-) HMG1, domains A and B {Rat (*Rattus norvegicus*)}
FKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGKPDA
>d1hsm_ a.21.1.1 (-) HMG1, domains A and B {Hamster (*Cricetulus griseus*)}
NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKDIAAYRAKGKPDA
>d1qrva_ a.21.1.1 (A:) HMG-D {Drosophila melanogaster}
SDKPKRPLSAYMLWLNSARESIKRENPGIKVTEAKRGELWRAMKDSEWEAKAKDDYDRAVKEFEANG
>d1cg7a_ a.21.1.1 (A:) NHP6a {Baker's yeast (*Saccharomyces cerevisiae*)}
MVTPREPKKRTTRKKDPNAPKRALSAYMFANENRDIVSENPDITFGQVGKKLGEKWKALTPEEKQPYEAKAQADKKRYESEKELYNATLA

>d1hrza_a.21.1.1 (A:) SRY {Human (Homo sapiens)}

DRVKRPMMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKPWFQEAQKLQAMHREKYPNYKVR

>d1j46a_a.21.1.1 (A:) SRY {Human (Homo sapiens)}

MQDRVKRPMMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKPWFQEAQKLQAMHREKYPNYKVRPQQAKMLPK

>d1i11a_a.21.1.1 (A:) Sox-5 {Mouse (Mus musculus)}

PHIKRPMNAFMVWAKDERRKILQAFPDHMNSNISKILGSRWKAMTNLEKQPYYEEQARLSKQHLEKYPDY

>d2lef_a.21.1.1 (A:) Lymphoid enhancer-binding factor, LEF1 {Mouse (Mus musculus)}

MHIKKPLNAFMLYMKEMRANVAESTLKESAINQILGRRWHALSREEQAKYYELARKERQLHMQLYPGWSARDNYGKKKRKREK

>d1k99a_a.21.1.1 (A:) Upstream binding factor, the first HMG box {Human (Homo sapiens)}

MKKLKKHPDFPKPLTPYFRFFMEKRAKYAKLHPEMSNLDLKILSKYKELPEKKMKYIQDFQREKQEERNLARFREDHPDLIQNAKK

>d1eqza_a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus), erythrocytes}

SGRKQGGKARAKAKSRSSRAGLQFPVGRVHRLRKGNYAERVGAGAPVYLAALVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPK

>d1hioa_a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus), erythrocytes}

KSRSSRAGLQFPVGRVHRLRKGNYAERVGAGAPVYLAALVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLP

>d1hq3a_a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus), erythrocytes}

KAKSRSSRAGLQFPVGRVHRLRKGNYAERVGAGAPVYLAALVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPK

>d1aoic_a.22.1.1 (C:) Histone H2A {African clawed frog (Xenopus laevis)}

GKQGGKTRAKAKTRSSRAGLQFPVGRVHRLRKGNYAERVGAGAPVYLAALVLEYLTAEILELAGNAARDNKKTRIIPRHLQLAVRNDEELNKLLGRTVIAQGGVLPNIQSVLLPK

>d1f66c_a.22.1.1 (C:) Histone H2A {Human (Homo sapiens), variant H2A.Z}

AVSRQRAGLQFPVGRIRHRLKSRTTSHGRVGATAAVYSAILEYLTAEVLELAGNASKDLVKRITPRHLQLAIRGDEELDSLIKATIAGGGVIPHIHKSLI

>d1id3c_a.22.1.1 (C:) Histone H2A {Baker's yeast (Saccharomyces cerevisiae), H2A.1}

QSRSAKAGLTFPVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAAEILELAGNAARDNKKTRIIPRHLQLAIRNDDDELNLKGNTIAQGGVLPNIHQNLLPKKSAKAT

>d1eqzb_a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus), erythrocytes}

VTKTQKKGDKKRKKSRKESYSIYVYKVLQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAUTKHTSSVTKYTSSK

>d1hiob_a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus), erythrocytes}

SYISIYVYKVLQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAUTKHTSS

>d1hq3b_a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus), erythrocytes}

RKESYSIYVYKVLQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAUTKHTSS

>d1aoid_a.22.1.1 (D:) Histone H2B {African clawed frog (Xenopus laevis)}

KKRRKTRKESYSIYVYKVLQVHPDTGISSKAMSIMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAUTKHTSSAK

>d1id3d_a.22.1.1 (D:) Histone H2B {Baker's yeast (Saccharomyces cerevisiae), H2B.2}

RKETYSSYIYVYKVLQTHPDTGISQKSMSILNSFVNDIFERIATEASKLAAYNKKSTISREIQTAVRLLLPGELAKHAVSEGTRAVTKYSSST

>d1eqzc_a.22.1.1 (C:) Histone H3 {Chicken (Gallus gallus), erythrocytes}

APATGGVKKPHRYRPGTVALREIRRQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCIAIHAKRVTIMPKDIQLARRGERA

>d1eqzg_a.22.1.1 (G:) Histone H3 {Chicken (Gallus gallus), erythrocytes}

PRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCIAIHAKRVTIMPKDIQLARRGERA

>d1hq3c_a.22.1.1 (C:) Histone H3 {Chicken (Gallus gallus), erythrocytes}
YRP GTVALREIRRYQKSTELLIRKL PQR LREIAQDFKTDLRFQSSA VMA LQEASEAYLVGLFEDTNLC IAHAKRV TIMP KDIQLARR IRGERA
>d1id3a_a.22.1.1 (A:) Histone H3 {Baker's yeast (Saccharomyces cerevisiae)}
PHRYKPGTVALREIRRFQKSTELLIRKL PQR LREIAQDFKTDLRFQSSAIGALQESVEA YLVSLFEDTNLAIIHAKRV TIQKKEIKLARR LRGER
>d1eqzh_a.22.1.1 (H:) Histone H4 {Chicken (Gallus gallus), erythrocytes}
KGLGKGGAKRHRKVLRDN IQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFL ENVIRDAV TYTEHAKRKT VTAMDVVYALKRQGRTLYGFGG
>d1hq3d_a.22.1.1 (D:) Histone H4 {Chicken (Gallus gallus), erythrocytes}
KVL RDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFL ENVIRDAV TYTEHAKRKT VTAMDVVYALKRQGRTLYGFGG
>d1id3b_a.22.1.1 (B:) Histone H4 {Baker's yeast (Saccharomyces cerevisiae)}
DNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKS FLESVIRD SVTYTEHAKRKT VTSDL DVYALKRQGRTLYGFGG
>d1b67a_a.22.1.2 (A:) Archaeal histone {Archaeon Methanothermus fervidus, histone A}
GELPIAPIGRIK NAGAER VSDDARIALAKVLEEMGEEIA SEAVKLAKHAGRKT IKAEDI EILARKMFK
>d1a7w_a.22.1.2 (-) Archaeal histone {Archaeon Methanothermus fervidus, histone B}
MELPIAPIGRIKDAGAER VSDDARITLAKILEEMGRDIA SEAI KLA RHAGRKT IKAEDI ELAVRRFK
>d1f1ea_a.22.1.2 (A:) Archaeal histone {Archaeon Methanopyrus kandleri}
ELPKAAIERIFRQGIGERRLSQDAKDTIYDFVPTMAEYVANA AKSVLDAS GKKTMEEHLKALADV LMVEGV EYDGELFGRATV RRIK RAGIERAS
SDAVDLYNKLC RATEELGEKAAEYADE DGRKT VQGEDV EKAITYSMPKGEL
>d1tafa_a.22.1.3 (A:) TAF(II)42 {Fruit fly (Drosophila melanogaster)}
PKDAQVIMSILKELNVQ EYEP RVVNQLLEFTFRYVTSILDDAKVYANHARKKTIDL DDVRLATEVTLD
>d1tafb_a.22.1.3 (B:) TAF(II)62 {Fruit fly (Drosophila melanogaster)}
MLYGSSISAESMKVIAESIGVGSLSDAAKELAEDVSIKLKRIVQDAAKFMNHAKRQKLSVRDIDMSLK
>d1bh9a_a.22.1.3 (A:) TAF(II)18 {Human (Homo sapiens)}
LFSKELRCMMYGF GDDQNP YTESVDILEDVIEFIT EMTHKAMSI
>d1bh9b_a.22.1.3 (B:) TAF(II)28 {Human (Homo sapiens)}
FSEEQLNRYEMYRRSAFPKAAIKRLIQSITGTSVS QNVVIAMSGISKVFVGEVVEALDVCEKW GEMPLQPKHMREAVR RLKSKGQIP
>d1jfia_a.22.1.3 (A:) Negative cofactor 2, NC2, alpha chain {Human (Homo sapiens)}
ARFPPARIKKIMQTDEEIGKVA AVPVII SRAELFLESLLKKACQV TQS RNAK TMTSHLKQCIE
>d1jfib_a.22.1.3 (B:) Negative cofactor 2, NC2, beta chain {Human (Homo sapiens)}
DDLTIPRAAIN KMIKETLPN VRVANDAREL VNCCTEFIHLISSEANEICNKSEKKTISPEHVIQALESLGFGSYISEVKEV LQECKTVALK RRKASSRLENL
GIPEEELLRQQQELFAKARQQQAELAQ QEWLQ
>d1fpoa2_a.23.1.1 (A:77-171) HSC20 (HSCB), C-terminal oligomerisation domain {Escherichia coli}
FDLASEQHTVRDT AFLMEQ LREELDEEQAKDEARLESFIKRVKKMF DTRHQLMVEQLDNETW DAAADCRKL RFLDKL RSSAEQ LEEKLLDF
>d1eexg_a.23.2.1 (G:) Diol dehydratase, gamma subunit {Klebsiella oxytoca}
SARVSDYPLANKHPEWVKTATNKLDDFTL ENVLSNKVTAQDMRITP ETLRLQ ASIAK DAGRDR LAMNFERAA ELTAVPDDR ILEIYNALRPYRSTKE
ELLAIAADDLESRYQAKICAAFVREAATLYVERKKLGDD
>d1mtyg_a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit {Methylococcus capsulatus}
LGIHSNDTRDAWVN KIAHVNTLEKAAEMLKQFRMDH TTPFRNSYELDNDYLWIEAKLEEKVAVL KARAFNEVDFRH KTA FGEDA KS VLDGT VAKM
NAAKDKWEAEKI HIGFRQAYKPPIMPV NYFLDGERQLGTRLMELRNLYD TPLEELRK QRG VRV VH
>d1mhyg_a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit {Methylosinus trichosporium}
AKREPIHD NSIRTEWEAKIAK L TSVDQATKFIQDFR LAYTSPFRK SYD IDVYQYIERKIEEKLSVLK TEKLPVADL ITKATTG EDAA VEA TWIA KIAA KS
KYEAEAIHIEFRQLYKPPVLPVN VFLRTDA ALGTVLMEIRNTDYYGTPLEGLRK ERGVKVLHLQ
>d1om2a_a.23.4.1 (A:) Mitochondrial import receptor subunit Tom20 {Rat (Rattus norvegicus)}
RAGLSKLPDLKDAEAVQKFFLEEQLGEELLAQGDYEGV DHLTN AIAVCGQPQQLLQVLQ QTLP PPPFQMLLTKLPTISQRIVSAQSLGEDDVE
>d1jw2a_a.23.5.1 (A:) Hemolysin expression modulating protein HHA {Escherichia coli}

MSEKPLTKTDYLMRLRCQTIDTLERVIEKNKYELSDNELAVFYSAADHRLAELTMNKLYDKIPSSVW/KFIR
>d1fnf__ a.24.1.1 (-) Apolipoprotein E3 {Human (Homo sapiens)}
GQRWELALGRFWDYLRWVQTLSEQVQEELLSSQVTQELRALMDETMKEALKAYKSELEEQLTPVAEETRARLSKELQAAQARLGADMEDVCGLVQ
YRGEVQAMLGQSTEELRVRLASHLRKLKRLLRDADDLQKRLAVYQA
>d2asr__ a.24.2.1 (-) Aspartate receptor, ligand-binding domain {Escherichia coli}
KSFVVSNLREQQQELSTWDMLQTRINLSRSAVRMMMDSSNQQSNAKVELLDARKTLAQAAATHYKKFKSMAPLPEMVATSRNIDEKYKNYYT
ALTELEIDYLDYGNNTGAYFAQPTQGMQNAMEGERFAQYALSSEKLYRDI
>d1vta_ a.24.2.1 (A:) Aspartate receptor, ligand-binding domain {Salmonella typhimurium}
GFVISNELRQQQSELSTWDMLQTRINLSRSAARMMMDASNQQSSAKTDLQNAKTTLAQAAAHYANFKNMTPLPAMAESANVDEKYQRYQ
AALAEIQFLDNGNMDAYFAQPTQGMQNALGEALGNYARVSENLYRQTF
>d2liga_ a.24.2.1 (A:) Aspartate receptor, ligand-binding domain {Salmonella typhimurium}
MGGLLFSSLQHCQQGVISNELRQQQSELSTWDMLQTRINLSRSAARMMMDASNQQSSAKTDLQNAKTTLAQAAAHYANFKNMTPLPAM
AEASANVDEKYQRYQAALAEIQFLDNGNMDAYFAQPTQGMQNALGEALGNYARVSENLYRQTFD
>d256ba_ a.24.3.1 (A:) Cytochrome b562 {Escherichia coli}
ADLEDNMETLNDNLVIEKADNAAQVKDALTMRAAALDAQKATPPKLEDKSPDSPEMKDFRHGFDILVGQIDDALKLANEGKVKEAQAAAQLK
TTRNAYHQKYR
>d2ccya_ a.24.3.2 (A:) Cytochrome c' {Rhodospirillum molischianum}
QSKPEDLLKLRQGLMQTLKSQWVPIAGFAAGKADLPADAQRAENMAMVAKLAPIGWAKGTEALPGETKPEAFGSKSAEFLGWKALATESTKL
AAAAAKAGPDALKQAQAAATGKVCKACHEEFKQD
>d1bbha_ a.24.3.2 (A:) Cytochrome c' {Chromatium vinosum}
AGLSPEEQIETRQAGYEFMGWNMGKIKANLEGEYNAAQVEAAANVIAAIANSGMGALYGPDTKNGDVKTRVKPEFFQNMEDVGKIAREFVG
AANTLAEVAATGEAEAVKTAFGDVGAAACKSCHEKYRAK
>d1e85a_ a.24.3.2 (A:) Cytochrome c' {Alcaligenes sp.}
EFAKPEDAVKYRQSALTLMASHFGRMTPVVKGQAPYDAAQIKANVEVLKTLALPWAAGPGTEGGDARPEIWSDAASFQKQQQAFQDNIVKLSA
AADAGDLDKLRAAFGDVGASCKACHDAYRK
>d1jafa_ a.24.3.2 (A:) Cytochrome c' {Rhodococcus gelatinosus}
QFQKPGDAIEYRQSAFTLIANHGRVAAMAQGKAPFDAKVAENIALVSTSLKLPLTAFGPGTDKGHGTEAKPAVWSDAAGFKAAADKFAAAVDKL
DAAGKTGDFAQIKAAVGETGGACKGCHDKFKE
>d1cpq__ a.24.3.2 (-) Cytochrome c' {Rhodobacter capsulatus}
ADTKVEAREAYFKSLGGSMKAMTGVAKFDAEAAKVEAAKLEKILATDVAPLFPAGTSSTDLPQTEAKAAIWANMDDFGAKGKAMHEAGGAV
IAAANAGDGAAGFAALQKLGTCACKHDDYREED
>d1a7va_ a.24.3.2 (A:) Cytochrome c' {Rhodopseudomonas palustris}
QTDVIAQRKAILKQMGEATKPIAAMLGEAKFDQAVVQSLAAIADDSKKLPALFPADSKTGGDTAALPKIWEDKAKFDDLFAKLAATAAQGTIK
DEASLKANIGGVLGNCNSCHDDFRAKKS
>d2hmza_ a.24.4.1 (A:) Hemerythrin {Sipunculid worm (Themiste dyscrita)}
GFPPIPDPYVWDPDFRTFYSIIDDEHKTLFNGIFHLAIDNNADNLGELRRCTGKHFLNEQQLMQASQYAGYAEHKKAHDDFIHKLDTWGDVTVAKN
WLVNHIKTIDFKYRGKI
>d1hrb__ a.24.4.1 (-) Hemerythrin {Phascolopsis gouldii}
GFPPIPDPYVWDPDFRTFYSIIDDEHKTLFNGIFHLAIDNNADNLGELRRCTGKHFLNEQVLMQASQYQFYDEHKKEHDGFINALDNWKGDVKWAKA
WLVNHIKTIDFKYKGKI
>d1i4ya_ a.24.4.1 (A:) Hemerythrin {Phascolopsis gouldii}
GFPPIPDPYVWDPDFRTFYSIIDDEHKTLFNGIFHLAIDNNADNLGELRRCTGKHFLNEQVLMQASQYQFYDEHKKEHETFIHALDNWKGDVKWAKS
WLVNHIKTIDFKYKGKI
>d2mhr__ a.24.4.1 (-) Myohemerythrin {Sipunculan worm (Themiste zostericola)}

GWEIPEPYVWDESFRVFYEQLDEEHKKIFKGIFDCIRDNSAPNLATLVVTTNHFTHEEAMMDAAKYSEVVPHKKMHKDFLEKIGGLSAPVDAKNV
DYCKEWLVNHIKGTDKYKGKL

>d1ei7a_a.24.5.1 (A:) Tobacco mosaic virus coat protein {Tobacco mosaic virus, vulgare strain}

SYSITPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSEVWKPSHQVTRFPDSDFKVYRYNAVLDPVTALLGAFDTRNRIIEVEN
QANPTTAETLDATRRVDDATVAIRSAINNLIVEIRGTGSYNRSSFESSGLVWTSGPAT

>d1vtmp_a.24.5.1 (P:) Tobacco mosaic virus coat protein {Tobacco mosaic virus, vulgare strain}

PYTINSPSQFVYLSSAYADPVELINLCTNALGNQFQTQQARTTVQQFADAWKPSPVMTVRFPASDFYVYRYNSTLDPLITALLNSFDTRNRIIEVN
QPAPNTTEIVNATQRVDDATVAIRASINNLANELVRGTGMFNQAGFETASGLVWTTPAT

>d1cgme_a.24.5.1 (E:) Cucumber green mottle mosaic virus {Cucumber green mottle mosaic virus, strain watermelon}

AYNPITPSKLIASFASVYVVRTLLNFLVASQGTAFQTQAGRDSFRESLSALPSSVDINSRFPDAGFYAFLNGPVLRPIFVSLSSSTDTRNRVIEVVDPNSP
TTAESLNAVKRRTDDASTAARAEIDNLIESISKGFVDYDRASFEAFSVVWEATTSKA

>d1rmva_a.24.5.1 (A:) Ribgrass mosaic virus {Ribgrass mosaic virus}

SYNITNSNQYQYFAAVWAEPPTMLNQCVSALSQSYQTQAGRDTVRQQFANLSTIVAPNQRFPDTGFRVYVNSAVIKPLYEALMKSFDTRNRIETEE
ESRPASEVANATQRVDDATVAIRSQIQLLNELSNGHGYMNRAEFEAILPWTTAPAT

>d3fapb_a.24.7.1 (B:) FKBP12-rapamycin-binding domain of FKBP-rapamycin-associated protein (FRAP) {Human (Homo sapiens)}

VAILWHEMWHEGLEASRLYFGERNVKGMFEVLEPLHAMMERGPQLKETSFNQAYGRDLMEAQEWCRKYMKGNSNVKDLTQAQDWLYHVFRRI
S

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

LRVQPEAQAKVDFREDLCTKTENLLGSYFPKKISELDAFLKEPALNEANLSNLKAPLDIXAVNCNEKIVVLLQLRKPEIKDVIEQLNLVTTWLQLQIPRIE
DGNNFGVAVQEKFELMTSLHTKLEGFTQISKYFSERGDAVTKAAKQPHVGDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKNFEKLKKPR
G

>d1dova_a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}

ESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCSSVKRGNMVRAARALLSAVTRLLIADMDVYKLLVQLKVEDGILKLRNAGNEQDLGIQYK
ALKPEVDKLNIMAAKRQQELKDVGNDQMAARGILQKNVPILYTAQSACLQHPDVAAYKANRDLIYKQLQQAVTGISNAAQAT

>d1dowa_a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}

KAHVLAASVEQATENFLEKGDKIAKESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCSSVKRGNMVRAARALLSAVTRLLIADMDVYKLLVQ
LKVEDGILKLRNAGNEQDLGIQYKALKPEVDKLNIMAAKRQQELKDVGNDQMAARGILQKNVPILYTAQSACLQHPDVAAYKANRDLIYKQLQ
QAVTGISNAAQAT

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

DLRRQLRKAVMDHVSFSLETNPVLLVIEAKNGNEKEVKEYAQVFREHANKLIEVANLACSISSNEEVKLVRMSASQLEALCPQVINAALALA
PQSKLAQENMDLFKEQWEEKQVRVLTDAVDDITS

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

IDDFLAVSENHILEDVNKCIALQEKDVGDLRTAGAIRGRAARVIHVTSEMDNYEPGVYTEKYLEATKLLNTVMPPRFTEQVEAAVEALSSDPAQP
MDNEFIDASRLVYDGIRDIRKAVLM

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

DSFLETNVPLLVIEAKNGNEKEVKEYAQVFREHANKLIEVANLACSISSNEEVKLVRMSASQLEALCPQVINAALALA
PQSKLAQENMDLFKEQWEEKQVRVLTDAVDDITS

>d1qkra_a.24.9.1 (A:) Vinculin {Chicken (Gallus gallus)}

KDEEFPEQKAGEAINOPMMMAARQLHDEARKWSSKGNDIIAAKRMALLMAEMSRLVRGGSGNKRALIQCAKDIASKDEVTRLAKEVAKQCT
DKRIRTNLLQVCERIPTISQLKILSTVKATMLGRTNISDEESEQATEMLVHNQNLMQSVKETVREA
AASIIRTDAFTLWRVVK
>d1k04a_a.24.14.1 (A:) FAT domain of focal adhesion kinase {Human (Homo sapiens)}

EISPPPTANLDRSNDKVYENVTGLVKAVIEMSSKIQPAPPEYVPMVKEVGLALRTLLATVDEIPLL
PASTHREIEMAQKLLNSDLGELINKMKLAQQY
VMTSLQQEYKKQMLTAAHALAVDAKNLLVIDQARLKMLGQT

>d1k40a_a.24.14.1 (A:) FAT domain of focal adhesion kinase {Mouse (Mus musculus)}

NDKVYENVTLVKAIVIEMSSKIQPAPPEEYVPMVKEVGLALRTLLATVDETIPALPASTHREIEMAQKLLNSDLGELISKMKLAQQYVMTSLQQEYKK
QMLTAAHALAVDAKNLLVIDQARLKML

>d2a0b__ a.24.10.1 (-) Aerobic respiration control sensor protein, ArcB {Escherichia coli}

SKSEALLDIPMLEQYLEVGPKLITDGLAVFEKMMPGYVSLESNLTAQDKKGIVEEGHKIKGAAGSVGLRHLQQLGQQIQSPDLPAWEDNVGEWIE
EMKEEWHRHDVEVLKAWAKAT

>d1c02a_ a.24.10.2 (A:) Phosphorelay protein ypd1 {Baker's yeast (Saccharomyces cerevisiae)}

STIPSEIIINWILNEIISMDDDDSFSKGLIIFIDQAQTTFAQMQRQLDGEKNLTELDNLGHFLGSSAALGLQRIAWVCERIQNLGRKMHQFFPNK
TELVNTLSDKSIINGINIDEDEEIKIQVDDKDENSILYLIAKALNQSRLEFKLARIELSYYNTNL

>d1i5na_ a.24.10.3 (A:) Chemotaxis protein CheA P1 domain {Salmonella typhimurium}

DISDFYQTFFDEADELLADMEQHLLDVPEPDAEQLNAIFRAAHSIKGGAGTFGFTILQETTHLMENLDEARRGEMQLNTDIINLFLETKDIMSEQ
LDAYKNSEEPDAASFYICNALRQLALEAK

>d1he1a_ a.24.11.1 (A:) ExoS toxin {Pseudomonas aeruginosa}

ASSAVVFQMVVLQQALPMTLKGDKASELATLTPEGLAREHSRLASGDGALRSISTLAGIRAGSQVEESRIQAGRLLERSIGGIALQQWGTTGGAAS
QLVLDASPELRREITDQLHQVMSEVALLRQAVESEVS

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

SKQPLLDIALKGLKRTLQPQEYMDGNSLRENQEMASGNGPLRSIMTNLQNLNKIPEAKQLNDYVTTLNIQVGVARFSQWGTGGEVERWVDKA
STHELTQAVKKIHVIAKELKNVTAEELEKIEAGAPM

>d1hy5a_ a.24.11.1 (A:) YopE {Yersinia pestis}

TSFSDSIKQLAAETLPKYMQQLNLSDAEMLQKNHDQFATGSGPLGSITQCQGLMQFCGELQAEASAILNTPCGIPFSQWGTIGGAASAYVASG
VDLTQAANEIKGLAQQMVKLLSM

>d1f1ma_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}

PNLTEISKKITESNAVVLAVKEVETLLSIDEALAKIGKKIKSDVSLDNEADHNGSLMSGAYLISTLTKKISAIKDSGELKAEIEKAKKCSEFTAKLKGEHTD
LGKEGVTDNAKKAILKTNNDKTGAADEKLFEVKNLKAAKEMLTNSVKELTSP

>d1g5za_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}

PNLTEISKKITESNAVVLAVKEVETLLASIDEATKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNLKNEELKEKIDTAKQCSTEFNKLSEHA
VLGLDNLTDDNAQRAILKKHANKDKGAAELEKLFKAVENLSKAAQDTLKNNAVKELTSPIVA

>d1ggqa_ a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}

GPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGDTENNHNHSLLAGAYAISTLIKQKLDGLKNEGLKEKIDAACKCSETFTNKLKE
KHTDLGKEGVTDADAKEAILKNTGKGAELGKLFEVVKNLKAAKEMLANSVKELTS

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

MFQQQLSARLQEAIGRLRGRGRITEEDLKATLREIRRALMDADVNLLEVARDFVERVREEALGKQVLESITPAEVILATVYEALKEALGG

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

LLDNLRLDTVRKFLTGSYYDKAVEDFIKELQKSLISADVNVKLVFSLTNKKERLKNEKPPTYIERREWFIKIVYDELSNLFGG

>d1fts_1 a.24.13.1 (201-284) Signal recognition particle receptor, FtsY {Escherichia coli}

RSLLKTKENLGSFISLFRGKKIDDLFEELEEQLLIADVGVETRKIITNLTEGASRKQLRDAEALYGLLKEEMGEILAKVDE

>d1jr8a_ a.24.15.1 (A:) Thiol oxidase Erv2p {Baker's yeast (Saccharomyces cerevisiae)}

DDKVKEVGRASWKYFHTLLARFPDEPTPEEREKLHTFIGLYAELYPCGECSYHFVKLIEKYPVQTSSRTAAAMWGCHIHNKVNEYLKKDIYDCATILED
YDCGC

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

GAMEKFKTLLYDIPCMEVSEEIISYAKLQLGKKLNDIYVSLTDHINFAIQRNQKGDIKNALLWETKRLYKDEFAIGKEALVMVKNKTGVSLPEDEAG
FIALHIVNAELNEE

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

MPNIINITKVMEEILSIVKYHFKIEFNEESLHYYRFVTDLKFFAQRLFNGTHMESEDDFLLDTVKEKYHRAYECTKKIQTYIEREYEHKLTSDELLYLTIDIER
VVK

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

MKSLKGSRTEKNILTAFAGESQARNRYNYFGGQAKKDGFVQISDIFAETADQEREHAKRLFLEGGLDEIVAAFPAGIIADTHANLIASAAGEHHEYTEMYPSFARIAREEGYEEIARVFASIAVAEEFHKEKFLDFARNIKEGRV

>d1bcfa_a.25.1.1 (A:) Bacterioferritin (cytochrome b1) {Escherichia coli}

MKGDTKVINYLNKLLGNELVAINQYFLHARMFKNWGLKRLNDVEYHESIDEMKHADRYIERILFLEGLPNLQDLGKLNIGEDVEEMLRSDLALELDGAKNLREAIGYADSVHDYVSRDMMIEILRDEEGHIDWLETLDLIQKMGLQNYLQAQIREEG

>d1jgca_a.25.1.1 (A:) Bacterioferritin (cytochrome b1) {Rhodobacter capsulatus}

MKGDAKVIIEFLNAALRSELTAISQYWVHFRLQEDWGLAKMAKSREESIEEMGHADKIIARILFLEGHPNLQKLDPLRIGEGPRETLECDLAGEHDALKLYREADYCAEVGDIVSKNIFESLTDIEEGHVDLFLETQISLYDRLGPQGFALLNAAPMDAA

>d1euma_a.25.1.1 (A:) Non-hem ferritin {Escherichia coli, ecFtnA}

LKPEMIEKLNEQMNLLEYSSLLYQQMSAWCSYHTFEGAAAFLRRHAQEEMTHMQRLFDYLTDTGNLPRINTVESPAEYSSLDEFQETYKHEQLITQKINELAHAAMTNQDYPTFNFLQWVYSEQHEEEKLFSIIDKLSLAGKSGEGLYFIDKELSTLD

>d1krqa_a.25.1.1 (A:) Non-hem ferritin {Campylobacter jejuni}

MLSKEVVKLLNEQINKEMYAANLYLSMSSWCYENSLSGAGAFLFAHASEESDHAKKLITYLNETDSHVELQEVVKQPEQNFKSLLDVFECTYEHEQFITKSINTLVEHMILTHKDYSTFNFLQWVYSEQHEEEALFRGIVDKKLIGEHNGNLYLADQYIKNIALSR

>d1dpsa_a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Escherichia coli}

SKATNLLYTRNDVSDSEKKATVELNRQVIQFIDLSSLTKQAHWNMRGANFIAVHEMLGFRITALIDHLDTMERAVALGGVALGTTQVINSKPLKSYPLDIHNVQDHLKELADRYAIVANDVRKAIGEAKDDDTADILTAASRDLKFLWFIECNIE

>d1qgha_a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Listeria innocua}

VDTKEFLNHQVANLVNFTVKIHQIHWYMRGHNFFTLHEKMDDLYSEFGEQMDEVAERLLAIGGSPFSTLKEFLENASVEEAPYTKPKTMDQLMEDLVGTLELLRDEYKQGIELTDKEGDDVTNDMLIAFKASIDKHIWMFKAFLGKAPLE

>d2fha_a.25.1.1 (-) (Apo)ferritin {Human (Homo sapiens), H chain}

TSQVRQNYHQDSEAINRQINLELYASYVLSMSYYFDRDDVALKNFAKYFLHQSHEREHAEKLMLQNLQRGGRIFLQDIQKPDCCDWESGLNAMECALHLEKNVNQSLLEHKLATDKNDPHLCDFIETHYLNEQVKAIKELGDHVTNLRKGMPESGLAEYLFDKHTLG

>d1aew_a.25.1.1 (-) (Apo)ferritin {Horse (Equus caballus), L chain}

SQIRQNYSTEAAVNRLVNLHRSAYTYSLGFYFDRDDVALEGVCHFFRELAEKREGAERLLKMQNQRGGRALFQDLQKPSQDEWGTPDAMKAAIVLEKSLNQALLDLHALGSAQADPHLCDFLESHFLDEEVKLIKMGDHLTNIQRLVGSQAGLGEYLFERLTL

>d1h96a_a.25.1.1 (A:) (Apo)ferritin {Mouse (Mus musculus)}

TSQIRQNYSTEVEAAVNRLVNLHRSAYTYSLGFFFDRDDVALEGVGHFFRELAEKREGAERLLEFQNDRGGRALFQDVQKPSQDEWGKTQEAMEAAALAMEKLNQALLDLHALGSARADPHLCDFLESHYLDKEVKLIKMGHNLTNLRRVAGPQPAQTGAPQGSLGEYLFERLTL

>d1bg7_a.25.1.1 (-) (Apo)ferritin {Bullfrog (Rana catesbeiana)}

DSQVRQNFHRDCEAAINRMVNMLEYASYTYLSMAFYFDRDDIALHNVAFFKEQSHEEREHAEKLMDQNKRGGRIVLQDVQKPERDEWGNTLEAMQAALQLEKTVNQALLDLHKVGSDKVDPHLCDFLETEYPEEQVKSICKQLGDYITNLKRLGLPQNGMGEYLFDKHTMGE

>d1mfra_a.25.1.1 (A:) (Apo)ferritin {Bullfrog (Rana catesbeiana)}

VSQVRQNYHSDCEAAVNRLNLELYASYTYSSMYAFFDRDDVALHNVAEFFKEHSHEEREHAEKFMKYQNKRGGRVVLQDIKKPERDEWGNTLEAMQAALQLEKTVNQALLDLHKLATDKVDPHLCDFLESEYLEEQQVKDIKRIGDFITNLKRLGLPENGGMGEYLFDKHHSV

>d1rcd_a.25.1.1 (-) (Apo)ferritin {Bullfrog (Rana catesbeiana)}

SQVRQNFHQDCEAGLNRVTNLKFHSSYYLSMASYFNRRDVALNSNFAKFFRERSEEKEHAEKLIYEQNQRGGRVFLQSVEKPERDDWANGLEALQTALKLQKSVNQALLDLHAVAADKSDPHMTDFLESPTYLSESvetiklgdhitlkkllwsshpmaeylfnkhtlg

>d1mtyb_a.25.1.2 (B:) Methane monooxygenase hydrolase, beta and alpha subunits {Methylococcus capsulatus}

ERRRGLTDPEMAAVILKALPEAPLDGNMKMGYFVTPRWRKLTEYEALTVYQPNADWIAGGLWDWTQKFHGRPSWGNETTELRTVDWFKHRDPLRWHAPYVKDAAEWRYTDRFLQGYSADGQIRAMNPTRDEFINRYWGAFLNEYGLFNAHSQGAREALSDVTRVSLAFWGFDKIDIAQMIQLERGFIAVPGFDESTAVPKAEWTNGEVYKSARLAVERGLWQEVFDWNESAFAVHAYDALFGQFVRREFFQRLAPRFGDNLTFFINQAQTYFQIAKQGVQDLYYNNCLGDDPEFSDYNRTVMRNWTGKLEPTIAALRDFMGLFAKLPAGTTDKEEITASLYRVDDWIEDYASRIDFKADRDQIVKAV

LAGLK

>d1mtyd_a.25.1.2 (D:) Methane monooxygenase hydrolase, beta and alpha subunits {Methylococcus capsulatus}

AANRAPTSVNAQEVRWLQSFNWDKFKNRTKYKMANETKEQFKLIAKEYARMEAVKDERQFGLSQLVALTRLNAGVRVHPKWNETMKVVS
NFLEVGEYNAIAATGMLWDSAQAAEQKNGYLAQVLDEIRHTHQCAYVNYYFAKNGQDPAGHNDARRRTIGPLWKGMKRVFSDGFISGDAVECS
LNQLVLGEACFTNPLIVAVTEWAANGDEITPTVFLSIEITDELRHMANGYQTUVSIANDPASAKYLNTDLNNAFWTQQKYFTPVLGMLFEYGSKFKV
EPWVKTWDRWVYEDWGGIWIGRLGKYGVESPRSLKDAKQDAYWAHHDLYLLAYALWPTGFFRLALPDQEEMEWFANEYPGWYDHYGKIYEW
RARGCEDPSSGFIPLMWIFIENHPIYIDRSVQVFPCSLAKGASTLRVHEYNGEMHTFSDQWGERMIWLAEPERYECQNIFEQYEGRELSEVIAELH
GLRSDGKTLIAQPHVRGDKLWTLDIQLNCVFKNPVKAF

>d1mhyb_a.25.1.2 (B:) Methane monooxygenase hydrolase, beta and alpha subunits {Methylosinus trichosporium}

KRGLTDPERAAIIAAVPDHALDTQRKYHYFIQPRWKPLSEYEQLSCYAQPNDWIAGGLDWGDWTQKFHGRPSWGNESTELRTTDWYRHRDP
ARRWHHPYVKDKSEEARYTQRFLAAYSSEGSIRTIDPYWRDEILNKYFGALLYSEYGLNAHSSVGRDCLSDTIRQTAFAALDKVDNAQMIQMERLF
IAKLVPGFDASTDVPKKIWTTDPIYSGARATVQEIWQGVQDWNEILWAGHAVYDATFGQFARREFFQRLATVYGDTLTPFTAQSQTYFQTTRGAI
DLFVYCLANDSEFGAHLRTFLNAWTEHYLASSVAALKDFVGLYAKVEKAGATDSAGVSEALQRVFGDWKIDYADKIFRVDVDQKVDAVLAGY

>d1mhyd_a.25.1.2 (D:) Methane monooxygenase hydrolase, beta and alpha subunits {Methylosinus trichosporium}

NRAPVGVERPQEVKWLQSFNWDKFNRTKYHMANETKEQFKVIAKEYARMEAKDERQFGTLLDGLTRLGAGNKHPRWGETMKVISNF
LEVGEYNAIASAMLWDSATAAEQKNGYLAQVLDEIRHTHQCAFINHYSKHYHDPAHNDARRTRAIGPLWKGMKRVFADGFISGDAVECSVNL
QLVGEACFTNPLIVAVTEWASANGDEITPTVFLSVEDELRHMANGYQTUVSIANDPASAKFLNTDLNNAFWTQQKYFTPVLGMLFEYGSKFKVEPW
VKTWNRWVSEDWGGIWIGRLGKYGVESPRSLRDAKRDAYWAHHDLALAAVAMWPLGFARLALPDEEDQAWFEANEYPGWADHYGKIFNEWKKL
GYEDPKSGFIPYQWLLANGHDVYIDRVSQVFPISLAKGTGSLRVHEFNGKKHSLDDWGERQWLIEPERYECHNVFEQYEGRELSEVIAEGHGVR
DGKTLIAQPHTRGDNLWTLEDIKRAGCVFPDPLAKF

>d1jqca_a.25.1.2 (A:) Ribonucleotide reductase R2 {Escherichia coli}

AYTTFSQTKNDDQLKEPMFFGQPVNARYDQQKYDIFEKLIEQLSFFWRPEEVDSRDRIDYQALPEHEKHIFISNLKYQTLLDSIQGRSPNVALLPLISI
PELETWVETWAFSETIHRSYTHIIRNIVNDPSVVFDIVTNEQIQRKRAEGISSYYDELIEMTSYWHLLGEGHTVNGKTVTSLRELKKLYLCMSVN
ALEAIRFYVSFACSFAFAERELMEGNAKIRLARIARDEALHLTGTQHMLNLLRGADDPEMAEIAEECKQECYDLFVQAAQKEKDADYLFRDGSIMIGL
NKDILCQYVEYITNIRMQAVGLDPFQTRSNSPIPINTWLV

>d1r2fa_a.25.1.2 (A:) Ribonucleotide reductase R2 {Salmonella typhimurium}

ISAINWNKIQDDKDLEVWNRLTSNFWLPEKVPLSNIDIPAWQTLSAEQQLTIRVFTGLLTDIQNIAGAPSLMADAIPHEEAVLSNISFMEAVERHAR
SYSSIFSTLCQTKEVDAAYAWSEENPPLQRKAQILAHYVSDEPLKKKIASVFLSGFWLPMYFSSRGKLTNTADLIRLIIRDEAHGYYIGYKYQJA
LQKLSAIEREEELKLFALDLIMELYDNEIRYTEALYAETGWVNDVKAFLCYNANKALMNLGYEALFPPMADVNPAILAALSP

>d1kgna_a.25.1.2 (A:) Ribonucleotide reductase R2 {Corynebacterium ammoniagenes}

SNEYDEIANHTDPVKAINWNVIPDEKMLEVWDRITGNFWLPEKIPVSNDIQSWNKMTPEQLATMRVFTGLLTDIQGTVGAISSLPAETMHE
EAVYTNIAFMESVHAKSYSNIFMTLASTPQINEAFRWEENENLQRKAKIIMSYYNGDDPLKKVASTLLESFLYSGFWLPMYFSSRALKLTNTADIIRLII
RDESVHGYYIGYKYQQGVKKLSEAEQEEYKAYTFDLMYDLYENEIEYTEDIYDDLGWTEDVKRFLRYNANKALNNLGYEGLFPTDETKVSPAILSSL

>d1xsm_a.25.1.2 (-) Ribonucleotide reductase R2 {Mouse (Mus musculus)}

NPSVEDEPLLRENPRRFVVFPIEYHDIWQMYKKAEASFWTAAEVDSLKDQHWEALKPDERHFISHVLAFFAASDGIVNENLVERFSQEVTQVTEARC
FYGFQIAMENIHSEMSLLIDTYIKDPKEREYLNFNAITMPCKVKKADWALRWIGDKEATYGERVVAFAAAVEGIFSGSGFASIFWLKKRGLMPGLTSN
ELISRDEGLHCDFACLMFKHLVHKPAEQRVREIITNAVRIEQEFLTEALPVKLIGMNCLMKQYIEFVADRLMLELGFNKIFRVENPDFM

>d1jk0a_a.25.1.2 (A:) Ribonucleotide reductase R2 {Baker's yeast (Saccharomyces cerevisiae)}

LNKELETIREENRVKSMDLKEKLSKDAENHKAYLKSQVHRHKLKEMEKEPLLNEDKERTVLFPIKYHEIWQAYKRAEAASFWTAAEIDLSDKIDHWN
NRMNENERFFISRVLAFFAASDGIVNENLVENFSTEVQIPEAKSFYGFQIMIENIHSETYSLLIDTYIKDPKESEFLFNIAHTIPEIGEKAEWALRWIQLAD
ALFGERLVAFASIEGVFFSGSFASIFWLKKRGMMPGLTSNELICRDEGLHTDFACLLFAHLKNKPDPDAIVEKIVTEAVEIEQRYFLDALPVALLGMNADL
MNQYVEFVADRLVAFGNKKYYKVENPFDFMEN

>d1jk0b_a.25.1.2 (B:) Ribonucleotide reductase R2 {Baker's yeast (Saccharomyces cerevisiae)}

FQKERHDMKEAKDEILLMENSRRVMFPIKYHEIWAAYKKVEASFWTAAEIELAKDTEDFQKLTDQKTYIGNLLALSISSDNLVNKYLIENFSAQQLQ

NPEGKSFYGFQIMMENIYSEVYSMMVDAFFKDPKNIPLFKEIANLPEVKHKAAFIERWISNDDSLYAERLVAFAAKEGIFQAGNYASMFWLTDKKIM
PGLAMANRNICRDRGAYTDFSCLLFAHLRTKPNPKIIEKIITEAVEIEKEYNSLPVEKGMDLSIHTYIEFVADGLLQGFGNEKYY
>d1afra_a.25.1.2 (A:) delta 9-stearoyl-acyl carrier protein desaturase {Castor bean (*Ricinus communis*)}
MPPREVHVQVTHSMPPQKIEIFKSLDNWAEEENILVHLKPVEKCWQPQDFLPDPASDGFDEQVRELRERAKEIPDDYVVVLGDMITEALPTYQTM
LNTLDGVRDETGASPTSWAIWTRAWTAEENRHGDLLNKYLGRVDMRQIEKTIQYLIGSGMDPRTEENSPYLGFIYTSFQERATFISHGNTARQAK
EHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKSMPAHLMYDGRDDNLFDHFSAVAQR LGVTAKDYADILEFLVGRW
KVDKLTGLSAEGQKAQDYYCRLPPRIRLEERAQGRAKEAPTMPFSWIFDRQVKL
>d1rhga_a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF) {Human (*Homo sapiens*)}
LPQSFLLKCLEQVRKIQGDGAALQEKLCAKYKLCHPEELVLLGHSGIPWAPLSSCPSQLQLAGCLSQLHSGLFLYQGLLQALEGISPELGPLTLQLD
VADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHLQSFLEVSYRVLH LA
>d1bgc_a.26.1.1 (-) Granulocyte-colony stimulating factor (G-CSF) {Cow (*Bos taurus*)}
SLPQSFLLKCLEQVRKIQADGAEQLERLCAAHKLCPEELMLLRHSLGIPQAPLSSCSSQLQRGCLNQLHGGFLFLYQGLLQALAGISPELAPLDTLQ
LDVTDFA TNIWLQMEDLGAAPAVQPTQGAMPTFTSAFQRRAGGVLVASNLQSFLELAYRALRHFAK
>d1bgea_a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF) {Dog (*Canis familiaris*)}
PLPQSFLLKCLEQMRKVQADGTLQETLCATHQLCHPEELVLLGHALGIPQAPLSSCSSQLQLMGCLRQLHSGLFLYQGLLQALAGISPELAPLDTL
QLD TTDFAINIWQQMEDLGMAPAVPPTQGTMFTAFTSAFQRRAGGVLVASNLQSFLELAYRALRHFAK
>d1alu_a.26.1.1 (-) Interleukin-6 {Human (*Homo sapiens*)}
LTSSERIDKQIRYILDGISALRKETCNKSNMCESSKEALAENNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEVYLEYLQNRFESSEEQARAVQMST
KVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSFKEFLQSSLRALRQM
>d1i1rb_a.26.1.1 (B:) Interleukin-6 {Human herpesvirus 8, Kaposi's sarcoma herpes-virus}
EFEKDLLIQLRNWMWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAIN DTDHCGLIGFNETSCLKLADGFFEVLFKFLTTEFGKSVINV DVMELLTK
TLGWDI QEELNKLTKTHSPPKFDRG LQLK YWVRHFASFYVLSAMEK FAGQAVRVLDSIP
>d1a7m_a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (*Mus musculus*)}
SPLPITPVNATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEFPNNVEKLCAPNMTDFPSFHNGTEKTLVELYRMVAYLSASLTNITRDQKV
RDQKVLNP SAVSLHSKLNATIDVMRGLLS NVLCRLCNK YRVGHVDVPPVDPHSDKEVFQKKLGCQLLGTYKQVISVVQAF
>d1lki_a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (*Mus musculus*)}
NATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEFPNNVEKLCAPNMTDFPSFHNGTEKTLVELYRMVAYLSASLTNITRDQKV
PTAVSLQVKLNATIDVMRGLLS NVLCRLCNK YRVGHVDVPPVDPHSDKEVFQKKLGCQLLGTYKQVISVVQAF
>d1emra_a.26.1.1 (A:) Leukemia inhibitory factor (LIF) {Human (*Homo sapiens*)}
LMNQIRSQLAQLNGSANALFILYYTAQGEFPNNLEKLCGPVN TDFPPFHANGTEKAKLVELYRIVVYLGTS LGNITRDQKILNPSALS LHSKLNATADI
LRG LLSNVLCRLCSKYHVGHDVTVGPDTSGKDVFKKKLGCQLLGKYKQVISVLAQAF
>d1a22a_a.26.1.1 (A:) Growth hormone, somatotropin {Human (*Homo sapiens*)}
FPTIPLSRLFDNAMLRAHRLHQLAFDTYQE FEEAYIPKEQKYSFLQNPQTSLCFSEIPTPSNREETQQKS NLELLRISL LLIQS WLEPVQFLRSV
FANS LV
YGASDSNVYD LLDKLEERI QTLMGRLEGQIFKQTYAKFD TDALLKN YG LLYC FRKDM DKVETFLRIVQCRS VEGSCGF
>d1axia_a.26.1.1 (A:) Growth hormone, somatotropin {Human (*Homo sapiens*)}
TIPLSRLFDNAMLRAHRLHQLAFDTYQE FEEAYIPKEQKYSFLQNPQTSLCFSEIPTPSNREETQQKS NLELLRISL LLIQS WLEPVQFLRSV
FANS LV
ASDSNVYD LLDKLEERI QTLMGRLEGQIFKQTYAKFD TDALLKN YG LLYC FRKDM DKVETFLRIVQCRS VEGSCGF
>d1hgu_a.26.1.1 (-) Growth hormone, somatotropin {Human (*Homo sapiens*)}
PTIPLSRLFQNAMLRAHRLHQLAFDTYQE FEEAYIPKEQKYSFLQAPQASLCFSEIPTPSNREQAQQKS NLQ L RISL LLIQS WLEPVQFLRSV
FANS LV
YGASDSNVYD LLDKLEERI QTLMGRLEGQIFKQTYAKFD TDALLKN YG LLYC FRKDM DKVETFLRIVQCRS VEGSCGF
>d1huw_a.26.1.1 (-) Growth hormone, somatotropin {Human (*Homo sapiens*)}
FPTIPLSRLFDNAMLRAHRLHQLAFDTYQE FEEAYIPKEQKYSFLQAPQASLCFSEIPTPSNREETQQKS NLELLRISL LLIQS WLEPVQFLRSV
FANS LV
VGASDSNVYD LLDKLEERI QTLMGRLE ALLKN YG LLYC FNKDM SKVSTY RTVQCRS VEGSCGF
>d1f6fa_a.26.1.1 (A:) Placental lactogen {Sheep (*Ovis aries*)}

AQHPPYCRNQPGKQCIPQLSFLDRATTVANYNSKLAGEMVNRFDQEYQGGINSESKVINCHTSSITTPNSKAEAITEDKILFKLVISLLHSWDEPLHH
AVTELANSKGTPALLTKAQEIKEAKVLVDGVEVIQKRIPHGEKNEPYPVWSEQSSLTSQDENVRRAFYRLFCLHRDSSKIYTYLRLKCRLTSC
>d1cnt1_a.26.1.1 (1:) Ciliary neurotrophic factor (CNTF) {Human (Homo sapiens)}
PHRRDLCSRSIWLARKIRSDLTALTESYVKHQGLNKNINLDSADGMPVASTDQWSELTEAERLQENLQAYRTFHVLLARLLEDQQVHFPTEGDFHQ
AIHTLLLQVAFAQYQIEELMILLEYKIPRNEADGMPINVGGGLFEKKLWGLVQLQELSQWTVRSIHDLRFISSHQTGIP
>d1ax8_a.26.1.1 (-) Leptin (obesity protein) {Human (Homo sapiens)}
IQKVQDDDTKTLIKTIVTRINDISHTQSFSKQKVGTGLDFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRDLLHVLAFSKSCHLPEASGL
ETLDLGGVLEASGYSTEVALSRLQGSLOQMLWQLDLSPGC
>d1evsa_a.26.1.1 (A:) Oncostatin M {Human (Homo sapiens)}
GSCSKEYRVLLGQLQKQTDLMQDTSRLLDPYIRIQLDVPKLREHCRERPGAFPSEETLRLGLGRRGFLQTLNATLGCVLHRLADLEQRLPKAQDLERS
GLNIEDLEKLQMARPNIQLGRNNIYCMAQLLSDTAEPTKAGRASQPPTPTPASDAFQRKLEGCRFLHGYYHFRMHSGVRVFSKW
>d1f45b_a.26.1.1 (B:) Heterodimeric interleukin-12 alpha chain {Human (Homo sapiens)}
QNLLRAVSNMLQKARQTLFYPCTSEEIDHEDITKDSTVEACLPLETKNESCLNSRETTSFITNGSCLASRKTSFMMALCLSSIYEDLKMVQVEFKTM
NAKLLMDPKRQIFLDQNMILAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS
>d1eera_a.26.1.2 (A:) Erythropoietin {Human (Homo sapiens)}
APPRICDSRVLERYLLEAKEAKITTGCAEHCSLNEKITVPDTKVNFYAWKRMEVGQQAVEVWQGLALLSEAVLRGQALLVKSSQPWEPLQLHVDK
AVSGLRSLLRALGAQKEAISNSDAASAAPLRTITADTRKLFVYSNFLRGKLKLYTGEACRTGDR
>d2gmfa_a.26.1.2 (A:) Granulocyte-macrophage colony-stimulating factor (GM-CSF) {Human (Homo sapiens)}
RSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETEVISEMFDLQEPCTLQTRLELYKQGLRGSLLKGPLTMMASHYKQHCPPTPETSCATQII
TFESFKENLKDFLLVIPFDCWEP
>d1hzia_a.26.1.2 (A:) Interleukin-4 (IL-4) {Human (Homo sapiens)}
HKCDITLQAIKTLNSLTEQKTLCTELTVTDIFASKNTTEKETFCRAATVLRQFYSHHEKDTRCLGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCP
KEANQSTLENFLERLKTIMREKYSKCSS
>d1hula_a.26.1.2 (A:) Interleukin-5 {Human (Homo sapiens)}
IPTSALVKETLALLSTHRTLLIANETLRIPVPHKNHQLCTEEIFQGIGTLESQTVQGGTVERLFKNLSLIKYYDGQKKCGEERRRNQFLDYLQEFLGV
MNTEWI
>d1hmca_a.26.1.2 (A:) Macrophage colony-stimulating factor (M-CSF) {Human (Homo sapiens)}
SEYCSHMGSGHLQLQRLLIDSQMETSCQITFEVDQEQQLKDPVCYLKKAFLLVQDIMEDETMRFRDNTPNAAIVQLQELSLRKSCFTKDYEHDKA
CVRTFYETPLQLLEKVKNVFNETKNLLDKDWNIFSNCNNNSFAECSSQGH
>d1etea_a.26.1.2 (A:) Flt3 ligand {Human (Homo sapiens)}
TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDDELCGGLWRLVLAQRWMERLKTVAGSKMQLLERVNTEIHFTKCAFQPPPCLR
QTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP
>d1scfa_a.26.1.2 (A:) Stem cell factor, SCF {Human (Homo sapiens)}
NVKDVTKLVANLPKDYMITLKVVPGMDVLPSCWWISEMVVQLSDSLTLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKSFKSPEPRL
TPEEFFRIFNRSIDAFKDFVVASETSDCVVS
>d1scfc_a.26.1.2 (C:) Stem cell factor, SCF {Human (Homo sapiens)}
NVKDVTKLVANLPKDYMITLKVVPGMDVLPSCWWISEMVVQLSDSLTLLDKFSNISEGLSNYSIIDKLVNIVDDLVECVKENSSKDLKSFKSPEPRL
TPEEFFRIFNRSIDAF
>d3inkc_a.26.1.2 (C:) Interleukin-2 (IL-2) {Human (Homo sapiens)}
STKKTQLQLEHLLDLQMLNGINNYKNPKLRLMLTFKFYMPKKATELKHLQCLEELKPLEEVNLNAQSKNFHLRPRDLISNINVLELGSETTFMC
YADETATIEFLNRWITFAQSIISTLT
>d1jli_a.26.1.2 (-) Interleukin-3 (IL-3) {Human (Homo sapiens)}
ANCSIMIDEIIHHLKRPPNPLDPNNLNSEDMDILMERNLRTPNLLAFVRAVKHENASAIESILKNLLPCPLATAAPTRHPIHKDGDWNEFRRKLT
YLTLENAQAQQ

>d1ga3a_a.26.1.2 (A:) Interleukin-13 (IL-13) {Human (Homo sapiens)}

GGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINSGCSAIEKTQRMLSGFCPHKVSAQFSSLHVRDTKIEVAQFVKD
LLHLKKLFREGRFN

>d2ilk__ a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory factor, CSIF) {Human (Homo sapiens)}

TQSENSCTHFPGNLPNMLRDLRDAFSRVKTFQMKDQLDNLLLKESLLEDFKGYLGQCQALSEMIQFYLEEVMPQAENQDPDIKAHVNSLGENLKTL
RLRLRRCHRFPCENKSKEAVQVKNAFNKLQEKGIVKAMSEFDIFINYIEAYMTMKIRN

>d1vlk__ a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory factor, CSIF) {Epstein-Barr virus}

CDNFPQMLRDLRDAFSRVKTFQTKDEVDNLLLKESLLEDFKGYLGQCQALSEMIQFYLEEVMPQAENQDPPEAKDHVNSLGENLKTLRLRRCHRF
PCENKSKEAVQVKNAFNKLQEKGIVKAMSEFDIFINYIEAYMTIK

>d1au1a_a.26.1.3 (A:) Interferon-beta {Human (Homo sapiens)}

MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPIEIKQLQQFKQEDAALTIYEMLQNIIFRQDSSSTGWNETIVVRLDELHQQTFLKTVL
LKTVEEKKLEDFTRGKLMSSLHLKRYYGRILHYLKAKEYSHCAWTIVRVEILRNFYFINRLTGYLRN

>d1rmi__ a.26.1.3 (-) Interferon-beta {Mouse (Mus musculus)}

INYKQLQLQERTNIRKCQELLEQLNGKINLTYRADFKIPMEMTEKMQKSYTAFAIQEMLQNVFLVFRNNFSSTGWNETIVVRLDELHQQTFLKTVL
EEKQEERLTWEMSSTALHLKSYYWRVQRYLKLMKYNSYAWMVVRAEIFRNFLIIIRRLTRNFQ

>d1rh2a_a.26.1.3 (A:) Interferon-alpha 2b {Human (Homo sapiens)}

THSLGSRRTLMLLAQMRRIISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLSTKDSSAAWDETLLDKFYTELYQQLNDEACVIQGV
GVTETPLMNEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLSTNLQE

>d1b5l__ a.26.1.3 (-) Interferon-tau {Sheep (Ovis aries)}

CYLSRKLMILDARENKLDRMNRSLSPHSCLDKDFGLPQEMVEGDQLQKDQAFPVLYEMLQQSFNLFYTEHSSAADTTLEQLCTGLQQQLD
HLDTCRGQVMGEEDSELGNMDPIVTVKYFQGIYDYLQEKGYSDCAWEIVRVEMMRALTVSTTLQKRLTK

>d1d9ca_a.26.1.3 (A:) Interferon-gamma {Cow (Bos taurus)}

QGQFFREIENLKEYFNASSPDVAKGGPLFSEILKNWKDESDKKIIQSIVSFYFKLFENLKDQVIQRSMDIIQDMFOKFNGSSEKLEDFKKLIQIPV
DDLQIQRKAINELIKVMNDLS

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

MQDPYVKEAENLKKYFNAGHSVDADNGTLFLGILKNWKEESDRKIMQSIVSFYFKLFKNFKDDQSIQSVETIKEDMVNKFFNSNKKRDDFEKLT
NYSVTDLNVQRKAIDELIQVMAELGANV

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

SGEFVKEAENLKKYFNAGHSVDADNGTLFLGILKNWKEESDRKIMQSIVSFYFKLFENLKDHEVIKSMESIKEDIFVKFFNSNLTKMDDFQNLTRIV
SVTDLNVQRKAIDELIQVMAELSPA

>d2rig__ a.26.1.3 (-) Interferon-gamma {Rabbit (Oryctolagus cuniculus)}

QDTLTRETEHLKAYLKANTSDVANGGPLFLNIRNWKEESDNKIIQSIVSFYFKLFNLKDHEVIKSMESIKEDIFVKFFNSNLTKMDDFQNLTRIV
DDRLVQRKAVSELSNVLNF

>d1a8h_1 a.27.1.1 (349-500) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}

LADDLGNLVQRTRAMILFRFAEGRIPEPVAGEELAEGTGLAGRPLVRELKFHVALEEAMAYVKALNRYINEKKPWELFKEPEEARAVLYRVVEGLRI
ASILLTPAMPDKMAELRRAALGKKEEVRLAERWGLAEPPIPEEAPVLFPKK

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

VVNLASRNAGFINKRFDGVLASLADPQLYKTFDAAEVIGEAWESREFGKAVREIMALADLANRYVDEQAPVVAKQEGRDADLQAICSMGINLF
RVLMTYLKPVLPLTERAEAFNLTELWDGIQQPLLGHKVNPFKALYNRIDMRQVEALVEASKE

>d1ile_1 a.27.1.1 (642-821) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}

YFLTLWNVYSSFTYANLDRPDLKNPPPKEKRPEMDRWLLARMQDLIQRVTEALEAYDPTTSARALRDFVVEDLSQWYVRRNRRRFWKNEDALDR
EAAYATLYEALVLVATLAAPFTPFLAEVLWQNLVRSRLEAKESVHLADWPEADPALADEALVAQMRAVLKVVDLARAARAKSGV

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

YRKIRNTRFMLGNINDFNPDTDSDPESELLEVDRYLLNRLREFTASTINNYENFDYLNQYQEVQNFINVLSNFYLDYGKDILYIEQRDSHIRRSMQTVLY

QILVDMTKLLAPIVHTAEEVWSHTPHVKEESVHLADMPKVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNASEF
LTSFDALHQLFIVSQVKVVKLDDQATAYEHGDIVIEHADGEKCERCWNYSEDLGAVDELTHLCPRCCQQVVKSLV
>d1qu3a1 a.27.1.1 (A:645-881) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}
YRKIRNTLRFMLGNINDFPDTSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNIYQEVENFINVELSNFYLDYGKDILYIEQRDSHIRRSMQTVL
QILVDMTKLLAPIVHTAEEVWSHTPHVKEESVHLADMPKVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNASEF
LTSFDALHQLFIVSQVKVVKLDDQATAYEHGDIVIEHA
>d1gaxa1 a.27.1.1 (A:579-862) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}
ANKLYNAARFVLLSREGFQAKEDPTLADRMRSLRGVEEITALYEALDLAQAAREVYELVWSEFCDWYLEAAKPALKAGNAHTLRTLEEVLA
LLHPMMPLTSELYQALTGKEELALEAWPEPGRDEEAERAFAEALKQAVTAVRALKAEGLPPAQEVRYLEGETAPVEENLEVFRFLSRADLLPERPA
KALVKAMPRVTARMPLEGLLDVEEWRRRQEKRKELLALAERSQRKLASPGFREKAPKEVVAEEARLENLEQAERIREALSQIG
>d1f7ua1 a.27.1.1 (A:484-607) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast (Saccharomyces cerevisiae)}
DTGPYLYQAHSLRSVERNASGITQEWINADFSLLKEPAKLLIRLLQYPDVLRNAIKTHEPTTVTYLFKLTHQVSSCYDVLWVAGQTEELATARLA
LYGAARQVLYNGMRLGLTPVERM
>d1iq0a1 a.27.1.1 (A:467-592) Arginyl-tRNA synthetase (ArgRS) {Thermus thermophilus}
GDTGPYVQYAHARAHSILRKAGEWGAPDLSQATPYERALADLLDFEEAVLEAAEERTPHVLAQYLLDAASWNAYYNARENGQPATPVLTAPGLR
ELRLSLVQLQRTLATGLDLLGIPAPEVM
>d1acp__ a.28.1.1 (-) Acyl carrier protein {Escherichia coli}
STIEERVKKIIIGEQLGVKQEEVTNNASFVEDLGADSLDTVELVMALEEEFDTEIPDEEAEKITTQAAIDYINGHQAA
>d1f80d_ a.28.1.1 (D:) Acyl carrier protein {Bacillus subtilis}
SADTLERVTKIIVDRLGVDEADVKLEASFKEDLGADXLDVVELVMELEDEFDMEISDEDAEKIATVGDAVNYIQ
>d1af8__ a.28.1.1 (-) Actinorhodin polyketide synthase acyl carrier protein, ACT ACP {Streptomyces coelicolor, A3(2)}
MATLTTDDLRRALVECAGETDGTDLSGDFLDLRFEDIGYDSLALMETAARLESRYGVIPDDVAGRVDPRELLDLINGALAEAA
>d1dnya_ a.28.1.2 (A:) Peptidyl carrier protein (PCP), thioester domain {Bacillus brevis}
YVAPTNVESKLAEIWERVLGVSGIGILDNFFQIGGHSLKAMAVAAQVHREYQVPLKVLFAQPTIKALAQYVAT
>d1dv5a_ a.28.1.3 (A:) apo-D-alanyl carrier protein {Lactobacillus casei}
ADEAIKNGVLDILADLTGSDDVKKNLDLNLFETGLLDSMGTVQLLELOQSQFGVDAPVSEFDRKEWDTPNKIIAKVEQAAQ
>d1unka_ a.28.2.1 (A:) ImmE7 protein (Im7) {Escherichia coli}
MELKNSISDYTEAEFVQLLKEIEKENVAATDDVLDVLLEHFVKITEHPDGTDLIYYPDSNRDDSPPEGIV/KEIKEWRAANGKPGFKQG
>d1imy__ a.28.2.1 (-) ImmE8 (Im8) {Escherichia coli}
MELKNSISDYTEEFKKIIEDIINCEGDEKKQDDNLEHFISVTEHPSGSDLIYYPEGNNNDGSPEAV/KEIKEWRAANGKSGFKQG
>d1emva_ a.28.2.1 (A:) ImmE9 protein (Im9) {Escherichia coli}
LKHSISDYTEAEFLQLVTTICNADTSSEEEVLKLVTHFEEMTEHPSGSDLIYYPKEGDDDSPSGIVNTVKQWRAANGKSGFKQ
>d2eiaa1 a.28.3.1 (A:148-222) EIAV capsid protein p26 {Equine infectious anemia virus}
PKAQNRQGAKEPYPEFVDRLLSQIKSEGHPQEISKFLDTLTIQNANECCRNAMEHRLRPEDTLEEKMYACRDIG
>d1qrjb1 a.28.3.1 (B:131-214) HTLV-I capsid protein {Human T-cell leukemia virus type 1}
PSWASILQGLEEPYHAFVERLNIALDNGLPEGTPKDPILRSLAYSNANKECQKLLQARGHTNSPLGDMILRACQTWTPKDKT
>d1a8o__ a.28.3.1 (-) HIV capsid protein, dimerisation domain {Human immunodeficiency virus type 1}
MDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMETLLVQNANPDCKTILKALGPGATLEEMMTACQG
>d1d1da1 a.28.3.1 (A:151-230) RSV capsid protein {Rous sarcoma virus}
GPWADITQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRAPSTLTPGEIIKYVLD
>d1eoqa_ a.28.3.1 (A:) RSV capsid protein {Rous sarcoma virus}
MDIMQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRAPSTLTPGEIIKYVLD
>d1e6ia_ a.29.2.1 (A:) GCN5 {Baker's yeast (Saccharomyces cerevisiae)}
RGPHDAAIQNLTELQNHAAPWFLQPVNKEEVPDYDFIKEPMDSLTMIEKLESNKYQKMEDFIYDARLVFNCRMYNGENTSYKYANRLEKFF

NNKVKEIPEYSHLID

>d1f68a_a.29.2.1 (A:) GCN5 {Human (Homo sapiens)}

GDQLYTTLNLLAQIKSHPSAWPFMEPVKKSEAPDYYEVIRFPIDLKTMTERLRSRYVTRKLFADLQRVIANCREYNPPDSEYCRCASALEKFFYFKL
KEG

>d1b91a_a.29.2.1 (A:) P300/CAF histone acetyltransferase bromodomain {Human (Homo sapiens)}

GSHMSKEPRDPDQLYSTLKSILQQVKSHQSAPFMEPVKRTEAPGYYEVIRSPMDLKTMSERLKNRYYVSKKLFADLQRVFTNCKEYNAPESEYY
KCANILEKFFFSSIKEAGLID

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

GTTVHCDYLNRPDKSIHRRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVKDYYKIITRPMQLTRENRKRLYPSREEFREHLELIVKNSAT
YNGPKHSLTQISQSMLDLCDEKLKEKEDKLARLEKAINP

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

LLDDDDQVAFSFILDNIVTQKMMAVPDSPFHHPVNKKFVPDYYKVIVNPMDLETIRKNISKHKYQSQRESFLDDVNLLANSVKYNGPESQYTKTAQ
EIVNVVCYQTLTEYDEHLTQLEKDICTAKEAA

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

FTSSLFLWGEALPTLLEFLNEVEKMLKNQVNTRRIHQLLKELEDDPLLENKDLEEKLQAFLDYVKEIPNLPEARAKRYRIQSKLEMIEKLRSWFIDYLE

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

VRLTPTMMILYSGRSQDGSHLLKSGRYLQQELPVRIAHRIGFRSLPFIIGCNPTILHVHELYIRAFQKLTDFFPKDQADEAQYCQLVRQLLDDHKDVVT
LAEGLRESRKHIEDEKLVRYFLDKTLTSRLGIRMLATHHLALHEDKP

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

ASLAGAPKYIEHFSKFSPSPLSMKQFLDFGSSNACEKTSFTLRQELPVRLANIMKEINLLPDRVLSTPSVQLVQSWVQSLLDIMEFLDKDPEDHRTLS
QFTDALVTIRNRHNDVVPTMAQGVLEYKDTYGDDPVSNQNIQYFLDRFYLRSIRMLINQHTLIFD

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

GKGFKIAMMTLDGGGRIGVAAQALGIAEAALADAVEYSKQRVQFGKPLCKFQSFKLADMKMQIEARNLVKAACKKQEGKPFTVDAAIAKRVAS
DVAMRVTTEAVQIFGGGYSEEYPVARHMRDAKITQIYEGTNEVQLMVTGGALLR

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

MGFKIAMQTLDMGRIGIASQALGIAQASLDCAVKYAENRHAFGAPLTKLQNIQFKLADMALALESARLLTWRAAMLKDNPFTKESAMAKLAAS
EAATAISHQAIQILGGMGYVTEMPAERYYRDARITEIYEGTSEIQRVLIAGHLLRSYR

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

GAGFKIAMGTDFKTRPPVAAGAVGLAQRALDEATKYALERKTFGKLLAEHQGISFLADMAMKVELARLSYQRAWEIDSGRRNTYYASIAKAYAAD
IANQLATDAVQVFGGNFNTTEYPVEKLMRDAKIYQIYEGTAQIQRIIIAREHIGRYK

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

GAGFKVAMGAFDKERPVVAAGAVGLAQRALDEATKYALERKTFGKLLVEHQAFQKIGHFQLMQGKADMYTRLMACRQYVNVAKACDEGHCTAKDCAGVILY
AGDIANQLATDAVQIILGGNGFNTEYPVEKLMRDAKIYQIYGGTSQIQRLLIVAREHIDKYKN

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

KGVYVLMMSGLDLERLVLAGGPLGLMQAVLDHTIPYLHVREAFCQKIGHFQLMQGKADMYTRLMACRQYVNVAKACDEGHCTAKDCAGVILY
AECATQVALDGIQCFGNGYIINDFPMGRFLRDAKLYEIGAGTSEVRRLVIGRAFNAD

>d1b6q_a.30.1.1 (-) ROP protein {Escherichia coli}

MTKQEKTALNMARFIRSQTLLNEKLNELPDEQADICESLHDHADELYRSCLARF

>d1f4na_a.30.1.1 (A:) ROP protein {Escherichia coli}

GTKQEKTILNMARFIRSQALTILEKANELADEIADEIADIAESIHDHADEIYRSALARFDDG

>d1f4nb_a.30.1.1 (B:) ROP protein {Escherichia coli}

EKTILNMARFIRSQTLLNEKLNELGADEQADICESLHDHADELYRSCLARFGDDGEN

>d1gtoa_a.30.1.1 (A:) ROP protein {Escherichia coli}

GTKQEKTALNMARFIRSQTLLNEKLNELGADEQADICESLHDHADELYRSCLARFGDDGEN

>d1nkd__ a.30.1.1 (-) ROP protein {Escherichia coli}
MTKQEKTALNMARFIRSQTTLLEKLNLADAADEQADICESLHDHAELYRSCLARFG
>d1joya_ a.30.2.1 (A:) EnvZ histidine kinase {Escherichia coli}
MAAGVKQLADDRLLMAGVSHDLRPTLIRLATEMMSEQDGYLAESINKDIEECNAIEQFIDYLR
>d1b3qa1 a.30.2.1 (A:293-354) Histidine kinase CheA {Thermotoga maritima}
SQTVRV DIEKLDNLMDLMGELVIARSRILETLKKNIKELDESLSHLSRTLDLQNVVMKIR
>d1r2aa_ a.31.1.1 (A:) Dimerization-anchoring domain of cAMP-dependent type II PK regulatory subunit {Mouse (Mus musculus)}
HMGHIQIPPGLTLLQQYTVEVLRQQPPDLVDFAVEYFTRLREARR
>d1ytfb1 a.32.1.1 (B:) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
SNAEASRVYEIIVESVVNEVREDFENAGIDEQTLQDLKNIWQKKLT
>d1ytd1 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}
WSTIVKLTCPTLKSMAKKCEGSIATMIKKCDK
>d1b0na1 a.34.1.1 (A:74-108) SinR repressor (dimerisation domain)-SinI anti-repressor complex {Bacillus subtilis}
LDSEWEKVLRDAMTSGVSKQFREFLDYQKWRKSQ
>d1b0nb1 a.34.1.1 (B:) SinR repressor (dimerisation domain)-SinI anti-repressor complex {Bacillus subtilis}
FELDQEWEVLMVEAKEANISPEEIRKYLLLN
>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)}
MVSKLSQLQTELLAALLESGLSKEALIQALGE
>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)}
SKLSQLQTELLAALLESGLSKEALIQAL
>d1e3oc2 a.35.1.1 (C:1-75) Oct-1 {Human (Homo sapiens)}
EEPSDLEELEQFAKTFKQRRIKLGFTQGDVGLAMGKLYGNDFSQTTSRFEALNLSFKNMSKLKPILLEKWLNDAE
>d1au7a2 a.35.1.1 (A:5-76) Pit-1 {Rat (Rattus norvegicus)}
GMRALEQFANEFKVRRIKLGYTQTNVGEALAAVGSEFSQTTICRFENLQLSFKNACKLKAILS KWLEEAQ
>d1llib_ a.35.1.2 (B:) lambda C1 repressor, DNA-binding domain {Bacteriophage lambda (Escherichia coli)}
STKKKPLTQEQLEDARRLKAIYEKKKNELGLSQESLADKLGGMQSGIGALFNGINALNAYNAALLAKILKVSVEEFSPSIAREIYEMYEAVS
>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)}
SISSRVKS KRIQLGLNQAELAQKVGT TQQSIEQLENGKTPRFLPELASALGVSVDWLLNGT
>d2cro__ a.35.1.2 (-) cro 434 {Bacteriophage 434}
MQTLSERLKKRRIALKMTQTELATKAGVKQQSIQLIEAGVTKRPRFLFEIAMALNCDPVWLQYGT
>d1adr__ a.35.1.2 (-) P22 C2 repressor, DNA-binding domain {Salmonella bacteriophage P22}
MNTQLMGERIRARRKKLIRQAALGKMGVGSVNAISQWERSETEPNGENLLALSKALQCSPDYLLKGDSLQTNVAY

>d1copd_a.35.1.2 (D:) cro lambda repressor {Bacteriophage lambda (Escherichia coli)}

MEQRITLKDYAMRGQTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAAEVKPFPSNKKTTA

>d1d1la_a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda (Escherichia coli)}

MEQRITLKDYAMRGQTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAAEVKPWPSN

>d3orca_a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda (Escherichia coli)}

EQRITLKDYAMRGQTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAAEVKDGEVKPFPSN

>d1ner__a.35.1.2 (-) Ner {Bacteriophage mu}

CSNEKARDWHRADVIAGLKKRKLSSLRSRQFGYAPTLANALERHWPKGEOIIANALETKPEVIWPSRYQAGE

>d1b0na2_a.35.1.3 (A:1-68) SinR repressor, DNA-binding domain {Bacillus subtilis}

MIGQRRIKQYRKEGYSLSELAEKAGVAKSYLSSIERNLQTNPSIQFLEKVSALDVSVHTLLDEKHET

>d1dw9a1_a.35.1.4 (A:1-86) Cyanase N-terminal domain {Escherichia coli}

MIQSQINRNIRLDLADAILSKAKKDLSFAEIADGTGLAEAFVTAALLGQQALPADAARLVGAKLDLDEDSILLQMIPLRGCIDD

>d1pru__a.35.1.5 (-) Purine repressor (PurR), N-terminal domain {Escherichia coli}

MATIKDVAKRANVSTTVSHVINKTRFVAEETRNAVWAAIKELHYSPSAVARSLKV

>d1vpwa1_a.35.1.5 (A:3-58) Purine repressor (PurR), N-terminal domain {Escherichia coli}

TIKDVAKRANVSTTVSHVINKTRFVAEETRNAVWAAIKELHYSPSAVARSMKVNH

>d1efaa1_a.35.1.5 (A:2-60) Lac repressor (LacR), N-terminal domain {Escherichia coli}

KPVPTLYDVAEYAGVSYQTCSRNNQASHVSAKTREKVEAACMAELNYIPNRVAQQLAGKQ

>d1lcca_a.35.1.5 (A:) Lac repressor (LacR), N-terminal domain {Escherichia coli}

MKPVPTLYDVAEYAGVSYQTCSRNNQASHVSAKTREKVEAACMAELNYIPNR

>d1uxc__a.35.1.5 (-) Fructose repressor (FruR), N-terminal domain {Escherichia coli}

MKLDEIARLAGVSRTTASYVINGKAKQYRVSDKTVEKVMADVREHNYHPNAVAAGLRLQ

>d1dula_a.36.1.1 (A:) Signal sequence binding protein Ffh {Escherichia coli}

FDLNDLFLEQVKVLVRMEAINSMTMKERAKPEIIKGSRKRIAAGSGMQVQDVNRLLKQFDDMQRMMKKM

>d1hq1a_a.36.1.1 (A:) Signal sequence binding protein Ffh {Escherichia coli}

GFDLNDLFLEQLRQMKNMGGMASLMGKLPGMGQIPDNVKSQMDDKVLRMEAINSMTMKERAKPEIIKGSRKRIAAGSGMQVQDVNRLLKQ

FDDMQRMMKKMK

>d2ffha2_a.36.1.1 (A:319-418) Signal sequence binding protein Ffh {Thermus aquaticus}

ELSLEDFLKQMQLKRLGPSEILGLPGVPQGLKVDEKAIRLEAIVSMTPEERKDPRILNGSRKRKIAKGSGTSVQEVRNRFIKAFFEMKALMKSLEK

>d1qb2a_a.36.1.1 (A:) SRP54M {Human (Homo sapiens)}

QFTLRDMYEQFQNIMKMGPFSQLGMIPFGTDFMSKGNEQESMARLKKLMTIMDSMNDQELDSTDGAVKFSKQPGRQVARGSGVSTRDV

QELLTQYTKFAQMVK

>d1sknp_a.37.1.1 (P:) Binding domain of Skn-1 {Caenorhabditis elegans}

GRQSKDEQLASDNELPVSAFQISEMSLSELQQVLKNESLSEYQRQLIRKRRRGKNKVAARTCRQRRTDRHDKM

>d1hloa_a.38.1.1 (A:) Max protein {Human (Homo sapiens)}

NDDIEVESDADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRKHNTHQQDIDDLKRQN

>d1an2a_a.38.1.1 (A:) Max protein {Mouse (Mus musculus)}

ADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRKHNTHQQDIDDLKRQN

>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)}

MDEKRRRAQHNEVERRRKINNWIVQLSKIIPDSSMESTKSGQSKGGILSKASDYIQELRQSNHR

>d1a0aa_a.38.1.1 (A:) Pho4 B/HLH domain {Baker's yeast (*Saccharomyces cerevisiae*)}
MKRESHKHAEQARRNRLAVALHELASLIPAEWKQQNVSAAPSKATTVEAACRYIRHLQNGST

>d1am9a_a.38.1.1 (A:) SREBP-1a {Human (*Homo sapiens*)}
QSRGEKRTAHNAIEKRYRSSINDKIIELKDLVVGTEAKLNKSAVLRAIDYIRFLQHSNQKLQENLSRTAVHKSLK

>d1bod__a.39.1.1 (-) Calbindin D9K {Cow (*Bos taurus*)}
MKSPEELKGIFEKYDKEGDGQLSKEELKLLQTEFPSLLKGMSLDLFEELDKNGDGEVSFEEFQVLVKKISQ

>d1ig5a_a.39.1.1 (A:) Calbindin D9K {Cow (*Bos taurus*)}
KSPEELKGIFEKYAAKEGDPNQLSKEELKLLQTEFPSLLKGPSLDLFEELDKNGDGEVSFEEFQVLVKKISQ

>d1cb1__a.39.1.1 (-) Calbindin D9K {Pig (*Sus scrofa*)}
SAQKSPAELKSIFEKYAAKEGDPNQLSKEELKQLIQAEPSSLKGPTLDDLFQELDKNGDGEVSFEEFQVLVKKISQ

>d1a03a_a.39.1.2 (A:) Calcyclin (S100) {Rabbit (*Oryctolagus cuniculus*)}
MASPLDQAIGLLIGIFHKYSKGEGDKHTLSKKELKELIQKELTIGSKLQDAEIVKLMDDLDRNKDQEVFNFQEVITFLGALAMIYNEALKG

>d1k2ha_a.39.1.2 (A:) Calcyclin (S100) {Rat (*Rattus norvegicus*), s100a1}
GSELETAMETLINVFHAFHSGKEGDKYKLSKKELKDLLQTELSSFLDVQKDADAVDKIMKELDENGDGEVDFQEFVVLVAALTVCNNFFWENS

>d1qlka_a.39.1.2 (A:) Calcyclin (S100) {Rat (*Rattus norvegicus*), s100b}
MSELEKAMVALIDVFHQYSREGDKHKLKSELKELINNELSHFLEEIKEQEVVVKVMETLDEDGDGECDFQEFMAFVSMVTACHEFFEHE

>d1mho__a.39.1.2 (-) Calcyclin (S100) {Cow (*Bos taurus*), s100b}
SELEKAVVALIDVFHQYSREGDKHKLKSELKELINNELSHFLEEIKEQEVVVKVMETLDEDGDGECDFQEFMAFVAMITTACHEFF

>d1a4pa_a.39.1.2 (A:) Calcyclin (S100) {Human (*Homo sapiens*), P11 s100a10, calpastatin}
PSQMEHAMETMMFTFHFKAGDKGYLTKEDLRVLMEKEPGFLENQKDPLAVDKIMKDLDDQCRDGKVGQFSFFSLIAGLTIACNDYFVVMKQ

>d1psra_a.39.1.2 (A:) Calcyclin (S100) {Human (*Homo sapiens*), psoriasin s100a7}
SNTQAERSIIGMIDMFHKYTRRDDKIDKPSLLTMMKENFPNFLSACDKKGTNYLADVFEKKDNEDKKIDFSEFLSLLGDIATDYHKQSHGAAPCSGG
SQ

>d1qlsa_a.39.1.2 (A:) Calcyclin (S100) {Pig (*Sus scrofa*), calgizzarin s100c (s100a11)}
PTETERCIESLIAIFQKHAGRGNNTKISKTEFLIMNTELAAFTQNQKDPGVLDRMMKKLDLSDGQLDFQEFLNLIGGLIACHDSFIKSTQK

>d1mr8a_a.39.1.2 (A:) Calcyclin (S100) {Human (*Homo sapiens*), calgranulin s100a8, MRP8}
MLTELEKALNSIIDVYHKYSLIKGNFHAVYRDDLKKLLETCPQYIRKGADVWFKELDINTDGAVNQFQFLILVIKMGVAAHKKSHEES

>d1e8aa_a.39.1.2 (A:) Calcyclin (S100) {Human (*Homo sapiens*), calgranulin C, s100a12}
TKLEEHLEGIVNIFHQYSVRKGHDTLSKGELKQLLTKELEANTIKNIKDAVIDEIFQGLDANQDEQVDFQEFISLVAIALKAHYH

>d1irja_a.39.1.2 (A:) Calcyclin (S100) {Human (*Homo sapiens*), s100a9 (mrp14)}
TCKMSQLERNIETIINTFHQYSVKGHDPTLNQGEFKEVLRKDLQNFLKENKNEKVIEHIMEDLTDNADKQLSFEEFIMLMARL

>d1sra__a.39.1.3 (-) C-terminal (EC) domain of BM-40/SPARC/osteonectin {Human (*Homo sapiens*)}
PPCLDSELTEFPLRMRDWLKVLVTLTYERDEDNNLTEREKQKLRVKKIHENEKRLEAGDHPVELLARDFEKNYNMYIFPVHWQFGQLDQHPIDGYLSH
TELAPLRAPLIPMEHCTTRFFETCDLDNDKYIALDEWAGCFGIKQKDIDKDLVI

>d1rro__a.39.1.4 (-) Oncomodulin {Rat (*Rattus norvegicus*)}
SITDILSAEDIAAAALQECQDPDTFEPQKFFQTSGLSKMSASQVKDFRFIDNDQSGYLDGDELKYFLQKFQSDARELTESETKSLMDAADNDGDGKIG
ADEFQEMVHS

>d1cdp__a.39.1.4 (-) Parvalbumin {Carp (*Cyprinus carpio*)}
AFAGVLNDADIAAALEACKAADSFNHKAFFAKVGLTSKSADDVKKAFAIIDQDKSGFIEEDELKLFLOQFKADARALTDGETKTFKAGDSGDGKIG
VDEFTALVKA

>d1pvaa_a.39.1.4 (A:) Parvalbumin {Pike (*Esox lucius*)}
AAKDLLKADDIKKALDAVKAEGSFNHKKFFALVGLKAMSANDVKKVFKIADADASGFIEEEELKFVLSFAADGRDLTDAETKAFLKAADKGDGKIGI
DEFETLVHEA

>d2pvba_a.39.1.4 (A:) Parvalbumin {Pike (*Esox lucius*)}

SFAGLKDADVAAALAAACSAADSFKHKEFFAKVGLASKSLDDVKKAFYVIDQDKSGFIEEDELKLFLQNFSPSARALTDAETKAFLADGDKGDGGMIGV
DEFAAMIKA

>d5pal__ a.39.1.4 (-) Parvalbumin {Leopard shark (*Triakis semifasciata*)}

PMTKVLKADDINKAISAFKDPGTFDYKRFFHLVGLKGKTDQAQVKEVFEILDKDQSGFIEEEELKGVLKGSFSAHGRDLNDETAKALLAAGDSDHDGKIG
ADEFAKMVAQA

>d1a75a_ a.39.1.4 (A:) Parvalbumin {Whiting (*Merlangius merlangus*)}

AGILADADCAAALKACEAADSFSYKAFFAKCGLSGKSADDIKKAFVFIDQDKSGFIEEDELKLFLQVFKAGARALTDAETKAFLKAGDSDGDGAIGVEE
WVALVKA

>d1bu3__ a.39.1.4 (-) Parvalbumin {Silver hake (*Merluccius bilinearis*)}

AFSGILADADVAAALKACEAADSFSNYKAFFAKVGLTAKSADDIKKAFFVIDQDKSGFIEEDELKLFLQVFSGSAGARALTDAETKAFLKAGDSDGDGAIGV
DEWAALVKA

>d1g33a_ a.39.1.4 (A:) Parvalbumin {Rat (*Rattus rattus*)}

MKSADDVKKVFHILDKDKGFIIEDELGSILKGFSSEDLSAKETKTLMAAGDKDGKIGVEEFSTLVAES

>d1rtp1_ a.39.1.4 (1:) Parvalbumin {Rat (*Rattus rattus*)}

SMTDLSAEDIKKAGFTAADSFDFDHKKFFQMVGKKSADDVKKVFHILDKDKGFIIEDELGSILKGFSSEDLSAKETKTLMAAGDKDGKIG
VEEFSTLVAES

>d1avsa_ a.39.1.5 (A:) Troponin C {Chicken (*Gallus gallus*)}

QAEARAFLSEEMIAEFKAADFMDADGGGDISTKELGTVMRMLGQNPTKEELDAIIIEVDEDGSGTIDFEEFLVMMVRQMK

>d1ctda_ a.39.1.5 (A:) Troponin C {Chicken (*Gallus gallus*)}

KSEEELANAFRIFDKNADGYIDIEELGEILRATG

>d1dtla_ a.39.1.5 (A:) Troponin C {Chicken (*Gallus gallus*)}

YKAADVQLTEEQKNEFKAAFDFVLAEGDSISTKELGVKVRMLGQNPTPEELQEMIDEVDEDGSGTDFDEFLVMMVRSMKDDSKGKSEEELSDL
FRMFDFKNADGYIDLEELKIMLQATGETITEDIEELMKDGDKNNDRIDYDEFLEFMKG

>d1jc2a_ a.39.1.5 (A:) Troponin C {Chicken (*Gallus gallus*)}

EDAKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVIEEDIEDLMKDSKDNNDGRIDFDEFLKMMEGVQ

>d1ncx_ a.39.1.5 (-) Troponin C {Chicken (*Gallus gallus*)}

ASMTDQQAEARAFLSEEMIAEFKAADFMDADGGGDISTKELGTVMRMLGQNPTKEELDAIIIEVDEDGSGTIDFEEFLVMMVRQMKEDAKGK
EEELANCFRIFDKNADGFIDIEELGEILRATGEHVTEEDIEDLMKDSKDNNDGRIDFDEFLKMMEGVQ

>d1smg_ a.39.1.5 (-) Troponin C {Chicken (*Gallus gallus*)}

ASMTDQQAEARAFLSEEMIAEFKAADFMDADGGGDISTKALGTVMRMLGQNPTKEELDAIIIEVDEDGSGTIDFEEFLVMMVRQMKEDA
KGS

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

KSEEELANAFRIFDKNADGYIDIEELGEILRATGXVTEEDIEDLMKDSKDNNDGRIDFDEFLKMMEGVQ

>d1tn4__ a.39.1.5 (-) Troponin C {Rabbit (*Oryctolagus cuniculus*)}

TDQQAEARSYLSEEMIAEFKAADFMDADGGGDISVKELGTVMRMLGQTPTKEELDAIIIEVDEDGSGTIDFEEFLVMMVRQMKEDAKGKSEEEL
AELFRIFDRNAADGYIDAELAEIFRASGEHVTDEEIESLMKDGDKNNDRIDFDEFLKMMEG

>d1fi5a_ a.39.1.5 (A:) Troponin C {Chicken (*Gallus gallus*), cardiac isoform}

MVRCMKDDSKGKTEEELSDLFRMFDFKNADGYIDLEELKIMLQATGETITEDIEELMKDGDKNNDRIDYDEFLEFMKGVE

>d1ap4__ a.39.1.5 (-) Troponin C {Human (*Homo sapiens*), cardiac isoform}

MDDIYKAAVEQLTEEQKNEFKAAFDFVLAEGDCISTKELGVKVRMLGQNPTPEELQEMIDEVDEDGSGTDFDEFLVMMVRCMKDDS

>d1ih0a_ a.39.1.5 (A:) Troponin C {Human (*Homo sapiens*), cardiac isoform}

GKSEEELSDLFRMFDFKNADGYIDLEELKIMLQATGETITEDIEELMKDGDKNNDRIDYDEFLEFMKGVE

>d2scpa_ a.39.1.5 (A:) Sarcoplasmic calcium-binding protein {Sandworm (*Nereis diversicolor*)}

SDLWVQKMKTYFNRIDFDKDGAIIRMDFESMAERFAKESEMKAHEAKVLMDSLTVWDNFLTAVAGGKGIDETTFINSMKEMVKNPEAKSVVEG
PLPLFFRAVDTNEDNNISRDEYGIFGMLGLDKTMAPASFDAIDTNNDGLSLEEFVIAGSDFFMNDGSTNKVFWGPLV

>d2sas__ a.39.1.5 (-) Sarcoplasmic calcium-binding protein {Amphioxus (*Branchiostoma lanceolatum*)}
GLNDFQKQKIKFTDFFLDMNHDSIQDNDFEDMMTRYKEVNKGSLSDADYKSMQASLEDEWRDLKGRADINKDDVVSWEYLAMWEKTIATC
KSVADLPAWCQNRPFLFKGMDVSGDGIVDLEEFQNYCKNFQLQCADVPNAVNVITDGGKVTFDLNRYKELYRLLSPAADAGNTLMGQKP
>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*)}
AAPKARALGPEEKDEC MKI FIDFDRNAENIA PVSDTMDMLT KLGQTYTKRETEAIMKEAR GPKGDKKNIGP EEWLTLC SKWVRQDD
>d1j7ra_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (*Branchiostoma lanceolatum*)}
LGPEEKDEC MKI FIDFDRNAENIA PVSDTMDMLT KLGQTYTKRETEAIMKEAR GPKGDKKNIGP EEWLTLC SKWVRQ
>d1ej3a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Jellyfish (*Aequorea aequorea*), aequorin}
LTSDFDNPRWIGRH KHM FNFL DVNH NGKIS LDEM VYK AS DIVIN NLGAT PEQAK RHDA VEAFF GAGM KYG VET DW PAYIE GWKL ATDE LEKY
AKNEPTLIRIWGD ALF DIVDK DQNG AITL DEW KAY TKA AGII QSS EDCE ETFR C DIDE SGQL DVDEM TRQHL GFW YTM DP ACE KLY GGAVP
>d1el4a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa (*Obelia longissima*), obelin}
SSKYAVKLKTD FDN PRWIKR H KHM FDL DING NGK I TLDE I VSK AS DDIC A KLE ATPE QT KR HQVC VE AFF RGC GM EY GKEI AFP QFL DGW KQL AT S
ELKKWARNEPTLIREWGDAVFDIFDKDGS GTITL DEW KAY GKIS GPS QDCE ATFRH C LD NSG DLD VDEM TRQHL GFW YTL DPE AD GLY GNG VP
P
>d1jf0a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa (*Obelia geniculata*), obelin}
KYAVKLQ TD FDNP KWIKR H KMF DYLD ING NGQ ITL DE I VSK AS DDIC KNL GAT PAQ TQR HQDC VEAFF RGC GLEY G KET K PEFLEG WKN LANADL
AKWARNEPTLIREWGDAVFDIFDKDGS GTITL DEW KAY GRIS GISP SEED CE KT FQHC LD NSG ELD VDEM TRQHL GFW YTL DPE AD GLY GNG VP
>d1jfja_ a.39.1.5 (A:) EHCBP {Entamoeba (*Entamoeba histolytica*)}
MAEALFKEIDVNGDGA VSYEEVKAFVSKKRAIKNEQLLQIFKSIDADGN GEIDQNEFAK FYG SIQG QDLS DD KIGLK VLYK LMDV DGDG KLT KEEV T
SFFKKH GIEKVAEQVM KADANGDGYIT LEEF L EFL S L
>d1cmg__ a.39.1.5 (-) Calmodulin {Cow (*Bos taurus*)}
MKDTDSEEEIREAFRVFDKDGNGYISAAELRH VMTNLGEKLT DEEVDEMIREADIDGDGQV NYEEFVQMM TAK
>d1fw4a_ a.39.1.5 (A:) Calmodulin {Cow (*Bos taurus*)}
SEEI REAFRVFDKDGNGYISAAELRH VMTNLGEKLT DEEVDEMIREADIDGDGQV NYEEFVQMM
>d1g4yr_ a.39.1.5 (R:) Calmodulin {Rat (*Rattus rattus*)}
ADQLTEEQIAEFKEA FSLFDKDG DGT ITT KELGT VMRS LGQ NPTEAE LQDM INEV DADG NGT IDFPE FL MM MARK M KTD SEEEIREAFRVFDKDG
NGYISAAELRH VMTNLGEKLT DEEVDEMIREADIDGDGQV NYEEFVQMM TA
>d1f70a_ a.39.1.5 (A:) Calmodulin {African frog (*Xenopus laevis*)}
ADQLTEEQIAEFKEA FSLFDKDG DGT ITT KELGT VMRS LGQ NPTEAE LQDM INEV DADG NGT IDFPE FL MM MARK M
>d1exra_ a.39.1.5 (A:) Calmodulin {Ciliate (*Paramecium tetraurelia*)}
EQLTEEQIAEFKEA FALFDKDG DGT ITT KELGT VMRS LGQ NPTEAE LQDM INEV DADG NGT IDFPE FL SL MARK M KEQD SEE ELIE AFK VFD RDNG
LISAAELRH VMTNLGEKLT DEEVDEMIREADIDGDG HINYEEF VRMM VS
>d1ggwa_ a.39.1.5 (A:) Cdc4p {Fission yeast (*Schizosaccharomyces pombe*)}
STDDSPYKQAFSLFDRHGTGRIPKTSIGDLLRACGQNPTLA EITEIESTLPAEV DM EQFLQVLNRPN GFDMPGDP EEFVKG FQVFDK DATGMIGVG E
LRYVLTSLGEKLSNEEMDELLKGVPVKDGMVNYHDFVQMILAN
>d1wdcb_ a.39.1.5 (B:) Myosin Essential Chain {Bay scallop (*Aequipecten irradians*)}
LPQKQIQEMKEAFSMIDVDRDGFVSKEDIKAISEQLGRAPDDKELTAMLKEAPGPLNFTMFLSIFSDKLSGT DSEETIRNAFAMFDEQETK KLNIEYIK
DLLENMGDNFNKDEM RMTFKEAPVEGGKFDYV KFTAMI KGS GE
>d1br1b_ a.39.1.5 (B:) Myosin Essential Chain {Chicken (*Gallus gallus*)}
FSEEQTAEFKEA FQLFDRTG DKI LYSC QGD VMRAL GQNP TNAEV MKVL GNPK SD EMNL KTLK FEQFL PMM QTI AKN KDQG CFEDY VEGL RVFDK
EGNGTV MGAEIRH VLV TLGE KMTEEVEQLVAGHED SNGCINYEELVRMVL SG
>d2mysb_ a.39.1.5 (B:) Myosin Essential Chain {Chicken (*Gallus gallus*)}

FDETEIEDFKEAFTVIDQNADGIIDKDDLRETFAAMGRNVNEELDAMIKEASGPINFTVFLTMFGEKLKGADPEDVIMGAFVLDPDGKGSIKSF
LEELLTTGGGRFTPPEEIKNMWAAFPDVAGNVDYKNICYVITHGEDA
>d1wdcc_a.39.1.5 (C:) Myosin Regulatory Chain {Bay scallop (*Aequipecten irradians*)}
LSQDEIDDLKDVFELFDWDGRDGAVIDAKLGDVCRLGINPRNEDVFAVGTHKMGEKSLPFEELPAYEGLMDCEQGTADYMEAFKTFDREG
QGFISGAEHLRVLTALGERLSDEDVDEIILTDLQEDLEGNVKYEDFKVKVMAGYP
>d2mysc_a.39.1.5 (C:) Myosin Regulatory Chain {Chicken (*Gallus gallus*)}
AAADDKFCAEFLFDRTGDAKITASQVGDIAKGQNPTNAEINKLGNPSKEEMNAAAITFEEFLPMQAAANNKDQGTFEDFVEGLRVFDKEGNG
TVMGAELRHVLATLGKEMTEEEVEELMKGQEDSNGCINYEAFKHIMSV
>d1auib_a.39.1.5 (B:) Calcineurin regulatory subunit (B-chain) {Human (*Homo sapiens*)}
SYPLEMCSHFDAEKRLGKRFKKLDLNSGSLVEEFMSLPELQQNPLVQRVIDIFDTDGNGEVDKEFIEGVSQFSVKGDKEQLRFAFRIYDMDK
DGYISNGELFQVLKMMVGNNLKDQLQQIVDKTIINADKDGDRISFEEFCAVVGGLDIHKKMVVD
>d1rec_a.39.1.5 (-) Recoverin {Cow (*Bos taurus*)}
LSKEILELQLNTKFTEEELSSWYQSFLKECPGSRITRQEFTIYSKFFPEADPKAYAQHVFRSFANDSGTLDFKEYVIALHMTSAGKTNQKLEWAFSL
YDVGNGTISKNEVLEIVTAIFKMISPEDTKHLPEDENTPEKRAEKIWGFFGKKDDDKLTERFIEGTLANKEILRLIQFEPQKVKEKL
>d1g8ia_a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Human (*Homo sapiens*)}
SNSKLKPEVVEELTRKTYFTEKEVQQWYKGFIKDCPSGQLDAAGFQKIYKQFFPGDPTKFATFVNVDENKDGRIEFSEFIQALSVTSGTLDEKLR
WAFKLYDLDNDGYITRNEMLDIVDAIYQMVGNTELPEEENTPEKRVDRIFAMMDKNAKGKLTQEFQEGSKADPSIVQALSLYDGLV
>d1fpwa_a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Baker's yeast (*Saccharomyces cerevisiae*)}
MGAKTSKLSKDDLCLKQSTYFDRREIQQWHKGFLRDCPSGQLAREDFVKIYKQFFPGSPEDFANHFTVFDKDNNGFIHFEEFITVLSTTSRGTLLEE
KLSWAFELYDLNHDGYITFDEMLTIVASYKMMGSMVTLNNEATPEMVRKKIFKLMKDNEGDYITLDEFREGSKVDPSSIIGALNLYDGLI
>d1jbaa_a.39.1.5 (A:) Guanylate cyclase activating protein 2, GCAP-2 {Cow (*Bos taurus*)}
GQQFSWEEAENGAVGAADAAQLQEWWYKKFLEECPSGTLFMHEFKRFFKVPDNNEATQYVEAMFRAFDTNGDNTIDFLEYVAALNLVRGTLLEHK
LKWTFKIYDKDRNGCIDRQELLDIVESIYKLKKACSVAVEAEQQGKLTPEEVVDRIFLLVDENGDGQLSNEFVEGARRDKWVMKMLQMDLNP
>d1bjfa_a.39.1.5 (A:) Neurocalcin {Cow (*Bos taurus*)}
NSKLRPEVMQDLLESTDFTFHEIQEWYKGFLRDCPSGHSMEFKKIYGNFFPYGDASKFAEHVFRTFDANGDTIDFREFIIALSRTGKLEQKLF
WAFSMYDLDGNGYISKAEMLEIVQAIYKVMSSVMKMPEDESTPEKRTEKIFRQMDTNRDGKLSLEEFIRGAKSDPSIVRLLQC
>d1dqua_a.39.1.5 (A:) Calcium- and integrin-binding protein, CIB {Human (*Homo sapiens*)}
SKELLAEQYQDLTFLTKQEILLAHRRFCCELLPQEQRSSVESSLRAQVPFEQJLSLPELKANPFKERICRVFSTSPAKDSLFSFEDFLLLSVFSDTATPDIKSHYAF
RIFDFDDGTNREDLSRLVNCLTGEGEDTRLASEMKQLIDNIILEESDIDRDTGTLNSELSEQHVISRSPDFASSFKIVL
>d1qjta_a.39.1.6 (A:) Eps15 {Mouse (*Mus musculus*)}
LSLTQLSSGNPVYEKYYRQVEAGNTGRVLALDAAFLKKSGLPDLILGKIWDLADTDGKGVL SKQEFFVALRLVACAQNGLEVSLSSSLAVPPPRFHD
>d1c07a_a.39.1.6 (A:) Eps15 {Human (*Homo sapiens*)}
TWVVSPAEKAKYDEIFLTKDMDGFVSGLEVREIFLKTGLPSTLLAHIWSLCDTKDCGKLSKDQFALAFHLISQKLIKIDPPHVLTPEMIPPS
>d1f8ha_a.39.1.6 (A:) Eps15 {Human (*Homo sapiens*)}
PWAVKPEDKAKYDAIFDSLSPVNGFLSGDKVVPVLLNSKLPDILGRVWELSDIDHDGMLRDEFAVAMFLVYCALEKEPVPMSPALVPPSKR
>d1iq3a_a.39.1.6 (A:) Pob1 {Human (*Homo sapiens*)}
GSLQDNSSYPDEPWRITEEQREYYVNQFRSLQPDPSSFISGSVAKNFTSKLSIPELSYIWELSDADCAGALTPEFCAAFHLIVARKNGYPLPEGLPPT
LQPEFIVTD
>d1fi6a_a.39.1.6 (A:) Reps1 {Mouse (*Mus musculus*)}
WKITDEQRQYYVNQFKTIQPDQFLWNVFQRVDKDRSGVISDNELQQALSNGTWTPFNPVTRSIISMFDRENKAGVNFEFTGVWKYITDWQNVFRT
>d1hqva_a.39.1.8 (A:) Apoptosis-linked protein alg-2 {Mouse (*Mus musculus*)}
PGPGGGPGPAAGAALPDQSFLWNVFQRVDKDRSGVISDNELQQALSNGTWTPFNPVTRSIISMFDRENKAGVNFEFTGVWKYITDWQNVFRT
YDRDNSGMIDKNEKLQALSGFGYRLSDQFHDLIRKFDRQGRGQIAFDDFIQGCIVLQLRTDIFRRYTDQDGWIQSYEQYLSMVF
>d1juoa_a.39.1.8 (A:) Sorcin {Human (*Homo sapiens*)}

FPGQTQDPLYGYFAAVAGQDGQIDAELQRCLTQSGIAGGYKPFNLETCLMVSMLRDMSGTMGFNEFKELWAVLNGWRQHFISFDTRS GTV
DPQELQKALTTMGFRSPQA VNSIAKRYSTNGKITFDDYIACCVKLRA L TDSFRRRTAQQGVNF PYDDFIQCVMSV
>d1dxb1 a.39.1.7 (B:158-298) Phosphoinositide-specific phospholipase C, isozyme D1 (PLC-D!) {Rat (Rattus norvegicus)}
NKMNFKELKDFLKE LNIQVDDGYARKIFRECDHSQTSLEEEIETFYKMLTQRAEIDRAFEEAGSAETLSVERLVTFLQHQQREEAGPALALSLIER
YE PSETAKAQRQMTKDGFLMYLLSADGNAFSLA HRRVYQDM
>d1qasa1 a.39.1.7 (A:205-298) Phosphoinositide-specific phospholipase C, isozyme D1 (PLC-D!) {Rat (Rattus norvegicus)}
YKMLTQRAEIDRAFEEAGSAETLSVERLVTFLQHQQREEAGPALALSLIER YEPSETAKAQRQMTKDGFLMYLLSADGNAFSLA HRRVYQDM
>d1k94a_a.39.1.7 (A:) Grancalcin {Human (Homo sapiens)}
SVYTYFSAVAGQDG EVDAEELQRCLTQSGINGTYS PFSLET CRIMI AMLDRDHTGKMGFNAFKELWAALNAWKENFMTVDQDGSGTV EHH ELRQ
AIGLMGYRLSPQTLTTIVKRYSKNGR IFFDDYVACCVKLRA L DFFRK RDHLQQGSANFIYDDFLQGTMAI
>d1kfus_a.39.1.7 (S:) Calpain small (regulatory) subunit (domain VI) {Human (Homo sapiens)}
THYSNIEANESEEV RQFRLFAQLAGDDMEVSATELMN IILNKVVTRHPDLKT DFGIDTCSRMVAVMDSDTTGKLGFE FKYLWNNIKRWQAIYKQ
FDTDRSGTICSS ELPGA FEAAGFHLNEHLYNMII RRSDEGNMDFDNFISCLVR LDAMFRAFKSLKDGTGQIQVNIQE WLQLTMYS
>d1dvia_a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI) {Rat (Rattus norvegicus)}
EEERQFRKLFVQLAGDDMEVSATELMN IILNKVVTRHPDLKT DFGIDTCSRMVAVMDSDTTGKLGFE FKYLWNNIKRWQAIYKQFDVDRSGTIGS
NELPGAFEAAGFHLNQH IYSMII RRSDETGNMDFDNFISCLVR LDAMFRAFRSLDKNGT GQIQVNIQE WLQLTMYS
>d1alva_a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI) {Pig (Sus scrofa)}
EEVRQFRLFAQLAGDDMEVSATELMN IILNKVVTRHPDLKT DFGIDTCSRMVAVMDSDTTGKLGFE FKYLWNNIKRWQAIYKQFDVDRSGTIGS
SELPGAFEAAGFHLNEHLYSMIIRRYSDEGGNMDFDNFISCLVR LDAMFRAFKSLKDGTGQIQVNIQE WLQLTMYS
>d1kul1 a.39.1.7 (L:515-700) Calpain large subunit, C-terminal domain (domain IV) {Human (Homo sapiens)}
EIEANLEEF DISEDDIDDGV RRLFAQLAGEDAEISAFELQ TILRRVLA KRDQDIKSDGFSIETCKIMVDM L DSGSGK LGLKEFYI LWTKI QKYQKIY REIDV
DRSGTMNSYEMRKALEEAGFK MPCQLHQVIVARFADDQ LIIDFDNFVR CLRLETLF KIFKQLDPENTGTIQLDLISWLCSVL
>d1df0a1 a.39.1.7 (A:515-700) Calpain large subunit, C-terminal domain (domain IV) {Rat (Rattus norvegicus)}
EIEANIEEIEAN EEDIGDGFR RLFAQLAGEDAEISAFELQ TILRRVLA KREDIKSDGFSIETCKIMVDM L DSGSGK LGLKEFYI LWTKI QKYQKIY REIDV
DRSGTMNSYEMRKALEEAGFKLPCQLHQVIVARFADDELIIDFDNFVR CLRLETLF KIFKQLDPENTGTIQLDLISWLCSVL
>d1eg3a1 a.39.1.7 (A:85-209) Dystrophin {Human (Homo sapiens)}
HPKMTELYQSLADLNNVRFSAYRTAMK LRLQKALCL DLLS AACD ALDQHNLKQNDQPM DILQIINCLTTIY DRLEQEHNNLVNVPLCVD MCLN
WLLNVYDTGRTGRIRVLSFKT GII SLCKA
>d1eg3a2 a.39.1.7 (A:210-306) Dystrophin {Human (Homo sapiens)}
HLEDKYR LFQVASSTGFC DQRRLG LLLHD SIQIPRQLGEV ASFGGS NIEPS VRSC FQFANNKPE IEA ALFL DWMR LEQSMV WLPV LHRV AAA ET
>d2cbla1 a.39.1.7 (A:178-263) Cbl {Human (Homo sapiens)}
TFRITKADA EAFWRKA FG EKTIV PWKSFR QALHEV HPISSGLEAMALK STIDL CNDY ISV FEF DIFT RLFP QPWSSL RNW NSL AV
>d1h8ba_a.39.1.7 (A:) alpha-Actinin {Human (Homo sapiens)}
MAD TDTAEQVIASFRILASDKPYI LAEE RRELPPDQ AQC YCIRKMPA YSGPGS VP G ALD YAA FSSA LYGE SDL
>d1c3za_a.39.2.1 (A:) Thp12-carrier protein {Yellow mealworm (*Tenebrio molitor*)}
ETPREKLKQHSDACKAEGGVSEESLNKVRNREEVDDPKLKEHAFCILK RAGFIDASGEFQLDH KTKF KENSEHPEKV DDLVAKCAVKKDTPQHSSAD F
FKCVHDNRS
>d1dqe a.39.2.1 (A:) Pheromone binding protein {Silkworm (*Bombyx mori*)}
SQEV MKNLSNFGK ALDECK KEMT L TDAIN ED FYN FWKE GYEIKN RETG C AIM CLST KLN MLD PEGN L HHG NAME FAKK HGA DETMA QQ LIDIV
HGCEKSTP AND DKCIW TLGVATCFK AEI HKLN WAPSMDV AVGE
>d1iioa_a.39.4.1 (A:) Hypothetical protein MTH865 {Archaeon Methanobacterium thermoautotrophicum}
GSHMKM GV KED IRGQI GALAGA DGPINSPEELMA ALPNGPD TCKSGD VELKASD AGQVLT ADDFP FKSA EEVADTIVN KAGL
>d1cpo_1 a.39.3.1 (0-119) Cloroperoxidase {Fungus (*Caldariomyces fumago*)}
EEPGSGIGYPYDNNTLPYVAPGPTDSRAPCPALNALAHGYIPHDGRAISRETLQNAFLNHMGIAN SVIELALTN AFVVCEYVTGSDCGDSL VNLTLL

AEPHAFEHDHSFSRKDYKQGVA

>d1cpo_2 a.39.3.1 (120-298) Cloroperoxidase {Fungus (Caldariomyces fumago)}

NSNDFIDNRNFDAETQTSLVVAGKTHFDYADMNEIRLQRESLSNELDFPGWFTESPKIQNVESGFIFALVDFNLPDNDENPLVRIDWWKYWFT

NESFPYHLGWHPPSPAREIEFVTASSAVLAASVTSTPSSLPSGAIGPGAEAVPLSFASTMTPFLATNAPYYAQDPTLGPN

>d1h67a_a.40.1.1 (A:) Calponin {Chicken (Gallus gallus)}

MPQTERQLRVWIEGATGRRIGDNFMDGLKDGVLCELINKLQPGSVQKVNDPVQNWHKLENIGNFLRAIKHYGVKPHDIFEANDLFENTNHTQVQ

STLIALASQAKTK

>d1bkra_a.40.1.1 (A:) beta-spectrin {Human (Homo sapiens)}

KSAKDALLWCQMKTAGYPNVNIHNFTTSWRGMAFNALIHKRPDLIDFDKLKKSNAHYNLQNAFNLAEQHGLTKLLDPEDISVDHPDEKSIITY
VVTYYHYFSKM

>d1aoa_1 a.40.1.1 (121-251) N-terminal actin-crosslinking domain from fimbrin {Human (Homo sapiens)}

YSEEKYAFVNWKALENDPDCRHVIPMNPNTDDLFKAVGDGIVLCKMINLSVPDTIDERAINKKLTPFIQENLNIALNSASAIGCHVNIGAEDL
RAGKPHLVLGLLWQIICKIGLFADIERSNEAL

>d1aoa_2 a.40.1.1 (260-375) N-terminal actin-crosslinking domain from fimbrin {Human (Homo sapiens)}

TLEELMKSPEELLRWANFHLENSGWQKINNFSADIKDSKAYFHLLNQIAPKGQKEGEPRIDINMSGFNETDDLKRAESMLQQADKLGRQFVTPA
DVSGNPKLNLAFAVANLFN

>d1bhda_a.40.1.1 (A:) Utrophin {Human (Homo sapiens)}

LQQTNSEKILLSWVRQTRPYSQNVNLNTTSWTDGLAFNAVLHRHKPDLFSWDKVVKMSPIERLEHAFSKAQTYLGIEKLLDPEDAVRLPDKSSII
MYLTSLFEV

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

DVQKKTFTKWINARFSKSGKPPINDMFTDLKDRKLLDLLEGLTGTLKERGSTRVHALNNVNRVLQVLHQNNVELNIGGDIVDGNHKLTGLL
WSIILHWQVKDVMKDVMSDLQQTN

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

DSYEREDVQKKTFTKVVNAQFSKFGKQHIENLFSDLQDGRRLLLEGLTGQKLPKEKGSTRVHALNNVNKAALRVLQNNNVDLVNIGSTDIVDGNH
KLTLGLIWNIIILHWQ

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

VKNVMKNIMAGLQQTNSEKILLSWVRQSTRNYPQVNINFTTSWSDGLALNALIHSHRPDLFDWNSVSQQSATQRLEHAFNIARYQLGIEKLLDP
EDVDTTYPDKKSILMYITSLFQVLPQQVSI

>d1a26_1 a.41.1.1 (662-796) Domain of poly(ADP-ribose) polymerase {Chicken (Gallus gallus)}

KSCLKAKPIQDLIKMIFDVESMKKAMVEFEIDLQKMPGLKLSKRQIQSAYSILNEVQQAVSDGGSESQILDLSNRFYTLIPHDFGMKKPPLSNLEYIQAK
VQMLDNLLDIEVASYLLRGGNEDGDKDPIDINYEK

>d1ycqa_a.42.1.1 (A:) MDM2 {African clawed frog (Xenopus laevis)}

EKLVQPTPLLSLLKSAGAQKETFTMKEVIYHLGQYIMAKQLYDEKQQHIVHCSNDPLGELFGVQEFSVKEPRLYAMISRNLVSANV

>d1ycra_a.42.1.1 (A:) MDM2 {Human (Homo sapiens)}

ETLVRPKPLLKLLKSVGAAQKDTYTMKEVLFYLQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIYTMIRNLVV

>d1b28a_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}

MKGMSKMPQFNLRWPREVLDLVRKVAEENGMSVNSIYQLVMESFKKEGRIGA

>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}

KMLQFNLWRPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIG
>d1myla_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
KMPQFNLWRPREVLDLVRKVAEENGMSVNSYIYQLVMESFKKEGR
>d1mylb_a.43.1.1 (B:) Arc repressor {Salmonella bacteriophage P22}
MPQFNLWRPREVLDLVRKVAEENGMSVNSYIYQLVMESFK
>d1mpta_a.43.1.1 (A:) Mnt repressor {Salmonella bacteriophage P22}
ARDDPHFNFRMPMEVREKLKFRAEANGRSMNSELLQIVQDALSKPSPVTGYNDAERLADEQSELV
>d2cpga_a.43.1.2 (A:) Transcriptional repressor CopG {Streptococcus agalactiae}
MKKRLTITLSESVLENLEKMAREMGLSKSAMISVALENYKKQ
>d1irqa_a.43.1.2 (A:) Omega transcriptional repressor {Streptococcus pyogenes}
IMGDKTVRVRADLHHIIKIETAKNGGNVKEVMDQALEEYIRKLPDKL
>d1cmba_a.43.1.2 (A:) Met repressor, MetR {Escherichia coli}
AEWSGEYISPYAEHGKKSEQVKKITVSIPLKVLKILTDERTRRQVNRLHATNSELLCEAFLHAFTGQPLPDDADLRKERSDEIPEAAKEIMREMGINPE
TWEY
>d1fvka1_a.44.1.1 (A:65-128) Disulphide-bond formation facilitator (DSBA), insertion domain {Escherichia coli}
GGDLGKDLTQAWAVAMALGVEDKVTVPFLFEGVQKTQTIRSASDIRDVFINAGIKGEYDAAWNS
>d1bed_1_a.44.1.1 (63-126) Disulphide-bond formation facilitator (DSBA), insertion domain {Vibrio cholerae}
GNMGQAMSKAYATMIALEVEDKMPVMFNRHTLRKPPKDEQELRQIFLDEGIDAALKFDAAYNG
>d1aqwa1_a.45.1.1 (A:77-209) Glutathione S-transferase {Human (Homo sapiens), class pi}
GLYGKDQQEAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDYVKALPGQLKPFETLLSQNQGGKTFIVGDQISFADYNLLDILLIHEVLAPGCLDAFPPL
LSAYVGRILSARPKLKAFLASPEYVNLPINGNGKQ
>d2gsra1_a.45.1.1 (A:77-207) Glutathione S-transferase {Pig (Sus scrofa), class pi}
YGKDQKEAALVDMVNDGVEDLRCKYATLIYTNYEAGKEKYVKELPEHLKPFETLLSQNQGGQAFVVGQSQISFADYNLLDILLIHQVLNPSCLDAPPLL
SAYVARLSARPKIKAFLASPEHVNRPINGNGKQ
>d1glqa1_a.45.1.1 (A:79-209) Glutathione S-transferase {Mouse (Mus musculus), class pi}
YGKNQREAAQMMDMVNDGVEDLRGKYVTLYIYTNYENGKNDYVKALPGHLKPFETLLSQNQGGKAFIVGDQISFADYNLLDILLIHQVLAPGCLDNFP
LLSAYVARLSARPKIKAFLSSPEHVNRPINGNGKQ
>d1gtua1_a.45.1.1 (A:85-217) Glutathione S-transferase {Human (Homo sapiens), class mu}
LCGETEEEKIRVDILENQTMNDNHMQLGMCYNPPEFEKLKPYLEELPEKLKLYSEFLGKRPWFAGNKITFVDFLVYDVLDRHIFEPKCLDAFPNLKDF
SRFEGLEKISAYMKSSRFLPRPVFSKMAVGK
>d1hna_1_a.45.1.1 (85-217) Glutathione S-transferase {Human (Homo sapiens), class mu}
LCGESEKEQIREDILENQFMDSRMQLAKLCYDPDFEKLKPYLEELPTMMQHFSQFLGKQPWFAGDKITFVDFLYDILDQNRIFDPKCLDEFPN
ISRFEGLKISAYMKSSRFLPKPLYTRAVVWGNK
>d3gtub1_a.45.1.1 (B:85-224) Glutathione S-transferase {Human (Homo sapiens), class mu}
RKHNMCGETEEEKIRVDIENQVMDFRQLIRLCYSSDHEKLKPQYLEELPGQLKQFSMFLGKFWAGEKLTFVDFLYDILDQNRIFDPKCLDEFPN
LKAFMCRFEALEKIAAYLQSDQFCMPINNKMAQWGNK
>d4gtua1_a.45.1.1 (A:85-217) Glutathione S-transferase {Human (Homo sapiens), class mu}
LCGETEEEKIRVDILENQAMDVSNQLARVCYSPDFEKLKPYEELPTMMQHFSQFLGKRPWFAGDKITFVDFLAYDVLDRHIFEPNCLDAFPNLKD
FISRFEGLEKISAYMKSSRFLPKPLYTRAVVWGNK
>d2gstaa1_a.45.1.1 (A:85-217) Glutathione S-transferase {Rat (Rattus norvegicus), class mu}
LCGETEEERIRADIVENQVMDNRMQLIMLCYNPDFFEKLKPQEFLKTIPEKMKLYSEFLGKRPWFAGDKITFVDFLAYDILDQYHIFEPKCLDAFPNLKD
FLARFEGLKKISAYMKSSRYLSTPIFSKLAQWSNK
>d1gsua1_a.45.1.1 (A:85-217) Glutathione S-transferase {Chicken (Gallus gallus), class mu}
MCGETEVKQRVDVLENHLMQLRMAFARLCYSPDFEKLKPAYEQLPGKLRQLSRFLGSRSWFVGDKLTVDLAYDVLQQRMFVPDFCPELQGNL

SQFLQRFEALEKISAYMRSGRFMKAPIFWYTALWNNK
>d1gsea1 a.45.1.1 (A:81-222) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}
LYGKDIKERALIDMYIEGIADLGEMILLPVCPEEKDAKLALIKEKIKNRYFPAFEKVLKSHGQDYLGVGNKLSRADIHLVELYYVEELDSSLSSFPPLLKAL
KTRISNLPTVKKFLQPGSPRKPPMDEKSLEARKIFRF
>d1gula1 a.45.1.1 (A:81-220) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}
LFGKNLKERTLIDMYVEGTLDLLELLIMHPFLKPDDQQKEVVNMAQKAIIRYFPVFEKILRGHGQSFLVGNCQLSLADVILLQTILAEEKIPNILSAFPFL
QEYTVKLSNIPTIKRFLEPGSKKKPPDEIYVRTVYNIF
>d1ev4a1 a.45.1.1 (A:80-222) Glutathione S-transferase {Rat (Rattus norvegicus), class alpha (a1-1)}
DLYGKDMKERALIDMYSEGILDTEMIMQLVICPPDQEAKTALAKDRTKNRYLPAFEKVLKSHGQDYLGVGNKLTVDIHLLELLYVEEFDASLLTSFPL
LKAFKSRISLSPNVKKFLQPGSQRKLPMDAKQIEEARKIYKF
>d1ev4c1 a.45.1.1 (C:80-208) Glutathione S-transferase {Rat (Rattus norvegicus), class alpha (a1-1)}
DLYGKDMKERALIDMYSEGILDTEMIMQLVICPPDQEAKTALAKDRTKNRYLPAFEKVLKSHGQDYLGVGNKLTVDIHLLELLYVEEFDASLLTSFPL
LKAFKSRISLSPNVKKFLQPGSQRKLP
>d1f3aa1 a.45.1.1 (A:80-221) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-1)}
LYGKDMKERALIDMYSEGILDTEMIGQLVLCPPDQREAKTALAKDRTKNRYLPAFEKVLKSHGQDYLGVGNRTRVDIHLLEVLLYVEEFDASLLTPFPL
KAFKSRISLSPNVKKFLQPGSQRKPPMDAKQIQEARAKAFKI
>d1b48a1 a.45.1.1 (A:80-222) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-4)}
NLYGKDLKERVIRIDMYADGTQDLMMMIAVAPFKTPKEESEYDLISRALKTRYFPVFEKILKDGHGEAFLVGNQLSWADIQLLEAILMVEELSAPVLSDF
PLLQAFKTRISNIPTIKFLQPGSQRKPPPDGPYVEVVRIVLKF
>d1jra1 a.45.1.1 (A:80-244) Glutathione S-transferase {Human (Homo sapiens), class theta}
TPDHWYPSDLQARARVHEYLGWHADCIRGTFGIPLWVQVLGPLIGVQVPEEKVERNRTAMDQALQWLEDKFLGDRPFLAGQQVTADLMAEEL
MQPVALGYELFEGRPRLAAWRGRVEAFLGAELCQEAHISIISILEQAAKTLPTPSPEAQAMLLRIARIP
>d1pd211 a.45.1.1 (1:76-199) Glutathione S-transferase {Rat (Rattus norvegicus), class sigma}
DLAGKTELEQCQVDAVVDTLDDFMSLFPWAEEENQDLKERTFNDLRTQAPHLLKLDLTYLGDKEWFIGNYVTWADFYWDICSTTLLVLPDKLLGIYP
RLVSLRNKVQAIPASAWILKRPQTKL
>d2gsq_1 a.45.1.1 (76-202) Glutathione S-transferase {Squid (Ommastrephes sloani pacificus), class sigma}
LDGKTSLEYRVDEITETLQDIFNDVVKIKFAPEAAKEAVQQNYEKSCKR LAPFLEGLLVSNGGDGFFVGNSMTLADLHCYVALEVPLKHTPELLKDC
PKIVALRKRAECPKIAAYLKKRPVRDF
>d1eema1 a.45.1.1 (A:103-241) Glutathione S-transferase {Human (Homo sapiens), class omega}
LPDDPYEKACQKMLEFSKVP SLVGSFIRSQNKEDYAGLKEEFRKEFTKLEEVLNTKKTFFGGNSISMIDYLIWPWFERLEAMKLNECVDHTPKLKL
WMAAMKEDPTVSALLSEKD WQGFELYLQNSPEACDYGL
>d1fw1a1 a.45.1.1 (A:88-212) Glutathione S-transferase {Human (Homo sapiens), class zeta}
LLPQDPKKRASVRMISDLIAGGIQPLQNLSVLKQVGEEMQLTWAQNAITCGFNALEQILQSTAGIYCVGDEVTMADLCLVPQVANAERFKVDLTPYP
TISSINKRLLVLEAFQVSHPCRQPDPT
>d1bg5_1 a.45.1.1 (81-254) Glutathione S-transferase {Schistosoma japonicum}
MLGGCPKERA EISMLEGAVLDI RYGV SRI AYSKDFETLK VDF LSKLPEMLKMFEDRLCHK TYLNGD HVT PDF MLYDAL DVV LYMDPMCLDAFPKLV
CFKKR IAEIPQIDKYLKSSKYIAWPLQGWQATF GGGD HPPKSDLV PRGSSYY QEA KSSKIMESFKNM VPQ QALVNSS
>d1duga1 a.45.1.1 (A:81-220) Glutathione S-transferase {Schistosoma japonicum}
LGGCPKERA EISMLEGAVLDI RYGV SRI AYSKDFETLK VDF LSKLPEMLKMFEDRLCHK TYLNGD HVT PDF MLYDAL DVV LYMDPMCLDAFPKLV
KKR IAEIPQIDKYLKSSKYIAWPLQGWQATF GGGD HPPKSDLV PRGSMELDKWA
>d1gne_1 a.45.1.1 (80-232) Glutathione S-transferase {Schistosoma japonicum}
MLGGCPKERA EISMLEGAVLDI RYGV SRI AYSKDFETLK VDF LSKLPEMLKMFEDRLCHK TYLNGD HVT PDF MLYDAL DVV LYMDPMCLDAFPKLV
CFKKR IAEIPQIDKYLKSSKYIAWPLQGWQATF GGGD HPPKSDLV PRGSMELDKWA
>d1fhe_1 a.45.1.1 (81-214) Glutathione S-transferase {Fasciola hepatica}

LGTTPEERARISMIEGAAMDLRIGFGRVCYNPKFEEVKEEYVKELPKTLKMWSDFLGDRHYLTGSSVSHVDFMLYETLDSIRYLAPHCLDEFPLKKEFK
SRIEALPKIKAYMESKRFIKWPLNGWAASFGAGDA

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

IGTTSEERARVSMIEGAAVDLRQGISRISYQPKEQLKEGYLKDLPTTMKWMSDFLGKNPVLRGTSVSHVDFMVYEALDAIRYLEPHCLDHFPNLQQ
FMSRIEALPSIKAYMESNRFIKWPLNGWAQFGGGDAPP

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

LQTDSKNISQYAIMAGMQVEDHQFDPVASKLAFEQIFKSIYGLTDEAVVAEEEAKLAKVLDVYEARLKEFKYLAGETFTLTDLHHIPAIQYLLGPTKK
LFTERPRVNEWVAEITKRPASEKVQ

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

ELLREGNLEEAAMVDVWIEVEANQYTAALNPILFQVLSPMLGGTTDQKVVDENLELKKVLEVYEARLTCKYLAGDFSLADLNHVSVTLCFLATPY
ASVLDAYPHVKAWWSGLMERPSVQKVAALM

>d1aw9_1 a.45.1.1 (83-217) Glutathione S-transferase {Maize (Zea mays), type III}

GTDLLPATASAALKLEVWLEVESHHFYPNASPLVFQLLVRPLLGGAPDAAVVDKHAEQLAKEVYEAHLARNKYLADANHASYLLYSKTP
KAGLVAARPHVKAWWEAIVARPAFKQTVAAIPLPPPP

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

PLLPRDLHKRAVNYQAMSIVLSGIQPHQNLAVIRYIEEKINVEEKTAVVNNAITKGFTALEKLLVNCAGKHATGDEIYLADLFLAPQIHGAINRFQINM
EPYPTLAKCYESYNELPAFQNALPEKQPDAPSST

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

QLLAPVNSISRYKTIEWLNYIATELHKGFTPLFRPDTPEEYKPTVRAQLEKKLQYVNEALKDEHWICGQRFTIADAYLFTVLRWAYAVKLNLEGLEHIAA
FMQRMAERPEVQDALSAEGLK

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

LLGGCPKERAISEMLEGAVLDIYRGVSRIAYSQDFETLKVDFSKLPEMLKFEDRLCHKTYLNGDHVTDPDFMLYDALDVLYMDPMCLDAFPKLVCF
KKRIEAIPOQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLVPRGSRRASVGSRMHYPGAFTYSPTPVTSGIGIGMSAMGS

>d1pmt_1 a.45.1.1 (81-201) Glutathione S-transferase {Proteus mirabilis}

NLIAPPKALERHQIEWLNFLASEVHKGSPLFSSDTPESYLPVVKNKLKSFKFYINDVLSQKQCVCGDHFTVADAYLFTLSQWAPHVALDLDLHSQ
DYLARIAQRPNVHSALVTEGLI

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

GLAPAEGSLDRYRLLSRLSFLGEFHKAFLVPLFAPATSDEAKAAAESVKNHLAALDKELAGRDHAGNAFSVADIYLYVMLGWPAYVGIDMAAYPAL
GAYAGKIAQRPAVGAAALKAEGLA

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

PLLTGKRSPAIEEWLRKVNGYANKLLPRAFKSAFDEFSTPAARKYFVDKKEASAGNFADLLAHSDGLIKNISDDLRAVDKLIVKPNAVNGELSEDDIQLF
PLLRNLTAVGINWPSRVADYRDNMAKQTQINLLSSMAI

>d1k0da1 a.45.1.1 (A:201-351) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}

LWSDDLADQSQINAWLFFQTSGHAPMIGQALHFYRFSQKIASAVERYTDEVRRVYGVVEMALAERREALVMELDTENAAAYSAGTPMSQRFF
DYPVWLVDKLTIAIDLAFVPWNVVDRIGINIKIEFPEVYKWTKHMMRRAPIKAL

>d1k0ma1 a.45.1.1 (A:92-240) Chloride intracellular channel 1 (clic1) {Human (Homo sapiens)}

RYPKLAALNPESNTAGLDIFAKFSAYIKNSNPALNDNLEKGLLKALKVLDNYLTSPLPEGVDETSAEDEGVSRKFLDGNELTACNLLPKLHIVQVVC
KKYRGFTIPEAFRGVHRYLSNAYAREFASTCPDDEIELAYEQVAKAL

>d1bmta1 a.46.1.1 (A:651-740) Methionine synthase domain {Escherichia coli}

QAЕWRSWEVNRKLEYSLVKGITEFIEQDTEEARQQATRPIEVIEGPLMDGMNVVGDLFEGKMFPLQVVKsarVMKQAVAYLEPFIEASK

>d2tpt_1 a.46.2.1 (1-70) Thymidine phosphorylase {Escherichia coli}

LFLAQEIIRKKRDGHALSDEEIRFFINGIRDNTISEGQIAALAMTIFFHDMDTMRPERVSLTAMRDGTVL

>d1brwa1 a.46.2.1 (A:1-70) Pyrimidine nucleoside phosphorylase {Bacillus stearothermophilus}

MRMVVDLIAKKRDGKALTKEEIEWIVRGYTNGDIPDYQMSALAMAIFRGMTEEETAALTMAMVQSGEMLD

>d1bf5a1 a.47.1.1 (A:136-316) STAT-1, coiled coil domain {Human (Homo sapiens)}

LDKQKELDSKVRNVKDKVMCIEHEIKSLEDLQDEYDFKCKTLQNREHLLLKKMYLMDNKRKEVVKIIELNVTELTONALINDELVEWKRRQQSAC

IGGPPNACLDQLQNLQNWFTIAESLQQVRRQQLKKELEQKYTYEHDPITKNKQVLWDRTRFSLFQQLIQSS

>d1bg1a1 a.47.1.1 (A:136-321) STAT3b {Mouse (Mus musculus)}

VVTTEKQQMLEQHLQDVTKRQVQDLEQKMKVVENLQDDDFNYKTLKSQGDMQDLNGNNQS VTRQKMQQLEQMLTALDQMRRSIVSELAGLLS

AMEYVQKLTDEELADWKRRQQIACIGGPPNICLDRLENWITS LAESQLQTRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAF

>d1dn1b_a.47.2.1 (B:) Syntaxin 1A N-terminal domain {Rat (Rattus norvegicus)}

DRFMDEFFEQVEEIRGFIDKIAENVEVKRKHSAILASPNPDEKTKEEELMSDIKTANKVRSKLKSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKFV

EVMSEYNATQSDYRERCKGRIQRQLEITGRRTSEELEDMLESGNPAIFASGII MDSSISQALSEIETRHSEIILKLENSIRELHDMFMDMAMLVESQGE

MIDRIEYNVEHAVDYVERAV

>d1ez3a_a.47.2.1 (A:) Syntaxin 1A N-terminal domain {Rat (Rattus norvegicus)}

RDRFMDEFFEQVEEIRGFIDKIAENVEVKRKHSAILASPNPDEKTKEEELMSDIKTANKVRSKLKSIEQSIEQEEGLNRSSADLRIRKTQHSTLSRKF

VEVMSEYNATQSDYRERCKGRI

>d1fioa_a.47.2.1 (A:) Sso1 {Baker's yeast (Saccharomyces cerevisiae)}

MHDFVGFMNKISQINRQLDKYDHTINQVDSLHKRLTEVNEEQASHLRHSLDNFVAQATDLQFKLKNEIKSAQRDGHI DTNKQAQAENS RQRFKLI

QDYRIVDSNYKEENKEQAKRQYMIIQPEATEDEVAAISDVGQQQIFSQALLNANRGEAKTALAEVQARHQELLKLEKSMAELTQLFNDMEELVIE

QQ

>d1hs7a_a.47.2.1 (A:) Vam3p N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

TNQKTKELSNLIETFAEQSRVLEKECTKIGSKRDSKELRYKIE TELIPNCTS VRDKIESN I LHQNGKLSADFKNLKYQSLQQSYNQRKSLFPLK

>d2cbla2_a.48.1.1 (A:47-177) N-terminal domain of cbl (N-cbl) {Human (Homo sapiens)}

PPGTVDKMKVEKCWKLMDKVVRLCQNP KLA LKNSPPYILDLLPTYQHLRTILSRYEGKMETLGENEYFRVFMENLMKKTKQTISLFKEGKERM YEE

NSQPRRNLTLSLIFSHMLAELKGIFPSGLFQGD

>d1de4c1_a.48.2.1 (C:609-756) Transferrin receptor ectodomain, C-terminal domain {Human (Homo sapiens)}

LDYERYNSQLSFVRDLNQYRADIKEMG LSLQWL YSARGDFFRATSRLTDFGNAEK TDRVMKKLNDRVMR VEYHFLSPYVSPKESPFRHVFWGS

GSHTLPALLENLKLRQNNGAFNETLFRNQLALATWTI QGAANALSGDVWDI

>d1eo0a_a.48.3.1 (A:) Transcription elongation factor TFIIS N-domain {Baker's yeast (Saccharomyces cerevisiae)}

MDSKEV LVHVKNLEKNKSNDAAV LEILHVL DKEFVPTEKLL RETKVGV EVNKF KKSTNVE ISKL VKKMISSWKDA IN

>d1f6va_a.49.1.1 (A:) C-terminal domain of B transposition protein {Bacteriophage mu}

GSRIAKRTAINKTKKADVKAIADA WQINGE KELELLQQIAQKPGALRILNHSRLAAMTAHGKGERVNEDYL RQAFRE LDVDISTLLRN

>d1i6ve_a.143.1.1 (E:) RNA polymerase omega subunit {Thermus aquaticus}

MAEPGIDKLF GMVDSKYRLTVVVAKRAQQQLRHRFKNTVLEPEERPKMRTLEG LYDDPNAVTWAMKELLT GRLFFGENL VPEDRLOKEMERLYPT E

EE

>d1cfaa_a.50.1.1 (A:) C5a anaphylotoxin {Human (Homo sapiens)}

MLQKKIEEAKYKHSVVKKCCYDGASVNNDTCEQRAARISLGPRCIKAFTECCVVASQLRANISHKDMC

>d1c5a_a.50.1.1 (-) C5a anaphylotoxin {Pig (Sus scrofa domestica)}

MLQKKIEEAKYKYSAMLKKCCYDGAYRNDDETCEERAARIKIGPKCVKA FKDCCYIANQVRAEQS

>d0c3a_a.50.1.1 (-) C3a anaphylotoxin {Human (Homo sapiens)}

SVQLTEKRMNKGKYPKELRKCCEDGMRQNPMRFSQRRTRFISLGEACKVFLDCCN YITELRRQHARASHLGLAR

>d1ocrh_a.51.1.1 (H:) Cytochrome c oxidase subunit h {Cow (Bos taurus)}

KIKNYQTAPFD SRFPNQNQTRNCWQNYLDFHRCEKAMTA KGGDVSVC EYRRVYKSLCPISWVSTWDDRRAEGTFPGKI

>d1hyp_a.52.1.1 (-) Soybean hydrophobic protein {Soybean (Glycine max)}

PSCPDL SICLN ILGGSLGT VDDCCALIGGLDIEAIVCLCIQLRALGILNLRN LQLI NSCRS YPSNATCPRT

>d1bwoa_a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Wheat (Triticum aestivum), L. seeds}

IDCGHVDSLVRPCLSYVQGGPGPSGQC CDGVKNLHNQARSQSDRQSACNCLKG IARGIHNLNEDNARSIPP KCGVNL PYTISLNIDCSRV

>d1be2__ a.52.1.1 (-) Plant non-specific lipid-transfer protein (ns-LTP) {Barley (*Hordeum vulgare*)}
LNCGQVDSKMKPCLTYVQGGPGPSGECCNGVRDLHNQAQSSGDRQTCVNCLKGIAARGIHNLNNAASIPSKCNVNVPYTISPDIDCSRIY
>d1fk5a_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Maize (*Zea mays*)}
AISCGQVASAIAPCISYARGQGSGPSAGCCSGVRSNNAARTTADRRACNCLKNAAAGVSGLNAGNAASIPSKCGSIPYTISTSTDCSRVN
>d1rzl__ a.52.1.1 (-) Plant non-specific lipid-transfer protein (ns-LTP) {Rice (*Oryza sativa*)}
ITCGQVNSAVGPCLTYARGGAGPSAACSGVRSKAAASTTADRRACNCLKNARGIKGLNAGNAASIPSKCGSVSPYTISASIDCSRVS
>d1hssa_ a.52.1.2 (A:) 0.19 alpha-amylase inhibitor {Wheat (*Triticum aestivum*)}
MCYPGQAFQVPALPACRPLLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSILDSMYKEHGAQEGQAGTGAFFPRCRREVVKLTAASITAVC
RLPIVVDASGDGAYVCKDVAYPDA
>d1tmqb_ a.52.1.2 (B:) Trypsin/alpha-amylase inhibitor RBI {Ragi (*Eleusine coracana gaertneri*), seeds}
SVGTSCIPGMAIPHNPILDSCRWYVSTRTCVGPRLATQEMKARCCRQLEAIPAYCRCEAVRILMDGVVTSSQHEGRLLQDLPGCPQRQVQRAFAPK
LVTEVECNLATIHGGPFCLSL
>d1bea__ a.52.1.2 (-) Hageman factor/amylase inhibitor {Maize (*Zea mays*)}
SCVPGWAIPHNPPLPSCRWYVTSRTCGIGPRLPWPELKRRCCRELADIPAYCRCTALSILMDGAIPPGPDAQLEGRLEDLPGCPREVQRGFAATLVTEA
ECNLATISGVAECPWILG
>g1pn1.1 a.52.1.3 (A;B:) Napin BNIB {Rape (*Brassica napus*)}
QPQKCQREFQQEQHLRACQQWIRQQLAGSPFXQSGPQQGPWLREQCCNELYQEDQVCVCPTLKQAAKSVRVQGQHGPfqSTRYQIAKNLPNV
CNMKQIGTCPFIAI
>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*)}
KKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG
>d1k1fa_ a.147.1.1 (A:) Bcr-Abl oncoprotein oligomerization domain {Human (*Homo sapiens*)}
MVDPGFAEAWKAQFPDSEPPRMELRSVGDIEQELEKASIRRLEQEVNQERFRMIYLQTLAKEK
>d1adt_1 a.54.1.1 (176-265) Domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}
PIVSWEKGMEAARALMDKYHVNDLKANFKLDPQVEALAAVCKTTLNEEHRLQLFTSNKTFVTMMGRFLQAYLQSFAEVTYKHH
>d1ihfa_ a.55.1.1 (A:) Integration host factor (IHF) {Escherichia coli}
ALTAKEMSEYLFDKLGSKRDAKELVELFFEEIRRLENQEVKLSGFGNFDLDRDNQRPGRNPKTGEDIPITARRVVTFRPGQKLKSRVENASPK
>d1ihfb_ a.55.1.1 (B:) Integration host factor (IHF) {Escherichia coli}
MTKSELIERLATQQSHIPAKTVEDAOKEMLEHMASTLAQGERIEIRGFGFSLHYRAPRTGRNPKTGDKVELEGKYVPHFKPGKELRDRANIY
>d1hns__ a.55.1.1 (-) DNA-binding domain of H1 protein, (H-NS) {Escherichia coli}
AQRAKYSYVDENGETKTWTGQGRTPAVIKKAMDEQGKSLDDFLIKQ
>d1huua_ a.55.1.1 (A:) HU protein {Bacillus stearothermophilus}
MNKTELINAVAETGLSKKDATKAVDAVFDSITEALRKGDVKVQLIGFGNFVNRERAARKGRNPQTGEEMEIPASKVPAFKPGKALKDAVK
>d1b8za_ a.55.1.1 (A:) HU protein {Thermotoga maritima}
MNKKELIDRVAKKAGAKKKDVKLILDILETITEALAKGEKVQIVGFGSFEVRKAAARKGVNPQTRKPITPERKVPFKPGKALKEVK
>d1exe_ a.55.1.1 (A:) Transcription factor 1, TF1 {Bacteriophage SPO1 (Bacillus subtilis)}
MNKTELIAKAIAQDTGLTQSVSKMLASFKEIITETVAKGDVKVQLTGFLNIKPVARQARKGFNPQTQEALIAPS VGVVKPGESLKAAEGLKYEDFAK
>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}
QPNLHPLQKAWVLHGGAQCGFCSPGFIVSAKGLDTNADPSREDVRDWFQKHRNACRCTGYKPLDAVMDAAAVINGKKPETDLEFKMPADG
RIWGSKYPRPTAVAKVTGLT

>d1dgja1 a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2 {Desulfovibrio desulfuricans}
APDCLHPLQHAWIQHGAQCGFCTPGFIVSAKALLDENVAPSREDVRDWFQKHHNICRCTGYKPLDAVMDAAAILRGEKTVEISFKMPADGR
WGSSIPRPSAVAKVTGLA

>d1fo4a1 a.56.1.1 (A:93-165) Xanthine oxidase, domain 2 {Cow (Bos taurus)}
STKTRLHPVQERIAKSHGSQCGFCTPGIVMSMYTLRNQPEPTVEEIEDAFQGNLCRCTGYRPILQGFRFAK

>d1jroa1 a.56.1.1 (A:85-166) Xanthine dehydrogenase chain A, domain 2 {Rhodobacter capsulatus}
DGRLHPVQQAMIDHHGSQCGFCTPGFIVSMAAHDRDRKDYDDLALGNLCRCTGYAPIRAAEAAAGEPPADWLQADAFTL

>d1qj2a1 a.56.1.1 (A:82-161) Carbon monoxide (CO) dehydrogenase iron-sulfur protein, C-domain {Pseudomonas carboxydovorans}
APDGTLSALQEGFRMMHGLQCGYCTPGMIMRSRLLQENPSPTEAEIRFGIGGNLCRCTGYQNIVKAIQYAAAKINGVPF

>d1ffva1 a.56.1.1 (A:82-157) Carbon monoxide (CO) dehydrogenase iron-sulfur protein, C-domain {Hydrogenophaga pseudoflava}
NKGVLHAVQEGFYKEHGLQCGFCTPGMLRAYRFLQENPNTAEIRGMTGNLCRCTGYQNIVKAVQYAARKLQE

>d1dj8a_a.57.1.1 (A:) Protein HNS-dependent expression A; HdeA {Escherichia coli}
NNKPVNSWTCEDFLAVDESFPQTAVGFAEALNNDKPEDAVLDVQGIATVTPAIVQACTQDKQANFKDKVKGEWDKIKK

>d1g9la_a.144.1.1 (A:) poly(A) binding protein {Human (Homo sapiens)}
GPLGSAAAATPAVRTVPQKYAAGVRNPQQHLNAQPQVTMQQPAHVQQEPLTASMLASAPPQEQQMLGERLFPLIQAMHPTLAGKITGML
LEIDNSELLHMLESPELSRKVDEAVAVLQAHQAKEAAQKAVNSATGVPTV

>d1i2ta_a.144.1.1 (A:) hyperplastic discs protein {Human (Homo sapiens)}
HRQALGERLYPRVQAMQPAFASKITGMILLESPQAQLLLASEDSLRARVDEAMELIIAHG

>d1af7_1 a.58.1.1 (11-91) Chemotaxis receptor methyltransferase CheR, N-terminal domain {Salmonella typhimurium}
SVLLQMTQRQLALSDAHFRRICQLIYQRAGIVLADHKRDVMVNRLVRLRALGLDDFGRYLSMLEANQNSAEWQAFINALTT

>d1e91a_a.59.1.1 (A:) Sin3B {Mouse (Mus musculus)}
ESDSVEFNNAISYVNKIKTRFLDHPEIYRSFLEILHTYQKEQLHTKGRPFQGMSEEEVFTEVANLFRGQEDLLSEFGQFLPEAKR

>d1g1eb_a.59.1.1 (B:) Sin3A {Mouse (Mus musculus)}
SLQNNQPVEFNHNAINYVNKIKNRQFQGQPDIFYKAFLIEHTYQKEQRNAKEAGGNYTPALTEQEYVAQVARLFKNQEDLLSEFGQFLPDA

>d1bqv__ a.60.1.1 (-) Ets-1 transcription factor pointed domain {Mouse (Mus musculus)}
MECADVPLLTSSKEMMSQALKATFSGFTKEQQRLGIPKDPRTQWTETHVRDWVMWAVNEFSLKGVDQKFCMSGAALCALGKECFLELAPDFVG
DILWEHLEILQKEDVK

>d1b0xa_a.60.1.2 (A:) EphA4 receptor tyrosine kinases {Mouse (Mus musculus)}
FSAVVSGDWLQAIKMDRYKDNTAAGYTTLEAVVHMSQDDLARIGITAITHQNKILSSVQAMRTQMQQMHG

>d1b4fa_a.60.1.2 (A:) EphB2 receptor {Human (Homo sapiens)}
PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFVVSQMMMEDILRVGVTLAGHQKKILNSIQVMRAQMNMQIQS

>d1sgg__ a.60.1.2 (-) EphB2 receptor {Chicken (Gallus gallus)}
YTSFNTVDEWLDAIKMSQYKESFASAGFTFDIVSQMTVEDILRVGVTLAGHQKKILNSIQVMRAQM

>d1coka_a.60.1.2 (A:) C-terminal domain of p73 {Human (Homo sapiens)}
YHADPSLVSFLTGLCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGQLQDLKQGHHDY

>d1dxsa_a.60.1.2 (A:) C-terminal domain of p73 {Human (Homo sapiens)}
SLVSFLTGLCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRGQLQDL

>d1cuk_2 a.60.2.1 (65-142) DNA helicase RuvA subunit, middle domain {Escherichia coli}
NKQERTLFKELIKTNGVGPKLALAILSGMSAQQFVNAVEREEVGALVKLPGIGKKTAERLIVEMKDRFKGLHGDLFTP

>d1bvsaa.60.2.1 (A:64-134) DNA helicase RuvA subunit, middle domain {Mycobacterium leprae}

DAENRDLFLALLSVGVGPRALAMATLAVHDAAALRQALADSDVASLTRPGIGRRGAERIVLEADKVGPV
>d1dgsa1 a.60.2.2 (A:401-581) NAD+-dependent DNA ligase, domain 3 {Thermus filiformis}
RWPEACPECGHRLVKEGKVHRCPNPLCPAKRFEAIRHYASRKAMDIEGLGEKLERLLEKGVLVDADLYHLRKEDLLGLERMGEKSAQNLLRQIESK
HRGLERLLYALGLPGVGEVLARNLARRFGTMDRLLEASLEELIEVEEVGELTARAILETLKDPAFRDLVRLKEAGVSMESK
>d1coo__ a.60.3.1 (-) C-terminal domain of RNA polymerase alpha subunit {Escherichia coli}
FDPIIIRPVDDLELTVRSANCLKAECIAHYIGDLVQRTEVELLKTPNLGKSLTEIKDVLASRGSLGMRLENWPPASIADE
>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)}
EESFGPQPISRLEQCGINANDVKKLEEAAGFHTVEAVAYAPKKELINKGISEAKADKILAEEAKLVMG
>d1ci4a_ a.60.5.1 (A:) Barrier-to-autointegration factor, BAF {Human (Homo sapiens)}
MTTSQKHDFVAEPMEKEPVGSLAGIGEVLGKKLEERGFDKAYVVLQFLVLKKDEDLFREWLKDTGANAKQSRCDFGCLREWCDAFL
>d1bpya1 a.60.6.1 (A:10-91) DNA polymerase beta, N-terminal (8 kD)-domain {Human (Homo sapiens)}
TLNGGITDMLTELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKKLPGVGTKIAEKIDEFLATGKLKLEKIRQD
>d1dk2a_ a.60.6.1 (A:) DNA polymerase beta, N-terminal (8 kD)-domain {Rat (Rattus norvegicus)}
SKRKAPQETLNGGITDMLVELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKKLPGVGTKIAEKIDEFLATGKLKLEK
>d1jmsa1 a.60.6.1 (A:148-242) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}
KKISQYACQRRRTLNYYNQLFTDALDILAENDELRENEGSCAFMRASSVLKSLPFPITSMKDTEGIPCLGDKVKSIEGIEDGESSEAKAVLN
>d1tfr_1 a.60.7.1 (183-305) T4 RNase H {Bacteriophage T4}
GSAEIDCMTKILKGDKKDNNVASVKVRSDFWFTRVEGERTPSMKTTSIVEAIANDREQAKVLLTESEYNRYKENLVLIIDFYIPDNIASNIVNYNSYKLPP
RGKIYSYFVKAGLSKLTNSINEF
>d1bgxt1 a.60.7.1 (T:174-289) 5' to 3' exonuclease domain of DNA polymerase Taq {Thermus aquaticus}
LRPDQWADYRALTGDESDNLPGVKIGEKTARKLLEEWGSLEALLKNLDRKPAIREKILAHMDDLKLSWDLAKVRTDLPLEVDFAKRREPDRERLRA
FLERLEFGSLLHEFGILLE
>d1xo1a1 a.60.7.1 (A:186-290) T5 5'-exonuclease {Bacteriophage T5}
VDDVEQFISLKAIMGDLGNIRGVEGIGAKRGYNIIREFGNVLDIIDQLPLPGKQKYIQNLNASEELLFRNLILVLDPYCVDAIAAVGQDVLDKFTKDIL
EIAE
>d1a77_1 a.60.7.1 (209-316) Flap endonuclease-1 {Archaeon Methanococcus jannaschii}
ISLDDLDIAIFMGTDYNPGGVKGIGFKRAYELVRSGVAKDVLKKEVEYYDEIKRIFKEPKVTDNYSLSLKDKEGIKFLVDENDFNYDRVKKHVDKLYN
LIANKT
>d1b43a1 a.60.7.1 (A:220-339) Fen-1 nuclease {Archaeon Pyrococcus furiosus}
LTREKLIELAILVGTDYNPAGGKIGLKKALEIVRHSDKPLAKFQKQSDVDLYAIKEFFLNPPVTNDYNLVWRDPDEEGILKFLCDEHDFSEERVKNGLER
LKKAIKSGKQSTLESWFKR
>d1d8ba_ a.60.8.1 (A:) HRDC domain from RecQ helicase {Baker's yeast (Saccharomyces cerevisiae)}
ELNNLRMTYERLRELNLGNRMVPPVGNFMPDSILKKMAILPMNDSAFATLGTVEDKYRRRFKYFKATIADLSKKRSSE
>d1go3f_ a.60.8.2 (F:) RNA polymerase II subunit RBP7 (RpoF) {Archaeon Methanococcus jannaschii}
MIGKKILGERYVTSEAAEIMYNRAQIGELEYEQGCALDYLQKFAKLDKEEAKLVEELISLGIDEKTAVKIADILPEDLDDRRAIYYKRELPEAAEILEIV
RKYI
>d1f44a1 a.60.9.1 (A:20-129) Cre recombinase {Bacteriophage P1}
SDEVRKNLMDMFRDRQAFSEHTWKMLLSVCRSWAAWCKLNNRKWFPAEPEDVRDYLQARGLAVKTIQQHLGQLNMLHRRSGLPRPSDSNA
VSLVMRRIRKENVDAGE
>d1a0p_1 a.60.9.1 (3-100) Recombinase XerD {Escherichia coli}
QDLARIEQFLDALWLEKNLAENTLNAYRRDLSMMVEWLHHRGLTLATAQSDDLQALLAERLEGGYKATSSARLLSAVRLFQYLYREKFREDDPSAHL
>d1floa1 a.60.9.1 (A:2-129) Fip recombinase {Baker's yeast (Saccharomyces cerevisiae)}

PQFDILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWMITHNGTAIKRATFMSYNTIISNSLSFDIVNKSLSQFKYKTQKATILEASLKKLIPAWEFTII
PYYGQKHQSDDITDIVSSLQLQFES

>d1zyma1_a.60.10.1 (A:22-144) Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain {Escherichia coli}
DEIVIDRKKSADQVDQEVERTFLSGRAKASAQLETIKTKAGETFGEEKEAIFEGHIMLLEDEELEQEIIALIKDKHMTADAAHEVIEGQASALEELDEY
LKERAADVRDIGKRLRNILGL

>d1jyga_a.60.11.1 (A:) Hypothetical protein YbjJ {Escherichia coli}
MNMDEAGGNWKQFKGVKEQWGLKLTDDMTIIEGKRDQLVGKIQERYGYQKDQAEKEVVDWETRNEYRW

>d1hiwa_a.61.1.1 (A:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}
VLSGGELDKWEKIRLRPGGKKQYKLKHIVVWASRELERFAVNPGLETSEGCRQILGQLQPSLQTGSEELRSLYNTIAVLYCVHQRIDVKDTKEALDKIEEE
QNKSKKKAQQAAAD

>d1hiws_a.61.1.1 (S:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}
VLSGGELDKWEKIRLRPGGKKQYKLKHIVVWASRELERFAVNPGLETSEGCRQILGQLQPSLQTGSEELRSLYNTIAVLYCVHQRIDVKDTKEALDKIEEE
QN

>d1tam_a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}
MGARASVLSGGELDRWEKIRLRPGGKKQYKLKHIVVWASRELERFAVNPGLETSEGCRQILGQLQPSLQTGSEELRSLYNTAVLYCVHQRIDVKDTK
EALDKIEEEQNKSKKKAQQAAAD

>d2hmx_a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}
HMGARASVLSGGELDKWEKIRLRPGGKKQYKLKHIVVWASRELERFAVNPGLETSEGCRQILGQLQPSLQTGSEELRSLYNTAVLYCVHQRIDVKDTK
EALDKIEEEQNKSKKKAQQAAADTGNNSQVSQNY

>d1ed1a_a.61.1.1 (A:) SIV matrix antigen {Simian immunodeficiency virus}
SVLSGKKADELEKIRLRPGGKKYMLKHVVWAANELDRFGLAESLLENKEGCQKILSVAPLVPTGSENLSLYNTVCIVCIHAEEKVKHTEAKQIV
QRHLVVEGTGAETMP

>d1jvr_a.61.1.2 (-) HTLV-II matrix protein {Human T-cell leukemia virus type 2}
HMGQIHGLSPTPIPKAPRGLSTHHWLNFNLQAAYRLQPQPSDFDFQQLRRFLKLALKTPIWLNPIDYSLLASLIPKGYPGRVVEIINILKNQVSPSAPAA
PVPTPICPTTTPPPPPPSPEAHVPPPYVEPTTQCF

>d1bax_a.61.1.3 (-) Mason-pfizer monkey virus matrix protein {Simian mason-pfizer virus}
MGQELSQHERYVEQLKQALKTRGVVKYADLLKFFDFVKDTCWPFPQEGTIDIKRWRRVGDCFQDYYNTFGPEKVPVTAFSYWNLIKELIDKKE

>d1a6s_a.61.1.4 (-) GAG polyprotein M-domain {Rous sarcoma virus}
GEAVIKVISSACKTCGKTPSKKEIGAMLSLLQKEGLLMSPSDLSPGSWDPIAALSQRAMILGKSGELKTWGLVLGALKAAREE

>d1heka_a.61.1.5 (A:) EIAV matrix antigen {Equine infectious anemia virus, EIAV}
AMADIGSMGDPLTWSKALKLEKVTVQGSQKLTGNCNWALSLVDFHDTNFVKEKDWFQLRDVPLLEDVTQTLSGQEREAFERTWWAISAVKM
GLQINNVVDGKASFQLLRAYE

>d1qgta_a.62.1.1 (A:) Hepatitis B viral capsid (hbcag) {Hepatitis B virus}
MDIDPYKEFGATVELLSFLPSDFPSVDRLLDTASALYREALSPEHCSPHHTALRQAICLGELMTLATVGNNEPDASRDLVNYVNTNMGLKIR
QLLWFHISCLTFGRETVLEYLVSFGVWIRTPPAYRPPNAPIST

>d1aep_a.63.1.1 (-) Apolipophorin-III {African locust (Locusta migratoria)}
NIAEAVQQLNHTIVNAAHELHETGLPTDEALNLTEQANAFKTKIAEVTTSLKQEAEKHQGSVAEQLNAFARNLNNSIHDAATSLNLQDQLNSLQS
ALTNVGHQWQDIATKTQASAQEAWAPVQSAQLEAAEKTKEAAAANLQNSIQSAVQK

>d1eq1a_a.63.1.1 (A:) Apolipophorin-III {Manduca sexta}
DAPAGGNAFEEMEKHAKEFQKTFSEQFNSLVNSKNTQDFNKALKDGSDSVLQQLSAFSSLQGAISDANGKAKEALEQARQNVEKTAELRKAHPD
VEKEANAFKDKLQAAVQTTVQESQKLAKEVASNMEETNKKLAPKIKQAYDDFKVHAEEVQKLHEAATKQ

>d1nkl_a.64.1.1 (-) NK-lysin {Pig (Sus scrofa)}
GYFCESCRKIIQKLEMVGPQPNETVTQAASQVCDKLKILRGLCKKIMRSFLRRISWDILTGKKPQAICVDIKICK

>d1qdma1_a.64.1.2 (A:1S-104S) (Pro)phytepsin {Barley (Hordeum vulgare)}

VVSQECKTIVSQYQQILDLLAETQPKKICSVGLCTFDGTRGSAGIRSVVDEPVKSNGLRADPMCSACEMAVVMQNLQAQNKTQDLILDYVNQLCNRLP

>d1e68a_a.64.2.1 (A:) Bacteriocin AS-48 {Enterococcus faecalis}

MAKEFGIPAAVAGTVLNVEAGGWTTIVSILTAGSGGLSLAAAGRESIKAYLKKEIKKGKRAVIAW

>d1ain__ a.65.1.1 (-) Annexin I {Human (Homo sapiens)}

GSAVSPYPTFPSSDVAALHKAIMVKVDEATIIDLTKRNNNAQRQQIKAAYLQETGKPLDETLKKALTGHLEEVVLALLKTPAQFDAELRAAMKGLGTDDEDLIELASRTNKEIRDINRVYREELKRDALKDITSDFRNALLSLAKGDRSEDFGVNEDLADSARALYEAGERRKGTDVNFNTILTRSYQP LRRVFQKYTKYSKHDMDNKVLDLELKDIKCLTAIVKCATSKPAFFAEKLHQAMKGVGTRHKALIRIMVSREIDMNDIKAFYQKMYGISLCQAILDET KGDYEKILVALCGGN

>d1bo9a_a.65.1.1 (A:) Annexin I {Human (Homo sapiens)}

TFNPSSDVAALHKAIMVKVDEATIIDLTKRNNNAQRQQIKAAYLQETGKPLDETLKKALTGHLEEVVLALLK

>d1hm6a_a.65.1.1 (A:) Annexin I {Pig (Sus scrofa)}

AMVSEFLKQAWFIDNEEYIYIKTVKGSKGGPGSAVSPYPTFPSSDVEALHKAITVKVDEATIIEILT KRTNAQRQQIKAAYLQEKGKPLDEALKALT GHLEEVALALLKTPAQFDAELRAAMKGLGTDDELNEILASRTNREIREINRVYKEELKRDALKDITSDFGDYQKALLSLAKGDRSEDLAINDDLADT DARALYEAGERRKGTDLNVFITLRTSYPHLRRVFQKYSKYSKHDMDNKVLDLELKDIENCLTVVVKCATSKPMFFAEKLHQAMKGIGTRHKTIRIM VSRSEIDMNDIKACYQKLYGISLCQAILDET KGDYEKILVALCG

>d1axn__ a.65.1.1 (-) Annexin III {Human (Homo sapiens)}

SASIWVGHGRGTVRDYPDFSPSVDAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEYQAAYGKELKDDLGDSLGHFEHLVALVTPPAVFDAKQL KKSMKGAGTNEDALIEILTTSRQMCDISQAYYTYYKSLGDDISSETSGDFRKALLTADGRRDESLKVDDEHLAKQDAQILYKAGENRWGTDEDKF TEILCLRSFPQLKLTDFEYRNISQKDIVDSIKGELSGHFEDLLLIAIVNCVRNTPAFLAERLHRAKGIGTDETLNRIMVSREIDLLDIRTEFKHYGYSYS AIKSDTSGDYEITLLKICGGDD

>d1i4aa_a.65.1.1 (A:) Annexin IV {Cow (Bos taurus)}

ASGFNAEDAQLRKAMKGLGTDEDAINVLAYRSTAQRQEIRTAYKTTIGRDLMDLKSELSGNFEQVILGMMPTVLYDVQELRKAMKGAGTDE GCLIEILASRTPEEIRRINQTYQLQYGRSLEDDIRS TSFMQRVLVLSAGGRDESNYLDDALMRQDAQDLYEAGEKKWGTDEVKFLVLCRNRNH LLHVFDEYKRIAQKDIEQSICKSETSGSFEDALLAIVKCMRNSAYFAERLYKSMKGLGTDDETLIRVMVSRAEIDMLDIRANFRKRLYGKSLYSFIKGDTSG DYRKVLLILCGGDD

>d1ala__ a.65.1.1 (-) Annexin V {Chicken (Gallus gallus)}

KYTRGTVTAFSPFDARADAELRKAMKGMGTDEETILKILTSRNNNAQRQEIASFKTLFGRDLVDDLKSELTGKFETLMVSLMRPARIFDAHALKHAIK GAGTNEKVLTIELASRTPAEVQNIQKVYMQEYANLEDKITGETSGHFQRLLVLLQANRDPDGRVEALVEKDAQVLFRAGELKWGTDEETFITILG TRSVSHLRRVFDKYMISGFQIEETIDRETSGDLEKLLAVVKCIRSPAYFAETLYYSMKGAGTDDTLIRVMVSREIDLLDIRHEFRKNFAKSLYQMIQ KDTSGDYRKALLLCGG

>d1hvd__ a.65.1.1 (-) Annexin V {Human (Homo sapiens)}

VLRGTVTDFPGFDGRADAELRKAMKGLGTD EESILTTSRSNAQRQEISAAFKTLFGRDLVDDLKSELTGKFETLMVSLMRPARIFDAHALKGA GTNEKVLTIESARTPEELRAIKQVYEEYGSNLEDDVVGDTGYYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAGELKWGTDEEKFITIGTRS VSHLRKVFDKYMISGFQIEETIDRETSGNLEQLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSREIDLFNIRKEFRKNFATSLSYMIKGDT SGDYKKALLLCGG

>d1g5na_a.65.1.1 (A:) Annexin V {Rat (Rattus norvegicus)}

ALRGTVTDFSGFDGRADAELRKAMKGLGTD EDSILNLLTARSNAQRQQIACEEFKTLFGRDLVNDMKSELTGKFETLMVSLMRPARIFDAHALKGA GAGTDEKVLTIESARTPEELRAIKQAYEEYGSNLEDDVVGDTGYYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAGELKWGTDEEKFITILG RSVSHLRRVFDKYMISGFQIEETIDRETSGNLENLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSREIDLFNIRKEFRKNFATSLSYMIKGDT SGDYKKALLLCGGEDD

>d1avc_1 a.65.1.1 (10-350) Annexin VI {Cow (Bos taurus)}

YRGSI RDFPDFNPSQDAETLYNAMKGFGSDKEAIINLITSRSNKQRQEICQNYKSLYKDLIADLKYTELGKFERLIVGLMRPPAYADAKEIKDAISGIGT DEKCLIEILASRTNEQIHLQVAAYKDAYERLEADITGDTGHSFRKMLVLLQGTREEDDVSEDLVQQDVQDLYEAGELKWGTDEAQFIYILGNSRKQ

HLRLVFDEYLKTTGKPIEASIRGEGLSGDFEKLMLAVVKCIRSTAEYFAERLFKAMKGLGTRDNTLIRIMVSRSELDMDIREIFRTKYEKSLSMIKNDTSG
EYKKTLLKLCGGDDAAGQFFPEAAQVAYQMWEWSAVR

>d1avc_2 a.65.1.1 (351-671) Annexin VI {Cow (Bos taurus)}

VELKGTVRPAGDFNPDAKALRKAMKGLTDEDTIIDITHRSNAQRQQIRQTFKSHFGRDLMAIDLKSELSGDLARLILGLMMPPAHYDAQLKKA
MEGAGTDEKALIEILATRTNAEIQAINKAYKEDYHKTLEDALSSDTSGHFKRILISLATGNREEGGEDRERAREDAQVAEILEIADTSGDKSSLETRFM
MILCTRSYPDLRRVFQEJVMTNYDVEHTIKKEMSGDVRDVFAIVQSVKNKPLFFADKLYKSMKGAGTEEKTLTRIMVSRSEIDLNNIRREFIEKYDKS
LHQAIEGDTSGHFLKALLAICGG

>d1dm5a_a.65.1.1 (A:) Annexin XII {Hydra vulgaris}

VVQGTVKPHASFNSREDAETLRKAMKIGTDEKSITHILATRSNAQRQQIKTDYTLFGKHLEDELKSELSGNYAAAALALLRPDEFLAEQLHAAMK
GLGTDKNALIDILCTQSNAQIHAIAFKLLYKEDLEKEISETSGNFQRLVSMQLGGRKEDEPVNAAHAAEDAAIYQAGEGQIGTDESRFNAVLAT
RSYPLHQIFHEYSKISNKTLQAIENEFGDIKNGLLAIVSVENRFAYFAERLHHAMKGLTSKTLIRILVSRSEIDLANKETFQAMYGKSLYEFIADD
CSGDYKDLLLQITGH

>d1dk5a_a.65.1.1 (A:) Annexin 24(ca32) {Bell pepper (Capsicum annuum)}

HHHHMASLTVPAPHVPSAEDCEQLRSAFKGWGTNEKLIISLAHRTAAQRKLIRQTYAETFGEDLLKELDRELTHDFEKLVWTLPSERDAHLAKEA
TKRWTCSNVLVELACTRSPKELVLAHEYHARYKKSLEEDVAYHTTGDHRKLLVPLSSYRGGEVDLRLAKAESKILHEKISDKAYSDEVIRILATRS
KAQLNATLNHYDEHGEDILKQLEDGDEFVALLRATIKGLVYPEHYFVEVRDAINRRGTEEDHLTRVIATRAEVDLKIADEYQKRDSIPLGRAIAKDTR
GDYESMILLALLGQE

>d1azsc1 a.66.1.1 (C:86-201) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}

GEKATKVQDIKNNLKEAIETIVAAMSNLVPPVELANPENQFRVDYILSVMNVPDFDPPEFYEHAKALWEDEGVRCYERSNEYQLIDCAQYFLDKID
VIKQDDYVPSDQDPLLRCR

>d1tada1 a.66.1.1 (A:57-177) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}

YSLEECLEFIAIYGNTLQSLIAVRAVAMTTLNQYQDSARQDDARKLMHMADTIEEGTMPKEMSDIIQRLWKDSGIQACFDRASEYQLNDSAGYYLSDL
ERLVTPGYVPTEQDVLSRVKT

>d1cipa1 a.66.1.1 (A:61-181) Transducin (alpha subunit), insertion domain {Rat (Rattus norvegicus)}

YSEECKQYKAVVYSNTIQSIIAIRAMGRLKIDFGDAARADDARQLFVLAGAAEEGFMTAELAGVIKRLWKDSGVQACFNRSREYQLNDSAAYYLND
LDRIAQPNEYIPTQQDVLRLTRVKT

>d1ej5a_a.68.1.1 (A:) Wiscott-Aldrich syndrome protein, WASP, C-terminal domain {Human (Homo sapiens)}

SGFKHVSHVGWDPQNGFDVNNDPDLRSLFSRAGISEAQLTDAETS KLIYDFIEDQGGLEAVRQEMRRQGGSGGSQSEGVLGALMHVMQKRSR
AIHSSDEGEDQAG

>d1e79a1 a.69.1.1 (A:380-510) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

TRAMKQVAGTMKLEAQYREVAFAQFGSDLDAATQQLLSRGVRLTLLKQGQYSPMAIEEQVAVIYAGVRGYLDKLEPSKITKFENAFLSHVISQHQ
ALLGKIRTDGKISEESDAKLKEIVTNFLAGFEA

>d1e79d1 a.69.1.1 (D:358-475) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

MDPNIVGSEHYDVARGVQKILQDYKSLQDIIAILGMDELSEEDKLTCSRARKIQRFLSQPFQVAEVFTGHLGKLVPLKETIKGFQQILAGEYDHLPEQAF
YMVGPIEEAVAKADKLAE

>d1skyb1 a.69.1.1 (B:372-502) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

IKAMKKVAGTLRLDAAYRELEAFAQFGSDLKATQANVARGARTVEVLKQDLHQPIPVEKQVLIIYALTRGFLDDIPVEDVRRFEKFYIWLQDQNGQ
HILLEHIRTTKDLPNEDDLNQIAEAKKTFVVSQ

>d1skye1 a.69.1.1 (E:357-470) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

EIVGEEHYQVARVQQTLEYKELQDIIAILGMDELSDEDKLVVHRARRIQFFLSQNFHVAEQFTGQPGSYVPVKETVRGFKEILEGKYDHLPEDRFL
VGRIEEVVEKAKAMG

>d1fx0a1 a.69.1.1 (A:373-501) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

IKAMKKVAGKLKLEAQFALEAFAQFASDLKATQNQLARGQLRELLKQPQSAPLTVEEQVMTIYTGTNGYLDLSLELDQVRKYLVELRTYVKTNKP

EFQEIISSKTFTEEAELLKEAIQEQMERT

>d1fx0b1 a.69.1.1 (B:378-485) C-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

RIVGEEHYEIAQRVKETLQRYKELQDIIAIGLDELSEEDRLTVARARKIERFLSQPFFVAEVFTGSPGKYVGLAETIRGFQLILSGELDSLPEQAFYLVGNI
DEATA

>d1fkma1 a.69.2.1 (A:249-442) Ypt/Rab-GAP domain of gyp1p {Baker's yeast (Saccharomyces cerevisiae)}

NSIIQRISKFDNILKDKTIINQQDLRQISWNGIPKIHRPVWKLIGYLPVNTRQEGFLQRKRKEYRDSLKHTFSDQHRSRDIPTWHQIEIDIPRTNPHIP
LYQFKSVQNSLQRILYLWAIRHPASGYVQGINDLVTPFFETFLTEYLPPSQIDDVEIKDPSTYMVDEQITDLEADTFWCLTKLLEQITDNYIH

>d1fkma2 a.69.2.1 (A:443-630) Ypt/Rab-GAP domain of gyp1p {Baker's yeast (Saccharomyces cerevisiae)}

GQPGILRQVKNLSQLVKRIDADLYNHFQNEHVEFIQFAFRWMNCLLMREFQMGTIVRMWDTYLSSETSQEVTSSYMSNDIKPPVTPEPRVASFV
TPTKDFQSPTTALSNTPNNAVEDSGKMRQSSLNEFHVFVCAALIKWSDQLMEMDFQETITFLQNPPTKDWTETDIEMLLSEAFIWQSLYK

>d1k5ha1 a.69.3.1 (A:301-398) 1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain {Escherichia coli}

KLSALTFAAPDYDRYPCLKLAMEAFEQQQAATTALNAANEITVAAFLAQHQIRFTDIAALNLSVLEKMDMREPQCVDVLSVDANAREVARKEVMRL
AS

>d1abv__ a.70.1.1 (-) N-terminal domain of the delta subunit of the F1FO-ATP synthase {Escherichia coli}

SEFITVARPYAKAAFDFAVEHQSVERWQDMILAFAAEVTKNEQMAELSGALAPETLAESFIAVCGEQLDENGNQLIRVMAENGRLNALPDVLEQFI
HLRAVSEAT

>d1g7da_ a.71.1.1 (A:) Endoplasmic reticulum protein ERP29, C-domain {Rat (Rattus norvegicus)}

PGCLPAYDALAGQFIEASSREARQAILKQQGDGLSGVKETDKKWasQYLKIMGKILDQGEDFPASELARIKSLNEMSEGKKEELQRSNLILTAFRKKG
AEKEEL

>d1dvka_ a.72.1.1 (A:) Functional domain of the splicing factor Prp18 {Baker's yeast (Saccharomyces cerevisiae)}

MRIQEIAQDKTISVIIDPSQIGSTEGKPPLSMKCNLHYHEILSRWKASLEAYHPELFLDTKALFPLLLQLRRNQLAPDLLISLATVLYHLQPKEINLAVQ
SYMKL SIGNVAWPIGVTSGIHARSAHSKIQGGRNAANIMIDERTRLWITSIKRLITFEEWYTSNH

>d1ak4c_ a.73.1.1 (C:) HIV-1 capsid protein {Human immunodeficiency virus type 1}

PIVQNLQQGMVHQAlSPRTLNAWVKVVEEKAFSPEVIMFSALSEGATPQDLNTMLNTVGGHQAMQMLKETINEEAAEDRHPVHAGPIAPGQMREPRGSD
GQMREPRGSDIAGTTSTLQEIQIGWMTNNPIPVGElYKRWIILGLNKIVRMYSP

>d2eiaa2 a.73.1.1 (A:17-147) EIAV capsid protein p26 {Equine infectious anemia virus}

PRGYTTWVNTIQTNGLLNEASQNLFGILSVDCNSEEMNAFLDVPGQAGQKQILDAIDKIAADDWDNRHPLPNAPIVAPPQGPIMTARFIRGLGV
PRERQMEPAFDQFRQTYRQWIIEAMSEGIKVMIGK

>d1g03a_ a.73.1.1 (A:) HTLV-I capsid protein {Human T-cell leukemia virus type 1}

PVMHPHGAPPNHRPWQMCKDLQAIKQEVSQAAPGSPQFMQTIHLAVQQFDPTAKDLQDQLQYLCSLVALHHQQQLDSLISEAETRGITGYNPLAG
PLRVQANNPQQQGLRREYQQLWLAAFAALPGSAKDPWSA

>g1qrj.1 a.73.1.1 (A:,B:16-130) HTLV-I capsid protein {Human T-cell leukemia virus type 1}

HHHHHSSGHIEGRHMXQMKDLQAIKQEVSQAAPGSPQFMQTIHLAVQQFDPTAKDLQDQLQYLCSLVALHHQQQLDSLISEAETRGITGYNPLAG
PLRVQANNPQQQGLRREYQQLWLAAFAALPGSAKDPWSA

>d1d1da2 a.73.1.1 (A:11-150) RSV capsid protein {Rous sarcoma virus}

WTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVLGPAPYALWMDAWGVQLQTIAAATRDPHPANGQGRGERTNLD
LKGLADGMVGNPQGQAALLRPGEVITASALQAFREVARLAEPA

>d1em9a_ a.73.1.1 (A:) RSV capsid protein {Rous sarcoma virus}

PVVIKTEGA PAWTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVLGPAPYALWMDAWGVQLQTIAAATRDPHPANGQGRGERTNLD
RGERTNLNRLKGLADGMVGNPQGQAALLRPGEVITASALQAFREVARLAEPA

>d1jsub2 a.74.1.1 (B:310-432) Cyclin A {Human (Homo sapiens)}

TVNQFLTQYFLHQQPANCKVESLAMFLGEISLIDADPYLKYLPSVIAGAAFHLALYVTGQSWPESLIRKTGYTLESLKPCLMDLHQTYLKAPQHAQQ
SIREKYKNSKYHGVSLNNPPETLNL

>d1vin_1 a.74.1.1 (181-308) Cyclin A {Cow (Bos taurus)}

DIHTYLREMEVKCKPKVGYMKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYIDRFLSSMSVLRGKLQLVGTAAMLASKFEEIYPPEVAEF
VYITDDTYTKKQVLRMEHVLVLAFLDAA

>d1vin_2 a.74.1.1 (309-432) Cyclin A {Cow (Bos taurus)}

PTINQFLTQYFLHQQPANCKVESLAMFLGEISLIDADPYLKYLPSVIAAAAFHLALYVTGQSWPESLVQKTGYTLETLKPCLLDLHQTYLRAPQHAQQ
SIREKYKNSKYHGVSLNNPPETLNL

>d1jkw_1 a.74.1.1 (11-161) Cyclin H (mcs2) {Human (Homo sapiens)}

WTFSEEQLARLRADANRKFRCKAVANGKVLNPDPVFPHEEMTLCKYYEKRLLFCFSVFKPAMPRSVVGTACMYFKRFYLNNSVMYEHPRIIMLT
CAFLACKVDEFNVSSPQFVGVLRESPLGQEKALEQILEYELLIQQQLNFHLIVH

>d1jkw_2 a.74.1.1 (162-287) Cyclin H (mcs2) {Human (Homo sapiens)}

NPYRPFEGFLIDLKTRYPILENLPEILRKTAADDFLNRIALTADYLTPSQIALTAILSSASRAGITMESYLSLESMLKENRTCLSQLLDIMKSMRNLVKYEPP
RSEEVAVLKQKLDRCHSALAL

>d1bu2a1 a.74.1.1 (A:22-148) Viral cyclin {Herpes virus saimiri}

RVLNNLKLRELLLPKFTSLWEIQTEVTVDNRILLTMHLLCESFELDKSVFPLSVSILDRLCKKQGTKTLQKIGAACVLIGSKIRTVKPMTVSKLTYLS
CDCFTNLELINQEKDILEALKWDTE

>d1bu2a2 a.74.1.1 (A:149-250) Viral cyclin {Herpes virus saimiri}

AVLATDFLIPLCNALKIPEDLWPQLYEAASTTICKALIQPNIAALLSPGLICAGGLTTIEDNTNCRPWTCTYLEDLSSILNFNSTNTVRTVKDQVSEAFSLYD

>d1f5qb1 a.74.1.1 (B:6-146) Viral cyclin {Murine herpes virus gamma 68}

FQGFLDSSLNEEDCRQMIYRSEREHDARMVGVNQDHFTSQYRKVLTWMFCVKDLRQDNVFPLAVALLDEFLSTRIDRENYQSTAVALHI
AGKVRAYMPIKATQLAYLCGGATTADKLTLLEVKSLSLTSWVADR

>d1f5qb2 a.74.1.1 (B:147-252) Viral cyclin {Murine herpes virus gamma 68}

CLSTDLYCILHIMHAPREDYLNINLCRPKIFCALCDGRSAMKRPVLITLACMHLMNQKYDYYENRIDGVCKSLYTKEELHQCCDLVDIAIVSFDENY
FKINA

>d1g3nc1 a.74.1.1 (C:16-147) Viral cyclin {Kaposi sarcoma-associated virus}

LCEDRIFYNILEIEPRFLTSDSVFGTFQQSLTSRMRKLLGTWMF SVCQEYNLEPNVVALALNLLDRLLLQVSKEHFQKTGSACLLVASKLRSLTPISTSSL
CYAAADFSRQELIDQEKEKELLEKLAWRTE

>d1g3nc2 a.74.1.1 (C:148-253) Viral cyclin {Kaposi sarcoma-associated virus}

AVLATDVTSLLLKLVGGSQHDFWHHEVNTLITKALVDPLTGSPLASIISAAGCALLVPANVIPQDTHSGGVPQLASILGCDVSVLQAAVEQILTSVD
FDLRI

>d1vola1 a.74.1.2 (A:113-207) Transcription factor IIB (TFIIB), core domain {Human (Homo sapiens)}

AMMNNAFEITTMDRINLPRNKVDRTNNLFRQAYEQKSLKGRANDAIASACLYIACRQEGVPRTFKEICA VRISKKEIGRCFKLILKA LETSVD

>d1vola2 a.74.1.2 (A:208-316) Transcription factor IIB (TFIIB), core domain {Human (Homo sapiens)}

LITTDGFMSRFCNSNLCPQVQMAATHIARKAVELDLVPGRSPISVAAAAYMASQASA EKRTQKEIGDIAGVADVTIRQSYRLIYPRAPDLFPTDFKFDT
TPVDKLPQL

>d1aisb1 a.74.1.2 (B:1108-1205) Transcription factor IIB (TFIIB), core domain {Archaeon Pyrococcus woesei}

NLAFASELDRITAQLKPRHVEEEARLYREAVRKGLIRGRSIESVMAACVYACRLLKV PRTLDEIADIARVDKKEIGRSYRFIARNLNLT PKKLF

>d1aisb2 a.74.1.2 (B:1206-1300) Transcription factor IIB (TFIIB), core domain {Archaeon Pyrococcus woesei}

VKPTDYVNKFADELGLSEKVRRAIEILDEAYKRGLTSGKSPAGLVAALYIASLLEG EKRTQREVAEVARTEVTRNRYKELVEKLKIKVPIA

>d1guxa_a.74.1.3 (A:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}

NTIQLMMILNSASDQPSEN LISYFNNTCTVNPKESILKRVKDIGYIFKEKFAKAVGQGCVEIGSQRYKLGVRLYYRVMESMLKSEEERLSIQNFSKLLND
NIFHMSLLACALEVV MATYSRSTS QNLDSGTDLSFPWILNVNLKAFDFYKVIESFIKAEGNL TREMIKH LERCEHRIMESLAWLSDSPLFDLIKQSK

>d1guxb_a.74.1.3 (B:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}

TSLSLFYKKVYRLAYLRLNLTCELRLSEHPELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKVKNIIDLKFKIVTAYKDLPHAVQETFKRVLIK
EEYDSIIVFYNSVFMQRQLTKTNILQYASTRPPTLSPIPHI

>d1k8ke_a.148.1.1 (E:) Arp2/3 complex 21 kDa subunit ARPC3 {Cow (Bos taurus)}

PAYHSSLMDPDTKLIGNMALLPIRSQFKGPAPRETKDTDIVDEAIYYFKANVFFKNEYIKNEADRTLIYITLYISECLKKLQKCNSKSQGEKEMYTLGITNF
PIPGEPGFPLNAIYAKPANKQEDEVMRAYLQQLRQETGLRLCEKVFDQNDKPSKWWTFCVRQFMNKSLSG

>d1jfza_a.149.1.1 (A:) RNase III endonuclease domain {Aequorea aeolicus}

GMKMLEQLEKKLGTYFKDKSLLKALTHVSYSKKEHYETLEFLGDALVNFFIVDLLVQYSPNKREGFLSPKAYLISEEFFNLLAQKLELHKFIRIKRGKINE
TIIGDVFEALWAAYIDSGRDANFTRELKYKLFKEDILSAIKEGR

>d1hus_a.75.1.1 (-) Ribosomal protein S7 {Bacillus stearothermophilus}

RDVLPDIYNSKLVTRLINKIMDGKSKAQKILYTAFDIIRERTGKDPMEVFQALKNVMPVLEVRARRVGGANYQVPVEVRPDRRVSLGLRWLVQY
ARLRNEKTMEERLANEIMDAANNTGAAVKKREDTHKMAEAN

>d1rss_a.75.1.1 (-) Ribosomal protein S7 {Thermus thermophilus}

LQPDLVYGDVLVTAFINKIMRDGKKNLAAIRFYDACKIIQEKTGQEPLKVFQAVENVKPRMEVRSSRVGGANYQVPMEVSPRRQQSLARLWLVQA
ANQRPERRAAVRIAHELMADAEGKGGAVKKREDVERMAEANRAYAHYRW

>d1iqlva_a.75.1.1 (A:) Ribosomal protein S7 {Archaeon Pyrococcus horikoshii}

IKVMGRWSTEDVEVKDPSLKPYINLEPRLLPHTHGRHAKKHFGKANVHIVERLINKVMSRGGSHYKVAGHFMRREHRSLSKKVRAYEVVKEAFKII
EKRTGKNPIQVLVVAIENAAPREDTTSVMFGGIRYHVADISPLRLDVALRNIALGASAKCYRTKMSFAEALAEIILAANKDPKSYASKKLEIERIAE
SSR

>d1jr3a1 a.80.1.1 (A:243-368) gamma subunit {Escherichia coli}

TLDDDQALSLVEAMVEANGERVMALINEAAARGIEWEALLVEMGLHRIAMVQLSPAALGNDMAAIELRMRELARTIPPTDIQLYQTLLIGRKEL
PYAPDRRMGVEMTLLRALAFHPRMPLPE

>d1a5t_1 a.80.1.1 (208-330) delta prime subunit {Escherichia coli}

DNWQARETLCQALAYSVPSGDWYSLAALNHEQAPARLHWLATLMDALKRHHGAAQVTNVDPGLVAELANHLSPSRLQAILGDVCHIREQLM
SVTGINRELLITDLLRIEHYLQPGVVLP

>d1jr3d1 a.80.1.1 (D:212-338) delta subunit {Escherichia coli}

FTPFWVDALLMGKSKRALHILQQLRLEGSEPVILLTLQRELLLVLNLKQSAHTPLRALFDKHRVWQNRRGMMGEALNRLSQQLRQAVQLTR
TELTLKQDYGQSVWAELEGLSLLCHKPLAD

>d1iqlva_a.80.1.1 (A:233-327) Replication factor C {Archaeon Pyrococcus furiosus}

RARPEDIREMMLALKGNFLKAREKLREILLKQGLSGEDVLVQMHKEVFNLPPIEPPKKVLLADKIGEYNFRIVEGANIEIQLAELAQFTLIGKK

>d1jr5a_a.150.1.1 (A:) Anti-sigma factor Asia {Bacteriophage T4}

MNKNIDTVREIITVASILIKFSREDIVENRANFIABLNEIGVTHEGRKLQNQNSFRKIVSELTQEDKKTLDNEGFEGVYRLEMYTNK

>d1f5ta2 a.76.1.1 (A:1065-1121) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}

TPTGRTLATAVMRKHRLAERLLTDIIGLDINKVHDEADRWEHVMSDERVERRLVKVLKDVSRSFGNPIPGLDELGV

>d1g3sa2 a.76.1.1 (A:65-140) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}

TPTGRTLATAVMRKHRLAERLLTDIIGLDINKVHDEASRWEHVMSDERVERRLVKVLKDVSRSFGNPIPGLDELGV

>d1fx7a2 a.76.1.1 (A:65-144) Iron-dependent regulator {Mycobacterium tuberculosis}

TEKGRALAIAVMRKHRLAERLLVDVIGLPWEEVHAEACRWEHVMSEDVERRLVKVLNNPTSPFGNPIPGLDELGVGPEP

>d1gpja1 a.151.1.1 (A:303-404) Glutamyl tRNA-reductase dimerization domain {Archaeon Methanopyrus kandleri}

EIPKVEKLIIEEEELKERRLVADVAKSLHEIKDRELERALRRLKTGDPENVLQDFAEYTKRLINVLTSAIMELPDEYRRAASRALRRASELNG

>d1ngr_a.77.1.1 (-) p75 low affinity neurotrophin receptor {Rat (Rattus norvegicus)}

GNLYSSLPLTKREEVEKLLNGDTWRHLAGELGYQPEHIDSFTHEACPVRALLASWGAQDSATLDALLAALRRIQRADIVESLCSE

>d1ddf_a.77.1.1 (-) Fas {Human (Homo sapiens)}

METVAINLSDVDSLKYITTIAVGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTII

KDITSDSENSNFRNEIQSLVLEHHHHHH

>d1a1w_a.77.1.1 (-) FADD (Mort1) {Human (Homo sapiens)}

MDPFLVLLHSVSSSLSSELTELKYLCGRVGKRKLERVQSGLDLFSMLLEQNDLEPGHTELLRELLASLRRHDLLRVDDFE

>d1e41a_a.77.1.1 (A:) FADD (Mort1) {Human (Homo sapiens)}

GSHMGEEIDLCAAFNVICDNVGKDWRRLARQLKVSDFKIDSIEDRYPRNLTERVRESLRWKNTKEENATVAHLVGALRSCQMNVLADLVQEQQARDLQRSGA

>d1fada_a.77.1.1 (A:) FADD (Mort1) {Mouse (Mus musculus)}

AAPPGEAYLQVAFDIVCDNVGRDWKRLARELKVEAKMDGIEEKYPRSLSERVRESLKVVKAEEKKNASVAGLVKALRTCRNLVADLVEEAQES

>d3crd_a.77.1.1 (-) Rайд CARD domain {Human (Homo sapiens)}

MEARDKQVLRLSLRELGAEVOLVEGLVLQYLYQEGILTENHIQEINAQTTGLRKTMLLDILPSRGPKAFDTFLDSLQEFPWVREKLKKAREEAMTDLPG

G

>d1cy5a_a.77.1.1 (A:) Apoptotic protease activating factor 1, APAF-1 {Human (Homo sapiens)}

MDAKARNCLLQHREALEKDIKTSYIMDHMISDGFLTISEEKVRNEPTQQQRAAMLIKMILKKNDSYVSFYNALLHEGYKDLAALLHDGIPV

>d3ygsp_a.77.1.1 (P:) Procaspsase 9 prodomain {Human (Homo sapiens)}

SMDEADRRLRRRLRLLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRRDQARQLIIDLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAG

>d1dgna_a.77.1.1 (A:) Iceberg {Human (Homo sapiens)}

ADQLLRKKRRIHHSVAGTINALLDCLLEDEVISQEDMNKVRDENDTVMDKARVLIDLTGKGPKSCCFIKHLCEEDPQLASKMGLH

>d1d2za_a.77.1.1 (A:) Pelle death domain {Drosophila melanogaster}

LDNTMAIRLLPLPVRAQLCAHLDALDVWQQLATAVKLYPDQVEQISSQQKQRGRSASNEFLNIWGGQYNHTVQTLFALKKLKLHNAMRLIKDYVSE
DLHKYI

>d1d2zb_a.77.1.1 (B:) Tube death domain {Drosophila melanogaster}

LSSKYSRNTELRVEDNDIYRLAKILDENSRCRKLMSSIIPKGMDVQACSGAGCLNFPAEIKKGFKYTAQDVFQIDEAAANRLPPDQSNSQMMIDEWKT
SGKLNERPTVGVLQLLVQAELSAADFVALDFLNESTPARPVDPGPALISLE

>d1hw1a2_a.78.1.1 (A:79-230) Fatty acid responsive transcription factor FadR, C-terminal domain {Escherichia coli}

GLNILETLARLDHESVPQLIDNLLSVRTNISTIFIRTAFRQHPDKAQEVLATANEVADHADAFELDYNIFRGLAFASGNPIYGLLNGMKGLYTRIGRHY
FANPEARSLALGFYHKLSALCSEGAHQDQVYETVRRYGHESGEIWHRMQKNL

>d1eyva_a.79.1.1 (A:) Antitermination factor NusB {Mycobacterium tuberculosis}

GRHQARKRAVALLFEAEVRGISAEEVVDTRAALAEAKPDIARLHPYTAAVARGVSEHAHIDDITAHLRGWTLDRPAVDRAILRVSVWELLHAAD
VPEPVVVDEAVQLAKELSTDDSPGFVNGLGQVM

>d1ey1a_a.79.1.1 (A:) Antitermination factor NusB {Escherichia coli}

MKPAARRRARECAVQALYSWQLSQNDIADVEYQFLAEQDVKDVDVLYFRELLAGVATNTAYLDGLMKPYLSRLLELGQVEKAVLRIALYELSKRSVD
PYKVAINEAIELAKSFGAEDSHKFVNGVLDKAAPVIRPNKK

>d1b79a_a.81.1.1 (A:) N-terminal domain of DnaB helicase {Escherichia coli}

PPHSIEAEQSVLGGMLDNERWDDVAERVVADDFYTRPRHIFTEMARLQESGSPIDLITLAESLERQGQLDSVGGFAYLAELSKNTPSAANISAYADI
VRE

>d1jwea_a.81.1.1 (A:) N-terminal domain of DnaB helicase {Escherichia coli}

MKVPPHSIEAEQSVLGGMLDNERWDDVAERVVADDFYTRPRHIFTEMARLQESGSPIDLITLAESLERQGQLDSVGGFAYLAELSKNTPSAANIS
AYADIVRERAVVREMIS

>d1qc7a_a.82.1.1 (A:) FliG C-terminal domain {Thermotoga maritima}

MFVFEDILKDDRSIQLVLREVDTRDALALKGASDELKEKIFKNMSKRAAALLKDELEYMGPVRLKDVEEAQQKIINIIRRLEEAGEIVIARGGGEELIM

>d1qc7b_a.82.1.1 (B:) FliG C-terminal domain {Thermotoga maritima}

MFVFEDILKDDRSIQLVLREVDTRDALALKGASDELKEKIFKNMSKRAAALLKDELEYMGPVRLKDVEEAQQKIINIIRRLEEAGEIV

>d1crka1_a.83.1.1 (A:1-98) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), mitochondria}

TVHEKRKLPPSADYPDLRKHNNCMAECLTPAIYAKLRDKLTPNGYSLDQCIQTGVNDPGHPFIKTVGMVAGDEESYEVFAEIFDPVIKARHNGYDPR

>d1qh4a1 a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), brain-type}
PFSNSHNLKMVKYVSDDEYPDLSVHNHHMAVKLTLDLYKKLRDRQTSSGFTLDDVIQTVVDNPGHPFIMTVCVAGDEESYEVFKELFDPVIEDRH
GGYKP

>d1qk1a1 a.83.1.1 (A:1-102) Creatine kinase, N-terminal domain {Human (Homo sapiens), mitochondria}
AASERRRLYPPSAEYPDLRKHNNCMASHLTPAVYARLCDKTTPTGWTLQCIQTVGDNPNGHPFIKTVGMVAGDEETYEVFAFLDFPVIQERHNGYD
PRTMKH

>d2crka1 a.83.1.1 (A:8-102) Creatine kinase, N-terminal domain {Rabbit (Oryctolagus cuniculus)}
NKYKLNYKSEEEYPDLSKHNNHMAVKLTPDLYKKLRDKETPSGFTLDDVIQTVGDNPNGHPFIMTVCVAGDEESYTFKDLFDPPIQDRHGGFKP

>d1g0wa1 a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Cow (Bos taurus), retinal isoform}
PFSNSHNTLKRPAEDEFPDLSGHNNHMAVKLTPELYALRAKSTPSGFTVDDVIQTVGDNPNGHPYIMTVCVAGDEESYDVFKELFDPIEDRHGG
YKP

>d1bg0_1 a.83.1.1 (2-95) Arginine kinase {Horseshoe crab (Limulus polyphemus)}
VDQATLDKLEAGFKKLQEASDKSLLKKHLTKDVFDSIKNKKTGMATLLDIQSGVENLDSGVGIYAPDAESYRTFGPLFDPIDIYHGGFKL

>d1al01_a.84.1.1 (1:) Scaffolding protein gpD of bacteriophage procapsid {Bacteriophage phi-X174}
EQSVRFQTALASIKLIQASAVALDTEDDFDFTSNKVWIATDRSRARRCVAECVYGTDFVGYPRFPAPEFIAAVIAYYVHPVNIQTACIMEGAFTEN
IINGVERPVKAELFAFTLVRAGNTDVLDAEENVQRQLRA

>d1l1_1 a.85.1.1 (1-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus polyphemus)}
TLHDQIRVCHLFQLSSATVIRLNVGKLQPGAIIFSCFHPDHLEEARHLYEVFWEAQDFNDIEIAKEARTFVNNEGLFAFAAEVAVLHRDDCKGLYVP

>d1lla_1 a.85.1.1 (2-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus polyphemus)}
LHDQKIRICHLFQLSSATVIGDGDKHKHSRDLKNVGKLQPGAIIFSCFHPDHLEEARHLYEVFWEAQDFNDIEIAKEARTFVNNEGLFAFAAEVAVLHR
DDCKGLYVP

>d1hc2_1 a.85.1.1 (5-135) Hemocyanin, N-terminal domain {Spiny lobster (Panulirus interruptus)}
TGNAQKQQDINHLLDKIYEPTKYPDLKDIENFNPLGDTIYNDHAAVETLMKELNDHRLLEQRHWYSLFNTRQRKEALMLFAVLNQCKEWYCFR
SNAAYFRERMNEGEFYALYVSVIHSKLGDGIVLP

>d1lla_2 a.86.1.1 (110-379) Hemocyanin {Horseshoe crab (Limulus polyphemus)}
PVQEIFPDKFIPSSAINEAFKKAHVRPEFDESPILVDVQDTGNILDPEYRLAYREDVGINAHWHWHLVYPSTWNPKYFGKKDRKGELFYMHQQ
MCARYDCERLSNGMHRMLPFFNDEPLAGYAPHLTVASGKYYSRPGDGLKLRDLGDIIESEMVRMRERILDSIHLYVISEDGSHKTLDELHGTDL
GALVESSYESVNHEYGNLHNWGHVTMARIHPDPGRFHEEPVMSTSLRDPIFYNWHRFIDNIFHEYKNTLK

>d1hc2_2 a.86.1.1 (136-398) Hemocyanin {Spiny lobster (Panulirus interruptus)}
PLYQITPHMFTNSEVIDKAYSAKMTQKPGTFNVSFGTNNREQRVAYFGEDIGMNIHHVTWHMDPFWWEDSYGYHLDRKGELEFWVHHQLTA
RFDFERLSNWLDPVDELHWDRIREGFAPLTSYKGGFPVRPDNIHFEDVDGVAHVHDLEITESRIHEAIDHYITDSGHTIDIRQPKGIELLDIIES
SKYSSNVQYYGSLHNTAHVMLGRQGDHGKFNLPPGMMEHFETATRDPSSFRLHKYMDNIFKKHTDSF

>d1js8a1 a.86.1.1 (A:2503-2791) Functional unit from octopus hemocyanin {Giant octopus (Octopus dofleini)}
AIIRKNVNSLTPSDIKELRDAMAKVQADTSNDNGYQKIASYHGIPLSCHYENGTYACCQHGMVTFPNWHRLTKQMEDALVAKGSHVGIPYWDWT
TTFANLPVLVTEKDNSFHHAIDVANTDTTRSPRAQLFDDPDKGDKSFFYRQIALALEQTDFCDFEIQFEIGHNAIHSWVGSSPYGMSTLHYTSYD
PLFLYHHSNTDRIWSVWQALQKYRGLPYNTANCEINKLVKPLKFNFNLDTPNAVTKAHSTGATSFYHKLGYDYDNLNFHGMТИPEEEHLKEIQH
>d1bt3a_a.86.1.2 (A:) Catechol oxidase {Sweet potato (Ipomoea batatas)}
APIQAPEISKCVVPPADLPPGAVVDNCPPVASNIVDYKLPAVTTMKVRPAHTMDKDAIAKFAKAVELMKALPADDPRNFYQQALVHCAYCNGGY
DQVNFPDQEIQVHNSWLFFPFRWYLYFYERILGKLIGDPSFGLFWNWDNPGGMVLPDFLNDSTSSLYDSNRNQSHLPPVVDLGYNGADTDV
TDQQRITDNLALMYKQMVTNAGTAELFLGKAYRGDAPSPGAGSIETSPHIPIHRWVGDPRNTNNEDMGNFYSAGRDIAYCHHSNVDRMWI
WQQLAGKPRKRDYTDSDWLNATFLFYDENGQAVKVRIGDSDLNQKMGYKYAKTPLPWL

>d1dbha1 a.87.1.1 (A:198-404) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}
EQTYYDLVKAFMAEIRQYIRELNLIKVFRPFVSNSKLFANDVENIFSRIVDIHELSVKLLGHIEDTVEMLTDEGSPHPLVGSCFEDAEELAFDPYESYA
RDILRPGFHDRFLSQLSKPGAALYQLSIGEGFKEAVQYVLPRLLLAPVYHCLHYFELLKQLEEKSEDQEDKECLKQAITALLNVQSGMEKCSKSLAKRRL

SESA

>d1by1a_a.87.1.1 (A:) beta-pix {Human (Homo sapiens)}

MKGFDTTAINKSYYNVQLNILETENEYSKELQTVLSTYRLPLQTSEKLSSANISYLMGNLEEICSFQQMILVQSLEECTKLPQAQQRVGGCFNLMPQ
MKTLYLTYCANHPSAVNVLTEHSEELEGFMETKGASSPGILVTTGLSKPFMRLDKYPTLLKELERHMEDYHTDRQDIQKSMAAFKNLSAQCQEVRK
KELELQILTEAIR

>d1f5xa_a.87.1.1 (A:) RhoGEF Vav {Mouse (Mus musculus)}

MKGDEIYEDLMRLESVPTPKMTEYDKRCCCLREIQQTEEKYTDTLSIQQQHFMKPLQRFLKPQDMETIFVNIEELFSVHTHFLKELKDALAGPGT
LYQVFIFYKERFLVYGRYCSQVESASKHLDQVATAREDVQMKLEECQRANNGRFTLRDLMVPMQRVLKYHLLQELVKHTQDATEKENLRLAD
MRDLAQCVNEVKR

>d1foea1 a.87.1.1 (A:1034-1239) GEF of TIAM1 (T-Lymphoma invasion and metastasis inducing protein 1) {Mouse (Mus musculus)}
QLSDADKLRKVICELLETERTYVKDLNCLMERYLKPLQKETFLTQDELDVFGNLTEMVEFQVEFLKTLEDGVRLVPDLEKLEVDQFKKVLFLGGSFL
YYADRFKLYSAFCASHTKVPKVLVKAKTDATAFKAFLDAONPRQQHSSTLESYLIKPIQRVLKYPLLRELFALTAESEEHYHLDVAIKTMNKVASHINE
MQKIHE

>d1boua_ a.88.1.1 (A:) LigA subunit of an aromatic-ring-opening dioxygenase LigAB {*Sphingomonas paucimobilis*, formerly *Pseudomonas paucimobilis*}

IDVHAYLAFFDDIPGTRVFTAQRKRGYNLNQFAMSLMKAENRERFKADESAYLDEWNLTTPAAVFLSKLFSTDGKF
QFAAGSMTGMQTQEYEAQMIMDGGGRSPAGVRISIKGGY

>d1hbna1 a.89.1.1 (A:270-549) Alpha chain {Archaeon Methanobacterium thermoautotrophicum}

RRARGENEPPGVPGYLA
DICQSSRVNYEDPVRVSLDVATGAMLYDQIWLSYMSGGVGFTQYATAAYTDN
ILDDFTYFGKEYVEDKYGLCEAPN
NMDTVLDVATEVTYGLEQEYEPALLE
DQFGGSQRAAVAAAAGCSTAFATGNA
QTGLSGWYLSMYLHKEQHSRLGFYGYDLQDCGASN
VFSI
RGDEGLPLELRGPNPYNYAMNVGHQGEYAGISQ
PHAARGDAFVNPLVKIAFADDNLVFD
FTNVRGEFAKGALREFEPAGERALITPA

>d1e6va1 a.89.1.1 (A:273-552) Alpha chain {Archaeon Methanopyrus kandleri}

RRARGENEPPGVPFGVLADCVQTMRKYPDDPAKVALEVIAGAMLYDQIWLGSYMSGVGFTQYATAVPDNILDDYVYGLEYVEDKYGIAEAEP
SMDVVKDVAETVTLGYLEQYERYPAAMETHFGGSQRRAAVCAAAGCSTAFATGHQAQGLNGWYLSQLHKEGQGRLGFYGYALQDQCGAANSL
VRSDEGLPLELRGPNPNYAMNVGHLGEYAGIVQAAHAARGDAFCVHPVIKVAFADENLVFDTEPRKEFKAGALREFEPAGERDLIVPA

>diegyai a.89.1.1 (A.1284-1369) Alpha chain {Archaeon Methanosaerica barkeri}

RRARGPNEPGGLSPGHLSIVQTSRVSEDPAKIALEVGAGCMYLDQWLGSYMSGGVFTQYAAIYDDIDLNNTYYDVIDKYNGAATVGG
DNVKVKASLEVVKDIATESTLYGIETYKFPTALEDHFGGSQRATVLAAGAVCSLATGNANAGLSGWYLSMYLHKAEWGRLGFFGFDLQDCGAT
NVLSYQGDEGLPDELRGPNYPNYAMNVGHQGGYAGIAQAAHSGRGRDAFTVNPLLKVCFADDLLPFNFAEPRREFGRGAIREFPAGERSLVPA
>d1hbhb1 a.89.1.1 (B:189-443) Beta chain {Archaeon Methanobacterium thermoautotrophicum}

GYALRNUMVNHVVAATLKNTLOAAALSTILEOTAMEEFMGDAVGAFERMHLLUGIAYOGMNADNLVEDLVKAN

VEKELETDYKVYGTDDLAMWNAYAAAGLMAATMVNQGAARAAQGVSSLLYYNDLIEFETGLPSVDFGKVEGTAVGFSFFSHSIYGGGGPGIFNGNHIVTRHSKGFAIPCVAAAMALDAGTQMFSPEATSGLIKEVFSQVDEFREPLKYVVVEAAAIEKNEI

>d1e6vb1 a.89.1.1 (B:190-442) Beta chain {Archaeon *Methanopyrus kandleri*}

GYALRNIMVNHIAA1RKNTMQAVC1AA1LQQ1AMFEMGDALGPFLRLHLLGAYQGLNADNMVYDIVKKHGKEGVGT1VVREVVERALEDGVIE
VKEELPSFKVYKANDMDLWNAAYAAAGLVAAVMVNQGAARAAQGVSATILYYNDLLEYETGLPGVDFGRAEGTAVGFSFFSHIYGGGGPGIFHGN
HIVTRHSKGFAIPPVAAMALDAGTQMFSPEVTSKLIGDVFGFEIDEFRPMKYITEAAAAEAK
>d1e6vb1_a.89.1.1 (B:2186-2433) Beta chain {Archaeon Methanoscincus barkeri}

GESLRNIMANHVAALISRNAMNASALSSIXEOSGIEMGGAVGMFEERHOUIGLAYOGIN

TAPSGYNFYKANDVPKWNAACAVGTLAATLVNCAGRAAQNVSSLLYFNDILEKETGLPGCDYGKVEGTAVGSFFSHSIYGGGGPGVFNGNHVV
TRHRSRGFAIPCVCAVALDAGTQMFSIESTSGLIGDVFGAIPFREPIKAVAGV
> d1hb5 - e 0.01 1.1 (-) Transcription factor STAT-4 N-domain [Mouse (Mus musculus)]

CGSOWNOVQOLEIKEFOVDOFYRDNERMEIRULLAOIWFTODWEVASNNETMATHILLONL

GNPMHVAVVISNCLREERRILAAANMPI

>d1agre_a.91.1.1 (E:) Regulator of G-protein signalling 4, RGS4 {Rat (Rattus norvegicus)}

VSQEEVKKWAESLENLINHEGLAFLKSEYSEENIDFWISCEEYKKIKSPSKLSPKAKKIYNEFISVQATKEVNLDSTREETSRNMLEPTITCFDEAQKKIFNLMEKDSYRRFLKSFRYLDLT

>d1fqia_a.91.1.1 (A:) RGS9, RGS domain {Cow (Bos taurus)}

KLVDPDKMRVERWAFNFSLIRDPKGRLQSFQHFLRKEFSGENLGFWEACEDLKYGDDQSKVKEKAEEYKLFLAPGARRWINIDGKTMDITVKGLKHPHYVLDAAQTHIYMLMKDSDYARYLKSPIYKEMILAKAIEP

>d1cmza_a.91.1.1 (A:) Galpha interacting protein, GaIP {Human (Homo sapiens)}

PSPEEVQSWAQSFDFKLMHSPAGRSVFRAFLRTYESEENMLFWLACEELKAEANQHVVDERLKYEDYVSILSPKEVSLDSRVREGINKKMQEPAHTFDAAQLQIYTLMRDSDYPRFLSSPTYRALL

>d1dk8a_a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}

GSASPTPPYLKWAESLHSLLDDQDGISLFRFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAIYRKYILDNNNGIVSRQTKPATKSFIFGCIMKQLIDPKQLDPAMFDQAQTEIQATMEENTYPSFLKSDIYLEYTRTGSESPKV

>d1emua_a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}

PPYLKWAESLHSLLDDQDGISLFRFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRLKLARAIYRKYILDNNNGIVSRQTKPATKSFIFGCIMKQLIDPMFDQAQTEIQATMEENTYPSFLKSDIYLEY

>d1iapa_a.91.1.1 (A:) p115RhoGEF {Human (Homo sapiens)}

SQFQSLEQVKRRPAHLMALLQHVALQFEPGPLLCLHADMLGSLGPKEAKKAFLDFYHSFLEKAVLVPVPPNVAFELDRTRADLISEDVQRFFVQEVVQQQVAVGRQLEDFRSKRLMGMTPEQELAQLEAWVGRDRASYEARERHVAERLLMHEEMQHTISTDEEKSAAVVAIGLYMRHLGVRT

>d1htjf_a.91.1.1 (F:) Pdz-RhoGEF RGS-like domain {Human (Homo sapiens)}

ESDIIFQDLEKLKSRPAHLGVFLRYIFSQADPSPLLFYLCAEVYQQASPKDSRSLGKDIDIWNIIFLEKNAPLRVKIPEMLQAEIDSRLRNSEDARGVLCEAQEAAMPEIQEIQIHDYRTKRTLGLSLYGENDLDDLGDPPLRERQVAEKQLAALGDILSAYAADRSAPMDFALNTYMSHAGIRL

>d1a9xa1_a.92.1.1 (A:403-555) Carbamoyl phosphate synthetase, large subunit connection domain {Escherichia coli}

EVGATGFDPKVSLLDPEALT KIRRELKDAGADRIWIYIADAFRAGLSVDGVFNLTNIDRWFLVQIEELVLEEKVAEVGITGLNADFLRQLKRKGFADARLAKLAGVREAEIRKL RDQYDLPVYKRVDTCAAFAEFTDTAYMYSTYEEECEANP

>d1b80a_a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete (Phanerochaete chrysosporium)}

VIEKRATCSNGKTVGDASCCA FWVLDIQQNLFHGGQCGAEAHESIRLVFHDSIAISPAMEAKGKFGGGGADGSIMIFDDIETAFHPNIGLDEIVKLQKPFVQKHGVTPGDFIAFAGAVALSNCPGAPQMNFTRGRPATQPAPDGLVPEPFHTVDQIINRVNDAGEFDELELVWMLS AHSVAAVNDVDPTVQGQGLPF DSTPGIFDSQFFFETQLRGTA FPGSGGNQGEVESPLPG EIRI QSDHTIARDSRTACEWQSFVNNQSKLVDDFQFIFLALTQLGQDPNAMTDCSDVIPQSKPIPGNLPFSFPAGKTIKDVEQACAETPFPTLTLPGPETSVQRI PPPGA

>d1llp_a.93.1.1 (-) Lignin peroxidase {White rot basidiomycete (Phanerochaete chrysosporium)}

ATCANGKTVGDASCCA FWVLDIQQNMFHGGQCGAEAHESIRLVFHDSIAISPAMEAKGKFGGGGADGSIMIFDTIETAFHPNIGLDEVVAMQKPFVQKHGVTPGDFIAFAGAVALSNCPGAPQMNFTRGRPATQPAPDGLVPEPFHTVDQIINRVNDAGEFDELELVWMLS AHSVAAVNDVDPTVQGLPF DSTPGIFDSQFFFETQLRGTA FPGSGGNQGEVESPG EIRI QSDHTIARDSRTACEWQSFVNNQSKLVDDFQFIFLALTQLGQDPNAMTDCSDVIPQSKPIPGNLPFSFPAGKTIKDVEQACAETPFPTLTLPGPETSVQRI PPPGA

>d1qpa_a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete (Phanerochaete chrysosporium)}

VACPDGVHTASNAACC AWFPVLDIQQNLFHGGQCGAEAHESIRLVFHDSIAISPAMEAKGKFGGGGADGSIMIFDTIETAFHPNIGLDEVVAMQK FIAKHGVTPGDFIAFAGA VGVSNCPGAPQMFFLGRPEATQAAPDGLVPEPFHTIDQVLARMLDAGGFDEIETVWLLSAHSIAANDVDPTISGLPFDSTPGQFD SQFFFETQLRGTA FPGSGGNQGEVESPG EIRI QSDHTIARDSRTACEWQSFVNNQSKLVDDFQFIFLALTQLGQDPNAMTDCSDVIPQSKPIPGNLPFSFPAGKTIKDVEQACAETPFPTLTLPGPETSVQRI PPPGA

>d1aru_a.93.1.1 (-) Peroxidase {Arthromyces ramosus}

SVTCPGGQSTSNSQCCVWFVLDLQTNFYQGSKCESVRKILRIVFHDAIGFSPALTAAGQFGGGGADGSIIAHSNIELAFPANGLTDIEALRAVG INHGVSFGDLIQFATAVGMNSNC PGSPRLEFLTGRSNSSQSPPSLIPGP GNTVTAILDRM GDAGFSPDEVV DLLAHSLASQEGLNSAIFRSPLDSTPQVFDTQFYIETLLKGTTQPGPSLGF AEELSPFPGEFRMRS DALLARD SRTACRWQSM TSSNEVMGQRYRAAMAKMSVLGFD RNALT CSDVIPS AVSNNAAPVIPGGLTVDI EVCSPSEP FPEIATASGPLSLAPAP

>d1jdra_a.93.1.1 (A:) Cytochrome c peroxidase, CCP {Baker's yeast (*Saccharomyces cerevisiae*)}
TTPLVHVASVEKGRSYEDFQKVYNAIALKLREDDEYDNYIGYGPVLVRLAWHTSGTWKHDNTGGSYGGTYRFKEFNDPSNAGLQNGKFLEPIHK
EFPWISSGDLFLSLLGGVTAQVEMQGPKIPWRCGRVDTPEPDTPDNGLPDAKDADYVRTFFQRLNMNDREVVALMGAHTLGKTHLKNSGYEGP
WTANNVFDNSFYLNLLNEDWKEKNDANNEQWDSKSGYMMILPTDYSLIQDPKYLSIVKEYANDQDKFFKDFSKAFEKLLENGITFPKDAPSPFIF
KTLEEQGL

>d1mn2_a.93.1.1 (-) Manganese peroxidase {Basidiomycetos fungus (*Phanerochaete chrysosporium*)}
AVCPDGTRVSHAAACAFIPLAQDLQETIFQNECGQDAHEVIRLFHDIAISRSQGPKAGGGADGSMILLPTVEPNFSANGIDDSVNNLIPFMQK
HNTISAADLVQFAGAVALSNCPGAPRLEFLAGRPNKIAAVDGLIPEPQDSVTKILQRFEDAGGFTPFEVSVLLASHSVARANKVDQTIDAAPFDSTPF
TFDTQVFLEVLLKGVGFGPSANNTGEVASPLPLGSQSDTGEMLRLQSDFAAHDPRTACIWQGFVNEQAFMAASFRAAMSKLAVLGHNRNSLIDCS
DVVPVPKPATGQPAMFPASTGPQDLELSCPSERFPTLTQPGASQSLIAHCPDGMSCPGVQFNGPA

>d1apxa_a.93.1.1 (A:) Ascorbate peroxidase {Pea (*Pisum sativum*)}
GKSPTVSPDYQKAIEKAKRKLRGFIAEKKCPLILRLAWHSAGTFDSKTKTGGPFGTIKHQAELAHGANGLDIAVRLEPIKEQFPIVSYADFYQLAG
VVAVEITGGPEVFPHPGREDKPEPPPREGRLPDATKGSIDLRLDVFGKAMGLSDQDIVALSGGHTIGAAHKERSGFEGPWTSNPLIFDNSYFTELLGEK
DGLLQLPSDKALLTDSVFRPLVEKYAADEDVFFADYEAHLKLSELGFAEA

>d7atja_a.93.1.1 (A:) Plant peroxidase {Horseradish (*Armoracia rusticana*)}
QLPTFYDNCNPVSNIVRDTIVNELSDPRIASILRLHFHDCFVNGCDASILLNTTSRTEKDAFGNANSARGFPVIDRMKAIVESACPRTVSCAD
LLTIAAQSVTLAGGPSWRVPLGRRDSLQAFQLDLANANLPAPFFTLPLQLKDSFRNVGLNRSSDLVALSGGHTFGKNQCRFIMDRLYNFSNTGLPDTL
NTTYLQLRGLCPLNGNL SALVDFDLRTPTIFDNKYYVNLEEQKGLIQSDQELFSSPNATDTIPLVRSFANSTQFFNAFVEAMDRMGNITPLTGQGQ
IRLNCRVVN

>d1scha_a.93.1.1 (A:) Plant peroxidase {Peanut (*Arachis hypogaea*)}
ELSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFVQGCDASVLLDDTSNFTGEKTAGPNANSIRGFEVIDTIKSQVESLCGVVSCADI
LAVAARDSVVALGGASWNVLLGRRDSTSASLSSANSDLPAPFFNLSGLISAFSNKGFTTKEVLTSGAHTIGQAQCTAFRTRIYNESNIDPTYAKSLQAN
CPSVGGDTNLSPFDVTPNKF DNAYYINLRNKKGLLHSQQLFNGVSTDQSQTAYSNNAATNTDFGNAMIKMGNLSPLTGTSGQIRTNCRKTN

>d1fhfa_a.93.1.1 (A:) Plant peroxidase {Soybean (*Glycine max*)}
QLPTFYRETCPNLPIVFGVIFDASFTDPRIGASLMRLHFHDCFVQGCDGSVLLNNTDIESEQDALPNINSIRGLDVNDIKTAVENSCPDTVSCADI
LAIAAEIASVGGPGWPVPLGRRDSLANTLANQNLAPFFNLTKASFAVQGLNTLDLVTSGGHTFGRARCSTFINRLYNFSNTGNPDPTLNTT
YLEVLRARCPQNATGDNLTNLDLSTPDQFDNRYSNLLQNLQSDQELFSTPGADTIPIVNSFSNQNTFFSNFRVSMIKMGNIGVLTGDEGEIRL
QCNFVNG

>d1bgp_a.93.1.1 (-) Plant peroxidase {Barley (*Hordeum vulgare*), peroxidase 1}
AEPPVAPGLSFDFYWQTCPRAESIVREFVQEAVRKDIGLAAGLLRLHFHDCFVQGCDASVLLDGSATGPGEQQAPPNLTLPASFKA VNDIRDRLERE
CRGAVVSCSDILALAARDSVVVSGGPDYRVPLGRRDSLFASTQDVLSLPGPSSNVQSLALLGRGLDADTLVTISGGHTIGLAHCSSFEDRLFPRP
DPTISPTFLSRLKRTCPAKGTDRTVLDVRTPNVFDNKYYIDLNVREGLFVSDQDLFTNAITRPIVERFAQSQQDFFEQFGVSIGKMGQMRVRTSDQG
EVRRNCSVNPGPG

>d1qgja_a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (*Arabidopsis thaliana*), peroxidase N}
QLSPDIYAKSCPVLQIVRKQVAIALKAEIRMAASLIRLHFHDCFVNGCDASLLDGADSEKLAIPNINSARGFEVIDTIKA AVENACPGVVSCADILTA
ARDSVVLSGGGPGWVALGRKDGLVANQNSANNLSPFEPLDAIIAKFVAVNLNITDVVALSGAHTFGQAKCAVFSNRLNFNTGAGNPDATLETSLL
NLQTVPLGGNSNITAPLDRSTTDTFDNNYFKNLLEGKGLSSDQILFSSDLAVNTKKLVEAYSRSQSLFFRDFTCAMIRMGNI SNGASGEVRTNCRV
INN

>d1pa2a_a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (*Arabidopsis thaliana*), peroxidase A2}
MQLNATFYSGTCPNASIVRSTIQQALQSDTRIGASLIRLHFHDCFVNGCDASILLDDTSI QSEKNAGPNVSARGFNVVDNIKTALENACPGVVSC
SDVLALASEASVSLAGGPSWTVLLGRRDSLANTLAGANSSIPSPIESLSNITFKFSAVGLNTNDLVALSGAHTFGRARC GVNNRLNFSGTGNPDPTL
NSTLLSTLQQLCPQNGSSTITNLSTPDADFNYYFANLQSN DGLLQSDQELFSTTGSSTIAIVTSFASNQTLFFQAFQAFQMINMGNISPLTGSNGE
RLDCKKVNGS

>g1cxp_1 a.93.1.2 (A;C;) Myeloperoxidase {Human (*Homo sapiens*)}

CPEQDKYRTITGMCNNRRSPTLGSNRFAVRWLPAEYEDGFSLPYGWTPGVKRNGFPVALARAVSNEIVRFPTDQLTPDQERSLMFMQWGQLLD
HDLDFTPEPAXNCETCSVQQPPCFPLKIPPNDPRIKNQADCIPFFRSCPACPGSNITIRNQINALTSFVDASMVGSEELARNLRNMSNQLGLAV
NQRFDQNGRALLPFDNLHDDPCLLTNSARIPCFLAGDTRSSEMPELTSMHTLLLREHNRLATELKSLNPRWDGERLYQEARKIVGAMVQIITYRDYL
PLVLGPTAMRKYLPTYRSYNDSDVPRIANVFTNAFRYGHTLIQPFMFRLDNRYQPMEPNPRVPLSRVFFASWRVLEGGIDPIRGLMATPAKLNRQ
NQIAVDEIRERLFEQVMRIGLDPALNMQRSDRGHLPGYNAWRRFCGLPQPETVQGLGTVRNLKLA
RKLMEQYGTNNIDIWMGGVSEPLKRKG
RVGPLLACIIGTQFRKLRDGDRFWWENEGVFSMQQRQALAQLSPRIICDNTGITT
VSKNIFMSNSYPRDFVCSTLPALNLASWREA

>d1eqga1 a.93.1.2 (A:74-583) Prostaglandin H2 synthase {Sheep (Ovis aries)}

IWTWLRTTLPSPSFIHFLTHGRWLWDFVNATFIRDTLMRLVLT
RSNLI
PSPTYNIAHDYISWESFSNVSYTRILPSVPRDCPTPMGK
KKQLPD
AEFLSRRFLRRKFIPDPQGTNLMFAFFAQHFTQHFFKTS
GKM
PGFTKALGHGV
DLGH
HIYGDNLERQYQLRLFKDGKLKYQMLN
GEVYPPSVEEA
PVLMHYPRGIPQS
QMAVGQE
VFGLPGL
MLYATI
WLREHN
RVC
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>d1cvua1 a.93.1.2 (A:74-583) Prostaglandin H2 synthase {Mouse (Mus musculus)}

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>d1jj2o_a.94.1.1 (O:) Ribosomal protein L19 (L19e) {Archaeon Haloarcula marismortui}

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>d1aa7a_a.95.1.1 (A:) Influenza virus matrix protein M1 {Influenza virus}

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>d2abk_a.96.1.1 (-) Endonuclease III {Escherichia coli}

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>d1mun_a.96.1.2 (-) Catalytic domain of MutY {Escherichia coli}

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>d1keaa_a.96.1.2 (A:) Thymine-DNA glycosylase {Archaeon Methanobacterium thermoformicicum}

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>d1mpga1_a.96.1.3 (A:100-282) 3-Methyladenine DNA glycosylase II (gene alkA or aidA) {Escherichia coli}

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>d1ko9a1_a.96.1.3 (A:136-323) 8-oxoguanine glycosylase {Human (Homo sapiens)}

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>d1gln_1 a.97.1.1 (306-468) Anticodon-binding (C-terminal) domain of glutamyl-tRNA synthetase (GluRS) {Thermus thermophilus}
DLEKLRWMNGKYIREVLSLEEVAVKPFLEAGLSEWEAYLRRRAVELMRPRFDLKEFPEKARYLFTEDYPVSEKAQRKLEEGPLLKELYPRLRAQE
EWTEAALEALLRGFAAKGVKLGQVAQPLRAALTGSLETPLGLFEILALLGKERALRRLERALA

>d1rlr_1 a.98.1.1 (10-221) R1 subunit of ribonucleotide reductase, N-terminal domain {Escherichia coli}
RDGSTERINLDKIHRVLDWAAEGLHNVSISQVELRSHQFYDGIKTSIDIHETIIKAAADLSRDAPDYQYLAARLAIFHLRKKAYQQFEPALYDHVVKM
VEMGKYDNHLLEDYEEFKQMDFIDHDRDMTFSYAAVKQLEGKYLVQNRVTGEIYESAQFLYILVAACLFSNYPRETRLQYVKRFYDAVSTFKISLPT
PIMSGVRTPTRO

>d1dnpa1 a.99.1.1 (A:201-469) FAD-binding (C-terminal) domain of DNA photolyase {Escherichia coli}
PVEEKAIAQLRQFCQNGAGEYEQQRDFPAVEGTSLASLATGGLSPRQCLHRLLAEQPQALDGGAGSVWLNEIWFYRHLITYHPSLCKHRPFI
AWTDRVQWQSNSPAHLQAWQEGKTGPIVDAAMRQLNSTGWMHNRLRMITASFLVKDLLIDWREGERYFMSQLIDGDLAANNGGWQWAAST
GTDAAPYFRIFNPTTQGEKFDFHEGEFIRQWLPELRDVGKVVHEPWKWAQKAGVTLDYPQPIVEHKEARVQTAAAYEARK

>d1iqra1 a.99.1.1 (A:172-416) FAD-binding (C-terminal) domain of DNA photolyase {Thermus thermophilus}
LPLPEPGEAAALAGLRAFLEAKLPRYAEERDRLDGEGBSRLSPYFALGVSPRLAAWEAERRGGEGARKWVAELLWRDFSYHLLYHFPWMAERPLDP
RFQAFPWQEDEALFQAWYEGKTGVPLVDAAMRELHATGFLSNRARMNAAQFAVKHLLPWRKCEAFRHLLDGDRAVNLQGWQWAGGLGV
DAAPYFRVFNPLQGERHDPEGRWLKRWAPEYPSYAKDPVVVDLEARRRYLRLARD

>d1qnf_1 a.99.1.1 (205-475) FAD-binding (C-terminal) domain of DNA photolyase {Anacystis nidulans}
PVEPGETAAIARLQEFCDRAIADYDPQRNFPAEAGTSGLSPALKFGAIGIRQAWQAASAHALRSDEARNSIRVWQQELAWREFYQHALYHFPSLA
DGPYRSLWQQFPWENREALFTAWTQAQTGYPIVDAAMRQLTETGWMHNRCRMIVASFLTKDLIIDWRRGEQFFMQHLVDGLAANNGGWQ
WSASSGMMPKPLRIFNPASQAKKFDATATYIKRWLPELRHVHPKDLISGEITPIERRGPAPIVNHNLRQKQFKALYNQLKAAI

>d2pgd_1 a.100.1.1 (177-473) 6-phosphogluconate dehydrogenase (6PGD) {Sheep (Ovis orientalis aries)}
GAGHFVKMVHNGIEYGDMLICEAYHLMKDVLGLGHKEMAKAFEEWNKTELDSFLIEITASILKFQDADGKHLLPKIRDSAGQKGTGKWTIALEY
GVPVTLIGEAVFARCLSSLKDERIQASKKLKGPKQNPIFEQDKKSFLEDIRKALYASKIISYAQGFMLRQAATEFGWTLNYGGIALMWRGCCIERSVFLGK
IKDAFDRNPGQLQNLLDDFFKSAVENCQDSWRRRAISTGVQAGIPMPCTTALSFYDGYRHAMLPAULQIQAQRDYFGAHTYELLAKPGQFIHTNWTC
HGG

>d1pgja1 a.100.1.1 (A:179-478) 6-phosphogluconate dehydrogenase (6PGD) {Trypanosoma brucei}
GAGSCVKMYHNSGEYAILQIWGEVFDILRAMGLNNDEVAAVLEDWKSKNFLKSYMLDISIAAARAKDKDGSYLTTEHVMDRIGSKGTGLWSAQEAL
EIGVPAPSLNMAVSRQFTMYKTERQANASNAPGITQSPGYTLKNKSPSGPEIKQLYDSVCIAIISCYAQMFQCLREMDKVHNFGNLNPATIATFRAG
CILQGYLLKPMTEAFEKKNPNISNLMCAFQTEIRAGLQNRYRDMVALTSKLEVSPVLSASLNVYTAMFTPTLKYGQLVSLQRDVFGRHGYERVDKDR
ESFQWPELQ

>d1qmga1 a.100.1.2 (A:308-595) Acetohydroxy acid isomeroreductase, ketoacid reductoisomerase (KARI) {Spinach (Spinacia oleracea)}

LEQEYKSDIFGERGILLGAVHGIVECLFRRTESGMSEDLAYKNTVECITGVISKTISTKGMLALYNSLSEEGKKDFQAAYSASYYPSMDILYECYEDVASG
SEIRSVVLAGRRFYKEGLPAFPMGKIDQTRMWKVGEKVRSPAGDLGPLYPFTAGVYVALMMAQIEILRKKGHYSIEINESVIEAVDSLNPFMHA
RGVSFMVDNCSTTARLGSRKWAPRFDYIILSQQALVADNGAPINQDLISNFLSDPVHEAIGVCAQLRPSVDISVTADDFVRPELRQA

>d1f0ya1 a.100.1.3 (A:204-302) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (Homo sapiens)}

GFIVNRLLPYLMEAIRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIIDGWHEMDSQNPLFQSPSPAMNKLVAEKGKKTGEGFYKY
YK

>d3hdha1 a.100.1.3 (A:204-302) Short chain L-3-hydroxyacyl CoA dehydrogenase {Pig (Sus scrofa)}

GFIVNRLLPYLIEAVRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIIDGWHEMDSQNPLFQSPSPAMNKLVAEKGKKTGEGFYKY
K

>d1dlja1 a.100.1.4 (A:197-294) UDP-glucose dehydrogenase (UDPGDH), middle domain {Streptococcus pyogenes}

ASEAEAVKLFANTYLALRVAYFNELDTYAESRKLN SHMIIQG ISYDDRIGMH YNNPSFGYGGYSLPKDTKQLLANYNNIPQTLIEAVSSNNVRKSYI

>d1bg6_1 a.100.1.5 (188-359) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}

NVLHTSLTNVNAVHMPLPTLLNAARCESGTPFQYYLEGITPSVGS LAEKVDAERIAIAKAFDLNVPSVC EWYKESY GQSPATIYEAVQGNPAYRGIAGP

INLNTRYFFEDVSTGLVPLSELGRAVNVTPLIDAVLDLSSIIDTDFRKEGRTEKLGSGLTAAGIRSAVE
>d1evya1 a.100.1.6 (A:189-357) Glycerol-3-phosphate dehydrogenase {Trypanosome (Leishmania mexicana)}
DRSFVCWATTDTVGCEVASAVKNVLAIGSGVANGLMGLNARAALIMRLLEIRDLTAAALGGDGSAVFGLAGLQLTCSELSRNFTVGKKLGKG
LPIEEIQRTSKAVAEGVATADPLMRLAKQLVKMPLCHQIYEIVYKKKNPRDALADLLSCLQDEGLPPLFK
>d1ks9a1 a.100.1.7 (A:168-291) Ketopantoate reductase PanE {Escherichia coli}
NIRAEWRKLA VNCVINPLTAIWNCPNGELRHHPQEIMQICEEVAAVIEREGHHTSAEDLRDYVMQVIDATAENISSMLQDIRALRHTEIDYINGFLR
RARAHGIAVPENTRLFEMIVKRKESE
>d1utg__ a.101.1.1 (-) Uteroglobin {Rabbit (Oryctolagus cuniculus)}
GICPRFAHVIENLLLGPSSYETSLKEFEPDDTMKDAGMQMKVLDSPQTTRENIMKLTEKIVKSPLCM
>d1ccd__ a.101.1.1 (-) Clara cell 17kDa protein {Rat (Rattus norvegicus)}
SSDICPGFLQVLEALLGSSESNYEAALKPFNPASDLQNAGTQLKRLVDTLPQETRINIVKLTEKILTSPLCEQDLRV
>d1utra_a.101.1.1 (A:) Clara cell 17kDa protein {Rat (Rattus norvegicus)}
ICPGFLQVLEALLGSSESNYEAALKPFNPASDLQNAGTQLKRLVDTLPQETRINIVKLTEKILTSPLC
>d1gai__ a.102.1.1 (-) Glucoamylase {Aspergillus awamori, variant x100}
ATLDWSLSNEATVARTAILNNIGADGAWVSGADSGIVASPSTDNPDYFTWTRDGLVIKTLVLDLFRNGDTDLLSTIEHYISSQAIQGVSNPSGDSL
SGGLGEPKFNVDETAYTGSWGRPQRDGPA RLTAMIGFGQWLNDNGYTSAAEIVWPLVRNDSYVAQYWNTGYDLWEEVNGSSFTIAVQHR
ALVEGSAFATAVGSSCSWCDSQAPQILCYLQSFWTGSYILANFDSSRSGKDTNTLLGSIHTFDPEAGCDDSTFQPCSPRALANHKEVVDSFRSIYTLND
GLSDSEAVAVGRYPEDSYNNGNPWFLCTLAAAEEQLYDALYQWDKQGSLEITDVS LDFFKALYSGAATGTYSSSTYSSIVSAVKT FADGFV SIVETHAA
SNGSLSEQFDKSDGDELSARDLTWSYALLTANNRRNSVPPSWGETSASSVPGTCAATSASGTYSSVTWSWPSIVATG
>d1ayx__ a.102.1.1 (-) Glucoamylase {Baker's yeast (Saccharomyces cerevisiae)}A YPSFEAYS NYKVDRTDLETFLDKQKEVSLYYLLQNIAYPEGQFNNGVPGTVIASPSTSNDYYYQWTRDSA ITFLTVLSELEDNNFNTLAKAVEYYIN
TSYNLQRTSNPSGSFDDENHKGLGEPKFNTDGSAYTGAWGRPQNDGPA RRAYAISRYLNDVNSLNEGKLVTDSDGDNFSSTEDIYKNIKP DLEYVIG
YWDSTGFDLWEENQGRHFFTSLVQQKALAYADIAKSFDGDFANTLS TASTLESYLSGSDGGFNTDVNHIVENPDLLQNSRQGLSATYIGPL
LTHDIGESSSTPF D VDNEYVLQSYLLLEDNKDRY SVNSAYSAGAAIGRPEDVYNGDGSSEGNPWFLATAYAAQVPYKLAYDAKSASNDTINKINYD
FFNKYIVDLSTINSAYQSSDSVTIKSGSDEFNTVADNLVTFGDSFLQVILDHINDD GSLNEQLNRTGYSTGAYSLTWSSGALLEAIRLRN KVKALA
>d1cem__ a.102.1.2 (-) CelA cellulase {Clostridium thermocellum}
AGVPFNTKPYGPTSIADNQSEVTAMLKAEWEDWKS KRITSNGAGGYKRVQR DASTNYDTVSEG MGYGLLAVCFNEQALFDDLYRYVKS HFNGN
GLMHWHIDANNVNTSHDGGDGAATDADE DIALALIFADKQWGSSGAINYQEARLTINNLYNHCVEHGSYVLKPGDRWGGSSVTNP SYFAPAW
YKVAQYTGDTRWNQVADKCYQIVEEVKKYNNGTGLV PDWCTASGTPASGQSYDYKYDATRGWRTAVDYSWFGDQRAKANC DMLTKFFARDG
AKGIVDGYTIQGSKISNNHNASFIGPVAAASMTGYDLNFAKELYRETAVK DSEYYGGYGNLSRLLTLYITGNFPNPLSDL
>d1tf4a1 a.102.1.2 (A:1-460) Endo/exocellulase: cellobiose E-4, N-terminal domain {Thermomonospora fusca}
EPAPNYAEALQKSMFFYEAQRSGKLPENN RSVWRGDSGLNDGADVGLDTGGWYDAGDHVFKGFPMAFTATMLAWGAI ESPEGYIRSGQMPYL
KDNLRWVNDYFIKAHPSPNVLYVQVG DGDADHKWW GPAEVMPMERPSFKVDPSCPGSDVAAETAAMAASSIVFADDPAYAATLVQHAKQLY
TFADTYRGVYSDCVPAGAFYNSW SGYQDELWVGAYWLYKATGDDSYLAKAEYEYDFLSTEQ QTDLSRWTIAWDDKSY GTYVLLAKETGKQKYID
DANRWLDYWTGVNGQ RV PYSPGM A VLD TWG AL RYA ANT AFVALVYAKV IDP VRK QRYHDF AVR Q IN YAL GDN PRN SSYV VFG NN P RNP
HHRTAHGSW TDSI AS PAENR HVLYG ALVGGPGSPN DAYT D RDQD YVANE VATD YNAGFSSA LAM IVEE YGGT PLAD FPPT EEPD G
>d1clc_1 a.102.1.2 (135-575) CelD cellulase {Clostridium thermocellum}
AMNVYEDAFKTAM LGMYLLRCG TS VSAT YNGIHY SHGP CHTNDAYL DINGQ HKT K D STKG WHD AGD YN KYV V NAGITV GS MFLA WEH FK DQL
EPVALEIPEKNN SIPDF L DELK YEIDW ILTM QY PDGSGR VA HKVSTRNFGG FIMPENE HDER FFV PW SSA ATADF VAM TAMA ARIF RP YDPQ YAEKCI
NAAKVSYEFLKNN PANV FAN QSGF STGEY ATV SD ADD RLWAAA EMW ET LGD EY LR DF EN RAAQ FS K KIE ADF DW DN V ANL GMFT YLL SER PGK
NPALVQSIKDSLL STADSIV RT SQN HGY GRT LG TYY WCG NGT VVR QTM ILQ VANK IS PN NDYV NA AL DAISHV FG RNN YN RS Y VT GLG IN PPM NP
H D RRSGADGIWEPWPGYLVGGWPGPKD WVDI QD SYQT NEI AIN WNA ALI YAL AGF V NYN
>d1faea_a.102.1.2 (A:) Processive endocellulase CelF (Cel48F) {Clostridium cellulolyticum}
ASSPANKVYQDRFES MYSKIKDPANGYFSEQGIPYHSIETLMVEAPDYGHVTTSEAMSYMWLEAMHGRFSGDFTGFDKSW SVTEQYLI PTEK DQP

NTSMSRYDANKPATYAPEFQDP SKYPSPLDTSQPVGRDPINSQLTSAYGTSMLYGMHWILDVDNWYGF GARADGTSKPSYINTFQRGEQESTWETI
PQPCWDEHKFGGQYGFLLFTKDTGTPAKQFKYTNA PDADARAVQATYWADQWAKEQGKS VSTSGKATKMGDYL RYSFFDKYFRKIGQPSQAG
TGYDAAHYLLS WYYAWGGGIDSTWSWIIGSSHNF GYQNPFAAWV LSTDANFKPKSSNGASDWAKSLDRQLEFYQWLQSAEGAIAGGATNSWN
GRYEAVPSGTSTFYGMGYVENPVYADPGSNTWFGMQVWSMQRVAE LYKTGDARAKL LDWKAWINGEIKFNADGTFQIPSTIDWEGQPD
WNPTQGYTGNNALHVKVNVNGTDLGCASSLANTLYAAKSGDETRSQRQNAQKL DAMWNNYSDSKGISTVEQRGDYHRFLDQE VFVPAGWTGK
MPNGDVIKSGVKFIDIRSKYKQDPEWQTMVAALQAGQVPTQLRHFWAQSEFAVANGVYAILFPD

>d1fp3a_a.102.1.3 (A:) N-acyl-D-glucosamine 2-epimerase {Pig (Sus scrofa)}

MEKERETLQAWKERVGQELDRVMAFWLEHS HDREHGGFTCLGRDGRVYDDLKYVWLQGRQVWMYCR LYR KLERFHRPELDAKAGGEFLR
HARVAPPEKKCAFVLT RDGRP VKVQR SIFSECFTMAM NELWRVTA EARYQSEAVDMMDQIVHWWREDPSGLR PQLPGAVASESMAPMMIL
CLVEQLGEED ELAGRYAQLGHWCARRILQHVQRDGQAVLENVSE DGEELSGCLGRHQNP GHALEAGWFLLRHSSRS GDAKLAHVIDTFLLPFR
SGWDADHGGLFYFQDADGLCPTQLEWAMKLWWPHSEAMIAFLMGYSE SGDPA LLRFYQVAE YTFRQFRDPEYGEWFGYLNREGKVALTIKG
FKGCFHVP RCLAMCEEMLSALLSRLA

>d1h54a1_a.102.1.4 (A:269-753) Lactobacillus maltose phosphorylase, central domain {Lactobacillus brevis}

DTQESLTAAMHQLSDKVAQSSYEDLLNAHTAIWAQRWEKSDVVIKGDDESQQGIRFNLQFLSTYYGEDARLNIGPKGFTGEK YGGATYWDTEAFA
FPVYLGITDPKVTRNLLMYR KQLDGAYINA QEQGLKG ALFPMVTFDGI ECHENEIT FEEI HRNGDIAFAI NYTRYT GDDSYV LHEGA KVLT EISRF
WADRVHFSKRNNQYMIHGVTGADEYENNVDNNW DTNMLAQWTLKYTLEILGKV DQDTAKQLDVSDEEKTKWQD IVDRM YLPYKD LNIFVQH
DGFLDKDIEPVSSIPADQRPINQNWSWDKILRSPYIKQGDVLQGIWDFIDDYTP EQKKANFDFYEP LT VHESSL SPAIH SVLAADLHYEDKA
ARL LDNYNNDTDGLHITSMTGAWIAVVQGFAGMVRDGQLHYAPFLPKTW TSYTFRQVFRDR LIEV SVHADGPHKLLSGEPLT IDVAGAAAA
AAAAA

>d1dl2a_a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

GAGEMRDRIESMFLESWRDYSKHGWGYDVYGP IEHTSHNM PRGNQPLGWIIVDSVDTLMLM YNSSTLYKSEFEAEIQRSEH WINDV LDFDIDAEV
NVFETTIRMLGGLLSAYH LSDV LEVGNKTVYLNKAIDL GDR LALAFL STQTGIP YSSINL HSGQAVKNHADG GA STAEFTT LQMEF KLAYLT GNR TY
WELVERVYEP LYKNN DLLNTYD GLVPIYTF PDTG KFGA STIRFG SRGS DFY EYLLKQY LLTHE TLYD LYR KS MEGM KKHL AQS KPSL WYIGER EQGL
HGQLSPKMDH LVCFM GLLAS GSGT EGLSI HEARRPFFSKSDWDLA KGITD TCYQMYKQSSG LAPEI VV FN DGNIKQDG WWRSSVG DFFV KPLD
RHNLQRPETV ESIM FMYHLSHDH KYREW GAEI ATSF FENT CVD CNDPKL RRFTS LDCI LPTK KSNM ESFW LAETLK YI LFDEF DLT KVV FNTE
AHPFPV LDEE ILKS QSLTT GWSL

>d1hcua_a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Trichoderma reesei}

KRGSPNPTRAAVKA AFQTSW NAYHHFAFPH DDLHPV SNSF DDER NGW GSSA IDGL DTA ILMG DADIV NTI LQY VPQ INFTT AVAN QGSS V FET
NIRY LGGLSAY DLLR GPF SS LATN QTLV NSLL RQA QT LANGL KVAFTT PGS VP DP TVF FN PTV RSGA SNN VAEIG S L VEW TRLS DLT GNP QY AQL
AQKGE SYLLN PKGSPE AW PGLIG T FV STNG T FQD SSG WSGL MDSF YE LIK MY LY DP VAF A HYK DRW VL GAD STI GH LG SHP STR KDL TF LSSYN
GQST SPNS GHL AS FGGG NFIL GGILL NEQ K YID FG IKL ASSY FG YT QT AS GIG PEG FAW VD S V T GAGG S PSS QSG FY SSAG FW V TAP YYI LR PET LES
LYY ARV TGDS K WQD LAWE A SAIE D C RAGS AY SS IN D VT QANG GGAS DDMES FW FAE ALK YAY L IFA EES DV QV AT GG NK FV F NTE AH PFS IRS

>d1krea_a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Fungus (Penicillium citrinum)}

SNQAKADA VKEA FQHAW NGYM KYA FPH D ELPV SNGH AD RS RNGW GAS A D V A L S T A V I M G K A D V N A I L E H V A D I F S K T S D T V S L F E T T I R Y L A G
ML SGYD L L QGP A K N L V D N Q D L I D G L L D Q S R N L A D V L K F A D T P S G V P Y N N I N I T S H G N D G A T T N G L A V T G T L V L E W T R L S D L T G D E E Y A K L S Q K A E S
YLLK P QP S S E P F P G L V G S S I N I D Q G F A D R S V W N G G D D S F Y E Y L K M Y V D P K R F E T Y K D R W V L A A E S T I K H L K S H P K S R P D L T F L S S Y S N R N Y D L S
SQHL TCF DGG S FLL GGT VLD RQDF IDF GLE L VDG CEAT YN S T L K I G P D S W G W D P K K V P S D Q K E F Y E K A G F Y I S S G S Y V L R P E V I E S F Y Y A H R V T G K E I Y
RDW V W N A F V A I N S T C R T D S G F A A V S D V N K A N G G S K Y D N Q E S F L F A E V M K Y S L A H S E D A A W Q V Q K G G K N T F V Y N T E A H P F S V A R

>d1fo3a_a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Human (Homo sapiens)}

QGPVHLN YRQKG VIDV FLHAW KG YRK FAW GH DELK P VSR SF SEW FGL GLT LID ALDT M W I L G R K E F E A R K W V S K K L H F E K D V D V N L F E S T I R I L G
G L L S A Y H L S G D S L F L R K A E D F G N R L M P A F R T P S K I P Y S D V N I G T G V A H P P R W T S D S T V A E V T S I Q L E F R E L S R L T G D K K F Q E A V E K V T Q H I H G L S G K K D
G L V P M F I N T H S G L F T H L G V F T L G A R A D S Y Y E Y L L K Q W I Q G G K Q E T Q L L E D Y V E A I E G V R T H L L R H E P S K L T F V G E L A H G R F S A K M D H L V C F L P G T L A L
G V Y H G L P A S H M E L A Q E L M E T C Y Q M N R Q M E T G L S P E V H F N L Y P Q P G R D V E V K P A D R H N L R P E T V E S L F Y L Y R V T G D R K Y Q D W G W E I L Q S F S R F
T R V P S G G Y S S I N N V Q D P Q K P E P R D K M E S F F L G E T K Y L F L L F S D D P N L L S D A Y V F N T E A H P L I W T

>d1qaza_a.102.3.1 (A:) Alginate lyase A1-III {Sphingomonas sp., A1}

GSHPFDQAVVKDPTASYVDVKARRTFLQSGQLDDRLKAALPKYDCTTEATPNPQQGEMVIPRRYLSGNHGPVNPDYEPVVTLYRDFEKISATGNLYVATGKPVYATCLNMILDKWAKADALLNYDPKSQSWSYQVEWSAATAAFALSTMMAEPNVTAQRRERVKWLNRVARHQTSFPGGDTCCNNHSYWRGQEATIIGVISVKDELFRWGLGRYVQAMGLINEDGSFVHEMTRHEQLHYQNYAMLPLTMIAETASRQGIDLYAYKENGRDIHSARKFVFAAVKNPDLIKYYAEPQDTRAFKPGRGDLNWIEYQRARFGFAELGFMTVPIFDPRTGGSATLLAYKP

>d1cb8a1 a.102.3.2 (A:26-335) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

GTAELIMKRVMLDLKKPLRNMDKVAEKNLNTLQPDGSWKDVPKDDAMTNWLPNHHLLQLETIIQAYIEKDISHYYGDDKVFDQISKAFKYWYDSDPKSRNWWHNEIATPQALGEMILMRYGKKPLDEALVHKLTERMKRGEPEKKTGANKTDIALHYFYRALLTSDEALLSAVKELFYPVQFVHYEEGLQYDYSYLQHGPQLQISSYGAFFITGVLKLANYVRDTPYALSTEKLAIFSKEYRSYLNKAIRGSYMFNFNVEGRGVSRPDILNKKAEKKRLLVAKMIDLKTHEEWADAIARTDSTVAAGYK

>d1egua1 a.102.3.2 (A:171-540) Hyaluronate lyase {Streptococcus pneumoniae}

KDTYTDRLDDWNGIIAGNQYYDSKNDQMAKLNQELEGKVALDSLSSISQADRIYLWEKFSNYKTSANLTATYRKLEEMAKQVTNPSSYYQDETVRRTVRDSMEWMHKHVYNSEKSIVGNWWDYIEGTPRAINNTLSMKEYFSDEEIKKYTDVIEKFVDPHEFRKTTDNPFKALGGNLVDMGRVKVIAGLRKDDQEISSTIRSIEQVFKLVDQGEGFYQDGSIYDHTNVAYTGANVNLIDGLSQLLPVIQTKKNPIDKDKMQTMYHWIDKSFAPLLVNGELMDMSRGRSGRISIRANSEGHVAAVEVLRGFIHRIADMSEGETKQRQLQSLVKTIVQSDSYDVFKNLKTYKDISLMSQSLSDAGVASVPR

>d1f1sa1 a.102.3.2 (A:249-619) Hyaluronate lyase {Streptococcus agalactiae}

EDNFTKLLDKWNNDVTIGNYVYDTNDNMQKLNQKLDETRANKIEAKLDSNRTFLWKDLNLNNSAQLTATYRRLEDIAKQITNPHTIYKNEKAIRTVKESLAWLHQNFYVNWKDIEGSANWWDFEIGVPRSITGTLSLMNNYFTDAEIKTYTDPIEHFVPAEYFRKTLVNPFKALGGNLVDMGRVKIIEGLLRKDNTIIEKTSKSLKLNFTTATKAEGFYADGSYIDHTNVAYTGANVNLIDGLTQLLPIIQETDYKISNQELDMVYKWINQSFPLIVKGELMDMSRGRSISREAASSHAAADEVLRGLRLANMSNEERNLDLKSTIKTIITSNKFYFNVLNNLKSYSDIANMNKLLNDSTVATKP

>d5eau_1 a.102.4.1 (21-220) 5-Epi-aristolochene synthase, N-terminal domain {Tobacco (Nicotiana tabacum)}

SPSLWGQDFLSFSIDNQVAEYAKEIEALKQETRNMLLATGMKLADTLNLIDTIERLGIYHFEKEIDDILDQIYNQNSNCNDLCTSALQFRLRQHGFIISPEIFSKFQDENKGKFESLASDVLGLNNYEASHVRTHADDILEDALAFSTIHLESAAPHLKSPREQVTHALEQCLHKVPRVETRFFISSYDKEQS

>d2sqca1 a.102.4.2 (A:8-36,A:308-630) Squalene-hopene cyclase {Alicyclobacillus acidocaldarius}

APAYARTLDRAVEYLLSCQKDEGYWWGPLXISPVWDTGLAVLALRAAGLPADHDRLVKAGEWLLDRQITVPGDWAVKRPNLKPGGFAQFDNVYYPDVCDTAVVVVWALNTLRLPDERRRDAMTKGFRWIVGMQSSNGGWGAYDVNTSDLNHIPFSDFGEVTDPSEDEVTAHVLECFGSGYDDAWKVIRRAVEYLKREQKPDGSWGRWGVNYLYGTGAVVSAKAVGIDTREPYIQKALDWVEQHQNPDDGGWGECRSYEDPAYAGKGASTPSQTAWALMALIAGGRAESEAARRGVQYLVETQRPDGGWDEPYYTGTGFPDFYLGTYMRYHVFPTLALGRYKQAIR

>d2sqca2 a.102.4.2 (A:37-307) Squalene-hopene cyclase {Alicyclobacillus acidocaldarius}

LSNVTMMEADEVLLCHILDRVRDRRMEKIRYLLHEQREDGTWALYPGGPPDLDTTIEAYVALKYIGMSRDEEPMQKALRFIQSQGGIESSRVFRMWLALVGEYPWEKVPMPVPPIMEFLGKRMPLNIYEGSWARATVVALSIVMSRQPVFPLPERARVPELYETDVPPRRGAKGGGWIFDALRALHGYQKLSVHPFRRAAEIRALDWLLERQAGDGSWGGIQPPWFYALIAKILDMTQHPAFIKGWEGLYVVELDYGGWMFQAS

>d1d8db_a.102.4.3 (B:) Protein farnesyltransferase, beta-subunit {Rat (Rattus norvegicus)}

PVWSEPLYSRPEHARERLQLDDS VETVTSIEQAKVEEKIYEQVFSSYKFNHLVPRVLVQREKFHFLKRLQLTDAYECLDASRPWL CYWILHSLELLDEPIPQIVATDVCQFLELCQSPDGGFGGGPGQYPHLAPTYAAVNALCIIGTEEAYNVINREKLLQYLSLKQPDGSFLMHVGGEVDVRSAYCAASVASLTNIITPDLFEGTAEWIARCQNWEGLGGVGPMEMAHGGYTFGLAALVILKKERSLNLKSLQWVTSRQMRFEGGFGQGRCNKLVDGCYSFWQAGLLPLLHRALHAQGDPALSMSSHWMFHQQALQEYILMCCQCAGGLLDKPGKSRDFYHTCYCLSGLSIAQHFSGAMLHDVVMGVPEVNLQPTHPVYNIGPDKVIQATTFLQKPVPGF

>d1ceb_a.102.4.3 (B:) Rab geranylgeranyltransferase, beta subunit {Rat (Rattus norvegicus)}

TQQKDVITKSDAPDTLLEKHADYLASYGSKKDDYEYCMSEYLRMSGVYWLGLTVMMDLMQLHRMNKEEILVFIKSCQHECGGVSASIGHDPHLLYTL SAVQILTLYDSIHVINVDKVVAYVQSLQKEDGSFAGDIWGEIDTRFSFCAVATALLGKLDAINVEKAIEFVLCMNFDDGGFCRPGSESHAGQIYCTGFLAITSQQLHQNVSNDLLGWLCERQLPSGGLNGRPEKLPDVCSWWVLASLKIIGRLHWIDREKLRSFILACQDEETGGFADRGDMVDPFHTLFGIAGLSLLGEEQIKPVSPVFCMPEEVLRVNVQPELVS

>d1c3d_a.102.4.4 (-) C3D, a C3 fragment and ligand for complement receptor 2 {Human (Homo sapiens)}

MLDAAERLKHLIVTPSGAGEQNMIGMPTVIAHYLDETEQWEKFGLEKRQGALELIKGYTQQLAFRQPSSAFAAFVKRAPSTWLTAYVVKVFSLV
NLIAIDSQVLCGAVKWILEKQKPDGVFQEDAPVIHQEMIGGLRNNNEKDMLATAFVLISLQEAKDICEEQVNSLPGSITKAGDFLEANYMNQLQRSYT
VIAIAGYALAQMGRLGPLLNUKFLTTAKDKNRWEDPGKQLYNVEATSYALLQLKDFDFVPPVVRWLNEQRYYGGGYGSTQATFMVFQALAQYQK
DAP

>d1qqfa_ a.102.4.4 (A:) C3D, a C3 fragment and ligand for complement receptor 2 {Rat (*Rattus norvegicus*)}

CGEQNMIGMTPVIAVHYLDQTEWKFGLERKQEALELIKGGYQTQLAFKQPISAYAFAFNRRPSTWLTA
YVSRVFSLAANLIAIDSQVLGAVKW
ILEKQKPDGVFQEDGPVIHQEMIGGFRNTKEADVSLTAFVLIALQEARDICEGQVN
SLPGSINKAGEYLEASYNLQRPYTVIA
GYALALMNKLEPY
LT
KFLNTAKDRNRWE
EPGQQLYNVE
ATSYALL
LLLKD
FDVPPV
RWL
NDERYYGG
G
STQATFM
VFQ
LAQYR
ADV

>d1csc_ a.103.1.1 (-) Citrate synthase {Chicken (Gallus gallus)}

ASSTNLKDVLALIPEQARIKTFRQQHGGTLGQITVDMSYGGMRGMKGLVYETSVLDPDEGIRFRGSIPECQKLLPKGGXGGEPLEGLFWLLVT
GQIPTGAQVSWLSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAITALNSESNFARAYAEGILRTKYWEMVYESAMDLIAKLPVAAKIYRNLYR
AGSSIGAIDSKLDWSHNFTNMIGYTDQAFTELMRLYLTIHSDHEGGNVSAHTSHLVGSALSDPVLFAAAMNGLAGPLHGLANQEVLGWLAQLQK
AXXXAGADASLRDYIWNTLNSGRVVPGYGHAVLRKTDPRYTCQREFALKLPGDPMFKLVAQLYKIVPNVLEQGAAANPWPNVDAHSGVLLQYY
GMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPKSMSTDGLIAL

>d1csh__ a.103.1.1 (-) Citrate synthase {Chicken (Gallus gallus)}

STNLKDVLASLIPKEQARIKTFRRQQHGNTAVGQITVDMSSYGGMGRGMKGLIYETSVLDPDEGIRFRGFSIPECQKLLPKAGGGEEPLPEGLFWLLVTQQ
IPTPEQVSWVSKEWAKRAALPSHVVTMLDNFPTNLHPMSQLSAITALNSESNFARAYAEGINRTKYWEFVYEDAMDLIAKLPVAAKIYRNLYRAG
SSIGAIDSKLWDHSNFTNMLGYTDPQFTELMRFLYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLLWLSQLQKD LG
ADASDEKLRDYIWNTLNSGRVVPGYGHAVLRKTDPRTQCREFALKHLPSPMFKLVAQLYKIVPNVLLEQGKAKNPWPNVDAHSGVLLQYYGMT
EMNNYTVLFGVSRALGVLAOLIWSRALGPRLPKSMSTAGLEKLSAGG

>d2cts a.103.1.1 (-) Citrate synthase {Pig (*Sus scrofa*)}

ASSTNLKDILADLIPKEQARIKTFRQQHGNTAVGQITVDMYGGMGRGMKGLVYETSVLDPDEGIRFRGYSIPECQKMLPKAKGGEPLPEGLFWLL
TGQIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFTNLHPMSQLSAITALNSESNFARAYAEGIHRTKYWEIYEDCMDLIAKLPCVAAKIYRNLY
EGSSIGAIDSKLDWSHNTNMGLYDTAQFTELMRILYLTIHSDHEGGNVSAHTSHLVGSALSDPYLSFAAMNGLAGPLHGLANQEVLVWLTLQKE
VGKDVSDEKLRYIWNTLNSGRVVPGYGHAVLRKTDPRTQCREFALKLPHDPMFKLVAQLYKIVPNVLL_EQGKAKNPWPVNDAHSGVLLQYYG
MTFMNYTVTLEGVSRAIQLWISRAI_KEPLERPKSMSSTDGLIKI_VDSK

>d1ai8a a.103.1.1 (A:) Citrate synthase {Archaeon Pyrococcus furiosus}

LAKGLEDVYIDQTNICYIDGKEGKLYYRGYSVEELAELSTFEVVYLLWWGKLPSLSELENFKKELAKSRGLPKEVIEIMEALPKNTHPMGALRTIISYLG
NIDDSDGIDPVPEEVYRIGISVTAKIPTIVANWYRIKNGLEYVPPKEKLSHAANFLYMLHGEEPKEWEKAMDVALILYAEHEINASTLAVMTVGSTLSD
YYSAILAGIGALKGPIHGGAVEEAIKQFMEIGSPEKVEEWFFKALQQKRKIMGAGHRVYKTVDPRARIFKKYASKLGDKLFEIAERLERLVEEYLSKKGI
SINVVDYWSGLVFYGMKIPIELYTTFAMGRIGWTAHLAEVSHNRIIRPRLOYVGEIGKKYLPIELRR

>d1a59 a.103.1.1 (-) Citrate synthase {Antarctic bacterium DS2-3R}

EPTIHKGLAGVTADVTISKVNSDTNSLLYRGYPVQELAKCSFEQVAYLLWNSELPNDSELKAFVNFRSHRKLDENVGAIDLLSTACHPMVDVARTA
VSVLGANHARAQDSSPEANLEKAMSLLATFPSVVAYDQRRRGEELIEPREDLDYSANFLWMTFGEEAAPEVVEAFNVSMLYAEHSFNASTFTARVI
TSTLADLHSAVTGAIGALKGPLHGGANEAVMHTFEEIGIRKDESLDEAATRSKAWMVDAQKKVMGFGRHVYKNGDSRVPTMKSALDAMIKH
YDRPEMILGlyNGLEAAMEEAKQIKPNLDYPAGPETYNLMGFDTEMFTPLFIAARITGWTAHIMEQVADNALIRPLSEYNGPEQRQVP

>d1dz4a_a.104.1.1 (A:) Cytochrome P450-CAM {Pseudomonas putida}

LAPLPPHPVPEHLFDFDMYNPNSLNSAGVQEAWA/LQESNPVDLVWTRCNGGHWIATRGQLIREAYEDYRHSSECPFIPREAGEAYDIFPTSMMDP
EQRQFRALANQVVGMPVVDKLENRIQELACSLIESLRPQGQCNFTEDYAEFPPIRFMLLAGLPEEDIPHLYKLTQDMTRPDGSMTFAEAKEALYDYLI
PIIEQRRQKPGTDAISIVANGQVNNGRPITSDEAKRMCGLLVGGLDTVVNFLSFSMEEFLAKSPEHRLQELIQRPERIPAACEFLLRRFLSVADGRILTSDEY
FHGVQLKKGDQILLPPQMLSGLDERENACPMHVDFSRQKVSHTFHGSHLCLGQHLARREIIVTLKEWLTRIPDFSIAPGAQIQHKSGIVSGVQALPL
VWDPATTKAV

>d1jpza a.104.1.1 (A:) Cytochrome P450 bm-3 {Bacillus megaterium}

TIKEMPQPKTGFELKNPLNNTDKPVQALMKIADELGEIFKFEEAPGRVTRYLSSQRLIKEACDESRFDKNLSQLQALKFVRDFAGDGLFTSWTHEKNWKK

AHNILLPSFSQQAMKGYHAMMVMDIAVQLVKWLERLNADEHIEVPEDMTRLTLDTIGLCGFNYRFNSFYRDQPHPFITSVMRALDEAMNKLQRAN
PDDPAYDENKRQFQEDIKVMNDLVKIIADRKAQSEQSDDLLHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLSFALYFLVKNPHVLQKAA
EEAARVLVDVPVSYKQVKQLKYVGMLVNEARLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMLVLPQLHARDKTIWGDDVEEPRPERFNPSAIPQH
AFKPGNGQRACIGQQFALHEATLVLGMMKLHDFDFTEDHTNYELDIKETTLKPEGFVVAKSKKIPLGGI
>d1jfba_a.104.1.1 (A:) Cytochrome P450-NOR, nitric reductase {Fungus (*Fusarium oxysporum*)}
APSFPFSRASGPEPPAEFAKLRATNPVSQVKLFDSLAWLVTKHDKVCFVATSEKLSKVTRQGFPELSASGKQAACKPTFVDMDPPEHMHQSRM
VEPTFTPEAVKNLQPYIQRTVDDLEQMCKQKGANGPDLVKEFALPVSYIYTLLGVPPNDLEYLTQQNAIRTNGSSTAREASAANQELLDYLAILVE
QRLVEPKDDISKLCTEQVKPGNIKSDAVQIAFLLVAGNATMVNMIALGVATLAQHPDQLAQLKANPSLAPQFVEELCRYHTASALAIKRTAKEDV
MIGDKLVRANEIIASNQSANDEEVFENPDEFNMNRKWPPQDPLGFGFDHRCIAEHLAKAELTTVFSTLYQKFPLKAVPLGKINYTPLNRDVG
IVDLPVIF
>d1jipa_a.104.1.1 (A:) Cytochrome P450-ERYF {Saccaropolyspora erythraea}
TTVPDLESDFHVDWYRTYAEIERTAPTPVRLGQDAWLVTGYDEAKAALSDLRLSSDPKKYPGVEVEFPAYLGFEDVRNYFATNMGTSDPPTH
TRLRKLVSQEFTVRRVEAMPRRVEQITAELLEVGDSGVVDIVDRFAHPLPIKVICELLGVDEKRYGEFGRWSSEILVMDPERAEQRGQAAREVNFI
DLVERRTEPGDDLSALIRVQDDDDGRLSADELTSIALVLLAGFESSVSLIGITYLLTHPDQLALVRRDPSALPNAVEEILRYIAPPETTRFAAEEVEI
GGVAIPQYSTVLVANGAANRDPKQFPDPHRFDVTRDTRGHLSFGQGIHFCMGRPLAKLEGALVALRALFGRFPALSLGIDADDVVWRRSLLRGIDHL
PVRLDG
>d1cpt_a.104.1.1 (-) Cytochrome P450-TERP {Pseudomonas sp.}
MDARATIPEHIARTVILPQGYADDEVIYPAFKWLREQPLAMAHIEGYDPMWIATKHADVMQIGKQPGFLSNAEGSEILYDQNNEAFMRSISGGCP
HVIDSLTSMDDPPTHTAYRGTLNWFPQASIRKLEENIRRIAQASVQRLDFDGECDMFMTDCALYYPLHVVMTALGVPPEDDEPLMLKLTQDFFGVEAA
RRFHETIATFYDYFNGFTVDRRSCPDDVMSLLANSKLDGNYIDDKYINAYVIAITAGHDTSSSSGAIIGLSRNPEQLALAKSDPALIPRLVDEAVR
WTAPVKSFMRTALADTEVRGQNIKRGDRIMLSYPSANRDEEVSNPDEFIDTRFPNRHGFVWGAHMCLGQHLAKLEMKIFFEELLPKLKSVELSG
PPRLVATNFVGGPKNVPIRFTKA
>d1e9xa_a.104.1.1 (A:) Cytochrome p450 14 alpha-sterol demethylase (cyp51) {Mycobacterium tuberculosis}
MSAVALPRVSGGHDEGHLEFRDPIGLMQVRDECVDGTFQLAGKQVVLSGSHANEFFRAGDDDDQAKAYPFMTPIFGEGVVFADSPER
RKEMLHNAALRQEQMKGHAATIEDQVRRMIADWGEAGEIDLDDFAELTYTSSACILGKFRDQLDGRFAKLYHELERGTDPLAYVDPYLPIESFRR
DEARNLVALVADIMNGRIANPPTDKSDRMLDVIAVKAETGTPRFSADEITGMFISMFMAGHHTSSGTASWTLIELMRHRDAYAAVIDELDELYG
DGRSVSFHALRQIPQLENVLKETLRLHPPILMRVAKGEFEVQGHRIHEGDLVAASPAISNRPEDFPDPDFVPARYEQPRQEDLLNRWTWIPFGA
GRHRCVGAFAIMQIKAIIFSVLLREYEFEEMAQPPESYRNDHSKMVVQLAQPACVRYRRRT
>d1io7a_a.104.1.1 (A:) CYP119 {Archaeon Sulfolobus solfataricus}
MYDWFSERMKKDPVYDGNIWQVFSYRTKEVLFNNFKFSSDLTGYHERLEDLRNGKIRFDIPTTRYMLTSDDPLHDELRSMSADIFSPQKLQTLLET
IRETTRSLLSDSIDPREDDIVKKLAVPLPIIVISKILGLPIEDKEKFKEWSDLVAFRLGKPGEIFELGKYLELIGYVKDHLSGTEVSRVVSNSNLSDEIKLGYI
LLLIAGNETTNLISNSVIDFTRNLWQRIREENLYLKAIEEARYSPPVMRTVRKTKERVKLGDTIEEGEYRVVVIASANRDEEVFHDGEKFIPDRNP
NPHLSFGSGIHLCLGAPLARLEARIAIEEFSKRFRHIEILDTEKPVNEVLNGYKRLVVRKLS
>d1dt6a_a.104.1.1 (A:) Mammalian cytochrome p450 2c5 {Rabbit (*Oryctolagus cuniculus*)}
PPGPTPFPIIGNILQIDAKDISLTKFSECYGPVFTVYLMKPTVVLHGYEAVKELAVDLGEEFAGRGSVPILEVKSKGLGIAFSNAKTWKEMRRFSLM
TLRNFGMGKRSIEDRIQEEARCLVEELRKTNASPCDPTFILGCAPCNVICSFIFHNRFDYKDEEFLKLMESLHENVELLGTWPLQVYNNFPALLDYFPGI
HKTLKNADYIKNFIMEKVKEHQKLLDVNNPRDFIDCFLIKMEQENNLEFTLESLVIAVSDLFGAGTETTSTLRYSLLLLKHPEVAARVQEEIERVIGR
HRSPCMQDRSRMPYTDVIAHEIQRFDLPLTNPFLHAVTRDVRFRNYFIPKGTDITSLTSVLHDEKAFPNPKVFDPGHFLDESGNFKKSDYFMPFSAGK
RMCGEGLARMELFLFLTSILQNFKLQSLVEPKDLDITAVVNGFVSVPPSYQLCFIPIHH
>d1etob_a.105.1.1 (B:) FIS protein {Escherichia coli}
MFEQRVNSDVLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEEVQPLDMVMQYTRGNATRAALMMGINRGTLRKKLK
KYGMN
>d1etxa_a.105.1.1 (A:) FIS protein {Escherichia coli}

>d1fipa_a.105.1.1 (A:) FIS protein {Escherichia coli}
PLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVQEALDMVMQYTRGNQTRAALMMGINRGTLRKKLKYGMN

>d1ntca_a.105.1.1 (A:) DNA-binding domain of NTRC {Salmonella typhimurium}
MDLPGELEFASTPDSPSHLPPDSWATLLAQWADRALRSGHQNLSEAQPTELRTLLTALRHTQGHKQEAARLLGWAATLTAKLKELGME

>d1g8ea_a.145.1.1 (A:) Flagellar transcriptional activator FlhD {Escherichia coli}
MHTSELLKHIYDINLSYLLAQRLIVQDKASAMFRLGINEEMATTLLAALTPQMVKLAETNQLVCHFRFDHQITQLTQDSRVDDLQQIHTGIMLST

>d1g8eb_a.145.1.1 (B:) Flagellar transcriptional activator FlhD {Escherichia coli}
TSELLKHIYDINLSYLLAQRLIVQDKASAMFRLGINEEMATTLLAALTPQMVKLAETNQLVCHFRFDHQITQLTQDS

>d1jhga_a.107.1.1 (A:) Trp repressor {Escherichia coli}
SAAMAEQRHQEWLRFDLLKNAYQNDLHLPLLNLMITPDEREALGTRVRIEELLRGEMSQRELKNELGAGIATITGSNSLKAAPVELRWLEEVLL
KSD

>d1trra_a.107.1.1 (A:) Trp repressor {Escherichia coli}
AQQSPYSAAMAEQRHEEWLRFDLLKNAYQNDLHLPLLNLMITPDEREALGTRVRIVEELLRGEMSQRELKNELGAGIATITGSNSLKAAPVELRQ
WLEEVLLK

>d1dd3a1_a.108.1.1 (A:1-57) Ribosomal protein L7/12, oligomerisation (N-terminal) domain {Thermotoga maritima}
MTIDEIIIAIEKLTVSELAELVKKLEDKFGVTAAAPVAVAAAPVAGAAAAGAAQEEKT

>d1dd3c1_a.108.1.1 (C:) Ribosomal protein L7/12, oligomerisation (N-terminal) domain {Thermotoga maritima}
MTIDEIIIAIEKLTVSELAELVKKLEDKFGVTAAAPVAVA

>d1iiea_a.109.1.1 (A:) MHC class II-associated invariant chain ectoplasmic trimerization domain {Human (Homo sapiens)}
YGNMTEDHVMHLLQNADPLKVVPLKGSPENLRHLKNTMETIDWKVFESWMHHWLLFEMRSRHSLEQKPTDAPPK

>d1aora1_a.110.1.1 (A:211-605) Aldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}
IADKQKFMLVREKVNLNRDPVAGGGLPKYGTAVLVNIINENGLPVKNFQTVYPYAEQSGEAMAACKYLRNKPCYACPIGCGRNRLPTVGET
EGPEYESVWALGANLGINDLASICANHMCDELGLDTISTGGTLATAMELEYEKGHIKDEELGDAPPFRWGNTEVLHYIEKIAKREGFGDKLAEWSYRL
AESYGHPELSMTVKKLELPAYDPRGAEGHGLGYATNNRGGCHIKNYMISPEILGYPYKMDPHDVSDDKIKMLIFQDLTALIDSAGLCLFTTFGLGADD
YRDLLNAALGWDFTTEDYLKIGERIWNAERLFNLKAGLDPARDTLPKRFLLEPMPEGPNKGHTVRLKEMLPRYYKLRGWTEDGKIPKEKLEELGIAE
FY

>d1b25a1_a.110.1.1 (A:211-619) Formaldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}
DKEELKKLSQLEAYNEILNSPGPFWKRQGTMAAVEWCNTNYALPTRNFSQDGYFEFARSIDGTYMEGMVKVQQRGCPCNMPGCVNVLDQEQSE
LDYENVALLGSNLGIGKLNEVSVLNRIADEMGMDTISLGVSIAHVMVERGILKEGPTFGDFKGAKQLALDIAYRKGEGLNLAAEGVKAMAEKLGT
HDFAMHVKGLEVSGYNCYIYPAMALAYGTSAGAHKEAWVIAWEIGTAPIEGEKAEKVEYKISYDPIKAQKVVELQRLRGGLFEMLTACRLPWVEV
GLSLDYYPKLLKAITGVTYTWDDLYKAADRVYSLIRAYVVREFNGKWDRKMDYPPKRWFTEGLKSGPHKGEHLDEKKYDELLSEYYRIRGWDERGIP
KKETLKELLDFTVIPELEKVTNLE

>d1d2ta_a.111.1.1 (A:) Acid phosphatase {Escherichia blattae}
GNDTTTKPDLYYLKNSEAINSLALLPPPVAVGSIABLNDQAMYEQGRLRNTERGKLAEDANLSSGGVANAFSGAFGSPITEKDAPALHKLLTNMIE
DAGDLATRSAKDHMRIRPAFYGVSTCNTTEQDKLSKNGSYPSGHTSIGWATALVLAEPQRQNEILKRGYELGQSRVICGYHWQSDVDAARVV
GSAVVATLHTNPAFQQQLQAKAEAFAQHQK

>d1qj9a_a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Ascophyllum nodosum}
TCSTSDDADDPTPPNERDDEAFASRVAAKRELEGTGTVQINNGETDLAAKFHKSLPHDDLGQVDADAFAALEDCLNGDLSICEDVPVGNSEGDP
VGRLVNPTAAFAIDISGPFSATTIPPVPTLPSPELAQLAEVYWMALARADVPMQYGTDDITVAAANLAGMEGFPNLDASIGSDGTVDPQLSF
RATFVGVETGPFISQLLNSFTIDSITVEPKQETFAPDVNMVDFDEWLNIQNGGPPAGPELLDDELRFVRNARDLARVTFTDNINTEAYRGALILLGL
DAFNРАGNGPFIDROAGFVNFGISHYFRLIGAAELAQRSSWYQKQWVHRFARPEALGGTLHLTIGELENADFDSLLENAELLKRVAAINAQN
PNNEVTVLLPQAIQEGSPTHPSYPSGHATQNGAFATVLKALIGLDRGGDCYPDPVYPDDGLKLIDFRGSCLTFEGEINKLAVNVAFGRQMLGIHYRF

DGIQGLLLGETITVRTLHQELMTFAEESTFEFRLFTGEVIKLFQDGTFIDGFKCPGLVYTGVENC

>d1qhba_a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Red algae (*Corallina officinalis*)}

GIPADNLQSRAKASFTRAAELALARGAVPSFANGEELLYRNSETGDPFIGSFTKGKLPHDDNGAIIDPDDFLAFVRAINSGDEKEIAALTLGPARDP
ETGLPIWRSIDLANSLDLEVRGWENSSAGLTDFLEGPAQSVAMPPAPVLTSPELIAEMAELYLMALGRDIEFSEFDSPKNAAFIRSAIERLNGLEWFN
TPAKLGDPPEIIRRGEVTGNLFRGILPGSEVGPYLSQFIIVGSKQIGSATVGNKTLVSPNADEFDGEIAGYSITISQRVRIATPGRDFMTDLKVFLD
VQDAADFRGFESYEPGARLIRTIRDLATWVHFDSLYEAYLNACILLANGVPFDPNLPFQQEDKLDNQDVFNFGSAHVLSLVTEVATRALKA
FNIHRRRLRPEATGGLISVNKNANFLKSESVPVEVDVLVEELSSILDDASSNEKQNIADGDVSPGKSFLPMAFAEGSPFHPSYGS
GHAVVAGACVTILKA
FFDANFQIDQVFV редуктаза

>d1vns_a.111.1.3 (-) Chloroperoxidase {Curvularia inaequalis}

VTPILPKIDEPEEYNTNYILFWNHVGLELNRTHTVGGPLTGPPLSARALGMLHLAIHDAYFSICPPTDFTFLSPDTENAAYRLPSPNGANDARQAV
AGAALKMLSSLYMKPVEQPQNPNGPANISDNAYAQLGLVLDRSVLEAPGGVDRESASFMFGEDVADVFALLNDPRGASQEGYHPTPGRYKFDD
THPVVLIPVDPNNPNGPKMPFRQYHAFYKGTTKRATQSEHFLADPPGLRSNADETAEYDDAVRVAIAMGGAQALNSTKRSPWQTAQGLYWAY
DGSNLIGTPPRFYNQIVRRIAVTYKKEEDLANSEVNNA
DFAFRLFALVACTDAGIFSWKEKW
EFWRPLSGVRDDGRPDHGDPFWLTGAPATN
TNDIPFKPPFPAYPSGHATFGGAVFQMVRYYNGRVGTWKDDEPDNIAIDMMISEELNGVNRLRQPYDPTAPIEDQPGIVRTRIVRFDSA
MENFAISRFLGVHWRDAAAARDILPI
TTKD
VYAVDNNGATVFQNV
EDIRYTRG
TREDEEGLFPIGGVPLGIEIADEIFNNGLKPTPPEIQP

>d1sig_a.112.1.1 (-) sigma70 subunit fragment from RNA polymerase {Escherichia coli}

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AREKFA
ELRAQYV
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IKAKGR
SHATAQ
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LPVKQ
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VNSMR
VMMDR
VRTQER
LIMKLC
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WFNA
AAIM
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LHDV
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HRALQ
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IEET
GLTIE
QVKD
INRR
MSIG
EAKARR
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RLVIS
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TNRGL
QFLDIQ
EGNIGLM
KAVDK
FEYRR
GYKF
STYAT
WWV
IRQA
ITRS
IADQ

>d1ewqa1_a.113.1.1 (A:267-541) DNA repair protein MutS, domain III {Thermus aquaticus}

RGQDTLFSV редуктаза
LDETRAPG
RRLLQSWL
RHPLLD
RGPLEAR
LDRVEG
FVREGAL
REGV
VRLAD
LERLAT
RLEGRAS
PKDLG
ALRRSL
QILPEL
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>d1e3ma1_a.113.1.1 (A:270-566) DNA repair protein MutS, domain III {Escherichia coli}

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>d1f5na1_a.114.1.1 (A:284-583) Interferon-induced guanylate-binding protein 1 (GBP1), C-terminal domain {Human (Homo sapiens)}

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PLPNQQFGVSLQHLQEKNPEQEPIPIVLRETVAYLQAHALTTEGIFRRSANTQVVREVQQKYNMGLPVDFDQYNALHLPAVILKTFRLRELPEPLLTFDLYPHVGFLNIQDESQRVPATLQLQTLPEENYQVLRLTAFLVQISAHSQDNKMTNTNLAVVFGPNLLWAKDAITLKAINPINTFTKFLLDHQGEFL>d1pbwa_a.116.1.1 (A:) p85 alpha subunit RhoGAP domain {Human (Homo sapiens)}

LPDLAEQFAPPDIAPPLIILKVEIAEKKGLECSTLYRTQSSNLAELRQLLCDCTPSVDEMDVHLADAFKRYLLDLPNPVPAAVYSEMSLAPEVQSSEEYIQLKKLIRSPSIPHQWLQYLLKHHFKLSQTSSKNLLNARVLSEIFSPMLFRFSASSDNTENLIKVIEILISTEW>d1f7ca_a.116.1.1 (A:) Graf {Chicken (Gallus gallus)}

AQLDSIGFSIIKKCIHAVETRGINEQGLYRIVGNSRVQKLLSILMDPKTATECTEICAEWEIKTITSALKTYLRMLPGPLMMYQFQRSFIKAALKLENQESRVSEIHSVHLRPEKNRQMLHLLMNHLAKVADNHKQNLMTVANLGVFGPTLLRPQEETVAAIMDIKFQNIVIEILHENHEKIFNTVPE>d1wer_a.116.1.2 (-) p120GAP domain {Human (Homo sapiens)}

MPEEEYSEFKELILQKELHVYVALSHVCQGDRTLLASILLRIFLHEKLESLLLCTLDREISMEDEATTLFRAATLASTLMEQYMKATATQFVHHALKDSILKIMESQSCELSPSKLEKNEDVNTNLTHLLNILSELVEKIFMASEILPPTRLYIYGLQKSVQHKWPTNTMRTRVSGFVFLRLCPAINPRMFNIISDSPSPIAARTLILVAKSVQNLANLVEFGAKEPYMEGVNPFIKSINKHRMIMFLDELGNVPELPDTTEHSRTDSLRLAALHEICVAHSDELRTLSNERGAQQHVLKKLLAITELLQQKQNNQYT>d1nf1a_a.116.1.2 (A:) GAP related domain of neurofibromin {Human (Homo sapiens)}

ERLVELTMMGDQGELPIAMALANVVPCSQWDELARVLVTLFDSRHLYQLLWNMFSKEVELADSMQTLFRGNSLASKIMTFCFKVYGATYLQKLIDPLLRIVITSSDWQHVSFEVDPTRLEPSSELENQRNLLQMTEKFHAISSSEFPPQLRSVCHCLYQVVSQRFQNSIGAVGSAMFLRFINPAIVSPYEAGILDKKPPIERGLKLMSKIQSIANHVLFKEEHMRPFNDFVKSNFDAARRFFLDIASDCPTSDAVNHSLSFISDGNVLAHRLWWNNQEKGQYLSNRDHKAvgrrpfdkmatllylgppe>d1bkds_a.117.1.1 (S:) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}

RLPSADVYRFAEPDSEENIIIEEGIPIIKAGTVIKLIERLTYHMYADPNFVRTFLTTYSRSCPQCELLIIEERFEIPEPRFRKEYIQPVQLRVLNVCRHWVEHFYDFERDAYLLQRMEEFIGTVRGKAMKKWVESITKIIQRKKITFQSSPPTVEWHISRPGHIETFDLLTLPPIEARIQLTLESPLYRAVQPSELVGSVWTKEDKEINSPNLLKMRHTTNLTLWFEKCVIETENLEERAVAVSVRIIIEILQVFQELNNFNGVLEVSAMNSPVYRLDHTFEQIPSRQKKILEEAHESDHYKKYLAKRSINPPCPFFGIYLTNLKTEEGNPEVLKRHGKELINFSKRRKVAEITGEIQQQNQPYCLRVESDIKRFENLNPMGNSMEKEFTDYLFNKSLEIEPRNPKPPLPRFPKKSYPLKSPGVVRPSN>d1h6oa_a.146.1.1 (A:) TRF1 {Human (Homo sapiens)}

EDAGLVAEAEAVAAGWMDFLCLSLCRAFDGRSEDFFRTRNSAEAIHGSSLTACQLRTIYCQFLTRIAAGKTLDAQFENDERITPLESALMIWGSIEKEHDKLHEEIQNLIQIAIVCMENGNFKEAEEVFERIFGDPNSHMPFKSKLLMIIISQKDTFHSSFFQHFSYNHMMEKIKSYVNYVLSEKSSTFLMKAALKVVE>d1h6pa_a.146.1.1 (A:) TRF2 {Human (Homo sapiens)}

AGEARLEEAVNRWVLKFYFHEALRAFRGSRYGDFRQIRDIMQALLVRPLGKEHTVSRLRVMQCLSRIEEGENLDCSFDMEAELTPLESAINVLEMICKTEFTLTEAVVESSRKLVKEAAVIIICNKEFKASKILKKHMSKDPTTQKLRNDLNNIREKNLAHPVIQNFSYETFQQKMLRFLESHLDDAEPYLLTMAKKALK>d1g3jc_a.118.1.1 (C:) beta-Catenin {Human (Homo sapiens)}

HHREGLLAIFKSGGIPALVKMLGPVDSVLFYAITTLHNLLHQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLIILASGGPQALVNIMRTTYEKLLWTSRVLKVLSVCSNKPAIVEAGGMQALGLHLDPSQRLVQNCWLRLNSDAATKQEGMEGLLGTQVQLGSDDINVVTCAGILSNLTCCNNYKNKMMVCQVGIGEALVRTVLРАГДРЕДИТЕПАICALRHLTSRHQEАЕМАQNAVRЛHYGLPVVКLLHPPSHWPLIKATVGLIRNLALCPANLALCPANHAPLREQGAIPRLVQLLVRAHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRIVGLNTIPLFVQLLYSPENIQRVAAGVLCEAGVLCELAQDKEAAEIAEAGATAPILELHSRNEGVATYAAAVLFRMSE>d1jdha_a.118.1.1 (A:) beta-Catenin {Human (Homo sapiens)}

AVVNINQDDAELATRAIPELTKLLNDEDQVVNKAAMVHQLSKKEASRHAIMRSPQMVSAILVTMQNTNDVETARCTAGTLHNLSHHREGLLAIFKSGGIPALVKMLGPVDSVLFYAITTLHNLLHQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKLIILASGGPQALVNIMRTTYEKLLWTSRVLKVLSVCSNKPAIVEAGGMQALGLHLDPSQRLVQNCWLRLNSDAATKQEGMEGLLGTQVQLGSDDINVVTCAGILSNLTCCNNYKNKMMVCQVGIGEALVRTVLРАГДРЕДИТЕПАICALRHLTSRHQEАЕМАQNAVRЛHYGLPVVКLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNRIVGLNTIPLFVQLLYSPENIQRVAAGVLCEL

AQDKEAAEIAEAEGATAPLTELLHSRNEGVTYAAAVLFRMS

>d1ala_a.118.1.1 (A:) Importin alpha {Mouse (Mus musculus)}

DEQMLKRRNVSSFPDDATSPHQNRNNQGTNVWSVEDIVKGINSNNLESQLQATQAARKLLSREKQPPIIDNIIAGLIPKFVSLGKTDCSIQFESA
WALTNIASGTSEQTKAVVDGGAIPAFISLLASPHAHISEQAVWALGNIAGDGSARLDVIKHGAIDPLALLAVPDLSTIACGYLRNLTWLSNLCRNK
NPAPPLDAVEQILPILTVRLHHNDPEVLADSCWAISYLTDPNTERIEMVVKKGVPQLVKLLGATELPALRAIGNVTGTDEQTQKVIDAGALAVF
PSLLTPKTNIQKEATWTMSNITAGRQDQIQQQVNHGLPFLVGVLSKADFKTQKEAAWAITNYTSGGTVEQIVYLVHCGIEPLMNLLSAKDTKIIQ
VILDAISNIFQAAEKLGETEKLSIMIEECGGGLDKIEALQRHENESVYKASLNLIKEYF

>d1ibrb_a.118.1.1 (B:) Importin beta {Human (Homo sapiens)}

ELITILEKTVSPDRLEAAQKFLERAIVENLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLTSKDPDIKAQYQQRWLAI DANARREVKNYVLQTLGT
ETYRPSSASQCVCAGIACAEIPVNQWPFLPQLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTIIQGMRKEEPSNNVLAATNALLN
SLEFTKANFDKESERHFIMQVVCATQCPDTRVRVAALQNLVKIMSYYQYMETYMGPAFAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEAS
EEAEQGRPPEHTSKFYAKGALQYLPILTQTLKQDENDDDDWNPKAAGVCLMILATCCEDDIVPHVLPFIKEHIKNPDWRYRDAAVMAFGCILE
GPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTVGRICELLPEAAINDVY LAPLQLCIEG

>d1qgra_a.118.1.1 (A:) Importin beta {Human (Homo sapiens)}

MELITILEKTVSPDRLEAAQKFLERAIVENLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLTSKDPDIKAQYQQRWLAI DANARREVKNYVLHTL
GTETYRPSSASQCVCAGIACAEIPVNQWPFLPQLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTIIQGMRKEEPSNNVLAATNAL
LNSLEFTKANFDKESERHFIMQVVCATQCPDTRVRVAALQNLVKIMSYYQYMETYMGPAFAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIE
ASEAAEQGRPPEHTSKFYAKGALQYLPILTQTLKQDENDDDDWNPKAAGVCLMILATCCEDDIVPHVLPFIKEHIKNPDWRYRDAAVMAFGC
ILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTVGRICELLPEAAINDVY LAPLQLCIEGLSAEPRVASNCWFSSLAEAAYEADVADDQ
EEPATYCLSSSFELIVQLLETTDRPDGHQCNLRLSSAYEALSMEIVKNSAKDCYPAVQKTTLIMERLQQVLMQESHIQSTS DRIQFNDLQSLLCATLQN
VLRKVQHQDALQISDVVMASLLRMFQSTAGSGVQEDALMAVSTLVEV LGGEFLKYMEAFKPFLIGLK NYAEYQVCLAAVGLVGDL CRALQSNIIP
FCDEVMQLLLENGNENVRSPVQPKIQLS VFGDIALIGGEFKKYLEVVLNTLQQASQAQV DKSDYDMV DYLNLRESCLEAYTGIVQGLKDQENVH
PDVMLVQPRVEFILSFIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLKLVEARPMIHELLTEGRRSKTNKAKTLARWATKELRKLKNQA

>d1qbkb_a.118.1.1 (B:) Karyopherin beta2 {Human (Homo sapiens)}

YEWKPDEQGLQQILQLLKESQSPDTTIQRTVQQKLEQLNQYPDFNNYLIVPLVLTKLSEDEPTRSLSGLILKNNVKAHFQNFPNGVTDFIKSECLNNIGD
SSPLIRATVGILITIASKGELQNWPDLPLKCLSLLS DEDYNTCEGAFGALQKICEDSAEILDSDVLDRLPNIMIPKFLQFFKHSSPKIRSHAVACVNQFIIS
RTQALMLHIDSFTENLFALAGDEEPEVRKNVCRALVMLEVRMDRLLPHMHNIVEYMLQRTQDQDENVALEACEFWLTLAEQPICKDVLVRHLPKL
IPVLVNGMKYSDIDIILLKGDV EEDETIPDSEQDIRPRFHRSRTVAQQHQEDGIEEE DDDDEIDDDDTISDWNLRKCSAAALDV LANVYRDELLPHIL
PLLKELLFHHEWVVKESGILVLGAI AEGCMQGMIPYLPELPHIQLCSDKKALVRSITCW TLSRYAHWVSQPPDTYLKPLMTELLKRILDSNKRVQE
AACSAFATLEEACTELV PLYI DTLVFAFSKYQHKNLLILYDAIGTLADSVGHHLNKPEIYQMLMPPLIQKWNMLKDEDKDLFPLLECLSSVATALQS
GFLPYCEPVYQRCVNLVQKTLAQAMLNNAQPDQYEAPDKFMIVALDLSGLAEGLGGNIEQLVARSNILTLMYQCMQDKMPEVRQSSFALLGDLT
KACFQHVVKPCIADFMPILG TNLNPEFISVCNNATWAIGEISIQMGIEMQPYIPMVLHQ LVEIINRPNTPKTLLENTAITIGRLGYVCPQEVAPMLQQFI
RPWCTSLRNIRDNEEKDSA FRGI CTMISVNPSGV IQDFIFFCD AVASWINPKDDL RDMFCKILHGFKNQVG DENWRRFSDQFPLPLKERLA AFYGV

>d1ee4a_a.118.1.1 (A:) Karyopherin alpha {Baker's yeast (Saccharomyces cerevisiae)}

QELPQMTQQLNSDDMQUEQLSATVKFRQILSREHRPPIDVVIQAGVVPRLVEFMRENQPEMLQLEAAWALTNIASG TS AQTKV VV DADAVPLFIQLL
YTGSVEVKEQAIWALGNVAGDSTDYRDYVLCQNAMEPILGLFNSNKPSLIRTATW TLSNLCRGKKPQDWSVVSQALPLTAKLIYSMDTETLV DAC
WAISYLSDPQEAIQAVIDV RPKRLVELLSHESTLV QTPALRAVGNIVTGN DLQTVV INAGVLPALRLLSSPKENIKKEACWTISNITAGNTEQI QAVI
DANLIPPLVKLLEVAEDKTKEACWAISNASSGGLQRPDIYLVSQGCICPLCDLLEIADRIIEVTL DALENILKMGEADKEARGLNINENADFIEKAG
GMEKIFNCQQNENDKIYEKAYKIIETYF

>d1b3ua_a.118.1.2 (A:) Constant regulatory domain of protein phosphatase 2a, pr65alpha {Human (Homo sapiens)}

AAADGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSTIALALGVERTRSELLPFLTDITYDEDEVLLALAEQLGTFTLVGGPEYVHCLLPPLES LATVEETVV
RDKAVESLRAISHEHSPSDLEAHFVPLVKRLAGGDWFTSRTSACGLFSVCYPRVSSAVKAELRQYFRNLCSDDTPMV RRAASKLGEFAKVLELDNVK
SEIIPMFSNLASDEQDSVRLAVEACVNIAQLLPQEDLEALVMPTLRQAAEDKSWRVRYMVA DKFTELQKAVGPEITKTDLVP A FQNL MKDCEAEVR
AAASHKVKEFCENLSADC REN VIMS QLPCIKELVSDANQHVKSALASVIM GLSPILGKDNTIEHLLPLFLAQLKDECPEVRLNII S NLCVNEVIGIRQL

SQSLPAIVELAEDAKWRVRLAIIEYMPPLLAGQLGVFFDEKNSLCMAWLVDHVYAIRERAATSNLKKLVEKFGKEWAHATIIPKVЛАMSGDPNYLHR
MTTLFCINVЛSEVCGQQDITTKHMLPTVLRMAGDPVANVRFNVAKSLOQKIGPILDNSTLQSEVKPILEKLTDQDVKYFAQEALTВLSA
>d1hu3a_a.118.1.2 (A:) Eukaryotic initiation factor eIF4G {Human (Homo sapiens)}
SDPENIKTQEFLRKVRSILNKLTPQMFnQLMKQVSGLTVDTEERLKGVIDLVFEKAIDEPFSVAYANMCRLVTLKVPMAKPGNTVFRKLLNRC
QKEFEKDКАDDDVFEKKQKELEAASAPEERTRLHDELEAKDKARRSIGNKFIGELFKLKMЛTEAIMHDСVVKLLKNHDEESLECLCRLTTIGKLD
FEKAKPRMDQYFNQMEKIVKERKTSSRIRFMLQDVIDLRLCNWVS
>d1h6ka1_a.118.1.2 (A:27-290) CBP80, 80kDa nuclear cap-binding protein {Human (Homo sapiens)}
TEDHLESЛИCKVGEKSACSLESNLELAGVLEADLPNPKSKILRLCTVARLLPEKLTITTLVGLLNARNYNFGGEFVEAMIRQLKЕSLKANNYNEAVYL
RFLSDLVNCVIAAPSMVAMFENFVSVTQEEDVPQVRRDWYVYAFSLSPWVGKELYKKDAEMDRIFANTESYLKRRQKTHVPMQLQVWTADKP
HPQEEYLDCWAQIQKLKDRWQERHILRPYLAФSILCEALQHNLPPTPPHTEDSVYPMPRVIFR
>d1h6ka2_a.118.1.2 (A:291-480) CBP80, 80kDa nuclear cap-binding protein {Human (Homo sapiens)}
MFДYTDDPEGPVMPGSHSVERFVIEENLHCIIKSHWKERKTCAAQLVSPGKNKIPLNYHIVEVIFAEFLQPAPPHIDVMYТLLIELCKLQPGSLPQV
LAQATEMILYMRLLTMNTTCVDRFINWFSHHSNFQRWSWEDWSDCLSQDPESPКPKFVREVLEKCMRLSYHQRIIDIVPPTFSALCPN
>d1h6ka3_a.118.1.2 (A:481-790) CBP80, 80kDa nuclear cap-binding protein {Human (Homo sapiens)}
PTCIYKGDESSNSLPGHСVALCLAVAFKSKATNDEIFSIKLDVNPNPNQDDDDDEGFSNPLKIEFVFTQTLHлаKSFHSFSAKHFЕVFKTLAESDE
GKLHVLRVMFVWRNHPQMIAVLVDKMI RTQIVDCAAVANWFSSELSDRFTRLFVWEILHSTIRKMNKHVLKIQKELEEAKELARQHDGVLEEQI
ЕRLQEКVESAQSEQKNLFLVIFQRFIMLITEHLVRCETDGTSVLTПWYKNCIERLQQIFLQHHQIIQQYMTLENLLFTAELDPHILAVFQQFCALQA
>d1hs6a1_a.118.1.7 (A:461-610) Leukotriene A4 hydrolase C-terminal domain {Human (Homo sapiens)}
DMTLTNACIALSQRWITAKEDDLNSFNATDLKDLSSHQLNEFLAQTLQRAPLPLGHИKRMQEVYNFNAINNSEIRFWLRLCIQSKWEDAIPLALKM
ATEQGRMKFTRPLFKDЛAФDKSHDQAVRTYQEHKASMHPVTAMLVGKDLKVD
>d1b89a_a.118.1.3 (A:) Clathrin heavy chain proximal leg segment {Cow (Bos taurus)}
RЛАELEEFINGPNNAHQVQGDRCYDEKMYDAAKLЛNNVSNGRЛАSTLVHLGEYQAAVGARKANSTRTWKEVCFAСVDGKEFRLAQMCGLHI
VVHADEEELINYQDRGYFEELITMLEAALGLERAHMGMFTELAILYSKFKPQKMREHLELFWSRVNIPKVLRAAEQ AHLWAEЛVFLYDKYEYDNA
IITMMNHPTDAWKEGQFKDIITKVANVЕLYYRAIQFYLFKPLLNDLLMVLSPRLDHTRAVNYFSKVKQLPLVKPylRSVQNHNNSVNEСLNNLFIT
EEDYQALRTSIDAYDNFDNISLAQRLEKHELIEFRRIAAYLFKG
>d1bpoa1_a.118.1.4 (A:331-487) Clathrin heavy-chain linker domain {Rat (Rattus norvegicus)}
EENIIPYITNVLQNPDLALRMAVRNNLAGAEELFARKFNALFAQGNYSEAAKVAANAPKGIL RTPDTIRRFQSVPАQPGQTSPLLQYFGIILDQGQLN
KEYSLELCРPVLQQGRKQЛLEKWLKEDKLECESEELGDLVKSVDPLTLSVYLRANVPNK
>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}
TPIGDCRVCFSFRMSLLTGRCTPGDACVAVESGRQIDRFFRNPHLAVQYLADPFWERRAIAVRYSPEALTPLIRDSDEVRRAYRLPREQLSAL
MFDEDREVITVADRLPLEQMAADRDYLVRAYVVQRIPPGRLFRFMРDEDRQVRKLVAKRLPEESLGLMTQDPЕPEVRRIVASRLRGDDLELL
HDPDWTVRLAAVEHASLEALRELDEPDPEVRLAIAGRL
>d1e8xa1_a.118.1.6 (A:525-725) Phosphoinositide 3-kinase (PI3K) helical domain {Pig (Sus scrofa)}
HPIALPKHRPTPPEGDRVRAEMPNQLRKQLEAIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLSSVKWGGQЕIVAKTYQLAKREVWDQSAL
DVGLTMQLDCNFSDENVRAIAVQKLESLEDDVLHYLLQLVQAVKFEPYHDSALARFLLKRLRNKRIGHFLFWLRSEIAQSRHYQQRFAVILEAYL
RGCG
>d1ib2a_a.118.1.8 (A:) Pumilio 1 {Human (Homo sapiens)}
GRSRLLEDFRNNRYPNLQLREIAGHIMEFSQDQHGSRFIQLKLERATPAERQLVFNEILQAAYQLMVDVFGNYVIQKFFEGSLEQKLALAERIRGHVL
SLALQMYGCRVIQKALEFIPSQQNEMVRELDGHVLKCVKDQNGNHVVQKICЕVQPQSLQFIIDAFKGQVFAЛSTHPYGRVIQRILEHCLPDQTL
PILEELHQHTEQLVQDQYGNVYIQHVLEHGRPEDKSIVAEIRGNVLVLSQHKFASNVЕKCVTHASRTЕAVLIDEVCTMNDGPHSALYTMMDQ
YANYVVQKМIDVAEPGQRKIVMHKIRPHIA
>d1ho8a_a.118.1.9 (A:) Regulatory subunit H of the V-type ATPase {Baker's yeast (Saccharomyces cerevisiae)}

GATKILMDSTHFNEIRSIIRSRSVAWDALARSEELSEIDASTAKALESILVKKNIGDGLSSNNAHSGFKVNGKTLIPLIHLSTSNDNECKSVQNLIAELL
SSDKYGDDTVKFFQEDPKQLEQLFDVSLKGDFQTVLISGFNVVSLVQNGLHNVKLVEKLLKNNNLINILQNIEQMDTCYVCIRLLQELAVIPEYRDVI
WLHEKKFMPTLFKILQRATDSQLATRIVATNSNHLDIQLQYHSLLIWLTFNPVFANELVQKYLSDFLDELLKLVKITIKEVSRLCISIILQCCSTRVKQHK
KVIKQLLLGNALPTVQSLSERKYSDEELRQDISNLKEILENEYQELETSFDEYVAELDSKLLCWSPPHVDNGFWSDNIDEFKKDNYKIFRQLIELLOAKVR
NGDVNAKQEKIIIQVALNDITHVVELLPESIDVLDKTGGKADIMELLNHSDSRVKEYEALKATQAIIGYTFK

>d1ycsb1 a.118.2.1 (B:327-456) 53BP2 {Human (Homo sapiens)}

PLALLDSSLEGEFDLVQRIIYEVDDPSLPNDEGITALHNACAGHTEIVKFLQFGVNVAADSDGWTPHLCAASCNNVQVCKFLVESGAASFAMT
YSDMQTAADKCEEMEEGYTQCSQFLYGVQEKM

>d1awcb_a.118.2.1 (B:) GA bindinig protein (GABP) beta 1 {Mouse (Mus musculus)}

DLGKKLLEAARAGQDDEVRLMANGAPFTDWLGTSPHLAAQYGHFSTTEVLLRAGVSRDARTKVDRTPLHMAASEGHANIEVLLKGADVNA
KDMILKMTALHWATEHNHQEVVELLIKYGADVHTQSKFCFKTAFDISIDNGNEDLAEILQ

>d1bd8_a.118.2.1 (-) Cell cycle inhibitor p19ink4D {Human (Homo sapiens)}

RAGDRLSGAAARGDVQEVRLLLHRELVHPDALNRFGKTAQVMMFGSTAIALELLKQGASPNVQDTSGTSPVHDAARTGFLDTLKVLVEHGADV
VPDGTGALPIHLAVQEGHTAVVSFLAAESDLHRRDARGLTPLEALQRGAQDLDILQGHM

>d1blxb_a.118.2.1 (B:) Cell cycle inhibitor p19ink4D {Mouse (Mus musculus)}

VCVGDRLSGAAARGDVQEVRLLLHRELVHPDALNRFGKTAQVMMFGSPAVALLELLKQGASPNVQDASGTSPVHDAARTGFLDTLKVLVEHGADV
NALDSTGSPLIHLAIREGHSSVVSFLAPESDLHRRDASGLTPLELARQRGAQNLMDILQGHMMIP

>d1ihba_a.118.2.1 (A:) p18ink4C(ink6) {Human (Homo sapiens)}

WGNELASAARGDLEQLTLLQNNVNNAQNGFGRATALQVMKLNPEIARRLLRGANPDLKDRGFAVIHDAARAGFLDTLQTLLEFQADVNI
DNEGPNLPLHLAAKEGHHLRVEFLVKHTASNVGHRNHKGDTACDLARLYGRNEVVSLMQANG

>d1a5e_a.118.2.1 (-) Cell cycle inhibitor p16ink4A {Human (Homo sapiens)}

MEPAAGSSMEPSADWLATAAAGRVEEVRALLEAGALPNAPNSYGRRIQVMMMGSAVARAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTL
VVLHRAGARLDVRDAWGRLPVDLAELGHHRDVARYLRAAGGTRGSNHARIDAEGPSDIPD

>d1bi7b_a.118.2.1 (B:) Cell cycle inhibitor p16ink4A {Human (Homo sapiens)}

EPSADWLATAAAGRVEEVRALLEAGANPNAPNSYGRRIQVMMMGSAVARAELLLLHGAEPNCADPATLTRPVHDAAREGFLDTLVLHRAGARL
DVRDAWGRLPVDLAELGHHRDVARYLRAAA

>d1iknd_a.118.2.1 (D:) I-kappa-B-alpha {Human (Homo sapiens)}

DGDSFLHLAIIEEKALTMEVIRQVKGDALFLNFQNNLQQTPLHLAVITTNQPEIAEALLGAGCDPELRDFRGNTPLHLACEQGCLASVGVLQSCTTP
HLHSILKATNYNGHTCLHLASIHYGLGIVELLVSLGADVNAQEPNGRTALHLAVDLQNPDLVSLLCGADVNRTYQGSPYQLTWGRPSTRIQQQ
LGQLTLENLQMLPESEDEESYDTES

>d1k1aa_a.118.2.1 (A:) bcl-3 {Human (Homo sapiens)}

EDGDTPLHIAVVQGNLPAVHRLVNLFFQGGRELDIYNNLRLQTPLHLAVITLPSVVRLLTAGASPMALDRHGQTAHLACEHRSPTCLRALDSAAP
GTLDLEARNYDGLTALHVAVNTECQETVQLLERGADIDAVDIKSGRSPLIHAVENNLSMVQLLQHGANVNAQMYSGSSALHSASGRGLLPLVRT
LVRSGADSSLKNCHNDTPLMVARSRRVIDL RG

>d1myo_a.118.2.1 (-) Myotrophin {Rat (Rattus norvegicus)}

MCDKEFMWALKNGDLDDEVKDYVAKGEDVNRTLEGGRKPLHYADCGQLEILEFLLKGADINAPDKHHITPLLSAVYEGHVSCVKLLSKGADKTVK
GPDGLTALEATDNQAIKALLQ

>d1sw6a_a.118.2.1 (A:) Swi6 ankyrin-repeat fragment {Baker's yeast (Saccharomyces cerevisiae)}

GPIITFTHDLSDFLSSPLKIMKALPSPVNDNEQKMKLEAFLQRLLFPEIQEMPTSNNNDSSRNSEGGSSNQQQQHVSFDSLQEVNDAFPNTQL
NLNIPVDEHGNTPLHWLTSIANLELVKHVKHGSNRLYGDNMGESCLVKAVKSNNYDSGTFEALLDYLYPCLIEDSMNRTILHHIIITSGMTGCSAA
AKYYLDILMGWIVKKQNRPIQSGTNEKESKPNDKNGERKDSENLDLKWIIMLNAQDSNGDTCLNIAARLGNISIVDALLDYGADPFIAKSGLR
PVDFGAG

>d1dcqa1_a.118.2.1 (A:369-522) Pyk2-associated protein beta {Mouse (Mus musculus)}

ADTAALKLHSLCEAVKTRDIFGLLQAYADGVDLTEKIPLANGHEPDETALHLAVRSVDRTLSHVDFLVQNSGNLDKQTGKGSTALHYCCLTDNAECLKLL

LRGKASIEIANESGETPLDIAKRLKHEHCEELLTQALSGRFNSHVHVEYEWRLL
>d1pbv__ a.118.3.1 (-) Exchange factor ARNO {Human (Homo sapiens)}
ANE GTKLQRNRKMAMGRKKFNMDPKKGIQFLVENEQQNTPEEIRFLYKGEGLNKTAIGDYLGEREEELNLA
VLSFAIMLNTSLHNPVNRDKPGLERFVAMNREGINEGGDLPEELLRNLYDSIRNEPFKI
WSFRLPGEAQKIDRMMEAFAQRYCLCNPGVFQSTDTCYVLSFAIMLNTSLHNPVNRDKPGLERFVAMNREGINEGGDLPEELLRNLYDSIRNEPFKI
P
>d1bc9__ a.118.3.1 (-) Cytohesin-1/b-2-1 {Human (Homo sapiens)}
MKNMQRNKQVAMGRKKFNMDPKKGIQFLIENDLLKNTCEDIAQFLYKGEGLNKTAIGDYLGERDEFNIQLV
HAFVELHEFTDLNLVQALRQFLWSF
RLPGEAQKIDRMMEAFAQRYCLCNPGVFQSTDTCYVLSFAIMLNTSLHNPVNRDKPGLERFVAMNREGINEGGDLPEELLRNLYDSIRNEPFKI
HHHHHH
>d1qsaa1 a.118.5.1 (A:1-450) 70 KDa soluble lytic transglycosylase (SLT70), superhelical domain {Escherichia coli}
DSLDEQRSRQAQKWA
DNRQMDVVEQMMMPGKDYPLYPYLEYRQITDDLMNQPAVTVNFVRANPTLQSRVNE
LARREDWRGLAF
SPEKPGTTEAQCNYYAKWNTGQSEEAWQGA
KEWL
TGSQPNACDKLFSVWRASGKQDPLAYLERIRLAMKAGNTGLTVLAGQMPADYQTIA
SAIISLANNPNTVLT
FARTTGATDFTRQMAAVAFASVARQDAENARLMIPS
LAQAQQLNEDQI
QELRDI
VAWRLMGNDV
TDEQAKWRDDAIMRS
QSTS
LIERRVRMALGTGDRRGLNTW
LARLP
MEAKEKD
EWRYWQADLLERG
REA
AEAKIELHQLMQQRGF
YPM
AAQRIGEYE
LKIDKAPQNVD
SALTQGPEMARV
REL
MYW
NLDNT
TAR
SE
WANLV
KS
SKTE
QAQ
LARYAF
NNQW
DLSV
QATIAG
KLWDH
LEERFP
>d1d8da_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Rat (Rattus norvegicus)}
FLS
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>d1jcqa_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Human (Homo sapiens)}
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>d1dcea1 a.118.6.1 (A:1-240,A:351-443) Rab geranylgeranyltransferase alpha-subunit, N-terminal domain {Rat (Rattus norvegicus)}
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GRL
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>d1qjba_ a.118.7.1 (A:) zeta isoform {Human (Homo sapiens)}
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>d1a17__ a.118.8.1 (-) Protein phosphatase 5 {Human (Homo sapiens)}
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>d1elra_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}
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>d1elwa_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}
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>d1qqa_a.118.8.1 (A:) Vesicular transport protein sec17 {Baker's yeast (*Saccharomyces cerevisiae*)}
ISDPVELLKRAEKKGVSSGMKLFSGSDSYKFEAAADLCVQAATYRLKELNLAGDSFLKAADYQKKAGNEDEAGNTYVEAYKCFKSGGNSVNAVD
SLENIAQIFTHRGQFRRGANFKFELGEILENDLHDYAKAIDCYELAGEWEYAQQDQSVALSNKCFIKCADCALDGQYIEASDIYSKLICKSMGNRLSQWS
LKDYFLKKGLCQLAATDAVAARTLQEGQSEDPNFADSRESNFLKSLIDAVNEGDSLSEQLEHCKEFDNFMRLDKWKITLNKIKESIQQQEDD
>d1hh8a_a.118.8.1 (A:) Neutrophil cytosolic factor 2 (NCF-2, p67-phox) {Human (*Homo sapiens*)}
SLVEAISLWNEGVLAAADKKDWKGALDAFSAVQDPHSRICFNIGCMYTIKNMTEAEKAFTRSINRDKHLAVAYFQRGMILYYQTEKYDLAIKDLKEALI
QLRGNQLIDYKILGLQFKLFACEVLYNIAFMYAKKEEWKKAEEQLALATSMKSEPRHSKIDKAMECVWQKLYEPVVIPVGRFRPNERQVAQL
>d1fcha_a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Human (*Homo sapiens*)}
SATYDKGYQFEEENPLRDHPQPFEEGLRRLQEGDLPNAVLLFEAAVQQDPKHMEAWQYLGTTQAENEQELLAISALRRCLELKPDNQTALMALAVS
FTNESLQRQACEILRDWLRYTPAYAHVTPAEEGAGGAGLGPSKRILGSLLSDSLFLEVKEFLAFLAVERLDPTSIDPDVQCGLGVLFNLSEYDKAVDCFT
AALSVRPNDDYLLWNKLGATLANGQSEEAVAAYRRALELQPGYIRSRYNLGISCINLGAHREAVEHFLEALNMQRKSRGRGEGGAMSENIWSTLRL
ALSMLGQSDAYGAADARDLSTLLTMFGLPQ
>d1hxia_a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Trypanosoma brucei}
NNTDYPFEANNPYMYHENPMEEGLSMKLANLAEALAFEAVCQKEPEREEAWRSLGLTQAENEKGLAIILNHARMLDPKDIAVHAALAVSHT
NEHNANAALASLRALL
>d1ihg1_a.118.8.1 (A:197-365) Cyclophilin 40 {Cow (*Bos taurus*)}
GSGDSHPDFPEDADVLKDVKILLISEDLKNIGNTFKSQNWE MAIKKYTKVLRYVEGSRAAAEDADGAKLQPVALCVLNIGACKLKMSDWQGA
VDSCLEALEIDPSNTKALYRRAQGWQGLKEYDQALADLKKAAQEIAPEDKAIQAEELLKVQKQKIKAQKDKEKAAY
>d1ipa1_a.118.8.1 (A:197-298) Cyclophilin 40 {Cow (*Bos taurus*)}
GSGDSHPDFPEDADVLKDVKILLISEDLKNIGNTFKSQNWE MAIKKYTKVLRYVEGSRAAAEDADGAKLQPVALCVLNIGACKLKMSDWQGA
VDSCL
>d1hz4a_a.118.8.2 (A:) Transcription factor MalT domain III {Escherichia coli}
EIKDIREDTMHAEFNALRAQVAINDGNPDEAERLAKLAELPPGWFYSRIVATSVLGEVLHCKGELTRSLALMQQTEQM MARQHDVWHYALWSLIQ
QSEILFAQGFLQTAWETQEKAQFLINEQHLEQLPMHEFLVRIRAAQLLAWARLDEAEASARSGIEVLSYQPQQQLQCLAMLIQCSLARGDLDNARS
QLNRLENLLNGNGKYHSDWISNANKVRVYWQMTGDAAAANWLRHTAKPEFANNHFLQGQWRNIARAQILLGEFEPAEIVLEELNENARSLRM
SDLNRNLLLNQLYWQAGRKSDAQRVLLDALKLANRTGFISHFVIEGEAMAQQLRQLIQLNLTPELEQHRAQRILREIN
>d1eyha_a.118.9.1 (A:) Epsin 1 {Rat (*Rattus norvegicus*)}
HNYSEAEIKVREATSNDPWPSSSLMSEIADLTNVVAFSEIMSMIWKRNDHGKNWRHVYKAMTLMEYLIKTSERVSQQCKENMYAVQTLKDF
QYVDRDGKDQGVNVREKAKQLVALLRDEDRLREERAHALKTKEKLAQTA
>d1inza_a.118.9.1 (A:) Epsin 1 {Human (*Homo sapiens*)}
GSSRMSTSSLRQMKNIVHNYSEAEIKVREATSNDPWPSSSLMSEIADLTNVVAFSEIMSMIWKRNDHGKNWRHVYKAMTLMEYLIKTSER
VSQQCKENMYAVQTLDFQYVDRDGKDQGVNVREKAKQLVALLRDEDRLREER
>d1dvpa1_a.118.9.2 (A:1-145) Hrs {Fruit fly (*Drosophila melanogaster*)}
MFRSSFCNKLNENATSHLRLEPDWPSILLICDEINQKDVTPKNAFAIKKKMNSPNPHSSCYSLVLESIVKNCAPVHEEVFTKENCEMFSSFLESTPHE
NVRQKMELVQTWAYAFRSSDKYQAIKDTMTILKAKGHTFPELRE
>d1elka_a.118.9.2 (A:) Tom1 protein {Human (*Homo sapiens*)}
SDFLLGNPFSSPVGQRIEKATDGLQSEDWALNMEICDIINETEEGPKDALARVKKRIVGNKNFHEVMLALTVEBCVKNCGHRHVVLVASQDFVESV
LVRTILPKNNPPTIVHDVKVNLNLIQSWADAFRSPDLTVIYEDLRRKGLEFPM
>d1juqa_a.118.9.2 (A:) Gga3 {Human (*Homo sapiens*)}
ESLESWLNKATNPSNRQEDWEYIIGFCQDQINKELEGQPQIAVRLLAHKIQSPQEWEALQALTVEACMKNCGRFHNEVGKFRFLNELIKVVS PKYLG
RVSEKVTKVIELLYSWTMLPPEAKIKDAYHMLKRQGIVQSDPPIPVDRTLI
>d1hf8a_a.118.10.1 (A:) Clathrin assembly lymphoid myeloid leukaemia protein, Calm {Rat (*Rattus norvegicus*)}
GSAVSKTVCKATTHEIMGPKKHLDYLIQCTNEMNVNIPQLADSLFERTTNSSVVVFKSLITTHLMVYGNERFIQYLASRNTLFNLSNFLDKSGLQ
GYDMSTFIRRYSRYLNEKA VSYRQVAFDFTKVKRGADGMRTMNTEKLLKTVPIIQNQMDALLDFNVNSNELTNGVINA AFMLFKDAIRLFAA YNE

>d1hx8a_a.118.10.1 (A:) AP180 (Lap) {Fruit fly (*Drosophila melanogaster*)}

QGLAKSVCKATTEECIGPKKKHLDLVHCANECPNVSIPHANLLIERSQNANVVYKSLITTHHLMAYGNERFMQYLASSNSTNLSSFLDKGTQVD
GGMGVPGGRMGYDMSPFIRRYAKYLNEKSLSYRAMAFDFCKVKRGKEEGLSRSMNAEKLLKTLPVLCQAQLDALLEFDQSNDLSNGVINMSFMILL
FRDLIRLFACYNDGIINLLEKYFDMNKKHARDALDLYKKFLVRMDRVGEFLKVAENVGIDKGDIPDLTKAPSSLLDALEQHLATL
>d1kpsb_a.118.12.1 (B:) Ran-GTPase activating protein 1 (RanGAP1), C-terminal domain {Mouse (*Mus musculus*)}

TDLSTFLSFPSPEKLLRLGPKVSVLIVQQTDTSPEKVVSAFLKVASVFRDASVTKAVLDAIDALMKKAFCSCSFSNTFLTRLLIHMGLLKSEDKIAIP
SLHGPLMVLNHVVRQDYFPKALAPLLAFVTKPNGALETCSFARHNLLQTLINYI
>d1k8kg_a.118.13.1 (G:) Arp2/3 complex 16 kDa subunit ARPC5 {Cow (*Bos taurus*)}

ARFRKVDVDEYDENKFVDEDGGDGQAGPDEGEVDSCLRQGNMTAAQALKNPPINTKSQAVKDAGSIVLKVLISFKANDIEKAVQSLDKNGV
DLLMKYIKGFESPDNSAVLLQWHEKALAAGGVGSIVRVLTARKTV
>d1ocre_a.118.11.1 (E:) Cytochrome c oxidase subunit E {Cow (*Bos taurus*)}

SHGSHETDEEF DARWV TYFN KPDIDAW ELRK GMNT LVGY DLV PEPKI IDA ALRAC RRL NDFAS A VRILE VVK DKAG PH KEI YPY VI QEL RPT LNE LGIS
TPEELGLDKV
>d1f8na1 a.119.1.1 (A:150-839) Lipoxigenase, C-terminal domain {Soybean (*Glycine max*), isozyme L1}

VPSETPAPLVSYREEELKSLRGNGTGERKEYDRIYDYDVYNDLGNPDKSEKLARPVLGGSSTFPYPRRGRTGRGPTVD PNT EKQGEVFYVPRDENLG
HLKSKDALEIGTKSLSQIVQPAFESA FDLKSTPIEFHSFQDVHDLYEGGIKLP RDVISTIPLPV KI ELYRTDGQHILKFPQPHVQVS QSAWMTDEEFARE
MIAGVNPCVIRGLEEFP PKSNLDPAIYGDQSSKITADSL DLDGYTMDEALGSRRLFM LDYHDIFMPYVRQINQLNSAKTYATRTI FLREDGTLKPVAIE
LSLPHSAGDL SAAV SVVLP AKEGVESTI WLLAKAYVIVNDSCYHQLMSHWLNTHAAMEP FVIATHR HLSV LHPIYKL LTPHYRN NMNINALARQSLI
NANGIIETTFLPSKYSVEMSSAVYKNWVFTDQALPADLIKRGVAIKDPSTPHGVRLIEDPYA ADGLEIWAIAKTWVQEYVPLYYARDDDVKN DSEL
QHWWKEAVEKG HGD LKDPWPKLQ TLLEDLV EVC LIIWI ASALHA AVNF GQPYGG LIMNRPTAS RRL PEKG TPEYE MMINNHE KAYL RTITSK
PTLISL SVEI LSTHASDEV YLG QRD NPHWT SD SKALQ AFQ KFGN KLKEIEE KLV RRN NDPSL QGN RL GPVQL PYTLL YPSSE EGLT FRG I PNSI
>d1ik3a1 a.119.1.1 (A:168-857) Lipoxigenase, C-terminal domain {Soybean (*Glycine max*), isozyme L3}

LPSETPAPLVKYREEELHNL RG DGT GERKEWE RIYDYDVYNDL GPD KGENHAR PV LGND TFPY PR RG RT GRK PTKD PN SE RSNDV YL PRDE AF
GHLKSSDFLT YGLKS VSNV LP LQSAF DLNFT P RFDS FDEV HG L YSGG I KLP TD IIS KIS PLV KLE I FRTD GEQ ALK FPPPK V IQV SKS AWMT DEEFAR
EMLAGVNPNLIRCLKDFFRSKLD SQVY GDHTS QTKEH LEPN LEG LT VDEAIQNKRL FLLD HHDP IM PYL RRI N ATSKAYA TRT IFLKND GTL RPLAI
E LSLPH PQGDQSGAFSQVFLPADEGV ESSI WLLAKAYV VVNDSCYHQLV SHWL NT HA VVEPF IATRN R HLSV VHPIYKL LPHYR DT MN INGLARL S
VNDGGVIEQTFLWGRYSVEMSAVYKDWVFTDQALPADLIKRGMAI ED PSCP HGIRL VIEDPYTV DGLEI WDAIKT W VHEY VFLY KSD TL REDP
E LQACW KEL VEVG HGD KKNEP PWPKM QTREEL VEAC AII WTAS LHA AVNF GQPYGG LILN RPTLS RRFMPEK GS AYE ELR KNPQ KAYL KTIP
K FQTLID LS VIEI SRH ASDEV YLGERDN PWT SDTRA LEAF KRG FNK LAQ JEN KLS ERN INDE KLR NR CGPV QM PTLL PSS KEGL TFRG I PNSI
>d1lox_1 a.119.1.2 (113-663) 15-Lipoxygenase {Rabbit (*Oryctolagus cuniculus*)}

TGCTTVGDPQGLFQKHREQEERRKLYQWGSWKEGLILNVAGSKLT DLPVDERFLED K KIDFEASLAWGLAELAKNSLN ILAPWKT LDDFN RIFW
CGRSKLARRVRD SWQEDSLFGYQFLNGANPMLLRSVQLPARLVFP PGMEELQ AQL E KELK AGT L FEA D FAL LDN IKA NVI LYC QQYLAAPLVMKL
QPDGKLM PMV IQLHLPKIGSSPPPLFLPTDPPMVWLLAKCWV RSSDFQVHELN SHL RGHL MAEVFTVATMR CLPSIHPVFKLIVPHL RY TLEIN VR
ARNGLVSDFG IFDQIMSTGGGGHVQLQQAGAFLTYRSFCPPD DLADRG LLGV ESSFYAQ DAL RLWEIISRYVQGIM GLY YTDEA VRD DLELQ SWC
REITEIGLQGAQKQGFP TSLSQVAQACHF VTM CIFTCTGQHSSII LGQL DWFTW VPNA PC TMRL PPPT KDAT LETV M ATLP NLKQSSLQMSIVW
QLGRDQPIMVPLGQHQEEYFSGPEPRAVLEKFREE LAIMDKEIEVRNEKLDIPYELRPSIVEN SVAI
>d1c1ka_a.120.1.1 (A:) gene 59 helicase assembly protein {Bacteriophage T4}

MIKLRMPAGGERYIDGKSVYKLYLMIKQHMNGKYDVIKYNWCMRVSDAAYQKRRDKYFFQKLSEK YKL KELALI FISNLVANQDAWIGDISDADALV
FYREYIGRLQKJFKFEE DIRNI YYFSKKVEVSAFKEI FEYNP KVQSSYIFKLLQ SNIIS FETFILL DSFL NIIDK HDE QTDN LVWNN YSIKL KAYR KILNIDSQK
AKN VFIETV KSCKY
>d2tct_2 a.121.1.1 (68-208) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}

LPAAGESWQSFLRN NAMS FRR ALL RYRD GAKVHL GTRP DEKQYDTV ETQL RFM TENG FSL RD GLY AISA VSHFTL GA VLEQ QEH TA ALT DRP AAPDE
NL PPLL RREAL QIMD SDD GEQ A F LH GLE SLIRG FEV QLT ALL QIV

>d1jt6a2 a.121.1.1 (A:73-187) Multidrug binding protein QacR {Staphylococcus aureus}
KTNREKFYLYNELSLTTEYYPLQNAlIEFYTEYYKTNsINEKMNKLENKYIDAYHVFKEGNLNGEWSINDVNAVKIAANAVNGIVTFTHEQNIERIK
LMNKFSQFLNGLS

>d1fqva1 a.122.1.1 (A:107-145) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}
VSWDSLPELLLGIFSCCLCPELLKVSGVCKRWYRLASD

>d1fqb1 a.122.1.1 (B:85-160) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}
IPVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPPEIRKTFNIKNDFTEEEEAQVRKENQWC

>d1fs1a1 a.122.1.1 (A:109-149) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}
WDSLPDELLLGIFSCCLCPELLKVSGVCKRWYRLASDES LW

>d1fs1b1 a.122.1.1 (B:86-140) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}
PVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPPEIRKTFN

>d1fs2b1 a.122.1.1 (B:80-146) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}
KRTDDIPVWDQEFLKVDQGTLFELILAANYLDIKGLLDVTCKTVANMIKGKTPPEIRKTFNKNDF

>d1g5ya_a.123.1.1 (A:) Retinoid-X receptor (RXR-alpha) {Human (Homo sapiens)}
PVERILEAELAVEPKTETYVEANMGLNPSSPNDPVTCQAADKQLFTLVEWAKRIPHFSPLDDQVILLRAGWNELLIASFSHRSIAVKDGILLATGL
HVHRNSAHSAGVGAIFDRVLTLSKMRDMQMMDKTELGLRAIVLFNPDSKGLSNAEVEALREKVVASLEAYCKHYPEQPGRAKLLRLPALRSI
GLKCLEHLFFFKLIGDTPIDTFLMEMLEAP

>d1dkfb_a.123.1.1 (B:) Retinoic acid receptor alpha (RAR-alpha) {Human (Homo sapiens)}
PEVGELIEKVRKAHQETFPALCQLGKYTTNNSSQRVSLIDLWDKFSELSTKCIIKTVEFAKQLPGFTTLIADQITLLKAACLDILRLICTRYTPEQDTM
TFSDDGLTNRTQMHNAGFGPLTDLVAFANQLLPLEMDDAETGLSAICLICGDRQDLEQPDRVDMQLQEPLLEALKVYVRKRRPSRPHMFPMKMLMK
ITDLRSISAKGAERVITLKMEIPGSMPPLIQEMLEN

>d1fcya_a.123.1.1 (A:) Retinoic acid receptor gamma (RAR-gamma) {Human (Homo sapiens)}
ASPQLEELITKVSKAHQETFPALCQLGKYTTNNSSQRVSLIDLWDKFSELSTKCIIKTVEFAKRLPGFTGLSIADQITLLKAACLDILRLICTRYTPEQ
DTMTFSDDGLTNRTQMHNAGFGPLTDLVAFAGQQLPLEMDDTETGLSAICLICGDRMDLEEPEVKDKLQEPLLEALRLYARRRPSQPYMFPRML
MKITDLRGISTKGAERAITLKMEIPGPMPPLEM

>d1a28a_a.123.1.1 (A:) Progesterone receptor {Human (Homo sapiens)}
QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSLLTSNQLGERQLLSVWKWSKSLPGFRNLHIDDQITLQYSWMSLMVFLGWRSYKHVGQMLYFA
PDLILNEQRMKESSFYSLCLTMWQIPQEFVKLQVSQEEFLCMKVLLNNTIPLEGLRSQTFEEMRSSYIRELIKAIQLRKQGVSSSQRFYQLTKLDDNL
HDLVKQLHLYCLNTFIQSRLSVEFPEMMSEVIAAQLPKILAGMV/KPLLFHK

>d3erda_a.123.1.1 (A:) Estrogen receptor alpha {Human (Homo sapiens)}
SLALSLTADQMVSALLDAEPPILYSEYDPTRPFSEASMMGLTNADRELVHMINWAKRVPGFVDLTLHDQVHLLECAWLEILMIGLVWRSMEHPG
KLLFAPNLLDRRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEFFVCLKSIIILNSGVYTFLSSTLKSLEEKDHIIHRVLKDITDTLHLMAGLTLQQQ
HQRLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEMLDAHRLH

>d1qkma_a.123.1.1 (A:) Estrogen receptor beta {Human (Homo sapiens)}
LDALSPEQLVLTLEAEPPHVLISRPSAPFTEASMMMSLTKLADKELVHMISWAKKIPGFVELFDQVRLL ESCWMEVLMGMLWRSIDHPGKLIF
APDLVLDRLDEGKCVEGILEIFDMLLATTSSRFRELKLQHKEYLCVKAMILLNNSMYPLVTADSSRKLAHLLNAVTDALVWVIAKSGISSQQSMSRL
ANLLMLLSHVRHASNKGMEHLLNMKCKNVVVPYDLLLEMLNAHVL

>d1qkna_a.123.1.1 (A:) Estrogen receptor beta {Rat (Rattus norvegicus)}
TLSPEQLVLTLEAEPPNVLSRPSMPTEASMMMSLTKLADKELVHMIGWAKKIPGFVELSLLDQVRLL ESCWMEVLMVGLWRSIDHPGKLIFA
PDLVLDRLDEGKCVEGILEIFDMLLATTSSRFRELKLQHKEYLCVKAMILLNNSMYPLASANQEASSRKLTHLLNAVTDALVWVIAKSGISSQQSVRLA
NLLMLLSHVRHISNKGMEHLLSMKCKNVVVPYDLLLEMLNA

>d1i37a_a.123.1.1 (A:) Androgen receptor {Rat (Rattus norvegicus)}
IFLNVLEIAIEPGVVCA GHDDNNQPSFA ALLSSLNELGERQLVHVV KWAKALPGFRNLHVDDQMAVIQYSWMGLMV FAMG WRSFTNVNSRMLYF
APDLVFNEYRMHKS RMYSQCVRMRLSQEFGWLQITPQEFLCMKALLFSIIPV DGLKNQKFFDEL RMNYIKELDRIIACKRKNP TCSRRFYQLTKL

LDSVQPIARELHQFTFDLLIKSHMVSVDPEMMMAEIISVQVPKILSGKVKPIYFH

>d1k7la_a.123.1.1 (A:) Peroxisome proliferator activated receptor alpha, PPAR-alpha {Human (Homo sapiens)}

DLKS LAKRIYE AYLKNFNMNKVKARVILSGKASNNPPFVIHD M ETLCMAE KTLVAKLVANGIQNKEAE VRIF HCC QCTS VET VTEL FAKA IPGFANL
DLNDQVTLLKGVYEAIFAMLSVMNKDGMLVAYGNNGFITREFLKSLRKPFCDIMEPKDFAMKFNALELDDSDISLFVAAIICGDRPGLLNVGHIEK
MQEGIVHVRLHLQSNHPDDIFLPKLLQKMA DL RQLVTEHAQLVQIIKKTESDAALHPLLQEYRDMY

>d2prga_a.123.1.1 (A:) Peroxisome proliferator activated receptor gamma, PPAR-gamma {Human (Homo sapiens)}

ESADLR ALAKHLYDSYIKSPLTKAKARAILTGTTDKSPFIYDMNSLMMGEDKIKFKHITPLQEQSKEAIRIFQGCQFRSVEAVQEITEYAKSIPGFV
NL DLNDQVTLLKGVYHEIYTMLASLMNKDGVLISEGQGFMTREFLKSLRKPF GDFMEPKFEFAVKFN ALELDDSDLAIFI AVIILSGDRPGLLNVKPIE
DIQDNLLQALELQLKLHNHPESSQLFAKLLQKMTDLRQIVTEHVQLQVIKKTETDMSLHPLLQEYKDLY

>d2gwxa_a.123.1.1 (A:) Peroxisome proliferator-activated receptor delta, PPAR-DELTA {Human (Homo sapiens)}

LKA FS KHI YNAYLKNFNMK KARS ILT GKA SHAP FV IHD IELW QAE KGLVW KQLVNGLPPYKEISVHFYRCQCTT VET VREL TEFAK SIPS FSSLFL
NDQVTLLKGVYHEA IFAM LASIVNK DGLL VANG SGF VTR EFLR SLRK PFS DIIEPK FEFAV KFN ALELDDSDLA LFIAA II CGDRPG LMN VPR VEA IQDT
ILRA LEFH LQAN HPDA QQ LPK LLQKMA DL RQLVTE HAQM MQR IKKTET TSLH PLLQEY KDM

>d1ilga_a.123.1.1 (A:) Pregnane x receptor, PXR {Human (Homo sapiens)}

GLTE EQRM IMIRELMDAQMKTFDTTFSHKNFRLPGVLSGGCELPESLQAPSREEAAKWSQVRKDLSLKVSLQLRGEDGSVWN YKPPADSGGKEIF
SLLPHMADMSTYMFKG IISFAK V ISYFRDLP IEDQISLLKGAA FELCQLRFNTV FNAETGTWECGR LS CLED TAGG FQQLL EPMLKFHYMLKKLQLH
EEYVLMQAI SLFSPD RPGV LQH RVV DQLQEQ FAITLKSYIE CNRPQPAH RFLKIMAMLTELRSINAQHTQRLLRIQDIHPFATPLM QELFGI

>d1ie9a_a.123.1.1 (A:) Vitamin D nuclear receptor {Human (Homo sapiens)}

D SLP KI LSE QQ RII AIL DAHH KT YD PT YSDFCQFRPPVRVNDGGGSVTLELSQLSMLPHI ADLV SYI QKVIGFAK MIPGFRDLTSEDQIVLLKSSAIE
VIML RSNESFTMDDMSWTCGNQDYK YRVSDVT KAGHS LEI EPLIKFQV GLKLN LHEEEHVLL MAICIVSPDRPGVQDA ALIEAIQDRLSNTLQTYI
RCR HPPP GS HLLYAKM IQKLADL RSLN EHS KQYR CLSF QPEC SMKLT PLV LEVFG

>d1bsxa_a.123.1.1 (A:) Thyroid hormone receptor beta (TR-beta) {Human (Homo sapiens)}

KPEPTDEEWELIKTVTEAH VATNAQGSHWKQKRKF LPEDIGQAPIVNAPEGGKV DLEAFSHFTK ITPA ITRVV DFAKKLPMFC ELP CEDQI ILLKGCC
MEIMSLRAAVRYDPESETLTNGEMAVTRGQLKNGGLGVSVDAIFDLGMSLSSFNLDDEV ALLQAVLL MSSDRPG LACVERIE KYQDSFLLA FEHYI
NYRKHHVTHFWPKLLMKVT DLRMIGACHASRFLHMKVECPTELFPPFLFLEV FED

>d1hg4a_a.123.1.1 (A:) Ultraspiracle protein, usp {Drosophila melanogaster}

FSIERIIAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVSALCQVVNKQLFQMVEYARMMPHFAQVPLDDQVILLKA AWIELIANVA WCSIVSLD
DGGAGGGGGGLGDGSFERRSPGLQPQQFLNQSFSYHRNSAIKAGVSAIFDRILSELSVKM KRLN DRRELSCLKAI ILYNPDIRGIKSRAEIMCRE
K VYACLDEHC RLEHPGDDGRFAQ LLLR PA LRSIS LKCQDHFL FRITS DRP LEELF LEQLE APPPPG

>d1g2na_a.123.1.1 (A:) Ultraspiracle protein, usp {Heliothis virescens}

AAVQELSIERLLEMESLVADPSEEFQFLRVGPDSNVPPKFRAPVSSL CQIGNKQIAALVVWARDIPHFSQLEMEDQI LLIKGSW NELLFAIAWRSMEF
LTEERDGV DGTGNRTTSPQQLMCLMPGM TLH RNSALQAGVGQIFDRVLSELSLKMRTL RDQAEYVALKAI ILLNP DVKG LKNRQEVEV LRE KMFL
CL DEYCRRSRSSEEGRFA ALLRLPA LRSIS LKSFEH LFFFHLVADTSIAGYIRDALRNHA

>d1ah7_a.124.1.1 (-) Bacterial phospholipase C {Bacillus cereus}

WSAEDKHKEGVNSHLWIVNRAIDIMSRTT LVKQDRVAQLNEW RTELENGIYAADYENPYDN STFASHFYDPDNGKTYIPFAKQAKETGA KYFKL
AGESYK NKDMKQAFFYLG LSLH YLG DVNQ PMHA ANFT NL SYPQGFHSKYEN FVDTI KDN YKV TDG NGYWNWKG TNPEE WIHG AAVVAKQDYS
GIVNDNTKDWFVKA AVSQEYADK WRAEV TPM TGK RLMDA QRV TAGYIQLW FD TYGDR

>d1ca1_1_a.124.1.1 (1-249) Alpha-toxin, N-terminal domain {Clostridium perfringens}

WDG KID GTG THAM IVT QGV SILE NLS KNEPE SVR KN LIE LKEN MHE LQLG STY PDY DK NAY DLY QDH FWDP DT DNN FSK DNS WYLA YSIP DT GES
QIRK FSA LARYE WQ RG NYK QAT FYLGE AMH YFG D IDT PYH PAN VT AVD SAG HV KFET FA ER KEQ YK INT VG CKT NED F YADIL K NKDF NAW SKEYA
RGFAK T GKS IYY SHAS MSH SW DDW DYAA KV TL ANS QKG TAGYIYR FLHD VSEG ND P

>d1ak0_a.124.1.2 (-) P1 nuclease {Penicillium citrinum}

WG ALGH AT VAYVAQH YV SPEA ASWA QG ILG SSSSY LASIAS WADE YRL TSAG KWSA SLH FIDA EDN PPT NC NV DYER DC GSS GCS ISAI ANY T QRV
SDS SSEN HAE ALRFLV H FIG DM T QPL HDE AYAVGGN KIN VTF DGYH DNL HS DW DT Y MPQ KLIG GH AL SD AE SWAK TLV QNIE SG NY TAQA IG WI

KGDNISEPITTATRWASDANALVCTVMPHAAALQTGDLYPTYYDSVIDTIELQIAKGGYRLANWINEIH

>d1f0ja_a.125.1.1 (A:) Catalytic domain of cyclic nucleotide phosphodiesterase 4b2b {Human (Homo sapiens)}

SISRGVNTENEDHLAKELEDLNKGGLNIFNAGYSHNRPLTCIMYAIQERDLLKTFRISSDTITYMMTLEDHYHSVDAYHNSLHAADVQSTHVL
LSTPALDAVFTDLEILAAIFAAIHDVDHPGSNQFLINTNSEALMYNDESVLENHHLAGFKLLQEEHCDIFMNLTKQRQLRKMVIDMVLATD
MSKHMSLLADLKTMVETKKVTSVQVLLDNYTDRIQVLRNMVHCADLSNPKSLEYRQWTDRIMEEFFQQGDKERERGMIEISPMCDKHTASVEK
SQVGFIDYIVHPLWETWADLVQPDAQDILDTLEDNRNWYQSMIPQAPAPPLDEQNRCQGLMEKFQF

>d1gnia1 a.126.1.1 (A:3-196) Serum albumin {Human (Homo sapiens)}

HKSEVAHRFKDLGEENFKALVIAFAQYLQQCPFEDHVKLNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNE
CFLQHKDDNPNPLPRLVRPEVDVMCTAFHDNEETFLKKLYEIARRHPFYAPELFFAKRYKAFTECQAADKAACLLPKDELRDEGKASSAKQ

>d1gnia2 a.126.1.1 (A:197-388) Serum albumin {Human (Homo sapiens)}

RLKASLQKFGERAFAVARLSQRFPKAFAEVSKLVTDLTKVHTECCHGDLLEADDRADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVEND
EMPADLPSLAADFVESKDVCKNYAEAKDVFLGMFLYEYARRHPDYSVVLRLAKTYETTLKCCAADPHECYAKVFDEFKPLVEEPQNLI

>d1gnia3 a.126.1.1 (A:389-584) Serum albumin {Human (Homo sapiens)}

KQNCELFEQLGEYKFQNALLVRYTKKPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMPACAEDYLSVVLNQLCVLHEKTPVSDRVTKCTESLVNRRP
CFSALEVDETYVPKEFNAETFTFHADITLSEKERQIKKQTALELVELVKHKPKATKEQLKAVMDDFAAFVEKCKADDKETCFAEGKKLVAASQAALG

>d1j78a1 a.126.1.1 (A:13-198) Vitamin D binding protein {Human (Homo sapiens)}

CKEFSHLGKEDFTSLSLVLYSRKFPSTFEEQVSQLVKEVVSITEACCAEGADPDYDRTSALSAKSCESNSPFPVHPGTAE CCTKEGLERKLCMAALKH
QPQEFTPTYVEPTNDEICEAFRKDPKEYANQFMWEYSTNYGQAPLSLLSYTKSLSMVGSCCTSASPTVCFLKERLQLKHLSSLLT

>d1j78a2 a.126.1.1 (A:199-386) Vitamin D binding protein {Human (Homo sapiens)}

LSNRVCSQYAYGEKKSRSLSNLKLAQKVPADLEVLPLAEDITNILSKCCESASEDCMAKELPEHTVKLCDNLSTKNSKFEDCCQEKTAMDVFVCTYF
MPAAQLPELPDVELPTNKDVCDPGNTKVMKDQYTFELSRRTHLPEVFLSKVLEPTLKLGECCDVEDSTTCFNAGPLLKKELSSFIDK

>d1j78a3 a.126.1.1 (A:387-457) Vitamin D binding protein {Human (Homo sapiens)}

GQELCADYSENTFTEYKKKLAERLKAKLPDATPTELAKLVNKRSDFA SNCCSINSPPLYCDSEIDAELKNI

>d1jswa_a.127.1.1 (A:) L-aspartate ammonia lyase {Escherichia coli}

MSNNIRIEEDLLGTREVPADAYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKAAAMANKELQTIPKS VANAIIAACDEVLNNGKCMDQFPVDV
YQGGAGTSVNMTNEVLANIGLELMGHQKGEYQYLNPNPDHVNCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAVEFQDILKMGRQLQ
DAVPMTLGQEFRAFSILLKEEVKNIQRATAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPAEDLIEATSDCGAYVMVHGALKRALVKMS
KICNDLRLSSGPRAGLNEINLPELQAGSSIMPAKVNPPVPEVVNVQCFKVGNDTTVTMAAEAGQLQNVMEPVIGQAMFESVHILTNACYNLLEK
CINGITANKEVCEGYVYNSIGIVTYLNPFIGHHNGDIVGKICAETGKSREVVLERGLTEAELDDIFS

>d1jswc_a.127.1.1 (C:) L-aspartate ammonia lyase {Escherichia coli}

IRIEEDLLGTREVPADAYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKAAAMANKELQTIPKS VANAIIAACDEVLNNGKCMDQFPVDVYQGG
AGTSVNMTNEVLANIGLELMGHQKGEYQYLNPNPDHVNCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAVEFQDILKMGRQLQDAVP
MTLGQEFRAFSILLKEEVKNIQRATAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPAEDLIEATSDCGAYVMVHGALKRALVKMSKICND
LRLSSGPRAGLNEINLPELQAGSSIMPAKVNPPVPEVVNVQCFKVGNDTTVTMAAEAGQLQNVMEPVIGQAMFESVHILTNACYNLLEK
CINGITANKEVCEGYVYNSIGIVTYLNPFIGHHNGDIVGKICAETGKSREVVLERGLTEAELDDIFS

>d1fura_a.127.1.1 (A:) Fumarase {Escherichia coli}

VRSEKDSMGAIDVPADKLWGAQTQRSLEHFRISTEKMPSTSIIHALALT KRAAKVNEDLGLSEEKASAIRQADEVLAGQHDDEFPLAIWQTGSGT
QSNNMNMNEVLANRASELLGGVRGMERKVHPNDDVNKSQSSNDVPTAMHVAALLRKLQIPQLKLTQTLNEKSRAFADIVKIGRTNLQDATPL
TLGQEISGWVAMILEHNLKHI EYSLPHVAELALGGTAVGTGLNTHPEYARRVADELAVITCAPVTAPNKFEALATCDALVQAHGALKGLAASLMKIAN
DVRWLASGPRCGIGEISIPENEPEGSSIMPVKVNPTQCEALTMCCQVMGNDVAINMGGASGNFELNVFRPMVIHNFLQSVRLADGMESFNKHC
AVGIEPNRERINQLNESLMLVTALNTHIGYDKAAEIAKKAHKEGLTLKAAALALGYLSEAFDSWVRPEQM

>d1yfm_a.127.1.1 (-) Fumarase {Baker's yeast (Saccharomyces cerevisiae)}

SFRTE TDAFGEIHVPADK YWGAQTQRSFQNFKIGGARERMPPLPVHAFGVLKSAIVNESLGGLDPKISKAIQQADEVASGKLDHFPLVFQ
SGTQSNNMNAEVISNRAIEILGGKIGSKQVHPNNHCNQS QSSNDTFTVHMIAASLQI QNELIPELTNLKNALEAKSKEFDHIVKIGRTHLQDATPL

GQEFGYVQQVENGIQRVAHSLKTLFLAQGGTAVGTGLNTKPGFDVKIAEQISKETGLKFQTAPNRFEALAAHDAIVECSGALNTLACSLFKIAQDIR
YLGSGPRCGYHEMLPENEPEGSSIMPGKVNPQTQNEALTQCVQVMGNNAITFAGSQGQFELNVFKPMIANLLNSIRLITDAAYSFRVHCVEGIK
ANEPRIHELLTKSLMLVTALNPKIGDYAASKVAKNAHKKGITLKESALEGLVLTKEFDEWVVPHEML

>d1k62a_a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Human (Homo sapiens)}

GAVDPIMEKFNASIAYDRHLWEVDVQGSKAYRSRGLKAGLLTAKAEMDQILHGDKVAEEWAQGTFKLNSNDEDIHTANERRLKEIGATAGKLHTGR
SRNDQVVTDLRLWMRQTCSTLSGLLWEIRTMVDRAEAERDVLFPGYTHLQRAQPIRWSHWILSHAVALTRDSERLLEVRKRINVLPLGSGAIAGNP
LGVDRELLRAELNFNGAITLNSMDATSERDFVAEFLFWRSLCMTHLSRMAEDLILYCTKEFSFVQLSDAYSTGSSLMPKKNPDSELIRSKAGR VFGR
AGLLMTLKGPLSTYNKDLQEDKEAVFEVSDTMSAVLQVATGVISTLQIHQENMGQALSPDMLATDLAYYLVRKGMPFRQAHEASGKAVFMAETKG
VALNQLSLQELQTISPLSGDVICVWDYRHSEVQYGA LGGTARSSDWQIRQVRALLQQAA

>d1auwa_a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas platyrhynchos), delta-crystallin}
TDPIIMEKLNSSIAYDQRLESDIQGS MAYAKALEKAGILTKELEKISGLEKISEEWSKGVFVVKQSDEDINTANERRLKEIGDIAGKLHTGRSNDQV
VTDLKLFMKNLSIISTHLLQLIKTLVERAAIEIDVILPGYTHLQKAQPIRWSQFLSHAVA LTRDSERLGEVKKRINVLPLGSGALAGNPLDIDREMLRSE
LEFASISLN SMDAISERDFVVEFLSFATLLMIHLSKMAEDLIIYSTSEFGFTLSDAFSTGSSLMPKKNPDSELIRSKAGR VFGRLASILMV LKG
NKDLQEDKEAVFDVVDTLAVLQVATGVISTLQISKENMEKALPEMLATDLALYLV RKGVPFRQAHTASGKAVH LAETKGITINKL SLEDLKSI SPQFSS
DVSQVFNFVNSVEQYTALGGTAKSSVTTQIEQLRELMKKQK

>d1dcnb_a.127.1.1 (B:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas platyrhynchos), delta-crystallin}
DPIMAKLNSSIAYDQRLESDIQGS MAYAKALEKAGILTKELEKISGLEKISEEWSKGVFVVKQSDEDINTANERRLKEIGDIAGKLNTGRSNDQV
STHLLQLIKTLVERAAIEIDVILPGYTNLQKAQPIRWSQFLSHAVA LTRDSERLGEVKKRINVLPLGSGALAGNPLDIDREMLRSE
ERDFVVEFLSFATLLMIHLSKMAEDLIIYSTSEFGFTLSDAFSTGSSLMPKKNPDSELIRSKSGRVFGRLASILMV LKG
LQISKENMEKALPEMLATDLALYLV RKGVPFRQAHTASGKAVH LAETKGITINNL SLEDLKSI SPQFSSDVSQVFNFVNSVEQYTALGGTAKSSVTTQ
EQLRELMKKQK

>d1hy0a_a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas platyrhynchos), delta-crystallin}
DPIMQMLSTSISTEQRLESDIQASIAYAKALEKAGILTKELEKISGLEKISEEWSKGVFVVKQSDEDINTANERRLKEIGDIAGKLHTGRSNDQV
LKLFMKNLSIISTHLLQLIKTLVERAAIEIDVILPGYTHLQKAQPIRWSQFLSHAVA LTRDSERLGEVKKRINVLPLGSGALAGNPLDIDREMLRSE
SISLN SMDAISERDFVVEFLSVATLLI HLSKMAEDLIIYSTSEFGFTLSDAFSTGSSLMPKKNPDSELIRSKSGRVFGRLASILMV LKG
EDKEAVFDVVDTLAVLQVATGVISTLQISKENMEKALPEMLATDLALYLV RKGMPFRQAHTASGKAVH LAETKGIAINNL TLEDLKSI SPFSSDVSQ
FNFVNSVEQYTALGGTAKSSVTTQIEQLRELMKKQK

>d1i0aa_a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Turkey (Meleagris gallopavo), delta-crystallin}
GRFVGSDPIMEILSSISTEQRLESDIQAS MAYAKALEKASILTKELEKISGLEKISEESSKGVLVMTQSDEDIQTAIERRLKEIGDIAGKLQTGRSRN
EQVVTDLKLLLKSSISVISTHLLQLIKTLVERAAIEIDVILPGYTHLQKAQPIRWSQFLSHAVA LTRDSERLGEVKKRITVLPLGSGVLAGN PLEIDRELLRS
ELDMTSITLNSIDAISERDFVVELISVATLLMIHLSKLAEDLIIYSTSEFGFTLSDAFSTGSSLMPKKNPDSELIRSKAGR VFGRLA ILMV LKG
DLQEDKEAVFDVVDTLAVLQVATGVISTLQINKENMEKALPELSTDALYLV RKGMPFRQAHTASGKAVH LAETKGITINNL TLEDLKSI SPFSSDVS
QVFVNSVEQYTAVGGTAKSSVTAQIEQLRELLKKQK

>d1c3ca_a.127.1.1 (A:) Adenylosuccinate lyase {Thermotoga maritima}

VERYSLSPMKDLWTEEAKYRRWLEVELAVTRAYEELGMIPKGVTTERIRNNAKIDVELFKKIEEKTNHDVVA FVEGIGSMIGEDSRFFHYGLTSSDVLD
ANSLALVEAGKILLESLK EFCDVWLWEVANRYKHTPTIGRTHGVHAEP TSFGLKVLGWYSEM KRN VQLRERAIEEVSYGKISGAVGN
LSYLGKPEPVSTQVVPDRHAFYLSLAIVAAGIERIAVEIRHLQRT E VLEVEEPFRKGQRGSSAMPHKKNPI CERLTGLSRMMRAYV
HERDISHSSVERYVFPDATQTLYMIVTATNVVRNMKVNEERMKKNIDLT KGLVFSQ RVLLKIEKG LTRKEAYDIVQRNALKTWNSEKH
EVKKLVTKEELEELFDISYLLKHVDHIFERFEK

>d1dofa_a.127.1.1 (A:) Adenylosuccinate lyase {Archaeon Pyrobaculum aerophilum}

HVSPFDWR YGSEEIRRLFTNEAIINAYLEVERALVCAEELGVAERGCCEVKNKASVSADEVYRLERETGH DILS VLLEQKSGCRYVHYGATSN
AWALLIRRALAAVKEKARAVGDQLASMARKYK TLEMVGRTHGQWAEPITLGKFANYYELYIACRQLAEEFIRAKIGGAVGTMASW
RRVAERLGLPHVITTQVAPRESFAVLASALALMAAVFERLAVEIRELSRPEIGEVVEGGGGSSAMPHKANPTASERIVSLARYVR
WHERDLTNSANERVWIPEALLDEILSALRVLKNVYIDEERITENLQKALPYILTEFH MNRMKI EGASRAEAYK
AKEVKALT FEYQKWPVERLIEDA

LSLKC

>d1f1oa_a.127.1.1 (A:) Adenylosuccinate lyase {Bacillus subtilis}

EMSAIWTDENRFQAWLEVILACEAWAELGVIPKEDVKVMRENASFIDINRILEIEKDTRHDVVAFTRAVSESLGEERKWVHYGLTSTDVVDTALSYLL
KQANDILLKDLERFVDIIKEAKEHKYTVMGRTHGVHAEPPTFGLKLA WHEEMKRNLERFKQAKAGIEVGKISGAVGTYANIDPFVEQYVCEKLG
LKAAPISTQLQRDRHADYMATLALIASIEKFAVEIRGLQKSETREVEEFFAKGQKGSSAMPHKRNPIGSENMTGMARVIRGYMMTAYENVPLWE
RDISHSSAERIILPDATIALNYMLNRFNSIVKNLTVPENMKRNMDRTLGLIYSQRVLLAIDTGLTREEAYDTVQPKAMEAWEKQVPFRELVEAEKIT
SRLSPEKIACDFDYN

>d1gk2a_a.127.1.2 (A:) Histidine ammonia-lyase (HAL) {Pseudomonas putida}

TELTLKPGTLAQLRAIHAAAPVRLQLDASAAPAIDASVACVEQIAEDRTAYGINTGFGLASTRIASHDLENLQRSVLSHAAGIGAPLDDLVRLIMVL
KINSLSRGSGIRRKVIDALIALVNAEVPHIPLKGSVGASGDLAPLAHMSLVL GEGKARYKGQWLSATEALAVAGLEPLTLAAKEGLALLNTQASTA
YALRGLFYAEDLYAAAICCGGLSVEAVLGSRSRPFDARIHEARGQRGQIDTAACFRDLLGDSSEVSLSHKNADKVQDPYSLRCQPQVMGACLTLRQA
AEVLGIEANAVSDNPLVFAAEQDVSGGGNGHAEPVAMAADNLALALIAEIGSLSERRISLMMDKHMSQLPPFLVENGGVNSGFMIAQVTAAALASEN
KALSHPHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVLIAEWLGACQGLDLRKGLKTSAKLEKARQALRSEVAHYDRDRFFAPDIEKAVL
LAKGSLTGLLPAGVLPPL

>d1uby_a.128.1.1 (-) Farnesyl diphosphate synthase {Chicken (Gallus gallus)}

SPVVVEREREFGVFFPQIVRDLTEDGIGHPEVGDavarLKVLQYNAPGGKCNRLTVAAAYRELSPGPKDAESLRCALAVGWCIELFQAASLVA
DDIMDQSLTRRGQLCWYKKEGVGLDAINDSFLESSVYRVLKKYCRQRPYVHLLEFLQTAYQTELQGQMLDLITAPVSKVDSLHFSEERYKAIVKYKTA
FYSYLPVAAAMYMGIDSKEEHENAKAILMEGEYFQIQDDYLDCFGDPALTGAvgTDIQDNKCSWLVVQLQRTPEQRQLLEDNYGRKEPEKV
AKVKELYEAVGMRAAFQQYEESYYRRLQELIEKHSNRLPKEIFLGLAQKIKRQK

>d1ezfa_a.128.1.2 (A:) Squalene synthase {Human (Homo sapiens)}

NSLKTCKYLNQTSRSFAAVIQALDGEMRNAVCIFYVLRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRFMESKEKDRQVLEDFTSLEFRNLA
EKYQTIVIADICRGMGMAEFLDKHVTSEQEWDKYCHYVAGLVGIGLSRLFSASEFEDPLVGEDTERANSMGLFLQKTNIIIRDYLEDQQGGREFWP
QEWSRYVKKLGDFAKPENIDLAVQCLNEITNALHHIPDVITYLSRLRNQSVFNFCAPQVMAIATLAACYNNQQVFKGAVKIRKGQAVTLMDAT
NMPAVKAIQYQYMEEIYHRIPDSDPSSKTRQIISTIRTQN

>d5eau_2 a.128.1.3 (221-548) 5-Epi-aristolochene synthase, C-terminal domain {Tobacco (Nicotiana tabacum)}

KNNVLLRFAKLDFNLLQMLHKQELAQVSRRWWKDLFVTTLPYARDRVVECYFWALGVYFEPQYSQARVMVLTISMISIVDDTFDAYGTVKELEYAT
DAIQRWIDINEIDRLPDYMKISYKAILDLYKDYKEKLSSAGRSHIVCHAIERMKEVVRNWNVESTWFIEGYTPPVSEYLSNALATTYYLATTSYLGMKS
ATEQDFEWLSKNPKILEASVIICRVIDDTAYEVEKSRGQIATGIECCMRDYGISTKEAMAKFQNMAETAWKDINEGLRPTVSTEFLTPILNLRARIVEV
TYIHNLDGYTHPEKVLKPHIINLLVDSIKI

>d1di1a_a.128.1.4 (A:) Aristolochene synthase {Fungus (Penicillium roqueforti)}

TPPPTQWSYLCHPRVKEVQDEVGYFLENWKPSFKAVRTFLDAKFSEVTCLYFPLALDDRIHFACRLTVLFLIDDVLEHMSFADGEAYNNRLIPISRG
DVLPDFRTKPEEFILYDLWESMRAHDAELANEVLEPTFVFMRAQTDRARLISIHELGHYLEREKDVKGKALLSALMRFMSGLRLSADELQDMKALEAN
CAKQLSVVNDIYSYDKEEASRTGHKEGAFLCSAVKVLAESKLGIPATKRLWMSMTREWETVHDEIVAEKIASPDGCSEAAKAYMKGLEYQMSGNE
QWSKTT

>d1ps1a_a.128.1.4 (A:) Pentalenene synthase {Streptomyces sp., UC5319}

QDVDFHPLPGRQSPDHARAEEQLAWPRSLGLIRSDAAERHLRGGYADLASRFYPHATGADLDLGVDLMSWFFLFDDLFGPRGENPEDTKQLT
DQVAAALDGPLDTAPPIAHGFADIWRRTCEGMPAWCARSARHWRNYFDGYVDEAESRFWNAPCDSAAQYLAMRRHTIGVQPTVDLAERAGR
FEVPHRFDSAIVSAMLIQIAVDVNLLNDIASLEKEEARGEQNNMVILRREHGWSRSVSHMQNEVRARLEQYLLLESCLPKVGEIYQLDTAER
EALERYRTDAVRTVIRGSYDWHRSSG

>d1jfaa_a.128.1.5 (A:) Trichodiene synthase {Fusarium sporotrichioides}

MENFPTEYFLNTTVRLLEYIRYRDSNYTREERIENLHYAYNKAHHFAQPRQQQLKVDPKRLQASLQTIVGMVVYSAKVSKECMADLSIHHTYTLV
LDDSKDDPYPTMVNFDDLQAGREQAHPWWALVNEHFPNVLRHGPFCSLNLRSTLDFFEGCWEQYNFGGFPGSHDYPFLRRMNGLGHCV
GASLWPKEQFNRSLFLEITSIAQAMENWMVVNDLMSFYKEFDDERDQISLKVKNYVSDEISLHEALEKLTQDTLHSSKQMVAVFSKDPQVM
TIECFMHGYVTWHLCDRRYRLSEIYEKVKEEKTEDAQKFCFYEQANVGAVSPSEWAYPPVAQLANV

>d1oela1 a.129.1.1 (A:2-136,A:410-525) GroEL {Escherichia coli}
AAKDVKGNDAGVKMLRGVNVLADAVKVTLGPGRNVVLDKSGAPITKDGVSAREIELEDKFENMGAQMVKEVASKANDAAGDGTATVL
AQAIITEGLKAVAAGMNPMDLKRGIDKAVTVAEELKALSVXGVVAGGGVALRIVASKLADLRQNEDQNVGIKVALRAMEAPLRQIVLNCGEPS
VVANTVKGGDNYGYNAATEEYGNMIDMGILDPTKVTRSLQYAASVAGLMITTECMVTDL
>d1ioka1 a.129.1.1 (A:2-136,A:410-526) GroEL {Paracoccus denitrificans}
AAKEVKFNSDARDMLKGVNILADAVKVTLGPGRNVVIDKSGAPITKDGVSAKEIELSDKFENMGAQMVRVASRTNDEAGDGTATVLAQ
AIVREGLKAVAAGMNPMDLKRGIDVATAKVEAIKSAARXGIVVGGVALVQGAKVLEGLSGANSDDQDAGIAIRRALEAPMRQIAENAGVDGAVV
AGKVRESSDKAFGFNAQTEEYGDMFKFGVIDPAKVVTALEDAASVAGLLTEAMIAEK
>d1a6da1 a.129.1.2 (A:17-145,A:404-519) Thermosome {Archaeon Thermoplasma acidophilum}
REQGKNAQRNNIEAAKAIADAVRTTLGPKGMDKMLVDSIGDIIISNDGATILKEMDVEHPTAKMIVEVSKAQDTAVGDGTTAVVLSGELLKQAETLL
DQGVHPTVISNGYRLAVNEARKIIDEIAKSXFLWGGGAVEELAMRLAKYANSVGGREQLAIEAFAKALEIIPRTLAENAGIDPINTLKLKADDEKGR
SVGVDLNNVGDMKAKGVVDPRLVKTHALESAVEATMILRIDDVI
>d1a6db1 a.129.1.2 (B:20-144,B:404-521) Thermosome {Archaeon Thermoplasma acidophilum}
KDAMKENIEAAIAISNSVRSSLGPRGMDKMLVDSLGDIVTNDGVTILKEMDVEHPAAKMMVEVSKTQDSFVGDGTTAVIAGGLLQQAQGLINQ
NVHPTVISEGYRMASEEAKRVIDEISTKIXAYAAGGGATAAEIAFLRSYAQKIGGRQQLAIEKFADAEIIPRALAENAGLDPIDILLKLRAEHAKGNKTY
GINVFTGEIEDMVKNVGVIEPIRVGKQAIESTAAIMILRIDDVIA
>d1ecma_a.130.1.1 (A:) Chorismate mutase domain of P-protein {Escherichia coli}
NPPLALREKISALDEKLLALLAERRELAVEVGKAKLLSHRPVRDIRERDLLERLITLGKAHHLDHYITRLFQLIIEDSVLTQQALLQQH
>d5csma_a.130.1.2 (A:) Allosteric chorismate mutase {Baker's yeast (Saccharomyces cerevisiae)}
MDFTKPETVLNLQNIRDELVRMEDSIIFKFIERSHFATCPVSEANHPGLEIPNFKGSFLDWALSNEIAHSRIRRFESEPDETPFFPDKIQKSFLPSINYPOQI
LAPYAPEVNYNDKIKKVIYEKIPLISKRDGDDKNNFGSVATRDIECLQSLRRIHFGKFVAEAKFQSDIPLYTKLIKSKDVEGIMKNITNSAVEEKILERLTK
KAEVYGVDPTERRIERRISPEYLVKIYKEIVIPITKEVEVEYLLRLEE
>d1pprm1 a.131.1.1 (M:1-156) Peridinin-chlorophyll protein {Dinoflagellate (Amphidinium carterae)}
DEIGDAAKKLGASYAFAKEVDWNNGIFLQAPGKLOPLEALKAIKDMIVMGAADPKLLKAAAEEAHHKAIIGSISGPNVTSRADWDNVNAALGRV
IASVPENMVMVDVDSVKITDPKVPAYMKSLVNGADAEEKAYEGFLAKDVKVKSQVTSAAG
>d1pprm2 a.131.1.1 (M:157-312) Peridinin-chlorophyll protein {Dinoflagellate (Amphidinium carterae)}
PATVPSGDIGVAAQQLSEASYPFLKEIDWLSDVYMKPLPGVSAQQLKAIDKMIVMGAQADGNALKAAAEEAHHKAIIGSIDATGVTSAADYAAVNA
ALGRVIASVPKSTVMDVYNAMEGVTDTISPLNMFSKVNPOLDANAAAKAFYTFKDVKVQAAQ
>d1qq8a_a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Human (Homo sapiens)}
PQDLSEALKEATKEVHTQAENAEFMRFNQKGQVTRDGFKLVMASLYHIYVALEEEIERNKQNPVYAPLYFPEELHRRAALEQDLAFWYGPRWQEVIP
YTPAMQRVYKRLHEVGRTEPELLVAHAYTRYLGLDSGGQVLKKIAQKALDLPSSGEGLAFTFPNIASATFKQLYRSRMNSLEMTPAVRQRVIEEAKT
AFLLNQLFEELQELLTH
>d1dvga_a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Rat (Rattus norvegicus)}
SQDLSEALKEATKEVHIRAENSEFMRFNQKGQVSRGFKLVVASLYHIYVALEEEIERNKQNPVYAPLYFPEELHRRAALEQDLAFWYGPRWQEAPIY
PATQHYVKRLHEVGGTHPELLVAHAYTRYLGLDSGGQVLKKIAQKALPSSGEGLASFTFPSIDNPTFKQLYRARMNTLELTPEVKHRVTEEAKTAFL
LNIELFEELQALLTE
>d1j77a_a.132.1.2 (A:) Gram-negative bacterial heme oxygenase {Neisseria meningitidis}
ALTFAKRLKADTTAVHDSVDNLVMSVQPFVSKENYIKFLQLQSVFHKAVDHYIKDAELNKAYPELEYMARYDAVTQDLKDLGEEPYKFDKELPYEAGN
KAIGWLYCAEGSNLGAALFKHAQKLDYNGEHGARHLAPHPDGRGKHWRADFVEHNLNALNLTPEAAEAIQGAREAFAFYKVVLRETFGLAADAE
PEGMMPH
>d1knca_a.152.1.1 (A:) Antioxidant defence protein AhpD {Mycobacterium tuberculosis}
SIEKLKAALPEYAKDIKLNSSITRSSVLDQEQLWGTLLASAAATRNPQVLADIGAEATDHSAAARHALGAAAIMGMNNVFYRGRGFLEGARYDDL
PGLRMNIIANPGIPKANFELWSFAVSAINGCSHCLVAHEHTLRTVGVDREAIFEALKAAIVSGVAQALATIEALS
>d1poa_a.133.1.2 (-) Snake phospholipase A2 {Taiwan cobra (Naja naja atra)}

NLYQFKNMIQCTVPSRSWWDFADYGCYCGRGSGTPVDDLDRCQVHDNCYNEAEKISGCPYFKTYSYECSGTLCKGGNNACAAAVCDCDR
LAAICFAGAPYNDNDYNINLKARC

>d1pp2l_a.133.1.2 (L:) Snake phospholipase A2 {Western diamondback rattlesnake (*Crotalus atrox*)}

SLVQFETLIMKIAGRSGLLWYSAYGCYCGWGGHGLPQDATDRCCFVHDCCYKGATDCNPKTVSYTSEENGIEICGGDDPCGTQICECDKAAAICFR
DNIPSYDNKYWLFPKDCREEPEC

>d1bjja_a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (*Agkistrodon halys pallas*), different isoforms}

NLLQFNKMIKEETGKNAIPFYAFYGCYCGWGGQGPKDGTDRCCFVHDCCYGRNLNCNTSDIYSYSLKEGYITCGKGTNCEEQICECDRVAACFR
NLDTYNNGYMFYRDSKCTETSEEC

>d1jiaa_a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (*Agkistrodon halys pallas*), different isoforms}

HLLQFRKMIKKMTGKEPVSYAFYGCYCGSGGRGKPKDATDRCCFVHDCCYEVTGCDPKWDDYTYSWKNGTIVCGGDDPKKECECDKAAAIC
FRDNLKTYKKRYMAYPDILCSSKSEKC

>d1psj_a.133.1.2 (-) Snake phospholipase A2 {Chinese water moccasin (*Agkistrodon halys pallas*), different isoforms}

SLIQFETLIMKVAKKSGMFWYSNYGCYCGWGGQGRPQDATDRCCFVHDCCYKGVTGCDPKMDVYSFSEENGDIVCGGDDPKKECECDRAAAIC
FRDNLTLYNDKKYWAFGAKNCPQESEPC

>d1ppa_a.133.1.2 (-) Snake phospholipase A2 {Eastern cottonmouth snake (*Agkistrodon piscivorus*)}

SVLELGKMLQETGKNAITSYGSYGCNCNGWGHGRGQPKDATDRCCFVHKCCYKKLDCNHKTDRYSWKNKAIICEEKNPCLKEMCECDKAVAICLR
ENLDTYNKKYKAYFKLCKKPDT

>d1vapa_a.133.1.2 (A:) Snake phospholipase A2 {Eastern cottonmouth snake (*Agkistrodon piscivorus*)}

NLFQFEKLICKMTGKSGMLWYSAYGCYCGWGGQGRPKDATDRCCFVHDCCYKGVTGCDPKMDSYTSEENGDIVCGGDDPKREICECDRAAAI
CFRDNLKTYDSKTYWKYPKKNCKEESEPC

>d1jla_a.133.1.2 (A:) Snake phospholipase A2 {Viper (*Deinagkistrodon acutus*)}

SLIQFETLIMVKVKSGMFWYSAYGCYCGWGGKGTPKDATDRCCFVHDCCYKGVTGCDPKMDSYTSEENGDIVCGGDDPKREICECDRVAAD
CFRDNLDTNSDTYWRYPRQDCEESPEC

>d1fe7a_a.133.1.2 (A:) Snake phospholipase A2 {Snake (*Daboia russelli pulchella*)}

SLLEFGKMLEETGKLAIPSYYGCYCGWGGKGTPKDATDRCCFVHDCCYGNLPDCNPKSDRYKYKRVNGAIVCEKGTSRENCECDKAAAICFRQ
NLNTYSKKYMLYPDFLCKGELKC

>d1ae7_a.133.1.2 (-) Snake phospholipase A2 {Mainland tiger snake (*Notechis scutatus scutatus*), notexin}

NLVQFSYLIQCANHGKRPTWHYMDYGCYCGAGGSFTPDELDRCCKIHDDCYDEAGKGCFPKMSAYDYYCENGPyCRNIKKCLRFVCDCDVE
AAFCFAKAPYNNANWNIDTKKRCQ

>d2nota_a.133.1.2 (A:) Snake phospholipase A2 {Mainland tiger snake (*Notechis scutatus scutatus*), notechis II-5}

NLVQFSYLIQCANHGRRPTRHYMDYGCYCGWGGSGTPVDELDRCCKIHDDCYSDAEKGCFPKMSAYDYYCENGPyCRNIKKCLRFVCDCDVE
AAFCFAKAPYNNANWNIDTKKRCQ

>d1qlla_a.133.1.2 (A:) Snake phospholipase A2 {Bothrops pirajai, Piratoxin-II (PRTX-II)}

SLFELGKMLQETGKNPAKSYGAYGCNCVGLRGKPKDATDRCCYVHKCCYKKLTGCPKSDRYSWKDFTIVCGENNPLKELCECDKAVAICLR
NLGTYNKKYRHLKPFCKKADKC

>d1vip_a.133.1.2 (-) Snake phospholipase A2 {Russell's viper (*Vipera russelli*)}

NLFQFAEMIVKMTGKNPLSSYSDYGCYCGWGGKGPKQDATDRCCFVHDCCYEVKSCKPKLSLYSFQNGGIVCGDNHSCKRAVCECDRVAATCF
RDNLNTYDKKYHNYPPSQCTGTEQC

>d1jta_a.133.1.2 (A:) Snake phospholipase A2 {Sand viper (*Vipera ammodytes meridionalis*), vipoxin}

NLFQFGDMILQKTGKEAVHSYAIYGCYCGWGGQARAQDATDRCCFAQDCCYGRVNDCNPKTATYTFENGDIVCGDNDLCLRVCEDRAAAICL
GENVNNTYDKNYEYYSISHCTEESEQC

>d1jltb_a.133.1.2 (B:) Snake phospholipase A2 {Sand viper (*Vipera ammodytes meridionalis*), vipoxin}

NLFQFAKMINGKLGAFSVWNYISYGCYCGWGGQGTPKDATDRCCFVHDCCYGRVRGCNPKLAIYSFKKGNIVCGKNNGLRDICECDRVAANC
HQNKNTYKFLSSSRCQTSEQC

>d1dpya_a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (Bungarus caeruleus), different isoforms}

NLIQFKNMICAGTRIWTAYVAYGCYCGKGGSGTPVDELDRCYCITHDHCYNEAEKIPGCNPNIKTYSYCTQPNLTCTDSADTC AFLCECDRTAAC

FASAPYNSNNIMLSSSTSCQ

>d1fe5a_a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (Bungarus caeruleus), different isoforms}

NLIQFKNMICAGTRPWTAYVNYGCYCGKGGSGTPVDELDRCYCITHDNCYNEAEKIPGCNPNIKTYSYCTEPNLCTDTADTCARFLCNCDRTAAC

CFASAPYNSNNVMISSSTNCQ

>d1kvoa_a.133.1.2 (A:) Phospholipase A2 {Human (Homo sapiens), synovial fluid}

NLVNFHRMICKLTTGKEAALSYGFYGCCHCGVGGRGSPKDADRCCVTHDCCYKRLEKRGCGTKFLSYKFSNGSRITCAKQDSCRSQLCECDKAAATCF

ARNKTTYNKKYQYYSNKHCRCGSTPRC

>d1g4ia_a.133.1.2 (A:) Phospholipase A2 {Cow (Bos taurus), pancreas}

ALWQFNGMIKCKIPSSEPLLDFNNYGCYCGLGGSGTPVDDLDRCQCQHDNCYKQAKKLDSCKVLDNPYTNNSYCSNNEITCSSENNACEAFICN

CDRRAAIIFSKVPYNKEHKNLDDKKNC

>d1hn4a_a.133.1.2 (A:) Phospholipase A2 {Pig (Sus scrofa), pancreas}

GISSRALWQFRSMIKCAIPGSHPPLMDFNNGCYCGLGGSGTPVDELDRCCEHDNCYRDAKNLDSCKFVDPYTESYSYCSNTEITCNSKNNACE

AFICNCRNAIIFSKAPYNKEHKNLDTKKYC

>d5p2pa_a.133.1.2 (A:) Phospholipase A2 {Pig (Sus scrofa), pancreas}

ALFQFRSMIKCAIPGSHPPLMDFNNGCYCGWGGSGTPVDELDRCCEHDNCYRDAKNLSGCPYTESYSYCSNTEITCNSKNNACEAFICNCDRN

AAICFSKAPYNKEHKNLDTKKYC

>d1buna_a.133.1.2 (A:) beta2-bungarotoxin, phospholipase A2 chain {Many-banded krait (Bungarus multicinctus), elapid}

NLINFMEMIRYTIPEKTVGEYADYGCGAGGSGRPIDALDRCCVHDNCYGDAEKKHKCNPKTQSYKLTKRTIICYGAAGTCARIIVCDCRTAA

LCFGNSEYIEGHKNIDTARFCQ

>d1goda_a.133.1.2 (A:) Myotoxin II {Bothrops godmani}

SMYQLWKMLQETGKNAVPSYGLYGCNCVGSRGPKDATDRCCVHKCCYKKLTDSCPDKTSYSWVDKTIVCGDNNPCLQEMCECDKAVAICL

RENLDTNYKNKYIYPKPLCKKADAC

>d1gmza_a.133.1.2 (A:) Myotoxin II {Snake (Bothrops pirajai), piratoxin III}

DLWQFGKMKLKGKLPFPYVTYGCYCGVGGRGGPKDATDRCCVHDCCYGKLTSCKPTDRYSRKDGTVCGENDPCRKEICECDKAAAVCFR

ENLDTNYKKYMSYLKSLCKXADD

>d1poc_a.133.1.1 (-) Phospholipase A2 {European honeybee (Apis mellifera)}

IIYPGTLWCGHGNKSSGPNELGRFKHTDACCRTHDMDCPDVMSAGESKHGLNTASHTRLSCDCDDKFYDCLKNSADTISYFVGKMYFNLIDTKCYK

LEHPVTGGERTEGRCLHYTVDKSKPKVYQWFDLRKY

>d1faza_a.133.1.3 (A:) Prokaryotic phospholipase A2 {Streptomyces violaceoruber}

APADKPQVLASFTQTASSQNAWLAANRNQSAWAAYEFDWSTDLCQAPDNPGFPNTACARHDFGYRNYKAAGSF DANKSRIDS AFYEDMKR

VCTGYTGEKNTACNSTAWTYYQAVKIG

>d1bxm_a.134.1.1 (-) beta-cryptogein {Phytophthora cryptogea}

RGTCTATQQTAAYHTLVSILSDASFNQCSTDGYSMLTAKALPTTAQYKLMCASTACNTMIKKIVTLNPPNCDLTVPTSGLVLNVSYANGFSNKCSSL

>d1g8qa_a.135.1.1 (A:) CD81 extracellular domain {Human (Homo sapiens)}

FVNKDQIAKDVKQFYDQALQQAVVDDANNAKAVVKTFHETLDCGSSTLTALTSVLKNNLCPGSNIISNLFKEDCHQKIDDLFSGKH

>d1dvoa_a.136.1.1 (A:) Repressor of bacterial conjugation Fino {Escherichia coli}

PPKWVKKKQKLAEKAREAEELAKKAQARQALSIYLNPLTLDEAVNTLKPWWPGLFDGDTPRLLACGIRDVLLEDVAQRNIPLSHKKLRRAMKAITR

SESYLCAMKAGACRYDTEGYVTEHISQEEEVYAAERLDKIRRQNRIKAEQAVLD

>d1jjsa_a.153.1.1 (A:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}

ALQDLLRTLKSPSSPQQQQVNLKSNPQLMAAFIKQRTAKYVAN

>d1kbhb_a.153.1.1 (B:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}

PNRSISPSALQDLLRTLKSPSSPQQQQVNLKSNPQLMAAFIKQRTAKYVANQPGMQ

>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}

GKKSKATKKRKAKLDNQNSRVPAYVMLKTREVQRNHRRHWRRNDTDE

>d1jj21_a.137.1.1 (1:) Ribosomal protein L39e {Archaeon Haloarcula marismortui}

GKKSKATKKRLAKLDNQNSRVPAWVMLKTDEVQRNHRRHWRRNDTDE

>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}

YDGTCKKAAGNCWEPKPGFPEKIAGSKYDPKHDPKELNKQADSIKOMEERNKKRVENFKKTGFYDVAKISA

>d1gg2g_a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

SIAQARKLVEQLKMEANIDRIKVSKAADLMAYCEAHAKEDPLLTPVPASENPF

>d1gotg_a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

LTEKDKLKMEVDQLKKEVTLERMLVSKCCEFRDYVEERSGEDPLVKGIPEDKNPFKEK

>d1tbge_a.137.3.1 (E:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}

APVINIEDLTEKDKLKMEVDQLKKEVTLERMLVSKCCEFRDYVEERSGEDPLVKGIPEDKNPFKEK

>d1hfes_a.137.4.1 (S:) Fe-only hydrogenase smaller subunit {Desulfovibrio desulfuricans}

VVKQJKDYMIDRINGVYGADAKFPVRASQDNTQVKALYKSYLEKPLGHKS HDLLHHTWFDKSKGVKELTTAGKLPNPRASEFEGPYPYE

>d1ef1c_a.137.5.1 (C:) Moesin tail domain {Human (Homo sapiens)}

AEASADLRADAMAKDRSEERTTEAEKNERVQKHLKALTSELANARDESKKTANDMIHAENMRLGRDKYKTLRQIRQGNTKQRIDEFESM

>d2prgc_a.137.6.1 (C:) Nuclear receptor coactivator Src-1 {Human (Homo sapiens)}

QTSHKLVQLTTAEQQLRHADITSCDKDVLSCGTTSNSASANSSGGSCPSSHSSLTERHKILHRLLQEGSPSDIT

>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 F1FO-ATP synthase {Cow (Bos taurus)}

VAYWRQAGLSYIRYSQICAKAVRDALKTEFKANAMKTGSTIKIVKV

>d1jjuc_a.137.9.1 (C:) Quinohemoprotein amine dehydrogenase C chain {Paracoccus denitrificans}

MNALVGCTTSFDPGWEVDAFGAVSNLCQPMEADLYGCADPCWXPAQVADTLNTYPNWSAGADDVMQDWRLQSVFPETK

>d1jmxg_a.137.9.1 (G:) Quinohemoprotein amine dehydrogenase C chain {Pseudomonas putida}

AVAGCTATTDPGWEVDAFGGVSSLCPMEADLYGCSGPCWXPAQVPDMMMSTYQDWNAQASNAEDWRNLGTVFPKDK

>d1aqe_a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

TFEIPESVTMSPKQFEGYTPKKGDVTFNHASHMDIACQQCHHTVPDTYTIESTEGCHDNIKERTEISSVERTFHTTKDSEKSCVGCHRELKRQGPS

DAPLACNSCHVQ

>d1i77a_a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

APAAPDKPLEFKGSQKTVMFPHAVHAKVECUTHHQVDGKESFAKGCGSSGCHDDLAGKQGEKSLYYVHTKELKHTNCIGCHSKVVEGKPELKDD

LTACAKSKCHP

>d2cy3_a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

ADAPGDDYVISAPEGMKAKPKGDKPGALQKTVFPFHTKATVECVQCHHTLEADGGAVKKCTTSGCHDSLEFRDKANAKDIKLVENAFHTQCDC

HKALKDKKPTGPTACGKCHTN

>d3cyr_a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}

APAVPNKPVEVKGSQKTVMFPHAPHEKVECTCHHLVDGKESYAKCGSSGCHDDLTAKKGEKSLYYVVAKGELKHTSCLACHSKVVAEKPELKKDL
TGCAKSCKHP

>d2cdv__ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio vulgaris}

APKAPADGLKMDTKQPVVFNHSTHKAVKCGDCHHPVNGKENYQKCATAGCHDNMDKKDKSAKGYYHAMHDKGTKFKSCVGCHLETAGADAA
KKKELTGCKSKCHS

>d2ctha_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio vulgaris}

APKAPADGLKMEATKQPVVFNHSTHKSVKCGDCHHPVNGKEDYRKCGTAGCHDSMDKKDKSAKGYYHVMHDKNFKSCVGCHVEVAGADAA
KKKDLTGCKSKCHe

>d1wad__ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio gigas}

VDVPADGAKIDFIAGGEKNLTVVFNHSTHKDVKCDDCHDPDKQYAGCTTDGCHNILDKADKSVNSWYKVVHDAKGGAKPTCISCHKDKAGDD
KELKKKLGTGCKGSACHP

>d3caoa_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio africanus}

EDMTHVPTDAFGKLERPAAVFNHDEHNEKAGIESCNACHHVVWVNGVLAEDEDSVGTPCSDCHALEQDGDTPLQLQDAYHQQCWGCHAKEQAKGP
VMCGECHVKN

>d1hh5a_ a.138.1.1 (A:) Cytochrome c7 (cytochrome c551.5) {Desulfuromonas acetoxidans}

ADVVTYENKKGNVTDFDKHAEKLGCDACHEGTPAKIAIDKSAHKDACKTCHKSNNGPTKCGGCHIK

>d19hca_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

AALEPTDSGAPSIVMFVGEKPNPKGAAMKPVVFNHЛИHEKKIADCETCHHTGDPVSCSTCHTVEGKAEGDYITLDRAMHATDIAARAKGNTPTS
CVSCHQSETKERRECAGCHAITTPKDEAWCATCHDITPSMTPSEMOKGIAGTLPGDNEALAAETVLAETVAPVSPMLAPYKVVIDALADKYEPS
DFTHRRHLTSLMESIKDDKLAQAFHDKPEILCATCHHRSPSLTPPKCGSCHTKEIDAADPGRPNLMAAYHLECMGCHKGMAVARPRDTDCTTCHK
AAA

>d1duwa_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 29577}

EPTDSGAPSIVMFVSAKPNPKGAAMKPAVFNHLAHEKKIANCETCHHTGDPVACSTCHTTEGKAEGNFVTLDRAMHATNIAKRAKGNTPVSCV
SCHEQQTKERRECAGCHAIVTPKRDQAWCATCHNVTSMTPEQMQQGIKGKLPPDQEALAAETVLNHPVQPLTAMQGPYKVSIDALADKYEP
SNFTHRRHMASLIMERIKGDKLAEAFHNKPETLCATCHHRSPSATPPKCGSCHTKEIDPANPNRPNLKAAYHLQCMGCHQGMNVGRPKNTDCTTC
HKARP

>d1dxrc_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit) {Rhodopseudomonas viridis}

CFFPPATTQTGFRLSMGEVLHPATVKAKKERDAQYPPALAAVKAEGPPVSQVYKVNVLGNLTEAEFLRTMTAITEWVSPQEGCTYCHDENNL
SEAKYPYVVARRMLEMTRAINTNWTQHVAQTGVTCYTCRGTPPLPPVRYLEPTLPLNNRETPTHVERVERSGYVRLAKYTAYSALNYDPFTMFL
ANDKRQVRVVPQTALPLVGVSRGKERRPLSDAYATFALMMSISDSLGNCTFCHNAQTFESWGKKSTPQRAIAWWGIRMVRDLNMNYLAPLNAS
LPASRLGRQGEAPQADCRTCHQGVTKPLFGASRLKDYPELGPIK

>d1eysc_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit) {Thermochromatium tepidum}

CEGPPPGTEQIGYRGVGMENYYVKRQRALSIQANQPESLPAADSTGPKASEVYQSVQLKDLGVGEFTRTMVAFTTWVSPKEGCNYCHVPGNW
ASDDIYTKVVSRRMFELVRAANSDWKAHVAETGVTCYTCRGNPVPKYAATVTDPPGPKPSGLKPTGQNYGSKTVAYASLPFDPLTPFLDQANEIRIT
GNAALAGSNPASLKQAEWTFGLMMNISDSLGVGCTSCHNTRAFNDWTQSTPKRTTAWYAIRHVRDINQNYIWPLNDVLPSRKGPYGDPLRVSC
MTCHQAVNKPLYGAQMAKDYPGLYK

>d1fgja_ a.138.1.3 (A:) Hydroxylamine oxidoreductase, HAO {Nitrosomonas europaea}

DISTVPDETYDALKDRGKATPKETYEAJVKRYKDPAGKGTMDYWEPIAISIYMDPNTFYKPPVSPKEVAERKDCVECHSDETPVWVRAWKR
STHANLDKIRNLKSDDPLYYKKGLEEVENNLRSMGKLEKETLKEVGCIDCHVDVNKKDKADHTKDIRMPTADTCGTCHLREFARESERDTMVW
PNGQWPAGRPSHALDYTANIETTVWATMPQREVAEGCTMCHTQNQNKCDNCNCHTRHEFSAAESRKPEACATCHSGVDHNNWEAYTMSKHGKLA
MN RDKWNWEVRLKDAFSKGGQNAPTCAACMEYEYEYTHONITRKTRWANYPFVPGIAENITSDWSEARLDSWLTCTQCHSERFARSYLDLMD
KGTLGLAKYQEANAIVKHMYEDGTLGQKTNRPNPPEKEKGFGIFTQLFWSKGNPASLELKLEMGENNLAKMHVGLAHVNPGGWTYEG
WGPMNRAYVEIQDEYTKMQELSALQARVN

>d1ft5a_ a.138.1.3 (A:) Cytochrome c554 {Nitrosomonas europaea}

ADAPFEGRKKCSSCHKAQASWKDTAHAKAMESLKPNVKKEAKQAKLDPAKDYTQDKDCVGCHVDGFGQKGTYIESPKPMLTGVGCESCHGP
GRNFRGDHRKSGQAFEGKKTGKDFHFEERCSACHLYEGSPWKGAKAPYTPFTPEVDAKYTFKFDEMVKAMHEHYKLEGVFE
GEPKFKFHDEFQASAKPAKKG

>d1ddca_a.138.1.3 (A:) Dimeric di-heme split-soret cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

RFDQVGGAFWKPHKLDPKECAQVAYDGYWYKGFGCGFAGFYISIVLMGEKYGAPYNQFPFAMLEANKGGISDWGTYGALYGAAATFSLFWGR
KEVHPMVNELFRWYEVTKLPIFNPGDAAQGVKGDLPMASDSVLCHISVKWCYENKIEATSKQRSERAGRITADAFAKAAEIINTKIDQGKDFKSTF
PMQASVSSCGECHMTKGNDANWAKGIMDCTPCHSGTAATQNKFVNH

>d1qdba_a.138.1.3 (A:) Cytochrome c nitrite reductase {Sulfurospirillum deleyianum}

GIAGKEKSEEWAKYYPHQFDWKKTKEYDSFTDMILAKDPALVIASGYAFSKDYNNSPRGHYYALQDNVNSLRTGAPVDAKTGPLTACWTCKSPDV
PRLIEDGELEYFTGKWAQYGSQIVNVIGCANCHDDKTAELKVRVPHLNRGLQAAGLKTFEESTHQDKRTLVCACQCHVEYYFKTEWKDAKGADKT
AMVVTLPWANGVGKDGNAGVEGMIKYYDEINFSDWTHNISKTPMLKAQHPGFEFWKGSIHGQKGKVSCADCHMPYTQEGSVKYSDHQVKENPL
DSMDQSCMNCHRESESKLRGIVHQKYERKEFLNKVAFDNIGKALETGKIAEAGASDEELKEVRKLIRHGQFKADMAIAAHGNYFHAPEETRLAA
GSDDAQKARLLLVKILAKHGVMDYIAPDFDTKDKAQKLAKVDIAALAAEKMFKQTLQEWEKKEAKAKGRANPELYKDVTINDKSSWNKK

>d1fs7a_a.138.1.3 (A:) Cytochrome c nitrite reductase {Wolinella succinogenes}

KTAHSQGIEGKAMSEEWARYPRQFDWKTKESDNITDMLKEKPALVVAWAGYPFSKDYNAPRGHYYALQDNINTLRTGAPVDGKTGPLPSACW
TCKSPDVPRIEQDGELEYFTGKWAQYGEIVNTIGCYNCHDDKSAELKSVPYLDRLGLSAAGFKTFAESTHQEKRSLVCAQCHVEYYFKTEWKDDK
GVDKTAMVVTLPWSKGISTEQMEAYYDEINFADWTHGISKTPMLKAQHPDWELYKTGIHGQKGVSCADCHMPYTQEGAVKYSDHKGVNPLDNM
DKSCMNCHRESEQQLKDKIVQKQFERKEFLQDIAFDNIKGKALETGKAMELGATDAELKEIRTHIRHAQWRADMAIAGHGSFFHAPEEVRLLLASGNE
EAQKARIKLVKVLAKYGAIDYVAPDFETKEKAQKLAKVDMEAFAEKLKFQTLQEWEKKQIAKGRLNPESLKGVDEKSSYYDKTKK

>d1e39a1_a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella frigidimarina}

ADNLAEFHVNQECDSCHTPDGELSNDLTYENTQCVSCHGTLAEVAETTKHEHYNASHFPGEVACTSCHSAHEKSMVYCDSCHSFDFNMPYA
KKWLRDE

>d1qo8a1_a.138.1.3 (A:2-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella frigidimarina}

TPDMGSFHADMGSQSCHAKPIKVTDSETHENAQCKSCHGEYAEELANDKLQFDPHNSHLDINCTSCHKGHEEPKFYCNECHSFEDIKPMFSDAK
KKKSWD

>d1d4ca1_a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella putrefaciens} APEVLADFHGEMGGCDSCHVSDKGVTNDNLTHENGQCVSCHGDLKELAAAAPDKVSPHKSHLIGEIACTSCHKGHEKSVAUCDACHSFGFDMP
FGGKWER

>d1neu_b.1.1.1 (-) Myelin membrane adhesion molecule P0 {Rat (Rattus norvegicus)}

IVVYTDREVYGAVGGSQVTLHCSFWSSSEWVSDDISFTWRYQPEGGRDAISIFHYAKGQPYIDEVGTFKERIQWVGDPWKDGSIIVHNLDYSDNGTFT
CDVKNPPDIVGKTSQVTLVVF

>d1eaja_b.1.1.1 (A:) Coxsackie virus and adenovirus receptor (Car), domain 1 {Human (Homo sapiens)}

FARSLSITTPEEMIEKAKGETAYLPCFKTLSPEDQGPLDIEWLISPADNQKVQVIIYSGDKIYDDYYPLKGRVHTSNLKSGDASINVNLQLSDIG
TYQCKVKKAPGVANKKIHLVLL

>d1qfoa_b.1.1.1 (A:) N-terminal domain of sialoadhesin {Mouse (Mus musculus)}

TWGVSSPKNVQGLGSCLLIPCIFSYPADVPVSNGITAIWYYDYSGKRQVVIHSGDPKLVDKRFRGRAELMGNMDHKVCNLLLKDLKPEDSGTYNFR
FEISDSNRWLDVKGTTVT

>d1akjd_b.1.1.1 (D:) CD8 {Human (Homo sapiens)}

SQFRVSPLDRTWNLGETVELKCQVLLSNTSGCSWLFQPRGAAASPTFLYLSQNPKAAEGLDTQRFSGKRLGDTFVLTSDLFRRENEGYYFCALS
NSIMYFSHFPVFLPA

>d1bqh_g_b.1.1.1 (G:) CD8 {Mouse (Mus musculus)}

KPQAPELRFPKKMDAELGQKVDLVCEVLGSVSQGCSWLFQNSSLQPTFVVYMASSHNKITWDEKLNSSKLFSAMRDTNNKYVLTNKFSKEN

EGYYFCSVISNSVMYFSSVPVLQKV
>d1cdy_1 b.1.1.1 (1-97) N-terminal domain of CD4 {Human (Homo sapiens)}
KKVVLGKKGDTVELCTASQKSIQFWKNSNQIKILGNQGSFLTKSPSKLNDRADSRRSLWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLV
>d1wioa2 b.1.1.1 (A:179-291) N-terminal domain of CD4 {Human (Homo sapiens)}
FQKASSIVYKKEGEQVEFSFPLAFTVEKLTSWQAERASSKSWITFDLNKEVSVKVTQDPKLQMGKKLPLHLLPQALPQYAGSGNLTLA
EAKTGKLHQEVNLVV
>d1cid_1 b.1.1.1 (1-105) N-terminal domain of CD4 {Rat (Rattus rattus)}
TSITAYKSEGESAEFSFPLNLGEESLQGELRWKAEPSSQSWITFSLKNQKVSVQKTSNPKFQLSETLPLTLQIPQVSLQFAGSGNLTLDRGILYQE
NLV
>d1hnf_1 b.1.1.1 (4-104) CD2, first domain {Human (Homo sapiens)}
TNALETWGALGQDINLDIPSQMSDDDDIKWEKTSDDKKIAQFRKEKTFKEKDLYKLFNGTLKIKHLKTDDQDIYKVSIYDTKGKVNLEKIFDLKI
E
>d1hnga1 b.1.1.1 (A:2-99) CD2, first domain {Rat (Rattus norvegicus)}
DSGVVWGAHGGINLNIPNFQMDDIDEVRWERGSTLVAEFKRKMKPFLKSGAFEILANGDLKIKNLTRDDSGTYNVTVYSTNGTRILNKALDLRILE
>d1ccza1 b.1.1.1 (A:1-93) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}
FSQQIYGVVYGNVTFHVPNSNPLKEVLWKKQKDKVAELENSEFRAFSSFKNRVYLDTVGSLSIYNLTSSDEDEYEMESPNTDMKFFLYVL
>d1qa9b_ b.1.1.1 (B:) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}
SSQQIYGVYGNVTFHVPNSNPLKEVLWKKQKDKVAELENSEFRAFSSFKNRVYLDTVGSLSIYNLTSSDEDEYEMESPNTDMKFFLYVGES
>d1dr9a1 b.1.1.1 (A:1-105) CD80, N-terminal domain {Human (Homo sapiens)}
VIHVTKEVATLSCGHNVSVEEAQTRIYWQKEKKMVLMMMSGDMNIWPEYKNRTIFDITNNLSIVALARPSDEGTYECSVVLKYEKDAFKREHLA
EVTLSVK
>d1i85a_ b.1.1.1 (A:) CD86 (b7-2), N-terminal domain {Human (Homo sapiens)}
MLKIQAYFNETADLPCQFANSQNQLSELVVFQWQDQENLVNEVYLGEKFDSVHSKYMGRSTSFDSDSRTLHNLIQDKGLYQCIHHKKPTGM
RIHQMNSELSVLA
>d1f97a1 b.1.1.1 (A:27-128) Junction adhesion molecule, JAM, N-terminal domain {Mouse (Mus musculus)}
KGSVYTAQSDVQVPENESIKLTCTYSGFSSPRVEWKVQGSTTALCYNSQTAPYADRVTFSGGITFSSVTRKDNGEYTCMVSEEGGQNYGEVSIHL
TVL
>d1jmaa_ b.1.1.1 (A:) HSV glycoprotein D {Herpes simplex virus type 1}
KYALADASLKMADPNRFRGKDPVLDQLTDPPGVRRVYHIQAGLPDPFQPPSLPITVYAVLERACRSVLLNAPSEAPQIVRGASEDVRKQPYNLTIA
WFRMGGNCAIPITVMEYTECSYNKSLGACPIRTQPRWNYYDSFAVSEDNLGFLMHAPAFETAGTYLRLVKINDWTEITQFILEHRAKGSCKYALPLR
IPPSACLSPQAYQQGVTVDSIGMLPRFIPENQRTVAVYSLKIAWHGPKAPYTSTLLPPELSE
>d1igta1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa
L chain}
DIVLTQSPSSLASLGDTITITCHASQINVVLSWYQQKPGNIPKLLIYKASNLTGVPNSRSGSGTGFTLTISSLQPEDIATYYCQQGQSYPLTFGGG
TKLEIKR
>d1igtb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa
L chain}
EVKLQESGGGLVQPGGSLKLSCATSGFTFSYDYYMYWVRQTPEKRLEWVAYISNGGGSTYYPTVKGRTISRDNAKNTLYLQMSRLKSEDTAMYCA
RHGGYYAMDYWGQQGTTVSSA
>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}
KCAHTVSKSMSMSVGERVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTISVQAEDLADYHCGQQGYSYPYTF
GGGTKEIK
>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}

VKLQESGAELARPGASVKMSCKASGYTFTTYTIHWIKQRPGQGLEWIGYINPSSVYTNYNQRFKDATALTRDRSSNTANIHLSLTSDSAYYCVRE
GEVPYWGQQGTTVTVSS

>d1hh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}
QVQLVQSGAEVKPGASVKVSCQASGYRFSNFVIHWVRQAPGQRFEWMGINPYNGNKEFSAKFQDRVTFTADTSANTAYMELRSLSADTAVY
YCARVGPYSWDDSPQDNYYMDVVGKGTIVVSS

>d1hzhl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}
EIVLTQSPGTLSPGERATFCSRSHSIRSRRVAWYQHKPGQAPRLVIHGVSNRASGISDRFSGSGSGTDFTLTIRVEPEDFALYYCQVYGASSYTFQG
GTKLERK

>d8faba1 b.1.1.1 (A:3-105) Immunoglobulin (variable domains of L and H chains) {Fab HIL (human), lambda L chain}
ELTQPPSVSPGQTARITCSANALPNQYAYWYQQKPGRAPVMVIYKDTQRPSGIPQRFSSSTGTTVLTISGVQAEDAEADYYCQAWDNSASIFGG
GTKLTV

>d8fabb1 b.1.1.1 (B:1-121) Immunoglobulin (variable domains of L and H chains) {Fab HIL (human), lambda L chain}
AVKLVQAGGGVVQPGRLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRYYGDSVKGRFTISRDNSKRTLYMQMNSLRTEDTAVY
YCARDPDILTAFSFIDWGGQVLTVSS

>d7fabh1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and H chains) {Fab NEW (human), lambda L chain}
AVQLEQSGPGLVRPSQLSLTCTVSGTSFDDYYWTWVVRQPPGRGLEWIGYVFYTGTLLDPSLGRVRTMLVNTSKNQFSRLSSVTAADTAVYYCAR
NLIAGGIDVWGQGSLVTVS

>d7fabl1 b.1.1.1 (L:1-103) Immunoglobulin (variable domains of L and H chains) {Fab NEW (human), lambda L chain}
ASVLTQPPSVGAPGQRTVISCTGSSNIAGHNVKWYQQLPGTAPKLLIFHNNARFSVSKSGTSATLITGLQAEDEADYYCQSYDRSLRVFGGGTK
LTVLR

>d1bafh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab ANO2 (mouse), kappa L chain}
DVQLQESGPGLVKPSQSCLTCTVTGYSITSDYAWNWRQFPGNKLEWMGYMSYSGSTRYNPSLRSRISITRDTSKNQFFLQLKSVTTEDTATYFCAR
GWPLAYWGQGTQVSVE

>d1bafl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab ANO2 (mouse), kappa L chain}
QIVLTQSPAAMSASPGEKVMTCSASSSVYYMYWYQQKPGSSPRLLIYDTSNLASGVPRFSGSGSGTSYSLISRMEAEDAATYYCQQWSSYPPITF
GVGTLKELKR

>d1a3rh1 b.1.1.1 (H:2-119) Immunoglobulin (variable domains of L and H chains) {Fab 8F5 (mouse), kappa L chain}
VQLQQSGAELVRPGASVKLSCTTSGFNKDIYIHWWVKQRPEQGLEWIGRLDPANGYTKYDPKFQGKATITVDSSNTAYHLSSLTSEDTAVYYCDGY
SYYDMDYWGPGTSVTTSAKTTAP

>d1a3rl1 b.1.1.1 (L:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 8F5 (mouse), kappa L chain}
DIVMTQSPSSLTVTTGEKVTMTCKSSQSLNSRTQKNYLWYQQKPGQSPKLLIYWASTRESGVPDFRTGSGSGTDFTLSISGVQAEDLAVYYCQNN
YNYPLTFGAGTKLELKRAADAAPT

>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}
EVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWAKQKPEQGLEWIGYISPGNDDIKYNEFKKGKATLTADKSSSTAYMQLNSLTSEDSAVYFCKRS
YYGHWGQGTTLVSSA

>d1bbj1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab B72.3 (mouse/human chimera), kappa L chain}
DIQMTQSPASLSVSVGETVTITCRASENIYSNLAWYQQKQGKSPQLLYAATNLADGVPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWGTPYTF
GGGTRLEIKRA

>d1hila1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 17/9 (mouse), kappa L chain}
DIVMTQSPSSLTVTAGEKVTMCTSSQSLFNSGKQKNYLWYQQKPGQPPKVLIYWASTRESGVPDFRTGSGSGTDFTLTISSVQAEDLAVYYCQND
YSNPLTFGGGTKELEKLR

>d1hilb1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 17/9 (mouse), kappa L chain}
EVQLVESGGDLVKPGGSLKLSCAASGFSSYGMWSVRQTPDKRLEVVATISNGGYTYPDSVKGRFTISRDNAKNTLYLQMSSLKSEDSAMYCA
RRERYDENGFAYWGQGTLVTS

>d1dbbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab DB3 (mouse), kappa L chain}
QIQLVQSGPELKPKGETVKISCKASGYAFTNYGVNWVKEAPGKELKWMGWINIYTGEPTYVDDFKGRFAFSLETSASTAYLEINNLKNEDTATYFCTR
GDYVNWYFDVVGAGTTVTVS

>d1dbbl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab DB3 (mouse), kappa L chain}
DVVMTQIPSLPVNLGDQASISCRSSQSLIHNSGNTYLHWYLQKPGQSPKLLMYKVSNRFYGVPDFSGSGSGTDFTLKISRVEAEDLGIFYFCQSSSH
VPPTFGGGTKLEIK

>d1dfbh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and H chains) {Fab 3D6 (human), kappa L chain}
EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDMALYY
CVKGRDYYDSGGYFTVAFDIWGQGTMVTSS

>d1dfbl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab 3D6 (human), kappa L chain}
DIQMTQSPSTLSASVGDRVTITCRASQSIWRWLAWYQQKPGKVPKLLIYKASSLESGVPSRFSGSGSGTEFTLTISLQPDDFATYYCQQYNSYSFGPGT
KVDIKR

>d1igfh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab B13I2 (mouse), kappa L chain}
EVQLVESGGDLVKPGGSLKLSCAASGFTSRCAMSWVRQTPKRLEVVAGISSGGSYTFYPDTVKGRFIISRNNAARNTLSQMSSLRSEDTAIYYCTRY
SSDPFYFDYWGQGTTLVSS

>d1igfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab B13I2 (mouse), kappa L chain}
DVLMQTPLSLPVSLGDQASISCRSSNQTILLSDGDTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDFSGSGSGTDFTLKISRVEAEDLGIVYYCFQGSHV
PPTFGGGTKLEIK

>d1igja1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 26-10 (mouse), kappa L chain}
DVVMTQTPSLPVSLGDQASISCRSSQSLVHSNGNTYLNWYLQKAGQSPKLLIYKVSNRFSGVPDFSGSGSGTDFTLKISRVEAEDLGIFYFCSQTHV
PPTFGGGTKLEIK

>d1igjb1 b.1.1.1 (B:2-114) Immunoglobulin (variable domains of L and H chains) {Fab 26-10 (mouse), kappa L chain}
VQLQQSGPELVKPGASVRMSCKSSGYIFTDFYMNWVRQSHGKSLDYIGYISPYSGVTGYNQFKKGATLTVDKSSTAYMELRSLTSEDAVYYCAGS
SGNKWAMDYWGHGASVTVSSA

>d1igmh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv POT (human) IgM, kappa L chain}
EVHLLESGGNLVQPGGSLRLSCAASGFTFNIFVMSWVRQAPGKGLEWVSGVFGSGNTDYADAVKGRFTITRDNKNTLYLQMNSLRAEDTAIYYC
AKHRVSYVLGFDSWGQGTLTVSSGSASAPTL

>d1igmI_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv POT (human) IgM, kappa L chain}
DIQMTQSPSSLSASVGDRVTITCQASQDISNYLAWYQQKPGKAPELRIYDASNLETGVPSRFSGSGSGTDFTTISSLQPEDIATYYCQQYQNLPFTFG
PGTKVDIKRTVAAPSV

>d1dqh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv MEZ (human) IgM, kappa L chain}
EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISSDGGNKYYTDSVKGRFTISRNDKNTLYLQMNSLRTEDTAVFYC
ARGNPPYSSGWGDDYWGQGTMVTSS

>d1dqll_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv MEZ (human) IgM, kappa L chain}
DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPGKAPKKLIYAASSLQSGVPSRFSGSGSGTDFTLTISLQPEDFATYYCLQQNSNWTFG
QGTTKVDIK

>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}
EIVLTQSPATLSPGERATLSCGASQSVSSNYLAWYQQKPGQAPRLLIYDASSRATGIPDFRGSGSGTDFTLTISLEPEDFAVYYCQQYGSPLTFGG
GTKVEI

>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}

EVQLQQWGAGLLKPSETLSLTCAVYGGFSDYYWSWIRQPPGKGLEWIGEINHSGSTNYNPSLKSRTVISVDTSKNQFLKLSSVTAADTAVYYCARPHDTSGHYWNWYGQGTLTVSS

>d1indh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab Cha255 (mouse), lambda L chain}

EVTLVESGGDSVKPGGLSLKSCAASGFTLSGETMSWVRQTPEKRLEWVATLSSGGFTFYSASVKGRTISRDNAQNNLYLQLNSLRSEDTALYFCASHRFVHWGHGTLTVSA

>d1faih1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Fab R19.9 (mouse), kappa L chain}

QVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGVNWVKQRPGQGLEWIGYINPGKGYSYNEFKGKTTLVDRSSSTAYMQLRSLTSEDAAVYFCARSFYGGSDLAVYYFDSWGQGTTLTVS

>d1fail1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab R19.9 (mouse), kappa L chain}

DIQMTQTPSSLASLGDRVITCRASQDISNYLNWYQQKPDGTVKLLIYTTSRLHSGVPSRFSGSGSGTDYSLTISNLEHEDIATYFCQQGSLPRTFGGGTKLEIKR

>d2fb4h1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab KOL (human), lambda L chain}

EVQLVQSGGGVVQPGRLRLSCSSGFIFSSYAMYWVRQAPGKGLEWVAAIWDDGSDQHYADSVKGRTISRNDSKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSSASCFCGPDYWGQGTPVTSSA

>d2fb4l1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab KOL (human), lambda L chain}

QSVLTQPPSASGTPGQRTISCGTSSNIGSSTVNWYQQLPGMAPKLLIYRDAWRPSGVPDFSGSKSGASASLAIGGLQSEDETDDYCAAWDVSNAYVFGTGTKVTLG

>d2fbjh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and H chains) {Fab J539 (mouse), kappa L chain}

EVKLLESGGGLVQPGGLSLKSCAASGFDTSKYWMSWVRQAPGKGLEWIGEIHEDSGTINYTPSLKDKFIISRDNAKNNSLYLQMSKVRSEDTALYCARLHYGYNAYWGQGTLTVSA

>d2fbjl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab J539 (mouse), kappa L chain}

EIVLTQSPAITAASLGQKVITCSASSVSSLHWYQQKSGTSPKPWIYEISKLASGVPARFSGSGSGTSYSLTINTMEAEDAAIYYCQQWTYPLITFGAGTKLELKRAD

>d1fgvh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab H52 (synthetic, humanised version), kappa L chain}

EVQLVESGGGLVQPGGLSLRLSCATSGYTFTETYTMHWMRQAPGKGLEWVAGINPKNGGTSYADSVKGRTISVDKSNTLYLQMNSLRAEDTAVYYCARWRLGLNYGFDVRYFDVVGQGTLTVSS

>d1fgvl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab H52 (synthetic, humanised version), kappa L chain}

DIQMTQSPSSLASVGDRVITCRASQDISNYLNWYQQKPGKAPKLLIYTSTLESGVPSRFSGSGSGTDYLTISLQPEDFATYYCQQGNTLPPTFGAGTKVEIK

>d2fgwh1 b.1.1.1 (H:1-124) Immunoglobulin (variable domains of L and H chains) {Fab H52 (synthetic, humanised version), kappa L chain}

EVQLVESGGGLVQPGGLSLRLSCATSGFTSDFYMEWVRQPPGKRLEWIAASRNKGKNTTEYSASVKGRTIVSRDTSQSILYLQMNALRAEDTAIYCARNYYGSTWYFDVVGAGTTVTS

>d1mcph1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab MCPC603 (human), kappa L chain}

EVKLVESGGGLVQPGGLSLRLSCATSGFTSDFYMEWVRQPPGKRLEWIAASRNKGKNTTEYSASVKGRTIVSRDTSQSILYLQMNALRAEDTAIYCARNYYGSTWYFDVVGAGTTVTS

>d2imn_ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Fab MCPC603 (human), kappa L chain}

DIVMTQSPSSLVSAGERVTMSCKSSQSLYKDGKNFLAWYQQKPGQPPKLLIYGASTRESGVPDFGSGSGTDFTLTISSVQAEDLAVYYCQNDHSYPLTFGAGTKLELKRT

>d1fvca_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Fab 4D5 (synthetic, humanised version), kappa L chain}

DIQMTQSPSSLASVGDRVITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFVSGVPSRFSRSRGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGAGTKVEIKRT

>d1fvcb_b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Fab 4D5 (synthetic, humanised version), kappa L chain}
EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCS
RWGGDGFYAMDYWGQQGTLVTSS

>d1ggbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 50.1 (mouse), kappa L chain}
QVQLQESGPGILQPSQSLTCSFGSFLSTYGMGVSWIRQPSGKGLEWLAHIFWDGDKRYNPSLKSRLKISKDTSNNQVFLKITSVDTADTATYYCVQ
EGYIYWGQGTSVTVS

>d1ggb1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 50.1 (mouse), kappa L chain}
DIVLTQSPGSLAVSLGQRATISCRASESVDDDGNSFLHWYQQKPGQPPKLLIYRSSNLISGIPDRFSGSGSRDFTLTINPVEADDVATYYCQQSNEDPL
TFGAGTKLEIK

>d1ai1h1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 59.1 (mouse), kappa L chain}
QVKLQESGPAVIKPSQSLTLCIVSGFSITRTNYCWHWIRQAPGKGLEWMGRICYEGSIYSPSIKSRTISRDLNKKFIQLISVTNEDTAMYCSREN
HMYETYFDVVGQGTTTVVS

>d1ai1l1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 59.1 (mouse), kappa L chain}
DIVMTQSPASLVVSLGQRATISCRASESVDSYGKSFMHWYQQKPGQPPKVLIYIASNLQESGVPARFSGSGSRDFTLTIDPVEADDAATYYCQQNNED
PPTFGAGTKLEMRR

>d1mamh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab Yst9.1 (mouse), kappa L chain}
EVKLVESGGGLVQPGGSLRLSCATSGFTTDYMSWVRQPPGKALEWLGFIRNKADGYTTEYSASVKGRTFISRDNQSILYLMNTLRAEDSATYYC
TRDPYGPAAVGQGTLVTVA

>d1maml1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab Yst9.1 (mouse), kappa L chain}
DIQMTQTSSLASLGDRVATICRASQDIYLNWYQQKPDGTVKLLIYTTSRLHSGVPSRSGSGTDSLTISLNQEDMATYICQQGNTLPFTFG
SGTKLEIKR

>d1mfa_1 b.1.1.1 (1L-111L) Immunoglobulin (variable domains of L and H chains) {Fab SE155-4 (mouse), lambda L chain}
QIVVTQESALTSPGETVLTCSRSGTSGNHANWVQEKPDLHLFTGLIGDTNNRAPGVPARFSGSLIGDKAALTITGAQPEDEAIYFCALWSNNH
WIFGGGTTKLTVLGQ

>d1mfa_2 b.1.1.1 (251H-367H) Immunoglobulin (variable domains of L and H chains) {Fab SE155-4 (mouse), lambda L chain}
EVQVQQSGTVVARPGASVKMSCKASGYTFTNYWMHWIKQRPGQGLEWIGAIYPGNSATFYNHKFRAKTKLTAVTSTTAYMELSSLTSEDSAVYYC
TRGGHGYGYDWGQGASLTVS

>d1nbv1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab BV04-01 (mouse), kappa L chain}
EVQPVETGGGLVQPKGSLKLSCAASGFSNTNAMNWVRQAPGKGLEWVARIRSKSNNTYADSVKDRFTISRDDSQNMLYLQMNNLKTEDTA
MYYCVRDQGTAWFAYWGQGTLVTVA

>d1teth1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab TE33 (mouse), kappa L chain}
QIQLVQSGPELKTPGETVRISCKASGYTFTTYGMSWVKQTPGKGFWMGWINTYSGVPTYADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFC
RRSWYFDVVGTTTVVS

>d1tetl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TE33 (mouse), kappa L chain}
DVLMQTPLSLPVSLGDQASISCKSSQSVHSSGNTYFEWYLQKPGQSPKLLIYKVSNRFSGVPDFSGSGSGTDFTLKISRVEAEDLGVYFCQGS
HTFGSGTKLEIK

>d1flrh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and H chains) {Fab 4-4-20 (mouse), kappa L chain}
EVKLDDETGGGLVQPGPRPMKLSGVASGFTSDYWMNWRQSPKGLEWVAQIRNKPYNYETYSDSVKGRFTISRDDSKSSVYLQMNNLRVEDMG
IYYCTGSYYGMDYWGQGTSVTVS

>d4fabl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 4-4-20 (mouse), kappa L chain}
DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSQGNTYLRWYLQKPGQSPKVLIIYKVSNRFSGVPDFSGSGSGTDFTLKISRVEAEDLG
VYFCQS

>d1jfqh1 b.1.1.1 (H:302-421) Immunoglobulin (variable domains of L and H chains) {Fab 36-71 (mouse), kappa L chain}
VQLQQSGVELVRAGSSVKMSCKASGYTFTSNGINWVKQRPGQGLEWIGYNPNPGNGYITYNEFKKGKTTLVDKSSNTAYMQLRSLTSEDS
AVYFC

RSEYYGGSYKFDYWGQGTTLVSS

>d1jfql1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 36-71 (mouse), kappa L chain}

DIQMTQIPSSLASLGDRVSIQRASQDINNFLNWYQQKPDGTIKLLIYFTSRSGVPSRFSGSGSGTDSLISNLEQEDIATYFCQQGNALPRTFGG
GKTLEIKR

>d1gigh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab HC19 (mouse), lambda L chain}

QVQLKESGPLVAPSQSLTCTVSGFLISNGVHWVRQPPKGLEWLGVIWAGGNTNYNSALMSRVISKDNSKSQVFLKMKSLQTDDTAMYCA
RDFYDYDVFYYAMDYWGQGTSVTW

>d2cgrh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Fab, anti-sweetener (mouse), kappa L chain}
RVQLLESGAELMKPGASVQISCKATGYTFSEYIEWVKERPGHGLEWIGEILPGSGRTNYREFKKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCTR
GYSSMDYWGQGTSVTVSAA

>d2cg1l1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab, anti-sweetener (mouse), kappa L chain}
ELVMTQSPLSLPVSLGDQASISCRPSQLVHSNGNTYLHWYLQKPGQSPKLLIYRVSNRFGVPDRFSGSGSGTAFTLKRISRVEAEDLGVYFCSQGTHV
PYTFGGGTKELK

>d1figh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 1F7 (mouse), kappa L chain}

DVQLQQSGPPELEKPGASVKISCKASGFLSPGHNINWIVQRNGKSLEWIGNIDPYGGTNFNPFKKGKATLTVDKSSSTLYMHLTSLOQSEDSAVYCAR
RRDGNYGFTYWQGTLVTVSA

>d1fig1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 1F7 (mouse), kappa L chain}

ENVTQSPAIMSASPGEKVTMACRASSVSSTYLHWYQQKSGASKLIIYSTNLASGVPARFSGSGSTSLSIISVEAEDAATYYCQQYSGYPLTFG
AGTKLELK

>d1frgh1 b.1.1.1 (H:218-336) Immunoglobulin (variable domains of L and H chains) {Fab 26/9 (mouse), kappa L chain}

EVLLVESGGDLVKPGFGLKLSCAASGFTFSSFGMSWVRHTPDFKRLEWVATISNGGGTYYYQDSVKGRFTISRDNAKNTLFLEMITSKSEDAGLYCAR
RERYDEKGFAYWGRGTLVTS

>d1frgl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 26/9 (mouse), kappa L chain}

DIVMTQSPSLVTAGEKVTMSCKSSQLFNSGKRKNFLTWHQKPGQPPKLIIWASTRESGVPDFRSGSGSGTDFTLTITSVQAEDLAIYYCQNDY
SHPLTFGAGTKLELK

>d1a2ya_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3 (mouse), kappa L chain}

DIVLTQSPASLSAVGETVTITCRASGNIHNYLAWYQQKQGKSPQLVYTTTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYYCQHFSTPRTFGGGTKLEIK

>d1a2yb_b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3 (mouse), kappa L chain}

QVQLQESGPLVAPSQSLSITCTVSGFSLTYGVNVWVRQPPGKLEWLGMIWGDGNTDYNALKSRLSISKDNKSQVFLKMNSLHTDDTARYYCA
RERDYRLDYWGQGTTLVSS

>d1a7ql b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3 (mouse), kappa L chain}

DIVLTQSPASLSAVGETVTITCRAGGNTHNYLAWYQQKQGKSPQLLVYTTLAAGVPSRSGSGTQYSLKINSLQPDDFGSYCQHFWSTPRSF
GGGTKEI

>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}

DIVMTQSHKFMSTVGDRVSITCKASQDVIAWYQQKPGQSPKLLIYWAISTRHTGVPDFRTGSGSGTDFLTISNVQSELDADYFCQHCGSYPT
FGSGTKEIK

>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}

QVQLQQPGSELVRPGASVVLCKASGYTFTNYWMHWVKQRPGQGLEWIGNIYPGSGDSNYDEKFKSATLTVDTSSSTAYMQLSGLTSEDSA VYYC
ARGIAFYEDHWGO GTTITVSS

>d1jhllh b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv D11.15 (mouse), kappa L chain}

OVOLOQOSGAEVLVRPGASVKLSCKASGYTFISYWINVVKORPGOGLEWIGNIYPSDSYTNYNOKFDKDALTVDKSSSTAYMQLSSPTSEDSAVYYCT

RDDNYGAMDYWGQQGTTVT

>d1jhll_b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv D11.15 (mouse), kappa L chain}

DIELTQSPSYLVASPGETITINCRASKSISKSLAWYQEKGKTNLLIYSGSTLQSGIPSRSFGSGSGTDFTLTISSEPEDFAMYICQQHNEYWPWTFGGGT
KLEIKR

>d1bqlh1_b.1.1.1 (H:2-116) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-5 (mouse), kappa L chain}

VQLQQSGAELMKPGASVKISCKASGYTFSDYWIEWVKQRPGHGLEWIGEILPGSGSTNYHERFKGKATFTADTSSTAYMQLNSLTSEDSGVYYCLH
GNYDFDGWQGQGTTLVSS

>d1bql1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-5 (mouse), kappa L chain}

DIVLTQSPAAMSASPGEKVMTCSASSSVNYMYWYQQKSGTSPKRWYDTSKLASGVPPRFSFGSGSGTSYSLTISSMETEDAATYYCQQWGRNPTF
GGGTKEIKR

>d1ic7h_b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-10 (mouse), kappa L chain}

DVQLQESGPSLVKPSQTLSTCSVGDSITSAYWSWIRKFPNRLEYMGYVSYSGSTYNNPSLKSRSITRDTSKNQYYLDLNSVTTEDTATYYCANWA
GDYWGQQGTLTVSAA

>d2jelh1_b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab JE142 (mouse), kappa L chain}

QVQLAQSGPELVRPGSVKISCKASGYTFTNYGMNVVKQAPGKGLEWMGWINTNTGEPTYGEEFKGRFAFSLETSASTANLQINNLKNEDKATFFC
ARGEDNFGSLSDYWGQQGTTLVSS

>d1ncbh1_b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab NC41 (mouse), kappa L chain}

QIQLVQSGPELKPKGETVKISCKASGYTFTNYGMNVVKQAPGKGLEWMGWINTNTGEPTYGEEFKGRFAFSLETSASTANLQINNLKNEDKATFFC
ARGEDNFGSLSDYWGQQGTTLVSS

>d1ncb1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab NC41 (mouse), kappa L chain}

DIVMTQSPKFMSTSVGDRVITCKASQDVSTAVVWYQQKPGQSPKLIYWASTRHIGVPDRFAGSGSGTDYTLISSVQAEDLALYYCQQHYSPPWT
GGGTKEIKR

>d1forh1_b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 17-1a (mouse), kappa L chain}

QGQLQQSGAELVRPGSSVKISCKASGYAFSSFWVNWKQRPGQGLEWIGQIYPGDDDNKYNGKFKGKATLTADKSSTAYMQLYSLTSEDSAVYFC
ARSGNYPYAMDYWGQQGTSVTVSSA

>d1forl1_b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 17-1a (mouse), kappa L chain}

QIVLTQSPAIMAASPGEKVITCSATSSVNYMHWFQQKPGTSPKLWYSSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYYCQQRSSYPITFGS
GTKLEIKR

>d1knoa1_b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Fab CNJ206 (mouse), kappa L chain}

QIQMTQSPSSLASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYAALDSGVPKRFSGSRSGSDYSLTISSLESEDFADYYCLQYASSPYTFGGGT
KLEILR

>d1knob1_b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Fab CNJ206 (mouse), kappa L chain}

DVKLVEGGGLVQPGGSRKLSAACGFTSSFGMHWWVRAPEKGLEWVAYISSGSSTIYADTVKGRTFISRDNPNTFLQMTSLRSEDTAMYYCA
RGDYYGSRGAYWGQQGTTLVSA

>d1eapb1_b.1.1.1 (B:1-124) Immunoglobulin (variable domains of L and H chains) {Fab 17E8 (mouse), kappa L chain}

EVQLQESGTELVKPGASVKISCKASGYISTDHAIHWVKQRPEQGLEWIGYISPGNGDIKYNEKFKVKATLTADQSSTAYMQLNSLTSEDSAVYFCR
YYGSSYVDYWGQQGTTLVSS

>d1mrhd1_b.1.1.1 (H:2-115) Immunoglobulin (variable domains of L and H chains) {Fab Jel 103 (mouse), kappa L chain}

VQLQQSGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGEIDPSDSYTNYNQKFKGKATLTVDTSSSTAYMQLNSLTSEDSAVYYCA
NLRGYFDYWGQQGTTLVSSAK

>d1fbih1_b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab F9.13.7 (mouse), kappa L chain}

QVQLQQPGAEVKGASVKLSCKASGYTFTSYWMHWVKQGPQGLEWIGEIDPSDSYPNNEKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYC
ASLYYYGTSYGVLDYWGQQGTSVTVS

>d1fbil1_b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab F9.13.7 (mouse), kappa L chain}

DIQMTQTSSLSASLGDRVTRISCRASQDISNYLNWYQQKPDGTVKLLIYTTSRLHSGVPSRFSGSQGTDYSLTIRNLEQEDIATYFCQQGYTPLPYTFGG
GTKLEIK

>d1rmfh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab R6.5 (mouse), kappa L chain}

QVQLQQSGPELVRPGVSKISCKGSGYTFIDYAIHWVKESHAKSLEWIGVISAYSGDTNYNQFKKGATMTVDKSSNTAYLEARLTSEDSAIYYCARG
GWLLSFDYWQGTTLTVSS

>d1rmf1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab R6.5 (mouse), kappa L chain}

DVVMTQSPSLPVLGDQASISCRSSQSLVHSNGNNYLHWYLQKSGQAPKLLIYKVSNRFSGVPDFSGSGSTDFTLKISRVEAEDLGVYFCSQSTH
VPLTFGGGTKEIK

>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}

QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIQWIKQRPGQGLEWIGVINPGSGGTDYNANFKGATLTADKSSIVYMQLSSLTSDDAVYFCA
RDFYDYDVGFDYWQGTTLTVSS

>d1fpt1 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}

DVVMTQTPSLPVSLGDQASISCRSSQSLVHSNGKTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDFSGSGSTYFTLKISRVEAEDLGVYFCSQSTH
PYTFGGGTKEIKR

>d1ikfh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and H chains) {Fab, anti-cyclosporin A, (mouse), kappa L chain}

EVKLVESGGGLVQPGGSLKLSCATSGFTFSDDYYMYWVRQNSEKRLEWWAFISNGGSAFYADIVKGRFTISRDNAKNTLYLQMSRLKSEDTAMYYCT
RHTLYDTLYGNYPVWFADWGQGTLTVSA

>d1ikfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab, anti-cyclosporin A, (mouse), kappa L chain}

DIQMTQTSSLSASLGDRVTRISCRASQDISTYLNWYQQKPDGTVKLLIFYTSRLRGVPSRFSGSQGTDYSLTISNLEQEDIATYFCQQGSRIPPTFGG
GTKLEIL

>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}

VQLQQSGTELMKPGRSLKISCKTTGYIFSNEYIEWVKQRPGHGLEWIGKILPGGGSNTYNDFKGKATFTADTSSNIAYMQLSSLTSEDSAVYYCARG
EDYYAYWYVLDYWQGTTVTVSSGGGGS

>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}

DIELTQSPLSLPVSLGDQASISCRSSQSLVHSNGNTSLHWYLKKPGQSPKLLIYKVSTRFSGVPDFRGSGSGSTDFTLKISRVEAEDLGVYFCSQSTHVPP
TFGSGTKLEKL

>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}

DIELTQTPLSLPVSLGDQASISCRSSQSIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDFRGSGSGSTDFTLKISRVEAEDLGVYCFQGSHP
YTFGGGTKEI

>d1igch1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab MoPC21 (mouse), kappa L chain}

DVQLVESGGGLVQPGGSRKLSCAASGFTFSSFGMHWVRQAPEKGLEWVAYISSGSTLHYADTVKGRFTISRDNPKNTFLQMTSLRSEDTGMYYC
ARWGNYPYYAMDYWGQGTSVTVS

>d1igcl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab MoPC21 (mouse), kappa L chain}

NIVMTQSPKSMSSMSVGERVTLCKASENVVTVWSWYQQKPEQSPKLLIYGAASNRYTGVPDFRGSGSATDFTLTSSVQAEDLADYHCGQGNSYPYT
FGGGTKEIKR

>d1ibgh1 b.1.1.1 (H:2-113) Immunoglobulin (variable domains of L and H chains) {Fab 40-50 (mouse), kappa L chain}

VHLVQSGPGLVAPSQSLSITCTVSGFSLTTYGVHWFRQPPGKGLEWLGLIWAGGNTDYNALMSRLSINKDNSKSQVFLKMNSLQADDTAMYYCAR
FRFASYYDYAVDYWGQGTSVTVSS

>d1ibgl1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and H chains) {Fab 40-50 (mouse), kappa L chain}

IVLTQSPASLA VSLGQRATISCRASKSVSTSGYSHIH WYQQKPGQPPKLLIYLASILESGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCQHSREYPLTFG
AGTELELK

>d1mlbb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and H chains) {Fab D44.1 (mouse), kappa L chain}

QVQLQESGAEV MKPGASVKISCKATGYTFSTYVIEWVKQRPGHGLEWIGEILPGSGSTYYNEKFKGKATFTADTSSNTAYMQLSSLTSEDSAVYYCAR
GDGNYGYWGQGTTLVSSA S

>d1a14h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab NC10 (mouse), kappa L chain}

QVQLQQSGAELVKPGASVRMSCKASGYTFTN MYWVKQSPGQGLEWIGIFYPGNGDTSYNQFKDKATLTADKSSNTAYMQLSSLTSEDSAVYY
CARSGGSYRYDGGFDYW GQGTTVTV

>d1a14l_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab NC10 (mouse), kappa L chain}

DIELTQTSSLSASLGDRV TICRASQDISNYLNWYQQNP DGTVKLLI YYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGG
TAA

>d1nmb1_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab NC10 (mouse), kappa L chain}

DIQMTQTSSLSASLGDRV TICRASQDISNYLNWYQQNP DGTVKLLI YYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGG
GTKLEIRRA

>d1bm3h1 b.1.1.1 (H:1-125) Immunoglobulin (variable domains of L and H chains) {Anti-integrin Fab OPG2 (mouse), kappa L chain}

EVQLVQSGGGLVNPGRS LKSCAASGFTFSSYGM SWVRQTP EKRLEWVAI SGGTYI HYPDSVKG RFTISRDNAKN NLYLQMSSLRSEDTALYYCTR
HPFYRYDGGNYYAMDHW GQGTSVTVA S

>d1nsnh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab N10 (mouse), kappa L chain}

DVQLQESGPGLVKPSQSLTCTV TGYSITS DYAWN WIRQFPGNKLEWMGYITYSGTTSYNPSLKS RISISRTSKNQFMQLNSVTTEDTGTFYCTR
GNGDWGQGTTLVSSA

>d1nsnl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab N10 (mouse), kappa L chain}

DIVLTQSPS SLA VSLGQRATISCRASQSVTSSFR YMH WYQQKPGQPRLLIKYASNLES GVPARFSGSGSGTDFTLNIHPVEEEDTATYYCQHSWEIPY
TFGGGT KLEIK

>d1iaih1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab 730.1.4 (mouse), kappa L chain}

QIQLVQSGPELKPGETVKISCKASGYTFTN YMGNWVKQAPGKGLKWM AINTYTG EPTYADDFKGRFAFSLETSASTYLQINNLKNEDTATYFC
RDGYYYENYYAMDYWGQGTSVTVA S

>d1iai1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 730.1.4 (mouse), kappa L chain}

DIVMTQSHKFMSTSVGDRVSITCKASQDV STAVAWYQQKPGQSPKLLIYSASYQ YTGV PDRFTGSGSRDFTFTINSVQAEDLAVYYCHQHYSTPFT
GSGTKLEIKR

>d1iaii1 b.1.1.1 (I:1-121) Immunoglobulin (variable domains of L and H chains) {Fab 409.5.3 (mouse), kappa L chain}

EVKLQESGGGLVQPGGSMK LSCVASGFTFNNWMSWVRQSPEK GLEWVAEIRLNSDNFATHYAESVKGKFIISRDDS KSR LYLQMNSLR AEDTGIY
YCVLRPLFYAVDYWGQGTSVTVA S

>d1iaim1 b.1.1.1 (M:1-109) Immunoglobulin (variable domains of L and H chains) {Fab 409.5.3 (mouse), kappa L chain}

DIQLTQSPAFMAASPGEKVITCSVSSSISSNLHWYQQKSETSPKPW IYGT SNLASGV PVR FSGSGSGTSYSLISSMEAEDAATYYCQQWNSYPYTF
GGGT KLEIKR

>d1plgh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Polysialic acid-binding Fab (mouse), kappa L
chain}

QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIH WVKQR PGEGLEWIGWIYPGSGNTKYNEKFKGKATLTVDTSS TAYMQLSSLTSEDSAVYFC
GGKFAMDYWGQGTSVTVA S

>d1plgl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Polysialic acid-binding Fab (mouse), kappa L
chain}

DVVMTQTPSLPVSLGDQASISCRSSQSLVHSNGNTLYWYLQKPGQSPKPLIYRVSNRFSGVPDRFSGSGSGTDFTL KISRVEAEDLGVYFCFQGTH
VPYTFGGGTRLEIK

>d1aj7h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 48G7 (mouse/human), kappa L chain}

QVQLQQSGAELVKPGASVLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITADTSSNTAYLQLSLTSEDTVYYCAS
YYGIYWGGTTLVSSA

>d1gafh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 48G7 (mouse/human), kappa L chain}

QVQLQQSGAELVKPGASVLSCTASGFNIKDTYMHWVKQRPKQGLEWIGRIDPANVDTKYDPKFQDKATITADTSSKTTYLQLSLTSEDTVYYCAS
YYGIYWGGTTLVSS

>d1gafl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab 48G7 (mouse/human), kappa L chain}

DIQMTQSPSSLSASLGERVSLTCRASQEINGYLGWLQQKPDGTIKRLIYAASLHSGVPKRSGSRGSYDYSLTISSEDFADYYCLQYASYPRTFGGG
TKVEIKRT

>d1vgeh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab TR1.9 (mouse/human), kappa L chain}

QVKLLEQSGAEVKKPGASVKSCKASGYSFTSYGLHWVRQAPGQRLEWMGWISAGTGNTKYSQKFRGRVTFRDTSATTAYMGLSLRPEDTAVY
YCARDPYGGGKSEFDYWGQGTLTVSS

>d1vgel1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TR1.9 (mouse/human), kappa L chain}

ELVMTQSPSSLSASVGDRVNIACRASQGISSALAWYQQKPGKAPRLLIYDASNLESGVPSRFSFGSGSGTDFTLTISLQPEDFAIYYCQQFNSYPLTFGG
GTKVEIK

>d1yuhb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and H chains) {Fab anti-nitrophenol (mouse), lambda L chain}

QVFQQSGAELVKPGASVLSCKASGYTFTSYLMHWIKQRPGRLWEWIGRIDPNNVTKFNEFKSKATLVDKPSSTAYMELSLTSEDSAVYYCAR
YAYCRPMMDYWGQGTTVTSS

>d1ucbh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab CBR96 (mouse/human), kappa L chain}

EVNLVESGGGLVQPGGSLKVSCVTSGFTSDYYMYWVVRQTPEKRLEWVAYISQGGDITDYPDTVKGRFTISRDNAKNSLYLQMSRLKSEDTAMYCA
RGLDDGAWFAYWGQGTTVTSS

>d1ucbl1 b.1.1.1 (L:4-108) Immunoglobulin (variable domains of L and H chains) {Fab CBR96 (mouse/human), kappa L chain}

MTQIPVSLPVSLGDQASICRSSQIIVHNNGNTYLEWYLQKPGQSPQLIYKVSNRFSGPDRFGSGSGTDFTLKISRVEAEDLGVYYCFQGSHVPFT
FGSGTKLEIKR

>d1dvfc_ b.1.1.1 (C:) Immunoglobulin (variable domains of L and H chains) {Fv E5.2 (mouse), kappa L chain}

DIQLTQSPSSLSASLGDRVТИСRASQDISNYLNWYQQKPDGTVKLLIYTSLRHSGVPSRFSFGSGSGTDYSLTISNLEQEDIATYFCQQGNTLPWTFGG
GTKLEIK

>d1dvd_ b.1.1.1 (D:) Immunoglobulin (variable domains of L and H chains) {Fv E5.2 (mouse), kappa L chain}

QVQLQQSGTELVKSGASVLSCTASGFNIKDTHMNWVKQRPEQGLEWIGRIDPANGNIQYDPKFRGKATITADTSSNTAYLQLSLTSEDTVYYCATK
VIYYQGRGAMDYWGQGTTTVSS

>d1ghfh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab GH1002 (mouse), kappa L chain}

VQLQQSGPELKPGETVKISCKLWYTFTDYGMNWVKQAPGKGLWMGWIQTNTEEPTYGAEFKGRFAFSLETAFTAYKQINNLKNEDMATYFC
RVEAGFDYWAQGTTTVSS

>d1ghfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab GH1002 (mouse), kappa L chain}

DIQMTQTTSSLASLGDRVТИСRESQDISNSLNWYQQKPDGTVKLLIYTSLRHSGVPSRFSFGSGTGTDYSLTISNLEQEDFATYFCQQGNTLPYTFF
GGTKLEIK

>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}

QVKLQQSGPGLVQPSQLSITCTVSGFSITCYGVHWVRQSPGKGLEWLGVIVSGGDTDYNAAFISRLSITKDNSKSQVFFKMNSLQPNDRAIYYCAR
RGGDFWGQGTTTVSS

>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}

DVVMTQTPLTLSVTIGQPASICKSSQLLDSDGKTYLNWLLQRPQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCWQGTHF
PRTFGGGTKLEIK

>d1kelh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab 28B4 (mouse), kappa L chain}

EVKLVESGGGLQPGGSLRLSCATSGFTFTDYYFNWARQPPGKALEWLGFIRNKAKGYTTEYSASVKGRFTISRDNSQGILYLMQNTLRAEDSATYYC
ARWGSYAMDYWGQGTSV

>d1kell1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 28B4 (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASISCRFSQSIVHSNGNTYLEWYLQKSGQSPKLLIYKVSNRFSGVPDFRGSGSGTDFTLKISRVEAEDLGVYYCFQGSHV
PRTFGGGTKLEIK

>d1osph1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}

EVQLQESGPLVVKPSQTLSTCSVTEPITSGFWDWIRKPGNKLEFMGYIRYGGGTYYNPSLKSPSITRDTSKNHYLLQNSVVTEDTATYYCARSRD
YYGSSGFAFWGEGLTVSA

>d1osp1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}

DIQMSQSSSFSVSLGDRVITCKASEDIYSRLAWYQQKPGNAPRLLISGATSLETWVPSRFSGSDSGKDYTLSITSLQTEDVATYFCQQYWSPPPTFG
GGTKLEIK

>d1fj1a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab LA-2 (mouse), kappa L chain}

DIQMTQSPSSLSATLGGKVTITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGNPSRFSGSGSGRDYSFSISNLEAEDIAIYYCLQYDNLQRTFGG
GTKVEIK

>d1fj1b1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Fab LA-2 (mouse), kappa L chain}

QIQLVQSGPELKPGETVKISCKASGYTFDYSMYWVKQAPGKGLKRMGWINTETGEPTYADDFKGRFALSLLTSASTAYLHISNLKNEDTATYFCAR
GLDSWGQGTSVTVSSA

>d1cloh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (mouse), kappa L chain}

EVKLVESGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISRDKSQSILYLMQNTLRAEDSATYY
CTRDRGLRFYFDYWGQGTTLVSS

>d1clo1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (mouse), kappa L chain}

QTVLQSPAILSASPGEVKVTMTCRASSSVTIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTYSLTISRVEAEDAATYYCQHWSSKPPTFGG
GTKLEIK

>d1ad0a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (engineered human construct), kappa L chain}

QTVLQSPSSLSVSVGDRVITCRASSSVTIHWYQQKPGLAPKSLIYATSNLASGVPARFSGSGSGTYSLTISRVEAEDAATYYCQHWSSKPPTFQGQ
TKVEVKR

>d1ad0b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (engineered human construct), kappa L chain}

EVQLLESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKGLEWLGFIGNKANGYTTEYSASVKGRFTISRDKSSTLYLMQNTLQAEDSAIYY
CTRDRGLRFYFDYWGQGTTLVSS

>d1mimh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab CHI621 (mouse), kappa L chain}

QLQQSGTVLARPGASVKMSCKASGYSFTRYWMHWIKQRPGQGLEWIGAIYPGNSDTSYNQKFEGKAKLTAVTSASTAYMELSSLTHEDSAVYYCSR
DYGYYDFWGQGTTLVSS

>d1miml1 b.1.1.1 (L:1-105) Immunoglobulin (variable domains of L and H chains) {Fab CHI621 (mouse), kappa L chain}

QIVSTQSPAAMSASPGEVKVTMTCASSRSYMQWYQQKPGTSPKRWIYDTSKLASGVPARFSGSGSGTYSLTISSMEAEDAATYYCHQRSSYTFGG
GTKLEIKR

>d1afvh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 25.3 (mouse), kappa L chain}

QVQLQQPGSQLVRPGASVKLSCKASGYFTSSWIHWAKQRPGQGLEWIGEIHPNSGNTNYNEFKKGKATLTVDTSSSTAYVDLSSLSEDASAVYYCAR
WRYGSPYYFDYWGQGTTLVSS

>d1afvl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 25.3 (mouse), kappa L chain}

DIVLTQSPASLAQSLQRATISCRASESVDNYGISFMNWFQQKPGQPPKLLIYAASNLSGVPARFSGSGSGTDFSLNIHPMEEEDTAMYFCQQSKEV
PLTFFAGTKVELKR

>d2mpah1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Bactericidal Fab MN12H2, (mouse), kappa L

chain}

EVNLQQSGTVLARPGASVRMSCKASGYSFTSYWLHWIKQRPGQGLEWIGGIYPGNRDTTRYTQRFKDKAKLTAVTSANTAYMELSLTNEDSAVYYC
SIIYFDYADFIMDYWGQGTTVTSS

>d2mpal1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Bactericidal Fab MN12H2, (mouse), kappa L chain}

DIVMTQTPLSLPVSLGDKASISCRSSQALHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFGVPDRFSGSGSTDFTLKISRVEAEDLGVFFCSQSTHV
PRTFGGGTKLEIK

>d1qkzh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab MN14C11.6 (mouse), kappa L chain}

DVKLVESGGGLVKPGRSLKLSCAASGFTSDYYMFWVRQTPEQRLEWWATISDGGAYTYPDSVKGRFTISRDNAKNLYLQMNSLKSEDTGMYYC
ARDPLEYYGMDYWGQGTTAVSS

>d1qkz1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab MN14C11.6 (mouse), kappa L chain}

NIVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYTVSNRFGVPDRFSGSGSTDFTLKISRVEAEDLGVYFCQSHTF
PTFGGGTKLEIK

>d1pskh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab against a ganglioside (mouse), kappa L chain}

EVQLQQSGPELVKPGASVKISCKTSGYTFKTYTMHWVKQSHGKSLEWIGDINPNNGTNYNQFKGTATLTVHKSSTTAYMELRSLTSEDSA VYYCTS
KSFDYWGQGTTLVSS

>d1pskl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab against a ganglioside (mouse), kappa L chain}
QIVLTQSPAAMSASPGEKVITCSASSSVNIHWFFQQKPGTFPKLWIYSTSTLASGVPGFRSGSGSTSYLTISRMGAEDAATYYCQQRSGYPFTFGS
GTKLEIK

>d1yejh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.3 (mouse), kappa L chain}

EMQLQQSGAELLRPQTSVLSCKTSGYIFTSYWIHWVKQRSGQGLEWIARIYPGTGSTYYNEKFKGKATLTADKSSTAYMQLSTLKSEDSA VYFCTR
WGFI PVREDYVMDYWGQGTLTVSS

>d1yejl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab D2.3 (mouse), kappa L chain}

DIVMTQSPLTSVTIGQPASICKSSQSLLYNGKTYLNWLQPGQSPKRLIHLVSKLDGVPDRITGSGSGSTDFTLKISRVEADLGVYYCVQGTHFP
YTFGGGTKLEIL

>d1yedb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.4 (mouse), kappa L chain}

AVKLQQSGPELVRPGTSVLSCKTSGYIFTSYWIHWVLQKSSQGLEWIARIYPGTGSTYYNEKFKGKATLTADKSSTAYMQLSSLKSEDSA VYFCTR
GFTTVRENYYAMDYWGQGTLTVSS

>d1yeeh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.5 (mouse), kappa L chain}

EVKLQESGAEVLRPGASVKLSCKTSGYIFTSYWIHWVKQRRAAGLEWIARIYPGTGSTYYNEKFKGKATLTADKSSTAYMQLSSLKSDDSAVYFCVR
WGFI PVREDYVLDYWGQGTLTVSS

>d1cfvh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv 4155 (mouse), kappa L chain}

QVQLQQSGGGLVNLGGSMTLSCVASGFTFNTYYMSWVRQTPEKTLVAAINSDGEPIYYPDTLKGRVTISRDNAKKTLYLQMSSLNFEDTALYYCAR
LNYAVYGM DYWGQGTTTVSS

>d1cfv1_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv 4155 (mouse), kappa L chain}

DIELTQSPPSLPVSLGDQVSICRSSQSLVNNRRNYLHWYLQKPGQSPKLVYKVSNRFGVPDRFSGSGSTDFTLKISRVAEADLG YFCQS SHVP
LTFGSGTKLEIKR

>d1hyxh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 6D9 (mouse), kappa L chain}

EVKLLESGGGLVKPGGSLKLSCAASGFTFSNYAMS WVRQTPEKRLEWVVSISGGSIYLYDSVKGRFTVSRDNARNILYLQM TSLRSEDTAMYFCAR
SHYDGSRDWYFDVVGAGTSVTSS

>d1hyxl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 6D9 (mouse), kappa L chain}

ELVMTQTPLSLPVSLGDQASISCRSSQTIVHSNGDTYLDWFLQKPGQSPKLLIYKVSNRFGVPDRFSGSGSTDFTLKISRVEAEDLGVYYCFQGS HV
PPTFGGGTKLEIK

>d2hrph1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab F11.2.32 (mouse), kappa L chain}
DVQLVESGGGLVQPGSRKLSCAASGFTFMRGMHWRQAPEKGLEWVAYISSSSTIYYADTVKGRFTISRDNPKNTLFLQMTSLRSEDTALYYCA
RSGGIERYDGTYYVMDYWGQGTSVTVSS

>d2hrpl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab F11.2.32 (mouse), kappa L chain}
DTVLTQSPASLAVLGQRATISCRASESDVYYGKSFMNWFQQKPGQPPKLLIYAASNQGSGVPARFSGSGSGTDFSLHIHPMEEDDSAMYFCQQSK
EVPWTFGGGTKLEIK

>d2ap2a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {scFv C219, (mouse sequence-based), kappa L chain}
FVRDIVMTQSPSSLTVAGEKVTMSCKSSQSLNSGNQKNYLWYQQKPGQPPKLLIYWASTRESGVPDFRTGSNSGTDFTLTISSVQAEDLAVYYC
QNDYSYPLTFGAGTKLEP

>d2ap2b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {scFv C219, (mouse sequence-based), kappa L chain}
EVQLQQSGAELVRPGAVKLSCTASGFNIKDDFMHWVKQRPEQGLEWIGRIDPANDNTKYAPKFQDKATIIADTSSNTAYLQMLSSLTSEDTAVYYCAR
REVYSYSPLDVVGAGTTVTPSG

>d1nfde1 b.1.1.1 (E:2-107) Immunoglobulin (variable domains of L and H chains) {Fab H57 (hamster), lambda L chain}
YEIQPSSASVTGETVKITCSGDQLPKNFAYWFQQKSDKNILLIYMDNKRPSGIPERFSGSTSGTTATLISGAQPEDEAAYCLSSYGDNNNDLVFGS
GTQLTVLR

>d1nfd1 b.1.1.1 (F:1-114) Immunoglobulin (variable domains of L and H chains) {Fab H57 (hamster), lambda L chain}
EVYLVESGGDLVQPGSSLKVSCAASGFTFSDFWMYWVRQAPGKLEWVGRIKNIPNNYATEYADSVRGRFTISRDDSRNSIYLQMNRRLRVDDTAIYY
CTRAGRFDHFHDYWGQGTMVTVSSA

>d2h1ph1 b.1.1.1 (H:301-420) Immunoglobulin (variable domains of L and H chains) {Fab 2H1 (mouse), kappa L chain}
DVKLVESGGGLVKLGGSLSKLSCAASGFTFSSYFLSWVRQTPKRLELVATINSNGDKTYHPDTMKGRFTISRDNAKNTLYLQMSSLKSEDTALYYCARR
DSSASLYFDYWGQGTTLVSS

>d2h1pl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 2H1 (mouse), kappa L chain}
DVVMTQTPLSLPVSLGDPASISCRSSQLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFGVPDKFSGSGSGTDFTLKISRVEAEDQGVYFCQSHT
VPWTFGGGTKLEIKR

>d1aqkh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}
EVQLVESGGGVQPGRLSRLSCAASGFTFNNYAIHWVRQAPGKLEWVAFISYDGSKNYYADSVKGRFTISRDNSKNTLFLQMNSLRPEDTAIYYCA
RVLFQQQLVLYAPFDIWGQGTMVTVSS

>d1aqkl1 b.1.1.1 (L:1-111) Immunoglobulin (variable domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}
ENVLTQPPSVGAPGQRVTISCTGSNSNIGAGFTVHWYQHLPGTAPKLLIFANTNRPSGVPDFSGSKSGTSASLAITGLQAEDADYYCQSYDSSLRA
RFGGGTRLTVLG

>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)}

ELVLTQSPSSMYASLGERVTITCKASQDINSYLNWFQQKPGKSPKTLIYRTNRLVDGVPSRFSGSGSGQDYSLTISSEYEDMGIYYCLQYDEFPYTFGS
GTKLEIK

>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)}

QVQLQQSGAELMKPGASVKISCKATGYTFSSYIEWVKQRPGHGLEWIGEILPGSGSTNYNEFKKGATFTADTSSNTAYMQLSSLTSEDSA VYYCA
RGHSYYFYDGDYWGQGTSVTVSS

>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)}

DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTISSEYEDMGIYYCLQYDEFPYTFGS
GTKLEIK

>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}

EVKLQESGGDLVQPGGSLKLSCAASGFTFSSYTMSWVRQTPEKRLEWVASINNGGRYYPPDTVKGRFTISRDNAKNTLYLQMSSLKSEDTAMYC
VRHEYYYAMDYWGQQGTTVTVSS

>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}

DIELTQTPVLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQFLVYNAKTLGEGVPSRSGSGSGTQFSLKINSLLPEDFGSYYCQHHYGTPLTFG
GGTKLEIK

>d1ae6h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab CTM01 (mouse), kappa L chain}

QIQLQQSGPELVKPGASVKISCKASGYTFTDYYINWMKQKPGQGLEWIGWIDPGSGNTKYNEKFKGATLTVDTSSSTAYMQLSSLTSEDTAVYFCA
REKTTYYYAMDYWGQQGTSVTVSAA

>d1ae6l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and H chains) {Fab CTM01 (mouse), kappa L chain}

DIVMTQAAPSVPVTPGESLSICRSSKSLLHSNGDTFLYWFLQRPGQSPQLIYRMSNLASGVPSRSGSGTAFLRVSRAEDVGVYCMQHLE
YPFTFGAGTKLELK

>d1ad9a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab CTM01 (human construct), kappa L chain}

DIQMTQSPSTLSASVGDRVTITCRSSKSLLHSNGDTFLYWFFQQKPGKAPKLLMYRMSNLASGVPSRSGSGTEFTLTISSLQPDDFATYYCMQHLE
YPFTFGQGKVEVKR

>d1ad9b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab CTM01 (human construct), kappa L chain}

EIQLVQSGAEVKKPGSSVKVSCKASGYTFTDYYINWMRQAPGQGLEWIGWIDPGSGNTKYNEKFGRATLTVDTNTAYMELSSLRSEDTAFYFCA
REKTTYYYAMDYWGQQGTLTVSS

>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}

EIQLQQSGAELVRPGALVLSCKASGFNIKDYMMHWVKQRPEQGLEWIGLIDPENGNTIYDPKFQGKASITADTSSNTAYLQLSSLTSEDTAVYYCARD
NSYYFDYWGQQGTTLVSS

>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}

DIKMTQSPSSMYASLGERVTITCKASQDIRKYLNWYQQKPKWPKPTLIYYATSLADGVPSRSGSGQDYSLTISSLESDDTATYYCLQHGESPYTFG
GGTKLEINR

>d1jpth1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-human tissue humanised factor Fab D3H44}

EVQLVESGGGLVQPGGSLRLSCAASGFNIKEYMHWWVQAPGKGLEWVGLIDPEQGNTIYDPKFQDRATISADNSKNTAYLQMNSLRAEDTAVYYC
ARDTAAYFDYWGQQGTLTVSS

>d1jptl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-human tissue humanised factor Fab D3H44}

DIQMTQSPSSLSASVGDRVTITCRASRDIKSYLNWYQQKPGKAPKVLIIYATSLAEGVPSRSGSGSGTDYTLTISSLQPEDFATYYCLQHGESPWTFG
QGKVEIK

>d1jrhh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A6 (mouse), kappa L chain}

AVKLQESGPILKPSQTLSTCSFGSLSLTYYGMGVWIRQSSGKGLEWLAHIWWDDDKYYNPSLKSRLTISKDTSRNQVFLKITSVATADTATYYCAR
RAPFYGNHAMDYWGQQGTTTVSS

>d1jrh1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A6 (mouse), kappa L chain}

SVEMTQSPSSFSVSLGDRVTITCKASEDIYNRLAWYQQKPGNAPRLLISGATSLETEVPSRSGSGSGKDYTLSLQTEDVATYYCQQYWSTWTFGG
GTKLEIK

>d1gpoh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab M41 (artificial design)}

EVKLQESGPILKPSQTLSTCSVTGDSITSDFWSWIRQFPGNRLEYMGFVQYSGETAYNPSLKSRSITRDTSKNQYYLDLNSVTTEDTAVYYCANWH
GDYWGQQGTTTVSS

>d1gpol1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab M41 (artificial design)}

DIELTQSPATLSVTPGNSVSICRASQSLVNEDGNTYLFWYQQKSHESPRLLIKYASQSISGIPSRSGSGSGTDFTLSINSVETEDLAVYFCQQITDWPF
TFFGGGKLEIK

>d1kb5h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab Desire-1 (mouse), kappa L chain}
EVQLQQSGPELEKPGASVKISCKASGYSGFTGYNMNWVKQSNKGSKLEWIGNIDPYGGISYNQKFKGRATLTVDKSSSTAYMQLKSLTSEDSAVYYCAR
SRTDLYYFDYWGGQGTTLVSS

>d1kb5l1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab Desire-1 (mouse), kappa L chain}
DIQMTQSPASLASVGETVTITCRASKNIYSALWYQQKQGKSPQLVNAKTLGEGVPSRFSGSQGTQFSLKINSLOPQEDFGSYYCQHHYGTPYTFG
GGTKLEIKR

>d1a4jb1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Diels alder catalytic Fab (mouse), kappa L chain}
QVQLLESGPELKPGETVKISCKASGYTFTNYGMNWKQAPGKGLKWMGWINTYGEPTYADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCV
QAERLRRTFDYWGAGTTVSS

>d1a4ka1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and H chains) {Diels alder catalytic Fab (mouse), kappa L chain}
ELVMTQTPLSLPVSLGDQASISCRSSQSLHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDFRGSGSGTDFILKISRVEAEDLGVYFCSQVTHV
PPTFGGGTKEIKRTVAA

>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}
QIQLVQSGPELKPGETVKISCKASGYMFTNYGMNWKQAPGKALKMGWINPYTGESTFADDFKGRFAFFLETSATTAYLQINNLKNEDMATYFC
ARGTTIVRAMDYWGQGTSLTVSSAKTPP

>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}
ELVMTQTPLSLPVSLGDQASISCRSSQSLHSNGNTYLHWYLQKPGQSPKFLIYKVSNRFSGVPDFRGSGSGTDFILKISRVEAEDLGVYFCQSTHF
FPTFGGGTKEIKSADAA

>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}
EVQLEESGPELVRPGTSVKISCKASGYTFTNYWLGVVKQRPGHGFEWIGDIYPGGVYTTNEKFRGKAILTADTSSSTAYMQLSSLTSEDSAVYFCAR
AGGYTGGDYWGQGTSVTSS

>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}
DIVLTQAAFSNPVTLGASASISCRSSKSLNSNGIIHMYWYLQKPGQSPQLLIYQMSKLASGAPDRFSGSGSGTDFILKISRVEAEDVGVYYCAQNLEL
PYTFGGGTKEIK

>d1ay1h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab TP7 (mouse), kappa L chain}
EVQLQESGPGLVKPYQSLSLCTVTGYSITSDYAWNIRQPGNKEWMGYITYSGTTDYNPSLKSRSITRDTSKNQFLQLNSVTTEDTATYYCARY
YYGYWYFDVWGGQGTTLVSS

>d1ay1l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TP7 (mouse), kappa L chain}
DIQMTQSPAAMSASPGEKVMTCSASSSVSYMWYQQKPGSSPRLLIYDSTNLASGVPRFSGSQGTSLISRMEAEDAATYYCQQWSTYPLTF
GAGTKLELK

>d1dsfh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anticancer Fv B1 (mouse)}
QLVESGGGLVKPGGSLKLSCAASGFIFSDNYMYWVRQTPEKCLEWVATISDGTYIDYSDSVKGRFTISRDNAKNNLYLQMSSLRSEDTGMYYCGRS
PIYYDYAPFTYWGQGTLTVSA

>d1dsf1_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anticancer Fv B1 (mouse)}
DVVMTQTPLSLPVSLGDQASISCRSSQNLVHSDGKTYLHWFLQKPGQSPTLLIYKVSNRFSGVPDFRGSGSGTDFILKISRVEAEDLGVYFCQSTHV
PLTFGCGTKEIK

>d1a6ta1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab Mab1-IA (mouse), kappa L chain}
QSVLSQLPAILSASPGEKVIMTSPSSVSYMWYQQKPGSSPKWIYSTNLASGVPRFSGSQGTSLISGVREAEDAATYYCQQYSSHPLTFG
GGTKLELK

>d1a6tb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab Mab1-IA (mouse), kappa L chain}

EVQLQQSGPDLVKPGASVKISCKASGYSFSTYYMHWVKQSHGKSLEIGRVDPDNGGTSFNQFKKGKAILTVDKSSSTAYMELGSLTSEDSAVYYCA
RRDDYYDFWGQGTSLTVSS

>d1a6wh_b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv B1-8 (mouse), lambda L chain}

QVQLQQPGAEVLKPGASVKLSCKASGYFTSYWMHWVKQRPGRGLEWIGRIDPNSSGGTKYNEKFKSATLTVDKPSSTAYMQLSILTSEDSAVYYC
ARYDYYGSSYFDYWQGQGTTVTVSS

>d1a6wl_b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv B1-8 (mouse), lambda L chain}

AVVTQESALTTSPGETVTLCRSSTGAVENTSNYANWVQEKPDLFTGLIGGTNNRAPGVPARFSGSLIGNKAALTITGAQTEDEAIYFCALWYSNHWW
FGGGTAKLTVLE

>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}

QVQLLESGAEVKPGSSVKVSCKASGDTFIRYSFTWVRQAPGQGLEWMGRITILDVAHYAPHLQGRVTITADKSTTVYLERNLRSDDTAVYFCAG
VYEGERGEYRNNGFLKHGWQGTLTVTSA

>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}

ELELTQSPATLVS PGERATLSCRASESVSSDLAWYQQKPGQAPRLIYGASTRATGVPARFSGSGAEFTLTISSLQSEDFAVYYCQQYNNWPPRTF
GQGTRLEIK

>d12e8h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 2E8 (mouse), kappa L chain}

EVQLQQSGAEVVRSGASVKLSCTASGFNIKDYYIHVVKQRPEKGLEWIGWIDPEIGDTEYVPKFQGKATMTADTSSNTAYLQLSSLTSEDTVYYCNA
GHDYDRGRFPYWGQGTLTVSAA

>d12e8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 2E8 (mouse), kappa L chain}

DIVMTQSQKFMSTSVDGRVSITCKASQNVGTAWAHQKPGQSPKLMYASNR YTGVPDFRTGS GSGTDFTLTISNMQSEDLADYFCQQYSSYPL
TFGAGTKLELK

>d1adqh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {IgM rheumatoid factor Fab (human), lambda L chain}

EVQLVESGGGLVQPGRLRLSCVTSGFTFDDYAMHWVVRQSPGKGLEWVG ISWNTGIIYADSVKGRFIISRDNAKNSLYLMNSLRVEDTALYYCA
KTRSYVVAEYYFHYWGQGILTVSS

>d1adql1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and H chains) {IgM rheumatoid factor Fab (human), lambda L chain}

YVLTQPPSVS VAPGQTARITCGGNIGSKSVHWYQQKPGQAPVLVYDDSDRPPGIPERFSGNSGNTATLTISRVEAGDEADYYCQVWDSSSDHA
VFGGGTAKLTVLG

>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}

DIQMTQTTSSLASLGDRV TISCSASQDISSYLNWYQQKPEGTVKLLIYTSSLHSGVPSAFSGSGSTDYSLTISNLEPEDFATYYCQQYSKFPWTFGG
GTKLEIK

>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}

QITLKESPGIVQPSQPFR LTCTFSGFSLSTSGIGVTWIRQPSGKGLEWL ATIWWDDNRYNPSLKSRLTVSKDTSNNQAFLNMMVTETADTAIYYCA
QSAITSVTDSAMDHWGQGTSVTVSS

>d1bvka_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Humanized anti-lysozyme Fv HuLys11 (mouse), kappa L chain}

DIQMTQSPSSLASVGDRVTITCRASGNIHNYLAWYQQKPGKAPKLLIYYTTLADGVPSRFGSGSGSTDYTFITSSLQPEDIATYYCQHF WSTPRTFG
QGTKVEIKR

>d1bvkb_b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Humanized anti-lysozyme Fv HuLys11 (mouse), kappa L chain}

QVQLQESGPGLVRPSQTLSTCTVSGFSLTG YGVNWVRQPPGRGLEWIGMIWGDGNTDYN SALKSRVTMLKDT SKNQFSRLSSVTAADTAVYYCA
RERDYRLDYWGQGSLTVSS

>d1a0qh1 b.1.1.1 (H:2-114) Immunoglobulin (variable domains of L and H chains) {Fab 29G11 (mouse), kappa L chain}
VQLQESDAELVKPGASVKISCKASGYTFTDHVIHWVKQKPEQGLEWIGYISPGNGDIKYNEFKGKATLTADKSSTAYMQLNSLTSEDSAVYLCKRGY
YGRSNVDYWGQQGTTLVSSA

>d1a0qI1 b.1.1.1 (L:2-108) Immunoglobulin (variable domains of L and H chains) {Fab 29G11 (mouse), kappa L chain}
IELTQSPSSLASLGGKVITCKASQDIKKYIGWYQHKPGKQPRLLIHYTSTLLPGIPSFRGSGSGRDYSFSISNLEPEDIATYYCLQYYNLRTFGGGTKE
IKR

>d1fnsh1 b.1.1.1 (H:215-336) Immunoglobulin (variable domains of L and H chains) {Fab NMC-4 (mouse), kappa L chain}
QVQLKESGPLVAPSQSLITCTVSGFLTDYGVWDVRQPPGKLEWLGMIWGDGSTDYNALKSRLSITKDNKSQVFLKMNSLQTDDTARYYCV
RDPADYGNYDYALDYWGQQGTSVTVSS

>d1fnsl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab NMC-4 (mouse), kappa L chain}
DIQMTQSPSSLASLGDRVTSICASQDINKYLNWYQQKPDGAVKLIFYSSLHSGVPSRFSGSGLTDYSLTISNLEPEDIATYYCQQYEKLPWTFGG
GTKLEVK

>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}
QVQLQQPGAEVLVRPGASVKLSCKASGYLTYYWMNWFKQRPDQGLEWIGRIDPYDSETHYNQFKDKAILTVDRSSSTAYMQLSSLTSEDSAVYYC
TRFLQITTIYGMWDYWGQQGTSVTVSS

>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}
QVQLQQSGAELMKPGPSVKISCKATGYSFSTYFIEWIRQRPGHGLEWIGEILPGSDNTNFNEKFDRATFTADTPSNTAYMQLSSLTSEDSAVYYCAR
PTGRLWFSYWGQQGTLVTVA

>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}
QIILTQSPAAMSASPGEVKVTMTCASSDISYMHWYQQKSDTSPKIWIYDTSKLASGVPARFSGSGSGTYSLTISTMEAEDAATYYCHQRSSYPTFGGG
TKLEIK

>d35c8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 5C8 (mouse), kappa L chain}
EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQKPEQGLEWIAQIDPANGNTKYDPKFQGKATITADTSSNTAYLHLSSLTSEDSAVYYCA
ADPPYYGHG DYWGQQGTTLVSS

>d35c8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 5C8 (mouse), kappa L chain}
DIVLTQSPAIMSASLGERVTMTCASSSVSSNLHWYQQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTYSLTISMEAEDAATYYCHQYHRSPYTF
GGGTKLEIK

>d1a5fh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Anti-E-selectin Fab (mouse), kappa L chain}
EVALQQSGAELVKPGASVKLSCAASGFTIKDAYMHWVKQKPEQGLEWIGRIDSGSSNTYDPTFKGKATITADSSNTAYLQMSSLTSEDTAVYYCAR
VGLSYWYAMDYWGQQGTSVTVSS

>d1axth1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 33F12 (mouse), kappa L chain}
EVKLEESGGGLVQPGGSMKLSCVSGLTSRFWMSWVRQSPEKGLEWVAEIRLKSDNYATHYAESVKGKFTISRDDSKSRLYLMNSLRTEDTGIYYC
KIYFYSFSYWGQQGTLVTVA

>d1axtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 33F12 (mouse), kappa L chain}
ELVMTQTPLSLPVSLGDQASISCRSSQSLVHSYGNFLNWYQKSGSPKLIYKVSNRFGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFC SQGTHV
PYTFGGGTKLEIK

>d1b2wh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Humanized and chimeric anti-gamma-interferon Fab}
EVQLVQSGGGVVQPGRSKLSCASGYIFTSSWINWVKQRPGRGLEWIGRIDPSDGEVHYNQDFKDRFTISRDKSKNTLYLQMNSLRPEDTAVYYCA
RGFLPWFWADWGQQGTLVTVSS

>d1b2wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Humanized and chimeric anti-gamma-

interferon Fab}

DIQMTQSPSTLASVGDRVTITCKASENVDTYVSWYQQKPGKAPKLLIYGASNRYTGVPNSRSGSGSGTDFTLTISSLQPDDFATYYCGQSINYPTFG
QGTKVEVK

>d1b4jh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Humanized and chimeric anti-gamma-interferon Fab}

EVQLQQPGADLVMPGAPVKLCLASGYIFTSSWINWVKQRPGRLWIGRIDPSDGEVHYNQDFDKATLTVDKSSSTAYIQLNLSLTSEDAVYYCA
RGFLPWFA DWGQGTLTVSA

>d1b4jl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Humanized and chimeric anti-gamma-interferon Fab}

NIVMTQSPKSMYVSIGERTLSCKASENVDTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFLTISSVQAEDLADYHCGQSINYPTF
GSGTKLEIK

>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}

DIKMTQSPSFLSASVGDRVTLNCKASQNIKYLNWYQQKLGE SPKLLIYNTNNLQTGIPSRSFSGSGSGTDFLTISSLQPEDVATYFCLQHISRPTFGT
GTKLELK

>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}

EVKLLESGGGLVQPGGSMRLSCAGSGFTFTDFYMNWIRQAGKAPEWLGFI RDKA KGYTTEYNPSVKGRFTISRDNTQNMLYLMNTLRAEDTAT
YYCAREGHTAAPFDYWQQGVMTVSS

>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}

QVQLQESGPGLVRPSQTLCTVSGFTFTDFYMNWVRQPPGRGLEWIGFIRDKA KGYTTEYNPSVKGRVTMVLVDTSKNQFSRLSSVTAADTAVYY
CAREGHTAAPFDYWQQGSLTVSS

>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}

DIQMTQSPSLSASVGDRVTITCKASQNIKYLNWYQQKPGKAPKLLIYNTNNLQTGVPNSRSGSGSGTDFLTISSLQPEDIATYYCLQHISRPTFG
QGTKVEIK

>d1bj1h1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {VEGF neutralizing Fab-12 (mouse), kappa L chain}

EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVRQAPGKGLEWVGWINTYTGEPTYAADFKRRFTSLDTSKSTAYLQMNSLRAEDTAVYY
CAKYPHYGGSSHWWYFDVVGQGTLTVSS

>d1bj1j1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and H chains) {VEGF neutralizing Fab-12 (mouse), kappa L chain}

DIQMTQSPSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIFTSSLHSGVPSRSFSGSGSGTDFLTISSLQPEDFATYYCQQYSTVWTFG
QGTKVEIK

>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}

DVLMQTQPVSLVSLGDQASISCRSSQSIVHSTGNTYLEWYLQKPGQSPKLLIYKISNRFSVGPDRFSGSGSGTDFTLKISRVEAEDLGYYCFQASHAP
RTFGGGTKLEIK

>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}

EVILVESGGGLVKPGGSLKLSCAASGFTFSSYMSWVRQTPEKRLEWVATISSGGNTYYPD SVKGRFTISRDNAKNNLYLQMSSLRSEDTALYYCARY
YRYEAWFASWGQGTLTVSA

>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}

DIKMTQSPSSMYTSLGERVTITCKASQDINSFLTWFQKPGKSPKTLIYRANRLMIGVPSRFSGSGQTYSLTISSLEYEDMGIYYCLQYDDFPLTFGA
GTKLDLK

>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}

QDQLQQSGAELVRPGASVKLSCKALGYIFTDYEIHWVKQTPVHGLEWIGGIHPGSSGTAYNQFKGKATLTADKSSTAFMELSSLSEDSAVYYCTRK
DYWGQGTLTVSA

>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}

DVQLQQSGPDLVKPSQSLTCTVTGYSITSGYSWHWIRQFPGNKLEWMGYIHYSAGTNYNPSLKSRSITRDTSKNQFFLQLNSVTTEDTATYYCAR
EEAMPYGNQAYYYAMDCWGGQGTTVSS

>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}

DIVLTQSPASLAvgQRATISCKASQGVDFDGASFMNWYQQKPGQPPKLLIFAASTLESGIPARFSGRGSGTDFTLNHVEEDAATYYCQQSHED
PLTFGAGTKLELK

>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}

EVQLQQSGAELVKPGASVKSCTASGFNIKDTYMHWWVKQRPEKGLEWIGRIDPASGNTKYDPKFQDKATITADTSSNTAYLQLSSLSEDTAVYYCAG
YDYGNFDYWGGT

>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}

DIQMTQSPASLSASVGETVTITCRASGNINHYLAWYQQKQGKSPQLVYNAKTLADGVPSRFSGSGSGTQYSLKINSQPEDFGSYYCQHFWSTPW
FGGGTKLEIK

>d1sbsh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Anti-HCG Fab 3A2, (mouse), kappa L chain}

EVNLEESGGGLVQPGGSMKLCVASGFTFSNYWMNWVRQSPEKGLEWVADIRLKSNNTYALYAESVKGRFTISRDDSKSSVYLQMNNLRAEDTGIY
YCTRGAYYRYDYAMDYWGQGTSVTSS

>d1sbsl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-HCG Fab 3A2, (mouse), kappa L chain}

DIVMSQSPSSLAVSVGEKVTMTCKSSQSLYSSNQMNLYAWYQQKPGQSPKLLIYWASTRESGVPDFRTGSGSGTDFTLTISVEAEDLAVYYCQQY
HSYPFTFGSGTKLEIK

>d1sm3h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Tumor-specific Fab SM3, (mouse), lambda L chain}

QVQLQESGGGLVQPGGSMKLCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSNNTYATHYAESVKGRFTISRDDSKSSVYLQMNNLRAEDTGI
YYCTGVGFAYWGQGTTVSS

>d2pcpa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 6B5, (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASICRSSQTIVHSNGNTYLEWYLQKPGQSPKLLIYKVTNRFGSVPDRFTGSGSGTDFTLKISRVEAEDLGVYYCFQGTHA
PYTGGGTTKLEIK

>d2pcpb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 6B5, (mouse), kappa L chain}

EVQLQQSGPELVKPGASVKMSCKASGYFTDYYIHWNKQSHGKSLEWIGIYIPNNGNGYNHKFKGKATLTVDKSSSTAYMDVRTLTSEDSAVYYC
GRSTWDDFDYWGGTTTVSS

>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}

ELVMTQTPKFMSTTVGDRVSITCKASQNVGTPVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTGSGSGTDFTLTISNMQSEDLADYFCQQYSSYPLT
FGGGTKVEIK

>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}

QVQLLESGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRGLEWIGMIDPNSGGTKYNEFKSKATLTVDKPSNTAYMQLSSLTSEDSAVYYC
TRRDMDYWAGTTVTVSS

>d1cf8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 19A4 (mouse), kappa L chain}

DVQLQESGPLVKPSQLSLTCTVGYSITSGYAWNWRQFPGNKLEWMGYIRYSGDTRYNPSLKSRSITRDTSKNQFFLQLNSVTTEDTATYYCAIG
YGNSDYWGQGTLTVSA

>d1cf8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 19A4 (mouse), kappa L chain}

DIVLTQSPTIMSVSPGEVKTLCSASSVSSNYVYWYQQKPGSSPKVWIYSTSNLASGVPARFSGSGSGTSYSLISSMEAEDAASYFCLQWSSFPYTFG
GGTKLELK

>d1c12a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab directed against the musk odorant traseolide, (mouse), kappa L chain}

DIELTQSPSSMSVSLGDTVSITCHASQGISSNIGWLQQKPGKSFKGLIYHGTNLEDGVPSRFSGSGSGADYSLTISSEDFA
DYYCVQYVQFPFTFGS
GTKLEIK

>d1c12b1 b.1.1.1 (B:301-413) Immunoglobulin (variable domains of L and H chains) {Fab directed against the musk odorant traseolide, (mouse), kappa L chain}

QVQLQESGPLVKPSQLSLTCTVGYSITSDYAWNWRQFPGNKLEWMGYISYSGSTSYSPSLKSRSITRDTSKNQFFLQLNSVTTEDTATYYCVTLS
TWLLRRKR SYWGQGTTVTVSS

>d1dlfh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv, (mouse), kappa L chain}

EVKLEESGGGLVQPGGSMKLSCATSGFTFSDAWMDWVRQSPEKGLEWVAEIRNKANNHATYYAESVKGRFTISRDDSKRRVYLQMNTLRAEDTGI
YYCTGIYYHYPWFAYWGQGTLTVS

>d1dlfl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv, (mouse), kappa L chain}

DVVMTQTPLSLPVSLGNQASISCRSSQLVHSNGNTYLHWYLQPGQSPKLIYKVSNRFSGVPDRFSGSGSGTDFTL
KISRVEAEDLGVYFCQS
TPFTFGSGTKLEIKR

>d43c9a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and amidolytic Fv 43c9, (mouse), kappa L chain}

DVVMQTTPSSLAMSVGQKVTMSCKSSQSLNISNQKNYLAWYQQKPGQSPKLLVYFASTRESGV
PDRFIGSGSGTDFLT
LISSVQAEDQADYFCQQ
HYRAPRTFGGGTKLEIK

>d43c9b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and amidolytic Fv 43c9, (mouse), kappa L chain}

GQVQLVESGPLVAPSQSLITCTVSGISLSRYNVHWRQSPGKLEWLGMIWGGGIEYNPAL
KSRLISKDN
KSQIFLKMNSLQTDDSAMYYCV
SYGYGGDRFSYWGQGTLTVS

>d1bz7a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab R24, (mouse), kappa L chain}

DIQMTQITSSLSVLGDRVII
SCRASQDIGNFLNWYQQKPD
GSLKLIY
TSRLQSGVPSRFSG
WGS
GTDYSLT
ISN
LEEEDIAT
FFC
CQQGKTLPYTFGG
GTKLEIK

>d1bz7b1 b.1.1.1 (B:1-122) Immunoglobulin (variable domains of L and H chains) {Fab R24, (mouse), kappa L chain}

DVQLVESGGGLVQPGGSRKL
CAASGFTFSNFG
MHWRQ
A
PEK
GLEW
VAY
ISSGG
SIN
YAD
TV
K
G
R
F
T
I
S
R
D
N
P
K
N
L
F
L
Q
M
T
S
L
R
S
E
D
T
A
I
Y
Y
C
T

RGGTGTRSLYYFDYWGQGATLIVSS

>d1ct8a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 7C8, (mouse), kappa L chain}

ELVMTQTPLSVTPGDSV
SLCRASQ
VS
N
K
L
H
W
Y
Q
Q
K
S
H
E
S
P
R
L
I
K
F
A
S
Q
I
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V
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F
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Y
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C
H
Q
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H
G
R
P
L
T
F
G
A

GTKLELK

>d1ct8b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 7C8, (mouse), kappa L chain}

QVKLLES
GAVLV
KPGAS
VKL
SCKT
SGFT
FSS
YIN
WL
K
Q
P
G
Q
S
L
E
W
I
A
W
I
Y
A
G
S
G
G
T
V
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T
E
D
S
A
I
Y
Y
C
A
R
Y
D
E
G
F
A
Y
W
G
Q
G
T
L
T
V
S

>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}

DIQMTQSPPLSASLGDKVTITCQASQDINKYIAWYQQKPGKAPRQLIRYTSILVLGTPSRSGSGSRDFSISNVASEDIASYYCLQYGNLYTFGAGTKLEIK

>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}

EVKLLESGPGLVQPSQTLSTCTVSGPLTTNGVSWVRQPPGKLEWIAAISGGSPYYNSALKSRLSINRDTSKSQVFLKMNSLQTEDTAIYFCTREDGWNYFDYWGPMTMVSS

>d1f3rb2 b.1.1.1 (B:139-257) Immunoglobulin (variable domains of L and H chains) {scFv MAB198, (rat), kappa L chain}

DIKLTQSPSLLSASVGDRVTLCKGSQNINNYLAWYQQKLGEAPKLLIYNTNSLQTGIPSRSRSGSGSGTDTLSINSVETEDFGMYFCQQNSWPYTFGGTKLEKAAEQKLISEEDLN

>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}

DIVLTQSPATLSVTPGDSVSLSCRASQSISSNNLHWYQQKSHESPRLLIKYASQSISGIPSRSGSGSGTDTLSINSVETEDFGMYFCQQNSWPYTFGGGTKLEIK

>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}

EVQLQESGPSLVKPSQTLSTCSVTGDSVTSYWSWIRKFPGNKLEYMGYISYSGSTYYHPSLKSRSITRDTSKNQYQLQNSVTTEDTATYYCASWGGDVWGAGTTTVSS

>d1ejoh1 b.1.1.1 (H:2501-2619) Immunoglobulin (variable domains of L and H chains) {Anti-FMDV Fab 4C4, (mouse), kappa L chain}

QMLVESGGDLVKPGGSLKLSCAAASGFTSSYMSWVRQTPEKRLEWVATISSGGAYTYPDSVKGRFTISDDNAESTLYLQMSSLRSEDTAMYYCVRRAFDSDVGFASWGHTLVSA

>d1ejol1 b.1.1.1 (L:2001-2111) Immunoglobulin (variable domains of L and H chains) {Anti-FMDV Fab 4C4, (mouse), kappa L chain}

DIVLTQSPASLAvgLQRATISCRASESVDSYGNFMHWYQQKPGQPKLLIYRASNLESGIPARFSGSGSRTDFTLTINPVEADDVATYYCQQSNEPLTGFAGTKLEK

>d1cr9h1 b.1.1.1 (H:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-prion Fab 3F4, (mouse), kappa L chain}

KVKLQQSGAELVRSGAVKLSCTASGFNIKDYYIQWVKQRPEQGLEWIGWIDPENGNSEYAPRFQGKATMTADTLSNTAYLQLSSLTSEDTAVYYCNADLHDYWGQGTTLVSS

>d1cr9l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and H chains) {Anti-prion Fab 3F4, (mouse), kappa L chain}

DVVMTQTPLSLSVTIGQPASISCKSSQSLSDGKTYLIWVFQRPQGSPKRLIFLVSKRDSVPDRFTGSGSGTDFTLKISRVEAEDVGVYYCWQGTHFPHTVGGGTKEIA

>d1qfwh_b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin alpha subunit] Fv, kappa L chain}

QLQQSGAELVKPGASVKLSCKASDYTFTSYWMHWVKQRPGQGLEWIGEINPTNGRTYYNEKF SKATLTVAA SASTAAMQASSLTSEDSAVYYCARRYGNSFDYWGQGTTTVSS

>d1qfwl_b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin alpha subunit] Fv, kappa L chain}

DIELTQSPDSLAVSLGQRATISCRASESVDSYGNFMQWYQQKPGQPKLLIYRASNLESGIPARFSGTGSRDFTLTINPVEADDVATYYCQQSDEPYMYTFFGGTKLEIKR

>d1qfwi_b.1.1.1 (I:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin beta subunit] Fv, kappa L chain}

QVQLQESGGHLVKPGGSLKLSCAAASGFAFSSFDMSWIRQTPEKRLEWVASITNVGTYTYPGSVKGRFSISRDNRNLTNLQMSSLRSEDTALYFCARQGTAAPQPYWFDWGAGTTTVSS

>d1qfwm_b.1.1.1 (M:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin beta subunit] Fv, kappa L chain}

DIELTQSPKSMMSMSVGERVTLCKASETVDVFVSWYQQKPEQSPKLLIFGASNRFSGVPDRFTGSGSATDFTLTISSVQAEDFADYHCGQTYNHPYTFGGGTKEIKR

>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}

DIVLTQSPASLAvgQRATiSCRASKSVSTGyGYMHWNQQKPGQPPrLLiYLVSNLESGVPARFSGSGSTDFTLNIPVEEDAATYYCQHIREPLT
FGGGTKLEIK
>d3c2b1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Fab 32C2 against P450-arom, (mouse), kappa L chain}
DVQLQESGPGLVKPSQSLTCTVTGYSISSDYAWNWRQFPGNKLEWMGYISYSGSTSYPNSLKSRSiTRDTSKNQFFLQLSSVTTEDTATYYCARGY
YGSSHSPVVGAGTTVTVSS
>d1dqdh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab HGR-2 F6, (mouse), kappa L chain}
EVQLQESGPSLVKPSQTLSLTCVTGDSiTSgyWNWIRKFPGNKLEYMGYISYSGSTYYNPSLKSRLSiTRDTSRNQYYLQLKSVPEDTATYYCASPPG
YGSGPYAMDYWGQGTSVTVSS
>d1dqdl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab HGR-2 F6, (mouse), kappa L chain}
DIVLSQSPAiMSASPGEKVTiTCASsSvSYMHWFQQKPGTSPKLCiYTTSNLASGVPARFSGSGSTSylSIRMEAEDAATYYCQRSTYPPTFGS
GTKLEIK
>d1deea1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}
DIQMTQSPSSLSASVGDRVTiCRTSQSiSSYLWYQQKPGKAPKLLiYAASSLQSGVPSRFSGSGSTDFLTiSSLQPEDFATYYCQQSYSAPRTFGQ
GTKVEIK
>d1deeb1 b.1.1.1 (B:501-621) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}
QVQLVESGGVVQPGKSLRLSCAASGFTSGYGMHWVRQAPGKGLEWVALiSYDESNYYADSVKGRTiSRDNskNTLYLQMNSLRAEDTAVYYC
AKVKFYDPTAPNDYWGQGTLVTVSS
>d1qnzh_b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fv 0.5B, (mouse), kappa L chain}
QVQLQQSGAELVKPGASVKMSCKASGYTFTTPIEWiMKQNHGKSLEWIGNFHPYSDDTNyNEFKFGKAkLTVEKSSSTVYLEFSRLTSDDSAVYYCA
IHYGSAYAMDYWGQGTSVTVSS
>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}
EVQLEESGGGLVTPGGSLRLSCAASGYVFSTYDMSWVRQTPeKRLEWVAFiSSGGRTSYPDTVKGRFTiSRDDAKNTLYLQMSSLQSEDtAMYYCT
RHFYAVLDYWGRTTlTVSS
>d1f4xh1 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}
QAVVTQESALTSPGETVLTCSRSTGTVTTsNYANWVQEKPDLHLFTGLiGATNNRAAGVPVRFGSLiGGKAALTiTGaqTEDEAIYFCALWYSGHW
VFGGGTKLTVLG
>d1f11b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-Pres2 Fab F124, (mouse), kappa L chain}
EVQLQQSGPELVKPGASVKMSCKASGYTFDYYMKWVKQSHGKSLEWIGDiNPNNGGTGYNQKFKGKATLTVDKSSSTAYMQLNSLTSEDAVYYC
CANDYGSTYGFAYWGQGTLTVSA
>d1f3dh1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}
EIQLQQSGPELVKPGASVKSCASGYFIDYNIHWVKQSHGKSLEWIGYiVPYSGGTTFNQKFKGKATLTVDKSSSTAFMHLNSLTFEDEAVYYC
YDGVYWGQGTTlTVSS
>d1f3dj1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}
DVLMQTPLSLPVSLGDQVSiCRSSQSIFHSDGKTYLEWHLQKPGQSPKLLiYKVSKRFGVPDRFSGSGSTDFTLKISRVEAEiLGYYCFQGSHV
PYTFGGGTKEIK
>d1fh5h1 b.1.1.1 (H:4-120) Immunoglobulin (variable domains of L and H chains) {Fab MAK33, (human), kappa L chain}
SGGGGLVKPAGSLKLSCAASGFTSSYYMYWVFRQTPDKRLEWVATiSDGGSYTYYPDsVKGRTiSRDNakNNLYLQMSSLKSEDTAMYYCARDAM
YWGQGTLTVSA
>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}
NIVLTQSPKSMsVsVGERVTLsCKASENVDTYVFWFQQKPDQSPKLLiYGPSNRYTGVpDRFTGSGSTTDFTLTiSSVQAEDLADYHCGQSYsPyT
GGGTKEIK

>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}
QVQLQQPGTELVRPGASVILSCKASGYTFTSYWINWVKQRPGQGLEWVGNIFPSDSYTNYNQFKDKATLTVDKSSSTAYMQVNSPTSEDAVYYC
TRGARDTWFAYWGQGTLVTVSV

>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)}

QVQLLEPGTELVKPGASVKSCLCRASGYSFTSYWMHWVKQRPGQGLEWIGLIDPSNGRTNFNDKFKSRATLTVDTSSTAYMQLSSLTSEDAVYYC
RIAYWGQGTLVTVSS

>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)}

EIQLTQSPSSLSASLGERVSLCRTSQEISGYLSWLQQKPDGTIKRLIYDATKLDSGAPKRSGSRSGSDYSLTISSLESEDFA
DYYCLQYASFPRTFGGGTK
LEIK

>d1etza1 b.1.1.1 (A:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-sweetener Fab NC10.14, (mouse), lambda L chain}

FAVVTQESALTTSPGETVLTCSRSTGA
VTTSNYAIWVQEKP
DHLFSGLIGGTNNRVP
GVPARFSGSLIGD
KAALT
VTA
GQTE
DEAIYFC
ALWYSNHW
VFGGGTKLTVLG

>d1etzb1 b.1.1.1 (B:1-126) Immunoglobulin (variable domains of L and H chains) {Anti-sweetener Fab NC10.14, (mouse), lambda L chain}

QVTLKESGPGI
LQPSQ
TLSCTSF
GSFLSTSG
MGVGW
IRQPS
GEGL
EWLADI
WWNDKK
YNP
SLKS
RTVSK
DTSSN
QVFL
KITSV
DTS
DTATY
HCA
RRTFS
YYY
GSS
YYFD
NWGQ
GTT
LVSS

>d1emth1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}

QVHLQESGPEL
VRPGASV
KISCKTSG
YVFSS
WMNW
VKQR
PGQGL
KIGRI
YPNG
NTNY
NEFK
KGKAT
LTAD
KSNT
AYMQ
LSSL
TSV
DSA
VFC
ATSS
AYWG
QGQ
GTL
TVSA

>d1emtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}

DIQMT
TQ
TSS
LSAS
LGDR
VT
FSC
ASQ
DIS
NYLN
WYQQ
KPD
GT
IKL
IYT
SSL
RS
GV
PSR
FSG
SG
GT
D
Y
SLT
IN
N
LE
P
EDI
ATY
FC
CQ
QY
SRL
P
TF
GSG
TK
LE
IK

>d1f13a1 b.1.1.1 (A:2-116) Immunoglobulin (variable domains of L and H chains) {Blue fluorescent Fab 19G2, (mouse), kappa L chain}

AALLES
GGGLV
KPG
GSL
KLS
CTAS
GIT
FSRY
IM
S
W
VR
Q
IPE
KR
LE
W
VA
ISS
GG
ITY
YP
DS
V
AGR
FT
IS
RD
NV
RN
I
LY
LQM
SSL
RSE
DT
AL
YY
CARG
QGR
PY
WG
QG
TS
TV
SA

>d1f13b1 b.1.1.1 (B:2-113) Immunoglobulin (variable domains of L and H chains) {Blue fluorescent Fab 19G2, (mouse), kappa L chain}

AALTQSPV
SNP
V
T
L
G
T
S
A
S
I
C
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K
R

>d1dzba1 b.1.1.1 (A:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}

QVKLQQSG
AEL
VKPG
ASV
KLS
CTAS
GFNI
KDT
YM
HW
VK
QR
PEQ
GLE
WIG
RID
PANG
NTKY
DPK
FQG
KAT
TAD
TSS
NTAY
LQ
LSSL
TSE
D
TAV
YY
CAR
WD
WY
FD
V
W
GQ
GTT
TV
SSG

>d1dzba2 b.1.1.1 (A:201-307) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}

DIELTQSP
SSMY
T
L
G
E
R
V
T
I
T
C
K
A
S
Q
D
I
N
S
Y
L
R
W
F
Q
Q
K
P
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L
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K

>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}

QVKLQQSG
AEL
VRSG
TSV
KLS
CTAS
GFNI
KDS
SYM
HW
L
RQ
GPE
Q
GLE
WIG
WID
PENG
D
TEY
A
PK
FQG
KAT
FT
T
D
T
S
S
NTAY
LQ
LSSL
TSE
D
TAV
YY
CN
EG
TPTGP
YY
FDY
WG
QG
GTT
TV
SSG

>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}

ENVLQSPAIMASAPGEKVTITCSASSSVSYMHWFFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYLTISRMEAEDAATYYCQQRSSYPLTFGA
GTKLELK

>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}

EVQLQQSGAELARPGAVKMSCKASGYTFTSYTMHWVKQRPGQGLEWIGYINPSSGYSYNQFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYC
SRPVVRLGYNFDYWGGSTLVSS

>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}

EIVLTQSPAITAASLGQKVITCSASSSVSYMHWYQQKSGTSPKPWYEISKLASGVPARFSGSGSGTSYLTISSMEAEDAAIYYCQQWNYPFTFGSGT
KLEIK

>d1dl7h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv M3C65, (human), lambda L chain}

QVQLKESGPGLVAPSQSLITCTVSGFSLTGYGVNWVRQPPGKLEWLGMIWGDGSTDYNALKSRLNISKDKSKSQVFLRMYSLQTDDTARYYCA
RDYGPYWGQGTLTVSS

>d1dl7l_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv M3C65, (human), lambda L chain}

QAVVTQESALTSPGETVLTCSRSTGAVTTSNYANWVQEKPDLFTGLIGGTKHRTPGAPARFSGSLIGDKAALTITGAQTEDEAIYFCALWYSNHW
VFGGGTKLTVL

>d1egjh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab against cytokine receptor common beta chain domain 4, (mouse), kappa L chain}

EVQLQQSGPELVKPGTSVKMSCKASGYTFTDYYMKWVKSHGKSLEWIGDINPSNGTLYNQFKKGKATLTVDKSSSTASMQLSRLTSEDSAVYYCS
RGDGIGHGGFAYWGQGTTVTVSS

>d1egj1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab against cytokine receptor common beta chain domain 4, (mouse), kappa L chain}

NIVLTQSPASLAvgQRATISCRANESVSYGDSFMHWYQQKPGQPKLIYLASNLSAGVPARFSGSGSRDFTLTIDPVETDDAATYYCQQNNED
PWTFGGGTKLEIK

>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}

EVQLQQSGTVLARPGASVKMSCKASGYSFTSFWMHWVKQRPGQGLEWIGTIYPGNSDTSYNQFKKGAKLTAVTSASTAYMEVSSLTNEDSAVYY
CTRSGYKYYALDYWGQGTSVTVSS

>d1fe8h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

DVKLVQSGPGLVAPSQSLITCTVSGFSLTYGVSWVRQPPGKLEWLGVIWGDGNTTYHSALISRLSISKDNRSQVFLKLNLSHTDDTATYYCAGNY
YGMDYWGQGTSVTVSS

>d1fe8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

DIAMTQTSSLASLGQKVTCRASQDIGNYLNWYQQKPDGTVRLLIYTSLRHSGVPSRFSFGSGSGTDYSLTISNLESEDIATYFCQNGGTNPWTFG
GGTKLEVKA

>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}

EVKLQESGAGLVQPSQSLTCSVGTYSITSGYYWNWIRLFPGNKLEWVGYISNVGDNNYNPSLKDRLSITRDTSKNQFFLKLNSVTTEDTATYYCARS
EYYSVTGYAMDYWGQGTTVSSAWRHP

>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}

DIELTQTPVSLAASLGDRVATICRASQDINNFLNWYQQKPDGTIKLLIYYTSRLHAGVPSRFSFGSGSGTDYSLTISNLEPEDIATYFCQHHIKFPWTFGAG
TKLEIK

>d1i1a1 b.1.1.1 (A:3-121) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fab G3-519, (mouse), kappa L chain}
QLQQSGAEVLRSGASVKLSCATSDFNIDYYIHWRQRPEQGLEWIGWLDPENGDTESAPKFQGKATMTADTSSNTAYQLSSLTSEASAVYYCNAI
STTRDYYALDYWGQGTSVTVSS

>d1i1b1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fab G3-519, (mouse), kappa L chain}
DIVMSQSPSSLAVSVEKVTMSCKSSQSLYSRNQMNYLSYQQKPGQSPKLLIYWASTRESGVPDFRTGSGSGTDFTLTISSVKAEDLAVYYCQY
YHYRTFGGGTRLEIR

>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}
GVQLQESGPGLVKPSQSLTCTVGYSITSDYAWNWRQFPGNKLEWMGYITYSGSTGYNPSLKSRSITRDTSKNQFFLQLNSVTTEDTATYYCASY
DDYTWTFTYWGQGTLTVSA

>d1f8t1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-IL2 Fab LNKB-2, (mouse), kappa L chain}
DVQMTQTPLTLSVTIGQPASISCESSQSLLSNGKTYLNWLQRPGQSPKRLIYLVSKLDGVPDRFTGSGSGTDFTLRISRVEAEDLGVYYCVQGTHFP
RTFGGGTKEIK

>d1e4wh1 b.1.1.1 (H:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-TGFalpha Fab TAB2, (mouse), kappa L chain}
QVQLQQPGAEVKGASVKLSCASGFTFTNYWMHWVKQRPGQGLEWIGEILPSNGRTNYNEKFKTATLTVDKSSNTAYMQLSSLTSEDSA VYYC
ARSPSDYWGQGTTLVSS

>d1e4wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-TGFalpha Fab TAB2, (mouse), kappa L chain}
DIQMTQTPSSLSASLGDRVTSRASQDISHYLNWFQQKPDGTVKLIIYTSTLHSGVPSRFSGS GSGTDYSLTISNLEEDIAFYFCQQGGALPFTFGS
GTKLAIK

>d1h8na1 b.1.1.1 (A:3-109) Immunoglobulin (variable domains of L and H chains) {Anti-ampicillin scFv, (mouse), kappa L chain}
KDIVLTQSHKFMSTSVGDRVSI TCKASQDVGTAVA WYQQKPGQSPKLLIYWASTRHTGVPDFRTGSGSGTDFTLTISNVQSED LADYFCQQYSSYPLT
FGAGTKLEI

>d1h8na2 b.1.1.1 (A:132-243) Immunoglobulin (variable domains of L and H chains) {Anti-ampicillin scFv, (mouse), kappa L chain}
QVQLQESGGEVLRPGASVKLSCASGYTFTSYWINWVKQRPGQGLEWIGNIYPSDSYTNQKFKD KATLTVDKSSSTAYMQLSSLTSEDSA VYFCA
RWGYWGQGTLTVSA

>d1i7za1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab GNC92H2, (mouse/human chimera), kappa L chain}
DLVLTQSPASLA VSLGQRATISCRASKSVTSGYNMHWYQQKPGQPPKLLIYL ASNLASGVPARFSGSGSGTDFTLNIHPVEEEDAATYYCLYSREFPP
WTFGGGTKEIK

>d1i7zb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab GNC92H2, (mouse/human chimera), kappa L chain}
QVQLQQSGPELKPGETVKISCKTSGSFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTYADDFRGRFAFSLATSASTAYLQIINLKNDTATYFCE
TYDSPLGDYWGQGTTTVSS

>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}
IALTQSPGTLSPGERATLSCRASQSFSSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYCQKYGTSAITFGQGT
RLEIK

>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}
QVQLVQSGAEVKKPGASVKVSCKVSGYLTLEPVHWVRQAPGKGLEWVGSDPESGESIYAREFQGSVTMTADTSTNIAYMELSSLRSDDTAVYYCA
VPDPDAFDIWGQGTMVTVSS

>d1fn4a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 198 against acetylcholine receptor, (rat)}
DIKLTQSPSLLSASVGDRVTLSCKG SQNINNYLAWYQQKLGEAPKLLIYNTNSLQ TGIPS RFS GSGSGTDYTLTISLQPEDVATYFCYQYNNNGYTFGAG
TKLELKR

>d1fn4b1 b.1.1.1 (B:1-106) Immunoglobulin (variable domains of L and H chains) {Fab 198 against acetylcholine receptor, (rat)}

QVQLLESGPGLVRPSETLSLTCTVSGFSLTSFSVSVRHPGKGPEWMGRMWYDGYTAYNSALKSRLSISRDTSKNQVFLKMNSLQTDDTGYYCTR
DLYGGYPLGFYWYDFWGP

>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}

QIQLVQSGPELKPGETVRISCKASDYSFMTSGMQWVQQMPGKGLKWIGWLNTQSGVPEYAEDFKGRFAFSLSTSATTAYLQINNLKNEDTATYFC
ATWGGNSAYWGQGTTLVSS

>d1jp5a1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and H chains) {scFv 1695, (mouse), kappa L chain}

DILMTQTPLYPVSLGDQASISCRSSQTIVHNNNGNTYLEWYLQKPGQSPQLIYKVSNRFGVPDRFSGSGSGTDFTLKRVEAEDLGYYCFQGSHP
PTFGGGTKLEIK

>d1jp5a2 b.1.1.1 (A:128-247) Immunoglobulin (variable domains of L and H chains) {scFv 1695, (mouse), kappa L chain}

EVQLQQSGPELKPGETVKISCKATNYAFDTDYSMHWVKQAPGGDLKYVGWINTETDEPTFADDFKGRFAFSLDTSTAFLQINNLKNEDTATYFC
RDRHDYGEIFTYWGQGTTVTSS

>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}

QVQLVESGGGLVQPGGSLRLCATSGFTFTDYYMSWVRQPPGKALEWLGFIRNKANGYTTEYSASVKGRFTISRDNSQSILYLMNTLRAEDSATYY
CARDGSYAMDYWGQGTTVTSS

>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}

QVQLQQPGAEVVKPGASVKLSCKASGYFTSDWIHWVKQRPGHGLEWIGEIIPSYGRANYNEKIQKKATLTADKSSTAFMQLSSLSEDASAVYYCAR
ERGDGYFAVVGAGTTVTSS

>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}

DILLTQSPAILSVPGERVSFSCRASQSIGTDIHWWYQQRTNGSPRLLIKYASESISGIPSRFGSGSGTDFTLSINSVEDIANYYCQOSNRWPFTFGSGT
KLEIK

>d1jguh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

EVKLVESRGGLVKPGGSQLSCAASGFTSGYAMSWFRLPEKRLEWVASIYNGFRIHYLDVKGRFTISSDYARNILYLMSTLRSEDTAMYCSRGD
AYSRYFDVVGAGTTVTSA

>d1jgul1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

EVVMTQSPSLPVSLGDQASISCRSSQLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFGVPDRFSGSGSGTDFTLKRVEAEDLGVYFCQSHTV
PPLTFGAGTKLELK

>d1i8ma1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Anti ssDNA Fab, (mouse), kappa L chain}

ELQMTQSPASLSASVGETVTITCRASENIYSLAWYQQKQGKSPQLVNAKTLAEGVPSRFGSGSGTQFSLKINSLQPEDFGSYCCQHHYGTPLTFG
AGTKLELK

>d1i8mb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Anti ssDNA Fab, (mouse), kappa L chain}

QVKLLESGPVELVKPGASVKMSCKASGYFTSYVMHWVKQKPGQGLEWIGYINPYNDGTYNEKFKGKATLTSKSSSTAYMELSSLSEDASAVYYCV
RGGYRPYYAMDYWGQGTTVTSS

>d1jv5b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Anti-blood group A Fv, (human), kappa L chain}

QVQLQQPGAEVVKPGTSVKLSCKASGYNFTSYWINWVKLRPGQGLEWIGDIYPGSGITNYNEKFKGKATLTVDTSSSTAYMQLSSLSEDASALYYCAG
QYGNLWFAYWGQGTLVTVS

>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}

QVQLQQPGAEVVKPGASVKLSCKASGYFTSYWMQWVKQRPGQGLEWIGEIDPSDSYTNQNQFKKGKATLTVDTSSSTAYMQLSSLSEDASAVYYC
ARNRDYSNNWYFDVVGAGTTVTSS

>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}

DIVLTQSPASLAVSLGQRATISCKASQSVYDGDSYMNVQQKPGQPPKLIYAASNLESGIPARFSGSGSGTDFTLNIHPVEEDAATYYCQQSNEDPRTFGGGTKLEIK

>d1jnha1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 10G6D6, (mouse), lambda L chain}

QAVVTQESALTTSPGETVLTCSRSSGAITTSHYANWIQEKPDLFTGLISGTNNRAPGVPARFSGSLIGDKAALTITGAQTEDEAIYICALWFSNQFIFSGTKVTV

>d1jnhb1 b.1.1.1 (B:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 10G6D6, (mouse), lambda L chain}

EVQLQQSGAELARPGASVKLCRTSGYSFTTYWMQWVRQRPQGLEWIAAIYPGDDDARYTQFKKGATLTADRSSIVYLQLNSLTSEDSAVYSCS
RGRSLYYTMDYWQGQGTSVT

>d1jnlh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}

EVQLQQSGAELVKPGASVRLCSASGFNIKDTYMFVVKQRPEQGLDWIGRINPANGISKYDPRFQGKATLTADTSSNTAYLQLDNLTSEDTAVYYCAI
EKDLPWGQGTLVTVS

>d1jnl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}

QIVMTQTPASLSASVGETVTITCRASGNIYNLYAWYQQKQGKSPQLLVNAKTLVDGVPLRFSGSGSGTQYSLKINSQPEDFGNYCHFWNTPYT
FGGGTKLEIK

>d1vhp__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {VH-P8 domain (human), camelized monomer}

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKEREIVSAVSGGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCA
RLKKYAFDYWGQGTLVTVSS

>d1jtpa_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-lysozyme antibody}

DVQLQASGGGSVQAGGSLRLSCAASGYTIGPYCMGWFRQAPGKEREVGVAAINMGGGITYYADSVKGRFTISQDNAKNTVYLLMNSLEPEDTAIYY
CAADSTIYASYYECGHGLSTGGYGYDSWQGQTQVTVSSRR

>d1bzqk_b.1.1.1 (K:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-RNase A antibody}

QVQLVESGGGLVQAGGSLRLSCAASGYAYTYIYMGWFRQAPGKEREVGVAAMDSGGGTLYADSVKGRFTISRDKGKNTVYLQMDSLKPEDTATYY
CAAGGYELDRDRTYGQWQGQTQVTVSSRR

>d1f2xk_b.1.1.1 (K:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), antibody cab-ca05}

QVQLVESGGGSVQAGGSLRLSCAASGYTVSTYCMGWFRQAPGKEREVGATILGGSTYYGDSVKGRFTISQDNAKNTVYLQMNSLKPEDTAIYYCAG
STVASTGWCRLRPYDYHYRGQGTQVTVSS

>d1hcv__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), anti-gonadotropin alpha subunit
VH domain}

VQLQESGGGLVQAGGSLRLSCAASGRTGSTYDMGWFRQAPGKERESVAAINWDSARTYYASSVRGFTISRDNAKKTQVYLQMNSLKPEDTAVYTC
GAGEGGTWDSWGQGTQVTVSS

>d1qd0a_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), anti-RR6 VH domain}

QVQLQESGGGLVQAGGSLRLSCAASGRAASGHGHYGMGWFRQVPGKEREFVAAIRWSGKETWYKDSVKGRFTISRDNAKTTVYLQMNSLKGED
TAVYYCAARPVRVADISLPGFDYWGQGTQVTVSS

>d1i3ua_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), the dye RR1-binding VH domain}

VQLQESGGGLVQAGDSLKLSCAESGDSIGTYVIGWFRQAPGKERIYLATIGRNLVGPSDFYTRYADSVKGRFAVS RDNAKNTVNLQMNSLKPEDTAV
YYCAAKTTWGGNDPNWNYWGQGTQVTV

>d1vla_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {VL domain (kappa) of antibody M29B, dimer synthetic}

DIELTQSPATLSVTPGNSVISCRASQSIGNRLFWYQQKSHESPRLLIKYASQSISGIPSRSFSGSGSGTDFTLSINSVETEDLAVYFCQQVSEWPFTFGGG
TKLEIK

>d1bwwa_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) dimer REI (human)}

TPDIQMTQSPSSLASVGDRVITCQASQDIKYLNWYQQKPGKAPKLLIYEASNQAGVPSRSGSGSTDFTFTISSLQPEDIATYYCQQYQSLPYTF
GQGTKLQIT

>d2rhe__b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda) dimer RHE (human)}

ESVLTQPPSASGTPGQRVTISCTGSATDIGSNSVIWYQQVPGKAPKLLIYNDLPSGVSDRFSASKSGTSASLAISGLESEDEADYYCAAWNDSLDEP
FGGGTGTKLTVLGQPK

>d1bjma1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and H chains) {Bence-Jones lambda L chain dimer LOC (human)}

ESVLTQPPSASGTPGQRVTISCGSSSNIGENSVTWYQHLSGTAPKLLIYEDNSRASGVSDRFSASKSGTSASLAISGLQPEDETDDYYCAAWDDSLVA
VFGTGTKTVLG

>d1wtla_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) dimer WAT (human)}

DIQMTQSPSSLASVGDRVITCQASQDISYLIWYQQQLKGAPNLLIYDASTLETGVPSRSGSGSTDFTFTISSLQPEDIATYYCQQYDTLPLTFG
GGTKVDIKR

>d1b0wa_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) dimer BRE (human)}

DIQMTQSPSSLASVGDRVITCQASQDISYLIWYQQQLKGAPNLLIYDASTLETGVPSRSGSGSTDFTFTISSLQPEDIATYYCQQYDDLPYTFGQ
GTKVEIKR

>d1eeqa_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa) domain LEN (human)}

DIVLTQSPDSLAVSLGERATINCKSSQSVDSSNSKNYLAWYQQKPGQPPKLLIYWASTRESGVPDFSGSGSTDFTLTISLQAEDVAVYYCQQYYS
HPYSFGQQGTKLEIK

>d1lila1 b.1.1.1 (A:2-107) Immunoglobulin (variable domains of L and H chains) {Bence-Jones lambda L chain dimer CLE (human)}

YEVTQPPSLSVSPGQTARITCSGEKLGDAYVCWYQQRPGQSPVVVIYQDNRRPSGIPERFSGSSSGNTATLTISGTQTLDEADYYCQVWDSNASV
FGGGTGTKLTVLG

>d1cd0a_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda) dimer JTO (human)}

NFMLNQPHVSSESPGKTVTISCTRSGNIDSNYVQWYQQRPGSAPITVIYEDNQRPSGPDRFAGSIDRSSNSASLTISGLKTEDEADYYCQSYDARN
VVFGGGTRLTVELG

>d2cd0a_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda) dimer WIL (human)}

NFLLTQPHSVSESPGKTVTISCTRSGSIANNVHWYQQRPGSSPTTIVFEDDHHRPSGVPDFSGSVDTSSNSASLTISGLKTEDEADYYCQSYDHNN
QVFGGGTGTKLTVLG

>d1b6da1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Bence-Jones kappa L chain DEL (human)}

DIQMTQSPSSLASVGDRVITCQASQDISSYLNWYQQKPGKAPKLLIHAASSLETGVPSRSGSGSTDFTFTISSLQPEDIATYYCQQYDSPLTFGG
GTKVEIK

>d1ek3a_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Kappa-4 VL REC (human)}

DIVMTQSPDSLAVSPGERATINCKSSQNLDSSFTNTLAWYQQKPGQPPKLLIYWASSRESGVPDFSGSGSTDFTLTISLQAEDVAVYYCQQY
STPPTFGGGTGTKVEIKR

>d1mcoh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Intact antibody (lambda) MCG (human)}

PLVLQESGPGLVKPSEALSITCTVSGDSINTILYYWSWIRQPPGKGLEWIGYIYSGSTYGNPSLKSRTVISVNTSKNQFYSKLSSVTAADTAVYYCARVPL
VVNPWGQGTLTVSS

>d1dcla1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and H chains) {Lambda L chain dimer MCG (human)}

PSALTQPPSASGSLGQSVTISCTGTSSNVGGYNVSWYQQHAGKAPKVIYEVNKRPSGVPDFSGSKSGNTASLTVSGLQAEDEADYYCSSYEGSDN
FVFGTGTKTVLG

>d1mcww1 b.1.1.1 (W:1-111) Immunoglobulin (variable domains of L and H chains) {Heterologous L chain dimer MCG-WEIR hybrid (human)}

ESALTQPSVSGSPGQSQITVSCAGHTSDVADSNSISWFQQHPDKAPKLLIYAVTFRPSGIPLRFSGSKSGNTASLTISGLLPDEADYFCMSYLSDASFV
GSGTGTKTVLR

>d1ac6a_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
DSVTQTEGVQVALSEEDFLTIHCNYSASGPALFWYVQYPGEQPQLFRASRDKEKGSSRGFEATYNKEATSFLQKASVQESDAVYYCALSGNNKL
TGFAGTKLTIKP

>d1b88a_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
MQQVRQSPQSLSLTVWEGETILNCSYENSAFDYFPWYQQFPGEGPALLISLSVNKKEDGRFTIFFNKREKKLSLHIADSQPGDSATYFCAASASFGD
NSKLIWGLGTSLVNP

>d1d9ka_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
QVRQSPQSLSLTVWEGETILNCSYEDSTFDYFPWYRQFPKGSPALLIAISLVSNNKKEDGRFTIFFNKREKKLSLHITDSQPGDSATYFCAATGSFNKLTFGA
GTRLA VSPY

>d1fo0a_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
KVTQTQTSISVMEKTTVTMDCVYETQDSSYFLFWYKQTASGEIVFLIRQDSYKKENATVGHSLNFQPKSSIGLIITATQIEDSAVYFCAMRGDYGG
GNKLIFGTGTLLSVKP

>d1h5ba_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
GDQVEQSPSALS LHEGTD SALRCNFTT MRSVQWFRQNSRGS LISLFY LASGT KENGRL KSAFD SERARY STL HIRDA QLED SGTY FCAA EASS GS
WLIFGSGTQLTVMPVT

>d1i9ea_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
QSVTQPDAR VTSEGASLQLRCKYSATPYLFWYVQYPRQGLQLLKYS G D P V V Q G V N G F E A E F S K S N S F H L R K A S V H W S D S A V Y F C A V S G F A S
ALT FGSGT KVIVLPYIQN

>d1kb5a_b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
QQVRQSPQSLSLTVWEGETILNCSYEDSTFNYFPWYQQFPGEGPALLISRSVSDKKEDGRFTIFFNKREKKLSLHITDSQPGDSATYFCAARYQGGRA
IFGTGTTSVSPGSAD

>d1nfda1_b.1.1.1 (A:1-117) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}
DSVTQTEGLVTVTEGLPVKLNCYQTTYLIAFFWYVQYLNEAPQVLLKSTDNKRT EH QGF HATLHKSSSFHLQKSSAQLSDS ALY CALSEG G NYK
YVFGAGTRLK VIAH

>d1bd2d1_b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}
QQVKQNNSPLSVQEGRISILNCDYTNMSMDYFLWYKKYPAEGPTFLISISSIKDKNADGRFTVFLNKSAKHLSLHIVPSQPGDSAVYFCAAMEGAQKL
FGQGTRLTINPN

>d1fytd1_b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}
QSVTQLGSHVSSEGALVLLRCNYSSVPPYLFWYVQYPNQGLQLLK YTSAATLVKGINGF EAEFKSETSFHLTKPSAHMS DAAEYFCAVSESPFGN
EKLTFGTGTRLTIPN

>d1qrnd1_b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}
KEVEQNNSGPLSVP EGAI ASLNCTYSDRGQSFFWYRQYSGK SPELIMSIYNGDKEDGRFTAQLNKASQYV SLLIRDSQPSD SATYLC AVTTDSWGKL
QFGAGTQVVTPD

>d1bec_1_b.1.1.1 (3-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
AVTQSPRNKVAVTGGKVTLSCQQTNNHNNMYWYRQDTGHGLRLIHSY GAGSTEKG DIPDG YKASRPSQEQFSLILELATPSQTSVYFCASGGGR
SYAEQFFGPGTRLT VLE

>d1fo0b_b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
VTLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLSPGDKEVSLPGADYLATRVTDT ELRLQVANMSQGRTLYCTCS
ADR VGNT LYFGE GSRLIV

>d1kb5b_b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
VTLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTLSPGDKEVSLPGADYLATRVTDT ELRLQVANMSQGRTLYCTCS
AAPDWGASAETLYFGSGTRLT VLE

>d1nfdb1_b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
DSGVVQSPRHIIKEKGGRS VLTCIPI SGHSNVVWYQQTLGKELKFLI QHYEKVERDKGFLPSRFSVQFDDYHSEMNNMSALELEDSAMYFCASSLRW

GDEQYFGPGTRLTVLE

>d1tcrb1 b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

EEAVTQSPRNKVAVTGGKVTLSNCNTNNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDIKPDKYKASRPSQENFSLILELATPSQTSVYFCASGGG
GTLFGAGTRLSVLE

>d1bd2e1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}

GVTQTPKFQVLTKGSMTLQCAQDMNHEYMSWYRQDPGMGLRLIHYSVGAGITDQGEVPNGYNVRSTTEDFPLRLSAAPSQTSVYFCASSYP
GGGFYEQYFGPGTRLTVTE

>d1fyte1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}

KVTQSSRYLVKRTGEKVFLCVQDMDHENMFWYRQDPGLGLRLIYFSYDVKMKKEKGDIPEGYSVSREKKERFSLILESASTNQTSMYLCASSSTGLPY
GYTFGSGTRLTVVE

>d1hxma1 b.1.1.1 (A:1-120) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}

AIELVPEHQTVPVSIGVPATLRCMKGAEIGNYYINWYRKTQGNTMTFIYREKDIYGPGBKDNFQGDIDIAKNLAVLKILAPSERDEGSYYCACDTLGM
GGEYTDKLIFGKGTRVTVEPR

>d1hxmb1 b.1.1.1 (B:1-123) T-cell antigen receptor {Human (Homo sapiens), delta-chain}

AGHLEQPQISSTKTSKARLECVVSGITISATSVVWYRERPGEVIQFLVISYDGTVRKESGIPSGKFEVDRIPETSTSTLIHNVEKQDIATYYCALWEAQ
QELGKKIKVFGPGTKLIIID

>d1tvda_b.1.1.1 (A:) T-cell antigen receptor {Human (Homo sapiens), delta-chain}

DKVTQSSPDQTAVSGSEVVLLCTYDTVSNPDLFWYRIRPDYSFQFVFYGGDSRSEGADFTQGRFSVKHILTQKAFHLISPVRTEDSATYYCAFTLPPP
TDKLIFGKGTRVTVEP

>d1ah1__ b.1.1.1 (-) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}

AMHVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLQRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVEL
MYPPYYLGIGNGTQIYVIDPEPCPDSDQEKP

>d18lc_b.1.1.1 (C:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}

MHVVAQPAVVLASSRGIASFVCEYASPGKATEVRVTVLQRQADSQVTEVCAATYMMGNELTFLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVEL
MYPPYYLGIGNGAQIYVIDPE

>d1dqta_b.1.1.1 (A:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Mouse (Mus musculus)}

IQVTQPSVVLASSHGVASFPCYSPSHNTDEVRTVLRQTNQMTVCATTTEKNTVGFLDYPFCSGTFNESRVNLTIQGLRAVDTGLYCKVELMY
PPPFVGMGNQIYVIDPE

>d3frua1 b.1.1.2 (A:179-269) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}

KEPPSMRLKARPGNGSSVLTCAAFSFYPPPELKFRLNRGLASGSGNCSTGPNGDSFHAWSLLEVKGDEHHYQCQVEHEGLAQPLTVSDL

>d3frub1 b.1.1.2 (B:) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}

IQKTPQIQVYSRHPPEENGPNFLNCYVSQFHPPQIEIELLKNGKKIPNIEMSDLSFSKDWSFYLAHTEFTPTETDVYACRVKHVTKEPKTVTWDRD

M

>d1bmg__ b.1.1.2 (-) Class I MHC, beta2-microglobulin and alpha-3 domain {Cow (Bos taurus)}

IQRPPKIQVYSRHPPEDGKPNYLNCYVYGFHPPQIEIDLKNGEKIKSEQSDLSFSKDWSFYLLSHAFTPNSKDQYSCRVKHVTLEQPRIVKWDRLD

>d1i4fa1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-A2.1}

TDAPKTHMTHHAVSDHEATLRCWALSFPYPAEITLTWQRDGEDQTQDTELVERPAGDGTQKWAADVPSGQEQRYTCHVQHEGLPKPLTRWE

>d1i4fb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-A2.1}

MIQRTPKIQVYSRHPAENGKSNFLNCYSGFHPSDIEVDLLKNGERIEKVEHSDLFSKDWSFYLLYYTEFTPTEKDEYACRVNHVTLSQPKIVKWDRD

M

>d1agda1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-B0801}

ADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVERPAGDRTFQKWAADVPSGEEQRYTCHVQHEGLPKPLTRWEP

>d1qqda1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-CW4}

AEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVERPAGDGTQKWAADVPSGEEQRYTCHVQHEGLPEPLTRW

>d1mhea1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-E}
LEPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQQDGEHTQDTELVERPAGDGTQKWAAVVPSGEEQRYTCHVQHEGLPEPVTLRW
>d1de4a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), hemochromatosis protein Hfe}
QQVPPLVKVTHVHTSSVTLRCRALNYPQNIITMKWLKDQPMDAKEFEPKDVLPNGDGTYQGWITLAVPPGEEQRYTQVEHPGLDQLIIVW
>d1fzka1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2KB}
TDSPKAHVTHHSRPEDKVTLCWALGFYPADITLTWQLNGEELIQDMELVERPAGDGTQKWASVVVPLGKEQYYTCHVYHQGLPEPLTLRW
>d1fzkb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2KB}
IQKTPQIQVYSRHPHENPKPNILNCYVTQFHPPHIEIQLMLNGKKIPKVEMSDMSFSKDWFSYILAHTEFPTETDTYACRVKHDSMAEPKTVWDR
DM
>d1jpfa1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2DB}
TDSPKAHVTHHPRSKGEVTLRCWALGFYPADITLTWQLNGEELTQDMELVERPAGDGTQKWASVVVPLGKEQNYTCRVYHEGLPEPLTLRWEP
>d1mhca1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2M3}
ADPPKAHVHHPRPKGDVTLRCWALGFYPADITLTWQKDEEDLTQDMELVERPAGDGTQKWAAVVPSGEEQRYTQVHHEGLTEPLALKWRS
>d1qo3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2DD}
TDPPKAHVTHHRRPEGDVTLCWALGFYPADITLTWQLNGEELTQDMELVERPAGDGTQKWASVVVPLGKEQNYTCRVHHEGLPEPLTLRWG
>d1k8da1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), IB QA-2}
TDPPKAHVTHHPRSYGAVTLCWALGFYPADITLTWQLNGEELTQDMELVERPAGDGTQKWASVVVPLGKEQNYTCRVHHEGLPEPLTLRW
>d1ed3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Rat (Rattus norvegicus), RT1-AA}
SDPPEAHVTLHPRPEGDVTLCWALGFYPADITLTWQLNGEELTQDMELVERPAGDGTQKWASVVVPLGKEQNYTCRVEHEGLPKPLSQRWE
>d1zaga1 b.1.1.2 (A:184-277) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}
QDPSSVVTSHQAPGEKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGDLHNGNGTYQSWWAVPPQDTAPYSCHVQHSSLAQPLVWPWEA
>d1hyrc1 b.1.1.2 (C:181-274) MHC I homolog {Human (Homo sapiens), Mic-a}
TVPPMVNVTRSEASEGNITVTCRASGFYPWNITLSWRQDGVLHDTQQWGDVLPDGNGTYQTWWATRICQGEEQRFTCYMEHSGNHSTHPVP
S
>d1c16a1 b.1.1.2 (A:181-276) MHC I homolog {Mouse (Mus musculus), t22}
RSDPPKAHVTRHPRPEGDVTLCWALGFYPADITLTWQLNGEELTQDMELVERPAGDGTQKWAAVVVPLGKEQSYTCHVYHEGLPEPLILRWG
G
>d1exua1 b.1.1.2 (A:177-267) MHC-related Fc receptor {Human (Homo sapiens)}
KEPPSMRLKARPSSPGFSLTCSAFSFYPPELQLRFLRNLAAAGTGQGDFGPNSDGSFHASSSLTVKSGDEHHYCCIVQHAGLAQPLRVEL
>d1igtb3 b.1.1.2 (B:236-361) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}
PCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQTTQHREDYNSTLRVSALPIQHQDWMSGKEF
KCKVNNNKDLPAPIERTISKPKG
>d1igtb4 b.1.1.2 (B:363-474) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}
SVRAPQVYLVPPPEEMTKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCVVHEGLHNH
HTTKSFSR
>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}
GCKPCICTVPEVSSVFIFPPKPKDTLLITVTPKTCVVVDISKDDPEVQFSWFVDNVEVHTAQTPREEQFNSTFRVVSALPIMHQDWLNGKEFKCRV
NSAAFPAPIEKTIKKG
>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}

KPRAPQVYTI PPPKEQMAKDKVSLTCMITDFFPEDITVEWQSDGQAPENYKNTQPIMTDGSYFVYSKLNVQKSNW EAGNTFTCSV LHEGLHNHH
TEKSLSH

>d1hzhh3 b.1.1.2 (H:236-359) Immunoglobulin (constant domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}

HTHCPPCPAPELLGGPSVFLFPKPKD TL MISRTPEVTCV VDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKE
YKCKVSNKALPAPIEKTISKA

>d8faba2 b.1.1.2 (A:106-208) Immunoglobulin (constant domains of L and H chains) {Fab HIL (human), lambda L chain}

LGQPKAAPS VTLFPPSSEELQANKATLV CLISDFYPGAVTV AWKADSSPIKAGVETT PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEK
TVAP

>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}

GSASAPTLFPLVSCENS P S D T S S V A V G C L A Q D F L P D S I T F S W K Y K N N S D I S S T R G F P S V L R G G K Y A A T S Q V L L P S K D V M A G T D E H V V C K V Q H P N G N K
EKNVPLPV

>d2fb4l2 b.1.1.2 (L:110-214) Immunoglobulin (constant domains of L and H chains) {Fab KOL (human), lambda L chain}

QPKANPTVTLFPPSSEELQANKATLV CLISDFYPGAVTV AWKADGSPV KAGVETT PSKQSNNKYAASSYLSLTPEQWKSHRSYSCQVTHEGSTVEKT
VAPTECS

>d2ig2h2 b.1.1.2 (H:120-231) Immunoglobulin (constant domains of L and H chains) {Fab KOL (human), lambda L chain}

STKGPSVF LAPSSKSTSG GTAALGCLVKDYFPQPVTWSN GALTSGVHTFP AVLQSS GLYLS SSVV TVPSS SLGTQTYICNVN HKPSNTKV DKR VEP
KSCDKTHTCPCP

>d2fbjh2 b.1.1.2 (H:119-220) Immunoglobulin (constant domains of L and H chains) {Fab J539 (mouse), kappa L chain}

ESARNPTIYPLTLPALSSDPVIIGCLIHDYF PSGTMNVTWGKSGKDITTVNFPPALASGGRTMSNQLTPAVECPEGESVKCSVQHDSNPVQELDV
NCSG

>d1mfb1b b.1.1.2 (L:112-212) Immunoglobulin (constant domains of L and H chains) {Fab SE155-4 (mouse), lambda L chain}

PKSSPSVTLFPPSSEELETNKATLV CTIDFYPGVVT DWKVDGTPV TQGMETT QPSKQSNNKYMASSYLT LTARAWERHSSY SCQVTHEGHTVEKSL
SRA

>d1teth2 b.1.1.2 (H:113-213) Immunoglobulin (constant domains of L and H chains) {Fab TE33 (mouse), kappa L chain}

SAKTPPSVYPLAPGSMVTLGCLVKGYFPEPVTVWN SGS LSSGVHTFP AVLQSDLYT LSSV TVPSS PRPSETVTCNVAHPAS STKVDKKIVPR

>d2jelh2 b.1.1.2 (H:114-226) Immunoglobulin (constant domains of L and H chains) {Fab JE142 (mouse), kappa L chain}

AATT PPSVYPLAPGSGGQGN SMVTLGCLVKGYFPEPVTVWN SGS LSSGVHTFP AVLAADLYT LSSV TVPSS PRPSETVTCNVAHPAS STKVDKKIA
PG

>d2jell2 b.1.1.2 (L:109-212) Immunoglobulin (constant domains of L and H chains) {Fab JE142 (mouse), kappa L chain}

ADAAPTVSIFPPSSEQ LSGGASVCF LNNF YPKD INVKW KIGDGA RQNGV LNSW TDQDSK DSYMSSTL T KDEYERHNSYTCEATHKT SDSPIV
KSFNRN

>d1eapb2 b.1.1.2 (B:125-221) Immunoglobulin (constant domains of L and H chains) {Fab 17E8 (mouse), kappa L chain}

AKTT PPSVYPLAPGC GDTGSSV TLGCLVKGYFPEPVTVWN SGG LSSV HTP ALLQSG LYTMSSV TVPGGGWPSATVTCVAHPAS STTV DKKL

>d1yuhb2 b.1.1.2 (B:119-218) Immunoglobulin (constant domains of L and H chains) {Fab anti-nitrophenol (mouse/human), lambda L chain}

AATT PPSVYPLAPGSA AQTN SMVTLGCLVKGYFPEPVTVWN SGS LSSGVHTFP AVLQSDLYT LSSV TVPASTWPSGTVTCNVAHPAS STAVDKKIV
PR

>d1clzh2 b.1.1.2 (H:115-231) Immunoglobulin (constant domains of L and H chains) {Fab MBR96 (mouse), kappa L chain}

TTTAPS VYPLVPGCSDTGS S VTLGCLVKGYFPEPVTVKWN YGALSSG VRTVSSVLQSGFYSLSSLV TVPSSTWPSQTVICNV AHPASKTEL KRIE PR

>d1nl dh2 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}

SASTTAPS VYPLAPVSGD QTNT S VTLGCLVKGYFPEPVTLWNSG S LSSGVHTFP AVLQSDLYT LSSV TVTSS WPSETITCNVAHPAS STKVDKKIEP

RGC

>d1kelh2 b.1.1.2 (H:116-218) Immunoglobulin (constant domains of L and H chains) {Fab 28B4 (mouse), kappa L chain}
TVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVPSSPRPSETTCNVAHPASSTKVDK
KIVP
>d1osph2 b.1.1.2 (H:121-218) Immunoglobulin (constant domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}
AKTTPPSVYPLAPGCGDTGSSVTLGCLVKGYFPESVTVWNSGSLSSVHTFPALLQSGLYTMSSSVTVPSSWPSQTVTCVAHPASSTTVDKLE
>d1nfde2 b.1.1.2 (E:108-215) Immunoglobulin (constant domains of L and H chains) {Fab H57 (hamster), lambda L chain}
GPKSPKVTVFPPSPEELRTNKATLVCLVNDFYPGSATVWKANGATINDGVKTTKPSKQGQNYMTSSYLSLTADQWKSHNRVSCQVTHEGETVEKS
LSPAECI
>d1nfdf2 b.1.1.2 (F:115-228) Immunoglobulin (constant domains of L and H chains) {Fab H57 (hamster), lambda L chain}
TTTAPSVDLAPACDSTTSTTDVTLGCLVKGYFPEPVTVWNSGALTSVGHTFPSVLHSGLYLSSSVTVPSTWPQKQITCNVAHPASSTKVDKKIEP
R
>d1aqkl2 b.1.1.2 (L:112-216) Immunoglobulin (constant domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}
QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVNAGVETTKPSKQSNNKYAASSYLSLTPEQWKSHKSQCVTHEGSTVEKT
VAPAECI
>d1a4kh2 b.1.1.2 (H:120-211) Immunoglobulin (constant domains of L and H chains) {Diels alder catalytic Fab (mouse), kappa L chain}
SVF LAPSSKTSGGTAALGCLVKDYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVPSSSLGTQTYICNVNHKPSNTKVDKKV
>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}
SVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVPSSPRPSETTCNVAHPASSTKVDKKIVPR
>d2hmc2 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}
RADAAPTVSIFPPSSEQTSGGASVVCFLNNFYPKDINVWAIDGSAANGVLNSWTQDSKDSTYSMSSTLTADYEANSYCAATHKTSTSPI
VKSFNANEC
>d1a5fh2 b.1.1.2 (H:121-217) Immunoglobulin (constant domains of L and H chains) {Anti-E-selectin Fab (mouse), kappa L chain}
AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVPSTETTCNVAHPASSTKVDKKIVPR
>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}
RANAAPTVSIFPPSTEQLATGGASVVCLMNKFYPRDISVKWKIDGTERNGVLNSVTDDQDSADSTYSMSSTLSLKADYQSHNLYTCQVVHKTSSPV
VAKNFNRNEC
>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}
AKTTAPSVDLAPVCGGTTGSSVTLGCLVKGYFPEPVTLWNSGSLSSGVHTFPALLQSGLYTLSSSVPSTSNTWPSQITCNVAHPASSTKVDKKIEPR
V
>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}
LTVSSAETTTPSVYPLAPGTAALKSSMVTLGCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVPSSWPSQTVTCNVAHPASSTKVD
KKIVPRNCGGDC
>d1sm3h2 b.1.1.2 (H:114-213) Immunoglobulin (constant domains of L and H chains) {Tumor-specific Fab SM3, (mouse), lambda L chain}
AKTTPPPTVYPLAPGSNAASQSMVTLGCLVKGYFPEPVTVWNSGSLASGVHTFPAVLQSDLYTLSSSVPSSWPSQETTCNVAHPASSTKVDKIV
PR
>d1c12b2 b.1.1.2 (B:414-513) Immunoglobulin (constant domains of L and H chains) {Fab directed against the musk odorant}

traseolide, (mouse), kappa L chain}

ASTKGPSVYPLAPGSKAAASMVTLGCLVKGYFPEPVTVWNSGSLSSGVHTFPVLQSDLYTLSSSVTVPSSPRPSETTCNVAPHASSTKVDKKIVPE

>d1r24b2 b.1.1.2 (B:123-217) Immunoglobulin (constant domains of L and H chains) {Fab R24, (mouse), kappa L chain}

ATTTAPSVDPLVPGCSDTSGSSVTLGCLVKGYFPGPVTWKWNYGALSSGVRTVSSVLQSGFYSLSLTVPSSTWPSQTVICNVAPHASPTKTDLIK

>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}

RADAAPTVSIFPPSTEQLATGGASVVCLMNNFYPRDISVKWKIDGTERRDGVLDSTQDSKDSTYSMSSTLTLKADYESHNLYTCEVVHKTSSPV
VKSFNRNEC

>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}

AQTTAPSVDPLAPCGDTSSTVTLGCLVKGYFPEPVTVWNSGALSSDVHTFPAVLQSGLYTLSSSVTSSWPSQTVCNVAPHASSTKVDKKLERR

>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}

AKTPPPVYPLVPGSLAQTNSMVTLGCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSETVCNVAPHASSTKVDKKIEP

>d1deeb2 b.1.1.2 (B:622-723) Immunoglobulin (constant domains of L and H chains) {Fab of human IgM RF 2A2}

GSASAPTLFPLVSCENSNPSSTVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKGYAATSQVLLPSKDVQAQGTNEHVCKVQHPNGNKEK
DVPL

>d1f3dh2 b.1.1.2 (H:122-223) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}

AKTPPPSVDPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSETVCNVAPHASSTKVDKKIV
PRDC

>d1fh5h2 b.1.1.2 (H:121-215) Immunoglobulin (constant domains of L and H chains) {Fab MAK33, (human), kappa L chain}

AKTPPPSVDPLATLGCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVTSSWPSETVCNVAPHASSTKVDKKIVPR

>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)}

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPVLQSSGLYSLSSVTVPSSTLGTQTYICNVNHKPSNTKVDKKVEP
KSC

>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)}

RTVAAPSVFIFPPSDEQLKSGTASV р VCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLKADYEKHKVYACEVTHQGLSSPV
TKSFNRGEC

>d1fe8h2 b.1.1.2 (H:116-216) Immunoglobulin (constant domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

AETTAPSVDVKLEPVSSV р LGCLVKGYFPEPVTLWNSGSLSSGVHTFPAVLQSDLYTLSSSVTSSWPSQSITCNVAHPASSTKVDKKIEPRG

>d1ifdb2 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}

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVWSNSGALTSGVHTFPVLQSSGLYSLSSVTVPSSTLGTATYTCNVVDHKPSNTKVDKRV

>d1fn4b2 b.1.1.2 (B:107-208) Immunoglobulin (constant domains of L and H chains) {Fab 198 against acetylcholine receptor, (rat)}

TMVTVSSV р PLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNSGALSSGVHTFPAVLQSGLYLTSSV р PSSTWSSQAVTCNVAPHASSTKVDKKI
VPRDC

>d1jguh2 b.1.1.2 (H:114-212) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

AKTTAPSVDPLAPVGCGDTTGSSV р LGCLVKGYFPEPVTLWNSGSLSSGVHTFPAVLQSDLYTLSSSVTSSWPSQSITCNVAHPASSTKVDKKIEP

>d1jgul2 b.1.1.2 (L:108-214) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

RADAAPTVSIFPPSSEQLTSGGASVVCFLNНFYPKDINV р WKIDGSERQNGVLNSWTDQDSKDSTYSMSSTLTLKDEYERHNSYTCEATHKTSTSPI
VKSFNRNEC

>d1mcoh2 b.1.1.2 (H:118-219) Immunoglobulin (constant domains of L and H chains) {Intact antibody (lambda) MCG (human)}

ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPQPVTVSWNSGALTSGVHTFPALQSSGLYLSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVA
PEL

>d1adqa1 b.1.1.2 (A:238-341) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgG1 class}

PSVFLFPPPKDTLmisrtpevtcvvvdvsqedpqvfnwyvdgqvvhnaaktkpreqqfnstyrvsvltvlhqnwldgkeykckvsnkglpssi
EKTISAKG

>d1dn2a1 b.1.1.2 (A:237-341) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgG1 class}

GPSVFLFPPPKDTLmisrtpevtcvvvdvshenpevkfnwyvdgvevhnaaktkpreeqynstyrvsvltvlhqdwlngkeykckvsnkalpapi
EKTISAKG

>d1dn2a2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgG1 class}

QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDGSFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYT
QKSLSL

>d1fc2d1 b.1.1.2 (D:238-341) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgG1 class}

PSVFLFPPPKDTLmisrtpevtcvvvdvshedpqvkfnwyvdgqvvhnaaktkpreqqyntstyrvsvltvlhqnwldgkeykckvsnkalpapi
KTISAKG

>d1fp5a1 b.1.1.2 (A:336-438) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgE}

VSAYLSRPSPFDLIRKSPTITCLVVDLAPSKGTVNLTSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTT
KTSG

>d1fp5a2 b.1.1.2 (A:439-543) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgE}

PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSFFVSRLEVTRAWEQKDEFICRAVHEAASPS
QTQRAVSV

>d1i1ca1 b.1.1.2 (A:239-341) Immunoglobulin (constant domains of L and H chains) {Fc (rat) IgG}

SVIFPPKTDVLGGGLTPKVTCVVVDISQNDPEVRFSWFIDDVEVHTAQTHAPEKQSNTRSVSELPIVERDWLNGKTFKCKVNSGAFAPIEKSI
KPEG

>d1i1ca2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L and H chains) {Fc (rat) IgG}

TPRGHQVYTMAPPKEEMTQSQVSITCMVKGFYPPDIYTEWKMNGQPQENYKNTPPTMDTDGSYFLYSKLNVKETWQQGNTFTCSVLEHEN
EHTEKSLSH

>d1pfc__ b.1.1.2 (-) Immunoglobulin (constant domains of L and H chains) {Fc (guinea pig)}

RTISKAKGPPRIPEVYLLPPRNELSKKKVSLTCMITGFYPADINVEWDSEPSDYKNTPPVFDTDGSFFLYSRLKVDTDAWNNGESFTCSVMEALPN
HVIQKSIISRSPG

>d1cqka_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {Fc MAK33 (mouse)}

PAAPQVYTIIPPLEQMAKDLVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMTDGSYFVYSKLNVQKSNWAEAGNTFTCSVLEGLHNHH
EKSLSH

>d1g84a_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {C epsilon2 domain from IgE (human)}

SRDFTPPVTKILQSSSDGGGHFPPTIQLLCVSGYTPGTINITWLEDGQVMVDVLSTASTTQEGERLASTQSELTSQKHWSRDRYTQVYQGHTFE
DSTKKSA

>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}

IQNPDPAVYQLRDSKSSDKSVCLTDFDSQTNVSQSKDSDDVYITDKTVLDMRSMDFKNSAVAWSNKSDFACANAFNNSIIPEDTF

>d1bec_2 b.1.1.2 (118-246) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

DLRQVTPPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVVELSWWVNGKEVHSGVSTDPPQAYKESNYSYCLSSRLRVSATFWHNPRNHFRQCQVQFH
GLSEEDKWPEGSPKPVTQNISAEAWGRAD

>d1bd2e2 b.1.1.2 (E:119-247) T-cell antigen receptor {Human (Homo sapiens), beta-chain}

DLKNVFPPEAVFEPSEAEISHTQKATLVCLATGFYPPDHVELSWWVNGKEVHSGVSTDPPQPLKEQPALNDSRYALSSRLRVSATFWQDPRNHFRQC

VQFYGLSENDEWTQDRAKPVTQIVSAEAWGRAD
>d1hxma2 b.1.1.2 (A:121-206) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}
SQPHTKPSVFMKNGTNVACLVKEFYPKDIRINLVSSKKITEFDPAVISPSGKYNAV/KLGKYEDSNSVTCSVQHDNKTvhstdfe
>d1hxmb2 b.1.1.2 (B:124-230) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLEKFFPDVIKIHWEEKSNTILGSQEGNTMKTNDTMYKFSWLTVPPEKSLDKEHRCIVRHENNKGVD
QEIIFPPI
>d1cd1a1 b.1.1.2 (A:186-279) CD1, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus)}
QEKPVAWLSSVPSSAHGHRQLVCHSGFYPKPVWVMWMRGDQEQQGTHRGDFLPNADETWYLQATLDVEAGEEAGLACRVKHSSLGGQDIILY
W
>d1hdma1 b.1.1.2 (A:94-196) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}
SRGFPIAEVFTLKPLEFGKPNTLVCVSNLFPMLTVNWHDHSVPEGFGPTFSAVDGLSFQAFSYLNFTPEPSDIFSCIVTHEPDRTAIAYWVPRN
ALPS
>d1hdmb1 b.1.1.2 (B:88-185) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}
TRPPSVQAVAKTPNTREPVMLACYVWGFYPAEVITWRKNGKLMHSSAHKTAQPNGDWYQTLSHLALTPSYGDTYTCVVEHIGAPEPILRDW
TPG
>d1aqdb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR1}
RRVEPKVTVYPSKTQPLQHHNLLCVSGFYPGSIEVRWFRNGQEEKAGVVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSVTSPLTVEW
RA
>d1fv1a1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}
ITNPPEVTVLTNSPVELREPNVLICFIDKFTPPVVNVTVLRNGKPVTGVSETVFLPREDHLFRKFHYLPFLPSTEDVYDCRVEHWGLDEPLLKHWEF
D
>d1fv1b1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}
RRVEPKVTVYPARTQTLQHHNLLCVSGFYPGSIEVRWFRNGQEEKAGVVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSVTSPLTVEW
RA
>d1d5zb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR4}
RRVYPEVTVYPAKTQPLQHHNLLCVSGFYPGSIEVRWFRNGQEEKAGVVSTGLIQNGDWTFQTLVMLETVPRSGEVYTCQVEHPSLTSPLTVEW
RA
>d1jk8a1 b.1.1.2 (A:85-181) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}
EVPEVTFSKSPVTLQPNTLICLVDNIFPPVNVITWLSNGHSVTEGVSETSFLSKSDHSFFKISYLTFLPSDDEIYDCKVEHWGLDEPLLKHWEP
>d1jk8b1 b.1.1.2 (B:95-192) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}
VEPTVTISPSRTEALNHHNLLCVSDFYPAQIKVRWFRNDQEETGVVSTPLIRNGDWTFQILVMLEMTPQRGDVYTCHVEHPSLQNPIIVEWRA
QS
>d1iaka1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}
ATNEAPQATVFPKSPVLLQPNTLICFVDNIFPPVINITWLRNSKSVDGIVSFTGQYETSVNRDYSFHKLISYLTIPSDDDIYDCKVEHWGLEPVLKHWE
E
>d1iakb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}
RLEQPSVVISRTEALNHHTLVCSVTDFYPAKIKVRWFRNGQEETGVVSTPLIRNGDWTFQVLMLEMPRRGEVYTCHVEHPSLTSPITVEWR
A
>d1fnga1 b.1.1.2 (A:82-182) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}
DANVAPEVTVLSRSPVNLGEPNILICFIDKSFPPVNVTWLRNGRPTEGVSETVFLPRDDHLFRKFHYLTFLPSTDDFYDCEVDHWGLEEPLRKHWE
FEE
>d1fnbg1 b.1.1.2 (B:93-188) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}
RRVEPTVTYPTKTQPLEHHNLLCVSDFYPGNIEVRWFRNGKEEKTGIVSTGLVRNGDWTFQTLVMLETVPRSGEVYTCQVEHPSLTDPTVWEW
>d2iada1 b.1.1.2 (A:83-186) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AD}

TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTGVYETSFVN RDHSFKLSQLTFIPSDDDIYDCKVEHWGLEEPVLKHWEPEI
SSADLVPR

>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)}

TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTGVYETSFVN RDHSFKLSQLTFIPSDDDIYDCKVEHWGLEEPVLKHWS

>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)}

RLEQPNAISLSRTEALNHHTLVCVTDFYPAKIKVRWFRNGQEETGVSSQLIRNGDWTFQVLVMLEMTPHQGEVYTCHVEHPSLKSPITVEW
S

>d1k8ia1 b.1.1.2 (A:93-191) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

VSRGLPVAEVFTLKP LEFGKPNTLVCFSNLFPPTLTNVWQLHSAPVEGASPTSISAVDGLTFQAFSYLNFTPEPFDLYSCTVTHEIDRYTAIAYWVPQ

>d1k8ib1 b.1.1.2 (B:95-190) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

APSVRVAQTTPFNTREPVMILACYVWGFYPADVTITWMKNGQLVPSHSNKEKTAQPNGDW TYQT VSYLALTPSYGDVYTCVVQHSGTSEPIRGDW
TP

>d1vcaa1 b.1.1.3 (A:91-199) Second domain of vascular cell adhesion molecule-1 (VCAM-1) {Human (Homo sapiens)}

FPKDPEIHL SGPLEAGK PTVKCSVADVYPFDRLEIDL KGDHLMKSQEFLEDADRKSLETKSLEV TFTPVIEDIGKVLCRAKLHIDEMDSVPTVRQAV
KELQVYISP

>d1iam_1 b.1.1.3 (83-185) Second domain of intercellular cell adhesion molecule-1 (ICAM-1) {Human (Homo sapiens)}

YWTPERVELAPLPSWQPGKQLTLRCQVEGGAPRAQLTVLLRGEKELKREPAVGEP AEVTTTVLVRDHHGAQFSCRTELDLRPQGLELFENTSAP
YQLQTF

>d1ic1a1 b.1.1.3 (A:83-190) Second domain of intercellular cell adhesion molecule-1 (ICAM-1) {Human (Homo sapiens)}

YWTPERVELAPLPSWQPGKQLTLRCQVEGGAPRANLTVLLRGEKELKREPAVGEP AEVTTTVLVRDHHGAQFSCRTELDLRPQGLELFENTSAP
YQLQTFVLPAT

>d1zxq_1 b.1.1.3 (87-192) Second domain of intercellular cell adhesion molecule-2 (ICAM-2) {Human (Homo sapiens)}

PPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGH RNFSCLA VLDLMSRGGNIFHKHSAP
KM LEIY

>d1cdy_2 b.1.1.3 (98-178) CD4 {Human (Homo sapiens)}

FGLTANS DTHLLQGQS LTTL ESSP PGSV QCRSPRGKNIQGGKTL SVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLA

>d1wioa4 b.1.1.3 (A:292-363) CD4 {Human (Homo sapiens)}

MRATQLQKNLTCEVWGPSPKLM LSLKLENKEAVSKREKAVWV LNP EAGMWQCLLSDSGQV LLESNIKVLP

>d1cid_2 b.1.1.3 (106-177) CD4 {Rat (Rattus rattus)}

VMKVTQPDNSTLTCVMNGTDPELNL YQDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVSKESSVEPVSCPEK

>d1hnf_2 b.1.1.3 (105-182) CD2, second domain {Human (Homo sapiens)}

RVSKPKI SWT CINTTLCEVMNGTDPELNL YQDGKHLKLSQRVITHKWTTSLSAKFKCTAGNKVSKESSVEPVSCPEK

>d1ccza2 b.1.1.3 (A:94-171) CD2-binding domain of CD58, second domain {Human (Homo sapiens)}

EMVSKPMIYWECSNATLCEVLEG TDV EKL YQGK EHL RSLRQK TMS YQWTNLRAPFKCAVN RV SQE SEME VVNCPE

>d1dr9a2 b.1.1.3 (A:106-200) CD80, second domain {Human (Homo sapiens)}

ADFPTPSISDFEIPTSNIRRIICSTS GGFPEPHLSWLEN GEEL NAI TT VSQDPETELYAVSSK LDFNMTTNHSFMCLI KYGHL RVN QT FWNTA

>d1vcaa2 b.1.1.4 (A:1-90) N-terminal domain of vascular cell adhesion molecule-1 (VCAM-1) {Human (Homo sapiens)}

FKIETTPESRYLAQIGDSVSLTCSTTGCESPFFSWRTQIDSPNGKVTNEGTTSTLMNPV SFGNEHSYLTACESRKLEKG I QV EYIS

>d1iam_2 b.1.1.4 (1-82) N-terminal domain of intracellular adhesion molecule-1, ICAM-1 {Human (Homo sapiens)}

QTSVSPSKVILPRGGSVLVTCSTCDQPKLLGIETPLPKKE LLPGNNRKVYELSNVQEDSQPM CYSNCPDGQSTA KTF LT

>d1zxq_2 b.1.1.4 (1-86) N-terminal domain of intracellular adhesion molecule-2, ICAM-2 {Human (Homo sapiens)}

KVFEVHVRPKKLA VE PKGSLEV NCSTTCNQPEVGG LETSLN KILLDEQAQWKH YL VS NISH DTVLQCHFTCSGKQESMNSNV SYQ

>d1epfa1 b.1.1.4 (A:1-97) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}

LQDIVPSQGEISVGESKFFLCQVAGDAKD KDISWFSPNGEKLSPNQQRISVVWN DDSSTLTIY NANIDDAGIYKC VVTAED GTQSEATVN VKIFQ

>d1epfa2 b.1.1.4 (A:98-189) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}

KLMFKNAPTPQEFKEGEDAVIVCDVSSLPTIIWKHGRDVILKKDVRFIVLSNNYLQIRGIKKTDEGTYRCEGRILARGEINFKDIQVIV

>d1ie5a_ b.1.1.4 (A:) Neural cell adhesion molecule (NCAM) {Chicken (Gallus gallus)}

GKDIQVIVNVPPSVRARQSTMNATANLSQSVTLACADGFPEPTMTWTKDGEPIEQEDNEEKYSFYNDGSELIIKKVDKSDEAEYICIAENKAGEQD
ATIHLKVF

>d1gsma1 b.1.1.4 (A:1-90) Mucosal addressin cell adhesion molecule-1 (MADCAM-1) {Human (Homo sapiens)}

VKPLQVEPPEPVAAVLGASRQLTCRLACADRGASVQWRGLDTSLGAVQSDTGRSVLTVRNASLSAAGTRVCVGSCGGRTFQHTVQLLVY

>d1gsma2 b.1.1.4 (A:91-206) Mucosal addressin cell adhesion molecule-1 (MADCAM-1) {Human (Homo sapiens)}

AFPNQLTVSPAALVPGDPEVACTAHKVTVPDPNALFSLLVGGQELEGAQALGPEVQEEEEPQGDEDVLFRTERWRLPPLGTPVPPALYCQATMR
LPGLELSHRQAIPVIEGR

>d1fhga_ b.1.1.4 (A:) Telokin {Turkey (Meleagris gallopavo)}

AEEKPHVKPYFTKTILDMEVVEGSAARFDCKVEGYPDPEVMWFKDDNPVKESRHFQIDYDEEGNCNLTISEVCGDDDAKYTCKAVNSLGEATCTAEI
LVETM

>d1g1ca_ b.1.1.4 (A:) Titin {Human (Homo sapiens), different modules}

SMEAPKIFERIQSQTVQGQSDAHFRVRVVGKPDPECEWYKNGVKIERSDRIYWYWPEVNCELIRDVTGEDSASIMVKAINIAGETSSHAFLLVQA
K

>d1nct__ b.1.1.4 (-) Titin {Human (Homo sapiens), different modules}

SKTTLAARILTKPRSMVTYEGESARFSCDTDGEPPVTWLRKGQVLSTSARHQVTTTKYKSTFEISSVQASDEGNYSVVENSEGKQEAFTLTIQK

>d1koa_1 b.1.1.4 (6265-6361) Twitchin {Nematode (Caenorhabditis elegans)}

QPRFIVKPYGTVEGEGQSANFYCRVIASSPPVVTWHKDDRELKQSVKYMKRYNGNDYGLTINRVKGDDKGEYTVRAKNSYGTKEEIVFLNVTRHSEP

>d1wiu__ b.1.1.4 (-) Twitchin {Nematode (Caenorhabditis elegans)}

LKPKILTASRKIKIKAGFTHNLEVDFIGAPDPTATWVGDGAAALAPELLVDAKSSTSIFFPSAKRADSGNYKLKVKNELGEDEAIFEVIVQ

>d1tiu__ b.1.1.4 (-) Twitchin {Human (Homo sapiens), Ig repeat 27}

LIEVEKPLYGVFVGETAHFEIELSEPDVHGQWKLKGQPLTASPDCIEIEDGKKHILHNCQLGMTGEVSFQAANAKSAANLKVKEL

>d1iray1 b.1.1.4 (Y:1-101) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

DKCKEREKIIIVSSANEIDVRCPCLNPNEHKGTITWYKDDSKTPVSTEQASRIHQHKEKLWVPAKVEDSGHYYCVVRNSSYCLRIKISAKFVENEPNL
C

>d1iray2 b.1.1.4 (Y:102-204) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

YNAQAIKFQKLPVAGDGLVCPYMEFFKNENNELPKLQWYKDCKPLLDNIHFGVKDR利VMNVAEKHRGNYTCHASYTLGKQYPITRVIEFITLE
ENKPT

>d1iray3 b.1.1.4 (Y:205-311) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

RPVIVSPANETMEVDLGSQIQLICNTGQLSDIAYWKWNGSVIDEDDPVLGEDYYSEN PANKRRSTLITVLNISEIESRFYKHPFTCAKNTHGIDAAY
IQLIYPV

>d1cvsc1 b.1.1.4 (C:149-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}

MPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPQPTLRWLKNGKEFKPDHRIGGYKVRYATWSIIMDSVPSDKGNYTCIVENEYGSINHTYQL
DVVER

>d1cvsc2 b.1.1.4 (C:251-359) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}

SPHRPILQAGLPANKTVVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPPVQILKTAGVNNTDKEMEVLHLRNVSFEDAGEYTCAGNSI
GLSHHSAWLTVL

>d1ev2e1 b.1.1.4 (E:150-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR2}

NKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPTMRWLKNGKEFKQEHHRIGGYKVRNQHWSLIMESVPSDKGNYTCVVENEYGSIN
HTYHLDVVE

>d1ev2e2 b.1.1.4 (E:251-360) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR2}

RSPHRPILQAGLPANASTVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDPGLPYLKVLKAAGVNNTDKEIEVLYIRNVTFEDAGEYTCAGNSI

GISFHSAWLTVL

>d1biha1 b.1.1.4 (A:5-98) Hemolin {Moth (Hyalophora cecropia)}

KYPVLDQPAEVLFRENNPTVLECIIEGNDQGVKYSWKKDGKSYNQEHNAAALKDEGSVFLRPQASDEGHYQCFAETPAGVASSRVISFRKT

>d1biha2 b.1.1.4 (A:99-209) Hemolin {Moth (Hyalophora cecropia)}

YLIASPAKTHEKTPIEGRPFQLCVPNAYPKPLTWKKRLSGADPNADVTDFDRITAGPDGNLYFTIVTKEDVSDIYKVCTAKNAAVDEEVVLVEYEIKGVTKDNGY

>d1biha3 b.1.1.4 (A:210-306) Hemolin {Moth (Hyalophora cecropia)}

KGEVPVPQYVKDMMAKAGDVTMIYCMYGSNPMGYPNYFKNGKDVGNGNPEDRITRHNRSGKRLFKTLPEDEVYTCEVDNGVGKPQKHSLKLTVV

>d1biha4 b.1.1.4 (A:307-395) Hemolin {Moth (Hyalophora cecropia)}

SAPKYEQQKPEKVIVVKQGQDVTPCKVTGLPAPNWWWSHNAKPLSGGRATVTDGLVIKGVKNGDKGYYGCRATNEHGDKYFETLVQVN

>d1cs6a1 b.1.1.4 (A:7-103) Axonin-1 {Chicken (Gallus gallus)}

RSYGPVFEEQPAHTLFPegasEEKVTLCRARANPPATYRWKMNGTELKGMPDSRYRLVAGDLVISNPVAKDAGSYQCVATNARGTVVSREASLRF

>d1cs6a2 b.1.1.4 (A:104-208) Axonin-1 {Chicken (Gallus gallus)}

GFLQEFSAEERDPVKITEGWGVMTCSPPPYPALSRYWLNEFPNFI PADGRRFVSQTTGNLYIAKTEASDLGNYSCATSHIDFITKSFSKSQLSAAEDA

>d1cs6a3 b.1.1.4 (A:209-299) Axonin-1 {Chicken (Gallus gallus)}

RQYAPSIIKAFPADTYALTGQMVTLECFAGNPVPQIKWRKLDGSQTSKWLSSEPLLHIQNVDFEDEGTYECEAENIKGRDTYQGRIIIHA

>d1cs6a4 b.1.1.4 (A:300-388) Axonin-1 {Chicken (Gallus gallus)}

QPDWLVDITDTEADIGSDLRWSCVASGKPRPAVRWL RDGQPLASQNRIEVSGGELRFSKLVLEDGMYQCVAEHKHTVYASAELTVQA

>d1g4b_ b.1.1.4 (B:) Perlecan Ig3 domain {Mouse (Mus musculus)}

PIMVTVEEQRQSQRPGADVTFICTAKSKSPAYTLVWTRLHNGKLPSRAMDFNGILTIRNVQPSDAGTYVCTGSNMFAMDQGTATLHQ

>d1f97a2 b.1.1.4 (A:129-238) Junction adhesion molecule, JAM, C-terminal domain {Mouse (Mus musculus)}

VPPSKPTISVPSSVTIGNRAVLTCEHDGSPPEYSWFKDGI SMLTADAKKTRAFMNSSFTIDPKSGDLIFDPVTAFDSEYYCQAQNGYGTAMRSEA AHMDAELNVGG

>d1fltx_ b.1.1.4 (X:) Second domain of the Flt-1 receptor {Human (Homo sapiens)}

GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLTCEATVNGHLYKTNYLTHRQT

>d1he7a_ b.1.1.4 (A:) NGF binding domain of trkA receptor {Human (Homo sapiens)}

SHMPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLRLNQPTHVNNGNYTLLAANPFGQASASIMA AFMDNPFEFNPE

>d1wwwx_ b.1.1.4 (X:) NGF binding domain of trkA receptor {Human (Homo sapiens)}

VSFPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLRLNQPTHVNNGNYTLLAANPFGQASASIMA FMDNP

>d1wwbx_ b.1.1.4 (X:) Ligand binding domain of trkB receptor {Human (Homo sapiens)}

VHFAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFNGAILNESKYICTKIHVTNHTEYHGCLQLDNP THMNNGDYTLIAKNEYGKDEKQISAHF MWPgid

>d1wwca_ b.1.1.4 (A:) NT3 binding domain of trkC receptor {Human (Homo sapiens)}

TVYYP RRVSLEPELRLEHCFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGERSEGCLFNKP THYNNNGNYTLLAANPFGQASASIMA FPVDE

>d1fcga1 b.1.1.4 (A:4-88) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIa}

APPKAVLKLEPPWINVLQEDSVTLCQGARS PESDSIQWFHNGNLIPHTQPSYRFKANNNDSGEYTCQTGQTSLSDPVHLTVLF

>d1fcga2 b.1.1.4 (A:89-174) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIa}

EWLVLTQTPHLEFQEGETIMLRCHSWKDKPLVKVTFQNGKSQKF SHLDPTFSIPQANHS HSGDYHCTGNIGYTLFSSKPVTITVQV

>d2fcba1 b.1.1.4 (A:6-90) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIb}

APPKAVLKLEPQWINVLQEDSVTLCRGTHSPESDSIQWFHNGNLIPTHTQPSYRFKANNNDSGEYTCQTGQTSLSDPVHLTVLS
>d2fcba2 b.1.1.4 (A:91-178) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIb}
EWLVLQTPHLEFQEGETIVLRCHSWKDKPLVKVTFQNGKSKFSRSDPNFSIPQANHSHSGDYHCTGNIGYTLYSSKPVTITVQAPA
>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}
HIGWLLLQAPRWVFKEEDIHLRCHSWKNTALHKVTLQNGKDRKYHHNSDFHIPKATLKDSGSYFCRGLVGSKNVSSETVNITITQA
>d1f2qa1 b.1.1.4 (A:4-85) IgE high affinity receptor alpha subunit {Human (Homo sapiens)}
PKVPSLNPPWNRFKGENDVLTNCNGNNFEVSSTKWFHNGLSEETNSSLNIVNAKFEDSGEYKCQHQHQVNESEPVYLEVFS
>d1f2qa2 b.1.1.4 (A:86-174) IgE high affinity receptor alpha subunit {Human (Homo sapiens)}
DWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIIYKDGEALKYWYENHNISITNATVEDSGTYCTGKVWQLDYESEPLNITVIKAPR
>d1efxd1 b.1.1.4 (D:4-103) Killer cell inhibitory receptor {Human (Homo sapiens), kir2d13}
VHRKPSLLAHPGRLVKSEETVILQCWSDVRFEHFLHREGKFKDTLHLIGEHHDGVSKANFSIGPMMDLAGTYRCYGSVTHSPYQLSAPSPLDIVI
TG
>d1efxd2 b.1.1.4 (D:104-200) Killer cell inhibitory receptor {Human (Homo sapiens), kir2d13}
LYEKPSLSAQPGPTVLAGESVTLSRSSYDMYHLSREGEAHECRFSAGPKVNGTFQADFLGPATHGGTYRCFGSFRDSPYEWNSSDPLLVSVI
>d1nkr_1 b.1.1.4 (6-101) Killer cell inhibitory receptor {Human (Homo sapiens), p58-cl42 kir}
RKPSLLAHPGPLVKSEETVILQCWSDVMFEHFLHREGMFNDTRLIGEHHDGVSKANFSISRMTQDLAGTYRCYGSVTHSPYQVSAPSPLDIVI
>d1nkr_2 b.1.1.4 (102-200) Killer cell inhibitory receptor {Human (Homo sapiens), p58-cl42 kir}
IGLYEKPSLSAQPGPTVLAGENVTLCSSRSSYDMYHLSREGEAHERRLPAGPKVNGTFQADFLGPATHGGTYRCFGSFHDSPYEWSKSSDPLLVS
T
>d1g0xa1 b.1.1.4 (A:2-97) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}
HLPKPTLWAEPGSVITQGSPVTLRCQGGQETQEYRLYREKKTAPWTRIPQELVKKGQFPIPSITWEHAGRYRCYGSDEGRSESSDPLELVVTG
>d1g0xa2 b.1.1.4 (A:98-198) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}
AYIKPTLSAQPSPVNSGGNVTLQCDSQVAFDGFILCKEGEDEHPQCLNSQPHARGSSRAIFSVGPVSPSRRWWYRCYAYDSNSPYEWSLPSDLLELL
VLG
>d1f42a1 b.1.1.4 (A:1-87) The p40 domain of interleukin-12 (IL-12 beta chain), N-terminal domain {Human (Homo sapiens)}
IWELLKKDVYVVELWDWPDAPGEMVVLCDTPEEDGITWLDQSSVEVLSGKTLTIQVKEFGDAGQYTCHKGGEVLHSLLLLHKKED
>d1bjba1 b.1.1.4 (A:101-186) CD3 gamma chain ectodomain fragment {Mouse (Mus musculus)}
KKDGTSQTNKAKNLVQVDGSRGDGSVLLTCGLTDKTWKLDGSIISPLNATKNTWLGNNAKDPRTGYCQCGAKETSNPLQVYYRM
>d1bjba2 b.1.1.4 (A:1-100) CD3 epsilon chain ectodomain fragment {Mouse (Mus musculus)}
DDAENIEYKVISGTSVELCPLSDENLKWEKNGQELPKHDKHLVLQDFSEVEDSGYYCYTPASNKNTYLYLKARVGSADDAAKKDAAKKDDAKK
DDA
>d1k3ia1 b.1.1.5 (A:538-639) Galactose oxidase, C-terminal domain {Fungi (Fusarium spp)}
GNLATRPKITRTSTQSVKGGRITISTSSISKASLIRYGTATHVNTDQRRIPLTLNNGGNSYFQVPSDSGVALPGYWMLFVMNSAGVPSASTIRV
TQ
>d1qba_1 b.1.1.5 (781-885) Bacterial chitobiase, c-terminal domain {Serratia marcescens}
GETHFVDTQALEKDWLRFANILGQRELAKLDKGGVAYRLPVPAGRAGGKLEANIALPGLGIESTDGGKQWQRYDAKAKPAVGSEVQVRSVSPDG
KRYSRAEKV
>d1svb_1 b.1.1.5 (303-395) Envelope glycoprotein, domain III (C-terminal) {Tick-borne encephalitis virus}
TYTMCDKFTWKRAPTDGHDVVMEVTFSGTKPCRIPVRAVHGSPDVNVAMLITPNPTIENNGGGFIEMQLPPGDNIIYVGELSHQWFQK
>d1cgt_1 b.1.1.5 (495-579) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans, different strains}
ETTPTIGHVGPVMGKPGNVVTIDGRGFGSTKGTVFYFGTTAVGAAITSWEDTQIKVTIPSVAAGNYAVKVAASGVNSNAYNNFTI
>d1kcla1 b.1.1.5 (A:496-581) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans, different strains}

TATPTIGHVGPMMAKPGVTITIDGRGFSSKGTVYFGTTAVSGADITSWEDTQIKVKIPAVAGGNYNIKVANAAGTASNVDNFEV
>d1cyg_1 b.1.1.5 (492-574) Cyclodextrin glycosyltransferase, domain E {Bacillus stearothermophilus}
ESTPIIGHVGPMGGQVGHQVTIDGEGFTNTGTVKFGTTAANVWSNNQIVVAVPNVSPGKYNITVQSSGQTSAAYDNFEV
>d1qhoal b.1.1.5 (A:496-576) Cyclodextrin glycosyltransferase, domain E {Bacillus stearothermophilus, maltogenic alpha-amylase}
ASAPQIGSVAPNMGIPGNVVTIDGKGFQGTQGTVTFGGVTATVKSWSNRIEVVYVNPMAAGLTDVKTAGGVSSNLNSYNI
>d1pama1 b.1.1.5 (A:497-582) Cyclodextrin glycosyltransferase, domain E {Bacillus sp., strain 1011}
TTPIIIGNVGPMMAKPGVTITIDGRGFSSKGTVYFGTTAVTGADIVAWEDTQIQVVKIPAVPGIYDIRVANAAGAASNIYDNFEVL
>d1ciu_1 b.1.1.5 (496-578) Cyclodextrin glycosyltransferase, domain E {Thermoanaerobacterium thermosulfurigenes, EM1}
SNSPLIGHVGPTMTKAGQTITIDGRGFQGTSGQVLFGSTAGTIVSWDDTEVKVKVPSVTPGKYNISLKTSSGATSNTYNNINI
>d1smaa1 b.1.1.5 (A:1-123) Maltogenic amylase, N-terminal domain {Thermus sp.}
MRKEAIHHRSTDNFAYADSETLHLRLQTKNDVDHVELLFGDPYEWHDGAWFQFQTMMPMRKTGSDGLFDYWLAEVKPPYRRLRYGFVLRAGGEK
LVYTEKGFYHEAPSDDTAYYFCFPFLHRV
>d1bvza1 b.1.1.5 (A:1-120) Maltogenic amylase, N-terminal domain {Thermoactinomyces vulgaris, TVAII}
MLLEAIFHEAKGSYAYPISETQLRVRLRAKKGDVVRCEVLYADRYASPEEELAHAGKAGSDERFDYFEALLECSTKRVKYVFLGPQGEAVYFGETG
FSAERSKAGVFQYAYIHRSE
>d1eh9a1 b.1.1.5 (A:1-90) Glycosyltrehalose trehalohydrolase, N-terminal domain {Archaeon Sulfolobus solfataricus, km1}
TFAYKIDGNEVIFTLWAPYQKSVKLKVKLEKGLYEMERDEKGYFTITLNNVKVRDRYKVVLDDASEIPDPASRYQPEGVHGPSQIQQESKE
>d1bf2_1 b.1.1.5 (1-162) Isoamylase, N-terminal domain {Pseudomonas amylofera}AINSMSLGASYDAQQANITFRVYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVVAUTVPVSSIKAAGITGAVYYGYRAWGPNPYASNWGKGS
QAGFVSDVDANGDRFNPNKLLDPYAQEVSQDPLNPSNQNQNVFASGASYRTTDSGIYAPKGVV
>d1lla_3 b.1.1.5 (380-628) Hemocyanin, C-terminal domain {Horseshoe crab (Limulus polyphemus)}
PYDHVDVLNFPDIQVQDVTLHARVDNVVHTFMREQELEKHGINPGNARSIKARYYHLDHEFSYAVNVQNNASDKHATVIRFLAPKYDELGNEIKA
DELRRTAIELDKFKTDLHPGKNTVVRHSLSSVTLSHQPTFEDLLHGVLNEHKSEYCSGWPShLLVPKGNIKGMEMYHLFVMLTDWDKDKVDGSES
VACVDAVSYCGARDHKYPDKPMGFPDFRPIHTEHISDFLTNNMFIKDIKIKFHE
>d1hc2_3 b.1.1.5 (399-653) Hemocyanin, C-terminal domain {Spiny lobster (Panulirus interruptus)}
PPYTHDNLEFSGMVVNGVAIDGELITFFDEFQYSLINAVDGENIEDVEINARVHRLNHNEFTYKITMSNNNDGERLATFRIFLCPIEDNNGITLDEA
RWFCIELDKFFQKVPSGPETIERSSKDSSVTPDMPSFQSLKEQADNAVNGGHDLDSAYERSCGIPDRMLLPKSKPEGMEFNLYVAVTDGDKDTEG
HNGGHDYGGTHAQCGVHGEAYPDNRPLGYPLERRIPPERVIDGVSNIKHVVVKVHH
>d1js8a2 b.1.1.5 (A:2792-2892) C-terminal domain of octopus hemocyanin {Giant octopus (Octopus dofleini)}
EDRVFAGFLLRTIGQSADVNFVCTKDGECTFGGTFCILGGEHEMFWAFDRLFKYDITTSKLHRLDAHDDFDIKVTIKGIDGHVLSNKYLSPPTVFLA
PA
>d1clc_2 b.1.1.5 (35-134) CelD cellulase, N-terminal domain {Clostridium thermocellum}
IETKVSAAKITENYQFDSRIRLN SIGFIPNHSKKATIAANCSTFYVVKEDGTIVYGTATSMFDNDTKEVYIADFSSVNEEGTYYLA PGVGKSVNF
>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}
AAPGKPTIAWGNTKFAIVEVDQAATAYNNLVKVNAAADVSVSWNLWNGDTTAKVLLNGKEAWSGPSTGSSGTANFKVNKGGRYQMVALCN
ADGCTASDATEIVVAD
>d1f13a1 b.1.1.5 (A:5-190) Transglutaminase N-terminal domain {Human (Homo sapiens)}
RTAFIGGRRAVPPNNSNAAEDDLPTVELQGVVPRGVNLQEFNVTSHLFKERWDTNKVDHHTDKYENNKLIVRRGQSFYVQIDFSRPYDPRRD
RVEYVIGRYPQENKGTYIPVPIVSELQSGKGAKIVMREDRSVRLSIQSSPKCIVGKFRMYVAWTPYGLRTSRNPETDTYILFNPWCED
>d1g0da1 b.1.1.5 (A:6-140) Transglutaminase N-terminal domain {Red sea bream (Chrysophrys major)}
GLIVDVNGRSHENNLAHRTREIDRERLIVRGGQPFSLQCSDSLPPKHHLEVLHLGKRDEVVIKVQKEHGARDKWWFNQQGAQDEILLTLHSPAN
AVIGHYRLAVLVMSPDGHIVERADKISFHMLFNPWCED

>d1eut_1 b.1.1.5 (403-505) Sialidase, "linker" domain {Micromonospora viridifaciens}

GICAPFTIPDVALEPGQQVTVPVAVTNQSGIAVPKPSLQLDASPDWQVQGSVEPLMPGRQAKGQVTITVPAGTPGRYRGATLRTSAGNASTTFT
VTVGLLD

>d1ksr__ b.1.1.5 (-) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}

ADPEKSYAEGPGLDGECFQPSFKIHAVDPGVHRTDGGDGFVVTIEGPAPVDPVMVDNGDGTYDVEFEPKEAGDYVINLTLDGDNVNGFPKT
TVKPA

>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}

KPAPSAEHSYAEAGEGLVKVFDNAPAEFTIFAVDTKGVARNDGGDPFEVAINGPDGLVDAKVTDDNNDGTYGVVYDAPVEGNYNVNTRLGNPIK
MPIDVKCIE

>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}

GANGEDSSFGSFTFTVAAKNKKGEVKTYGGDKFEVSITGPAEEITLDAIDNQDGTYTAAYSLVGNRFSTGVKLNGKIEGSPFKQVLGNPGKKNPEV
KSFTTTRTAN

>d1ds6b_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}

GNYKPPPQKSLKELQEMDKDESLIKTKTLLGDGPVVTDPKAPNVVTRTLVCESAPGPITMDLTGDEALKKETIVLKEGSEYRVKIHFKVNRD
IVSGLKYVQHTYRTGVKVDKATFMVGSYGRPPEEYEFITPVEEAPKGMLARGTYHNKSFTTDDKQDHLSWEWNLSIKKEWG

>d1fsoa_ b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}

MVPNVVVTGLTLVCSSAPGPLEDLTGDLFQSFVKEGVYERIKISFRVNREIVSGMKYIQHTYRAGVAIDATDYMVGSGYGPRAEYEFLTPVEEA
PKGMLARGSYSIKSRFTDDKTDHLSWEWNFTIKKDWK

>d1hh4e_ b.1.1.5 (E:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}

HSVNYKPPAQKSIQEIQELDKDDESLRKYKEALLGRAVASADPNVPNVVVTGLTLVCSSAPGPLEDLTGDLFQSFVKEGVYERIKISFRVNREIV
SGMKYIQHTYRKGVKIDKTDYMGSGYGPRAEYEFLTPVEEAPKGMLARGSYSIKSRFTDDKTDHLSWEWNLTICKDW

>d1rhoa_ b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}

VAVSADPNVPNVVVTGLTLVCSSAPGPLEDLTGDLFQSFVKEGVYERIKISFRVNREIVSGMKYIEHTYRKGVKIDKTDYMGSGYGPRAEYEFL
LTPVEEAPKGMLARGSYSIKSRFTDDKTDHLSWEWNLTICKDWK

>d1ajw__ b.1.1.5 (-) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}

AVSADPNVPNVVVTTRTLVCSTAPGPLEDLTGDLFQSFVKEGVYERIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMGSGYGPRAEYEFL
TPMEEAPKGMLARGSYSIKSRFTDDKTDHLSWEWNLTICKKEWD

>d1doab_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}

EPTAEQLAQIAAENEDEHSVNYKPPAQKSIQEIQELDKDDESLRKYKEALLGRAVASADPNVPNVVVTTRTLVCSTAPGPLEDLTGDLFQSFV
KEGVYERIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMGSGYGPRAEYEFLTPMEEAPKGMLARGSYSIKSRFTDDKTDHLSWEWNLTICK
WKD

>d1ayra2 b.1.1.5 (A:183-368) Arrestin {Cow (Bos taurus), visual arrestin}

DMGPQPRAEASWQFFMSDKPLRLAVSLSKIEIYHGEPIPVTAVTNSTEKTVKKIKVLVEQVTNVVLYSSDYYIKTVAAEEAQEKVPPNSSLTKTLV
LLANNRERRGIALDGKIKHEDTNLASSTIKEGIDKTVMGILVSQIKVKLTSGLLGELTSSEVATEVPFRLMHQPQPEDPDTAKA

>d1cf1a1 b.1.1.5 (A:10-182) Arrestin {Cow (Bos taurus), visual arrestin}

HVIFKKISRDKSVTIYLGKRDYIDHVERVEPVGVVLVDPVELVKGKRVVSLTCAFRYGQEDIDVMGLSFRRDLYFSQVVFPPVGASGATTRLQESLIK
KLGANTYPFLTFDYLPCSVMLQPAQDVGKSCGVDFEIKAFATHSTDVEEDKIPKKSSVRLLIRKVQHAPR

>d1cf1a2 b.1.1.5 (A:183-393) Arrestin {Cow (Bos taurus), visual arrestin}

DMGPQPRAEASWQFFMSDKPLRLAVSLSKIEIYHGEPIPVTAVTNSTEKTVKKIKVLVEQVTNVVLYSSDYYIKTVAAEEAQEKVPPNSSLTKTLV
LLANNRERRGIALDGKIKHEDTNLASSTIKEGIDKTVMGILVSQIKVKLTSGLLGELTSSEVATEVPFRLMHQPQPEDPDTAKESFQDENFVFEFARQ
NLKDAQEYKE

>d1g4ma1 b.1.1.5 (A:5-175) Arrestin {Cow (Bos taurus), beta-arrestin 1}
GTRVFKKASPNGKLTVYLGKDFVDHIDLVEPVGVVLDPEYLKERRVYVTLCAFRYGRELDLVGLTFRKDLFVANVQSFPPAPEDKKPLTRLQERL
IKKLGEHAYPFTFEIPPNLPCSVTLQPGPEDTGKACGVDEYEVAKFCAENLEEKIHKRNSVRLVIRKVQYAP

>d1g4ma2 b.1.1.5 (A:176-393) Arrestin {Cow (Bos taurus), beta-arrestin 1}
ERPGPQPTAETTRQFLMSDKPLHLEASLDKEIYYHGEPIVSNVHVTNNNTKTVKKIKISVRQYADICLFNTAQYKCPVAMEEADDTVAPSSTFCVKYTL
TPFLANNREKGLALDGKLKHEDTNLASSTLLREGANREILGIIVSYKVVKVLVSRGGLLGDASSDVAELPFTLMHPKPKEEPPHREVPEHETPVDT
NLIELDTNDDDIVFEDFAR

>d1a02n1 b.1.1.5 (N:577-678) Transcription factor NFATC, C-terminal domain {Human (Homo sapiens)}
LPMVERQDTSCLVYGGQQMILTQNFNTSESKVVFTKTTDQQIWEMEATVDKDKSQPNMLFVIEPEYRNKHIRTpvkvNFVINGKRKRSQPQ
HFTYHPV

>d1imhc1 b.1.1.5 (C:368-468) Transcription factor TONEBP, C-terminal domain {Human (Homo sapiens)}
VPEILKKSLHSCSVKGEEEVFLIGKNFLGKTKVIFQENVSDENSWKSEAEIDMELFHQNHLIVKVPPYHDQHITLPVSVGIYVVTNAGRSHDVQPFTY
PD

>d1bfs__ b.1.1.5 (-) p50 subunit of NF-kappa B transcription factor, C-terminal domain {Mouse (Mus musculus)}
ASNLKIVRMDRTAGCVTGGEEIYLLCDKVQKDDIQIRFYEEEENGWEGFGFSPTDVHQFAIVFKTPKYKDVNITKPASVQLRRKSDLETSEPK
PFLYYPE

>d1a3qa1 b.1.1.5 (A:227-327) p52 subunit of NF-kappa B (NFKB), C-terminal domain {Human (Homo sapiens)}
NLKISRMDKTAGSVRGGDEVYLLCDKVQKDDIEVRFYEDDENGWQAFGDFSPTDVHQFAIVFRTPYHKMKIERPVTVFLQLRKRGDVSDSKQ
FTYYP

>d1bfta_ b.1.1.5 (A:) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Mouse (Mus musculus)}
TAELKICRVNRNSGSCLGGEIFLLCDKVQKEDIEVYFTGPGWEARGFSFSQADVHRQVAIVFRTPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQ
YLPD

>d1ikna1 b.1.1.5 (A:192-303) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Mouse (Mus musculus)}
AELKICRVNRNSGSCLGGEIFLLCDKVQKEDIEVYFTGPGWEARGFSFSQADVHRQVAIVFRTPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQY
LPDTDDRHRRIEEKRK

>d1nfia1 b.1.1.5 (A:190-314) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Human (Homo sapiens)}
NTAELKICRVNRNSGSCLGGEIFLLCDKVQKEDIEVYFTGPGWEARGFSFSQADVHRQVAIVFRTPYADPSLQAPVRVSMQLRRPSDRELSEPMEF
QYLPDTDDRHRRIEEKRKRTYETFKSIMK

>d1ahm__ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides farinae), Der f 2}
DQDVVKDCANNEIKKVMVGCHGSDPCIIHRGKPFITLEALFDANQNTKAKIEIKASLDGLEIDVPGIDTNACHFKCPLVKGQQYDIKYTNVPKIA
PKSENVVVTVKLIGDNGVLACAIATHGKIRD

>d1a9v__ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides pteronyssinus), Der p 2}
SQVDVKDCANHEIKVLVPGCHGSEPCIIRGKPFQLEAVFEANQNTKAKIEIKASIDGLEVDVPGIDPNACHYMKCPLVKGQQYDIKYTNVPKIA
PKSENVVVTVKVMGDDGVLACAIATHAKIRD

>d1soxa1 b.1.1.5 (A:344-466) Sulfite oxidase, C-terminal domain {Chicken (Gallus gallus)}
ELPVQSAVTQPRPGAAVPPGELTVKGyawSGGGREVVRRDVSLDGGRTWKVARLMGDKAPPGRAWAWALWELTVVEAGTELEIVCKAVDSSY
VQPDSVAPIWNLGVLSAWHRVRSVQD

>d1cvra1 b.1.1.5 (A:351-432) Gingipain R (RgpB), C-terminal domain {Porphyromonas gingivalis}
PTEMQVTAPANISASAQTFEVACDYNGAIATLSDDGDMVGTAIVKDGKAIKLNESIADETNLTLTVVGYNKVTVIKDVKE

>d1h6ta1 b.1.1.6 (A:241-321) Internalin B {Listeria monocytogenes}
ECLNKPINHQSNLVPNTVKNTDGSVTPEIISDDGDYEKPNVKWHLPEFTNEVSFIFYQPVTIGKAKARFHGRVTQPLKE

>d1h6ua1 b.1.1.6 (A:263-343) Internalin H {Listeria monocytogenes}
TITNQPVFYNNNLVVPNVVKGPSGAPIPATISDNGTYASPNLTWNLTSPINNSYTFNQSVTFKNTTVPFSGTVTQPLTE

>d1ehxa_ b.1.1.6 (A:) Cellulosomal scaffoldin protein CipC, module x2.1 {Clostridium cellulolyticum}

MQDPTINPTSISAKGSFADTKITLTPNGNTFNGISELQSSQYTGTNEVTLASYLNTLPENTTKTLCDFGVGKKNPKLTIVLPKDIPGLE
>d1im3d_ b.1.1.6 (D:) Cytomegalovirus protein US2 {Human cytomegalovirus}
PWFQJEDNRCYIDNGKLFARGSVGNMSRFVFDPKADYGGVGENLYHADDVEFVGESLKWNVRNLDVMPIFETLALRLVLQGDVIWLRCVPEL
>d1jjua3 b.1.1.6 (A:274-351) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}
AAPQVLAVAPARLKIGEETQLRVAGTGLGSDLTPEGVAGSVESAGNGVTKLATGTPGPVSLELGGQKVDLVAYD
>d1jjua4 b.1.1.6 (A:352-489) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}
RPDRISIVPDLTIAIRIGGNGGPVKPAQFEAMGWLNPGDQPGTGDDIALGAFPASWATDNFDEEAEMQDAKYAGSIDDTGLFTPAAEGPNPER
PMQTNNAGNLKVIATVDAEAEPLSAEAHLYATVQRFDVAPIR
>d1jmxa3 b.1.1.6 (A:282-363) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Pseudomonas putida}
GKARLLAVQPAFIKAGGESEITLVGSGLAGKPDLGAGVEVTEVLEQTPTLVRKARAADAKPGQREAVGTLKGVNLAVYD
>d1jmxa4 b.1.1.6 (A:364-494) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Pseudomonas putida}
KVEEVKVVPAFSIARIGENGASVPKVQGRFEAEAWGKDANGQPLRIGYLPSWKVEPFNERAVEDEDVKFAGKMQADGVFVPGGAGPNPERKM
MTNNAGNLKVIATLADGGQTGEGHMIVTVQRWNPNPLP
>d2hft_1 b.1.2.1 (1-106) Extracellular region of human tissue factor {Human (Homo sapiens)}
SGTTNTVAAYNLTWKSTNFK TILEWEPKPVNVQYTVQISTKSGDWKSCKFCYTTDTECDLTDEIVKDVQTYLARVFSYPAGNVESTGSAGEPLYENSPE
FTPYLET
>d2hft_2 b.1.2.1 (107-211) Extracellular region of human tissue factor {Human (Homo sapiens)}
NLGQPTIQSFSEQVGTKVNVTVEDERTLVRRNNFLSLRDVFGKDLIYTLYWKSQQEKGEFRSGKKTAKTNTNEFLIDVDKGENYCFSVQAIPSRTV
NRKSTDSPVEMCG
>g1dan.1 b.1.2.1 (T.;U:91-106) Extracellular region of human tissue factor {Human (Homo sapiens)}
TVAAYNLTWKSTNFK TILEWEPKPVNVQYTVQISTKSGDWKSCKFCYTTDTECDLTDEIVKDVQTYLARVFSYPAXEPLYENSPEFTPYLET
>d1a21a1 b.1.2.1 (A:4-106) Extracellular region of human tissue factor {Rabbit (Oryctolagus cuniculus)}
TGRAYNLTWKSTNFK TILEWEPKSIDHVYTVQISTRLENWKSCKFLTAETECDLTDEVVKDVGQTYMARVLSYPARNGNTTGFPEEPFRNSPEFTPYL
DTNL
>d1a21a2 b.1.2.1 (A:107-208) Extracellular region of human tissue factor {Rabbit (Oryctolagus cuniculus)}
GQPTIQSFSEQVGTKLNVTVQDARTLVRRNGTFLSLRAVFGKDLNYTLYWRASSTGKKTATTNTNEFLIDVDKGENYCFSVQAIPSRKQRSPESLT
ECT
>d1fnf_1 b.1.2.1 (-) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
RDLEVVAATPTSLISWDAPAVTVRYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDYTITVYAVTGRGDSPASSKPIINYRTEI
>d1fnf_1 b.1.2.1 (1142-1235) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
PLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRITTPNGQQGSLEEVVHADQSSCTFDNLSPGLEYNVSVYTVKDDKESVPISDTIIPA
>d1fnf_2 b.1.2.1 (1236-1326) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
VPPPTDLRFTNIGPDTMRVTWAPPSIDLNFLVRYSPVKNEEDVAELSIISPSDNAVLTNLLPGTEYVVSVSSVYEQHESTPLRGRQKTC
>d1fnf_3 b.1.2.1 (1327-1415) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
LDSPTGIDFSIDTANSFTVHWIAPRATITGYRIRHHPEHFSGRPREDRVPHSRNSITLTNLTQPGTEYVVIVALNGREESPILLQQST
>d1fnha1 b.1.2.1 (A:3-92) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
PAPTDLKFTQVPTSLAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSSVVSGLMVATKYEVSYALKDTLSRPAQGVVTLE
>d1fnha2 b.1.2.1 (A:93-182) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
NVSPPRRARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKPDVRSYТИGLQPGTDYKIYLTNDNARSSPVVIDASTA
>d1fnha3 b.1.2.1 (A:183-271) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
IDAPSNLRLFLATTPNSLLVSWQPPRARITYIICKYEPKGSPPREVVRPRPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKT
>d1j8ka_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
NIDRPKGLAFTDVDVDSIKIAWESPQGQVSRYRTVYSSPEDGIHELPAPDGEEDELAELQGLRPGSEYTVSVALHDDMESQPLIGTQSTAIPA
>d2fnba_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}

MRGSEVPQLTDLFVDITDSSIGLRWTPLNSSTIIGYRITVVAAGEGIPIFEDFVDSSVGYVTVTGLEPGIDYDISVITLINGGESAPTTLTQQT
>d2mfn_1 b.1.2.1 (1-92) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}
GLDSPTGFDSIDTANSFTVHWVAPRAPITGYIIRHHAESVGRPRQDRVPPSRNSITLNLNPQTEYVVIIAVNGREESPPLIGQQATVS
>d2mfn_2 b.1.2.1 (93-184) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}
DIPRDLEVIASTPTSLLISWEPAPASVRYRITYGETGGNNSPQEFTVPGSKSTATINNIKPGADYTITLYAVTGRGDSPASSKPVSINYKT
>d1qr4a1 b.1.2.1 (A:1-87) Tenascin {Chicken (Gallus gallus)}
DNPKDLEVSPTETTLRLWRPPVAKFDRYRLTYVSPSGKKNEIMEIPVDSSTSFLRGLDACTEYTLISLVAEKGRHKSKPTTIKGSTV
>d1qr4a2 b.1.2.1 (A:88-175) Tenascin {Chicken (Gallus gallus)}
VGSPKGIFSDITENSATVSWTPPSRSRVDSYRVSYVPITGGTPNVVTDGSKTRTKLVKLPGVDYNVNIISVKGFESEPIGILKT
>d1ten__ b.1.2.1 (-) Tenascin {Human (Homo sapiens)}
RLDAPSQIEVKDVTDTTALITWFKPLAEIDGIELTYGIKDVGPDRTTIDLTEDENQYSIGNLKPDTYEVSISRRGDMSSNPAKETFTT
>d1cfb_1 b.1.2.1 (610-709) Neurogian, two amino proximal Fn3 repeats {Drosophila melanogaster}
IVQDVPNAPKLTGTCQADKAIEIHWEQQGDNRSPILHYTIQFNTSFTPASWDAAYEKVPTNDSSFVVQMSPWANYTRVIAFNKIGASPPSAHDSC
TTQ
>d1cfb_2 b.1.2.1 (710-814) Neurogian, two amino proximal Fn3 repeats {Drosophila melanogaster}
PDVPFKNPNDNVVGQGTEPNVLISWTPMPEIEHNAPNFHYYVSWKRDIPAAWENNIFDWRQNNIVIADQPTFVKYLIKVVAINDRGESNVAEE
EVVGYSGEDR
>d1qg3a1 b.1.2.1 (A:1126-1217) Integrin beta-4 subunit {Human (Homo sapiens)}
DLGAPQNPNAKAAGSRKIHFNWLPSSGKPMGYRVKYWIQGDSESEAHLDSKVPSVELTNLYPCDYEMKVCAYGAQGEGPYSSLVSCRTHQ
>d1qg3a2 b.1.2.1 (A:1218-1320) Integrin beta-4 subunit {Human (Homo sapiens)}
EVPSEPGRILAFNVSSVTQLSWAEPETNGEITAYEVYGLVNDDNRPIGPMKKVLVDNPKNRMILLIENLRESQPYRTVKARNGAGWGPEREAI
NLATQP
>d1axib1 b.1.2.1 (B:32-130) Growth hormone receptor {Human (Homo sapiens)}
EPKFTKCRSPERETFSCHWTDEVHHGTKNEGPIQLFYTRRNTQEWTQEWKECPDYVSAGENSCYFNSSFTSIAIPYCIKTSNGGTVDCKFSVDEIV
Q
>d1axib2 b.1.2.1 (B:131-236) Growth hormone receptor {Human (Homo sapiens)}
PDPIALNWTLNVSLLGHADIQVRWEAPRNADIQKGWMVLEYELQYKEVNETKWKMMDPILTTSVPVSLKVDKEYEVVRVSKQRNSGNYGEF
SEVLYVTLQPQ
>d1eerb1 b.1.2.1 (B:8-116) Erythropoietin (EPO) receptor {Human (Homo sapiens)}
DPKFESKAALLAARGPEELLCFTERLEDLVCWEEAASAGVPGQYSFYQLEDEPWKLCLRHQAPTARGAVRFWCSLPTADTSSVPLELRVTAASG
APRYHRVIHIN
>d1eerb2 b.1.2.1 (B:117-220) Erythropoietin (EPO) receptor {Human (Homo sapiens)}
EVVLLDAPVGLVARLADES GHVVLRLWLPPPETPMTSHIRYEVDVSAGQQGAGSVQRVEILEGRTECVLSNLRGTRYTFAVRARMAEPSFGFWSEW
SEPVSLLT
>d1bp3b1 b.1.2.1 (B:202-300) Prolactin receptor {Human (Homo sapiens)}
LPPGKPEIFKCRSPNKETFTCWWWRPGTDGLPTNYSLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVD
VTYI
>d1bp3b2 b.1.2.1 (B:301-404) Prolactin receptor {Human (Homo sapiens)}
VQPDPPLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTFWFTLLYEIRLKPEKAAEWEIHFAQQQTEFKILSLHPGQKYLVQVRCKPDHG YWSAWSPAT
FIQIPS
>d1f6fb1 b.1.2.1 (B:5-100) Prolactin receptor {Rat (Rattus norvegicus)}
GKPEIHKCRSPDKETFTCWWNP GTDGLPTNYSLTYSKEGEKTTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGSSSSDPLYVDVTYI
>d1f6fb2 b.1.2.1 (B:101-203) Prolactin receptor {Rat (Rattus norvegicus)}
VEPEPPRNLTLEVQLDKKTYLWVKWSPPTIDVKTGWFTMEYEIRLKPEEAEWEIHFTGHQTQFKVFDLYPGQKYLVQTRCKPDHG YWSRWSQ

ESSVEMP

>d1iarb1 b.1.2.1 (B:1-96) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}

FKVLQEPTCVSDYMSISTCEWMNGPTNCSTELRLLYQLVFLLSEAHTCIPENNGAGCVCHLLMDDVVSADNYTLWAGQQLLWKGSKPKSEHV

>d1iarb2 b.1.2.1 (B:97-197) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}

KPRAPGNTLVHTNVSDDLTSNPYPPDNYLYNHLYAVNIWSENDPADFRIYNVTLEPSLRIAASLKGSIYRARVRAWAQAYNTTWSEWPST
KWH

>d1egja_ b.1.2.1 (A:) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

IQMAPPSLNVTKDGDSYSLRWETMKMRYEHIDHTFEIQYRKDTATWKDSKTETLQNAHSMALPALESTRYWARVRVRSRTGYNGIWSEWSEAR
SWDTE

>d1gh7a1 b.1.2.1 (A:1-103) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

EEIPLQLRCYNDYTSHITCRWADTQDAQRLVNVTLIRRVNEDLLEPVSCDLSDMPWSACPHPRCVPRRCVIPCQSFVTDVDYFSFPDRPLGT
RLTVL

>d1gh7a2 b.1.2.1 (A:104-217) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

TQHVPQPPEPRDLQISTDQDHFLLTWSVALGSPQSHWLSPGDLEFEVVYKRLQDSWEDAIIILNTSQATLGPEHLMPSTYVARVRTRLAPGSRLSG
RPSKWSPEVCWDSQPGD

>d1gh7a3 b.1.2.1 (A:218-316) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}

EAQPQNLECFDGAAVLSCSWEVRKEVASSVSFGLFYKPSDAGSAVLLREECSPVLREGL GSLHTRHHCQIPVDPATHGQYIVSVQPRRAEKHIKS

>d1cd9b1 b.1.2.1 (B:1-107) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse (Mus musculus)}

AGYPPASPSNLSCLMHLLTNSLVCQWEPPGPETHLPTSFLKSFRSRADCQYQGDTIPDCVAKKRQNNCSIPRKNLLYQYMAIWVQAENMLGSSEPK
KLCLDPMDVV

>d1cd9b2 b.1.2.1 (B:108-213) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse (Mus musculus)}

KLEPPMLQALDIGPDVVSHQPGCLWLSWPWKPSEYMEQECELRYQPQLKGANWTLVFHLPSKQFELCGLHQAPVYTLQMRCIRSSLPGFWSP
PWSPGLQLRPTM

>d1fyhb1 b.1.2.1 (B:12-109) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}

VPTPTNVTIESYNMNPIVYWEYQIMPQPVFTVEVKNYGVKNSEWIDACINISHHYCNISDHVGDPNSLWVRVKARVGQKESAYAKSEEFAVCRD
GK

>d1fyhb2 b.1.2.1 (B:110-223) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}

IGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVDYDPETTCYIRVNVYVRMNGSEIQYKILTQKEDDCDEIQCQLAIPVSSLNSQYCVSAEGVLHWG
VTTEKSKEVCITIFN

>d1bqua1 b.1.2.1 (A:5-99) Cytokine receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

GLPPEPKPNLSCIVNEGKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTSCTVDYSTVYFVNIEVVVAEANALGVTSDFHINFDPV

>d1bqua2 b.1.2.1 (A:100-214) Cytokine receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

YKVKPNNPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDASTRSSFTVQDLKPFTEYVFRICRMKEDGKGWSDWSEEA
SGITYEDRPSKEPSF

>d1i1ra1 b.1.2.1 (A:2-101) Cytokine receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

LLDPCGYISPESPVQVLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIASLNIQLTCNLTFGQLEQNVTGQIISG

>d1j7vr1 b.1.2.1 (R:2-100) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}

GTELPSPPSVWFEAEFFHHILHWTPIPQQSESTCYEVALLRYGIESWNNSISQCSQTLSYDLTAUTLDLYHSNGYRARVRAVDGSRHSQWTNTRFSV
D

>d1j7vr2 b.1.2.1 (R:101-206) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}

EVTLTVGSVNLIEHNGFILGKIQLPRPKMAPAQDTYESIFSHFREYEIAIRKPGQFTFHKVKHEQFSLTSGEVGEFCVQVKPSVASRSNKGWWSK
EECISLT

>d1bpv__ b.1.2.1 (-) Type I titin module {Human (Homo sapiens)}

SPIDPPGKPVPLNITRHTVTLWAKPEYGGFKITSYIVEKRDLPNGRWLKANFSNILENEFTVSGLTEDAAYEFRVIAKNAAGAISPPSEPSDAITCRDD

VEA

>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)}

GIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWLTTLSTDLTFSVKSSRGSSDPQGVTCAATLSAERVRGDNKEYEYVSECQEDSACPAAEESLPI
EVMVDAVHKLKYE NYTSFFIRDII

>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)}

KPDPPKLNQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYSSSWEVASVPCS

>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}

TQISDFHVATRFNDDFSRAVLEAEVQMCGELRDYLRTVSLWQGETQVASGTAPFGGEIIDERGGYADRVTRLNVENPKLWSAEIPNLYRAVVELHT
ADGTLIEAEACDVGFR

>d1jz8a2 b.1.4.1 (A:626-730) beta-Galactosidase, domains 2 and 4 {Escherichia coli}

FFQFRLSGQTIEVTSEYLFRHSDNELLHWMVALDGKPLASGEVPLDVA PQGKQLIELPELPQPESAGQLWLTVRVVQPNA TAWSEAGHISAWQQW
RLAENLSVTL

>d1bhga1 b.1.4.1 (A:226-328) beta-Glucuronidase {Human (Homo sapiens)}

TYIDDITVTSVEQDSGLVNYQISVKGSNLFKLEVRLDAENKV VANGTGTQGQLKPGVSLWWPYLMHERPAYL SLEVQLTAQTS LGPVSDFYTL
VGIRT

>d1f13a2 b.1.5.1 (A:516-627) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}

SNVDMDFEVENAVLGKDFKLSITFRNNSHNRYTITAYLSANITFYTGVPKAEFKKETFDVTLEPLSFKKEAVLIQAGEYMGQLLEQASLHFFVTARINET
RDVLAKQKSTVL

>d1f13a3 b.1.5.1 (A:628-728) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}

TIPEIIKVRGTQVGSDMTVTEFTNPLKETLRNVVWHL DPGVTRPMKKMFREIRPNSTVQWEEVCRPWVGHRKLIA MSSDSLRHVY GELDV
QIQRR

>d1g0da2 b.1.5.1 (A:472-583) Transglutaminase, two C-terminal domains {Red sea bream (Chrysophrys major)}

RLQLSIKHAQPVFGTDFDIVEVKNEGGRDAHAQLTMLAMAVTYNSLRRGECQRKTISVTVAHKAHKEVMRLHYDDYVRCVSEHHLIRVKALLDA
PGENGPIIMTVANIPLS

>d1g0da3 b.1.5.1 (A:584-684) Transglutaminase, two C-terminal domains {Red sea bream (Chrysophrys major)}

TPELLVQPGKAVVWEPLTAYVSFTNPLPVPLKGGVFTLEGAGLLSATQIHNGAVAPSGKVS VKLSFSPMRTGVRKLLVDFSDRLKDVKGTTVV
HKK

>d1ncia_ b.1.6.1 (A:) N-cadherin (neural) {Mouse (Mus musculus)}

GSDWVIPPINLPENSRGPFQELVRIRSGRDKNLSSLRYSVTGPGADQPPTGIFIINPISGQLSVTKPLDRELIARFH LRAHAVDINGNQVENPIDIVINV
D

>d1ncja2 b.1.6.1 (A:102-215) N-cadherin (neural) {Mouse (Mus musculus)}

NDNRPEFLHQVWNGSVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRIVSQAPSTPSNMFTINNETGDIITVAAGLDREKVQQYTLIIQATDME
GNPTYGLSNTATAVITVTD

>d1edha1 b.1.6.1 (A:3-101) E-cadherin (epithelial) {Mouse (Mus musculus)}

VIPPISCPENEKGEFPKNLVQIKSNRDKETKVFYSITGQGADKPPVGFIIERETGWLKV TQPLDREIAKYI LYSHAVSSNGEAEDPMEIVITVTDQ

>d1edha2 b.1.6.1 (A:102-213) E-cadherin (epithelial) {Mouse (Mus musculus)}

NDNRPEFTQEVFEGSVAEGAVPGTSVMKVSATDADDDVN TYNAAIAYTIVSQDPELPHKNMFTVNRDTGVISVL TSGLDRESYPTTLVQAADLQ
GEGLSTTAKAVITVKD

>d2mcm__ b.1.7.1 (-) Macromycin {Streptomyces macromomyceticus}

APGVTVTPATGLSNGQTVTSATGLTPGTVYHVGQCAVVEPGVIGCDATTSTDVTADAAGKITAQLKVHSSFQAVVGADGTPWGTVNCKVVSCSA
GLGSDSGEGAAQA ITFA

>d1noa__ b.1.7.1 (-) Neocarzinostatin {Streptomyces carzinostaticus}

AAPATATVTPSSGLSDGTV/KVAGAGLQAGTAYDVGQCAWVDTGVACNPADFSSVTADANGSASTSLTVRRSFEGFLFDGTRWGTVDCTTAACQV
GLSDAAGNGPEGVAISFN
>d1acx__ b.1.7.1 (-) Actinoxanthin {Actinomyces globisporus, number 1131}
APAFSVSPASGASDGQSVSVAAGETYYIAQCAPVGGQDACNPATATSFTTDASGAASFSTVRKSYAGQTPSGTPVGSVDCATDACLNGAGNS
GLNLGHVALTFG
>d1hzka_ b.1.7.1 (A:) Antitumor antibiotic C-1027 apoprotein {Streptomyces globisporus}
APAFSVSPASGLSDGQSVSVSGAAAGETYYIAQCAPVGGQDACNPATATSFTTDASGAASFVVRKSYTGSTPEGTPVGSVDCATAACNLGAGN
SGLDLGHVALTFG
>d1akp__ b.1.7.1 (-) Kedarcidin (apo form) {Actimomycete, strain L585-6}
ASAAVSVSPATGLADGATVTSASGFATSTSATALQCAILADGRGACNVAEFHDFSLSGGEGETSVVRRSFTGYVMPDGPEVGA/DCDTAPGGCEI
VVGGBTGEYGNAAISFG
>d1cbja_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Cow (Bos taurus)}
ATKAVCVLKGDPVQGTHFEAKGDTVVVTGSITGLTEGDHGFLHVHQFGDNTQGCTSAGPHFNPLSKKHGGPKDEERHVGDLGNVTADKNGVAIV
DIVDPLISLSGEYSIIGRTMVVHEKPDDLGRGGNEESTKTGNAGSRLACGVIGIAK
>d1azva_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Human (Homo sapiens)}
ATKAVCVLKGDPVQGIIINFEQKESNGPVKVWGSIKRLEGLHGFHVHEFGDNTAGCTSAGPHFNPLSRKHGGPKDEERHVGDLGNVTADKDGVA
DVSIEDSVISLSDGDHCIIIGRTLVVHEKADDLGKGGNEESTKTGNAGSRLACGVIGIAQ
>d1xsoa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {African clawed frog (Xenopus laevis)}
VKAVCVLAGSGDVKGVVHFEQQDEGAVSVEGKIEGLTDGLHGFHIHVFGDNTNGCMSAGSHFNPNENKNHGAPGDTDRHVGDLGNVTAEggVA
QFKITDSLISLKGPNIIIGRTAVVHEKADDLGKGGNDESLKTGNAGGRLACGVIGYSP
>d1srda_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Spinach (Spinacia oleracea)}
ATKKAVAVLKGTNSVNVGTTQEDDGPTTVNRISGLAPGKHFHLHEFGDTTNGCMSTGPHFNPKTHGAPEDEVRHAGDLGNIVANTDGVA
EATIVDNQIPLTPNSVVGALVHELEDDLGKGHHELSPPTGNAGGRLACGVVGLTP
>d1jcv__ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Baker's yeast (Saccharomyces cerevisiae)}
VQAVAVLKGDAVGSGVVKFEQASESEPTVSYEAGNSPNAERGFHIHEFGDATNGCVSAGPHFNPKTHGAPTDEVRHVGDMGNVKTDENGV
AKGSFKDSLIKLIGPTSVVGRSVVIHAGQDDLGKDTESSLKTGNAGPRPACGVIGLTN
>d1yaia_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Photobacterium leiognathi}
QDLTVKMTDLQTGKPGTIELSQNKYGVVFTPELADLTPGMHGFHIHQNGSCASSEKDGVVLGGAAGGHYDPEHTNKHGFPTDDNHKGDL
ALFVSANGLATNPVLAPRTLKELKGHAIMIHAGGDNHSDMPKALGGGGARVACGVIQ
>d1eso__ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Escherichia coli}
ASEKVEMNIVTSQGVGQSIGSVTITEDKGLEFSPDLKALPPGEHGFFHAKGSCQPATKDGA
SAEASAGGHLDPQNTGKHEGPEGAGHLDPA
LVNNNDGKATDAVIAPRLKSLDEIKDKALMVHVGGDNMSDQP
KPLGGGGERYACGVIK
>d1eqwa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Salmonella typhimurium}
NTLTVKMNDALSSGTGENIGEITVSETPYGLLFTP
HLNLGTPGIHGFLHVHTNPSCMPGMKD
KEVPALMAGGHLDPEKTGKHLGPYNDKGHLGDL
PGLVVNADGTATYPLA
PRLKSLSELKGHS
LMIHKGDN
YNSDKP
A
PLGGGGARFACGVIE
>d2apsa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Actinobacillus pleuropneumoniae}
EKLVVQVQLDPVKGNKDVGTV
EITESAYGLVFTPHLHGLA
QGLHGFIHQNP
SCEPK
EKG
D
GKLV
VAGLGAGGH
WD
PKET
KQHGP
WSDNA
HLGD
LPAL
FVE
HD
GSAT
NPV
LAP
RLK
L
DEV
KG
H
SLMI
HEGG
DN
HSD
HP
A
PL
GGGG
PR
MAC
GVIE
>d1ej8a_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
SSAVAILETFQKYTIDQKKDTAVRGLARI
VQVGEN
KTL
FDIT
VNG
VPEAG
NYHASI
HEK
GDV
SKGV
EST
GK
VWHKF
DEPI
EFC
N
ESDL
GK
LYS
>d1jk9b1 b.1.8.1 (B:74-245) Copper chaperone for superoxide dismutase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
GKPNSSAVAILETFQKYTIDQKKDTAVRGLARI
VQVGEN
KTL
FDIT
VNG
VPEAG
NYHASI
HEK
GDV
SKGV
EST
GK
VWHKF
DEPI
EFC
N
ESDL
GK
LYS

GKTFLSAPLPTWQLIGRSFVISKSLNHPENEPESSVKDYSFLGVIARSAGVWENNKKVCACTGKTVWEERKDALA
>d1do5a_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase, C-terminal domain {Human (Homo sapiens)}
QNLGAAVAILGGPGTVQGVVRFLQLTPERCLIEGTIDGLEPLGHGLHVHQYGDLTNCNSCGNHFPNDGASHGGPQDSRHRGDLGNVRADADG
RAIFRMEDEQLKVVWDVIGRSLLIDEGEDDLRGHHPLSKITGNSGERLACGIIRSAGLF
>d1d7ca_ b.1.9.1 (A:) Cytochrome domain of cellobiose dehydrogenase {Fungus (Phanerochaete chrysosporium)}
ESASQFTDPTTGFQFTGITDPVHDVTYGFVFPLATSGAQSTEFIGEVVAPIASKWIGIALGGAMNNNDLLVAWANGNQIVSSTRWATGYVQPTAYT
GTATLTLPETTINSTHWKVVFCQCQCTEWNNGGIDVTSQGVLAWSNVAVDDPSDPQSTFSEHTDFGFFGIDYSTAHSANYQNYLNGDSG
>d1i8aa_ b.1.9.2 (A:) Xylanase 10A {Thermotoga maritima}
MVATAKYGTPVIDGEIDEWNNTTEEETKAVAMGSLDNATAKVRVLWDENLYVLAIVKDPVLNKDNNSNPWEQDSVEIFIDENNHHKTGYYEDDDA
QFRVNVMNEQTFTGGSPARFKTAKLIEGGYIVEAAIKWTKPNTVIGFNIQVNDANEKGQRVGIIWSDPTNNSWRDPSKFGNLRLIK
>d1qtsa1 b.1.10.1 (A:692-824) Alpa-adaptin AP2, N-terminal subdomain {Mouse (Mus musculus)}
GSPGIRLGSSEDNFARFVCKNNGVLFENQLLQIGLKEFRQNLGRMFIFYGNKTSTQFLNFTPLICADDLQTNLNLTQPKVDPTVDGGAQVQQVNN
IECISDFTEAPVNIQFRYGGTFQNVSVKLPI TLNK
>d1e42a1 b.1.10.1 (A:705-824) Beta2-adaptin AP2, N-terminal subdomain {Human (Homo sapiens)}
GGYVAPKAVWLPVAKAKGLEISGTFTHRQGHYMEMNFTNKALQHM TDFAIQFNKNSFGVIPSTPLAIHTPLMPNQSIDVSLPLNTLGPVMKMEPL
NNLQVAVKNNIDVFYFSCLIPLVN
>d1jv2a1 b.1.15.1 (A:439-598) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo sapiens)}
PVITVNAGLEVPSILNQDNKTCSPGTALKVSCFNRFLKADGKGVPLRNQVLELLDKLKQKGAI RALFLYSRSPSHSKNMTISRGGLMQCEE
LIAYLRDESEFRDKLTPITIMEYRLDYRTAADTTGLQPILNQFTPANISRQAHILLDCGE
>d1jv2a2 b.1.15.1 (A:599-737) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo sapiens)}
DNVCKPKLEVSDQDKKIYIGDDNPLTLIVKAQNQGEGAYEAELIVSIPLQADFIGVVRNNEALARLSCAFKTENQTRQVVCDLGNPMKAGTQLLA
GLRFSVHQQSEMDTSVKFDLQIQSSNLFDKVSPVVSHKVDA
>d1jv2a3 b.1.15.1 (A:738-956) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo sapiens)}
VLA AVEIRGVSSPDHVFLPIPWN EHENPETEEDVGPVQVHIYERLNNGPSSFSKAMLHLQWPYKYNNNNTLLYLHYDIDGPMNCTSDMEINPLRIK
SSLQTTEKNDTVAGQGERDHLLKRD LASEGDIHTLGCVAQCLKIVCQVGRDRGKSAILYVKSLLWTETFMNKENQHNSYSLKSSASFNVIEFPYK
NLPIEDITNSTLTTNVTWGIQ
>d1jv2b1 b.1.15.1 (B:55-106,B:355-434) Hybrid domain of integrin beta {Human (Homo sapiens)}
EFPVSEARVLEDPLSDKGSGDSSQVTQVSPQRIALRLRPDDSKNFNSIQVRQXVELEVRDLPEELS FNATCLNNEVIPGLKSCMGLKIGDTVSFSIEA
KVRGCPQEKEKSFTIKPVGFKDSLIVQVTFDCD
>d1qpxa1 b.1.11.1 (A:1-124) Pilus chaperone PapD, N-domain {Escherichia coli}
AVSLDRTRA VFDGSEKSMTLDISNDNQKLPYLAQAWIENENQE KIITGPVIATPPVQRLDPAKSMVRLSTTPDISLPQDRESLFYFNLREIPPRSEKA
NNVQIALCTKIKL FYRPAAIKTR
>d1quna1 b.1.11.1 (A:1-121) Periplasmic chaperone FimC {Escherichia coli}
GVALGATRVIPAGQKQVQLAVTNNDENSTYLIQS WVENADGVKDGRFIVTPPLFAMKGKKENTL RILDATNNQLPQDRESLFWMNVKAIPSMDK
SKLTENTLQLAIISRIKLYYRPAKLA
>d1mspa_ b.1.11.2 (A:) Major sperm protein, alpha isoform (recombinant), ph 4.6 {Pig roundworm (Ascaris suum)}
SVPPGDINTQPSQKIVFNAPYDDKHTYHIKITNAGGRRIGWAIKTTNMRRLSVDPPCGVLDPEKVLMAVSCDTFNAATEDLNNDRITIEWTNTPD
GAAKQFRREWFGDG MVRRKNLPIEYLN
>d4kbpa1 b.1.12.1 (A:9-120) Purple acid phosphatase, N-terminal domain {Kidney bean (Phaseolus vulgaris)}
RDMPLDSDVFRVPPGYNAPQQVHITQGDLVGRAMIISWVTMDEPGSSAVRYWSEKNGRKRIAKGKMSTYRFFNYSSGFIHHTTIRKLKYNTKYYE
VGLRNTRRFSFITPP
>d1dqia_ b.1.13.1 (A:) Superoxide reductase (SOR) {Archaeon Pyrococcus furiosus}
MISETIRSGDWKGEKHVPVIEYEREGELVKVKVQVGKEIPHNTTEHHIRYIELYFLPEGENFVYQVGRVEFTA HGESVNGPNTSDVYTEPIAYFVLKTK
KKKGKLYALS YCNIHGLWENEVTL

>d1dfx_1 b.1.13.1 (37-125) Desulfoferrodoxin C-terminal domain {Desulfovibrio desulfuricans}
VEGSTDGAMEKHVPVIEKVDGGYLIKVGSPHPMEEKHWIEWIELLAGRSYTKFLPGDAPEAFFAIDASKVTAREYCNLHGHWAEN

>d1f00i1 b.1.14.1 (I:658-752) Intimin {Escherichia coli}
ASITEIKADTTAVANGQDAITYTVKVMKGDKPVSQNQEVFTTTLGKLSNSTEKTDTNGYAKVLTSTPGKSLVSARVSDVAVDVKAPEVEFFT

>d1f00i2 b.1.14.1 (I:753-841) Intimin {Escherichia coli}
TLTIDDGNIIEIVGTGVKGKLPTVWLQYGQVNLSASGGNGKYTWRSANPAIASVDASSGQVTLKEGTTTISVISSDNQTATYTIATPNS

>d1cwva1 b.1.14.1 (A:503-596) Invasin {Yersinia pseudotuberculosis}
LTLTAAVIGDGAPANGKTAITVEFTVADFEGKPLAGQEVVITNNNGALPNKITEKTDANGVARIALNTTDGTVVTAEVEGQRQSVDTHFVKKG

>d1cwva2 b.1.14.1 (A:597-692) Invasin {Yersinia pseudotuberculosis}
TIAADKSTLAAPTSIIADGLMASTITLELKDTYGDPQAGANVAFDTTLGNMGVTDHNDGTYAPLSTTLGVATVTKVDGAASFSPVTVNFT

>d1cwva3 b.1.14.1 (A:693-795) Invasin {Yersinia pseudotuberculosis}
ADPIPDAGRSSFTVSTPDILADGTMSSLSFVPPDKNGHFISGMQGLSFTQNGVPVISPIEQPDSYATVVGNSVGDTVITPQVDTLILSTLQKKISL
FPV

>d1cwva4 b.1.14.1 (A:796-886) Invasin {Yersinia pseudotuberculosis}
PTLTGILNGQNFATDKGFPKTFKNATFQLQMDNDVANNTQYEWSSEFTPNVSVNDQGQVTITYQTYSEAVTAKSKKFPSYSYRFYP

>d1f0la1 b.2.1.1 (A:381-535) Diphtheria toxin, C-terminal domain {Corynebacterium diphtheriae}
SPGHKTQPFLHDGYAVSWNTVEDSIIRTGFQGESGHDIKITAENTPLPIAGVLLPTPGKLDVNKSCTHISVNGRKIRMRCAIDGDVTFCRPKSPVY
GNGVHANLHVAFHRSSSEKIHSNEISSDSIGVLGYQKTVDHTKVNSKLSLFFEIKS

>d1exh__ b.2.2.1 (-) Exo-1,4-beta-D-glycanase (cellulase, xylanase), cellulose-binding domain, CBD {Cellulomonas fimi}
ASSGPAGCQVLWGVNVQWNTGFTANVTVKNTSSAPVDGWTLTFSFPSGQQVTQAWSSTVTQSGSAVTRNAPWNGSIPAGGTAQFGFNGSHTG
TNAAPTAFLNLNGTPCTVG

>d1e5ba_ b.2.2.1 (A:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas fimi}
TGCSVTATRAEWSDFNVTYSVGSAAWTVNLAQNGSQTIQASWNANVTGSGSTRVTPNGSGNTFGVTVMKNGSSTTPAACAGS

>d1hejc_ b.2.2.1 (C:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas fimi}
TGSCSVSAVRGEEWADRFNVTYSVGSSSWVTLGLNGGQSVQSSWNAALTGSSGT TARPNSGNSFGVTFYKNGSSATPGATCATG

>d1nbca_ b.2.2.2 (A:) Cellulosomal scaffolding protein A, scaffoldin {Clostridium thermocellum}
NLKVEFYNSNPSDTTNSINPQFKVTNTGSSAIDLSQLTRYYTVDGQKDQTFWCDHAIIGSNGSYNGITSNVKGTFVKMSSSTNNADTYLEISFTG
GTLEPGAHVQIQGRFAKNDWSNYTQSNDYSFKSASQFVEWDQVTAYLNGVLVWGKEP

>d1g43a_ b.2.2.2 (A:) Cellulosomal scaffolding protein A, scaffoldin {Clostridium cellulolyticum}
AGTGVVSVQFNNGSSPASSNSIYARFKVTNTGSPINLADKLRLYYTQDADKPLTFWCDHAGYMSGNSYIDATSKVTGSFKAVSPAVENTADHYLEVA
LNSDAGSLPAGGSIEIQTRFARNDWSNFDQSNDWSYTAAGSYMWDWKQKISAFVGGTLAYGSTP

>d1tf4a2 b.2.2.2 (A:461-605) Endo/exocellulase:cellobiose E-4, C-terminal domain {Thermomonospora fusca}
PEIFVEAQINTPGTTFEIKAMIRNQSGWPARMQLDKGTFRYWFTLDEGVDPADITVSSAYNCATPEDVHHVSGDLYYVEIDCTGEKIFPGQQSEHR
REVQFRIAGGPGWDPNSNDWSFQGQIGNELAPAPYIVLYDDGVPVWGTAP

>d1anu__ b.2.2.2 (-) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}
VVVEIGKVTGSGVTTEIPVYFRGVPSPKGIANCDFVFRYDPNVLEIIGIDPGDIIVDPNPTKSFDTAIPDRKIIIVLFAEDSGTGAYAITKDGVFAKIRATV
KSSAPGYITFDEVGGFADNDLVEQKVFSIDGGVNV

>d1aoha_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}
AVRIKVDVTNAKPGDTVRIPVRFSGIPSKGIANCDFVSYDPNVLEIIIEPGEIIVDPNPTKSFDTAIPDRKMIIVLFAEDSGTGAYAITEDGVFATIVA
KVKSGAPNGLSVIKFVEVGGFANNDLVEQKTQFFDGGVNV

>d1g1ka_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}
ASLKVTVGTTANGKPGDTVTPVTFADVAKMKNVGTNCYLGYDASLLEVSVDAGPIVKNAAVNFSSASNGTISFLFLDNTITDELITADGVFANIKF
KLKSVTAKTTTPVTFKDGGAFGDTMSKIASVTKTNGSVTIDPG

>d1qba_2 b.2.2.3 (28-200) Bacterial chitobiase, n-terminal domain {Serratia marcescens}

DQQLVDQLSQLKLNVKMLDNRAGENGVDCAALGADWASCNRVLFTLSNDGQAIDGKDWWIYFHSPRQTLRVNDQFKIAHTGDLYKLEPTAKFS
GFPAGKAVEIPVVAEYWQLFRNDFLPRWYATSGDAKPKMLANTDTENLDQFVAPFTGDQWKRTKDDKNILMTPASRFV
>d1amx_ b.2.3.1 (-) Collagen-binding domain of adhesin {Staphylococcus aureus}
TSSVFYYKTGDMLPEDTTHVRWFNLINNEKSYVSKDITIKDQIQGGQQLDLSTLNINVGTHSNYSGQSAITDFEKAFPGSKITVDNTKNTIDVTIPQ
GYGSYNSFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVHN
>d1qunb1 b.2.3.2 (B:1-158) Mannose-specific adhesin FimH {Escherichia coli}
FACTTANGTAIPIGGGSANVYVNAPVVNVGQNLVVDLSTQIFCHNDYPETITDYVTLQRGSAYGGVLSNFSGTVKYSGSSYPFPTTSETPRVVNSRT
DKPWPVALYLPVSSAGGVAIKAGSLIAVLILRQTNNYNSDDFQFVWNIIYANNDVVPT
>d1qunb2 b.2.3.2 (B:159-279) Mannose-specific adhesin FimH {Escherichia coli}
GGCDSARDVTVTLPDYPGSVPIPLTVYCAKSQNLGYLSGTTADAGNSIFTNTASFSPAQGVGVQLTRNGTIIPANNTVSLGAVGTSAVSLGTANYA
RTGGQVTAGNVQSIIGVTFYQ
>d1pdkb_ b.2.3.2 (B:) PapK pilus subunit {Escherichia coli}
LLDRPCHVSGDSLKNHVVFKTRASRDFWYPPGRSPTESFVIRLENCHATAVGKIVTLFKGTEEAALPGHLKVTGVNAGRLGIALLTDGSSLKPGTS
HNKGQGEKVTGNSLELPFGAYVATPEALRTKSVVPGDYEATATFELTYR
>d1j8ra_ b.2.3.3 (A:) PapG adhesin receptor-binding domain {Escherichia coli}
WNNIVFYSLGDVNSYQGGNNVITQRQPQITSWRPGIATVTWNQCNGPEFADGFWAYYREYIAWVVFPKKVMQTQNGYPLFIEVHNKGWSSEENTG
DNDSYFFLKGYKWDERAFDAGNLCQKPGEIFLTFKVALPADLPLGDYSVKIPYTSQMQRHFASYL GARFKIPYNVAKLPRENEMLFLFKNI
GG
>d1edya_ b.2.4.1 (A:) alpha-1-macroglobulin {Rat (Rattus norvegicus)}
EAPFTLKVNLTPLNFDKAEEHRKFQIHNIVSYIGERPNNSNMIVDVKMVSGFIPVKPSVKKLQDQSNIQRTEVNTNHVLIYEKLTNQTMGFSFAVEQ
DIPVKNLKAPVKVYDYYETDEFAIEEYSAPFSSDS
>d1bv8a_ b.2.4.1 (A:) alpha-2-macroglobulin {Human (Homo sapiens)}
EEFPFALGVQLPQTCDEPKAHTSFQISLSVSYTGSRASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTEVSSNHLIYLDKVSNQTLSLFFTQLQ
DVPVRDLKPAIVKVYDYYETDEFAIAEYNAPCSKDLGNA
>d1ayoa_ b.2.4.1 (A:) alpha-2-macroglobulin {Cow (Bos taurus)}
EFPALEVQTLQTCDEPKAHTSFQISLSVSYIGSRPASNMAIVDVKMVSGFIPLKPTVKMLERSNVSRTEVSSNHLIYLDKVTNETLTLFTVLQDIP
VRDLKPAIVKVYDYYETDEFAVAEYSAPCS
>d1ycsa_ b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Human (Homo sapiens)}
VPSQKTYQGSYGFRLGLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPGTRVRAMAIYKQSQHMTEVRRCPHHERCSDSDGLAPP
QHLIRVEGNLRVEYDDRNTFRHSVVVPYEPPEVGSDCTTIHYNMCNSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCACPGRDRRTEEE
>d1hu8a_ b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Mouse (Mus musculus)}
TYQGNYGFHLGFLQSGTAKSVMCTYSPPLNKLFQLAKTCPVQLWVSATPPAGSRVRAMAIYKKSQHMTEVRRCPHHERCSDGDGLAPPQHLIR
VEGNAPEYLEDRQTRHSVVVPYEPPEAGSEYTTIHYKYMNCNSCMGGMNRRPILTIITLEDSSGNLLGRDSFEVRVCACPGRDRRTEEE
>d1a02n2 b.2.5.1 (N:399-576) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}
WPLSSQSGSYELRIEVQPKPHRAHYETEGSRGAVKAPTGGHPVVQLHGYMENKPLGLQFIGTADERILKPHAFYQVHRITGKTVTTSYEKIVGNT
KVKLEIPLEPKNNMRATIDCAGILKLRNADIELRKGETDIGRNTRVRLVFRVHPESSGRIVSLQTAASNPIECSQRS
>d1a66a_ b.2.5.1 (A:) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}
MKDWQLPSHSGPYELRIEVQPKSHHRARYETEGSRGAVKASAGGHPIVQLHGYLENEPMLQLFIGTADDRLRPHAFYQVHRITGKTVSTSHEAIL
SNTKVLEIPLLPENSMRAVIDCAGILKLRNSDIERKGETDIGRNTRVRLVFRVHVPQPSGRTLSQVASNPICCSQRS
>d1imhc2 b.2.5.1 (C:188-367) Transcription factor TONEBP, DNA-binding domain {Human (Homo sapiens)}
KKSPMLCGQYPVKSEGKELKIVVQPETQHRARYLTEGSRGSVKDRTQQGFPTVKLEGHNEPVVLQFVGNDSGRVKPHGFYQACRVTGRNTPCKE
VDIEGTTVIEVGLDPSNNMTLAVDCVGILKLRNADVEARIGAIGSKKKSTRARLVFRVNIMRKDGSTLQTPSSPILCTPAG
>d1nfka2 b.2.5.1 (A:39-250) p50 subunit of NF-kappa B (NFkB), N-terminal domain {Mouse (Mus musculus)}
GPYLQILEQPKQRGFRFRYVCEGPHGGLPGASSEKNKKSYPQVKICNYVGPARKVIVQLVTNGKNIHLHAHSLVGKHCEDGVCTVAGPKDMVVGFA

NLGLILHVTKKVFETLEARMTEACIRGYNPGLLVSDLAYLQAEGGGDRQLTDREKEIIRQAAVQQTKEMDLSVRLMFTAFLPDSTGSFTRRLEPVV
SDAIYDSKAPNASNLKI

>d1a3qa2 b.2.5.1 (A:37-226) p52 subunit of NF-kappa B (NFKB), N-terminal domain {Human (Homo sapiens)}

GPYLVIVEQPKQRGFRFRYCGPSHGGLPGASSEKGRKYPTVKICNYEGPAKIEVDLVTHSDPPRAHAHSLVGKQCSELGICAVSGPKDMTAQFN
NLGVLHVTKKNMMGTMIQKLQRQRRLSRPQGLTEAEQRELEQEAKKVMDSLIVRLRFAFLRSLPLKPVISQPIHDSKSPGAS

>d1ikna2 b.2.5.1 (A:19-191) p65 subunit of NF-kappa B (NFKB), N-terminal domain {Mouse (Mus musculus)}

PYVEIIEQPKQRGMFRYKCEGRSAGSIPGERSTDTKTHPTIKINGTGPGBTVRISLTKDPPHRPHPELVGKDCRDGYEADLCPDRSIHSFQNLGI
QCVKKRDLLEQAIQSRIQTNNNPFHVPIEQRGDYDLNAVRLCFQVTVRDPAGRPLLTPVLSPHIFDNRAPNT

>d1nfia2 b.2.5.1 (A:20-189) p65 subunit of NF-kappa B (NFKB), N-terminal domain {Human (Homo sapiens)}

YVEIIEQPKQRGMFRYKCEGRSAGSIPGERSTDTKTHPTIKINGTGPGBTVRISLTKDPPHRPHPELVGKDCRDGYEAEELCPDRCIHSFQNLGIQ
CVKKRDLLEQAIQSRIQTNNNPFQVPIEEQRGDYDLNAVRLCFQVTVRDPAGRPLLTPVLSPHIFDNRAPNT

>d1bvoa_b.2.5.1 (A:) Dorsal homologue Gambif1 {African malaria mosquito (Anopheles gambiae)}

PYVEITEQPHPKALRFRYECEGRSAGSIPGVNTTAEQKTFPSIQVHGRGRAVVVSCVTKEGPEHKPHPNLVGKEGCKKGVCVEINSTTMSYTFN
NLGIQCVKKDVEEARLRQEIRVDPFRFGHAKEPGSIDLNARLFCQVFLEGQQRGRFTEPLTPVVSIDIYDKK

>d1xbra_b.2.5.1 (A:) T domain from Brachyury transcription factor {African clawed frog (Xenopus laevis)}

ELKVSLEERDLWTRFKELTNEMIVTKNGRRMFPVLKVSMGLDPNAMYTVLLDFVAADNHRWKYVNGEWVPGKPEPQAPSCVYIHPDSPNFGA
HWMKDPVSFSKVLTNKMNNGGQIMLNSLHKYEPRHIVRVGGTQRMITSHPETQFIAVTAYQNEEITALKIHNPFAKFLDAKERN

>d1bf5a2 b.2.5.1 (A:317-568) STAT-1, DNA-binding domain {Human (Homo sapiens)}

FVVERQPCMPTHPQRPLVLTGVQFTVKLRLVVKLQELNYNLKVLFKDVKNERNTVKGFRKFNILGHTKVMNMEESTNGSLAAEFRHLQLKEQ
KNAGTRTNEGPLIVTEELHSLSFETQLCQPGLVIDLETTSPVVVISVSQLPSGWASILWYNMLVAEPRNLSFFLTPPCRWAQLSEVLSWFSSVTK
RGLNDQNLMLGEKLLGPNASPDGLIPWTRFCENINDKNPFWLWIESILELIKHH

>d1bg1a2 b.2.5.1 (A:322-575) STAT3b {Mouse (Mus musculus)}

VVERQPCMPMHDRPLVKTGVQFTTKVRLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMNMEESNNGLSAEFKHLTLREQRC
GNGGRANCDAVLTEELHLITFETEVYHQGLKIDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTQPIGTWDQVAEVLWSWFSSST
TKRGLSIEQLTTLAEKLLGPVNYSGCQITWAKFCENMAGKGFSFWWLDNIIDLVKKY

>d1e50q_b.2.5.1 (Q:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}

LVRTDSPNFLCSVLPTHWRNCNKLPIAFKVALGDVPDGTLTVMAGNDENYSAELRNATAAMKNQVARFNDLRFVGRSGRGKSFTLTIVFTNPP
QVATYHRAKITVD

>d1h9da_b.2.5.1 (A:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}

VLADHPGELVRTDSPNFLCSVLPTHWRNCNKLPIAFKVALGDVPDGTLTVMAGNDENYSAELRNATAAMKNQVARFNDLRFVGRSGRGKSFTLT
ITVFTNPPQVATYHRAKITVDGPREPRR

>d1hc1_1 b.2.6.1 (1-167,231-250) Cytochrome f, large domain {Turnip (Brassica rapa)}

YPIFAQQNYENPREATGRIVCANCHLASKPVDIEVPQAVLPDTVFEAVVKIPYDMQLKQVLANGKKGALNVGAVLILPEGFELAPPDRISPEMKEKIG
NLSFQNRYRPNKKNILVGPVPGQKYSEITFPILAPDPATNKDVHFLKPYIYVGGNRGRGQIYPDGSKSNXPVGGFGQDAEIVLQDPLR

>d1e2wa1 b.2.6.1 (A:1-168,A:233-251) Cytochrome f, large domain {Chlamydomonas reinhardtii}

YPVFAQQNYANPREANGRIVCANCHLAQKAVEIEVPQAVLPDTVFEAVIELPYDKQVKVQLANGKKGDLNVGMVLILPEGFELAPPDRVPAEIKEV
GNLYYQPYSPEQKNILVGPVPGKKYSEMVPILSPDPAKNKNVSYLYKPYIYFGGNRGRGQVYPDGKKSFXNVGGFGQAETEIVLQNP
>d1ci3m1 b.2.6.1 (M:1-169,M:232-249) Cytochrome f, large domain {Phormidium laminosum}

YPFWAQQNYANPREATGRIVCANCHLAAKPAEIEVPQAVLPDSVFKAVVKIPYDHSQLQVQVQADGSKGPLNVGAVLMLPEGFTIAPEDRIPEEMKEE
VGPSYLFQPYADDKQNIVLGPLPGDEYYEIVFPVLSNPATNKSVAFGKYSIHLGANRGRGQIYPTGEKSNNXNVGGFGQKDTEIVLQSPN

>d1i31a_b.2.7.1 (A:) Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor {Rat (Rattus norvegicus)}

IGWRREGIKYRRNELFLDLESVNLMSPGQQVLSAHSGRVMKSYLSGMPECKFGMNDKIVIEKQGKGTADETSKGKQKQSIADDCTFHQCVR
KFDSERSISIPIPGEFELMRYRTTDIILPFRVPLVREVGRKLEVKKVVIKSNFKPSLLAQKIEVRIPTPLNTSGVQVICMKGKAKYKASENAIVW
MAGMKESQISAEIELLPTNDKKKWARPPISMNFEVPFAPSGLKVRYLKVFEPKLNYSDDHDVIKWVRYIGRSGIYETRC

>d1cgt_2 b.3.1.1 (580-684) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}
LTGDQVTVRFVNNASTLGQNLYLTGNVAELGNWSTGSTAIGPAFNQVIHQYPTWYDVSVPAGKQLEFKFFKNGSTITWESGSNHTFTTPASGT
ATVTVNWQ

>d1kcl2 b.3.1.1 (A:582-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}
LSGDQVSVRFVNNATTALGQNVLGSVSELGNWDPAKAIGPMYNQVVYQYPNWWYDVSVPAGKTIEFKFLKKQGSTVTWEGGSNHTFTAPSSG
TATINVNWQP

>d1cyg_2 b.3.1.1 (575-680) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus}
LTNDQVSVRFVNNATTNLGQNIIYIVGNVYELGNWDTSKAIGPMFNQVVYSYPTWYIDVSVPAGEKTIIEFKFIKKDSQGNVTWESGSNHVYTTPTNT
TGKIIVDWQN

>d1qhoa2 b.3.1.1 (A:577-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus, maltogenic alpha-amylase}
LSGTQTSVVFTVKSAPPTNLGDKIYLGNIPLEGNWSTDTSKAVNNAQGPLAPNYPDWFYVFSVPAGKTIQFKFFIKRADGTIQWENGSNHVATTP
TGATGNITVTWQN

>d1pama2 b.3.1.1 (A:583-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus sp., strain 1011}
TGDQVTVRFVINNATTALGQNVLGTGNVSELGNWDPNNAIGPMYNQVVYQYPWYDVSVPAGQTIEFKFLKKQGSTVTWEGGANRTFTPTSG
TATVNWNWQP

>d1ciu_2 b.3.1.1 (579-683) Cyclodextrin glycosyltransferase, C-terminal domain {Thermoanaerobacterium thermosulfurigenes, EM1}
LTGNQICVRFVNNASTVYGENVYLTGNVAELGNWDTSKAIGPMFNQVVYQYPWYDVSVPAGTTIQFKFIKKNGNTITWEGGSNHTYTVPSST
GTVIVNWQQ

>d1acz__ b.3.1.1 (-) Glucoamilase, granular starch-binding domain {Aspergillus niger}
CTTPAVAVTFDLTATTYGENIYLGSISQLGDWETSDGIALSADKYTSSDPLWYVTVTLPPAGESFEYKFIRIESDDSVIEWESDPNREYTVPQACGTSTA
TVTDTWR

>d1cqya_ b.3.1.1 (A:) beta-amylase {Bacillus cereus}
TPVMQTIVKNVPTTIGDTVYITGNRAELGSWDTKQYPIQLYYDSHSNDWRGNVVLPAERNIEFKAFIKSKDGTVKSWQTIQQSWNPVPLKTTSHS
SW

>d1h8la1 b.3.2.1 (A:305-383) Carboxypeptidase D, a regulatory domain {Crested duck (*Lophonetta specularioides*)}
GIWGFVLADTGRGILNATISVADINHPVTTYKGDYWRLLVQGTYKVTASARGYDPVTKTEVDSKGQVQVNFTLSRT

>d1vcbc_ b.3.3.1 (C:) VHL {Human (*Homo sapiens*)}
LRSVNSREPSQVIFCRSPRVLPVWLNFGEPPYPTLPPGTGRRHYSRGLWLFRDAGTHDGLLNQTELFVPSLNVDGQPIFANITLPVYTLKE
RCLQVVRSLVKPENYRRLDIVRSIYEDLEDHPNVQKDLERLTQE

>d1f86a_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (*Homo sapiens*)}
CPLMVKVLDAVRGSPAINVAVHFRKAADDTWEPFASGKTSESGELHGLTTEEFVEGIYKVEIDTKSYWKALGISPFWHEHAEVVFTANDSGPRRYTIA
ALLSPYSYSTMAVVTN

>d1ttba_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (*Homo sapiens*)}
GPTGTGESKCPLMVKVLDAVRGSPAINVAVHFRKAADDTWEPFASGKTSESGELHGLTTEEFVEGIYKVEIDTKSYWKALGISPFWHEHAEVVFTAN
DSGPERRYTIATLLSPYSYTTAVVTPKE

>d1gkea_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Rat (*Rattus norvegicus*)}
SKCPLMVKVLDAVRGSPAVDVAVKVFKTADGSWEPFASGKTAESGEHLHGLTDEKFTEGVYRVELDTKSYWKALGISPFWHEYAEVVFTANDSGHRH
YTIAALLSPYSYTTAVVNPQN

>d1tfpa_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Chicken (*Gallus gallus*)}
CPLMVKVLDAVRGSPAANVAVKFKAADGTWQDFATGKTTEFGEIHELTTEEQFVEGVYRVEFDTSSYWKGGLSPFWHEYADVFTANDSGHRHY
TIAALLSPFSYTTAVVS

>d1d2oa1 b.3.5.1 (A:535-624) B repeat unit of collagen binding surface protein (cna) {Staphylococcus aureus}

ETTSSIGEVVWDDKDNQDGKRPEKVSVNLLANGEVKTLVDVSETNWVYEFKDLPKYDEGKKIEYTVTEDHVKYDFTTDINGTTITNKYTP
>d1d2oa2 b.3.5.1 (A:625-721) B repeat unit of collagen binding surface protein (cna) {Staphylococcus aureus}
GETSATVTKNWDDNNNQDGKRPEIKVELYQDGKATGKTAILNESNNWHTWTGLDEAKGQQVKYVEELTKVGYTTHVDNNDMGNLITTNK
YTP
>d1dmha_b.3.6.1 (A:) Catechol 1,2-dioxygenase {Acinetobacter calcoaceticus}
VKIFNTQDVQDFLRVASGLEQEGGNPRVKQIIHRVLSLDLYKAIEDLNITSDEYWAGVAYLNQLGANQEAGLLSPGLFDHYLDMRMDAEDAALGIEN
ATPRTIEGPLVAGAPESVGYARMDDGSDPNGHTLILHGTIFDADGKPLPNNAKVEIWHANTKGFYSHFDPTGEQQAFNMRRSIITDENGQYRVRTIL
PAGYGCPEGPTQQQLNQLGRHGNRPAHIHYFVSADGHRKLTQINVAGDPYTYDDFAYATREGLVVAVEHTDPEAIKANDVEGPFAEMVFDLKL
RLVDGVDNQVVDRPRЛАV
>d3pcca_b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Pseudomonas aeruginosa}
PIELLPETPSQTAGPYVHIGLALEAAGNPTRDQEWINRLAKPDAPGEHILLGQVYDGNNGHLVRDSFLEVWQADANGEYQDAYNLENANFSFRTA
TTFDAGEWTLHTVKPGVVNNAAAGVPMAPHINISLFARGINIHLHTRLYFDDEAQANAKCPVLNLIEQPQRRETIAKRCEVDGKTAYRFDIRIQGEGE
TVFFDF
>d1eo9a_b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Acinetobacter calcoaceticus, adp1}
ELKETPSQTGGPYVHIGLLPKQANIEVFEHNLDNNLVQDNTQGQRIRLEGQVFDSLPLRDVLINEIWQADTNGVYPSQADTQGKQVDPNFLGWG
RTGADFGTGFWSFNTIKPGAVPGRKGSTQAPHISLIIFARGINIGLHTRVYFDDEAEANAKDPVLSIEWATRRQTLVAKREERDGEVYVYRFDIRIQGE
NETVFFDI
>d3pccm_b.3.6.1 (M:) Protocatechuate-3,4-dioxygenase, beta chain {Pseudomonas aeruginosa}
PAQDNSRFVIRDRNWHPKALTPDYKTSIARSPRQALVSIPQSIETTGPNFSHLGFGAHDHDLNNFNNGGLPIGERIVAGRVDQYGKPVNPTLVE
MWQANAGGRYRHKNDRYLAPLDPNFGGVGRCLTDGYYSFRTIKPGPYWRNGPNDWRPAHHFGISGPSIATKLITQLYFEGDPLIPMCPIVKSI
ANPEAVQQLIAKLDMNNANPMDCLAYRFDIVLRGQRKTHFE
>d1eo9b_b.3.6.1 (B:) Protocatechuate-3,4-dioxygenase, beta chain {Acinetobacter calcoaceticus, adp1}
IIWGAYAQRNTEDHPPAYAPGYKTSVLRSPKNALISIAETLSEVTAPHFSADKFGPKDNDLILNYAKDGLPIGERIVVHGVRDQFGRPVKNALVEWWQ
ANASGRYRHPNDQYIGAMDPNFGGCGRMLTDDNGYYFRTIKPGPYWRNRINEWRPAHHFSIADGWAQRLISQFYFEGDTLIDSCPILKTIPSE
QQRRALIALEDKSNFIEADSRCYRFIDLRLRRATYFENDLT
>d1c3ga1_b.4.1.1 (A:180-259) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}
ETVQVNLPVSLEDLFVGKKSKFKIGRKPHGASEKTQIDIQLKPGWKAGTKITYKNQGDYNPQTGRRTLQFVIQEKSHP
>d1c3ga2_b.4.1.1 (A:260-349) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}
NFKRDGDDLIYTLPLSFKESSLGFSKTIQTIDGRTLPLSRVQPVQPSQTSTYPGQGMPTPKNPSQRGNLIVKYKVDPYISLNDAQKRAID
>d1hd8a1_b.105.1.1 (A:263-356) Penicillin-binding protein 5, C-terminal domain {Escherichia coli}
FETVNPPLVKGKEFASEPWWFGSDRASLGVDKDVLTIPRGRMKDLKASYVLSSELHAPLQKNQVVTINFQLDGKTEQRPLVVLQEIEPGN
>d1hoe_b.5.1.1 (-) alpha-Amylase inhibitor tendamistat {Streptomyces tendae}
DTTSEPAVSCVTLYQSWRYSQADNGCAETVTVKVVYEDDTEGLCYAVAPGQITVGDGYIGSHGHARYLARCL
>d1aac_b.6.1.1 (-) Amicyanin {Paracoccus denitrificans}
DKATIPSESPAAAEVADGAIVVDIAKMKYETPELHVKVGDTVTWINREAMPHNVHFVAGVLGEALKGPMMKKEQAYSLTFTEAGTYDYHCTPHP
FMRGKVVVE
>d1id2a_b.6.1.1 (A:) Amicyanin {Paracoccus versutus (Thiobacillus versutus)}
QDKITVTSEKPVAAADVPAVVGIEKMKYLTPEVTIKAGETVYWWNGEVMPHNVAFKKGIVGEDAFRGEMMTKDQAYAITFNEAGSYDYFCTP
HPFMRGKVIVE
>d1plc_b.6.1.1 (-) Plastocyanin {Poplar (Populus nigra), variant italica}
IDVLLGADDGSLAFVPSEFSISPGEKIVFKNNAGFPHNIVFDEDSIPSGVDASKISMSEEDLLNAKGETFEVALSNKGEYSFYCSPHQGAGMVGVKTVN
>d9pcy_b.6.1.1 (-) Plastocyanin {French bean (Phaseolus vulgaris)}
LEVLLGSGDGSLSVFPSEFSVPSGEKIVFKNNAGFPHNVFDEDEIPAGVDAVKISMPEEELLNAPGETYVVTLDKGTSFYCSPHQGAGMVGVKTV
N

>d1pla__ b.6.1.1 (-) Plastocyanin {Parsley (*Petroselinum crispum*)}
AEVKLGSDGGLVSPSSFTAAGEKITFKNNAGFPNIVFDEDEVPAVGNAEKISQPEYLNGAGETYEVLTKEGTYKFYCEPHAGAGMKGEVTNV
>d1ag6__ b.6.1.1 (-) Plastocyanin {Spinach (*Spinacia oleracea*)}
VEVLLGGDDGSALFLPGDFVASGEEIVFKNNAGFPNIVFDEDEIPSGVDAAKISMSEEDLLNAPGETYKVLTEKGYKFYCSPHQGAGMVGKVTVN
>d1bypa_ b.6.1.1 (A:) Plastocyanin {White campion (*Silene pratensis*)}
AEVLLGSSDGGLAFVPSDLIASGEKITFKNNAGFPNIVFDEDAVPAGVDADAIISYDDYLNKGTVRKLPGVYGVYCEPHAGAGMKMTITVN
>d1iuz__ b.6.1.1 (-) Plastocyanin {Sea lettuce (*Ulva pertusa*)}
AQIVKLGGDDGSALFVPSKISVAAGEAIEFVNNAGFPNIVFDEDAVPAGVDADAIISYDDYLNKGTVRKLPGVYGVYCEPHAGAGMKMTITVQ
>d2plt__ b.6.1.1 (-) Plastocyanin {Green alga (*Chlamydomonas reinhardtii*)}
DATVKLGADSGALEFVPKTLTIKSGETVNFGNNAGFPNIVFDEDAIPSGVNADAISRDDYLNAPGETYSVNLTAAGEYYCEPHQGAGMVGKIIIVQ
>d7pcy__ b.6.1.1 (-) Plastocyanin {Green alga (*Enteromorpha prolifera*)}
AAIVKLGGDDGSALFVPPNITVGAGESIEFINNAGFPNIVFDEDAVPAGVDADAIISYDDYLNKGTVRKLPGVYGVYCEPHAGAGMKMTITVQ
>d1kdj__ b.6.1.1 (-) Plastocyanin {Fern (*Adiantum capillus-veneris*)}
AKVEVGDEVGNFKYPDSITVSAGEAVEFTLVGETGHNIVFDIPAGAPGTVASELKAASMDENDLLSEDEPSFKAKVSTPGTYTFYCTPHKSANMKGTLTVK
>d1nin__ b.6.1.1 (-) Plastocyanin {Anabaena variabilis}
ETYTVKLGSDKGLLVFEPAKLTIKPGDTVEFLNNKVPPhNIVFDDKQPGASKELADKLSHSQLMSPQSTTTFPADAPAGEYTFYCEPHRGAGMV
GKITVAG
>d1bawa_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (*Phormidium laminosum*)}
ETFTVKMGADSGLLQFEPANVTVPAGDTVKWVNNKLPPhNIVFDADGPADTAALKLHSKGLFAAGESFTSTFEPGTYYCEPHRGAGMV
MVGKITVEG
>d1pcs__ b.6.1.1 (-) Plastocyanin {Cyanobacterium (*Synechocystis* sp.), pcc 6803}
ANATVKMGSDSGALVFEPESTVTIKAGEEVKWVNNKLPPhNIVFDADGPADTAALKLHSKGLFAAGESFTSTFEPGTYYCEPHRGAGMV
VE
>d1bxva_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (*Synechocystis* sp.), pcc 7942}
QTVAIKMGADNGMLAFEPSTIEIQAGDTVQWVNNKLPPhNIVFDADGPADTAALKLHSKGLFAAGESFTSTFEPGTYYCEPHRGAGMV
KIVVQ
>d2b3ia_ b.6.1.1 (A:) Plastocyanin {Photosynthetic prokaryote (*Prochlorothrix hollandica*)}
ASVQIKMGTDKYAPLYEPKALSISAGDTVEFVMNKVGPhNIVFDKVPAGESAPALSNTKLAIPGSFVTLGTPGTYSFYCTPHRGAGMV
GTITVE
>d1paz__ b.6.1.1 (-) Pseudoazurin {Alcaligenes faecalis, strain s-6}
ENIEVHMLNKGGAEGAMVFEPAYIKANPGDTVTIFPVDKGHNVESIKDMIPEGAEFKSKINENYVLTQPGAYLVKCTPHYAMGMIALAV
GDSPA
NLDQIVSAKKPKIVQERLEKVI
>d1pmv__ b.6.1.1 (-) Pseudoazurin {Methylobacterium extorquens, strain am1}
DEVAVKMLNSPGGMMVFDPALVRLPGDSIKFLPTDKGHNVETIKGMAPDGADYVKTGQEAFFKDEGVYGFKA
PHYMMGMVALVV
GDKRDNLAAKSQHNLTKQRDLPLFAQIQ
>d1bqk__ b.6.1.1 (-) Pseudoazurin {Achromobacter cycloclastes}
ADFEVHMLNKGKGAMVFEPASLKVAPGDTVTIFPTDKGHNVETIKGMPDGAEAFKSKINENYKVFTAPGVYGV
KCTPHGMGMVGVQVGD
APANLEAVKGAKNPKKAQERLDAALAALGN
>d1adwa_ b.6.1.1 (A:) Pseudoazurin {Thiosphaera pantotropha}
ATHEVHMLNKGESGAMVFEPAFVRAEPMGVINFVPTDKSHNVEAIKEILPEGVESFKSKINESY
TLVTEPGLYGVKCTPHGMGMVGLVQVGD
NLDAAKTAKMPKKARERMDAELAQVN

>d2cbp__ b.6.1.1 (-) Plantacyanin {Cucumber (*Cucumis sativus*)}
AVYVVGSGGWTNFNTESWPKGKRFRAGDILLFNYNPSMHNVVVVNQGGFSTCNTPAGAKVYTSGRDQIKLPKGQSIFYICNFPGHQCQGMKIAVN
AL
>d1f56a_ b.6.1.1 (A:) Plantacyanin {Spinach (*Spinacia oleracea*)}
AVYNIGWSFNVNGARGKSFRAGDVLFVKYIKGQHNVVAVNGRGYASCSAPRGARTYSSGQDRIKLTRGQNYFICSFPGHCGGGMKAINAK
>d1azca_ b.6.1.1 (A:) Azurin {Alcaligenes denitrificans}
AQCEATIESNDAMQYNLKEMVVDKSCQFTVLHKHVGKMAKVAMGHNWLTKEADKQGVATDGMNAGLAQDYVKAGDTRVIAHTKVIGGGS
DSVTFDVSKLTPGEAYAYFCSPGHWAMMKGTLKLSN
>d1dyza_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015), different isoforms}
AQCEATVESNDAMQYNVKEIVVDKSCQFTMHLKHVGKMAKVAMGHNLVTKDADKQAVATDGMGAGLAQDYVKAGDTRVIAHTKVIGGGS
DSVTFDVSKIAAGENYAYFCSPGHWAMMKGTLKLG
>d1rkra_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015), different isoforms}
AECSVDIAGNDGMQFDKKEITVSKSCQFTVNLKHPGKLAKNVMGHNWVLTQADMQGAVNDGMAAGLDNNYVKKDDARVIAHTKVIGGGET
DSVTFDVSKLAAGEDYAYFCSPGHFALMKGVLKLV
>d1cc3a_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}
AECSVDIQGNDQMQLQFNTNAITVDKSCQFTVNLSPGNLPKNVMGHNWVLTAAADMQGVTDGMASGLDKDYLKPDDSRVIAHTKLIGSKEK
DSVTFDVSKLKEGEQYMFCTFPGHSALMKGTLTLK
>d1jzga_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}
AECSVDIQGNDQMQLQFNTNAITVDKSCQFTVNLSPGNLPKNVMGHNWVLTAAADMQGVTDGMASGLDKDYLKPDDSRVIAHTKLIGSKEK
DSVTFDVSKLKEGEQYMFCTFPGHSALMKGTLTLK
>d1joi__ b.6.1.1 (-) Azurin {Pseudomonas fluorescens}
AECKVTVSTDQMSFNTKAIIDKSCKTFVELTHSGSLPKNVMGHNWVLTAAADMQPIADMPGIASDGMAAGIDKNYLKEGDTRVIAHTKIIGAGEKDSVT
FDVSKLAAAGTDYAFFCSFGHISMMKGTVTVK
>d1nwpa_ b.6.1.1 (A:) Azurin {Pseudomonas putida}
AECKVTVSTDQMSFNTKDIIDKSCKTFVELTHSGSLPKNVMGHNWVLTAAADMQPIADGLSAGIDKQYLKDGDARVIAHTKVIGAGEKDSVT
DVS KLAAGEKYGFCSFGHISMMKGTVTLK
>d1cuoa_ b.6.1.1 (A:) Azurin {Methylomonas sp. j}
ASCETTVTSGDTMTYSTRSISVPASCAEFVTNFEHKGHMPKTGMGHNWVLAKSADVGDVAKEGAHAGADNNFVTPGDKRVIAFTPPIIGGGEKTSV
KFKVSALKDEAYTYFCSYPGHFSMMRGTLKLEE
>d1qhqa_ b.6.1.1 (A:) Auracyanin {Chloroflexus aurantiacus}
ANAPGGSNVVNETPAQTVEVRAAPDALAFAQTSLSLPANTVVRDFVNQNNLGVQHNWVLVNGGDDAAAVENTAAQNNADALFVPPPDTPNA
LAWTAMLNAGESGSVTFRTPAPGTYLYICFPGHYLAGMKGTLTVPT
>d1e30a_ b.6.1.1 (A:) Rusticyanin {Thiobacillus ferrooxidans}
LDTTWKEATLPQVKAMLEKDTGKVSGDTVTYSGKTVHVVAALPGFPFPSFEVHDKNPTLEIPAGATVDVTINTKGFHSDITKKGPYAVM
PVIDPIVAGTGFSPVPKDGKFGYTNTFWHPTAGTYYVCQIPGHAATGQFGKIVVK
>d1jer__ b.6.1.1 (-) Stellacyanin {Cucumber (*Cucumis sativus*)}
MQSTVHIVGDNTPGSVPSSPNFSQWAAGKTFRVGDSLQFNFPANAHNVHEMETKQSFACNFVNSDNDVERTSPVIERLDELMHYFVCTVG
THCSNGQKLSINVVAAN
>d1ibya_ b.6.1.4 (A:) Red copper protein nitrosocyanin {Nitrosomonas europaea}
EHNFnVVINAYDTTIPELNVEGVTVKNIRAFNVLNEPETLVVKKGDAVKVVENKSPISEGFSIDAFGVQEVIKAGETKTISFTADKAGAFTIWQLHP
KNIHLPGTTLNVVE
>d1qnia1 b.6.1.4 (A:451-581) Nitrous oxide reductase, C-terminal domain {Pseudomonas nautica}
KIYERNDPYFASCRAQAQAEKDGVTLESNDKVIRDGNKVRVYMTSVAPQYGMTDFVKKEGDEVTVYITNLDMVEDVTHGFCMVNHGSMEISPQQT
ASVTFTAGKPGVYWYCNWFCHALHMEMVGRMLVEAA

>d1fwxa1 b.6.1.4 (A:452-581) Nitrous oxide reductase, C-terminal domain {Paracoccus denitrificans}
SVWDRNDPMWAETRAQAEADGVIDNWTEEVIRDGNKVRVYMSVAPSFSIESFTVKEGDEVTVITNLDEIDDLHGFTMGNYGVAMEIGPQ
MTSSVTFAANPGVYWWYCQWFCHALHMEMRGRMLVEPK

>d1cyx_ b.6.1.2 (-) Quinol oxidase (CyoA) {Escherichia coli}
KPITIEVVSMDWKFFIYPEQGIATVNEIAFPANTPVFKVTSNSVMHSFFIPRLGSQIYAMAGMQTRLHLIANEPGTYDGICAEICGPGHSGMKFK
AIATPDRAAFDQWVAKAKQSPNTMSDMAAFEKLAAPSEYNQVEYFSNVKPDFADINKFM

>d1fftb1 b.6.1.2 (B:118-283) Quinol oxidase (CyoA) {Escherichia coli}
KPLAHDEKPITIEVVSMDWKFFIYPEQGIATVNEIAFPANTPVFKVTSNSVMNSFFIPRLGSQIYAMAGMQTRLHLIANEPGTYDGISASYSGPGF
SGMKFKAIATPDRAAFDQWVAKAKQSPNTMSDMAAFEKLAAPSEYNQVEYFSNVKPDFADINKFM

>d1ocrb1 b.6.1.2 (B:91-227) Cytochrome c oxidase {Cow (Bos taurus)}
NNPSLTVKTMGHQWYWSYEYTDYEDLSFDSSYMIPTSELKPGELRLLEVNDNRVLPMEMTIRMLVSSEDVLHSWAVPSLGLKTDAPGRLNQTTLMS
SRPGLYYGQCSEICGSNHSFMPIVLEVLPLKYFEKWSASML

>d1ar1b1 b.6.1.2 (B:108-252) Cytochrome c oxidase {Paracoccus denitrificans}
NDPDLVIKAIGHQWYWSYEYPNDGVAFDALMLEKEALADAGYSEDEYLLATDNPVVVPVGKKVLVQVTATDVIHAWTIPAFAVKQDAVPGRIAQLW
FSVDQEGVYFGQCELCGINHAYMPIVVKAVSQEKYEAWLAGAKEFAA

>d2cuua_ b.6.1.2 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}
AGKLERVDPTTVRQEGPWADPAQAVVQTGPQNQYTYYLAFAFGYQPNPIEVPKQGAEIVFKITSPDVIGHFVEGTNINVEVLPGEVSTVRYTFKRP
EYRIICNQYCGLGHQNMFGTIVVKE

>d2cuab_ b.6.1.2 (B:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}
AYTLATHTAGVIPAGKLERVDPTTVRQEGPWADPAQAVVQTGPQNQYTYYLAFAFGYQPNPIEVPKQGAEIVFKITSPDVIGHFVEGTNINVEVLPGE
VSTVRYTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE

>d1nif_1 b.6.1.3 (8-166) Nitrite reductase, NIR {Achromobacter cycloclastes}
DISTLPRVKVDLVKPPFVHAHDQVAKTGPVVFTMIEKKVIDREGTEIHAMTFNGSVPGPLMVHENDYVELRLINPDNTLLHNIDFHAATGA
LGGGALTQVNPGEEETLRFKATKPGVFVYHCAEGMVPWHVHTSGMNGAIMVLPRDGLKDE

>d1nif_2 b.6.1.3 (167-340) Nitrite reductase, NIR {Achromobacter cycloclastes}
GQPLTYDKIYYVGEQDFYVPKDEAGNYKKYETPGEAYEDAVKAMRTLTPTHIVFNGAVGALTGDHALTAAVGERVLVHSQANRDTRPHLIGGHG
YVWATGKFRNPPLDQETWLIPGGTAGAAFYTFRQPGVYAYVNHNLIAFELGAAGHFKVGEWNDDLMTSVVKPASM

>d1j9qa1 b.6.1.3 (A:4-166) Nitrite reductase, NIR {Alcaligenes faecalis, strain s-6}
ATAAEIAALPRQKVVELDPPFVHAHSQVAEGGPKVVEFTMIEKKIVIDDAGTEVHAMAFNGTVPGPLMVHQDDYLELTLINPETNTLMHNINF
HAATGALGGGLTEINPGEKTIILRFKATKPGVFVYHCAEGMVPWHVSGMNGAIMVLPREGLHDGK

>d1j9qa2 b.6.1.3 (A:167-339) Nitrite reductase, NIR {Alcaligenes faecalis, strain s-6}
GKALTYDKIYYVGEQDFYVPRDENKGKYKYEAPGDAYEDTVKVMRTLTPTHVVFNGAVGALTGDKAMTAAVGEKVLIVHSQANRDTRPHLIGGHG
DYVWATGKFNTPPDVQETWFIPGGAAAGAAFYTFQQPGIYAYVNHNLIAFELGAAAHFKVGEWNDDLMTSVLAPSG

>d1gs7a1 b.6.1.3 (A:1-159) Nitrite reductase, NIR {Alcaligenes xylosoxidans}
QDADKLPTHKVTLVAPPQVHPHEQATKSGPKVVEFTMIEKKMVIDDKGTLQAMTFNGSMPGPTLVVHEGDYVQLTLVNPATNAMPHNVDHF
GATGALGGAKLTNVNPGEQATLRKADRSQTFVYHCAEGMVPWHVSGMNGAIMVLPRDGLKD

>d1gs7a2 b.6.1.3 (A:160-336) Nitrite reductase, NIR {Alcaligenes xylosoxidans}
QGKPLHYDRAYTIGEFDLYIPKPGPDGKYKDYATLAESYGDVTVQVMRTLTPSHIVFNGKVGALTGANALTAKVGETVLLIHSQANRDTRPHLIGGFDW
VWETGKFANPPQRDLETWFIRGGSAGAALYTFKQPGVYAYLNHNLIAFELGAAGHIKVEGKWNDLMKQIKAPAPIPR

>d1ndsa1 b.6.1.3 (A:11-166) Nitrite reductase, NIR {Alcaligenes xylosoxidans}
GLPRVAVDLVAPPLVPHSQVAAGAPKVVQFRMSIEKKMVADDGTTAQAMTFNGSVPGPTLVVHEGDIYELTLVNPATNSMPHNVDFHAATG
ALGGAGLTQVPGQEAVLRFKADRSQTFVYHCAPAGMVPWHVSGMNGAIMVLPRDGLRDA

>d1ndsa2 b.6.1.3 (A:167-340) Nitrite reductase, NIR {Alcaligenes xylosoxidans}
GAALAYDRVYTIGESDLYVPKAADGNYSYDYPALASAYADTVAVMRTLTPSHAVFNGAVGALTGANALTAAVGESVLIHSQANRDSRPHLIGGHGDW

VWTTGKFANPPQLNMETWFIPGGSAAAALYTFKQPGTYAYLSHNIEAMELGAAAQSVEGQWDDLMTSVAAPGPA
>d1kbva1 b.6.1.3 (A:13-163) Nitrite reductase, NIR {Neisseria gonorrhoeae, AniA}
ELPVIDAVTTHAPEVPPAIDRDPAKVRVKMETVEKTMKMDDGVEYRYWTFDGDVPGRMIRVREGDTVEEFSNNPSSTVPHNVDFAATGQGG
GAAATFTAPGRSTFSFKALQPGLIYIHCAVAPVGMHIANGMYGLILVEPKELPKV
>d1kbva2 b.6.1.3 (A:164-314) Nitrite reductase, NIR {Neisseria gonorrhoeae, AniA}
DKEFYIVQGDFYTKGKKGAQGLQPFDMDKAVAEQPEYVFNGHVGALTGDNALAKAGETVRMYVGNGGPNLVSSFHVIGEIFDKVYVEGGKLIN
ENVQSTIVPAGGSIAVEFKVDIPGNYTLVDHSIFRAFNKGALGQLKVEGAENPEIM
>d1kv7a1 b.6.1.3 (A:31-170) multi-copper oxidase CueO {Escherichia coli}
RPTLPIPDLLTDARNRIQLTIGAGQSTFGGKTATTWGYNGNLLGPAVKLQRGKAVTVDIYNQLEETTLHWHLGEVPGEVDGGPQGIIPPGGKRSVT
LNVDQPAATCWPHQHGKTGRQVAMGLAGLVIEDDEILKL
>d1kv7a2 b.6.1.3 (A:171-335) multi-copper oxidase CueO {Escherichia coli}
MLPKQWGIDDVPVIVQDKKSFADGQIDYQLDVMATAAVGWFGDTLLNGAIYPQHAAPRGWLRLRLLNGCNARSLNFATSDNRPLYVIASDGGLP
EPVKVSELPVLMGERFEVLVEVNDNKPFDLVTLPVSQMGMAIAPFDKPHPVMRIQPIASAGALPDTLS
>d1kv7a3 b.6.1.3 (A:336-516) multi-copper oxidase CueO {Escherichia coli}
SLPALPSLEGLTVRKLQLSMDPMILDMMGQMQLMEKYGDQAMAGMDHSQMMGHMGHGNMNHMNHGGKDFHHANKINGQAFDMNKP
MFAAAKGQYERWVISGVGDMMLHPFHIHGTQFRILENGKPPAAHRAGWKDTVKEGNVSEVLVFNHDAPKEHAYMAHCHLLEHEDTGMM
GFTV
>d1aoza1 b.6.1.3 (A:1-129) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}
SQIRHYKWEVEYMFWAPNCNENIVMGINQFPGPTIRANAGDSVVVELTNKLHTEGVVIWHWHLQRGTPWADGTASISQCAINPGETFFYNFTV
DNPGTFFYHGHLGMQRSAALYGSIVDPPQGKKE
>d1aoza2 b.6.1.3 (A:130-338) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}
PFHYDGEINLLSDWWHSQSIHKQEVGLSSKPIRWIGEPQTILLNRRGQFDCSIAAKYDSNLEPCKLKGSESCAPYIFHSPKKTYRIRIASTTALAALNFA
IGNHQLLVVEADGNYVQPFYSDIDIYSGESYSVLITTDQNPSENYWVGTRARHPNTPGTLNNYLNSVSKLPTSPPPQTPAWDDFDRSKNFTY
RITAAMGSPK
>d1aoza3 b.6.1.3 (A:339-552) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}
PPVKFNRRIFLLNTQN VINGYVKAINDVSLALPPTPYLGAMKYNLLHAFDQNPPPEVFPEDYDIDTPPTNEKTRIGNGVYQFKIGEVVVDVILQNA
MMKENLSETHPWHLHGDWFVLGYGDGKFSAEESSNLKNPPLRNTVVIFPYGWTAIRFVADNPGVWAFCIEPHLHMGMGVVFAEGVEKV
GRIPTKALACGGTAKSLINNPKNP
>d1hfua1 b.6.1.3 (A:1-131) Laccase {Inky cap fungus (Coprinus cinereus)}
AIVNSVDTMTLTNAVSPDGFTTRAGILVNGVHGPLIRGGKNDNFELNVVNDLNPTMLRPTSIIWHGLFQRGTNWADGADGVNQCPISPGHAF
LYKFTPAGHAGTFWYHSHFTQYCDGLRGPMDVYDDND
>d1hfua2 b.6.1.3 (A:132-303) Laccase {Inky cap fungus (Coprinus cinereus)}
PHAALYDEDDENTIITLADWYHIPAPSIQGAAQPDATLINGKGRYVGGPAELSIVNVEQGKKYRMRLISLCDPNWQFSIDGHELTIEVDGELTEPH
TVDRLQIFTGQRYSFVLDANQPVNDYWIRAQPNKGRNGLAGTFANGVNSAILRYAGAANADPTTSANPNPAQL
>d1hfua3 b.6.1.3 (A:304-503) Laccase {Inky cap fungus (Coprinus cinereus)}
NEADLHALIDPAAPGIPTGAADVNLRFQLGFSGGRFTINGTAYESPSPVTLQIMSGAQASANDLPPAGSVYELPRNQVVELVVPAGVLGGPHFHLH
GHAFSVRSAGSSTYNFVNPKRDVSLGVTGDEVTIRFTDNP GPWFFCHIEFHLMLNGLAIVFAEDMANTVDANNPPVEWAQLCEIYDDLPE
ATSIQTV
>d1kcw_1 b.6.1.3 (1-192) Ceruloplasmin {Human (Homo sapiens)}
KEKHYYIGIETTWDYASDHGEKKLISVDEHSNIYLQNGPDRIGRLYKKALYQYTDETFRTTIEKPVWLGLFLGPIIKAETGDKVYVHLKNLASRPYTFHS
HGITYYKEHEGAIYPDNTDFQRADDKVYPGEQYTYMILLATEEQSPGEGDGNCVTRIYHSHIDAPKDIASGLIGPLIICKKDSLKEKEK
>d1kcw_2 b.6.1.3 (193-338) Ceruloplasmin {Human (Homo sapiens)}
HIDREFVVMFSVVDENFSWYLEDNIKYCSEPEKVKDKDNEFQESNRMYSVNGYTFGSLPLGSMCAEDRVKWYLFMGNEVDVHAFFHGQALT
NKNYRIDTINLFATLFDAYMVAQNPGEWMLSCQNLNLKAGLQAFFQVQEC

>d1kcw_3 b.6.1.3 (347-553) Ceruloplasmin {Human (Homo sapiens)}

IRGKHVRHYIAAEEIIWNYAPSGIDIFTKENLTAPGSDAVFFEQGTTRIGGSYKKLVREYTDASFNRKERGPEEEHLGILGPVIWAEVGDITRVTFH
NKGAYPLSIEPIGVRFNKNNEGTYSPNYNPQSRSPVPPSASHVAPTTFTYEWTVPKEVGPTNADPVCLAKMYSADVPTKDIITGLIGPMKICKGS
LHANGRQK

>d1kcw_4 b.6.1.3 (554-705) Ceruloplasmin {Human (Homo sapiens)}

DVDKEFYLFPPTVFDENESLLLEDNIRMFTTAPDQVDKEDEDQESNMHSMNGFMYGNQPGLTMCKGDSVVWYLSAGNEADVHGIYFSGNTYL
WRGERRDATANLFPQTSLTHMWPDTEGTFNVECLTDHYTGGMKQKYTVNQCRRQSED

>d1kcw_5 b.6.1.3 (706-884) Ceruloplasmin {Human (Homo sapiens)}

STFYLGERTYYIAAVEVEWDYSPQREWKEKLHHLQEQQNSNAFLDKGEFYIGSKYKKVVRQYTDSTFRVPVERKAEEELGILGPQLHADVGDKVKI
IFKNMATRPYSIHAHGVTESSTVPTLPGETLTLYVWKIPERSGAGTEDSACIPWAYYSTVDQVKDLYSGLIGPLIVCRP

>d1kcw_6 b.6.1.3 (892-1040) Ceruloplasmin {Human (Homo sapiens)}

RRKLEFALLFLVFDENESWLDDNIKTYSDHPEKVNKDDEEFIESNKMHAINGRMFGNLQGLTMHVGDEVNWYLMGMGNEIDLHTVHFHGSFQ
YKHRCGVSSDVFDIFPGTYQTLEMFPRTPGIWLLHCHVTDHAGMETTYTVLQN

>d1qasa2 b.7.1.1 (A:626-756) PI-specific phospholipase C isozyme D1 (PLC-D1), C-terminal domain {Rat (Rattus norvegicus)}

WRPERLVRVIIISGQQLPKVKNKNSIVDPKIVIEHGVGRDTGSRQTAITNNGFNPRWDMFEFEVTPDIALVRFMVEDYDSSSKNDFIGQSTIP
WNSLKQGYRHVHLLSKNGDQHPSATLFVKISIQD

>d1rlw__ b.7.1.1 (-) Domain from cytosolic phospholipase A2 {Human (Homo sapiens)}

SSHKFTVVVLRATKVTGAFGMDMLDTPDPYVELFISTTPDSRKTRHFNNNDINPVWNETFEFILDPNQENVLEITLMDANYVMDETLGTATFTVSSM
KVGEKKEVPFIFNQVTEMVLEMSLEVASS

>d1d5ra1 b.7.1.1 (A:188-351) Pten tumor suppressor (Phosphoinositide phosphatase), C-terminal domain {Human (Homo sapiens)}

YRPVALLFKMMFETIPMFSGGTCNPQFVVQLKVKIYSSNSGPTRREDKFMYFEFPQPLPVCGDIKVEFFHKQNKKMFKMFHWVNNTFFIPGP
EEDVNDKEYLVLTKNDLKANKDKANRYFSPNFVKLYFTKTV

>d1e8xa2 b.7.1.1 (A:357-522) Phosphoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}

CDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLQSGKGEDQGSFNADKLTSATNPDKENSMSISILLDN
KAQLYYVNLLIDHRFLRLRGEGYVLHMWQLSKGKEDQGSFNADKLTSAATNPDKENSMSISILLDN

>d1e8ya2 b.7.1.1 (A:357-522) Phosphoinositide 3-kinase (PI3K) {Human (Homo sapiens)}

CDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGGQVLQSGKGEDQGSFNADKLTSAATNPDKENSMSISILLDN
VRLYYVNLLIDHRFLRLRGEGYVLHMWQISGKGEDQGSFNADKLTSAATNPDKENSMSISILLDN

>d1bdya_ b.7.1.1 (A:) Domain from protein kinase C delta {Rat (Rattus norvegicus)}

MAPFLRISFNSYELGSLQAEDDASQPFCAVKMKEALTTDRGKTLVQKPTMYPEWKFDAHIYEGRVIQIVLMRAAEDPMSEVTGVSVLAERCKK
NNNGKAEFWLDLQPQAKVLMCVQYFLE

>d1gmia_ b.7.1.1 (A:) Domain from protein kinase C epsilon {Rat (Rattus rattus)}

MVVFNGLLKKICEAVSLKPTAWSLRDAVGPRPQTFLLDPYIALNVDDSRIGQTAKQKTNPAWHDEFVTDCNGRKIELAVFHDAPIGYDDFVANC
TIQFEELLQNGSRHFEDWIDLEPEGKVYVIIDLSGSSG

>d1byna_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}

EKLGKLQYSLDYDFQNNQLVGIQAAELPALDMGGTSDPYVKVFLPDKKKFETKVRKTLNPVNEQFTFKVPYSELGGKTLVMAVYDFDRFSKH
DIIGEFKPMNTVDFGHVTEEWRLDQSAEK

>d1dqva1 b.7.1.2 (A:295-424) Synaptogamin I {Rat (Rattus norvegicus)}

GAPCGRISFALRYLYGSDQLVVRILQALDLPAKDSNGFSDPYVKYLLPDRKKKFETKVRKTLNPVNEQFTFKVPYSELGGKTLVMAVYDFDRFSRHL
IGQVVLNDNLLEAEQPPDRPLWRDILEGG

>d1dqva2 b.7.1.2 (A:425-569) Synaptogamin I {Rat (Rattus norvegicus)}

SEKADLGELNFSLCYLPTAGLLTVIJKASNLKAMDLTGFSDPYVKASLISEGRRLKKRKTISKNTLNPTYNEALVFDVAPESVENVGLSIAVVDYDCIGH
NEVIGVCRVGPEAADPHGREHWAEMLANPRKPVEHWQLVEEK

>d1k5wa_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}

KLGDICFSLRYVPTAGKLTIVILEAKNLKKMDVGGLSDPYVKIHLMQNGKRLKKKTTIKNTLPYNNESFSFEVPFEQIQKVQVVTVLDYDKGN
DAIGKVFVGYNSTGAELRHWSDMANPRPIAQWHTLQVEEVDAMLA

>d1rsy_ b.7.1.2 (-) Synaptogamin I {Rat (Rattus norvegicus)}

GGGILDMSMVEKEEPKEEEKLGLQLQSYLDYDFQNNQLLVIIQAAELPALDMGGTSDPYVKVFLLPDKKKFETKVRKTLNPVFNEQFTFKVPYSELG
GKTLVMAVYDFDRFSKHDIIGEFKVPMNTVDFGHVTEWRDLQSA

>d1dsya_ b.7.1.2 (A:) C2 domain from protein kinase c (alpha) {Rat (Rattus norvegicus)}

TEKRGRIYLKAEVTDKLVTVRDALKNLIPMDPGLSDPYVKLKLIPDPKNESKQKTIRSTLNPKWNESTFKLKPSDKDRLSVEIWWDWDRTRN
DFMGSLSGFGVSELMKMPASGWYKLLNQEEGEYYNVPIE

>d1a25a_ b.7.1.2 (A:) C2 domain from protein kinase c (beta) {Rat (Rattus norvegicus)}

ERRGRRIYIQAHQAHIDREVLIVVVRAKNLVPMMDPGLSDPYVKLKLIPDPKSESQKTKTICSLNPWEWNETFRFQLKESDKDRLSVEIWWDWDLTSRNDF
MGSLSGFGISELQKAGVDGWFKLLSQEEGEYFN

>d3rpba_ b.7.1.2 (A:) C2b-domain of rabphilin {Rat (Rattus norvegicus)}

RGKILVSLMYSTQQGGILVGIIRCVHAAAMDANGYSDPFVKLWLKPDMGKKAKHKTQIKKTLNPEFNEEFFYDIKHSIDLAKKSLDISVWDYDIGKSN
DYIGGCQLGISAKERLKHWWYECLKNKDKKIERWHQLQNEH

>d1qpxa2 b.7.2.1 (A:125-215) PapD {Escherichia coli}

NEVWQDQLILNKVSGGYRIENPTPYVTIVLGGSEKQAEEGEFETVMSLPRSEQTVKSANYNTPYLSYINDYGGRPVLSFICNGSRCVKG
>d1quna2 b.7.2.1 (A:122-205) FimC {Escherichia coli}

LPPDQAAEKLRFRRSANSLLINPTPYLTVTELNAGTRVLENALVPPMGESAVKLPSAGSNITYRTINDY GALTPKMTGVME

>d1who_ b.7.3.1 (-) Pollen allergen PHL P 2 {Timothy grass (Phleum pratense)}

VPKVTFTVEKGSNEKHLAVLVYEGDTMAEVELREHGSDEWVAMTKGEVVTFDSEEPLQGPNFRLTEKGMKNVFDVVPEKYTIGATYAP

>d1dcea2 b.7.4.1 (A:241-350) Rab geranylgeranyltransferase alpha-subunit, insert domain {Rat (Rattus norvegicus)}

PHDVLCVHVSREEACLSVCFSRPLTVGSRMGTLLMVDEAPLSVEWRTPDGRNRPSHVWLCDLPAASNDQLPQHTFRVIWTGSDSQKECVLLK
DRPECWCRCDSATDEQ

>d1czya1 b.8.1.1 (A:350-501) TNF receptor associated factor 2 (TRAF2) {Human (Homo sapiens)}

YDGVFIWKISDFPDKRQEAVGRIPAFSPAFYTSRYGYKMCRLIYNGDGTGRGTHLSLFFVMKGPNDALLRWPFKQVTLMLDDQNNREHVIDA
FRPDVTSSSFQRPVNDMNIASGPLFCPVSKMEA KNSYVRDDAIKIAVDLTGL

>d1flka1 b.8.1.1 (A:350-504) TNF receptor associated factor 3 (TRAF3) {Human (Homo sapiens)}

YNGVLIWKIRDYKRRKQEAVMGKTLQLSQPFYTGYFGYKMCARVYLNQGDGMKGTHLSLFFVIMRGEYDALLPWPKQVTLMLMDQGSSRRHL
GDAFKPDPNSSFKPKTGE MNIASGCPVFAQTVLENGTYIKDDTIFIKIVVDTSDLPDP

>d1k2fa_ b.8.1.2 (A:) SIAH, seven in absentia homolog {Mouse (Mus musculus)}

SVLFPCKYASSGCEITLPHTEKAHEELCEFRPYSCPCPGASCKWQGSLDAVMPHLMHQHKSI TLLQGEDIVFLATDINLPGAVDWVMMQSCFGFH
FMLVLEKQEYDGHQQFFAIVQLIGTRKQAENFAYRLENGHRRRLTWEATPRSIHEGIATAIMNSDCLVFDT SIAQLFAENGNLGINVTISM

>d2bn2a_ b.9.1.1 (A:) Neurophysin II {Cow (Bos taurus)}

AMSDLELRQCLPCPGGGKGRCFGPSICCGDELGCFVGTAEALRCQEENYLPS PCQSGQKPCGSGGRCAAAGICCNDSCVTEPEC

>d1kvp_ b.10.1.1 (-) Bacteriophage capsid proteins {Bacteriophage phi-X174}

SNIQTGAERMPHDLH LGFLAGQIGRLITSTTPVIAGDSFEMDAVGALRLSP LRRGLAIDSTVDIFTYVPHRHVYGEQWIKFMKDGVNATPLPTVN
TTGYIDHAFLGTINPD TNKIPKHLFQGYLNYYNFKAPWMPDRTEANPNEQNQDDARYGFRCCHLKNIWTAPLPPETRSRQM TTSTGMAPTT
KFRDVPNL SGTPLIFRDNKGRTIKTGQLGIGPV DAGFLVAQNTAQAANGERAI PSNLWADLSNATSIDIMGLQAA ANLHTDQERDYFMQR YRDVIS
SFGGKTSYDADNRPLL VMSRN LWASGYDVGTDQTSLGQFSGRVQQTYKHSVPRFFVPEHGT MFTLALVRFPTATKEIQYLNAKGALT YTDI AGDP
VLYGNLPPREISMKDVFRSGDSSKKFKIAEGQWYRYAPS YVSPAYHLLEGFPFIQEPPSGDLQERVLIRHH DQCFQS VQLLQWNSQVKFNVTVYR
NLPTTRDSIMTS

>d2bpa1_ b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage phi-X174}

SNIQTGAERMPHDLH LGFLAGQIGRLITSTTPVIAGDSFEMDAVGALRLSP LRRGLAIDSTVDIFTYVPHRHVYGEQWIKFMKDGVNATPLPTVN

TTGYIDHAAFLGTINPDNTKIPKHLFQGYLNYYFKAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPETELSRQMTTSTSIDIMGL
QAAYANLHTDQERDYFMQRYRDVISSFGGKTSYADNRPLLVMRSNLWASGYVDGTDQTSLGQFSGRVQQTYKHSVPRFFVPEHGTMFTLALV
RFPPTATKEIQYLNAGALTYTDIAGDPVLYGNLPPREISMKDVFRRSGDSSKKFIAEGQWRYAPSYPSPAYHLLEGFPFIQEPPSGDLQERVLIRHHD
YDQCFQSQVQLLWNSQVKFNVTYRNLPTRDSIMTS

>d2bpa_ b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage phi-X174}

MFQTFISRHSNFFSDKLVLTSVPASSAPVLQTPKATSSTLYFDSLTVNAGNGFLHCIMQDTSVNAANQVSVGADIAFDADPKFFACLRFESSV
PTTLPTAYDVPLNGRHGGYTVDKCVTIDVLPRTPGNVYVGFMVWSNFTAKCRLVSLNQVIKEIICLQPLK

>d1gff1_ b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage G4}

VPHDLSHLVFEAGKIGRLKTISWTPVVAGDSFECDMVGAIRSLPRLRGALAVDSRVDFSFYIPHRHIYQQWINFMKDGVNASLPPVCSSGWDSA
AYLGTIPSSTLKVPKFLHQGYLNYYFKPPWSDDLTYANPSNMPSEDYKGVRVANLSIWATPLPPDRTSENMTTGSTDIMGLQAAYAKLHT
EQERDYFMTRYRDIMKEFGGHTSYGDNRPLLMRSEFWASGYVDGTDQSSLGQFSGRVQQTFNKHVPRFYVPEHGVIMTLAVTRFPPTHEME
MHYLVGKENLTYTDIACDPALMANLPPREVSLLKEFFHSSPDSAKFIAEGQWYRTQPDRVAFPYNALDGFPFYSALPSTDLKDRVLVNTNNYDEIFQS
MQLAHWNMQTKFNINVYRHMPTRDSIMTS

>d1gff2_ b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage G4}

MFQKFISKNAPINSTLQAATKTPAVAAPVLSVPNLSRSTILINATTAVTTHSGLCHVVRIDETNPTNHHALSIAGSLSNVPADMIAFAIRFEVADGVV
PTAVPALYDVYPIETFNNGKAISFKDAVTIDSHPRTVGNDVYAGIMLWSNAWTASTISGVLSVNQNREATVLQPLK

>d1stma_ b.10.1.2 (A:) SPMV coat protein {Satellite panicum mosaic virus}

AAATSLVYDTCYVTLTERATTSFQRQSFPTLKGMGDRAFQVVAFTIQGVSAAPLMYNARLYNPGTDHSVATGVQLMGTVPRTVRLTPRGQNNW
FFGNTEEAETILAIDGLVSTKGANAPSNTIVTGCFLAPSELQSS

>d1a34a_ b.10.1.2 (A:) STMV coat protein {Satellite tobacco mosaic virus}

TGDNNSVVTMIRAGSYPKVNPTPTWVRAIPFEVSQSGIAFKVPVGSLFSANFRDSFTSVMSVRAWTQLPPVNEYSFVRLKPLKTDSTEEFF
GRASNINTRASVGYRPTNLRQNTVAADNVCEVRSCNRQVALVISCCFN

>d2stv__ b.10.1.2 (-) STNV coat protein {Satellite tobacco necrosis virus}

TMRAVKRMINTHLEHKRFAINSNTNATAGTVQNLNSNGIIQGDDINQRSGDQVRIVSHKLHVRGTAITVSQTFRFIWFRDNMNRGTTPTVLEVLN
TANFMSQYNPITLQQKRFTILKDTLNCSLTGESIKDRIINLPGQLVNYNGATAVAASNGPGAIFMLQIGDSLVLWDSSYEAVYD
>d1smva_ b.10.1.2 (A:) SMV coat potein {Sesbania mosaic virus}

GAITVLHCELTAEIGVTDSIVSSELVMPYTVGTWLRGVADNWSKYSWLSVRYTIIPSCSSTAGSIHMGFQYDMADTVPVSVNKLNSLRGYVSGQV
WSGSAGLCFINNSRCSDTSTAISTTLDVSELGKKWPYKTSADYATAVGVDVNIATDLVPARLVIALLDGSSSTAVAAGRIYDTYTIQMIEPTASALNL

>d1smvc_ b.10.1.2 (C:) SMV coat potein {Sesbania mosaic virus}

QAGISMAPSAQGAMVRIRNPVSSSRGAITVLHCELTAEIGVTDSIVSSELVMPYTVGTWLRGVADNWSKYSWLSVRYTIIPSCSSTAGSIHMGF
QYDMADTVPVSVNKLNSLRGYVSGQVWWSGAGLCFINNSRCSDTSTAISTTLDVSELGKKWPYKTSADYATAVGVDVNIATDLVPARLVIALLDGSS
TAVAAGRIYDTYTIQMIEPTASALN

>d1f2na_ b.10.1.2 (A:) RYMV capsid protein {Rice yellow mottle virus}

LSSNTWPLHSVEFLADFKRSSTSADATTYDCVPNLPRVWSLARCYSMWKPTRWDVYLPESATVAGSIEMCFLYDYADTIPRTGKMSRTAGFVT
SSVWYGAEGCHLSSGGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVNTILPARLAVRSSIKPTVSDTPGKLYVIASMVLRDPVDPLNT

>d1f2nc_ b.10.1.2 (C:) RYMV capsid protein {Rice yellow mottle virus}

AEPQLQRAPVAQASRISGTVPGPLSSNTWPLHSVEFLADFKRSSTSADATTYDCVPNLPRVWSLARCYSMWKPTRWDVYLPESATVAGSIEMC
FLYDYADTIPRTGKMSRTAGFVTSSVWYGAEGCHLSSGGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVNTILPARLAVRSSIKPTVSDTPGKL
YVIASMVLRDPVDPLNT

>d1bmv1_ b.10.1.2 (1:) BPMV coat protein {Bean pod mottle virus}

SISQQTVWNQMATVRTPLNFSSKQSFQFSVLLGGISDKTDWITLVQNSPISNLLRVAAWKKCLMVKVVMSGNAAVKRSDWASLVQVF
LTNSNSTEHDACRWTKSEPHSWELIFPIEVCGPNNGFEMWSSEANQTSWHLFLVDNPQKQSTTFDVLGGISQNFIEAGNTLMPAFSVPQ

>d1bmv2_ b.10.1.2 (2:) BPMV coat protein {Bean pod mottle virus}

METNLFKLSDDVETPKGSMLDLKISQSKIALPKNTVGGTILRSDLLANLTEGNFRASVLDQRTTHRIGMIKMVATVGIPENTGIALACAMNSSIRGR

ASSDIYTICSDQCELWNPACTKAMTMSFNPNPCSDAWSLEFLKRTGFHCDIICVTGWTATPMQDVQVTIDWFISSEQCVPRTYCVLNPQNPFLVNR
WMGKLTFPQGTSRSVKRMPPLSIGGGAGAKSAILMNMPNAVLSMWRVFVGLFVEVKMTSPYIKCTVSFFIAFGNLADDTINFEAFPHKLVQFGEI
QEKKVVLKFQSQEEFLAWSTQVRPATLADGCPYLYAMVHDSSVTPGDFIVGVKLTIENMCAYGLNPGISGSRLLGTPQ
>d1a6ca1 b.10.1.2 (A:1-176) TRSV capsid protein {Tobacco ringspot virus}
AVTVVPDPCTCCGTLFSFKVPKDAKGKHLGTFDIRQAIDYGGLHSQEWCAGKIVNPTFTVRMHAPRNAFAGLSIACTFDDYKRIDLALGNECPPSE
MFELPTKVFMKDADVHEWFNYGELTGHGLCNWANVATQPTLYFFVASTNQVTMAADWQCIVTMHVDMGPVIDRFELN
>d1a6ca2 b.10.1.2 (A:177-348) TRSV capsid protein {Tobacco ringspot virus}
PTMTWPIQLGDTFAIDRYYEAKEIKLDGSTSMLSISYNFGGPVKHSKKHAISYRAVMSRNLGWSGTISGSVSKVSSLCTASFVIFPWECEAPTLRQ
VLWGPHQIMHGDKQFEAIKTRLHSAATTEEGFGRGLGILPLSGPIAPDAHVGSYEFIVHINTWRPDQVHPPM
>d1a6ca3 b.10.1.2 (A:349-513) TRSV capsid protein {Tobacco ringspot virus}
FSSSELYNWFTLTNLKPDANTGVNFIDPGYIHDFAKDATVTLASNPLSLVAAATGWHYGEVDLCISWSRSKQAAQAEQSVSITTNYRDWGAYWQ
GQARIYDLRTEAEIPIFLGSYAGATPSGALKQNYVRISIVNAKDIVALRVCLRPKSIFWGRSATLF
>d4sbva_ b.10.1.2 (A:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}
SSMDVTILSHCELSTELAVTVTIVVTSELVMPFTVGTWLRGVAQNWSKYAWVAIRYTYLPSCPTTSGAIHMGFQYDMADTLPVSVNQLSNLKGYVT
GPVWEGQSGLCFVNNTKCPDTSRAITALDTNEVSEKYPFKTATDYATAVGVNANIGNILPRLVTAMEGGSSKTAVNTGRLYASYTIRLIEPIAAALN
L
>d4sbvc_ b.10.1.2 (C:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}
QAGVSMAPIAQGTMVKLRPPMLRSSMDVTILSHCELSTELAVTVTIVVTSELVMPFTVGTWLRGVAQNWSKYAWVAIRYTYLPSCPTTSGAIHM
GFQYDMADTLPVSVNQLSNLKGYVTGPVWEGQSGLCFVNNTKCPDTSRAITALDTNEVSEKYPFKTATDYATAVGVNANIGNILPRLVTAMEG
GSSKTAVENTGRLYASYTIRLIEPIAAALN
>d2tbva_ b.10.1.2 (A:) TBSV coat protein {Tomato bushy stunt virus}
GGVTVTSHREYLTVQVNNSGGFVVNGGIV/GNSLQLNPSNGTLFSWLPALASNFDQYSFNSVLDYVPLCGTTEVGRVALYFDKDSQDPEPADRVELA
NFGVLKETAPWAEAMRIPTDKVCRYCNDSATVDQKLIDLGLQLGIATYGGAGADAVGELFLARSVTLYFPQPTNTLLSKRDLTGSЛАДАТГРГЛВЛ
TRPTVLTHTFRATGTFNLSGGRLCLTSLLGATGAVVINDILAIDNVGTASDYFLNCTVSSLPATVTFTVSGVAAGILLGRARANVVNLL
>d2tbvc_ b.10.1.2 (C:) TBSV coat protein {Tomato bushy stunt virus}
IITHVGGVGGSIMAPVAWSRQLVGSKPCKTGRSGGVTSHREYLTVQVNNSGGFVVNGGIVGNSLQLNPSNGTLFSWLPALASNFDQYSFNSVLD
YVPLCGTTEVGRVALYFDKDSQDPEPADRVELANFGVLKETAPWAEAMRIPTDKVCRYCNDSATVDQKLIDLGLQLGIATYGGAGADAVGELFLARS
VTLYFPQPTNTLLSKRDLTGSЛАДАТГРГЛВЛTRPTVLTHTFRATGTFNLSGGRLCLTSLLGATGAVVINDILAIDNVGTASDYFLNCTVSSLPATVT
FTVSGVAAGILLGRARANVVNLL
>d1cwp_a_ b.10.1.2 (A:) Cowpea chlorotic mottle virus {Host: cowpea (*Vigna unguiculata*), (L.)}
KAIKAWTGYSVSKWTASCAAAEAKVTSAITISPNELSSERNKQLKVRVLLWLGLLPSVSGTVKSCVTETQTTAAASFQVALAVADNSKDVAAMYP
EAFKGITLEQLAADLTIYSSAALTEGDDVIVHLEVEHVRPFDDSFPTPVY
>d1c8na_ b.10.1.2 (A:) TNV coat protein {Tobacco necrosis virus}
NSTVVSNSELILNLTPIALAYTVQSLPLIATQPAWLGTIADNYSKWRWVSLRIIYSPKCPTTSGTVAMCLSYDRNDVAPGSRVQLSQTYKAINFPPYAG
YDGAAILNTDVTPTSAIYVDVDVTRFDKAWYSTIGTAAFAALTAFDQNQFCPCTVHIGSDGGPAVAVPPGDIFFKYVIELIEPINPTMN
>d1c8nc_ b.10.1.2 (C:) TNV coat protein {Tobacco necrosis virus}
GVSRAGGFVTAPVIGAMVTRPTVPRFGMRGNSTVVSNSELILNLTPIALAYTVQSLPLIATQPAWLGTIADNYSKWRWVSLRIIYSPKCPTTSGTV
MCLSYDRNDVAPGSRVQLSQTYKAINFPPYAGYDGAAILNTDVTPTSAIYVDVDVTRFDKAWYSTIGTAAFAALTAFDQNQFCPCTVHIGSDGGPAV
AVPPGDIFFKYVIELIEPINPTMN
>d1auya_ b.10.1.2 (A:) TYMV coat protein {Turnip yellow mosaic virus}
SPLTIKQPQFQSEVL FAGTKDAEASLTIANIDSVSTLTFYRHASLESLWVTIHPTLQAPTFTTVGVCWVPAQSPVTPAQITKTYGGQIFCIGGAIQTLSP
VKCPLEMMQPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTLMHSPLITDTST
>d1auyb_ b.10.1.2 (B:) TYMV coat protein {Turnip yellow mosaic virus}
MEIDKELAPQDRTVTATVLPAPGSPPLTIKQPQFQSEVL FAGTKDAEASLTIANIDSVSTLTFYRHASLESLWVTIHPTLQAPTFTTVGVCWVPAQS

PVTPAQITKYGGQIFCIGGAIQTLSPPLVKCPLEMMQPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTSLMHSPPLITDTST

>d1e57a_b.10.1.2 (A:) PHMV coat protein {Physalis mottle virus}

SPAIVLPFQEATTFGTAETAAQVSLQTADPITKLTA^PYRHAQIVECKAILPTDLAVSNPLTVYLAWVPANSPATPTQILRVYGGQSFLGGAISAAKTIE

VPLNLD^SVNRMLKDSVTYDTPKLLAYSRAPTNPSKIPTASIQISGRIRLSKPM^LIAN

>d1e57b_b.10.1.2 (B:) PHMV coat protein {Physalis mottle virus}

VVKVKQASIPAGSILSQPNTEQSPAIVLPFQEATTFGTAETAAQVSLQTADPITKLTA^PYRHAQIVECKAILPTDLAVSNPLTVYLAWVPANSPATPTQILRVYGGQSFLGGAISAAKTIEVPLNLD^SVNRMLKDSVTYDTPKLLAYSRAPTNPSKIPTASIQISGRIRLSKPM^LIAN

>d1ddla_b.10.1.2 (A:) DYMV coat protein {Desmodium yellow mottle tymovirus}

MEQDKILAHQASLNTKPSLLPPPVGNNPPVISYPFQITLASLGTEDAADS^SIASNSVLATYTALYRHAQLKHLKATIHP^TYMAPKYPTSV^ALVWVPANS

TATSTQVL^DTYGGHLFCIGGSVNSVKPIDVEANLTNLNPIIKASTTFTDTPKLLYYSKAQATAPSPTCYLTIQQQIELSSPLLQASS

>d1f15a_b.10.1.2 (A:) CMV coat protein {Cucumber mosaic virus, strain fny}

ERCRPGYFTTSITLKPPKIDRGSYGKRLLLPSVTEYDKKLVSRLQIRVNPLPKFDSTVVWVTVRKVPASSDLSVAISAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIGDMRKYAVLVSKDDAETDELVLHVDIEHQRIPTSGVLPV

>d1f15b_b.10.1.2 (B:) CMV coat protein {Cucumber mosaic virus, strain fny}

DANFRVLSQQQLSRLNKLAAGRPTINHPTFVGSERCPGYFTSITLKPPKIDRGSYGKRLLLPSVTEYDKKLVSRLQIRVNPLPKFDSTVVWVTVRKVPASSDLSVAISAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIGDMRKYAVLVSKDDAETDELVLHVDIEHQRIPTSGVLPV

>d2bbva_b.10.1.3 (A:) Nodavirus capsid protein {Black beetle virus}

LTRLSPQGLAFLKCAFAPPDFNTDPKGIPDRFEGKVTRKDVLNQSINFTANRDTFILIA^PTPGVAYWVADVPAGTFPISTTFNAVNFPGFNSMFGNAAASRSDQVSSFRYASMN^GVIYPTSNLMQFAGSITVW^KCPV^KLSNVQFPVATTPAT^SALVHTLVGLDGVLAVGPDNFSESFIKGVFQSVCNEPD^FEFSIDLEGIQLTPPANVTATSGQPFNLAAGAEAVSGIVGWGNMDTIVRVSAPTGA^NSAILKTWACLEYRPNPNA^MLYQFGHDSPPCDEVALQEYRTVARSLPVAVIAAQN

>d2bbvc_b.10.1.3 (C:) Nodavirus capsid protein {Black beetle virus}

TQ^TAPVPQQNVPKQPRRRRNARRNRRQGRAMNM^GALTRLSQ^GLAFLKCAFAPPDFNTDPKGIPDRFEGKVTRKDVLNQSINFTANRDTFILIA^PTPGVAYWVADVPAGTFPISTTFNAVNFPGFNSMFGNAAASRSDQVSSFRYASMN^GVIYPTSNLMQFAGSITVW^KCPV^KLSNVQFPVATTPAT^SALVHTLVGLDGVLAVGPDNFSESFIKGVFQSVCNEPD^FEFSIDLEGIQLTPPANVTATSGQPFNLAAGAEAVSGIVGWGNMDTIVRVSAPTGA^NSAILKTWACLEYRPNPNA^MLYQFGHDSPPCDEVALQEYRTVARSLPVAVIAAQN

>d1nova_b.10.1.3 (A:) Nodavirus capsid protein {Nodamura virus}

NMLKMSAPGLDFLKCAFASPDFNTDPKGIPDKFQGLVLPKKHCLTQSITFTPGKQTM^LVAPIPGIACLKAEANVGASFGVPLASVEFGFDQLFGT^ISATDTAANVTA^FRYASMAAGVYPTSNLMQFAGSIQVY^KPLKQVLNSYSQTVATV^PPTNLAQNTIA^IDGLEALDALPNNNYSGSFIEG^CYSQSVCNEPEFEFHPIMEGYASVPPANVTNAQASMFTNLTFSGARYTGLGMDAIALVTTPT^IARDIPIAVACKDN

>d1novc_b.10.1.3 (C:) Nodavirus capsid protein {Nodamura virus}

RRRAAPRQQQRQ^SNRASNQPRRRARRTRRQQRMAATNNMLKMSAPGLDFLKCAFASPDFNTDPKGIPDKFQGLVLPKKHCLTQSITFTPGK^ITM^LVAPIPGIACLKAEANVGASFGVPLASVEFGFDQLFGT^ISATDTAANVTA^FRYASMAAGVYPTSNLMQFAGSIQVY^KPLKQVLNSYSQTVATV^PPTNLAQNTIA^IDGLEALDALPNNNYSGSFIEG^CYSQSVCNEPEFEFHPIMEGYASVPPANVTNAQASMFTNLTFSGARYTGLGMDAIALVTTPT^IGAVNTAVLKWWACVEYRPNPNSTLYEFARES^PANDEYALAAYRKIARDIPIAVACKDN

>g1f8v.1 b.10.1.3 (A:,D:) Nodavirus capsid protein {Pariacoto virus}

NNRNKARKVVS^RSTALVPMAPASQRTGPAPRKPRKNQALVRNPR^LTAGLAFLKCAFAPDFSVDPKGIPDNFHGR^TLAIKDCNTTSV^VFTPNTDYIVVAPVPGFAYFRAEVAVGAQPTT^FVGVPYPTYATNFGAGSQNGLPAVN^NYSKFRYASMACGLYPTSNMMMFSGSVQVWRVDLN^LSEAVNP^AV^TTAITPAPGV^FANFV^DKR^INGLR^GIRPL^APRDN^YSGNFIDGAYTFAFDK^STDFEW^CDFV^RS^LEFS^EN^VGAATAM^KL^APGGGTD^TLTGLGN^VNTLV^YKISTPTGAVNTAILRTWN^CIELQPYTDSALFQSGV^SPPFDPLAECYHN^LKMR^FP^VAVSSREN^XSKFWEGV^LR^VL^NQISGTL^SV^IPG^PGTISAGVHQ^MLTGM^YMY

>g1f8v.2 b.10.1.3 (B:,E:) Nodavirus capsid protein {Pariacoto virus}

NPR^LT^DAGLAFLKCAFAPDFSVDPKGIPDNFHGR^TLAIKDCNTTSV^VFTPNTDTYIVVAPVPGFAYFRAEVAVGAQPTT^FVGVPYPTYATNFGAGS

QNGLPAVNNSKFRYASMACGLYPTSNNMQFSGSVQWRVDLNLSEAVNPVTAITPAPGVFANFVKRNGLRGIRPLAPRDNSGNFIDGAYTF
AFDKSTDWEWCDFVRSLEFSNVLAATAMKLLAPGGTDLLTGLGNVNTLVYKISTPTGAVENTAILRTWNCLIELQPYTDSALFQFSGVSPPFDPLA
LEYHNLKMRFPVAWSRENXSKFWEGVLRLNQISGTLSP

>d1dnv__ b.10.1.3 (-) Galleria mellonella densovirus capsid protein {Wax moth (Galleria mellonella), densovirus}

YYIIPRFSMFGKKLSTYKSHKFMIFGLANNVIGPTGTAVNRLLTCLAEIPWQKPLVMNQSEFDLLPPGSRVVECNVKVIFRTNRIAETSSVT
KQATLNQISNVQTAIGLNKGWGINRAFTAQSDQPMIPTATTAPKYPEVTGDTGYRGMIADYYGADSTNDTAFGNAGNYPHHQVSSFTLQNYYC
MYQQTNQGTGGWPCLAELHQFDSKTVNNQCLIDVTYKPKMGLIKSPLNYKIIGQPTVKGTISVGDNLNVNMRGAVVTNPPEATQNVIAESTHNLTR
NFPADLFNIYSDIEKSQVLHKGPWGHNPKIQPSVHIGIQAVPALTTGALLINSSPLNSWTDSMGYIDVMSSCTVMEAQPHTFPSTEANTNPGNTI
YRINLTPNSLTSAFNGLYGNGLTG

>d1b35a_ b.10.1.3 (A:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

VMGEDQQIPRNEAQHGVPISIDTHRISNNWSPQAMCIGEKVVSIQLIKRFGIFGDANTLQADGSSFVAPFTVTSTKLTSTRNTQFDYYYYLY
AFWRGSMRIKMAETQDGTGTPRKKTNFTWFVRMFNSLQDSFNSLISTSSAVTTVLPSGTINMGPSTQVIDPTVEGLIEVEPVYNNISHITPAVTI
DDGTPSMEDYLKGHSPPCLTFSPRDSISATNHITASFMRALGDDFSFMYLLGVPPVLNVARA

>d1b35b_ b.10.1.3 (B:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

ENSHIENEDKRLTSEQKEIVHFVSEGVPSTTALPDIVNLSTNYLDKNTREDRIHSIKDFLSRPIIIATNLWSVSDPVEKQLYTANFPEVLISNAMYQDKLK
GFVGLRATLVKVQVNSQPFQQGRMLQYIPIYAQMMPNRTVLINEQLQGRSGCPRTDLELSVGTEVEMRIPYVSPHLYNNLTGQGSFGSIYVVVYSQ
LHDQVSGTGSIEYTVWAHLEDVDVQYPTGANIFTGNEAYIKGTSRYDAAQAHAA

>d1b35c_ b.10.1.3 (C:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (Teleogryllus commodus)}

SKPTVQGKIGECKLRGQGRMANFDGMMDMSHKMALSSTNEIETNEGLAGTSLDVMDSRVLSPNYWDRFTWKTSDVINTVLWDNYVSPFKVKPY
SATITDRFRCTHMKGKANAFTYWRGSMVYTFKVKTQYHSGRLRISFIPYYNTTISTGTPDVSRTQKIVVDLRTSTAVSFTVPIGSRPWLYCIRPESS
WLSKDNTDGALMYNCVSGIVRVEVLNQLVAACQNFSEIDVICEVNGGPDEFAAGPTCPYVYAGDFTLADTRKIEARTQEYSNNED

>d1sida_ b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

KACPRPAPVPKLLIKGGMVEQLDVTGPDSVTEIEAFNPRMGQPPTPESLTEGGQYYGWSRGINLATSDTEDSPGNNTLPTWSMAKLQLPMLNEDLT
TCDTLQMWEAVSVKTEVVGSGLLDVHGFKPTDTVNTKGISTPVEGSQYHVFAVGGEPPLQGLVTDARTKYKEEVVTIKITKKDMVNKDQVL
NPISKAKLDKGGMYPVEIWHPDPAKNENTRYFGNYTGGTTPPVLQFTNTLTVLLDENVGPLCKGEGLYLSVDIMGWRVTRNYDVHHWRGLP
RYFKITLRKRWVKNPYPMASLISSLFNMLPQVQGQPMEGENTQVEEVRYDGTEPVPGDPDMTRYVDRFGKTKTVFPG

>d1vpsa_ b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

GGMEVLDLVGPDSVTEIEAFNPRMGQPPTPESLTEGGQYYGWSRGINLATSDTEDSPGNNTLPTWSMAKLQLPMLNEDLTQMLWEAVSV
KTEVVGSGLLDVHGFKPTDTVNTKGISTPVEGSQYHVFAVGGEPPLQGLVTDARTKYKEEVVTIKITKKDMVNKDQVLNPISKAKLDKGMY
PVEIWHPDPAKNENTRYFGNYTGGTTPPVLQFTNTLTVLLDENVGPLCKGEGLYLSVDIMGWRVTRNYDVHHWRGLPRYFKITLRKRWVK

>d1fmd1_ b.10.1.4 (1:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTTGESADPVTTVENYGETQVQRRHHTDVAFVLDRFVKVTVSDNQHTLDVMQAHKDNIVGALLRAATYYFSDEIAVHTGKLTWVPNGAPV
SALNNNTNPTAYHKGPVTRLALPYTAPHRVLATAYTGTTTASARGDLAHLTTAAHLPTSFNGAVKAETITELLVRMKRAELYCPRPILPIQPTGD
RHKQPLVAPAKQ

>d1fmd2_ b.10.1.4 (2:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

DKKTEETTLLERILTTRNGHTTSTQSSVGVTFGYATAEDSTSGPNTSALETRVHQAKERFFKMALFDWVPSQNFGHMHKVVLPHEPKGIVGGLVKS
YAYMRNGWDVEVTAVGNQFNGGCLLVALVPEMGDISDREKYQLTLYPHQFINPRTNMTAHITVPYGVNRYDQYKQHRPWTLVMMVVAAPLTNT
AGAQQIKVYANIAPIANTNVHVAGELPSKE

>d1fmd3_ b.10.1.4 (3:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

GIFPVACSDGYGNMVTDPKTADPAYGKVNPPRTALPGRFTNYLDVAEACPFLMFENVPVYSTRDGQRLLAKFDVSLAAKHMNTLAGLAQY
YTQYGTINLHFMTGPTDAKARYMVAVVPPGMDAPDNPEEAHCIAHEWDTGLNSKFTFSIPYISAADYTYTASHEAETTCVQGWVCVYQITHGK
ADADALVVASAGKDFELRLPVDARQQ

>d1qqp1_ b.10.1.4 (1:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTSGESADPVTTVENYGETQVQRRQHTDVSFIMDRFVKVTPQNQINILDLMQVPSHTLGALLRASYYFSDEIAVKGDLTWVPGNAPEKA

LDNTTNPTAYHKAPLTRLALPYTAPHRVLATVYNGECRYSRNAVPNLRGDLQVLAQKVARTLPTSFNYGAIKATRVTELLYRMKRAETYCPRPLLAIHPT
EARHKQKIVAPVK

>d1qqp2_ b.10.1.4 (2:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

DKKTEETTLLEDRLITTRNGHTTSTQSSVGVTYGYATAEDFVSGPNTSLETRVVQAERFFKTHLFDWTSDFGRCHLLEPTDHKGVYGS LTD SYAMRNGWDVEVTAVGNQFNGGCLVAMVPELCISIQKRELYQLTLPHQFINPRTNMTAHITVPFGVNRYDQYKVHKPWTLVVMVAPLVNTEGA
PQIKVYANIAPTNVHVAGEFPSKE

>d1qqp3_ b.10.1.4 (3:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

GIFPVACSDGYGGLVTTDPKTADPVYGKVNPPRNQLPGRFTNLLDVAEACPTFLRFEGGPVYVTTKTDSDRVLAQFDMSLAAKHMSNTFLAGLAQ
YYTQYSGTINLHFMTGPTDAKARYMVAYAPPGMEEPKTPPEAAAHCHIAEWDTGLNSKTFPSIPYLSAADYTYTASDVATTNVQGWVCLFQITHG
KADGDALVVLASAGKDFELRLPVDARAE

>d1c8da_ b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host: dog (Canis familiaris)}

GVGISTGTNNQTEFKFLENGWVYITANSSRLVHLNMPSENYRRVVNNMDKTA VNGNMA LDDIHA EITPWSLVDANA WGVWFNP GDWQL
IVNTMSELHLSFEQEIFNVVLKTVSESATQPPTKVYNNDLTASLMVALDSNNTMPPTAAMRSETLGFPWKPTIPTPWRYYFQWDR LIPSHTGT
SGPTNIYHGTDPPDVQFYTIENSVPVHLLRGDEFATGTF FDCKPCRLHTWQTNRALGLPFLNSLPQSEGDTNFGDIGVQQDKRRGV TQMGN
TNYITEATIMRPAEVGYSAPYYSFEASTQGPFTPIAAGRGAQTDENQAADGNPRYAFGRQHGQKTTTGETPERFTYIAH QDTGRYPEGDWIQN
INFNLPTNDNVLPTDPIGGKTGINYTNIFNTYGPLTALNNVPPVYPNGQIWDFKEFDTLKPRLHVNAFVCQNNCPQLFVKVAPNLTNQYDPD
ASANMSRIVTYSDFWWKGKLVFKAKLRASHTWNPIQQMSINVDNQFNYVPSNIGGMKIVYEKSQAPRKLY

>d1k3va_ b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host: pig (Sus scrofa)}

GVGVSTGTNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKRIHVLSNE SGVAGQMVQDDAHTQMVT PWSLIDANA WGVWFNPADWQLIS
NNMTEINLVSFEQEIFNVVLKTTESATSPPTKIYNNDLTASLMVALDTNNTLPYTPAAPRSETLGFPWLPTKPTQYRYYLSCIRNLNPPTYTGQSQQIT
DSIQTGLHSDIMFYTIENAVPIHLLRTGDEFSTGIYHFDTKPLKLTHSWC QTNRSLGLPPKLLTEPTTEGDQHPGTLPAANTRKGYHQTINNSY TEATAIRP
AQVGYNTPYMNFEYSNGGPFLTPIVPTADTQYNDEPNGAIRFTMDYQHGHLTSSQELERYTFNPQSKCGRAPKQQFNQQAPLNLENTNNGTLL
PSDPIGGKSNMHFMNTLNTYGPLTALNNTAPVFNGQIWDFKE DTLKPRLHVTA PFVCKNNPPGQLFVKIAPNL TDFNADSPQQPRIITYSNFW
WGKTLTFTAKMRSSNMWNP IQQH TTAEIGNYIPTNIGGIRMFPEYSQLIPRKLY

>d1mvma_ b.10.1.4 (A:) MVM coat protein {Murine minute virus, strain i}

GVGVSTGSYDNQTHYRFLGDWVETALATRLVHLNMPKSEN YCRIRVHNTTDSVKG NMA KDDAHEQIWTPWSLVDANA WGVWLQPSDWQY
ICNTMSQLNLVSLDQEIFNVVLKTVTEQDSGGQA IKIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFPWKPTIASPYRYYFCVDRDLSVTYEN
QE GTIEHNVMGTPKG MNSQFFT TIENTQQITLLRTGDEFATGTYYFDTNPV KLHTWQTNRQLGQ PPLSTFPEADT DAGTLTAQGSRH GATQMEV
NWVSEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADVTQGMDREANGSVRYSYGKQHGENWA AHGPAPER YT WDE TNFGSGRDTRDGFI
QSAPL VPPPLNGILT NANPIGTKNDIHSNFVNFSYGP LTFSHPSPVY PQGQIWDFKELD LEHKP RLHITAPFVCKNNAPGQMLVRLGP NLTDQYD
NGATLSRIVTYGTF FWKGKLTMR AKL RANTT WNPVYQVSVEDNGNSYMSV KWLP TATGNMQSVPLITRV VARNTY

>d1hx s1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}

GSSSTDNTVRETVAATS RDALPNT EASG PTHSKEIP ALTA VETGATNPLVPSDTVQTRHVVQHRSRSESSIESFFARGACVTIMTVDNPASTTNKDKL
FAVWKYKDTVQLRRKLE FFTYSRFD MELTFV VTANFTETNNGHALNQVYQIMYVPPGAPVPEK WDDYTWQTSSNPSIFYTYGTA PARIS VPYVG
NAYSHFYDGF SKVPLKDQSAALGDSLYGAASLND FGILAVRVVNDHNPTK VTSKIRVYLPKHIRVW C PRPPRAVAYYGP GVDYKDG TLPLSTKDLTT
Y

>d1hx s2_ b.10.1.4 (2:) Poliovirus {Poliovirus type 1, strain Mahoney}

ACGYSDRV LQLTGN STITTQEAANSV VAGRWEYLRDSEANPVDQPTEP DVACRFYLTDTV SWT KESRGWW KLP DALR DMGLF QNM Y
HYLGRSGYTVHVQCNASKFH QGALGV FAVPEM CLAGDSNTTMHTSYQ NAPG EKGGTFTGFTPDNNQ TSPARRFC PV DYL NGNTLL GNA F
FPHQIINLRTNNCATL VLPYVNSL SIDS MVKHNNW GIA LPLAPLNFA SESSPEI PTIAPMCCEFNGLRN ITL PRLQ

>d1hx s3_ b.10.1.4 (3:) Poliovirus {Poliovirus type 1, strain Mahoney}

GLPV MNTPGSNQYLTADNFQSPCALPEFDT PPI DIPGEVKNM MELAEIDTMIPFD LSATK NTM EMYRVRLSDKP HTDDPILCL SPASD PRL SH
TMLGEILNYYTHWAGSLKFTFLFCGSM MATGKLLV SYAPP GADPPKR KEAM LGTH V IWDIGLQSSCTM VV PWISNTT YRQ TIDD SFT EGGY ISF VY
QTRIVVPLSTPREMDILGF VSACN DFSV RLL RTT HIEQKA

>d1pov0_ b.10.1.4 (0:) Poliovirus {Poliovirus type 1, strain Mahoney}

GAQVSSQKVGAHENSNRAYGGSTINYTTINYRDSASNAASKQDFSQDPSKFTEPIDVLIKTAPEMLNSPNIEACGYSDRVQLTLGNSTITTQEAANS
VVAYGRWPEYLRDSEANPVDPQTEPDVAACRFYTLTVS这一切是ESRGWWKKLPDALRDMGLFGQNMYYHLYGRSGYTVHVQCNASKFHQGALG
VFAVPEMCLAGDSNTTMHTSYQNANPGEKGFTGFTPDNNQTSPARRFCPVDFLLNGNTLLGNAFVFPHQIINLRTNNCATLVPYVNSLSIDS
MVKHNNWGINAIALPLAPLNFASESSPEIPTLTIAPIMCCEFNGLRNITLPRLO

>d1pov1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}

QHRSRSESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRRKLEFFFTYSRFDMELTFVVTANFTETNNGHALNQVQIMYVPPGAP
VPEKWDDYTWTQTSNPSIFYTYGTAPARISVPYVGISNAYSHFYDGFSKVPLKDQSAALGDSLGAASLNDFGILAVRVVNDHNPTKVTSKIRVYLKPK
HIRVWCPRPPRAVAYYGPVVDYKDGTLPLSTKDLTT

>d1eah1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 2, strain Lansing}

ANNLPDTQSSGPAHSKETPALTAVENTGATNPVLPSDTVQTRHVIQKRTRSESTVESFFARGACVAlIEVDNDAPTKRASKLFSVWKITYKDTVQLRRKLE
FFFTYSRFDMEFTFVVTNTSYNDANNGHALNQVQIMYIPPGAPIPGKWNDYTWTQTSNPSVFTYGAAPPARISVPYVGIANAYSHFYDGFAKVPAG
QASTEGDSLGAASLNDFGSLAVRVVNDHNPTKLTISKIRVYMKPKHVRVWCPRPPRAVYYGPVVDYKDGAPLPGKGLTT

>d1eah2_ b.10.1.4 (2:) Poliovirus {Poliovirus type 2, strain Lansing}

SVRVMQLTLGNSTITTQEAANSVAVGRWPEYIKDSEANPVDPQTEPDVAACRFYTLDTVWRKESRGWWKKLPDALRDMGLFGQNMFYHYLG
RAGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSTTHMFTKYENANPGEKGGEFKGSFTLDTNATNPARNFCPVDFLGSGVLAGNAFVYPHQII
NLRTNNCATLVPVNSLSIDSMTKHNNWGINAIALPLAPLDFATESSTEIPITLTIAPIMCCEFNGLRNITVPRTO

>d1eah3_ b.10.1.4 (3:) Poliovirus {Poliovirus type 2, strain Lansing}

GLPVLNTPGSNQYLADNYQSPCAIPEFDVTPPIDIPGEVRNMMELAEIDTMIPNLNTQRKNTMDMYRVELNDAHSDTPILCLSLSPASDPRLAH
TMLGEILNYYTHWAGSLKFTFLFCGSMMATGKLLSYAPPAGEAPKSKEAMLGTHVIWDIGLQSSCTMVPWISNTTYRQTINDSFTEGGYISMFY
QTRVVVPLSTPRKMDILGFVSACNDFSVRLRDTHISQEA

>d1pvc1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 3, strain Sabin}

QDSLPTKASGPAHSKEVPALTAVENTGATNPVLAPSDTVQTRHVVQRRSESTIESFFARGACVAlIEVDNEQPTTRACQLFAMWRITYKDTVQLRRKLE
EFFFTYSRFDMEFTFVVTANFTNANNGHALNQVQIMYIPPGAPIPKWDDYTWTQTSNPSIFYTYGAAPPARISVPYVGIANAYSHFYDGFAKVPKLT
DANDQIGDSLAYSAMTVDDFGVLAVRVVNDHNPTKVTSKVRIYMKPKHVRVWCPRPPRAVYYGPVVDYRNNLDPLSEKGLTT

>d1pvc2_ b.10.1.4 (2:) Poliovirus {Poliovirus type 3, strain Sabin}

ACGYSDRVQLTLGNSTITTQEAANSVAVGRWPEFIRDEANPVDPQTEPDVATCRFYTLDTVMWGKESKGWWKKLPDALRDMGLFGQNMYY
HYLGRSGYTVHVQCNASKFHQGALGVFAIPEYCLAGDSDKQRYSYANANPGERGGKFYSQFNKDNAVTSPKREFCPVDFLLCGVLLGNAFVYPH
QIINLRTNNSATIVLPYVNALAIDSMVKHNNWGINAIALPLSPLDFAQDSSVEIPITVTIAPMCSEFNGLRNVTAPKFQ

>d1pvc3_ b.10.1.4 (3:) Poliovirus {Poliovirus type 3, strain Sabin}

GLPVLNTPGSNQYLTSNDNHQSPCAIPEFDVTPPIDIPGEVKNMMELAEIDTMIPNLESTKRNTMDMYRVTLSDSADLSQPILCISLSPAFDPRLSHT
MLGEVLNYYTHWAGSLKFTFLFCGSMMATGKLVAYAPPQAQPPTSKEAMLGTHVIWDIGLQSSCTMVPWISNTYRQTTQDSFTEGGYISMFY
YQTRIVVPLSTPKSMSMLGFVSACNDFSVRLRDTHISQSA

>d4rhv1_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 14}

TVASISGPKHTQKVPILTANETGATMPVLPDSIETRTTYMHFNGSETDVECFLGRAACVHVTEIQNKDATGIDNHREAKLFNDWKINLSSLVQLRKKE
LELFITYVRFDSEYTIATASQPDANSYSSNLVQAMYVPPGAPNPKEWDDYTWTQASNPSVFFKGDTSRFSVPYVGLASAYNCFYDGYSQHDDAET
QYGITVLNHMGMSAFRIVNEHDEHKTLVKIRVYHRAKHVEAWIPRAPRALPYTSIGRTNPKNTEPVIKRKGDIKSY

>d4rhv2_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 14}

GYSDRVQQITLGNSTITTQEAANANAVVCYAEWPEYLPDVADSVNKTSKPDTSCRFYTLDSKTWTGSKGCWKLKPDALRDMGVFGQNMFFHSI
GRSGYTVHVQCNATKFHSGCLLVIPIEHQLASHEGGNVSVKYTFHPGERGIDLSSANEVGGPVKDVLYNMNGTLLGNLLIFPHQFINLRTNNTATI
VIPYINSVPIDSMTRHNNVSLMVIPIALTVPTGATPSLPIVTIAPMCTEFSGIRSKSIVPQ

>d4rhv3_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 14}

GLPTTLPGSGQFLTTDRQSPSALPNYEPTPRIHIPGVHNLLEIIQVDTLIPMNNTHTKDEVNSYLIPLNANRQNEQVFGTNLFIGDGVFKTLLGEI
VQYYTHWSGLRSLMYTPALSSAKLILAYTPPGARGPQRREAMLGTHVVWDIGLQSTIVMTIPWTSGVQFRYTDPTDTSAGFLSCWYQTSLIL

PPE TTGQVYLLSFISACPDFKLRLMKDTQTISQTVALTE
>d1aym1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 16}
NPVERVDEVLNEVLPVNINQSHPTTNAVPLDAEATGHTNKIQPEDTIETRYVQSSQLDEMSVESFLGRSGCIHESVLDIVDNYNDQSFTKWNINLQEMAQIRRKFEMFTYARFDSEITMPSVAAKDGHIGHIVMQYMYVPPGAPIPTRDDYAWQSGTNASVFWQHQPFPRFLPFLSIASAYYMFYDGYDGTYSRGTWTNDMGLCSRITSEQLHKVVKVTRIYHKAKHTKAWCPRPPRAVQYSHTHTNYKLSSEVHNDVAIRPRTNLTTV
>d1aym2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 16}
SDRIIQITRGDSTITSQDVANAVVGYGVWPHYLTPQDATAIDKPTQPDTSNRFYTLDSKMWNSTSKGWWWKLPDALKDMGIFGENMFYHFLGRSGYTVHVQCNAASKFHQGTLVVMIPEHQLATVNKGNVNAGYKYTHPGEAGREVGTQVENEKQPSDDNWLNFDGTLGNLLIFPHQFINLRSNNSATLIVPVVNAVPMDSMLRHNNWSLVIPVCQLQSNNSNIVPITVSISPMCMAEFGARAKTVVQ
>d1aym3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 16}
GLPVYITPGSGQFMTTDDMQSPCALPWYHPTKEIFIPGEVKNLIEMCQVDTLIPINSTQSNIGNVSMYTTLSPQTKLAEEIFAIAKVDIASHPLATTI GEIASYFTHWTSLSRFSMFCGTANTTLKVLLAYTPPGIGKPRSRKEAMLGTHVWDVGLQSTVSLVVPWISASQYRFTTDYSSAGYITCWYQTNFVVPNTPTAEMLCFVGCKDFCLRMARDTDLHKQTGPITQ
>d1r1a1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 1A}
NYIDEVLNEVLPVNICKESHHHTSNSAPLLDAETGHTSNVQPEDAIETTRYVITSQTRDEMSIESFLGRSGCVHISRIKVDYTDNGQDINFCKWKITLQEMAQIRRKFELFTYVRFDSEITLVPICIAGRGGDIGHIVMQYMYVPPGAPIPSKRNDWSQSGTNMSIFWQHQPFPRFSIPFLSIASAYYMFYDGYDGDNTSSKGSSVVTNDMGTCSRIVTEKQKLSVVIITHIYHKAKHTKAWCPRPPRAVPTHSHVTNYMPETGDTTAIVRRNTITTA
>d1r1a2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 1A}
DRIMQITRGDSTITSSDDVANAVVGYGVWPHYLTPQDATAINKPTQPDTSNRFYTLESKHWNNGSSKGWWWKLPDALKDMGIFGENMYYHFLGRSGYTVHVQCNAASKFHQGTLVVMIPEHQLASAKHGSVTAGYKLTHPGEAGRDSQERDASLRQPSDDSWLNFDGTLGNLLIFPHQFINLRSNNSATLIVPVVNAVPMDSMLRHNNWCLVIIPIPLRSETTSSNIVPITVSISPMCMAEFGARAKNIQ
>d1r1a3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 1A}
GLPVYITPGSGQFMTTDDMQSPCALPWYHPTKEISIPGEVKNLIEMCQVDTLIPVNNVGNNVGNVSMYTQLGNQTGMAQKVFISIKVDITSTPLATTLIGEIASYTHWTSLSRFSMFCGTANTTLKLLAYTPPGIDEPTTRKDAMLGTHVWDVGLQSTISLVPWVSASHFRLTADNKYSMAGYITCWYQTNLVVPSTPQTADMCFVSACKDFCLRMARDTDLHIQSGPIEQ
>d1fpn1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 2}
LVVPNISSNPTTSNSAPALDAETGHTSSVQPEDVIETRYVQTQTRDEMSLESFLGRSGCIHESKLEVTLANYKENFTVWAINLQEMAQIRRKFELFTYTRFDSEITLVPICASLQSDIGHITMQYMYVPPGAPVNSRDDYAWQSGTNASVFWQHQAYPRFLSVAASAYYMFYDGYDEQDQNYGTA NTNNMGSLCSRIVTEKHIHKVHIMTRIYHKAKHVKAWCPRPPRALEYTRAHRTNFKIEDRSIQTAIVTRPIITTA
>d1fpn2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 2}
RIIQITRGDSTITSQDVANAIVAYGVWPHYLSSKDASAIDKPSQPDTSNRFYTLRSVTWSSSKGWWWKLPDALKDMGIFGENMFYHLYGRSGYTHVQCNAASKFHQGTLIVALIPEHQIASALHGNVNGYNYTHPGETGREVKAETRLNPDLPQTEYWLNFDTLLGNITIFPHQFINLRSNNSATIAPYV NAVPMDSMRSHNNWSLVIIPIPLETSSAINTIPITISISPMCMAEFGARAKRQ
>d1fpn3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 2}
GLPVFITPGSGQFLTDDFQSPCALPWYHPTKEISIPGEVKNLVEICQVDSLVPINNTDTYINSENMYSVVLQSSINAPDKIFSIRTDVASQLATTLEI SSYFTHWTSLSRFSMFCGTANTTVKLLAYTPPGIAEPTTRKDAMLGTHVWDVGLQSTISMVWPWISASHYRNTSPGRSTSGYITCWYQTRLVIPP QTPPTARLLCFVGCKDFCLRMARDTDLHLQSGAIAQ
>d1rhi1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 3}
QTLASVSSGPKHTQSVPALTANETGATLTPRPSDNVETRTTYMHFNGSETDVESFLGRAACVHTEIKNKNAAGLDNHRKEGLFNDWKINLSSLVQL RKKLELFYVRFDSEYTLATASQPEASSYSSNLTVQAMYVPPGAPNPKEWDDYTWSQASNPSVFKVGETSRFSVPFGIASAYNCFYDGYSHDDPD TPYGITVLNHMGMSMAFRVVNEHDVHTTIVKIRVYHRAKHVEAWIPRAPRALPYVSIGRTNYPRDSKTIKKRTNIKY
>d1rhi2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 3}
GYSDRVQQITLGNSTTQEARNIAVCYAEWPEYLSNDNADSVNKTSKPDISVCRFTLDSKTWKATSKGWCWKLPAKDMGVFGQNMFYHSLG RTGYTIHVQCNAKTFHSGCLLWVPIEHQLASHEGGTVSVKYKYTHPGDRGIDLDTVEAGGPTSDAIYNMDGTLGNLLIFPHQFINMRTNNNTATIV

VPYINSVPIDSMTTRHNNVSLMVPIAPLNAPTGSSTLPVTVTIAPMCTEFTGIRSRISVPQ

>d1rhi3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 3}

GLPTTLPMSGQFLTTDRQSPSALPSYEPTPRIHIPGKVRNLLEIIQVGTLIPMNNTGNDNVTNYLPLHADRQEIQFGTKLYIGDGVFKTLLGEIA
QYYTHWSGLRISLMLYTGPALSSAKIILAYTPPGTRGPEDKKEAMLGTHVVWDIGLQSTIVMTIPWTSQVQFRYTDPTYTSAGYLSWCWYLTSLILPPQ
TSGQVYLLSFISACPDFKLRLMKDTQTISQTDALTE

>d1bev1_b.10.1.4 (1:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

QAAGALVAGTSTHSVATDSTPAQLQAETGATSTARDESMIERTTIVPTHGIHETSVEFFGRSSLVGMPLLATGTSITHWRIDREFVQLRAKMSWF
TYMRFDVEFTIIATSSTGQNVTEQHTTYQVMVPPGAPVPSNQDSFQWQSGCNPSVFADTDGPPAQFSVPFMSSANAYSTVYDGYARFMDTDP
DRYGILPSNFLGFMFYFRTLEDAAHQVRFRYAKIKHTSCWIPRAPRQAPYKKRYNLVFGSDSDRICSNRASLTSY

>d1bev2_b.10.1.4 (2:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

EACGYSDRVQLTLGNSTITTQEAANICVAYGCWPAKLSDTDATSVDKPTEPGVSADRFYTLRSKPQADSKGWYWKLDALNNTMGFGQNAQF
HYLYRGGWAHVQCNAKHFHQGTLVLAYPEHQIATQEPAFDRTMPGSEGGTFQEPFWLEDGTSLGNSLIYPHQWINLRTNNSATLILPYVNAIP
MDSAIRHSNWTLAIIPLVAPLKYYAAETTPLVPTVTIAPMETEYNGLRRAIASNQ

>d1bev3_b.10.1.4 (3:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

GLPTKPGPGSYQFMTTDECSPCILPDFQPTPEIFIPGKVNNLLEIAQVESILEANNREGVEGVERYVIPVSVQDALDAQIYALRLELGGGPLSSLLGT
LAKHYTQWWSGVEITCMFTGTFMTGKVLAYTPPGDMPRNREEARLGTHVIWDFGLQSSITLVIPWISASHFRGVSNDDVNYQYYAGHVTI
WYQTNMVIPPFGFPNTAGIIMMIAAQPNFSFRIQKDREDMTQTAILQ

>d2mev1_b.10.1.4 (1:) Mengo virus {Host: monkey brain; middle size plaque variant}

GVENAEKGVTENTDATADFVAQPVYLPEENQTKVAFFYDRSSPIGAFAVKSGSLESGFAPFSNKACPNSVILTPGPQFDPAYDQLRPQRLTEIWGN
ETSEVFPLKTKQDYSFCLSPFVYYKCDELVTSPHTSGAHGLLVRWCPTGPTKPTTQLHEVSSLSEGRTPQVYSAGPGTSNQISFVVPPNSPLSVLP
AVWYNGHKRFDNTGDLGIAPNSDFGTLFFAGTKPDIKFTVYLRYKNMRVFCRPTVFFPWPTSGDKIDMT

>d2mev2_b.10.1.4 (2:) Mengo virus {Host: monkey brain; middle size plaque variant}

ENLSDRVSQLTAGNTVTNTQSTVGRLVGTVHDGEHPASCADTASEKILAVERYYTFKVNWTSTQPKFEYIRIPLPHVLSGEDGGVFGATLRRHYL
VKTGWRVQVQCNASQFHAGSLLVMAPEYPTLDVFAMDNRWSKDNLPGTRTQTNRKGPFAMDHQNFWQWTLYPHQFLNLTNTVDLEPV
YVNIAPTSWTQHASWTLVIAVVAPLTYSTGASTSLDITASIQPVRPVFNGLRHEVLSRQ

>d2mev3_b.10.1.4 (3:) Mengo virus {Host: monkey brain; middle size plaque variant}

SPIPVTIERHAGTWYSTLPDSTVPIYGKTPVAPANYMVGEYKDFLEIAQJPTFIGNKVPNAVPYIEASNTAVKTQPLAVYQVTLSCSCLANTFLAALS
AQYRGSLVYTFVFTGTAMMKGKFLIAYTPPGAGKPTSRDQAMQATYAIWDLGLNSSYFTVPFISPTHFRMVGTDQANITNDGWVTVWQLT
YPPGCPTSAKILMVSAKGDFSLKMPISPAPWSPQ

>d1cov1_b.10.1.4 (1:) Coxsackievirus B3 {Host: human (Homo sapiens)}

RVADTVGTGPTNSEAIPALTAETGHTSQVPSDTMQTRHVKNYHSRSESTIENFLCRSACVYFTEYENSGAKRYAEWVITPRQAAQLRRKLEFFT
RFDLELTFTVITSTQQPSTTQNQDAQILTHQIMYVPPGGVPDKVDSYVWQTSTNPSPVFWTEGNAPPMSVPFLSIGNAYSNFYDGWSEFSRNG
GINTLNNMGTLYARHVNAGSTGPIKSTIRIYFKPKHVKAZIPRPPRLCQYEAKNVNFQPSGVTTTRQSITMTNT

>d1cov2_b.10.1.4 (2:) Coxsackievirus B3 {Host: human (Homo sapiens)}

GYSDRVRSLGNSTITTQECANVVVGTVWPDPYLDKSEATAEDQPTQPDVATCRFTLDSVQWQKTPGWVWKLDPALSNLGLFGQNMQYHYL
GRTGYTIHVQCNCASFHQGCLLVVCVPEAMGCAVLNNTPSSAELLGDTAKEFADKPVASGSNKLVQRVYVAGMGVGVGNLIFPHQWINL
NNSATIVMPYTNSPMDNMFRHNNVTLMVIPFVPLDYCPGSTTYVPTVTIAPMCAEYNGLRLAGHQ

>d1cov3_b.10.1.4 (3:) Coxsackievirus B3 {Host: human (Homo sapiens)}

GLPTMNTPGSCQFLTSDFQSPSAMQPQYDVTPEMRIPEVGNVKNLMEIAEVDSVVPVQNVGEKVNNSMEAYQIPVRSNEGSGTQVFGPLQPGYSSV
SRTLLGEILNYYTHWSGSIKLTFMFCGSAMATGKFLAYSPPGAGAPTKRVDAMLGTHVVWDVGLQSSVLCIPWISQTHRYVASDEYTAGGFITC
WYQTNIVVPAQSSCYIMCFVSACNDFSVRLLKDTPFISQENFFQ

>d1d4m1_b.10.1.4 (1:) Coxsackievirus A9 {Host: human (Homo sapiens)}

GDVEEAIERAVVHVADTMRSGPSNSASPVALTAVETGHTSQTSPDTMQTRHVKNYHSRSESTVENFLGRSACVYMEYKTTDNDVNKKFVAWPI
NTKQMVMQMRKLEMFTYLRFDMEVTFVITSRQDPGTTLAQDMPVLHQIMYVPPGGPIPAPVDDYAWQTSTNPSIFWTEGNAPARMSIPFISIGN

AYSNFYDGWSNFDQRGSYGYNTLNNLGHIVRHVGSSPHIPITSTIRVFKPKHRAWVPRPPRLCQYKKAFSVDFTPTITDTRKDINTVTTV
>d1d4m2_b.10.1.4 (2:) Coxsackievirus A9 {Host: human (Homo sapiens)}
SDRVRSLTGNSTITTQECANVVVGYGRWPTYLDRDEATAEDQPTQPDVATCRFTLDSIKWEKGSGVWWWKFPEALSDMGLFGQNMQYHYLGR
AGYTIHVQCNASKFHQGCLLVCVPEAEMGAVVGQAFSATAMANGDKAYEFTSATQSDQTKVQTAIHAGMGVGVGNLTIYPHQWINLRTNNS
ATIVMPYINSVPMDNMFRHYNFTLMVIPFKLDYADTASTYVPIVTVPAPMCAYNGLRLAQAO
>d1d4m3_b.10.1.4 (3:) Coxsackievirus A9 {Host: human (Homo sapiens)}
GLPTMNTPGSTQFLTSDDFQSPCALPQFDVTPSMNIPGEVKNLMEIAEVDSVPVNQDQTMQEMFRIPVTINAPLQQVFGRLQPGLDVF
KHTLLGEILNYYAHWSGSMKLTFCGSAATGKFIAVSPPGANPKTRKDAMLGTHIIWDIGLQSSCVLCVPWISQTHYRLVQQDEYTSAGYVTC
WYQTGMIVPPGTPNSSIMCFASACNDFSVRMLRDTFISQDNKLQ
>d1ev11_b.10.1.4 (1:) Echovirus type 1 {Host: human (Homo sapiens)}
GDVQNAVEGAMVRVADTVQTSATNSERVPNLTAVENTGHTSQAVPGDMQTRHVINNHVRSESTIENFLARSACVFLEYKTGTKEDENSFNNWVI
TTRRAQLRRKLEMFTYLRFDMEITVVITSSQDQSTSQNQNAPVLTHQIMVPPGGPIPVSDDYSWTNSTNPSIFWTEGNAPARMSIPFISIGNAY
SNFYDGWSHFSQAGVYGFITLNMGQLFFRHVNKPNAITSVARIYFKPKHVRAWWPRPPRLCPYINSTNVNFEPKPVTEVRTNIITT
>d1ev12_b.10.1.4 (2:) Echovirus type 1 {Host: human (Homo sapiens)}
GYSDRVRSLTGNSTITTQECANVVVGYGEWPEYLDNEATAEDQPTQPDVATCRFTLDSQWENGSPGWWWWKFPDALRDMLFGQNMYYHY
LGRAGYTIHVQCNASKFHQGCILVVCVPEAEMGSAQTSGVVNYEHISKGEIASRFTTTAEDHGVAQAVWNAGMGVGVGNLTIFPHQWINLRTN
NSATIVMPYVNSVPMDNMFRHNTLMIIPFVPLDFSAGASTYVPIVTVPAPMCAYNGLRLAGHQ
>d1ev13_b.10.1.4 (3:) Echovirus type 1 {Host: human (Homo sapiens)}
GLPTMNTPGSNQFLTSDDFQSPSAMQPFDVTPEMHIPGEVRNLMEAEVDSVMPINNDSAAKVSSMEAYRVELSTNTNAGTQVFGQLNPGAES
VMNRTLMEIILNYYAHWSGSIKTFVFCGSAMTTGKFLSYAPPGAGAPKTRKDAMLGTHVVWDVGLQSSCVLCIPWISQTHYRFVEKDPTYTNAGF
VTCWYQTSVSPASNQPKCYMMCIVSACNDFSVRMLRDTKFIEQTSFYQ
>d1tme1_b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}
GSDNAEKGVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNIESTFVYQENDRLNCLLTLPSFCPDSTSGPVTKAPVQWRWV
RSGGTTNFPLMTKQDYAFLCFSPTYYKCDLEVTVSALGTDVAVSLRWAPTGAPADVTDLQIYTPSLGETRNPHMWLVGAGNTQISFVVPYNPL
SVLPAAWFNGWSDFGNTKDFGVAPNADFGRLWIQGNTSASVRIRYKKMKVFCRPTLFFPWV
>d1tme2_b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}
DRVASDKAGNSATNTQSTVGRLCGYGEAHGEHPASCADTATDKVLAERYYTIDLASWTTQEAFSHIRIPLPHVLAGEDGGVFGATLRRHYLCKT
GWRVQVQCNASQFHAGSLLVFMAPEFYTGKGTKTGMEPTDPFTMDTTWRAPQGAPTGYRYDSRTGFFAMNHQNQWQWTVYPHQILNLRT
NTTVLEVYVNIAPTSSWTQHANWTLVAVFSPLQYASGSSDVQITASIQPVNPVFNGLRHETVIA
>d1tme3_b.10.1.4 (3:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}
SPIAVTVREHKGFYSTNPDTTVPIYGKISTPNDYMCGEFSDLLELKPTFLGNPNNSNKRYPYFSATNSVPTSLVDYQVALSCCMNSMLAAVA
RNFNQYRGSLNFLVFTGAAMVKGKFLIAYTPPGAGKPTTRDQAMQATYAIWDLGLNSSFVFTAPFISPTHYRQTSYTSATIASVDGWVTVWQLTPL
TYPSTGTPVNSDILTVSAGDDFTLRMPISTKWWV
>d1tmf1_b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}
GVDNAEKGVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNMETTFNYQENDYRLNCLLTLPSFCPDSSGPQKTKAPVQWR
WVRSGGVNGANFPLMTKQDYAFLCFSPTFYKCDLEVTVSALGTDVAVSLRWAPTGAPADVTDLQIYTPSLGETRNPHMWLVGAGNSQVSFVV
PYNSPLSVLPAAWFNGWSDFGNTKDFGVAPNADFGRLWIQGNTSASVRIRYKKMKVFCRPTLFFPWPTPTTKINADNPVPILELE
>d1tmf2_b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}
DQNTEEMENLSDRVASDKAGNSATNTQSTVGRLCGYGKSHHGEHPASCADTATDKVLAERYYTIDLASWTTSQEAFSHIRIPLPHVLAGEDGGF
GATLRRHYLCKTGWRVQVQCNASQFHAGSLLVFMAPEFYTGKGTKTGMEPSDPFTMDTEWRSPQGAPTGYRYDSRTGFFATNHQNQWQWT
YPHQILNLRTNTTVLEVYVNVAPSSWTQHANWTLVAVSPLQYATGSSPDVQITASLQPVNPVFNGLRHETVIAQ
>d1sva1_b.10.1.4 (1:) Simian virus 40 (SV40) coat protein {Simian virus 40}
PKKPKEPVQVPKLVKGIEVLGVKTGVDSFTEVECFLNPQMGNPDEHQKGLSKLAAEKQFTDDSPDKEQLPCYSVARILPNINEDLTCGNILMWE
AVTVKTEVIGVTAMLNLHSGTQKTHENGAGKPIQGSNFHFAVGGEPELELQGVLANYRTKYPAAQTVTPKNATVDSQQMNTDHKAVIDKDNAYPVE

CWVPDPSKNENTRYFGTYTGGENVPPVLHITNTATTVLLDEQGVGPLCKADSLYSAVDICGLFTNTSGTQQWKGLPRYFKITLRKRSVKNPYPISFLL
SDLINRRRTQRVDGQPMIGMSSQVEEVRYEDTEELPGDPDMIRYIDEFGTTTRMQ

>d1dzla_b.10.1.4 (A:) L1 protein {Human papillomavirus type 16}

KVVSTDEYVARTNIYYHAGTSRLAVGHYPFIKKPNNNKILVPKVSGLQYRVRFRIHLPPDNKGFPDTSFYNPDTQRLWWACVGVEVGRGQPLGVGI
SGHPLLNKLDDEASAYAANAGVDNRECISMDYKQTQLCLIGCKPPIGEHWKGSPCTQVAQPGDCPPELEINTVIQDGDMVDTGFGAMDFTT
LQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRREQMVFVRHLFNRAVTGENVPDDLYIKGSGSTANLASSNYFPTPSGSMTSDAQIFNPKY
WLQRAQGHNNNGICWGNQLFVTVDTRSTNMSLCAAISTSETTYKNTNFKEYLHGEEYDLQFIFQLCKITLTADVMTYIHSMNSTILEDWNFGLQ
PPPGBTLEDTYRFVTSQAIACQKHTPPAPKEDPLKKYTFWEVNKEKFSADLDQFPLGRKFLLQLGL

>d1ihma_b.10.1.4 (A:) Calcivirus capsid protein {Norwalk virus}

DPLAMDPVAGSSTAVATAGQVNIPDWIINNFVQAPQGEFTISPNNTPGDVLFDSLGPFLHNPFLHLSQMYNGWVGNMRVRIMLAGNAFTAGKI
IVSCIPPGFGSHNLNTIAQATLFPHIADVRTLDPIEVPLEDRNVLFHNNDRNQQTMRLVCMLYTPLRTGGGTGDSFVAGRVMTCSPDFNLFVLP
PTVEQKTRPFTLPNLPLSSLSNSRAPLISSMGISPDNVQSVQFQNQRCILDGRVLGTTVSLSHVAKIRGTSNGTVINLTLEDGTPFHPFEGPAPIGF
DLGGCDWHINMTQFGHSSQTQYDVDTTPDTFVPHLSIQANGIGSGNYGVLSWISPPSHPSGSQVDLWKIPNYGSSITEATHLAPSVYPPGFGEV
LVFFMSKMPGPGAYNLPCLLPQEYISHLASEQAPTVGEAALLHYVDPTGRNLGEFKAYPDGFLTCVPNGASSGPQQLPINGVFVFWVSFRYQLK
PVGTA

>d1amm_1 b.11.1.1 (1-85) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GKITFYEDRGFQGHCYECSSDCPNLQPYSRCSNIRVDSGCWMLYERPNYQGHQYFLRRGDYPDYQQWMGFNDSIRSCRIPQHT

>d1amm_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GTFRMRIYERDDFRGQMSEITDDCPSLQDRFHLEVHSLNVLEGSWVLYEMPSYRGRQYLLRPGEYRRYLDWGAMNAKVGSLRRVMDFY

>d1elpa1 b.11.1.1 (A:1-85) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}

GKITFYEDRGFQGRHYECSSDHSLNQPYLGRCSNVRVDSGCWMIYEQPNYLPQYFLRRGDYPDYQQWMGLNDSIRSCRIPHAG

>d1elpa2 b.11.1.1 (A:87-174) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}

SHRLRLYEREDYRGQMIEITEDCSSLQDRFHNEIHSLNVLEGSWVLYELPNYRGRQYLLRPGEYRRYHDWGAMNAKVGSLRRVIDY

>d1a7ha_b.11.1.1 (A:) gamma-Crystallin {Cow (Bos taurus), isoform S}

MYKIQIFEKGDFNGQMHEETTEDCPSEMQFHMREVHSCKVLEGAWIFYELPNYRGRQYLLDKKEYRKPVDWGAASPAVQSFRRIIVE

>d1ha4a_b.11.1.1 (A:) gamma-Crystallin {Human (Homo sapiens)}

GQYKIQIFEKGDFSGQMYETTEDCPSEMQFHMREIHSCKVLEGWVIFYELPNYRGRQYLLDKKEYRKPIDWGAASPAVQSFRRIIVE

>d1a45_1 b.11.1.1 (1-84) gamma-Crystallin {Cow (Bos taurus), isoform F}

GKITFYEDRGFQGRHYECSSDHSLNQPYSRCSNIRVDSGCWMLYEQPNFQGPQYFLRRGDYPDYQQWMGLNDSIRSCRIPHT

>d1a45_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform F}

GSHRLRLYEREDYRGQMVEITEDCSSLHDFHFSEIHSFNVLEGWWVLYEMTNYRGRQYLLRPGDYRRYHDWGATNARVGSLLRAVDFY

>d2bb2_1 b.11.1.1 (-2-85) beta-Crystallin {Cow (Bos taurus)}

LNPKIIIFEQENFGHSHELGPCPNLKETGVEKAGSVLVQAGPWVGYEQANCKGEQFVFEKGEYPRWDSWTSSRTDSLSSLRPIKVD

>d2bb2_2 b.11.1.1 (86-175) beta-Crystallin {Cow (Bos taurus)}

QEHKITLYENPNFTGKKMEVDDDVPSFHAHGYQEKFVSSVRVQSGTWVGQYQPGYRGLQYLLKGDYKDSGDFGAPQPQVQSVRRIRDMQW

>d1a5da1 b.11.1.1 (A:1-84) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

GKITFYEDRGFQGRHYECSTDHSNLQPYSRCSNVRVDSGCWMLYEQPNFTGCQYFLRRGDYPDYQQWMGFSDSVRSCRLIPHS

>d1a5da2 b.11.1.1 (A:85-174) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

SSHRIIRIYEREDYRGQMVEITDDCPHLQDRFHFSDFHFMEGYWVLYEMPNYRGRQYLLRPGEYRRYHDWGAMNARVGSLLRIMDFY

>d1bd7a_b.11.1.1 (A:) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

EHKIIILYENPNFTGKKMEVDDDVPSFHAHGYQEKFVSSVRVQSGTWVGQYQPGYRGLQYLLKGDYKDSGDFGAPQPQVQSVRRIRDMQGNNPKIII

FEQENFGHSHELGPCPNLKETGMEKAGSVLVQAGPWVGYEQANCKGEQFVFEKGEYPRWDSWTSSRTDSLSSLRPIK

>d1npsa_b.11.1.1 (A:) Protein S {Myxococcus xanthus}

ANITVFYNEDFQGKQVDPPLPGNYTRAQLAALGIENNTISSVKVPPGVKAILYQNDGFAGDQIEVVANAEELGPLNNNVSSIRVISVPV

>d1prr_2 b.11.1.1 (91-173) Protein S {*Myxococcus xanthus*}

PRARFFYKEQFDGKEVDLPPGQYTQAELERYGIDNNNTISSVKPQGLAVLFKNDNFSGDTPVNSDAPTLGAMNNNTSSIRIS

>d1hdfa_b.11.1.1 (A:) Spherulin 3a (S3a) {Slime mold (*Physarum polycephalum*)}

SVCKGVSGNPAKGEVFLYKHVNFGDSWKVTGNVYDFRSVSGLNDVSSVKVGPNKAFIFKDDRFNGNFIRLEESSQVTDLTRNLNDAISSLIVATFE

>d1wkt__ b.11.1.2 (-) Yeast killer toxin {*Williopsis mrakii*}

GDGYLIMCKNCDPNTGSCDWKQNWNTCVGIGANVHWMTGGSTDGKQGCATIWEKGSGCVGRSTMCCPANTCCNINTGFYIRSYRVE

>d1bhu__ b.11.1.3 (-) Streptomyces metalloproteinase inhibitor, SMPI {*Streptomyces nigrescens*}

APSCPAGSLCTYSGTGLSGARTVIPASDMEKAGTDGVKLPASARSFANGTHFTLRYGPARKVTCVRFCYQYATVGKVAPGAQLRSLPSPGATVVGQDLGD

>d1f53a_b.11.1.4 (A:) Killer toxin-like protein SKLP {*Streptomyces* sp.}

IDHPCRGENFLKIWSHSGGQQSVDCYANRGRIDFGWWWDKISTGNNDIYYDANGDSVRVDRWHDITYPNRPPKVNSIEIL

>d1g6ea_b.11.1.6 (A:) Antifungal protein AFP1 {*Streptomyces tendae*, tu901}

MINRTDCNENSYLEIHNNERDRLCFANAGTMPVAIYGVNWVESGNVVTLQFQRNLSDPRLETITLQKWGSWNPGHIHEILSIRIY

>d1c01a_b.11.1.5 (A:) Plant antimicrobial protein MIAMP1 {*Macadamia* nut (*Macadamia integrifolia*)}

SAFTVWSGPCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGWKSIFIQC

>d1f8na2_b.12.1.1 (A:6-149) Plant lipoxygenase {*Soybean* (*Glycine max*), isozyme L1}

HKIKGTVVLMPKNELEVNPDGSAVDNLNAFLGRSVSLQLISATKADAHGKGKVGKDTFLEGINTSLPLTGAGESAFNIHFEDGSMGIPGAFYIKNYMQVEFFLKSLTLEISNQGTIRFVCNSWVYNTKLKYKSVRIFFANHTY

>d1ik3a2_b.12.1.1 (A:9-167) Plant lipoxygenase {*Soybean* (*Glycine max*), isozyme L3}

GHKIKGTVVLMRKNVLDNSVTSVGGIIGQGLDLVGSTLDTLTAFLGRSVSLQLISATKADANGKGKLGATFLEGIITSPLTGAGQSAFKINF EWDDSGIPGAFYIKNFMQTEFFLVS LTLEDIPNHGSIHFCVNSWIYNAKLFKSDRIFTANQTY

>d1lox_2 b.12.1.1 (2-112) 15-Lipoxygenase {*Rabbit* (*Oryctolagus cuniculus*)}

GVYRVCVSTGASIYAGSKNKVELWLVGQHGEVELGSCLRTRNKEEFKVNVSYLGSLLFVRLKKHFLKEDAWFCNWISVQALGAAEDKYWFPCYRWVVGDGVQSLPVG

>d1hpla1_b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain {*Horse* (*Equus caballus*)}

RWRYRVDVTLGKKTGHILVSLFGNKGNSRQYEIFQGTLKPDNTSNEFDSDEVDLQVFKFIWYNNVINLTPKGASKITVERNDGSVFNFCS EETVREDVLLTLAC

>d1etha1_b.12.1.2 (A:337-448) Pancreatic lipase, C-terminal domain {*Pig* (*Sus scrofa*)}

ARWRYKVSVTLSGKKVTGHILVSLFGNKGNSKQYEIFKGTLKPDNTSNEFDSDEVDLQVFKFIWYNNVINPTLPRVGASKITVERNDGKVYDFCS QETVREEVLLTNPC

>d1gpl_1_b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain {*Guinea pig* (*Cavia porcellus*)}

RWRYKVSVTLSGKKVTGHILVSLFGNKGNSKQYEIFKGTLKPDNTSNEFDSDEVDLQVFKFIWYNNVINPTLPRVGASKITVERNDGKVYDFCS ETVREEVLLTLPC

>d1rp1_1_b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain {*Dog* (*Canis familiaris*)}

RWRYGVSVTLSGKRATGQAKVALFGSKGNTHQFNIFKGILKPGSTSNEFDAKLDVGTIEKVFKFLWNNNNNPTFPKVGAAKITVQKGEETVHSFCSESTVREDVLLTLPC

>d1bu8a1_b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain {*Rat* (*Rattus norvegicus*)}

RWRYKVSVTLSGAKKLSGYILVALYGNNGNSKQYEIFKGSLKPEARHVRDIDVDINVGEIQVKFLWNINKVINLFRPTLQASQITVQSGVDGKEYNFCS SDTVREDVLLQSLYPC

>d1ca1_2_b.12.1.3 (250-370) Alpha-toxin, C-terminal domain {*Clostridium perfringens*}

SVGKNVKELVAYISTSGEKDAGTDDYMYFGIKTKDGKTQEWE MDNPGNDFMTGSKDTYTFKLKDENLKIDDIQNMWIRKRKYTAFPDAYKPE NIKVIANGKVVVDKDINEWISGNSTYNIK

>d1k5ja_b.13.3.1 (A:) Nucleoplasmin core {*Xenopus laevis*}

VSLIWGCELNEQNKTFEFKVEDDEEKCEHQLALRTVCLGDKADEFHIVEIVTQEEGAEKSVPIATLKPSILPMATMVGIELTPVTFRLKAGSGPLYISG

QHVA

>d1pgs_1 b.13.1.1 (4-140) Peptide:N-glycosidase F, PNGase F {*Flavobacterium meningosepticum*}

DNTVNICKFDKVNAFGDGLSQSAEGTFTFPADVTTVKTIKMFICNECPNKTCDEWDRYANVYVKNKTTGEWYEIGRFITPYWVGTEKLPRGLEIDV
TDFKSLLSGNTELKIYTETWLAKGREYSVDFDIVYGTDPY

>d1pgs_2 b.13.1.1 (141-314) Peptide:N-glycosidase F, PNGase F {*Flavobacterium meningosepticum*}

KYSAVVPVIQYNKSSIDGVPGKAHTLGLKKNIQLPTNTEKAYLRTTISGWGHAKPYDAGSRGCAEWCFRTHTIAINNANTFQHQLGALGCSANPIN
NQSPGNWTPDRAGWCPGMAPTRIDVLNNSLTGSTFSYEKFQSWTNNGTNGDAFYAISSFVIAKSNTPISAPVVTN

>d1phm_1 b.13.1.2 (45-198) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (*Rattus norvegicus*)}

NECLGTIGPVTPLDASDFALDIRMPGVTPKESDTYFCMSMRLPVDEEAVIDFKPRASMDTVHHMLFGNCNMPSTGSYWFCDEGTCTDKANILYA
WARNAPPTRLPKGVGFRVGGETGSKYFVLQVHYGDISAFRDNHKDCSGSVHLTRVPQ

>d1phm_2 b.13.1.2 (199-354) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (*Rattus norvegicus*)}

PLIAGMYLMMSVDTVIPPGEKVVNADISCQYKMYPMHVFAVRVHTHHLGKVVSGYRVNRNGQWTLIGRNPQLPQAFYPVEHPVDVTGDLIAAR
CVFTGEGRTEATHIGGTSSDEMCNLYIMYYMEAKYALSFMTCRKVNAPDMFRTPAENAPI

>d1hx6a1 b.13.2.1 (A:15-244) Coat protein p3 {Bacteriophage prd1}

LRNQQAMAANLQARQIVLQQSYPVIQQVETQTDFPANSVFDVTANVGIVKGFLVKTAAITNNHATEAVALTDFGPANLVQRVIYYDPDNQRHT
ETSGWHLHFVNTAKQGAPFLSSMVTDSPIKYGDVMNVIDPATIAAGATGELTMYYWVPLAYSETDLTGAVALANVPQSKQRLKLEFANNNTAFAAV
GANPLEAIYQGAGAADCEFEESİTYVQSYLDQLPVGQ

>d1hx6a2 b.13.2.1 (A:245-384) Coat protein p3 {Bacteriophage prd1}

NGYILPLIDLSTLYNLENSAQAGLTPNVDVFVQYANLYRYSTIAVFDNGGSFNAGTDINYLSQRTANFSDRKLDPKTAAQTRRIATDFPKGVVY
DNRDKPIYLTQYGNVGFVVNPKTVNQNARLLMGYEYFTSRT

>d1dhx_1 b.13.2.2 (44-650) Adenovirus hexon {Human adenovirus type 2}

FRNPTVAPTHDVTDRSQRRTLRFIPVDRDTASYKARFTLAVGDNRVLDMASTYFDIRGVLDRGPTFKPYSGTAYNALAPKGAPNSCEWEQTEDS
GRAVAEDEEEDEDEEEEEEEQNARDQATKKTHVYQAQPLSGETITKSGLQIGSDNAETQAKPVYADPSYQPEPQIGESQWNEADANAAGGRVLKK
TTPMKPCYGSYARPTNPFGGQSVLPVDEKGVPPLKVDLQFFSNTTSLNDRQGNATPKVVLYSEDVNMETPDTHLSYKPGKDENSKAMLGQQS
MPNRPNYIAFRDNFIGLMMYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLDSIGDRTRYFSMWQNQAVDSYDPDVRIIENHGTEDELPNYC
FPLGGIGVTDTYQAIKANGNGSGDNGDTTWKDETFRNEIGVGNNFAMEINLNANLWRNFLYSNIALYLPDKLKYNPTNVEISDNPNPTYDYMNK
RVVAPGLVDCYINL GARWSDLYMDNVNPFNHHRNAGLRYRSMLLNGNRYVPFH IQV P QKFFAIKNLLPGSYTYEWNFRKDVMVLQSSLGN
RVDGASIKFDSICLYATFFPMAHNTASTLEAMLR

>d1ruxa1 b.13.2.2 (A:5-636) Adenovirus hexon {Human adenovirus type 5}

MMPQWSYMHISGQDASEYLSPGLVQFARATETYFSLNNKFRNPTVAPTHDVTDRSQRRTLRFIPVDRDTASYKARFTLAVGDNRVLDMASTYF
DIRGVLDRGPTFKPYSGTAYNALAPKGAPNPCEWEAAATEINLEEEEDDNEDEVDEQAEQQKTHVFGQAPYSGINITKEGIQIGVEGQTPKYADK
TFQPEPQIGESQWYETEINHAAGRVLKTTPMKPCYGSYAKPTNENGQGQILVKQQNGKLESQVEMQFFSTEATAGNGDNLTPKVVLYSEDVDIE
TPDTHISYMPTEIKEGNSRELMGQQSMPNRPNYIAFRDNFIGLMMYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLDSIGDRTRYFSMW
QAVDSYDPDVRIIENHGTEDELPNYCFPLGGVINTETLTKVKPKTGQENGWEKDATEFSKNEIRVGNNFAMEINLNANLWRNFLYSNIALYLPDKLK
YSPSNVKISDNPNPTYDYMNRKVVAPGLVDCYINL GARWSDLYMDNVNPFNHHRNAGLRYRSMLLNGNRYVPFH IQV P QKFFAIKNLLPGSYTYE
WNFRKDVMVLQSSLGNL RVDGASIKFDSICLYATFFPMAHNTASTLEAMLRND

>d1ruxa2 b.13.2.2 (A:637-946) Adenovirus hexon {Human adenovirus type 5}

TNDQSFNDYLSAANMLYPIPANATNVPISPSRNWAAFRGWAFTRLKTKETPSLGSYDPYYTSGSIPYLDGTFYLNHTFKKVAITFDSSVSWPGND
RLLTPNEFEIKRSVDGEGYNVAQCNCMTKDWFLVQMLANYNIGYQGFYIPESYKDRMYSFFRNFQPMRSQVVDDTKYKDYQQVGILHQHNNNSGFV
GYLAPTMREGQAYPANFPYPLIGKAVDSITQKKFLCDRTLW RIPFSSNFMSMGALTDLGQNLLYANSAHALDMTVEVDPMDEPTLLYLFEVFDVV
RVHRPHRGVIETVYLRTPFSA

>d1kfu1 b.14.1.1 (L:356-514) Calpain large subunit, middle domain (domain III) {Human (*Homo sapiens*)}

WKLTKMDGNWRRGSTAGGCRNYPNTFWMNPQYLIKLEEDEDEEDGESGCTFLVGLIQKHRRRQRKMGEDMHTGFIYEVPEELSGQTNIHS

KNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFSEKKADYQAVDD
>d1df0a2 b.14.1.1 (A:356-514) Calpain large subunit, middle domain (domain III) {Rat (Rattus norvegicus)}
WKLTKMDGNWRRGSTALLGCRNYPNTFWMPNQPYLIKLEEEDEDDEGERGCTFLVGLIQKHRRQRKMGEDMHTIGFGIYEVPEELTGQTNIHL
KNFFLTTRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPHKNGDFCIRVFSEKKADYQTVDD
>d1f35a_b.94.1.1 (A:) Olfactory marker protein {Mouse (Mus musculus)}
AEDGPQKQQLEMPPLVDQDLTQQMRLRVEVKQRGEKKQDGKLRPAESVYRLDFIQQQLQFDHWNVVLDKPGKVITGTSQNWTPLTNLM
TRQLLDPAIAFWRKEDSDAMDWNEADALEFGERLSLAKRKVMYFLITFGEVGVEPANLKASVVFNL
>d1shsa_b.15.1.1 (A:) Small heat shock protein {Archaeon Methanococcus jannaschii}
TGIQISGKGFMPIISIEGDQHIKVIAWLPVNKEIIILNAVGDTEIRAKRSPLMITESERIIYSEIPEEEEYRTIKLPATVKEENASAKFENGVLVLPKA
SSIKKGINIE
>d1gmea_b.15.1.1 (A:) Small heat shock protein {Wheat (Triticum aestivum)}
SIVRRSNVFDPFADLWADPFDTFRSIVPAISGGSETAAFAANARMDWKETPEAHVFKADLPGVKKEEVKVEVEDGNVLVSGERTKEKEDKNDKW
HRVERSSGKFVRRFRLLEDAKVEEVKAGLENGVLTVPKAEVKKPEVKAIQISG
>d1gmeb_b.15.1.1 (B:) Small heat shock protein {Wheat (Triticum aestivum)}
NARMDWKETPEAHVFKADLPGVKKEEVKVEVEDGNVLVSGERTKEKEDKNDKWHRVERSSGKFVRRFRLLEDAKVEEVKAGLENGVLTVPKA
EVKKPEVKAIQISG
>d1ejfa_b.15.1.2 (A:) Co-chaperone p23 {Human (Homo sapiens)}
MQPASAKWYDRRDYVFIEFCVEDSKDVNVNFKEKSCLTFSCLGGSDNFKHLNEIDLFHCIDPNDSKHKRTDRSILCCLRKGESGQSWSRPLTKERAKLN
WLSVDFNNWKDWE
>d1ezsa_b.16.1.1 (A:) Ecotin, trypsin inhibitor {Escherichia coli}
PPYPQAEGGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGAAAAYVFDKVSSPVSTRMACPDGKKEKKFVTAYLGAGMLR
YNSKLPIVVYTPDNVDVKYRVWKAEEKIDNAVR
>d1slua_b.16.1.1 (A:) Ecotin, trypsin inhibitor {Escherichia coli}
IAPYPQAEGGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGYDYYFDKVSSPVSTMMHCPDGKKEKKFVTAYLGAD
MLRYNSKLPIVVYTPDNVDVKYRVWKAEEKIDNAVR
>g1fi8.1 b.16.1.1 (C;D:) Ecotin, trypsin inhibitor {Escherichia coli}
PLEKIAPYPQAEGGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGYDYYFDKVSSPIEPDXKFVTAYLGAGMLRNSK
LPIVVYTPDNVDVKYRVWKAEEKIDNAVR
>d1beha_b.17.1.1 (A:) Phosphatidylethanolamine binding protein, PEpb {Human (Homo sapiens)}
VDLSKWSGPLSLQEVDQCPQHPLHVYAGAAVDELGVLTPTQVKNRPTSISWDGLDSGKLYTLVTDAPSRSRKDPKYREWHHFLVNMKGNDIS
SGTVLSDYVGSGPPKGTLHRYVWLVEQDRPLKCDEPILSNRSGDHRGKFKVASFRKKYELRAPVAGTCYQAEWDDYVPKLYEQLSG
>d1a44_b.17.1.1 (-) Phosphatidylethanolamine binding protein, PEpb {Cow (Bos taurus)}
PVDSLKWGSPLSLQEVDERPQHPLQVKYGGAEVDELGVLTPTQVKNRPTSITWDGLDPGKLYTLVTDAPSRSRKDPKYREWHHFLVNMKGNNI
SSGTVLSDYVGSGPPKGTLHRYVWLVEQEGPLKCDEPILSNRSGDHRGKFKVASFRKKYELGAPVAGTCYQAEWDDYVPKLYEQLSG
>d1qoua_b.17.1.1 (A:) Centroradialis protein Cen {Garden snapdragon (Antirrhinum majus)}
GRVIGDVVDHFTSTVKMSVIYNSNNSIKVYNGHELPASVTSPRVEHGGDMRSFFTILMTDPVPGPSDPYLREHLHWIVTDIPGTTDSSFGKE
VVSYEMPRPNIGIHRVFLLFKQKKRGQAMLSPPVCRDGFNTRKFTQENEGLPVAAVFFNCQRET
>d1fjja_b.17.1.2 (A:) Hypothetical protein YbhB {Escherichia coli}
AMKLISNDLRDGDKLPHRHVFNGMGYDGDNISPFLAWDDVPAGTKSFVVTCDPDAUTGSGWWHHVVVNLPADTRVLPQGFGSGLVAMPDG
VLQRTDFGKTYGDGAAPPKGETHRYIFTVHALDIERIDVDEGASGAMVGFNVHFSLASASITAMFS
>d1fuxa_b.17.1.2 (A:) Hypothetical protein YbcL {Escherichia coli}
EFQVTSNEIKTGEQLTTSVFGFGCEGGNTSPSLTWSGVPEGTKSFAVTVYDPDAPTGSGWWHWTVVNIPATVTYLPDAGRRDGTKLPTGAVQ
GRNDFGYAGFGGACPPKGDKPHHYQFKVWALKTEKIPVDSNSSGALVGYMLNANKIATAEITPVYEIKLE
>d1g13a_b.95.1.1 (A:) Ganglioside M2 (gm2) activator {Human (Homo sapiens)}

SSFSWDNCDEGKDPAVIRSLTLEPDPIIVPGNVTLSVMGSTSVPLSSPLKVLVLEKEVAGLWIKIPCTDYIGSCTFEHFCVLDMLIPTGEPCPEPLRTY
GLPCHCPCFKEGTYSLPKSEFVVPDLEPSWLTTGNYRIESVLSGGKRLGCIKIAASLKGI

>d1i9ba_b.96.1.1 (A:) Acetylcholine binding protein (ACHBP) {Great pond snail (*Lymnaea stagnalis*)}

FDRADILYNIRQTSRPDVITQRDRPVAVSVSLKFINILENEITNEVDVVFHQQTWSRDLAWNSSHSPDQSVPISSLWVPDLAAISKPEVLT
PQLARVSDGEVLYMPSIRQRFSCDVSGVDTESGATCRIKIGSWTHHSREISVDPTTENSDDSEYFSQYSRFEILDVTQKKNSVTYSCCPEAYEDVEVSL
NFRKKG

>d1k3ia2 b.18.1.1 (A:-12-150) Galactose oxidase, N-terminal domain {Fungi (*Fusarium spp.*)}

IPEGSLQFLSLRASAPIGSAISRNNWAVTCDSAQSGNECNKAIDGNKDTFWHTFYANGDPKPPHTYIDMKTTQNNGLSMLPRQDGNGWI
GRHEVYLSSTGTNWGSPVASGSWFADSTTKYSNFETRPARYVRLVAITEANGQPWTIAEINVFQASS

>d1eut_2 b.18.1.1 (506-647) Sialidase, C-terminal domain {Micromonospora viridifaciens}

QARMSIADVSEETAREDGRASNVIDGNPSTFWHTEWSRADAPGYPHRISLDLGGHTISGLQYTRRQNSANEQVADYEIYTSNLGTTWDGPVAS
GRFTTSLAPQRAVFpardaryirlvalseqtghkyaavaelevegqr

>d1czsa_b.18.1.2 (A:) C2 domain of factor V {Human (*Homo sapiens*)}

GCSTPLGMENGKIEKQITASSFKKSWWGDYWEPFRARLNAQGRVNAWQAKANNKQWLEIDLKIKKITAIIQGCKSLSEMYVKSYTIHSEQ
GVEWKPYRLKSSMVDKIFEGNTNTKGVHNKFFNPPFIRVTPKTWNQSITLRLELFGCDIY

>d1d7pm_b.18.1.2 (M:) C2 domain of factor VIII {Human (*Homo sapiens*)}

LNSCSMPLGMESKAISDAQITASSYFTNMFAWSPSKARLHLQGRSNAWRPQVNNPKEWLQDFQKTMKVTVGTTQGVKSLLTSMYVKEFLISS
QDGHQWTLFFQNGKVKVQFQGNQDSFTPVNCLDPPLTRYLRIHPQSWVHQIALRMEVLGCEAQ

>d1jhja_b.18.1.9 (A:) APC10/DOC1 subunit of the anaphase-promoting complex {Human (*Homo sapiens*)}

ATPNKTPPGADPKQLERTGTVREIGSQAVWSLSSCKPGFGVDQLRDNLETWQSDGSQPHLVNIQFRKTTVKTLCIYADYKSDESYTPSKISVRVG
NNFHNLQEIRQLELVEPSGWIVPLTDNHKKPTRTFMIQIAVLANHQNGRDTHMRQIKIYTPV

>d1dlc_1 b.18.1.3 (500-644) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis tenebrionis, CRYIIA (BT13)}

FFNMIDSKKITQLPLVKAYKLQSGASVVAQPRFTGGDIQCTENSAATIVTPDVSYSQYRARIHYASTSQITFTLSLDGAPFNQYYFDKTINKGDTLT
YNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN

>d1ji6a1 b.18.1.3 (A:503-652) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis, CRY3bb1}

FFNTIDAEEKITQLPVVKAYALSSGASIIEGPGFTGGNLFLKESSNSIAKFKVTLNSAALLQRYVRIRYASTTNLRLFVQNSNNDFLVYINKTMNKDDDL
TYQTFDLATTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPVQL

>d1ciy_1 b.18.1.3 (462-609) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis, CRYIA (A)}

NNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTPGQJSTLRVNITAPLSQRYVRIRYASTTNLQFHTSIDGRPINQGNSATMSSGSNLQS
GSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV

>d1i5pa1 b.18.1.3 (A:473-633) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

NIYAANENGTMIHLAPEDYTGTISPIHATQVNNQRTFISEKFGNQGDSLRFEQSNTTARYTLRGNGNSNLYLRVSSIGNSTIRVTINGRVYTVSNV
NTTNNDGVNDNGARFSDINIGNIVASDNTNVTLIDINVTLNSGTPFDLMNIMFVPTNLPPLY

>d1nuka_b.18.1.4 (A:) Ligand-binding domain of the ephb2 receptor tyrosine kinase {Mouse (*Mus musculus*)}

EETLMDSTTATAELGWMVHPPSGWEVSGYDENMNTIRTYQVCNVFESSQNNWLRKFIRRRGAHRIHVEMKFSVRDCSSIPS PGSCKETFNLYY
YEADFDLAKTFPNWMENP WVVKD TIAADEFSQV D L G R V M K I N T E V R S F G P V S R N G F Y L A F Q D Y G G C M S I A V R V F Y R

>d1jz8a3 b.18.1.5 (A:13-219) beta-Galactosidase {Escherichia coli}

RRDWENPGVTQLNRALAHPPFASWRNSEEARTDRPSQQRLRSNGEWRFWFAPEAVPESWLECDLPEADTVVPSNWQMHGVD APIYTNV
PITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVNSAFHLWCNGRWVGYGQDSRLPSEFDLSAFLRAGENRLAVMVLRWSDGSYLEDQ
DMWRMSGIFRDVSLLHKPT

>d1bhga2 b.18.1.5 (A:22-225) beta-Glucuronidase {Human (*Homo sapiens*)}

GLQGGMLYPQESPSPRECKELDGLWSFRADFSNDNRRRGEEQWYRRLWESGPTVDMVPVSSFNDISQDWRLRHFVGWVWYEREVILPERWTQD
LRTRVVLIRGSAHSYAIWVNVGDTLEHEGGYLPFEADISNLQVGPLPSRLRITIAINNTLPTTLPPTIQYLTDTSKYPKGYFVQNTYFDFNYAGLQ
RSVLLYTTPT

>d1cx1a_b.18.1.6 (A:) Cellulose-binding domain {Cellulomonas fimi}
ASLDSEVELLPTSFAESLGPWSLYTSEPVFADGRMCVDLPGQGNPWDAGLVNGVPVGEGESYVLSFTASATPDMPVRVLVGEGGGAYRTAEE
QGSAPLTGEPATREYAFTSNLTFFPDGDAPGQVAFHLGKAGAYEFCISQVSLTTSAT

>d1ulo_b.18.1.6 (-) Cellulose-binding domain {Cellulomonas fimi}
ASPIGEGTFDDGPEGWVAVGTDGPLDTSTGALCVAVPAGSAQYGVGVNLNGVAIEEGTTYTLRYTATASTDVTVRALVGQNGAPYGTVDLTPALTSE
PRQVTETFTASATYPATPAADDPEGQIAFQLGGFSADAATLCLDDVALDSEVEL

>d1gmma_b.18.1.10 (A:) Carbohydrate binding module from xylanase U {Clostridium thermocellum}
FSKIESEEYNSLKSSTIQTIGTSDGGSGIGYIESGDYLVFNKINFNGANGANSFKARVASGADPTNIQLRLGSPGTGTLIGTLTVASTGGWNYYEKSCSITNT
TGQHDLYLVFSGPVNIDYFIFDSN

>d1gnya_b.18.1.11 (A:) Xylan-binding module from xylanase 10c {Pseudomonas cellulosa}
GNVIEVDMANGWRGNASGSTSHSGITYSADGVTFAALGDGVGAVF DIARP TTLED AVIAMVVNVSAEFKASEANLQIFAQLKEDWSKGEWDCL
AGSSELTADTDLTCTIDE DDKFQN QTARDVQVGIQAKGTPAGTITIKSVTITLAQE A

>d1j83a_b.18.1.12 (A:) Endo-1,4-beta glucanase EngF {Clostridium cellulovorans}
QPTAPKDFSSGFWD FNDGTTQFGVNPDSPITAINVENANNALKISLN SKGSNDLSEG NF WANVRISADIWGQSINIY GDTKLTMDVIA PT PVNV
SIAAIPQSSTHGWGNPTRAIRVWTNNFVAQTDGTYKATLTISTNDSPNFNTIAD AADSVTNMILFVGNSNDNISLDNIKFTK

>d1dyoa_b.18.1.7 (A:) Xylan-binding domain {Clostridium thermocellum}
PDAGYYYHDTFEGSVGQWTARGPAEVLLSGRTAYKGSESSLVRNRTA WNGAQRALNPRTFVPGNTYCF SVVASFIEGASSTTFCMKLQYVDGSGT
QRYDTIDMKTVGPNQWHLYNPQYRIPSDATDMYVYVETADDTINFYIDEAIGAVAGTVI

>d1xnaa_b.18.1.8 (A:) N-terminal domain of xrcc1 {Human (Homo sapiens)}
MPEIRLRHVVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTI SVV LQLEKEE QIHSV DINGDGS AFVEV LVGSSAGG AGEQDYEVLLV TSS FMSPSE
SRSGSNPNRVRMFGPDKLVRAAA EKRWDRVKIVCSQPSKDPFGLSFVRFHS

>d1ju3a1_b.18.1.13 (A:352-574) Bacterial cocaine esterase C-terminal domain {Rhodococcus sp. mb1}
PLPDTAYTPFYLGSGAANTSTGGGTLSISGTESADTYLYDPADPVP SLLGGTLLFHNGDNGPADQRP IHD RDDVLCYSTEVLDPVEVTGTVSARLF
VSSSAVTDFTA KLVDFVFDGRAIALCDGIVRMRYRET L VNPTLIEAGEIYEVAIDMLATSNVFLPGHRIMVQVSSSNFPKYDRNSNTGGVIAREQLEE
MCTAVNRIRHGPEHP SHIVLP IKR

>d1bvp12_b.19.1.1 (1:121-254) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {Bluetongue virus}
PARQP YGF FLEET FQ PGRWF MRAAQAV TAVV CGPDMIQV SLNAG ARG DVQQ IFQ GRND PMMI YLVW RR IN FAMA QG NSQQ TQAG VTV S
GGVDMRAGRIIAWDGQA ALHVHN P TQQNAMVQI QVVF YISM D

>d1ahsa_b.19.1.1 (A:) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {African horse sickness virus}
TGPYAGAVEVQ QSGRYY VPQGRTRGGYINSNIAEV CMDAGAAGQVN ALLAPRRGDAV MIYFV WRPLRIFCDPQGASLESAPGT FVT DGV NVAA
GDVVAWNTIAPVN VGNPGARRSILQFEV LWYT

>d1qhda2_b.19.1.1 (A:149-332) vp6, the major capsid protein of group A rotavirus {Bovine rotavirus}
GFTFH KPNIFPYSASFTLNRSQPAHDNLMTWLNAGSEI QVAGFDYSCAINAPANTQQFEHIVQLRRVLT TATILLPDAERFSF PRVITSADGATT
WYFNPVILRPNNVIEFLLNGQI INTYQARFGTIIARNFDTIRLSFQLMRPPNMTPAVAALFPNAQPFEHHATVGLTRIESAVCE

>d1jsda_b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
DKICIGYQSTNSTETVDTLTETNVPVTHAKELLHTSHNGMLCATNLGHPLILDTCIEGLIYGNPSCD LLLGGREWSYIVERPSAVNGMCYPGNVENLE
ELRSLFSSASSYQRIQIFPDTIWNVSYSGTSSACSDSFYRSMRWLTQKNNA YPIQDAQY TNRGKSI FMWGINHPPDTVQTNLYTRD TTSVTTE
DINRTFKPVIGPRPLVNGLHGRIDYYWSVLPGQTLRVRSNGNLIAPWYGHILSGESHGRILKTDLNSGNCVVCQC TERGGLNTTLPFHNVSKYAFG
NCPKVGVKSLKLAVGLRNVP AR

>d1jsma_b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDLNGVKPLILRDCS VAGWLLGNPM CDEF LN VPEWSYIVEKDNPVNGLCYP ENF
NDYEELKHLLSSTNHFEKIRIIPRSSWSNH DASSGVSSACPYNGRSSFFRN VVWLIKNNAYPTIKRSYNNTNQEDLILWGIHHPNDAAEQT KLYQNP
TTYVSGTSTLNQR SVPEIATPKVNGQSGRM EFFW TILKPNDA INFESNGNFI APEYAYKIVKKGGSAIMKSGLEYGN CNTKQ TPMGAINSSM PF
HNHPLTIGEC PKVGS RLV LATGLRNVP

d2visc_b.19.1.2 (C:) Hemagglutinin {Influenza A virus, different strains}
VQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFCNSCYPYDVPDYASLRSLVASSGTLFITEGFTWTGVIQNGGSNACKR
GPGSGFFSRLNWLTKSGSTYPVLNVTPNMPNNDFDKLYIWGIIHHPSTNQEQTSLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKP
GDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPICTCISECITPNGSIPNDKPFQNVNKITYGACPKYV
>d2viua_b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
STATLCLGHHAVPNGTLVKITDDQIEVTNATELVQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFCNSCYPYDVPDYASL
RSLVASSGTLFITEGFTWTGVIQNGGSNACKRGPGSGFFSRLNWLTKSGSTYPVLNVTPNMPNNDFDKLYIWGIIHHPSTNQEQTSLYVQASGRVTV
TRRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPICTCISECITPNGSIPNDKPFQNVNKITYGACP
KYVKQNTLKLATGMNRNPVEKQT
>d1flca1 b.19.1.3 (A:151-306) Hemagglutinin domain of haemagglutinin-esterase-fusion glycoprotein HEF1 {Influenza C virus}
CMSLVNALDKTIPLQVTAGNCNNFLKNPALYTQEVKPSENKGKENLAFFLTLPTQFGTYECKLHLVASCYFIYDSKEVYNKRGCDNYFQVIYDSF
GKVVGGLDNRVSPYTGNSGDTPTMQCDMLQLKPGRYSVRSSPRFLMPERSYCFDMK
>d1aol__ b.20.1.1 (-) F-MuLV receptor-binding domain {Friend murine leukemia virus}
QVYNITWEVTNGDRETVWAISGNHPLTWWPVLTDLCMLALSGPPHWGLEYQAPYSSPPGPCCSGSSAGCSRDCDEPLTSLTPRCNTAW
NRLKLDQVTHKSSSEGFYVCPGSHRPREAKSCCGPDSYCASWGCETTGRVYWKPSSWDYITVDNNLTSQAVQVCKDNKWCNPLAIQFTNAGK
QVTSWTTGHYWGRLYVSGRDPLTFGIRLRYQNLGPRVP
>d1knb__ b.21.1.1 (-) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 5}
NDKLTWTTPAPSPNCRLNAEKDAKTLVLTCKGSQILATVSLAVKGSLAPISGTVQSAHLIIRFDENGVLLNNSLDPEYWNFRNGDLTEGTAYTN
GFMPNLSAYPKSHGKTAKSNIISQVYLNQDKTPVTLTITLNGTQETGDTTPSAYSMSFSWDWSGHNYINEIFATSSYTFSYIAQE
>d1qhva_b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 2}
AITIGNKNDKLTWTTPDPSPNCRIHSNDCKFTLVLTKGSQVLATVAALAVSGDLSSMTGTVASVSIFLRFDQNGVLMENSSLKKHYWNFRNG
STNANPYTNAVGFMPLNLLAYPKTQSQTAKNNIVSQVYLNQDKTPVTLTITLNGTSESTETSEVSTYSMSFTWSWESGKYTTETFATNSYTFSYIAQE
>d1h7za_b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 3}
KNNLTWTGPKEANCIIEYGKQNPDSKLTLLVNGGIVNGYVTLMGASDVNTLFKNKNVSINVELYFDATGHILPDSSLKTDLELKVKQTADFSARG
FMPSTTAYPFVLPNAGTHNENYIFGQCYYKASDGALFPLEVTVMLNKRQLPDSRTSYVMTFLWSLNAGLAPETTQATLITSPFTFSYIREDD
>d1kaca_b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 12}
TPYDPLTLWTTPDPPPNCISIQLDAKTLCLTKNGSIVNGIVSLVGVKGNLLNIQSTTTVGVLVDEQGRLITSTPTALVPQASWGYRQGQSVSTNT
VTNGLGMPNVSAVPRNASEAKSQMVSLTYLQGDTSKPITMKVAFNGITSNGYSLTMWSGLSNYINQPFSTPSCSFSYITQE
>d1kkea1 b.21.1.2 (A:250-312) Reovirus attachment protein sigma 1 {Reovirus}
EQSYVASVTPLRLNSSTKVLDMIIDSSTLEINSSGQLTVRSTSPNLRYPIADVSGGIGMSPN
>d1aly__ b.22.1.1 (-) Extracellular domain of CD40 ligand {Human (Homo sapiens)}
GDQNPQIAAHVISEASSKTTSLQWAEGYYTMSNNLVTLENGKQLTVKRQGLYYIYAQVFCNRREASSQAPFIASLCLKSPGRFERILLRAANTHSS
AKPCGQQSIHLGGFELPGASVFNVTDPQSVMHGTGFTSGFLKKL
>d1c28a_b.22.1.1 (A:) 30 kd adipocyte complement-related protein {Mouse (Mus musculus)}
MYRSAFSVGLETRVTPNPIRFTKIFYNQQNHYDGSTGKFYCNIPIGLYYFSYHITVYMKDVVKVSLFKDKDAVLFTYDQYQEKNVDQASGSVLLHEV
GDQVWLQVYGDGDHNGLYADNVNDSTFTGFLLYHDT
>d1tnra_b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}
KPAALHIGDPSKQNSLLWRANTDRAFLQDGFLSNNSSLVPTSGIYFVYSQVFSGKAYSPKATSSPLYLAHEVQLFSSQYPFHVPOLLSSQKMVYPGLQ
EPWLHSMYHGAAFQLTQGDQLSTHTDGIPHVLSPSTVFFGAFAL
>d4tsva_b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}
DKPVAHVANPQAEGQLQWSNRRANALLANGVELRDNQLVPIEGLFLIYSQVLFKGQGCPSTHVLTHTISRIA SYQTKVNLLSAIKSPCQRETPE
GAEAKPWPYIPLGGVFQLEKGDRSLAESINRDPYLDFAESGQVYFGIIAL
>d2tnfa_b.22.1.1 (A:) Tumor necrosis factor (TNF) {Mouse (Mus musculus)}
SDKPVAHVANHQVEEQLEWLSQRANALLANGMDLKDNQVLPADGILYVSVQULFKGQGCPDYLVLTHTVSRFAISYQEKVNLLSAIKSPCPKD

PEGAEELKPWYEPYIYGGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL
>d1dg6a_b.22.1.1 (A:) Apoptosis-2 ligand, apo2l/TRAIL {Human (Homo sapiens)}
QRVAAHITGTRGRSNTLSSPNSNEKALGRKINSWESSRSGHSFLSNLHLRNGLVIEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKTSYPAP
ILLMKSARNSCWSKDAEYGLSIYQGGIFELKENDRIFSVTNEHIDMDHEASFFGAFLVG
>d1jtxz_b.22.1.1 (X:) TRANCE/RANKL cytokine {Mouse (Mus musculus)}
QPFAHLTINAASIPSGSHKVTLSSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFRHHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMKGG
STKNWSGNSEFHFSINVGFFKLRAAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID
>d1jh5a_b.22.1.1 (A:) Soluble part of TALL-1, sTALL-1 {Human (Homo sapiens)}
VTQDCLQLIADSETPTIQKGSYTFPVWLLSKRGSALEEKENKILVKETGYFFIYGQVLYTAKTYAMGHLIQRKKVHVFGDELSVTLFRCIQNMPELTP
NNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFGALKLL
>d1gr3a_b.22.1.1 (A:) Collagen X NC1 trimerisation domain {Human (Homo sapiens)}
MPVSAFTVILSKAYPAIGTPIPFDKILYNRQQHYDPRTGIFTQCIPGIYFSYHVHKGTHVWVGLYKNGTPVMYTDEYTKGYLDQASGAIIDLTEND
QVWLQLPNAESNGLYSSEYHVSSFGFLVAMP
>d1sfp__b.23.1.1 (-) Acidic seminal fluid protein (ASFP) {Cow (Bos taurus)}
LPRNTNCGILKEESGVATYYGPKTNCVWTIQMPPEYHVRVSIQYQLQNCNKESLEIIDGLPGSPVLGKICEGSLMDYRSSGSIMTVKYIREPEHPASF
YEVLYFQDPQA
>d1sppa_b.23.1.1 (A:) Major seminal plasma glycoprotein PSP-I {Pig (Sus scrofa)}
LDYHACGGLRTDDYGTIFTYKGPTECVTLQVDPKYKLLVIPTLNLCGKEYVEVLEGAPGSKSLGFCEGLSILNRGSSGMTVKYKRDSGHYPASPYE
IIFLRDSQG
>d1sppb_b.23.1.1 (B:) Major seminal plasma glycoprotein PSP-II {Pig (Sus scrofa)}
ARINGPDECGRVIKDTSGSISNTDRQKNLCTWTILMKPDQKVRMAIPYLNLAGCKEYVEVFDGLLSPSYGKLCAGAAIVLSTANTMTIKYNRISGN
SSSPFLIYFYGSSP
>d1cb8a2_b.24.1.1 (A:600-700) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}
PKVLANTNQLQAVYHQQLDMVQAIFYTAGKLSVAGIEIETDKPCAVLIKINGKQVIWAADPLQEKETAVLSIRDLKTGKTNRVKIDFPQQEFAGATV
ELK
>d1egua2_b.24.1.1 (A:815-893) Hyaluronate lyase {Streptococcus pneumoniae}
SSLIENNTELQSVYDAKQGVWGIVKYDDSVSTISNQFQLKRGVYTIRKEDEYKIAYYNPETQESAPDQEVFKLEQH
>d1f1sa3_b.24.1.1 (A:920-984) Hyaluronate lyase {Streptococcus agalactiae}
SKQQVIYDKNSQTWAVIKHDNQESLINNQFKMNKAGLYLVQKVGNNDYQNVYYQPQTMTKDQLAI
>d1iaza_b.97.1.1 (A:) Equinatoxin II (eqtII, tenebrosin C) {European sea anemone (Actinia equina)}
AGAVIDGASLSFDILKTVLEALGNVKRKIAVGVDNESGKWTALNTYFRSGTSIDVLPHKVPHGKALLYNGQKDRGPVATGAVGLAYLMSDGNTLA
VLFSPVYDYNWYSNNWWNVRIYKGKRRADQRMYEELYYNLSFRGDNGWHTRNLGYGLKSRGMNSSGHAILEHVSKA
>d1aun__b.25.1.1 (-) Pathogenesis-related protein 5d {Common tobacco (Nicotiana tabacum)}
SGVFEVHNNCPTYVWAAATPVGGGRRLERGQSWWFWAPPGKTMARIWGRTNCFDGAGRGWCQTGDCGGVLECKGWGKPPNTLAEYALN
QFSNLDFWDISVIDGFNIPMSFGPTKPGPKCHGIQCTANINGECPGSLRVPGCNNPCTTFGGQQYCCTQGPGCPTELSRWFKQRPCDAYSPQ
DDPTSTFTCTSWTTDYKVMFCPY
>d1du5a_b.25.1.1 (A:) Zeamatin {Maize (Zea mays)}
AVFTVVNQCPFTVWAASPVPGGRQLNRGESWRITAPAGTTAARIWARTGCKFDASGRGSCRTGDCGGVLQCTGYGRAPNTLAEYALKQFNLLD
FFDISLIDGFNVPMSPFLPDGGSGCSRPRCAVDVNARCPAELRQDGVCNNACPVFKDEYCCVGSANDCHPTNSRYFKGQCPDAYSPKDDATS
TFTCPAGTNKYKVVFCP
>d1thw__b.25.1.1 (-) Thaumatin {Ketemfe (Thaumatomoccus daniellii)}
ATFEIVNRCSTVWAAASKGDAALDAGGRQLNGESWTINVEPGTKGGKIWARTDCYFDDSGSGICKTGDCGGLRKRFGRPPTLAEFSLNQYG
KDYIDISNIKGFBVPMDFSPTRGCRGVRCAADIVGQCPAKLKAPGGCNDACTVFQTCYCCVGSANDCHPTNSRYFKGQCPDAYSPKDDATS
GSSNYRVTFCPTA

>d1dd1a_b.26.1.1 (A:) Smad4 tumor suppressor C-terminal domain {Human (Homo sapiens)}

NGHLQHHPPMPPHPGHYWPVHNELAFQPPISNHPAPEYWCSIAYFEMDVQVGETFKVPPSCPIVTVDGYVDPSSGDRFCLGQLSNVRTEAIERA
RLHIGKGVQLECKGEGDVWRCLSDHAVFVQSYYLDREAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQQQAATAQAAAAAQAAVAGNIPGPG
SVGGIAPAISLSAAAGIGVDDLRLCILRMSFVKWGPDPYPRQSIKETPCWIEIHLHRALQLLDEVLHTMP

>d1ygs_b.26.1.1 (-) Smad4 tumor suppressor C-terminal domain {Human (Homo sapiens)}

APEYWCSIAVFEMDVQVGETFKVPPSCPIVTVDGYVDPSSGDRFCLGQLSNVRTEAIERARLHIGKGVQLECKGEGDVWRCLSDHAVFVQSYYL
DREAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQQQAATAQAAAAAQAAVAGNIPGPGSVGGIAPAISLSAAAGIGVDDLRLCILRMSFVKW
GPDYPRQSIKETPCWIEIHLHRALQLLDEVLHTM

>d1khxa_b.26.1.1 (A:) Smad2 MH2 domain {Human (Homo sapiens)}

PVTYSEPAFWCSIAYYELNQRVGETFHASQPSLTVDGFTDPSNSERFCLGLLSNVNRNATVEMTRRHIGRGRVRLYYIGGEVFAECLSDSAIFVQSPNCN
QRYGWHPATVCKIPPGCNLKIFNNQEFAALLAQSVNQGFEAVYQLTRMCTIRMSFVKWGAEYRRQTVTSTPCWIEHLHGPLQWLDKVLTQMG
SPSVRCSSMS

>d1khua_b.26.1.1 (A:) Smad1 {Human (Homo sapiens)}

PKHWCSIVYYELNNRVGEAFHASSTSVLVDGFTDPSNNKNRFCCLGLLSNVNRNSTENRRHIGKGVHLYVGGEVYAECLSDSSIFVQSRNCNYHHG
HFPTTVCKIPSGCSLKIFNNQEFAQLLAQSVNHFETVYELTKMCTIRMSFVKWGAEYHRQDVTVTSTPCWIEHLHGPLQWLDKVLTQMGSPHNPI
SSVS

>d1dmza_b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

GNGRFLTLKPLPDSIIQESLEIQQQGVNPFFIGRSEDNCNKIEDNRNLSRVHCFIFKKRAVGKSMYESPAQGLDDIWYCHTGTNVSYLNRRMIQGKTF
LLQDGDEIKIIWDKNNKFVIGFKVEINDTTGLFNEGLGMLQEQRVVLKQTAEEKDLVKKL

>d1g6ga_b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

GENIVCRVICTTGQPIRDLSADISQLKEKRSIKKVVTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLNDISTNGTWLNGQKVEKNSNQLSQG
DEITVGVGVESDILSLVIFINDKFKQCL

>d1k3ja_b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

ATQRFLIEFKFSQEIQGENIVCRVICTTGQPIRDLSADISQLKEKRSIKKVVTFGRNPACDYHLGNISRLSNKHFQILLGEDGNLLNDISTNGTWLNG
QKVEKNSNQLLSQGDEITVGVGVESDILSLVIFINDKFKQCLEQNKVDRIR

>d1qu5a_b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

EAETREQKLLHSNNNTENVSSKKKGNGRFLTLKPLPDSIIQESLEIQQQGVNPFFIGRSEDNCNKIEDNRNLSRVHCFIFKKRAVGKSMYESPAQGLDDI
WYCHTGTNVSYLNRRMIQGKFLQDGDEIKIIWDKNNKFVIGFKVEINDTTGLFNEGLGMLQEQRVVLKQTAEEKDLVKKL

>d1cq3a_b.27.1.1 (A:) Soluble secreted chemokine inhibitor, VCCI {Cowpox virus}

SFSSSSCTEEENKHHMGIDVIKVTQDKDQTPTNDKICQSVTEVTESEDESEEVVKGDPTTYT VVGGGLTMDFGFTKCPKISSISEYSDGNTVNARLSS
VSPGQGKDSPAITLEALSMIKDCEMSINKCSEEKDSNIKTHPVLSNISHKKVSYEDIIGSTIVDTKCVKNLEISVRIGDMCKESSELEVKGDFKYVD
GSASEDAADDTSLINSAKLIAVC

>d1p35a_b.28.1.1 (A:) Paculovirus p35 {Nuclear polyhedrosis virus (*Autographa californica*), ACMNPV}

CVIFPVEIDVSQTIIRDQCVDKQTRRELVYINIKMNTQLTKPVLMMFNISGPIRSVTRKNNNLRDRIKSKVDEQFDQLERDYSQMDGFHDSIKYFKDE
HYSVSCQNGSVLKSFKAKILKSHDYTDKKSIEAYEKYCLPKLDERNDYYAVCVLKPGFENGNSNQVLSFEYNPIGNKIVPFAHEINDTGLYEYDVAYV
DSVQFDGEQFEEFVQSLILPSSFKNSEKVLYYNEASKNSMUYKALEFTTESSWGKSEKYNWKFICNGFYDJKSKVLYVNLHNVTSALKNVILNTIK
>d1nls_b.29.1.1 (-) Concanavalin A {Jack bean (*Canavalia ensiformis*)}

ADTIVAVELDTPNTDIGDPSYPHIGIDIKSRSKKTAKWMQMNGKVTGTAHIYNSVDKRLSAVVSYPNADSATVSYDVLNDVLPEWVRVGLSASTG
LYKETNTILWSFTSKLKSNSTHETNALHFMFNQFSKDKDQLLQGDATTGTDGNLELTRVSSNGSPQGSSVGRALFYAPVHIWESSAVVASFEATFTF
LIKSPDSDHPADGIAFFISNIDSSIPSGGSTGRLGLFPDAN

>d2cna_b.29.1.1 (-) Concanavalin A {Jack bean (*Canavalia ensiformis*)}

ADTIVAVELDTPNTDIGDPSYPHIGIDIKSRSKKTAKWMQMNGKVTGTAHIYNSVDKRLSAVVSYPNADSATVSYDVLNDVLPEWVRVGLSASTG
LYKETNTILWSFTSKLKSNSTHQTDALHFMFNQFSKDKDQLLQGDATTGTDGNLELTRVSSNGSPQGSSVGRALFYAPVHIWESSATVSAFEATFAF
LIKSPDSDHPADGIAFFISNIDSSIPSGGSTGRLGLFPDAN

>g2ltn.1 b.29.1.1 (A.;B;) Legume lectin {Garden pea (*Pisum sativum*)}

TETTSFLITKFSPDQQNLIFQGDGYTTKEKLTAKVAKNTVGRALYSSPIHIWDRETGNVANFVTSFTVINAPNSYNADGFTFIAPVDTKPQTGGY
LGVFNSAEYDKTTQTVAVEFDTFYNAAWDPSNRDRHIGIDVNSIKSVNTKSWKLQNGEANVIAFNAATNVLTVSLTPNXVTSYTLSDVVSLSKDV
VPEWVRIGFSATTGAEYAAHEVLSWSFHSELSG

>g1len.1 b.29.1.1 (A.;B;) Legume lectin {Common lentil (*Lens culinaris*)}

TETTSFSITKFSPDQQNLIFQGDGYTTKGKLTAKVAKSTVGRALYSTPIHIWDRDTGNVANFVTSFTVIDAPSSYNADGFTFIAPVDTKPQTGGY
LGVFNSKEYDKTSQTVAVEFDTFYNAAWDPSNKERHIGIDVNSIKSVNTKSWNLQNGERANVIAFNAATNVLTVTLTPNXVTSYTLNEVPLKDV
VPEWVRIGFSATTGAEFAAQEVHSWSFNSQLG

>d1led__ b.29.1.1 (-) Legume lectin {West-central african legume (*Griffonia simplicifolia*)}

ENTVNFTYPDFWSYSLKNNGTEITFLGDA TRIPGALQLTKTDANGNPVRSSAGQASYEPVFLWDSTGKAASFYTSFTFLKNYGAPTADGLAFFLAPV
DSSVKDYGGLGLFRHETAADPSKNQVVAVEFDTWINKDWNDPPYPHIGIDVNSIVSATTRWENDDAYGSSIATAHITYDARSKILTLLSYEHGRD
YILSHVVDLAKVLPQKVIRIGFSAGVGYDEVTYIISWHFFSTLDGTNK

>d1hqla_ b.29.1.1 (A;) Legume lectin {*Griffonia simplicifolia*, lectin I-b4}

SVSFTFPNFWSVEDSIIFQGDANTTAGTLQLCKTNQYGTPLQWSAGR ALYSDPVQLWDNKTESVASFYTEFTFLKITGNGPADGLAFFLAPPDSV
KDAGEYLGLFNKSTATQPSKNQVVAVEFDTWTNPNPPEPSYRHIGHINVNSIVSATTRWEDSDIFSGKIATARISYDGSAEILTVVLSYPDGSDYILSHSV
DMRQNLPESRVGISASTGNNQFLTVYIISWRFSSNL

>d1ax0__ b.29.1.1 (-) Legume lectin {Coral tree (*Erythrina corallodendron*)}

VETISFSFSEFEPGNDNLTLOQAA LITQSGVLQLTKINQNGMPAWDSTGRTLYAKPVHIIWDMTTGTVASFETRFSFSIEQPYTRPLPADGLVFFMGPT
KSKPAQGYGYLGIFNNSKQD NSYQTLGVEFDTFSNPWDPQVPHIGIDVNSIRS IKTQPFLDNGQVANVVIKYDASSKILHAVLVYPSSGAIYTIAEV
DVKQVLP EWVDVGLSGATGAQRDAETHDVYWSWSFQASLPE

>d1wbfa_ b.29.1.1 (A;) Legume lectin {Winged bean (*Psophocarpus tetragonolobus*), basic agglutinin}

KTISFNFCFHQN EEEQLKLQRDARISSNSVLELT KVVNGVPTWNSTGRALYAKPVHIIWDMTTGVASFETRFSFSIRQPFPRPHADGLVFFIAPPNT
QTGE GGGYFGIYNPLSPYPFVAVEFDTFRNTWDPQIPHIGIDVNSVISTKTVPTL DNGIANVVIKYDASTKILHVVLVFP SLGTIYTIA DIVDLKQVLPE
SVNVGFSAATGDPSGKQRNATEHDILSWSFSASLPG

>d1f9ka_ b.29.1.1 (A;) Legume lectin {Winged bean (*Psophocarpus tetragonolobus*), acidic lectin}

ETQS FNF DHFEENS KELN LQRQ ASIKS NGV LE LT KLT KNG VGP VWK STGR ALYA EPIK IWD STTG NVAS FETR FSFSN IT QPYA PEPAD GLTFM VPPNS
PQGEDGGNLGVFKPPEGDNAFAVEFDTFQNTWDPQVPHIGIDVNSIVSSKTLHFQLENGGVANVVIKYD SPTKILNVVLA FHS VGT VY TLS NIVDLK
QEFPNSEWWNVGLSATTG YQKNAV ETHEIISWSFTSSL

>g1loe.1 b.29.1.1 (A.;B;) Legume lectin {*Lathyrus ochrus*, isolectin I}

TETTSFSITKFGPDQQNLIFQGDGYTTKERLTLTAKVAKRNTVGRALYSSPIHIWDSKTGNVANFVTSFTVIDAPNSYNADGFTFIAPVDTKPQTGGY
YLGVFNSKD YDKTSQTVAVEFDTFYNTAWDPSNGDRHIGIDVNSIKSINTKSWALQN GKEANVIAFNAATNVLTVSLTPXTSYTLNEVPLKEFVPE
WVRIGFSATTGAEFAAHEVLSWYFHSELA

>d2pela_ b.29.1.1 (A;) Legume lectin {Peanut (*Arachis hypogaea*)}

AETVS FNF NFSFSEG NPAIN FQGD VTLSNGNIQLT NLK VNS VGRV LYAMPV RIWSSATGNV ASFL TSFS FEM KDI KDYDPADGI IFFIA PE DTQI PAGS
IGGGTLGVSDTKGAGHFVGVEFDTYSNSEYNDPPTDHVGIDVNSVDSVKTVPWNSVSGAVVKT VYIDSSTKTL SAVT NDNGDITTIAQVVDLKAK
LPERVKFGFSASGSLGGRQIHLIRWSFTSLTT

>d1g9fa_ b.29.1.1 (A;) Legume lectin {Soybean (*Glycine max*)}

AETVS FSWNK FVKQPNM ILQGDAIVTSSGKLQLNKV DENGTPKPSLGR ALYSTPIHIW DKETGSVASFAASFNFTYAPDTKRLADGLAFFLAPI DT
KPQTHAGYLGFLNENESGDQVVAVEFDTFRNSWDPPNPHIGINVNSIRS IKTT SWDLANNKVA KV LITYDASTSLLV ASL VPSQRTS NILSDVVDLK
SLPEW VRIGFS AATGLDIPGESHDVLSWSFASNLPHASSN IDPLDLTSF VLHE

>g1qmo.1 b.29.1.1 (A.;E;) Legume lectin {Field bean (*Dolichos lab lab*), Fril}

AQSLSF SFTKFD PNQ EDLIFQ GHAT STNNV LQVT KLD SAGNPVSSA GRVLYA PRL WEDSAV L TSFTI INFEIST PYTSRI ADGL AFFI APP DS VSYH
GGFLGLFP NANX SVVVA VEFD TYLPD YGDP NYIHIGIDVNSIRSKV TAKWDWQNGK IATAHIS YNSV SKRLS VTSYYAGSKPATLSYDIELHTV LP EW
VRVGLSASTGQD KERNTVHS WSFTSSLWTN

>d1g7ya_b.29.1.1 (A:) Legume lectin {Horse gram (Dolichos biflorus), different isoforms}

ADIQSFNKFNFNSSSFLQGATVSSKLRLTKVKGNGLPTLSSLGRAFYSSPIQYDKSTGAVASWATSFTANIFAPNKSSADGIAFALPVGSEPKSNS
GFLGVFDSDVYDNAQTVAVEFDTFSNTDWDPSTSRRHIGIDVNSIKSIRTASWGLANGQNAEILITNAATSLLVASLVHPSRTSYIVSERVDITNELPE
YVSIGFSATTGLSEGYTETHDVLWSFASKLPDDSTEPDIASYLVRNVL

>d1lu1_b.29.1.1 (-) Legume lectin {Horse gram (Dolichos biflorus), different isoforms}

ANIQSFNKFNFNSPSFLQGATVSSGKLQLTKVKENGIPPTSSLGRAFYSSPIQYDKSTGAVASWTSFTVKISAPSASFADGIAFALPVGSEPRNG
GYLGVFDSDVYNNSAQTVAVEFDTLSNSGWDPMSMKHIGIDVNSIKSIATVSWDLANGENAEILITNAATSLLVASLVHPSRTSYILSERVDITNELPE
YVSIGFSATTGLSEGYIETHDVLWSFASKLPDDSTAEPDIASYLVRNVL

>d1h9wa_b.29.1.1 (A:) Legume lectin {Duke (Dioclea guianensis)}

ADTIVAVELDSPNTDIGDPSYPHIGIDIKSIRSKSTARWMQTKVGTAHISYNSSVAKRSLAVSYTGSSSTVSYDVLNNVLPEWVRVGLSATTGLY
KETNTILSWSFTSKLKNTNSIADANSLHFNFQNFSQNPKDILQGDATTSDGNLELTKVSSGDPQGSSVGRALFYAPVHIWEKSAVVASFDATFTFLIK
SPDRDPADGITFFIANTDTSIPSGSGGRLGLFPDAN

>d1fx5a_b.29.1.1 (A:) Legume lectin {Furze (Ulex europaeus), UEA-I}

SDDSFKFKNFQNGKDLQFQGNASVIETGVLQLNKVGNLNPDETGGIARYIAPIHIWCNTGELASFITSFSFFMETSANPKAATDGLTFLAPPDSP
LRRAGGYFGLFNDTCKDSSQTVAVEFDTIGSPVNFWDPGPFHIGIDVNCVKSINAERWNKRYGLNNVANVEIIYEASSKLTASLTYPSDQTSISVTSI
VDLKEILPEWVSVGFSGSTYIGRQATHEVLNWYFTSTFINT

>d1qnwa_b.29.1.1 (A:) Legume lectin {Furze (Ulex europaeus), UEA-II}

SDDSFNFDKFVNPQNKKIIQGQDASVTTGVLQVTKVKPNTTSGRALYAAPIQIWDSITGKVASFATSFVVKADKSDGVDFLAFFPANSQIPSG
SSAGMFGLFSSSDSKSSNQIAVEFDTYFGKAYNPWDPPDFKHIGIDVNSIKTVKWDWRNGEVADVITYRAPTKSLTVCLSYPSDGTNSIITASVLD
KAILPEWVSVGFSGGVGMAAEFETHDVLWSWYFTSNLE

>d1dbna_b.29.1.1 (A:) Legume lectin {Maackia amurensis, leukoagglutinin}

SDELSFTINNFVPNEADLFLQGEAVSSTGVLQLTKVENGPQPKYSVGRALYAAPVRIWGNTGSVASFSTSFTFVVKAPNPDTSDGLAFYLAPPDSQ
IPSGSVSKYLGFLNNNSNSDSSNQIVAVEFDTYFAHSYDPWDPNRYRHIGIDVNGIESIKTVQWDWINGVAFATITYLAPNKTIALSVPSNQTTFVA
ASVDLKEILPEWVVRVGFSAATGYPTEVETHDVLWSFTSTL

>d1fnya_b.29.1.1 (A:) Legume lectin {Black locust (Robinia pseudoacacia)}

TGSLSFSPKFAPNQPYLINQGDALVTSTGVLQLTNVNGPSSKSLGRALYAAPFQIWDSITGNVASFVTSFTFIQAPNPATTADGLAFLAPVDTQP
LDLGGMLGIFKDGYFNKSNQIVAVEFDTFSNGDWDPKGRHLGINVNSIESIKTVPWNTNGEVANVFSYEASTKSLASLVPSLETSFIIDAIVDVKI
VLPEWVRFGFSATTGIDKGYVQTNDVLSWSFESNLPG

>d1avba_b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (Phaseolus vulgaris)}

SNDASFNVTFNKTNLILQGDATVSEGHLLTNVKGNEEDSMGRAFYSAPIQINDRTIDNLASFSTNFTFRINAKNIENSAYGLAFALPVGSRPKLKG
RYLGLFNTTNYDRDAHTVAVVFDTVSNRIEDVNSIRPIATESCNFGHNNGEKAEVRTYDSPKNDLRVSLLYPSSEEKCHVSATVPLEKEVEDWVSVG
FSATSGSKKETTETHNVLSWSFSSNFI

>d1dhkb_b.29.1.1 (B:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (Phaseolus vulgaris)}

ATETSFNIDAFNKTNLILQGDATVSSNGNLQLSYNSYDSMSRAFYSAPIQIRDSTTGTVASFATSTFTNIQVPPNAGPADGLAFALPVGQS
VEFDTLSRISIDVNNNDIKSVPWDVHDYDGQNAEVRTYNSSTKVFVSLSNPSTGKSNNVSTTVELEKEVYDWSVGFSAATSGAYQWSYETHDVL
WSFSSKF

>d1g8wa_b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (Phaseolus vulgaris)}

SNDIYFNQRFNETNLILQGDASVSSSGQLRLTNNGNGEPRVGSGLGRAFYSAPIQIWDTNTGTVASFATSTFTNIQVPPNAGPADGLAFALPVGQS
PKDKGGFLGLFDGSNSNFHTVAVEFDTLYNKDWDPTERHIGIDVNSIRSIKTRWDVNGENAEVLITYDSSTNLLASLVPSQKTSFIVSDTVDLKS
LPEWVSVGFSAATTGINKGNVETNDVLSWSFASKLS

>d1ioaa_b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (Phaseolus vulgaris), G02771, arcelin-5a}

ATETSFNFPNFHTDDKLILQGNATISSKGQLQLTGVGNSNELPRVDSLGRAFYSDPIQIKDSSNNVASFNTNFTFIIRAKNQISAYGLAFALPVNSPPQKK
QEFLGIFNTNNPEPNARTVAVVNTFKNRIDFDKNFIKPVYNENCDFHKYNGEKTDVQITYDSSNNDLRVFLHFTVSQVKCSVSATVHLEKEVDEWW
SVGFSPSGLTEDTTETHDVLWSFSSKFR

>d1gbg__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus licheniformis}
QTGGSFYEPFNNYNTGLWQKADGYSNGNMFNCTWRANNVSMTSLGEMRLSLTSPSYNKFDCEGENRSVQTYGYGLYEVNMKPAKNVGIVSSFTY
TGPTDGTPWEIDIEFLGKDCKVQFNYYTNGVGNHEKIVNLGFDAANSYHTYAFDWQPNSIKWYVDGQLKHTATTQIPQTPGKIMMNLWNGAG
VDEWLGSYNGVTPLAHYNWVRYTKR

>d2ayh__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Hybrid protein: residues 1-16 from Bacillus amyloliquefaciens and Bacillus macerans}
QTGGSFPEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKGLTSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFTYTGP
AHGTQWDEIDIEFLGKDCKVQFNYYTNGVGGHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDD
WLGSYNGANPLYAEYDWVKYTSN
>d1ajka_ b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}
NTGIVSSFTYTGPAAHGTQWDEIDIEFLGKDCKVQFNYYTNGVGGHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIM
MNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTSNQTGGSFPEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKGLTSSAYNK
FDCAEYRSTNIYGYGLYEVSMKPAK
>d1ajoa_ b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}
GHEKVISLGFDASKGFHTYAFDWQPGYIKWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTSNQTGGSFPE
PFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKGLTSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFTYTGPAAHGTQW
DEIDIEFLGKDCKVQFNYYTNG
>d1cpm__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}
FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFTYTGPAAHGTQWDEIDIEFLGKDCKVQFNYYTNGVGGHEKVISLGFDASKGFHTYAFDWQPGYI
KWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTSNQTGGSFPEPFNSYNSGTWEKADGYSNGGVFNCTW
RANNVNFTNDGKLKGLTSSAYNA
>d1cpn__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}
FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFTYTGPAAHGTQWDEIDIEFLGKDCKVQFNYYTNGVGGHEKVISLGFDASKGFHTYAFDWQPGYI
KWYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDDWLGSYNGANPLYAEYDWVKYTSNQFNSYNSGTWEKADGYSNGGVFNCTWRA
NNVNFTNDGKLKGLTSS
>d1dypa_ b.29.1.2 (A:) kappa-Carrageenase, catalytic {Pseudoalteromonas carrageenovora}
SMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQTEINYGVWSWKNEATVSKGKLKLTKEHQRTFWDGCNQQVANYPLYYTSGVAKSRAT
GNYGYEARIKGASTFPVGSPAFWMYSTDRSLTKEGDVQYSEIDVVELTQKSAVRESDHDLHNIVVKNGKPTWMRPGSFQTNHNGYHLPFDPRN
DFHTYGVNVTKDKITWYVDGEIVGEKDNLWHRQMNLTSQGLRAPHTQWKCNCQFYPNSANKSAEGFPTSMEVDYVRTWVKV
>d1sita_ b.29.1.3 (A:) S-lectin, different isoforms {Cow (Bos taurus)}
CGLVASNLNLKPGECLRVRGEVAADAKSFLNLGKDDNNLCLHFNPRAHGDVNTIVCNSKDAGAWGAEQRESAFPQPGSVVEVCISFNQTDLT
IKLPDGYEFKFPNRLNLEAINYLSAGGDFKIKCVAFE
>d1blkza_ b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}
SNVPHKSSLPEGIRPGTVLIRGLVPPNASRFHVNLGCQEEQGSDAALHFNPRLDTSEVVFSKEQGSWGREERGPVFPQRGPFEVLIIASDDGF
KAVVGDAQYHHFRHRLPLARVRLVEVGGDVQLDSVRIF
>d1hlca_ b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}
ELEVKNMDMKPGSTLKTSIADGTDGFVINLGQGTDKLNLFNPRFSESTIVCNSLDGSNWQEQREDHLCFSPGSEVKFTVTFESDKFKVCLPDG
HELTFPNRLGHSHLSYLSVRGGFNMSFFKLKE
>d1qmja_ b.29.1.3 (A:) S-lectin, different isoforms {Chicken (Gallus gallus)}
QGLVVTQLDVQPGECVKVKGKILSDAKGFSVNKGDSSTMLHFNPRLDCHGDVNTVCNSKEDGTWGEEDRKADFPFQQGDKVEICISFDAAEV
KVKVPEVEFEFPNRLGMEKIQYLAVEGDFKVKAIKFS
>d1a78a_ b.29.1.3 (A:) S-lectin, different isoforms {Toad (Bufo arenarum)}
ASAGVAVTNLNKPGHCVEIKGSIPPDCKGFAVNLLHFNARFDLHGDNKIVCNSKEADAWGSEQREEVFVFPFQQGAEVVMCFEYQTQ
KIIKFSSGDQFSFPVRKVLPSIPFLSLEGЛАFKSITTE

>d1hdka_b.29.1.3 (A:) Charcot-Leyden crystal (CLC) protein {Human (Homo sapiens)}

SLLPVPYTEAASLSTGSTVTIKGRPLVCFLNEPYLQVFDFHTEMKEESDIVFHfqvCFGRVVMMNSREYGAWKQQVESKNMPFQDGQEFLSISVLPD
KYQVMVNQGSSYTFDHRKPEAVKMVQVWRDISLTKFNVSYL

>d1a3k__ b.29.1.3 (-) Galectin-3 CRD {Human (Homo sapiens)}

LIVPYNLPLPGGVVPRMLITILGTVKPNANRIALDFQRGNDAFHNPRLFNENNRRVIVCNTKLDNNWGREERQSVPFESGKPKIQLVEPDHFK
VAVNDAHLLQYNHRVKKLNEISLGISGDIDLTSASYTMI

>d1c1la_b.29.1.3 (A:) Congerin I {Conger eel (Conger myriaster)}

GGLQVKNFDTVGKFLTVGGFINNSPQRFSVNVESMNSLSLHLDHRFNYGADQNTIVMNSTLKGDNGWETEQRSTNFTLSAGQYFEITLSYDINK
FYIDILDGPNLLEFPNRYSKELPFLSLAGDARLTLVKE

>d1d2sa_b.29.1.4 (A:) Sex hormone-binding globulin {Human (Homo sapiens)}

PPAVHLSNGPGQPEPIAVMTFDLTKITKTSSFEVRTWDPEGVIFYGDTNPKDDWFMLGLRDGRPEIQLHNHWAQLTVAGPRLDDGRWHQVEVK
MEGDSVLLEVGDGEEVRLRQVSGHPIMRIALGGLLFPASNLRPLVPALDGCLRRDSWLDKQAEISASAPTSLRSC

>d1dyka1 b.29.1.4 (A:2744-2932) Laminin alpha2 chain {Mouse (Mus musculus)}

HGPCVAESEPALLTGSKQFGLSRNSHIAIAFDDTKVKNRLTIELEVRTEAESGLLFYMARINHADFATVQLRNGFPYSYDLGSDTSTMPTKINDGQ
WHKIKIVRKQEGILYVDDASSQTISPKKADILDVVGILYVGGLPINYTRRIGPVTSYLDGCVRNHLHMEQAPVLDQPTSSFHVGTCFA

>d1dyka2_b.29.1.4 (A:2933-3117) Laminin alpha2 chain {Mouse (Mus musculus)}

NAESGTYFDGTGFAKAVGGFKVGLDLLVEFERTTRPTGVLLGVSSQKMDGMGIEMIDEKLMFHVDNGAGRFTAIIYDAEIPGHMCNGQWHKVTA
KKIKNRLELVVDGNQVDAQSPNSASTSADTPVFGFPGLNQFGLTTNIRFRGCIRSLKLTKGTGKPLEVNFAKALELRGVQPVCPT

>d1c4ra_b.29.1.4 (A:) Ligand-binding domain of neurexin 1beta {Rat (Rattus norvegicus)}

HAGTTYIFSKGGGQITYKWPVPPNDPSTRADRLAIGFSTVQKEAVLVRVDSSSGLGDYLELHIHQKGKIGVKFNVGTDIAIESNAIINDGKYHVVRFTR
SGGNATLQVDSWPVIERYPAGRQLTIFNSQATIIGGKEQGQPFQGQLSGLYYNGLKVLNMAAENDANIAIVGNVRLVGEV

>d1saca_b.29.1.5 (A:) Serum amyloid P component (SAP) {Human (Homo sapiens)}

HTDLSGKVVFVFPRESVTDHVNLITPLEKPLQNLTCFRAYSDLSRAYSLSFSYNTQGRDNELLVYKERVGEYSLYIGRHKVTSKVIEKFPAVHICVSWE
SGIAEFWINGTPLVKKGLRQGYFVEAQPKIVLGQEQQDSYGGKFDRSQSFVGEIGDLYMWDSVLPPENILSAYQGTPLPANILDWQALNYEIRGYVIIKP
LVWV

>d1b09a_b.29.1.5 (A:) C-reactive protein (CRP) {Human (Homo sapiens)}

QTDMSRKAFVFPKESDTSYVSLKAPLTKPLKAFTVCLHFYTELSSTRGYSIFSATKRQDNEILIFWSKDYGSEFTVGGSEILFEVPEVTAVPHICTSWES
ASGIEFWVWDGKPRVRKSLKKGYTVGAEEASIILGQEQQDSFGGNFEGSQSLVGDIGNVNWMDFVLPDEINTIYLGGPFSNVNLWRALKYEVQGEV
FTKPQLWP

>d1jhna1_b.29.1.12 (A:61-262) Calnexin {Dog (Canis familiaris)}

YKAPVPSGEVFADSFDRGTLGWLISLAKKDDTDDEIAKYDGKWEVDEMKEALKPGDKGLVMSRAKHHAISAKLNKPFLFDTKPLIVQYEVNFQN
GIECGGAYVKLSSKTPELNLDQFHDKPTYTIMFGPDCKGEDYKLHFIRHKNPKTGVYEKHAKRPDADLKTYFTDKTHLYTLINPDNSFEILVDQSI
VNSGN

>d1jhna2_b.29.1.12 (A:412-458) Calnexin {Dog (Canis familiaris)}

LEPFKMTPTFSAIGLELWSMTSDIFFDNFIVCGDRRVDDWANDGWGL

>d1a8d_1 b.29.1.6 (1-247) Tetanus neurotoxin {Clostridium tetani}

MKNLDCWVDNEEDIDVILKKSTILNLDINNDIISDISGFNSSVITYPDAQLVPINGKAIHLVNNESSEVIVHKAMDIYNDMFNNFTVSFWLRVPKVS
ASHLEQYGTNEYSIISMKHKHSLSIGSGWSVSLKGNNLIWTLKDSAGEVRQITFRDLPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGL
GAIREDNNITLKDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLS

>d3btaa1_b.29.1.6 (A:872-1078) Botulinum neurotoxin {Clostridium botulinum, serotype A}

IINTSILNLRYESNLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNNSGWK
VSLNYGEIWTIQLDTQEIQRVVFKYSQMINSDYINRWIFVITNNRLNNSKIYINGRLLDQKPISNLGNIHASNINMKLDGCRDTHRYIWIKYFNL
DKEL

>d1epwa1_b.29.1.6 (A:862-1079) Botulinum neurotoxin {Clostridium botulinum, serotype B}

NIIINLRYKDNNLIDLGYAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLEDFSVSFWRIPKYKNDGIQNYIHNNEYTIINCMKNNSG
WKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIIFKLDGDIDRTQFIWMKYFSIFNT
ELSQSNIEERYKIQSY

>d1ikpa1 b.29.1.7 (A:2-251) Exotoxin A, N-terminal domain {Pseudomonas aeruginosa}

EEAFDLWNECAKACVLDLKDGVRRSSRMSVDPAIADTNQGQLHYSMVLEGGNDALKLAIDNALSITSDGLTIRLEGGVEPNKPVRYSYTRQARGSW
SLNWLVPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDATFFVRAHESNEMQPTLAISHAGVSVMMAQAQPRREKRWSEWAS
GKVLCLLDQLDGVNYLAQQRCNLDDTWEKGKIVRLAGNPAKHLDIKPTVISHRLHFP

>d1kit_1 b.29.1.8 (25-216) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}

ALFDYNATGDTEDSPAKQGWMQDNTNNGSVLNTADGMPAWLVQGIGGRAQWTYSLTNQHAQASSFGWRMTTEMKVLSGGMITNYYAN
GTQRVLPIISLDSSGNLVFEGQTGRVLATGTAATEYHKFELVFLPGSNPSASFYFDGKLIRDNIQPTASKQNMIVWGNGSSNTDVAAYRDIKFEI
QGD

>d1kit_2 b.29.1.8 (347-543) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}

DVTDQVKERSFQIAGWGGSLEYRRNTSLSQQDWQSNAKIRIVDGAANQIQVADGSRKYVVTLSIDESGGLVANLNGVSAPIILQSEHAKVHSFHD
YELQYSALNHTTLFVGQQITTWAGEVSQENNIQFGNADAQIDGRHLVQKIVLTQQGHNLVEFDAFYLAQQTPEVEKDLKLGWTKIKTGNTMSL
YGNAS

>d2sli_1 b.29.1.9 (81-276) Leech intramolecular trans-sialidase, N-terminal domain {North american leech (Macrobdella decora)}

IPEGILMEKNNVDIAEGQGYSLDQEAGAKYVKAMTQGTIISYKSTSENGIQSLFSVGNSTAGNQDRHFHYITNSGGIGIELRNTDGVFNYTLDRPAS
VRALYKGERVFNTVALKADAANKQCRLFANGELLATLDKDAFKFISDITGVNDNTLGGTKRQGKIAYPFGGTIGDIKVYSNALDEELIQATGVTTY

>d6cel__ b.29.1.10 (-) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma reesei, Cel7A}

ESACTLQSETHPPLTWQKCSSGGTCTQQTGSVVIDANWRTHATNSSTCYDGNTWSSTLCPDNETCAKNCLDGAAYASTYGVTTSGNSLSDIFV
TQSAQKNVGarLYLMASDTTYQEFTLGNFSDVDVSQLPCGLNGALYFVSMADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQANVEG
WEPSSNNANTGIGGHGSCCSQMDIWEANSISEALTPHPCTTVQGEICEGDCGCGTYSNDNRGGTCDPGCDWNPYRLGNTSFYGPGSTLDTK
KLTVTQFETSGAINRYYVQNGVTFQQPNAELGSYSGNELNDDYCTAEAAEFGGSSFDKGGLTQFKKATSGGMVLVMSLWDDYYANMLWLDSTY
PTNETSSTPGAVRGSCSTSSGVPQAQVESQSPNAKVTFSNIKFGPIGSTGNPSG

>d1eg1a_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma reesei, Endoglucanase I}

EQPGTSTPEVHPKLTTCYCKSGGCVAQDTSVVLDWNYRWMHDANYNSCTVNGGVNTLCPDEATCGKNCIFIEGVDYAASGVTTSGSSLTMNQY
MPSSSGYSSVSPRLYLLSDGEYVMLKLNQELSFDVLSALPCGENGSLYLSQMDENGGANQYNTAGANYGSGYCDAQCPVQTWRNGTLNTS
HQGFCCNEMDILEGNSRANALTPHSCTACADSAAGCFNPYGSYKSYYGPDTVDTSKFTIITQFTNDNGSPSGNLVSITRKYQQNGVDIPSAQP
GGDTISSLPSASAYGGLATMGKALSSGMVLVFSIWNDNSQYMNWLDSGNAGPCSTEENPSNILANNPNTHVVFNSNIRWDIGSTT

>d3ovwa_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Fusarium oxysporum}

ETPDKAKEQHPKLETYRCTKASGCKKQTNYIVADAGIHGIRQKNGAGCGDWGQKPNAACPDDEASCACKNCILSGMDSNAYKNAGITSGNKLRQ
QLINNQLVSPRVYLLEENKKYEMLHLTGTEFSFDVEMEKLPCGMNGALYLSMPQDGGKSTSRSNKAGAYYAGACYDAQCYVTPFINGVGNIKGQ
GVCCNELDIWEANSRATHIAPHPCSKPGLYGCCTGDECSSGICDKAGCGWNHNRINVTDYGRGKQYKVDSTRKFTVTSQFVANKQGDLIELHRHY
IQDNKVIIESAVVNISGPPKINFINDKYCAATGANEYMRLGGTKQMGDAMSRGMVLAWSVWWSEGDFMAWLDQGVAGPCDATEGDPKNIVKVQ
PNPEVTFSNIRIGEIGSTSSV

>d1dyma_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Humicola insolens, Cel7b}

EKPGETKEVHPQLTFRCTKRGGCKPATNFIVLDSLSPHIHRAEGLPGGGCDWGNPPPDKVCPDVESCAKNCIMEGIPDYSQYGVTTNGTSRLQH
ILPDGRVPSPRVYLLDKTKRKYEMLHLTGFEFTFDVDAKLPCGMNSALYLSMPQDGGKSTSRSNKAGAYYAGACYDAQCYVTPFINGVGNIKGQ
NAMDIWEANSRASHVAPHTCNKKGLYCEGEECAFEGVCDKNGCGWNHYRNVTYYGRGEFKVNTLKPFVVTQFLANRRGKLEKIHRFYVQ
DGKVIESFYTNKEGVPYTNMIDDEFCEATGSRKYMELGATQGMGEALTRGMVLAMSIWWDQGGNMEWLHGEAGPCAKGEGAPSNIQVEPF
PEVITYTNLRWGEIGSTY

>d1gpla_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Phanerochaete chrysosporium, Cel7d}

EQAGTNTAENHPQLQSQQCTTSGGCKPLSTKVVLDNSNWRVHSTSGYTCYTGNEDTSLCDGKTCANCALDGADYSGTYGITSTGTALT
VTGSNVGSRVYLMADDTHYQLLKLNNQEFTFDVDMNSLPGLNGALYLSAMDADGGMSKYPGNKAGAYGTGYCDSQCPKDIKFINGEANVNG

WTETGSNTGTGSYGTCCSEMDIWEANNDAAAFTPHPCTTGQTRCGDDCARNTGLCDGDGFNSFRMGDKTFLKGKMTVDTSKPFTVVTQF
LTNDNTSTGTLSEIRRIYIQNGKVIQNSVANIPGVDPVNSITDNFCACQQKTAFGDTNWFAQKGGLKQMGEALGNGMVLALSIWDDHAANMLWLD
SDYPTDKDPSAPGVARGTCATTSGVPSPDVSQVPNSQVFSNIKFDIGSTFSGTS
>d1xnb__ b.29.1.11 (-) Xylanase II {Bacillus circulans}
ASTDYWQNWTDGGSIVNAVNGSGGNYSVNSNTGNFVVGKGTGSPRTINYNAGVWAPNGNGYLTYGWTRSPLIEYYVVDSWGTYRPTG
TYKGTVKSDGGTYDIYTTTRYNAPSIDGDRRTFTQYWSVRQSKRPTGSNATITFTNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTVW
>d1qh7a_ b.29.1.11 (A:) Xylanase II {Bacillus agaradhaerens}
EIVTDNSIGNHDGYDYEFWKDSGGSGTMILNHGGTSAQWNNVNNILFRKGKKFNETQTHQQVGNMSINYGANFQPNGNAYLCVYGWTVDPLV
EYYIVDSWGNWRPPGATPKGITVDGGTYDIYETLRVNQPSIKGIATFKQYWSVRRSKRTSGTISVSNHFRAWENLGMNMGKMYEVALTVEGYQSS
GSANVYSNTLRINGNPLS
>d1hixa_ b.29.1.11 (A:) Xylanase II {Streptomyces sp. s38, xyl1}
ITTNQTGTNNNGYYYSFWTDGGSVSMNLASGGSGTWSWTNCGNFVAGKGWANGARRTVNYSGSFNPNSGNAYLTLYGWTANPLVEYYIVDNWGT
YRPTGTYKGTVTSDDGGTYDVYQTTRVNAPSVEGKTTFNQYWSVRQSKRTGGSITAGNHFDAWARYGMPGFSNYYMIIMATEGYQSSGSSSIS
>d1xnd__ b.29.1.11 (-) Xylanase II {Trichoderma harzianum}
QTIGPGTGNSGYYYSYWNDGHAGVTYNGGGGSFTVNWNSNGNFVAGKGWQPGTKNKVINFSGSYNPNGNSYLSIYGWSRNPLIEYYIVENFG
TYNPSTGATKLGEVTSDDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNRSSGSVNTANHFNAWAHGLTGTMDYQIVAVEGYFSSGSASITVS
>d1xyn__ b.29.1.11 (-) Xylanase II {Trichoderma reesei, xyn1}
ASINYDQNYQTGGQVSYSPSNTGFSVNWNNTQDDFVVGVGWTGSSAPINFGGFSVNSGTGLSVYGWSTNPLVEYYIMEDNHNNYPAQGTVKGT
VTSDDGATYTIWENTRVNEPSIQGTATFNQYISVRNSPRTSVTQVNFNAWAASLGLHLGQMNYQVVAVEGGWSGSASQSVN
>d1enxa_ b.29.1.11 (A:) Xylanase II {Trichoderma reesei, xyn11}
ETIQPGTGNNNGYFYSYWNDGHAGVTYNGGGQFSVNSNSGNFVGGKGWQPGTKNKVINFSGSYNPNGNSYLSVYGWSRNPLIEYYIVENF
GTYNPSTGATKLGEVTSDDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNRSSGSVNTANHFNAWAQQGLTGTMDYQIVAVEGYFSSGSASITVS
>d1yna__ b.29.1.11 (-) Xylanase II {Thermomyces lanuginosus}
ETTPNSEGWHDGYYYSW/SDGGAQATYTNLEGGTYEISWGDDGNLVGGKGWNPGLNARAIHFEVYQPNGNSYLAvgwvNYPQAEEYYIVEDYGDYNPCSSATS
GTYDPSSGATDLGTVEDGSIYRLGKTRVNAPSIDGTQFDQYWSVRQDKRTSGTVQTCFHDAWARAGLNVNGDHYYQIVATEGYFSSGYARIT
VADVG
>d1bk1__ b.29.1.11 (-) Xylanase II {Aspergillus kawachii}
AGINYVQNYNGNLGDFTYDESAGTFSMYWEDGVSSDFVVGWLTTGSSNAITYSAEYASAGSSSYLAvgwvNYPQAEEYYIVEDYGDYNPCSSATS
LGTVYSDGSTYQVCTDRTNEPSITGTSTFTQYFSVRESTRSGTVTVANHFNFWAQHGFNSDFNYQVMAVEAWSGAGSASVTIS
>d1pvxa_ b.29.1.11 (A:) Xylanase II {Paecilomyces variotii bainier}
GTTPNSEGWHDGYYYSW/SDGGGDSTYTNNSGGTYEITWGNGGNLVGGKGWNPGLNARAIHFTGVYQPNGTSYLSVYGWTRNPLVEYYIVEN
FGSSNPSSGSTDLGTVSCDGSTYLGQSTRYNAPSIDGTQTFNQYWSVRQDKRTSGTVQTCFHDAWASAGLNVTGDHYYQIVATEGYFSSGYARIT
VADVG
>d1f5ja_ b.29.1.11 (A:) Xylanase II {Dictyoglomus thermophilum}
ALTSNASGTFDGYYELWKTGNTTMTVYTGQRFSCQWSNINNALFRGKKYNQNQSLGIRITYSATYNPGNSYLCIYGWSTNPLVEFYIVES
WGNWRPPGATSLGQVTIDGGTYDIYRTTRVNQPSIVGTATFDQYWSVRTSKRTSGTVTVTDHFRAWANRGLNLGTIDQITLCVEGYQSSGSANITQ
NTFSQSS
>d2n1ra_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Streptomyces lividans, CelB2}
DTTICEPFGTTIQGRYVVQNNRWGSTAPQCVTATDTGFRVTQADGSAUTNGAKPSVPSVNGCHYTNCSPGTDLPRVRLTVSAAAPSSISYGFVDG
AVYNASYDIWLDPTARTDGVNQTEIMIWFNRVGPPIQPIGSPVGTASVGGRTWEVWSGGNGSNDVLSFVAPSAISGWSFDVMDFVRATVARGLAE
NDWYLTsvQAGFEPWQNGAGLAVNSFSSTVET
>d1h8va_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain {Trichoderma reesei, Cel12A}
ETSCDQWATFTGNGYTVSNNLW GASAGSGFGCVTAVSLSGGASWHADWQWSSGGQNNVKS YQNSQIAIPQKRTVNSISSMPTTASWSYSGSNIR
ANVAYDLFTAANPNHVTYSGDYELMIWLKYGDIGPIGSSQGTNVGGQSWTLYYGYNGAMQVYSFVAQTNTTNSGDVKNFFNLRDNKGNA

AGQYVLSYQFGTEPFTGSGTLNVASWTASIN

>d1jz8a4 b.30.1.1 (A:731-1023) beta-Galactosidase, domain 5 {Escherichia coli}

PAASHAIPIHLLTSEMDFCIELGNKRWQFNQRSGFLSQMWIGDKQLLPLRDQFTRALDNDIGVSEATRIDPNAWVERWKAAGHYQAEAALLQC
TADTLADAVLTTAHAWQHQGKTLFISRKTYRIDGSGQMAITVDVEVASDTPHPARIGLNCQLAQVAERVNWLGLGPQENYPDRITAACFDRWDLP
LSDMYTPVVFPESEGLRCGTRELNYGPHQWRGDFQFNISRYSQQQLMETSHRHLHAEGTWLNIDGFHMGIGGDDSWSPSVSAEFQLSAGRYH
YQLVWCQK

>d1oaca1 b.30.2.1 (A:301-724) Copper amine oxidase, domain 3 (catalytic) {Escherichia coli}

PAVKPMQIIPEGKNYTITGDMIHWRNDFHLSMNSRVGPMISTVTYNDNGTKRKVMYEGSLGGMIVPYGDPIGWYFKAYLDSDGYGMGTLT
SPIARGKDAPSNAVLLNETIADYTGVPMEIFPRAIAFERYAGPEYKHQMGEQPNVSTERRELVRWISTVGNADYIFDWIFHENGTIGIDAGTGIEA
VKGVAKTMHDEAKDDTRYGLIDHNIVGTTHQIYNFRLDLVGENNSLVAMPVVKPNTAGGPRSTMQVNQYNIGNEQDAAQKFDPGTI
RLSNNPKENRMGNPVSQIIPYAGGTHPVAKGAQFAPDEWIYHRLSFMDKQLWVTRYHPGERFPEGKYPNRSTHTDGLGQYSKDNESLDNTAV
VWMTTGTTHVARAEEWPIMPTEWVHTLLKPWNFFDETPTLGALK

>d1ksia1 b.30.2.1 (A:207-647) Copper amine oxidase, domain 3 (catalytic) {Pea seedling (Pisum sativum)}

VSKQSPFPQKQHSLTSHPQPGPFQINGHSVSWANWKFHIGFDVRAGIVISLASIYDLEKHKSRRVLYKGYISELFVPYQDPTEEFYFKTFFDSGEFG
FGLSTVSLPNRDCPPHAQFIDTYVHSANGTPILLKNAICVFEQYGNIMWRHTENGIPNESIEESRTEVNLIVRTIVGNADNVIDWEFKASGSIKPSI
ALSGILEIKGNTNIKHKDEIKEDLHGKLVSANSIGYHDHFVYYLDFDIDGTHNSFEKTSLKTVRIKDGSSKRKSYWTETQAKTESDAKITIGLAPAEV
VNPNIKTAVGNEVGYRLAPIAHPPLTEDDYPQIRGAFTNYNVWVTAYNRTEKWAGGLYVDSRGDDTLAVWTKQNREIVNKDIVMWVVGIHH
VPAQEDFPIMPPLLSTSFLRPTNFFERNPVLKTLSPRDVAWPGC

>d1av4_1 b.30.2.1 (212-628) Copper amine oxidase, domain 3 (catalytic) {Arthrobacter globiformis}

PLRTTQKPISTQPEGPSFTVTGGNHIEWEKWSLDVGFDVREGVVLHNIAFRGDRLRPIINRASIAEMVVPYGDPSIRSWQNYFDTGEYLVGQYA
NSLELGCDCLGDITYLSPVISDAFGNPREIRNGICMHEEDWGILAKHSDLWSGINYTRRNRRMVISFFTIGNADYGFYWYLYLDGTIEFEAKATGVVF
TSAFPEGGSNDNISQLAPGLGAPFHQIFSARLDMAIDGFTNRVEEDVVRQTMGPGNERGNAFSRKRTVLRESEAVERADARTGRTWIISNPESK
NRLNEPVGYKLHAHNQPTLLADPGSSIARRAAFATKDLWVTRYADDERYPTGDFVNQHSGGAGLPSIAQDRDIDGQDIVVWHTGLTHFPRVED
WPIMPVDTVGFKLRPEGFFDRSPVLDVPAN

>d1a2va1 b.30.2.1 (A:237-672) Copper amine oxidase, domain 3 (catalytic) {Yeast (Hansenula polymorpha)}

PEAPPINVTPPEGVFSKMTGNVMEWSNFKFHIGFYREGIVLSDVSYNDHGNVRPIFHRISLSEMIIVPYGSPEFPHQRKHALDIGEYGAGYMTNPLS
LGCDCKGVYIYDAHFSDRAGDPITVKNAVCIHEEDDGLLFKHSDFRDNFATSLVTRATKLVVSQJFTAANAEYCLYWWFMQDGAIIRLDIILTGLNTYI
LGDDEEAGPWGTRVYPNVNAHNHQHFLSLRIDPRIDGDGNSAAACDAKSSPYPLGPSENMYGNAFYSEKTTFKTVKDSLNTYESATGRSWDIFPESK
NKVNPYSGKPPSYKLVSTQCPPLAKEGSLVAKRAPWASHSVNVVPYKDNRLYPSGDHVVPQWSGDGVRGMREWIGDSENIIDNTDILFFHTFGITH
FPAPEDFPLMPAEPITMLRPRHFFTENPGLDIQPSYAMTTSEAKRAV

>d1cb8a3 b.30.3.1 (A:336-599) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

IEPYHHQFWNGDYVQHLRPAYSFNRMVSKRTRSESGNKENLLGRYLSGATNIQLRGPEYYNIMPVWEWDKIPGITSRDYLTDPLTLWGEQG
SNDFAGGVSDGVY GASAYALDYDSLQAKKAWFFFKEIVCLGAGINSNAPENITTLNQSWLNGPVISTAGKTGRGKITTFAQGQFWLLHDAIGYY
FPEGANLSLTSQSKQKGWNFHINNSHKDEVSGDVFKLWINHGARPENAQYAYIVLPGINKPEEIKKYNGTA

>d1egua3 b.30.3.1 (A:541-814) Hyaluronate lyase {Streptococcus pneumoniae}

TSYLSAFNKMDFKTAMYNAEKGFGFLSSLSSRTLNYEHMNKENKRGWYTSMDGMFYLYNGDLSHYSDGYWPTVNPYKMPGTTEDAKRADSDTG
KVLPSAFVGTSKLDDANATATMDFTNWNNQTLAHKSWFMLDKIAFLGSNIQNTSTDATTIDQRKLESSNPYKVYVNDKEASLTEQEKDYPETQS
VFLESSDSKKNIGYFFFKKSSISMKSALQKGAWKDINEGQSDKEVENEFLTISQAHKQNGDSYGYMLIPNVDRATFNQMIKELE

>d1f1sa4 b.30.3.1 (A:620-919) Hyaluronate lyase {Streptococcus agalactiae}

LKSNLSTFNMSMDRLAYNNAKKDFGFLSLHSKRTLNYPEGMNDENTRGWYTGDGMFYIYNSDQSHYSNHFWPTVNPYK MAGTTEKDAKREDTTKE
FMSKHSKDAKEKTGQVTGTSDFVGSKLNDHFALAAMDFTNWDRITLAQKGWVILNDKIVFLGSNIKNTNGIGNVSTTIDQRKDDSKTPYTTVNV
GKTIDLKQASSQQFTDKSVFLESKEPGRNIGYIFFKNSTIDIERKEQTGTWNSINRTSKNTSIVSNPFITISQKHDNKGDSYGYMMVPNIDRTSFDKLA
NSKEVELLENS

>d1h54a2 b.30.4.1 (A:1-268) Lactobacillus maltose phosphorylase, N-terminal domain {Lactobacillus brevis}

MKRIFEVQPWNVITHFDPDKRQLQESMTSLNGYMGMRGDFEEGYSGDSLQGIYLGGWYPDKTRVGWWKNGYPKYFGKVNAVNFIKLPIE
NGEPVDLAKDKISDFTLDLMHQGVNRSFVERGAVRVALNFQRFLSAQPELSVQKVTVKNLSDAEVDVTLKPSIDADMNEEANYDERFWDV
LATDQQADRGSIWAKTPNPFGTPRFTSGMEMRLVTLKNVATQPNEKEVTTAYTGKLAPQASAELEKRVIVVTSRDY
>d1hs6a2 b.98.1.1 (A:1-208) Leukotriene A4 hydrolase N-terminal domain {Human (Homo sapiens)}
PEIVDTCSLASPASVCRTKHLHRCSDFTRRLTGTAALTQSQEDNLRSLVLDTKDLTIEKVVINGQEVKYALGERQSYKGSPMEISLPIALSKNQEIVI
EISFETSPKSSALQWLTPEQTSGKEHPYLFSQCQAIHCRAILPCQDTPSVKLTYAEVSVPKELVALMSAIRDGETPDPEPSRKIYKFIQKVPICLYIALV
VGA
>d1es6a_b.31.1.1 (A:) EV matrix protein {Ebola virus}
GDTPSNPLRPIADDTIDHASHTPGSVAFILEAMVNVISGPKVLMKQPIWLPLGVADQKTYSDSTAAIMLASYTITHFGKATNPLRVNRLGPGI
PDHPLRLLRIGNQAFLQEFVLPPVQLPQYFTFDLALKLITQPLPAATWTDDPTGSNGALRPGISFHPKLRPILLPNKSGKGNSDLTSPEKIQAIMTS
LQDFKIVPIDPTKNIMGIEVPETLVLKLTGKKVTSKNGQPIVLLPKYIGLDPVAPGDLTMVITQDCDTCHSPASLP
>d1qexa_b.32.1.1 (A:) gp9 {Bacteriophage T4}
MFIQEKKLIDTGEIGNASTGDLFDGGNキンSDFNAINAFGDQRKMAVANGTADGQIIHATGYYQKHSITEYATPVKVGTRHDIDTSTVGVKVII
RGEGLDCVEFINSNGSISVTNPLTIQAIKGVSGNLVTPSKVTLRCISSDNSTSVVNYSIESMFGQKESPAEGTWNISTGSVDIPLFHRTEYNM
AKLLVTCQSDGRKIKTAEINILVDTNVSEISSEYAVMRVGNETEDEIANIAFSIKENYVTATISSSTGMRAAVKVIATQKIGVAQ
>d1rie_b.33.1.1 (-) ISP subunit of the mitochondrial cytochrome bc1-complex, watersoluble domain {Cow (Bos taurus)}
AMSKIEIKLSDIPEGKNAFKWRGKPLFVRHRTKKEIDQEAABEVSQLRDPQHDLERVKKPEWVILIGVCTHLCVPIANAGDFGGYCPCHGSHYD
ASGRIRKGAPLNLEVPSYEFTSDDMVIVG
>d1ezve1_b.33.1.1 (E:87-215) ISP subunit of the mitochondrial cytochrome bc1-complex, watersoluble domain {Baker's yeast
(Saccharomyces cerevisiae)}
DVLAMAKVEVNLAAPLGKNNVVKWQGKPVIRHRTPHEIQEANSVDMMSALKDPQTDADRVKDPQWLIMLGICTHLCVPIGEAGDFGGWFPC
HGSHYDISGRIRKGAPLNLEIPAYEFDGDKVIVG
>d1rfs_b.33.1.1 (-) ISP subunit from chloroplast cytochrome bf complex {Spinach (Spinacia oleracea)}
TIAKDALGNDVIAAEWLKTHAPGDRLTQGLKGDPTYLVESDKTLATFGINAVCTHLCVVPFNAEENKFICPCCHGSQYNNQGRVVRGPAPLSAL
AHCDVDDGKVFVWPWTETDFRTGEAPWWA
>d1g8kb_b.33.1.1 (B:) Arsenite oxidase Rieske subunit {Alcaligenes faecalis}
RTTLAYPATAVSVAKNLAANEPEVSPYDSSPCAVKLGAPVPGGVGPDDIVASYVLCTHMGCPSTSVDSSKTFCPCCHTEFDAEKAGQMICGEA
TADLPRVLLRYDAASDALTAVGVDGLIYGRQANVI
>d1fqta_b.33.1.1 (A:) Rieske-type ferredoxin associated with biphenyl dioxygenase {Burkholderia cepacia}
MKFTRVCDRRDVPEGEALKVESGGTSVAIFNVDGELFATQDRCTHGDWSLSDGGYLEGDVVECSLHMGKFCVRTGKVKSPPPCEALKIFPIRIEDND
VLVDFEAGYLAP
>d1eg9a1_b.33.1.2 (A:1-154) Naphthalene 1,2-dioxygenase alpha subunit, N-domain {Pseudomonas putida}
MNYNNKILVSEGLSQKHLIHGDEELFQHELKTIFARNWLFLHDSLIPAPGDYVAKMGIDEVIVSRQNDGSIRAFLNCRHRGKTLVSVEAGNAKG
FVCSYHGWGFGSNGELQSPFEKDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQ
>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}
NPIPGLDELGVGNSDAAPGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLHNGKDVELLDDLAHTIRIEEL
>d1c0wa3_b.34.1.2 (A:165-223) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}
IVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLHNGKDVELLDDLAHTIRI
>d1g3sa3_b.34.1.2 (A:148-225) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}
PGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLHNGKDVELLDDLAHTIRIEE
>d1fx7a3_b.34.1.2 (A:145-230) Iron-dependent regulator IdeR {Mycobacterium tuberculosis}
GADDANLVRTELPGSPVAVVVRQLTEHVQGDIDLTRLKDAGVVPNARVTVETTPGGVTIVPGHENVTLPHEMAHAVKVEKV

>d1igqa_b.34.1.3 (A:) Transcriptional repressor protein KorB {Escherichia coli}
KKAIQVEHDERPARLILNRRPAEGYAWLKYEDEDGQEFEANLADVKLVALIEG

>d1igub_b.34.1.3 (B:) Transcriptional repressor protein KorB {Escherichia coli}
PDPDKLKKAIQVEHDERPARLILNRRPAEGYAWLKYEDEDGQEFEANLADVKLVALIEG

>d1ckaa_b.34.2.1 (A:) C-Crk, N-terminal SH3 domain {Mouse (Mus musculus)}
AEYVRALFDNGNDEEDLPFKKGDLRIRDKPEEQWWNAEDSEGKRGMIPVYVEKY

>d1efna_b.34.2.1 (A:) Fyn proto-oncogene tyrosine kinase, SH3 domain {Human (Homo sapiens)}
ALFVALYDYEAITEDDLSFHKGKEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPV

>d1shfa_b.34.2.1 (A:) Fyn proto-oncogene tyrosine kinase, SH3 domain {Human (Homo sapiens)}
VTLFVALYDYEARTEDDLSFHKGKEKFQILNSSEGDWWEARSLTTGETGYIPSNYVAPVD

>d1neb__b.34.2.1 (-) SH3 domain from nebulin {Human (Homo sapiens)}
TAGKIFRAMYDYMAADADEVSFKDGDAINVQAIDEWMYGTVQRTGRTGMLPANYVEAI

>d1bbza_b.34.2.1 (A:) Abl tyrosine kinase, SH3 domain {Human (Homo sapiens)}
NLFVALYDFVASGDNTLSITKGEKLRLVLGYNHNGEWCEAQTKNGQGWVPSNYITPVNS

>d2abl_1 b.34.2.1 (75-139) Abl tyrosine kinase, SH3 domain {Human (Homo sapiens)}
MGPSENDPNLFVALYDFVASGDNTLSITKGEKLRLVLGYNHNGEWCEAQTKNGQGWVPSNYITPVN

>d1pht__b.34.2.1 (-) Phosphatidylinositol 3-kinase (p85-alpha subunit, pi3k), SH3 domain {Human (Homo sapiens)}
AEGYQYRALYDYKKEREEDIDLHLDILTVNKGSVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEYIGRKKISPP

>d1g2ba_b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
MDRQGFVPAAYVKLDSTGTGKELVLALYDYQEKSREVTMKKGDLTLLNSTNKDWKVEVNDRQGFVPAAYVKLD

>d1pwt__b.34.2.1 (-) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
MGTGKELVLALYDYQEKSREVTMKKGDLTLLNSTNKDWKVEVNDRQGFVPAAYVKLD

>d1qkwa_b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
KELVLALYDYQEKSREVTMKKGDLTLLNSTNKDWKVEVNDRQGFVPAAYVKLD

>d1tuc__b.34.2.1 (-) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
MGPREVTMKKGDLTLLNSTNKDWKVEVNDRQGFVPAAYVKLDSTGTGKELVLALYDYQE

>d1awj__b.34.2.1 (-) IL-2 inducible T-cell (Itc) kinase {Mouse (Mus musculus)}
KKPLPPTPEDNRRSFQEPEEETLVIALYDYQTNDPQELALRCDEEYLYLDSSEIHWWWRVQDKNGHEGYAPSSYLVEKS

>d1bu1a_b.34.2.1 (A:) Hemopoetic cell kinase Hck {Human (Homo sapiens)}
IIIVALYDYEAIHHEDLSFQKGDQMVMVLEESGEWWKARSLATRKEGYIPSNYVARVD

>d1qcf1 b.34.2.1 (A:80-145) Hemopoetic cell kinase Hck {Human (Homo sapiens)}
SGIRIIIVVALYDYEAIHHEDLSFQKGDQMVMVLEESGEWWKARSLATRKEGYIPSNYVARVDSLET

>d1cska_b.34.2.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}
GTECIAKYNFHGTAEQDLPCKGDVLTIVAVTKDPNWYKAKKNVGREGIIPANYVQKR

>d1fmk_1 b.34.2.1 (82-145) c-src tyrosine kinase {Human (Homo sapiens)}
MVTTFVALYDYERSRTEDLSFKKGERLQIVNNTEGDWWLAHSLSTGQTGYIPSNYVAPSDSIQA

>d1nloc_b.34.2.1 (C:) c-src tyrosine kinase {Chicken (Gallus gallus)}
TFVALYDYERSRTEDLSFKKGERLQIVNNTEGDWWLAHSLSTGQTGYIPSNYVAPS

>d1awx__b.34.2.1 (-) Bruton's tyrosine kinase {Human (Homo sapiens)}
GSMSTSELKKVVALYDYMPMNANDLQLRKGDEYFILEESNLPWWRARDKNGQEGYIPSNYVTEAEDS

>d1qlxa_b.34.2.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}
LKKVVALYDYMPMNANDLQLRKGDEYFILEESNLPWWRARDKNGQEGYIPSNYVTEAE

>d1g15a_b.34.2.1 (A:) tyrosine kinase tec {Mouse (Mus musculus)}
GSEIVVAMYDFQATEAHDLRLERGQEYIILEKNDLHWWRARDKYGSEGYIPSNYVTGKSNLDQYD

>d1gcqa_b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}

STYVQALFDQDPQEDGELGFRRGDFIHVMNDNSDPNWWKGACHGQTGMFPRNYVTPV

>d1gria1 b.34.2.1 (A:1-56) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}

MEAIAKYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIKPKNYIEMK

>d1gria2 b.34.2.1 (A:157-217) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}

QPTYVQALFDQDPQEDGELGFRRGDFIHVMNDNSDPNWWKGACHGQTGMFPRNYVTPVNRNV

>d1gbra_b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Mouse (Mus musculus)}

GSRRASVGSMMEAIAKYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIKPKNYIEMKPHPEFIVTD

>d1sema_b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Caenorhabditis elegans, SEM-5}

ETKFVQALFDNPQESGELAFKRGDVITLINKDDPNWWEGQLNNRRGIFPSNYVCY

>d2hsp__b.34.2.1 (-) Phospholipase C, SH3 domain {Human (Homo sapiens)}

GSPTFKCAVKALFDYKAQREDELTIFIKSIIQNVEKQEGGWWRGDYGGKKQLWFPSNYVEEMVNPEGIHRD

>d1h92a_b.34.2.1 (A:) p56-lck tyrosine kinase, SH3 domain {Human (Homo sapiens)}

GSPLQDNLIVAHSYEPHDGLGFEKGEQLRILEQSGEWWKAQSLTTGQEGFIPFNFAKAN

>d1lcka1 b.34.2.1 (A:63-116) p56-lck tyrosine kinase, SH3 domain {Human (Homo sapiens)}

DNLVIALHSYEPHDGLGFEKGEQLRILEQSGEWWKAQSLTTGQEGFIPFNFAKAN

>d1ycsb2 b.34.2.1 (B:457-519) 53BP2 {Human (Homo sapiens)}

IMNKGVYIYLWDYEPQNDDELPMKEGDCMTIIHREDEDEIEWWWARLNDKEGYVPRNLLGLYP

>d1bb9__b.34.2.1 (-) Amphiphysin 2 {Rat (Rattus norvegicus)}

TTGRLDLPPGFMFKVQAQHDYTATDDELQLKAGDVVLVIFQNPSEEQDEGWLMGVKESDWNQHKELEKCRGVFPENFTERVQ

>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)}

GSHMPKMEVFQEYYGIPPPPAGFPFLRLNPGDIVELTKAEAEHNWWEGRNTATNEGVWFCNRVHPYV

>d1k1za_b.34.2.1 (A:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}

RAQDKKRNELGLPKMEVFQEYYGIPPPPAGFGFLRLNPGDIVELTKAEAEHNWWEGRNTATNEGVWFCNRVHPYVH

>d1i1ja_b.34.2.1 (A:) Melanoma inhibitory activity protein {Human (Homo sapiens)}

GPMPKTLADRKLCAQECSPHISMAVALQDYMAPDCRFLTIHRGQVVYFSKLKGRGRLFWGGSVQGDYYGDLAARLGYPSSIVREDQTLKPGKV

DVKTDKWDFYC

>d1kjwa1 b.34.2.1 (A:430-525) Psd-95 {Rat (Rattus norvegicus)}

GFYIRALFDYDKDCGFLSQALSFRFGDVLHVIDAGDEEWQARRVHSDSETDDIGFIPSKRRVERREWSRLKAKDWGSSGSQGREDSVLSYET

>d1br2a1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain {Chicken (Gallus gallus), pectoral muscle}

LWVVPSEKHGFEAASIKEKGDEVTVLQENGKKVTLSKDDIQKMN

>d2mysa1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain {Chicken (Gallus gallus), pectoral muscle}

AKSSVFVHPKQSFVKGTIQSKEGGKVTVKTEGGELTVKEDQVFS

>d1b7ta1 b.34.3.1 (A:29-76) Myosin S1 fragment, N-terminal domain {Bay scallop (Aequipecten irradians)}

DGKKNCWVVPDEKEGFASAEIQSSKGDEITVKIVADSSTRTVKKDDIQS

>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)}

YIWYNPDPKERDSYECGEIVSETSDSFTFKTSQDRQVKKDDANQ

>d1g5va_b.34.9.1 (A:) Survival motor neuron protein 1, smn {Human (Homo sapiens)}

QQWKVGDKCSAIWSEDCIYPATIASIDFKRETCVVYTGYNREEQNLSDLLSPI
>d1khca_ b.34.9.2 (A:) DNA methyltransferase DNMT3B {Mouse (Mus musculus)}
TEYQDDKEFGIGDLVWGKIKGFSWWPAMVVSWKATSKRQAMPGMWRVQWFQDGKFSEISADKLVALGLFSQHFNLATFNKLVSYRKAMYHTLE
KARVRAGKTFSSSPGESLEDQLKPMLEWAHGGFKPTGIEGLKPN
>d1vie__ b.34.4.1 (-) R67 dihydrofolate reductase {Escherichia coli, plasmid PLZ1}
PSNATFGMGDRVRKKSGAAWQQQIVGWYCTNLPEGYAVESEAHPGSVQIYPVAALERIN
>d1psf_ b.34.4.2 (-) Photosystem I accessory protein E (PsaE) {Cyanobacterium (Synechococcus sp.), pcc 7002}
AIERGSKVKILRKESYWYGDVGTAVSIDKSGIIYPVIVRFNKVNNGFSGSAGGLNTNNFAEHELEVVG
>d1qp2a_ b.34.4.2 (A:) Photosystem I accessory protein E (PsaE) {Cyanobacterium (Nostoc sp.), strain pcc8009}
MVQRGSKVRLRPESYWFQDVGTAVSDQSGIKYPVIVRFEKVNYSGINTNNFAEDELVEEAPKAKPKK
>d1jb0e_ b.34.4.2 (E:) Photosystem I accessory protein E (PsaE) {Synechococcus elongatus}
VQRGSKVILRPESYWYNEVGTAVSDQTPGVKYPVIVRFDKVNNTGSGSASGVNTNNFALHEVQEVA
>d1dj7b_ b.34.4.3 (B:) Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain {Synechocystis sp.}
MNVGDRVRVTSSVVVYHHPEHKKTAFLDLQGMEGEVAAVLTEWQGRPISANLPVLVKFEQRFAHFRPDEVTLI
>d2ahjb_ b.34.4.4 (B:) Nitrile hydratase beta chain {Rhodococcus erythropolis}
MDGVHDLAGVQGFGKVPHTVNADIGPTFHAWEHLPYSLMFLAGVAELGAFSVDEVRYVVERMEPRHYMMTPYYERYVIGVATLMVEKGILTQDE
LESLAGGPPLSRPSESEGRPAPVETTFFEVGQQRVRVRDEYVPGHIRMPAYCRGRVGTISHRTTEKWPFPAIGHGRNDAGEEPTYHVKFAAEELFGS
DTDGGSVVVDLFEGYLEPA
>d1jj2s_ b.34.5.1 (S:) Ribosomal proteins L24 (L24p) {Archaeon Haloarcula marismortui}
SKQPDQQRKSQRRAPLHERHKQVRATLSADLREEEYQQRNRVRVNAGDTVELRGDFAGEEGEVINVLDKAVIHVEDVTLEKTDGEEVPRPLDTSNV
RVTDLDLEDEKREARLESEDDSA
>d1jj2p_ b.34.5.1 (P:) Ribosomal proteins L21e {Archaeon Haloarcula marismortui}
PSSNGPLEGTRGKLKNKPRDRGTSPPQRAVEEFDDGEVKHLKIDPSVPNGRFHPRFDGQTGTVEGKQGDAYKVDIVDGGKEKTIITAAHLRRQE
>d2eifa1 b.34.5.2 (A:1-73) N-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Methanococcus jannaschii}
VIIMP GTKQNVGSLKVGQYVMIDGVPCEIVDISVSKPGKHGGAKARVVGIGIFEVKKEFVAPTSSKVEVPI
>d1kbk_1 b.34.5.2 (4-74) N-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Pyrobaculum aerophilum}
KWMSTKYVEAGELKEGSYVVVIDGEPCRVEIEKSKTGKHGSAKARIAVGVFDGGKRTLSLPVDAQVEVP
>d1rl2a1 b.34.5.3 (A:126-195) C-terminal domain of ribosomal protein L2 {Bacillus stearothermophilus}
GNALPLENPVGTLVHNIELKPGRGQLVRAAGTSAQVLGKEGKYIVRLASGEVRMILKCRATVGEVG
>d1jj2a1 b.34.5.3 (A:91-237) C-terminal domain of ribosomal protein L2 {Archaeon Haloarcula marismortui}
GNTLPLAEIPEGVPVCNVESSPGDGGKFARASGVNAQLLHDRNVAVVLPGEMLKRDPCRTIGVGGGRTDKPFVKAGNKKHMKARGT
KWPNVRGVAMNAVDPFGGGRQHPGPKKSISRNAPPGRKVGDIAKRTGRGG
>d3vub__ b.34.6.1 (-) CcdB {Escherichia coli}
MQFKVYTYKRESRYRLFVQSDIIDTPGRRMVIPLASARLLSDKVSRELYPVVHIGDESWRMMTTMASVPVSIGEEVADLSHRENDIKNAINLM
FWGI
>d1hyoa1 b.34.8.1 (A:1-118) Fumarylacetate hydrolase, FAH, N-terminal domain {Mouse (Mus musculus)}
MSFIPVAEDSDFPIQNLPYGVFSTQSNSPKPRIGVAIGDQILDLSVIKHLFTGPALSKHQHVFDETTLNNFMGLQAAWKEARASLQNLLSASQARLD
DKELRQRAFTSQASATMHP
>d1ex4a1 b.34.7.1 (A:223-270) DNA-binding domain of retroviral integrase {Human immunodeficiency virus type 1}
FRVYYRDSRNSLWKGPAKLLWKGEHAVVIQDNNSDIKVVPRRKAKIIRD
>d1ihva_ b.34.7.1 (A:) DNA-binding domain of retroviral integrase {Human immunodeficiency virus type 1}
MIQNFRVYYRDSRDPVWKGPALKWKGEGAVVIQDNNSDIKVVPRRKAKIIRD
>d1c0ma1 b.34.7.1 (A:217-269) DNA-binding domain of retroviral integrase {Rous sarcoma virus (RSV, avian sarcoma virus)}
VLTEGPPVKIRIETGEWEKGWNVLVWGRGYAAVKNRDTDVKIWVPSRKVKPDI

>d1c6vx_b.34.7.1 (X:) DNA-binding domain of retroviral integrase {Simian immunodeficiency virus}

KNSKFKNFRVYYREGRDQLWKGPGELLWKGEAVLLVKVGTDIKVVPRRKAKIKD

>d1aono_b.35.1.1 (O:) Chaperonin-10 (GroES) {Escherichia coli}

MNIRPLHDRVIVKRKEVETKSAGGIVLTGAAAKSTRGEVLAVGNRIELENGEVKPLDVKGDIVIFNDGYGVKSEKIDNEEVLIMSESIDLALIVEA

>d1jh2a_b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium tuberculosis}

AKVNIKPLEDKILVQANEAEETTASGLVIPDTAKEKPQEGTVVAVGPGRWDEDGEKRIPLDVAEGDTVIYSKYGGTEIKYNGEEYLISARDVLAVVSK

>d1lepa_b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium leprae}

AKVKIKPLEDKILVQAGEAEETMTPSGLVIPENAKEKPQEGTVVAVGPGRWDEDGAKRIPVDVSEGDIVIYSKYGGTEIKYNGEEYLISARDVLAVVSK

>d1g31a_b.35.1.1 (A:) GP31 co-chaperonin {Bacteriophage T4}

QQLPPIRAVGEYVILVSEPAQAGDEEVTESGLIIGKRVQGEVPELCVVHSVGPDVPEGFCEVGDLTSPLVGQIRNVPHFVALGLKQPKEIKQKFVTCHY
KAIPCLYK

>d1heta1_b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Horse (Equus caballus)}

STAGKVIKCKAAVLWEEKKPFSEEVEVAPPKAHEVRIKMWATGICRSDDHVSGTLVTPLPVIAGHEAAGIVESIGEGVTTVRPGDKVPLFTPQCGKC
RVCKHPEGNFCLKNLSPRGTMQDGTSRFTCRGKPIHHFLGSTFSQYTvvDEISVAKIDAASPLEKVCLIGCXKDSVPKLVADFMAKKFALDPLITH
VLPFEKINEGF DLLRSGESIRTILTF

>d1d1ta1_b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

GTAGKVIKCKAAVLWEQKQPFSEEIEVAPPKTKEVRIKILATGICRTDDHVIKGTMVSKFPVIVGHEATGIVESIGEGVTTVKPGDKVPLFLPQCRCN
ACRNPDGNCIRSDITGRGVLAGDTTRFTCKGKPVHHFLNTSTFTEYTVVDESSVAKIDAASPLEKVCLIGCXRDDVPKLVTEFLAKKFLDQLITHVLP
FFKISEGFELLNSGQSIRTVLTF

>d1hsoa1_b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

STAGKVIKCKAAVLWELKKPFSEEVEVAPPKAHEVRIKMWAVGICRTDDHVSGTMVTPLPVILGHEAAGIVESVGEGVTTVKPGDKVPLAIPQCGK
CRICKNPESNYCLKNDLVSNPQGTLQDGTSRFTCRRKPIHHFLGISTFSQYTvvDENAVAKIDAASPLEKVCLIGCXKECPVPLVADFMAKKFSLDALITH
VLPFEKINEGF DLLHSGKSIRTILMF

>d1hsza1_b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

STAGKVIKCKAAVLWEVKKPFSEEVEVAPPKAYEVRIKMWAVGICRTDDHVSGNLVTPLPVILGHEAAGIVESVGEGVTTVKPGDKVPLFTPQCGK
CRVCKNPESNYCLKNDLGNPRGTLQDGTRRFTCRGKPIHHFLGSTFSQYTvvDENAVAKIDAASPLEKVCLIGCXKEIPKLVADFMAKKFSLDALIT
HVLPFEKINEGF DLLHSGKSIRTVLTF

>d1ht0a1_b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

STAGKVIKCKAAVLWELKKPFSEEVEVAPPKAHEVRIKMWAVGICRSDEHVSGNLVTPLPVILGHEAAGIVESVGEGVTTVKPGDKVPLFTPQCGKC
RICKNPESNYCLKNDLGNPRGTLQDGTRRFTCRGKPIHHFLGSTFSQYTvvDENAVAKIDAASPLEKVCLIGCXKESVPKLVADFMAKKFSLDALIT
VLPFEKINEGF DLLRSGKSIRTVLTF

>d1teha1_b.35.1.2 (A:3-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

ANEVIKCKAAVAWEAGKPLSIEEIEVAPPKAHEVRIKIIATVCHTDAYTSGADPEGCFPVILGHEGAGIVESVGEGVTKLKAGDTVIPLYIPQCCKFC
LNPKTNLCQKIRVTQKGKLMPPDGTSRFTCKGKTLHYMGTSTFSEYTVVADISVAKIDPLAPLDKVCLLGCVXESVPKLVSEYMSKKIKVDEFVTHNLSF
DEINKAFELMHSGKSIRTVVKI

>d1e3ia1_b.35.1.2 (A:1-174,A:325-376) Alcohol dehydrogenase {Mouse (Mus musculus), class II}

GTQGKVIKCKAAIAWKGSPLCIEEIEVSPPKACEVRIQVIATCVCPTDINATDPKKKALFPVVLGHECAGIVESVGPGVTNFKPGDKVIPFFAPQCKRC
KLCSPLTNLCGKLRNFKYPTIDQELMEDRTSRFTCKGRSIYHFMGVSSFSQYTvvSEANLARVDEANLERVCXKSVDSPNLVSDYKNKKFDL DLL
THALPFESINDAIDLMKEGKSIRTILTF

>d1cdoa1_b.35.1.2 (A:1-175,A:325-374) Alcohol dehydrogenase {Cod (Gadus callarias)}

ATVGKVIKCKAAVAWEANKPLVIEEIEVDPHANEIRIKIIATGVCHTDLYHLFEGKHKDGFPVVLGHEGAGIVESVGPGVTEFQPGEKVIPLFISQCGEC
RFCQSPKTNQCVKGWANESPDMSPKETRFTCKGRKVLFQFLGSTFSQYTvvNQIAVAKIDPSAPLDTVCLLGCVXESVPKLVSEYMSKKIKVDEFVTHNLSF
THRMPLESVNDAIDLMKHGKCIRTVLSL

>d1keva1_b.35.1.2 (A:1-150,A:315-351) Bacterial secondary alcohol dehydrogenase {Clostridium beijerinckii}

MKGFAMILGINKLGWIEKERPVAGSYDAIVRPLAVSPCTSIDIHTVFEGALGDRKNMILGHEAVGEVVEVGSEVKDFKPGDRVIVPCPTPDWRSLEVQ
AGFQQHSNGMLAGWKFSNFKDGVFGFYFHVNADMNLAIPKDMPLENAVMITDXDLSKLVTYHGFDHIEEALLMKDKPKDLIKAVVIL
>d1ykfa1 b.35.1.2 (A:1-150,A:315-352) Bacterial secondary alcohol dehydrogenase {Thermoanaerobacter brockii}
MKGFAMILSIGKVWIEKEKPAPGPFDAIVRPLAVAPCTSIDIHTVFEGAIGERHNMLGHEAVGEVVEVGSEVKDFKPGDRVVAITPDWRTSEVQ
RGYHQHSGGMLAGWKFSNVKDGVFGEFFHVNDADMNLALHPKEIPLEAAVMIPDXDPSKLVTYFRGFDNIEKAFMLMKDKPKDLIKPVVILA
>d1e3ja1 b.35.1.2 (A:4-150,A:314-351) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}
DNLSAVLYKQNDLRLEQRPIPEKEDEVLQQMAYVGICGSDVHYYEHGRIADFIVKDPMVIGHASGTVVKGKVNHLKGDRVAVEPGVPCRC
QFCKEGKYNLCPDLTCATPPDDGNLARYYVHAADFCHKLDPDNVSLEEGALXNVKQLVTHSKLEQTVDafeAARKKADNTIKVMISCRQ
>d1qora1 b.35.1.2 (A:2-135,A:266-327) Quinone oxidoreductase {Escherichia coli}
ATRIEFHKHGGPEVLQAVEFTP PADPAENEI QVENKAIGINFIDTYIRSLYPPPSLPSGLTEAGIVSKVGSVVKHIKAGDRVVAQSLGAYSSVHNII
ADKAAILPAAISFEQAAASFLLKGLTVYYLLRKTXLQGYITTREELTEASNELFLSIASGVIVKVDVAEQQQKYLKDAQRAHEILES RATQGSSLIP
>d1uuu1_b.35.2.1 (A:) Sac Y {Bacillus subtilis}
MKIKRILNHNAIVVQDKNEEKILLGAGIAFNKKNDIVDPSKIEKTFIRKDTDPY
>d1pdr__ b.36.1.1 (-) Discs large protein homolog {Human (Homo sapiens)}
ITREPRKVVLHRGSTGLFNIVGGEDGEGIFISFILAGGPADLSGELRKGDRIISVNSVDLRAASHEQAAAALKNAGQAVTIVAQYRPEEYSRQHA
>d1kwa1_b.36.1.1 (A:) Cask/Lin-2 {Human (Homo sapiens)}
RSRLVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMIHRQGTLHVGEIREINGISVANQTV EQLQKMLREMRSITFKIVPSYREF
>d1be9a_b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}
FLGEDIPREPRRIIH RGSTGLGFNIIGGEDGEGIFISFILAGGPADLSGELRKGDQILSNGVDLRNASHEQAAIALKNAGQTVIIAQYKPEEYSRFEA
NSRVNSSGRIVTN
>d1qlca_b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}
AEKVMIEIKLIKGPGLFSIAGGGVGNQHPIGDNSIYVTKIIEGGAAHKDGRQIQGDKILAVNSVGLVEDVMHEDAVAALKNTYDVYLVAKPSNA
>d1qava_b.36.1.1 (A:) Syntrophin {Mouse (Mus musculus)}
GSLQRRRVTVRKADAGGLGISKGGRENKMPILISKFKGLAADQTEALFGDAILSVNGEDLSSATHDEAVQALKTGKEVVLEVVKYM
>d1b8qa_b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}
GSHMIEPNVISVRLFKRKVGGLGFLVKERVKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRPLVDSLDSALEVLRGIASETHVVLILRGPEGFTTHLE
TTFTGDGTPKTIRVTQPLGPPTKAV
>d1qaua_b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}
NVISVRLFKRKVGGLGFLVKERVKPPVIISDLIRGGAAEQSGLIQAGDIILAVNDRPLVDSLDSALEVLRGIASETHVVLILRGPEGFTTHLETTFTGDG
TPKTIRVTQP
>d3pdza_b.36.1.1 (A:) Phosphatase hPTP1e {Human (Homo sapiens)}
PKPGDIFEVELAKNDNSLGLSITGGVNTSRHGGIYVKAVIPQGAAESDGRHIKGDRVLAVNGSLEGATHKQAVETLNTGQVHVLLKGQSPT
>d1g9oa_b.36.1.1 (A:) Na+/H+ exchanger regulatory factor, NHERF {Human (Homo sapiens)}
RMLPRLCCKGPNGYGFHLHGEKGKLGQYIRLVEPGSPAECAGAGLDRIVEVNGENVEKETHQQVVSIRALA NAVRLLVDPETDEQL
>d1ihja_b.36.1.1 (A:) Inad {Fruit fly (Drosophila melanogaster)}
GELIHMVTLDKGKKSFGICIVRGEVKDPSNTKTTGIFIKGIVPDSPAHLCGRLKVGDRILSNGKDVRNSTEQAVIDLIKEADFKIELEIQT
>d1fc6a3_b.36.1.3 (A:157-248) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}
AGSVTGVGLEITYDGGSGKDVVLT PAPGGPAEKAGARAGDVIVTDGTAVKGMISLYDVS DLLQGEADSQVEVVLHAPGAPSNTRTLQLTRQ
>d1k32a1_b.36.1.3 (A:763-853) Tricorn protease {Archaeon Thermoplasma acidophilum}
GRIACDFKLDGDHYVVAKAYGDYSNEGEKSPIFYGIDPTGYLIEDIDGETVGAGSNIYRLSEKAGTSARI LSGKGGDKRDLMIDILD
>d1i16__ b.36.1.2 (-) Interleukin 16 {Human (Homo sapiens)}
MPDLSNSSTDSEAASASAASDVSVESTAEATVCTVTLKMSAGLGSLEGGKGS LHGDKPLTINRIFGAASEQSETVQPGDEILQLGGTAMQGLTRFEA
WNIIKALPDGPVTIVIRRKSLSKETTAAGDS
>d1g3p_1 b.37.1.1 (1-65) N-terminal domains of the minor coat protein g3p {Bacteriophage M13}

AETVESCLAKSHTENSFTNVVKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIP
>d1g3p_2 b.37.1.1 (91-217) N-terminal domains of the minor coat protein g3p {Bacteriophage M13}
EYGDTPIPGYTYINPLDGYPPGTEQNPANPNSLEESQPLNTFMQNRRNRQGALTIVTGTQGTDPVKTYQYTPVSSKAMYDAYWNGKF
RDCAFHSGFNEDIFVCEYQQQSSDLPQPPVNA
>d1fgp__ b.37.1.1 (-) N-terminal domains of the minor coat protein g3p {Bacteriophage fd}
ETVESCLAKPHTENSFTNVVKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIPENAAAH
>d1b34a_ b.38.1.1 (A:) D1 core SNRNP protein {Human (Homo sapiens)}
KLVRFLMKLSHETVTIELKNGTQVHGTTGVDVSMNTHLKAVKMTLNREPVLQLETLSIRGNNIRYFILPDSLPLDTLLV
>d1b34b_ b.38.1.1 (B:) D2 core SNRNP protein {Human (Homo sapiens)}
TGPLSVLTQSVKNNTQVLINCRNNKKLLGRVKAFCRHCNMVLENVKEMWTEVPKGKGKKSKPVNKDRYISKMFLRGDSIVVLRNPLIAGK
>d1d3ba_ b.38.1.1 (A:) D3 core SNRNP protein {Human (Homo sapiens)}
GVPIKVLHEAEGHIVTCNTGEVYRGKLLIEADNMNCQMSNITVYRDGRVAQLEQVYIRGCKIRFLILPD
>d1d3bb_ b.38.1.1 (B:) B core SNRNP protein {Human (Homo sapiens)}
SKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFRKIKPKNSKQAEREERKRVGLVLLRGENLVSMTVEGPPP
>d1d3bl_ b.38.1.1 (L:) B core SNRNP protein {Human (Homo sapiens)}
TVGKSSKMLQHIDYRMRCILQDGRIFIGTFKAFDKHMNLILCDCDEFRKIKPKNSKQAEREERKRVGLVLLRGENLVSMTVEGPPPDTG
>d1i81a_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium thermoautotrophicum}
RVNVQRPLDALGNSLNSPVIKKLGDRFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGDNIVYISP
>d1jria_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium thermoautotrophicum}
QRPLDALGNSLNSPVIKKLGDRFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGDNIVYISRGK
>d1i8fa_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Pyrobaculum aerophilum}
ATLGATLQDSIGKQVLVKLRLDSHEIRGILRSFDQHVNLLEDAEEIIDGNVYKRTGMVVRGENVLFISPVP
>d14k1_ b.38.1.1 (1:) Archaeal homoheptameric Sm protein {Archaeon Archaeoglobus fulgidus}
PPRPLDVLNRLSKSPVIVRLKGGRFRGTLGDIHMNLVLLDAEEIQNGEVVRKVGSVIRGDTVVFSPA
>d1h5pa_ b.99.1.1 (A:) Nuclear autoantigen Sp100b {Human (Homo sapiens)}
MDENINFQSELPVTCGEVKGTLYKERFKQGTSKKCIQSEDKKWFTPREFEIGDRGASKNWKLSIRC GGTLKVL MENKFLPEPPSTRKKVTIK
>d1whi__ b.39.1.1 (-) Ribosomal protein L14 {Bacillus stearothermophilus}
MIQQESRLKVADNSGAREVLVIKVLGGSGRRYANIGDVVVATVKDATPGGVVKKGQVVKA VVVRTKRGVRRPDGSYRFDENACVIIRDDKS PRGTR
IFGPVARELRDKDFMKIISLAPEVI
>d1jj2j_ b.39.1.1 (J:) Ribosomal protein L14 {Archaeon Haloarcula marismortui}
MEALGADVTQGLEKGSLITCADNTGARELKVISVGYSGTKRHPKAGLGDKITVSKGTPEMRRQVLEAVVVRQRKPIRRDPGTRVKFEDNAAVI
VDENEDPRGTELKGPIAREVAQRFGSVASAATMIV
>d1ez6a_ b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}
LHKEPATLIKAIDGDTVVKLMYKGQPMVFRLLVDPETKHPKKGVEKYGPEAAAFTKKMVENAKKIEVEFDKGQRTDKYGRGLAYIYADGKMVNEALV
RQGLAKVAYVYKGNNTHEQLLRKAEAQAKKEKLNIWS
>d1joqa_ b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}
ATSTKKLHKEPATLIKAIDGDTVVKLMYKGQPMTFRLLLVDTPETKHPKKGVEKYGPEASAFKKMVENAKKIEVEFDKGQRTDKYGRGLAYIYADGKM
VNEALVRQGLAKVAYVYKPNNTHEQLLRKSEAQAKKEKLNIWS
>d1sty__ b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}
KLHKEPATLIKAIDGDTVVKLMYKGQPMTFRLLLVDTPETKHPKKGVEKYGPEASAFKKMVENAKKIEVEFDKGQRTDKYGRGLAYIYADGKM
LVRQGLAKVAYVYKPNNTHEQHLRGKSEAQAKKEKLNIWS
>d2sob__ b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}
ATSTKKLHKEPATLIKAIDGDTVVKLMYKGQPMTFRLLLVDTPETKHPKKGVEKYGPEASAFKKMLENAKKIEVEFDKGQRTDKYGRV LAYIYADGKM
VNEAL

>d1djrd_b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}
APQTITELCSEYRNTQIYTINDKILSYTESMAGKREMVIIIFKSGETFQVEVPGSQHIDSQQKAIERMKDTRITYLTETKIDKLCVWNNTPNSIAISM
KN

>d1ltd_b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}
APQSITELCSEYHNTQIYTINDKILSYTESMAGKREMVIIIFKSGATFQVEVPGSQHIDSQQKAIERMKDTRITYLTETKIDKLCVWNNTPNSIAISM
EKLYAGA

>d1tiid_b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IIB}
GASQFFKDNCNRTTASLVEGVELKYISDINNNTDGMYVVSSTGGVWRISRAKDYPDNVMTAEMRKIAMAAVLSGMRVNMCASPSPNVIWAI
ELEA

>d3chbd_b.40.2.1 (D:) Cholera toxin {Vibrio cholerae}
TPQNITDLCAEYHNTQIHTLNDKIFSITESLAGKREMAIIIFKNGATFQVEVPGSQHIDSQQKAIERMKDTRIAYLTEAKVEKLCVWNNTPRAIAIS
MAN

>d1c4qa_b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}
TPDCVTGKVEYTKYNDDDTFTVKVGDKELATNRANLQLSLLSAQITGMTVTIKTNACHNGGFSEVIFR

>d2bosa_b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}
ADCAKGKIEFSKYNEDENTFTVKVSGREYWTRNLQPLQSAQLTGMTVTIISNTCSSGSGFAEVQFN

>d1prtb1_b.40.2.1 (B:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain {Bordetella pertussis}
TTRNTGQPATDHYYSNVTARLLSSTSRLCAVFVRSGQPVIGACTSPYDGKYWSMYSRLRKMLYLIYVAGISVRVHSKEEQYYDYEDATFETYALTGI
SICNPNGSSLC

>d1prtc1_b.40.2.1 (C:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain {Bordetella pertussis}
TIYKTGQPAADHYYSKVTATRLLASTNSRLCAVFVRDGQSVIGACASPYEGRYRDMYDALRRLYMIYMSGЛАVRVHSKEEQYYDYEDATFQTYALT
GISLCNPAASIC

>d1prtd_b.40.2.1 (D:) Pertussis toxin S4 subunit {Bordetella pertussis}
DPVYVLVTKTNMVVTSVAMPKYEVTPTRMLVCGIAAKLGAAASSPDAHVPCFGKDLKRPGSSPMEMLRAVFMQRPLRMFLGPQLTFEGKPAL
ELIRMVECSGKQDCP

>d1prtf_b.40.2.1 (F:) Pertussis toxin S5 subunit {Bordetella pertussis}
LPTHLYKNFTVQELALKLKGKNQEFCLTAFMSGRSLVRACLSAGHEHTWFDTMLGFAISAYALKSRIALTVEDSPYPTGPDLLELQICPLNGYCE

>d1esfa1_b.40.2.2 (A:1-120) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}
SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEAKTENKESHDQFLQHTILFKGFTDHSWYNDLLDFDSKDIVDKYKGKKVDLYGAYGYQCAGG
TPNKTACMYGGVTLHDNNRNL

>d1i4pa1_b.40.2.2 (A:1-120) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}
ESQPDPTPDELHKSSFTGMGNMKLYDDHYVSATKMSVDKFALHDLYNISDKKLKNYDKVKTELLNEDLAKKYKDEVVDVYGSNYYVCYFSS
KDNVGVKTGGKTCMYGGITKHEG

>d3tss_1_b.40.2.2 (5-93) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}
NIKDLLDWYSSGSDTFTNSEVLDNSLGSMRIKNTDGSISLIIFPSPYYSPAFTKGEKVDLNTKRIKKSQHTSEGTVIHFQISGVNTNEK

>d1sebd1_b.40.2.2 (D:2-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLISIKDTYDNVRVEFKNKDLADKYKDVKYVDFGANYYYQCYFSKKTCM
YGGVTEH

>d3seb_1_b.40.2.2 (1-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLISIKDTKLGNYDNVRVEFKNKDLADKYKDVKYVDFGANYYYQCYFSKK
TNDINSHQTDKRKTCMYGGVTEH

>d1jckb1_b.40.2.2 (B:1-121) Staphylococcal enterotoxin C3, SEC3 {Staphylococcus aureus}
ESQPDPMPPDDLHSSEFTGTMGNMKLYDDHYVSATKVKSVDKFALHDLYNINDKLNNDKVKTELLNEDLANKYKDEVVDVYGSNYYVCYFSS
SKDNVGVKTSGKTCMYGGITKHEGN

>d1enfa1 b.40.2.2 (A:2-101) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}
DLHDKSELTDLALANAYGQYNHPFIKENIKSDEISGEKDLIFRNQGDSGNDLRVKFATADLAQKFKKNVNDIYASFYKCEKISENISECLYGGTTLNS

>d1an8_1 b.40.2.2 (3-95) Streptococcal superantigen Spe-C {Streptococcus pyogenes}
KKDISNVKS DLLAYITPYDYKDCRVNFSTTHLNIDTQKYRGKDYYISSEMSYEASQKFKRDDHVDFGLFYILNSHTGEIYGGITPAQN

>d1et9a1 b.40.2.2 (A:1-95) Streptococcal superantigen Spe-H {Streptococcus pyogenes}
NSYNTTNRHNL ELSLYKHDSNLIEADSIKNSPDIVTSHMLKYSVKDKNL SVFFEKDWISQEFDKEVDIYALSAQEVC ECPGKRYEA FGGITLNS

>d1eu3a1 b.40.2.2 (A:2A-96) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}
GLEVDNNSSLRNIYSTIVYEYSDIVDFKTSHNLVTKKLDVRDARDFFINSEMDEYAANDFKTDKIAVFSVPFDWNYLSKGKV TAYTYGGITPYQK

>d1bxta1 b.40.2.2 (A:1-119) Streptococcal superantigen SSA {Streptococcus pyogenes}
SSQPDPTPEQLNKSSQFTGVMGNLRCLYDNHFVEGTNRSTGQLLHQHDLIFPIKDLKLKNYDSVKTEFNSKDLATKYKNKDVDIFGSNYYNCYYSEG
NSCKNAKKT C MYGGVTEHHRN

>d1fnua1 b.40.2.2 (A:1-107) Streptococcal pyrogenic exotoxin A1 {Streptococcus pyogenes}
QQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHE NVKSV DQLL SHDLIY NVSGP NYDKLKTELKNQEMATLFKDKNVDIYGV EYYHLCYL CENAERSAC
IYGGVTNHE

>d1d2ba_ b.40.3.1 (A:) TIMP-1 {Human (Homo sapiens)}
CTCVP PHPQTAFCNSDLVIRAKFVGTP EVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFV YTPAMESVCGYFHRSHNRSEEFIAGKLQDG LLHITT
CSFVAPWN SLSLAQR RGFTK TYTVGCEE

>d1ueab_ b.40.3.1 (B:) TIMP-1 {Human (Homo sapiens)}
CTCVP PHPQTAFCNSDLVIRAKFVGTP EVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFV YTPAMESVCGYFHRSHNRSEEFIAGKLQDG LLHITT
SFVAPWN SLSLAQR RGFTK TYTVGCEE CTVP CLSIPCKL QSGTHCLWT DQLL QGSEKG FQSRHLA CLPREP GLCT WQLRS

>d1br9__ b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}
CSCSPVHPQQAFCNADVIRAKAVSEKEV DSGNDIYGNPIKRIQYEIKQIKMF KGPEK DIFEIY TAPSSA VCGVSLDVGKKEYLIAGKAEGDGKMHIT
LCD FIVPWDTLSTTQKKS LN HRYQM GCECK ITRCP MIPC YISSP D ECLWMDWVTEK NINGHQAKFFACIKRSDGSCAWYRGAA

>d2tmp__ b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}
CSCSPVHPQQAFCNADVIRAKAVSEKEV DSGNDIYGNPIKRIQYEIKQIKMF KGPEK DIFEIY TAPSSA VCGVSLDVGKKEYLIAGKAEGDGKMHIT
CDFI VPWDTLSTTQKKS LN HRYQM GCECK ITRCP MIPC YISSP D ECLWMDWVTEK NINGHQAKFFACIKRSDGSCAWYRGAA APP

>d1bqqt_ b.40.3.1 (T:) TIMP-2 {Cow (Bos taurus)}
CSCSPVHPQQAFCNADIVIRAKAVNKKEV DSGNDIYGNPIKRIQYEIKQIKMF KGPDQ DIFEIY TAPAA VCGVSL DIGG KKEYLIAGKAEGNGNMHIT
LCD FIVPWDTLSATQKKS LN HRYQM GCECK ITRCP MIPC YISSP D ECLWMDWVTEK NINGHQAKFFACIKRSDGSCAWYRGAA APP

>d1jb3a_ b.40.3.2 (A:) The laminin-binding domain of agrin {Chicken (Gallus gallus)}
ELQRREEEANVLTGTEEIMNVDPVHHTYSCKVRVWRYLGKDITVTHEI LDGGN KV VIGGFGDPLICDNQVSTGDTRIFFVN PAPQYMWPAHRN
ELMLNSSLMRITLRN LEEVEHCV EHRKLLA

>d1k28a1 b.40.8.1 (A:6-129) Tail-associated lysozyme gp5, N-terminal domain {Bacteriophage T4}
NNLNWFVG VVEDRMDPLKLG RVR VRVGLHPPQRAQGDV MGIPTEKLPWMSIQPITSAMSGIGGSVTGP VEGTRV GHFLDKWKTNGIVLG
TYGGIVREKPNRLEGFS DPTGQYP RRLGNDT

>d1eova1 b.40.4.1 (A:71-204) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}
AKDNYGKLPLIQS RDSDRTGQK RVKFV DLDEAKD SDKEVLFRARVHNTRQQGATL AFLTRQQ ASL IQGLV KANKE GTISK NMV KWAGSLNLESIVL
VRGIVKKVDEPIK SATVQ NLIEI HITKI YSETPEAL

>d1b8aa1 b.40.4.1 (A:1-103) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus kodakaraensis}
MYRTHYSSEITEELNGQKV VAGWW EVKDLGGIKFLWIRD RGIV QITAPKKV DP EFLK LIPK LRSED VVA VEGVV NFTP KA KLGF EILPEKIVVLN
RAET

>d1c0aa1 b.40.4.1 (A:1-106) Aspartyl-tRNA synthetase (AspRS) {Escherichia coli}
MRTEYCGQLRLSHVGQQVTLCGWVNRRRLGSLIFIDMRDREGIVQVFDPDRADALKLASERNEFCIQVTGTVRARDEKNINRD MATGEIEVLA
SSLTIINRAD

>d1g51a1 b.40.4.1 (A:1-104) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}
MRRTHYAGSLRETHVGEEVVLEGWVNRRDLGGIFLDLDRREGLVQLVAHPASPAYATAERVRPEWWVRAKGLVRLRPEPNPRLATGRVEVELSAL
EVLAEEK

>d1bbua1 b.40.4.1 (A:11-154) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}
VVDLNNEKLTRREKLNRREQGIAFPNDFRRDHSDQLHAEFDGKENEEALEALNIEAVAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDLPEG
VYNEQFKWDLGDLGAKGKLFKTGTGELSIHCTELRLLTAKRPLPD

>d1krs__ b.40.4.1 (-) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}
FRRDHTSDQLHAEFDGKENEEALEALNIEAVAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDLPEGVYNEQFKWDLGDLGAKGKLFKTGTGE
LSIHCTELRLLTKA

>d1e1oa1 b.40.4.1 (A:11-153) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysU}
AIDFNDELNRNREKLAALRQQGVAFPNDFRRDHSDQLHEEFDAKDNQELESNLIEVSAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDLPEG
VYNDQFKWDLGDIIGARTLFTQTGELSIHCTELRLLTAKRPLP

>d1gm5a2 b.40.4.9 (A:106-285) RecG "wedge" domain {Thermotoga maritima}
CSGEEVDSLTDIQtyAKGVGPNRKKKKLGIELRDLLEFFPRDYEDRRKIFKLNDLLPGEKVTQGKIVSVETKKFQNMNILTAVLSDGLVHVPLKWFN
QDYLQTYLQLTGKEVFTGTVKSNAUTGQYIEHNAEVTPKEGEYVRRILPIYRLTSGISQKQMRKIFEENIPSLCCSLK

>d1cuk_3 b.40.4.2 (1-64) DNA helicase RuvA subunit, N-terminal domain {Escherichia coli}
MIGRLRGIIIEKQPPLVIEVGGVGYEVHMPMTCFYELPEAGQEAIVFTHFVVREDAQLLYGFN

>d1bvsa3 b.40.4.2 (A:1-63) DNA helicase RuvA subunit, N-terminal domain {Mycobacterium leprae}
MIFSVRGEVLEVALDHAVIEAAGIGYRVNATPSALATLNQGSQARLTAMVVREDSMTLYGFS

>d3ulla_b.40.4.3 (A:) ssDNA-binding protein {Human (Homo sapiens), mitochondria}
LERSLRVHLLGRVGQDPVLRQVEGKNPVTIFSLATNEMWRSGDSEVYQLGDVSQKTTWHRSVFRPGLRDVAYQVKKGSRIVLEGKIDYGEYMD
KNNVRRQATTIADNIIFL

>d1kawa_b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}
RGVNKVILVGNLNGDPEVRYMPNGGAVANITLATSESWRDKATGEMKEQTEWHRVLFGLAEVASEYLRKGSQVYIEGQLRTRKWTDSQGQDR
YTTEVVNVGGTMQML

>d1qvca_b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}
ASRGVNKVILVGNLNGDPEVRYMPNGGAVANITLATSESWRDKATGEMKEQTEWHRVLFGLAEVASEYLRKGSQVYIEGQLRTRKWTDSQGQ
DRYTTTEVVNVGGTMQMLGGRQGGGAPAGGNIGGGQPQGGWGQPQQPQGGN

>d1ewia_b.40.4.3 (A:) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}
MVGQLSEGAIAIMQKGDTNIKPILOVINIRPITTGNSPRYRLLMSDGLNTLSSFMLATQLNPLVEEQLSSNCVCQIHRFIVNTLKDGRRVVILMEL
EVLKSAEAVGVKIGN

>d1fgua1 b.40.4.3 (A:181-298) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}
MSKVVPIASLTPYQSKWTICARVTNKSQIRTWSNSRGEGLFSLELVDESGEIRATAFNEQVDKFFPLIEVNKVYYFSKGLKIANQFTA
VKNDYEMTFNNETSVMPCEDDHHLPTV

>d1fgua2 b.40.4.3 (A:299-426) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}
QFDFTGIDDLENKSKDLSVIIIGICKSYEDATKITVRSNNREVAKRNIIYLMDTSGKVVATLWGEDADKFDGSRQPVLAIKGARVSDFGGRSLSVLSSST
IIANPDIPEAKLRGWFDAEGQALDGVS

>d1quqa_b.40.4.3 (A:) Replication protein A 32 KDa subunit (RPA32) fragment {Human (Homo sapiens)}
HIVPCTISQLSATLVDEVFRIGNVEISQVTIVGIIRHAEKAPTNIVYKIDDMTAAPMDVRQWVDTDDTSSENTVVPPETYVKVAGHLRSFQNKKSLVA
FKIMPLEDMNEFTTHILEVINAHMVLSK

>d1quqb_b.40.4.3 (B:) Replication protein A 14 KDa (RPA14) subunit {Human (Homo sapiens)}
DMMDLPRSRINAGMLAQFIDKPVCVGRLEKIHPTGKMFILSDGEGKNGTIELMEPLDEEISGIVEVVGRVTAKATILCTS
YVQFKEDSHPFDLGLYNEAVKIIHDFPQFYPLG

>d1jb7a1 b.40.4.3 (A:36-204) Telomere end binding protein alpha subunit {Oxytricha nova}

YEYVELAKASLTSAPQPHFYAVVIDATFPYKTNQERYICSLKIVDPTLYLKQQKGAGDASDYATLVLAKRFEDLPIIHRAGDIIRVHRATLRLYNGQRQFN
ANVFYSSSWALFSTDKRSVTQEINNQDAVSDTTPFSKSHATIEKNEISILQNLRKWANQYFSSY

>d1jb7a2 b.40.4.3 (A:205-328) Telomere end binding protein alpha subunit {Oxytricha nova}
VISSDMYTALNKAQAQKGDFDVAKILQVHELDEYTNELKLKDASGQVFYTLSKLKFPHVRTGEVVRIRSATYDETSTQKKVLILSHYSNIITFIQSSKL
AKELRAKIQDDHSVEASLKKNV

>d1jb7a3 b.40.4.3 (A:329-495) Telomere end binding protein alpha subunit {Oxytricha nova}
SLNAVVLTEDKKHAALPSTSLLQDLFHADSDKELQAQDTFRQFYVTKIEPSDVKEWWKGYDRTKKSSLKGASGKGDNIFQVQFLVKDASTQLN
NNTYRVLVLTQDGLGANFFNVKADNLHKNADARKKLEDSAEELLTKFNSYVDAVVERRNGFYLIKDTKLIV

>d1k8ga2 b.40.4.3 (A:205-315) Telomere end binding protein alpha subunit {Oxytricha nova}
VISSDMYTALNKAQAQKGDFDVAKILQVHELDEYTNELKLKDASGQVFYTLSKLKFPHVRTGEVVRIRSATYDETSTQKKVLILSHYSNIITFIQSSKL
AKELRAKIQD

>d1jb7b_ b.40.4.3 (B:) Core domain of telomere end binding protein beta subunit {Oxytricha nova}
QQQSAFKQLYTELFNNEGDFSKVSSNLKKPLKCYVKESYPHFLVTDGYFFVAPYFTKEAVNEFHAKFPVNIVDLTDKVIVINNSLELRRVNSAEVFT
SYANLEARLIVHSFKPNLQERLNPTRYPVNLFRDEFKTTIQHFRHTALQAAINKTVKGDNLVDISKVADAAGKKGVDAIGIVKASASKGDEFSDFSK
EGNTATLKIADIFVQEKG

>d1jjcb3 b.40.4.4 (B:39-151) Domain B2 of PheRS-beta, PheT {Thermus thermophilus (Thermus aquaticus)}
FPIPRGVVFARVLEAHPIPGTRLKRLVLDAGRTEVVSGAENARKGIGVALALPGTELPGLGQKVGERVIQGVRSGMALSRELGVEYGGGLLEFP
EDALPPGTPLSEAWP

>d1f10a_ b.40.4.4 (A:) EMAP II {Human (Homo sapiens)}
IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVGVLNVHVPLEQMQRNMVILLCNLPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVP
GDRITFDAFPGEPDKELPKKIWEQIQPDLHTNDECVATYKGVPFEVKGKGVCRAQTMSNSGIKL

>d1gd7a_ b.40.4.4 (A:) CsaA {Thermus thermophilus}
MTPLEAFQILDLRVGRVLRAEPHEKARKPSYKLWVDLGPLGVKQSSAQITELYRPEDLVGRLLVCAVNIGAKRVAGFLSEVLVLGPDEAGRVVLLAP
DREVPLGGKVF

>d1mjc__ b.40.4.5 (-) Major cold shock protein {Escherichia coli}
SGKMTGIVKWFNADKGFGFITPDDGSKDVVFHFSAIQNDGYKSLDEGQKVSTIESGAKGPAAGNVTL

>d1csp__ b.40.4.5 (-) Major cold shock protein {Bacillus subtilis}
MLEGKVKWFNNEKGFGIEVEGGDDVFVHFSAIQGEGFKTLEEGQAVSFEIVEGNRGPQAANVTKEA

>d1c9oa_ b.40.4.5 (A:) Major cold shock protein {Bacillus caldolyticus}
MQRGKVKWFNNEKGFGIEVEGGSDVFVHFSAIQGEGFKTLEEGQEVSEIVQGNRGPQAANVVKL

>d1g6pa_ b.40.4.5 (A:) Major cold shock protein {Thermotoga maritima}
MRGKVKWFDSKKGYGFITKDEGGDVFWHSAIMEGFKTLKEGQVVEFIQEGKKGPQAAHVKVVE

>d1h95a_ b.40.4.5 (A:) Y-box protein 1 cold shock domain (YB1-CSD) {Human (Homo sapiens)}
MKKVIATKVLGTVKWFNRVNGYGFINRNRTDKEDVFVHQTAIKNNPRKYLRSVGVDGETVEFDVVEGEKGAEAANVTGPG

>d1sro__ b.40.4.5 (-) S1 RNA-binding domain of polyribonucleotide phosphorylase, PNPase {Escherichia coli}
AEIEVGRVYTGKVTRIVDFGAFVAIGGGKEGLVHISQIAKRVKVTDLQMGQEVPKVLEVDRQGRIRLSIKEA

>d1e3pa2 b.40.4.5 (A:656-717) S1 RNA-binding domain of polyribonucleotide phosphorylase, PNPase {Streptomyces antibioticus}
GSVVKTTFGAFVSLLPGKDGLLHISQIRKLAGGKRVENVEDVLGVGQKVQVEIAEIDSRKG

>d1hh2p1 b.40.4.5 (P:127-198) S1 domain of NusA {Thermotoga maritima}
FEKYSELKGTVTTAEIRVMGEWADIRIGKLETRLPKKEWIPGEEIKAGDLVVKVYIIDVVKTTKGPKILVSR

>d1k0ra1 b.40.4.5 (A:108-183) S1 domain of NusA {Mycobacterium tuberculosis}
STREGEIVAGVIQRDSRANARGLVVVRIGHTETKASEGVIPAAEQVPGESYEHGNRLRCYVVGVTRGAREPLITLSR

>d1go3e_ b.40.4.5 (E:) RNA polymerase II subunit RBP4 (RpoE) {Archaeon Methanococcus jannaschii}
MYKILEIADVVKVPPEFGKDLKETVKKILMEKYEGRLDKDVGFLSIVDVKDIGEGKVVHGDGSAYHPVVFETLVYIPEMYELIEGEVVVDVEFGSFV

RLGPLDGLIHVSQIMDDYVSYDPKREAIIGKETGKVLEIGDYVRARIVASLKAERKRGSKIALTMRQPYLGKLEWIEEKAKKQ
>d1ah9__ b.40.4.5 (-) Translational initiation factor 1, IF1 {Escherichia coli}
AKEDNIEMQGTLETLPNTMFRVELENGTHVVTAHISGKMRKNYIRILTGDVKTVELTPYDLSKGRIVFRS
>d1hr0w_ b.40.4.5 (W:) Translational initiation factor 1, IF1 {Escherichia coli}
AKEKDTIRTEGVVTEALPNATFRVKLDGSGPEILAYISGKMRMHYIRLPGDRVVEITPYDPTRGRIVYRK
>d1jt8a_ b.40.4.5 (A:) Archaeal initiation factor-1a, aIF1a {Archaeon Methanococcus jannaschii}
MAEQQQEQQQIRVIRPRKEENEILGIIEQMLGASRVRVRCLDGKTRLGRIPGRLKRNRIWVREGDVIVKPWEVQGDQKCDIIWRYTKTQVEWLKRKG
YLDELL
>d1d7qa_ b.40.4.5 (A:) Translation initiation factor-1a, eIF1a {Human (Homo sapiens)}
PKNKGKGGKNRRGKNENESEKRELVFKEGQYEAQVIKMLGNGRLEAMCFDGVKRLCHIRGKLRKKWINTSDIILVGLRDYQDNKADVLVYNA
DEARSLKAYGELPEHAKINETDTFGPGDDDEIQFDDIGDDDEDIDDI
>d1a62_2 b.40.4.5 (48-125) Rho termination factor, RNA-binding domain {Escherichia coli}
DIFGDGVLEILQDGFGFLRSADSSYLAGPDDIYVSPSQIRRNLRTGDTISGKIRPPKEGERYFALLKVNEVNFDKPE
>d2eifa2 b.40.4.5 (A:74-132) C-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Methanococcus jannaschii}
IDRRKGQVLAIMGDMVQIMDLQTYTELLEPIPEGIEGLEPGGEVEYIEAVGQQYKITRVI
>d1kbk_2 b.40.4.5 (75-139) C-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Pyrobaculum aerophilum}
IEKFTAQILSVSGDVQLMDMDRDYKTIEVPMKYVEEEAKGRLAPGAEVEVWQILDYKIIRVK
>d1rl2a2 b.40.4.5 (A:60-125) N-terminal domain of ribosomal protein L2 {Bacillus stearothermophilus}
QYRIIDFKRDKDGIPGRVATIEDPNRSANIALINYADGEKRYIIAPKNLKVGMEIMSGPDADI
>d1jj2a2 b.40.4.5 (A:1-90) N-terminal domain of ribosomal protein L2 {Archaeon Haloarcula marismortui}
GRRIQGQRGRGTSTFRAPSHRYKADLEHRKVEDGDIVAGTVVDIEHDPARSAPVAAVEFEDGDRRLILAPEGVGVGDELQVGVDAEIAP
>d1fjgl_ b.40.4.5 (L:) Ribosomal protein S12 {Thermus thermophilus}
PTINQLVRKGREKVRKSKVPALKGAPFRGVCTVVRTPKPNSALRKVAKVRLTSGYEVTAIPGEGHNLQEHSVVLIRGGRVKDLPGVRYHIVRG
VYDAAGVKDRKKSRSKYGTKKPEAA
>d1fjgq_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}
PKKVLTVVVSDKMQKTVLVERQFPHPLYGKVIKRSKKYLAHDPEEKYKLGDVVEIIESRPISKRKFRVRLVESGRMDLVEKYLIRRQNYQSLSKR
GGKA
>d1i94q_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}
PKKVLTVVVSDKMQKTVLVERQFPHPLYGKVIKRSKKYLAHDPEERYKVGDVVEIIEARPISKRKFRVRLVEEGRLDLVEKYLVRQNYASLSKR
GGKA
>d1rip__ b.40.4.5 (-) Ribosomal protein S17 {Bacillus stearothermophilus}
QRKVYVGRVVSDFKMDKTITVLTETYKKHPLYGKRVKYSKKYKAHDEHNEAKVGDIVKIMETRPLSATKRFRLVEIVEKAVR
>d1ckma1 b.40.4.6 (A:239-327) RNA guanylyltransferase (mRNA capping enzyme) {Chlorella virus, PBCV-1}
THHTIDFIIMSEDGTIGIFDPNLRKNVPGKLDGYYNKGSIVECGFADGTWKYIQGRSDKNQANDRLTYEKTLLNIEENITIDELLDLF
>d1a0i_1 b.40.4.6 (241-349) ATP-dependent DNA ligase {Bacteriophage T7}
PENEADGIQGLVWGTKGLANEKGKVIGFEVLLESGRLVNATNISRALMDEFETETVKEATLSQWGFFSPYIGDNDACTINPYDGWACQISYMEETPD
GSLRHPSFVMFR
>d1fvia1 b.40.4.6 (A:190-293) ATP-dependent DNA ligase {Chlorella virus, PBCV-1}
FKDAEATIISMALFKNTNTKDKNFGYSKRSTHKSGKVEEDVMGSIEVDYDGVVFSIGTFDADQRDFWQNKESYIGKMKVFKYFEMGSKDCPR
FPVFIGIR
>d1dgsa2 b.40.4.6 (A:315-400) NAD+-dependent DNA ligase {Thermus filiformis}
AEEKETRLLDVFQVGRTRVTPGVLEPVFIEGSEVSRTLHNESYIEELDIRIGDWVLVHAGGVIPLEVRLVKERRTGKERPI
>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}
MNIQITFTDSVRQGTSAGNPYTFQEGFLHLEDKPHPLQCQFFVESVIPAGSYQVPRINVNNRPELAFDFKAMKRA

>d1gpc_b.40.4.7 (-) Gene 32 protein (gp32) core {Bacteriophage T4}
GFSSEDKGEWKLKLDNAGNGQAVIRFLPSKNDEQAPFAILVNHGFKKNGKWKYIETCSSTHGDYDSCPVCQYISKNDLYNTDNKEYSLVKRKTSYWAN
ILVVKDPAAPENEKGKVKYRFGKKIWKINAMIAVDVEMGETPVDTCPWEGANFVLKVQVSGFSNYDESKFLNQSAIPNIDDEFQKELFEQMV
DLSEMITSKDKFKSFEELNTKFGQVM

>d1je5a_b.40.4.7 (A:) gp2.5 {Bacteriophage T7}
MAKKIIFTSALGTAEPYAYIAKPDYGNERGFGNPRGVYKVDLTIPNKDPRCQRMVDEIVKCHEEAYAAVEEYANPPAVARGKKPLKPYEGDMPPF
DNGDGTTTFKFKCYASFQDKKTKETKHINLVVDSKGKKMEDVPIIGGGSKLKVKYSLVPYKWNTAVGASVQLQLESVMLVELATFGGGEDDWADAE
VEEN

>d1i50h_b.40.4.8 (H:) RNA polymerase subunit RBP8 {Baker's yeast (Saccharomyces cerevisiae)}
SNTLFDDIFQVSEVDPGRYNKVCRIEAATTQDQCKLTIDINVELFPVAAQDSLTVTISSLNLEDTPANDSSATRSWRPPQAGDRSLADDYDYVMY
TAYKFEEVSKDLIAVYYSGFGLLMRLEGNYRNLLNLQENAYLLIRR

>d1e9ga_b.40.5.1 (A:) Inorganic pyrophosphatase {Baker's yeast (Saccharomyces cerevisiae)}
TYTTRQIGAKNTLEYKVYIEKDGKPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEITKEETLNPIQDTKKGKLRFRNCFPHGYIHNYGAFPQT
WEDPNVSHPETKAVGDNDPIDVLEIGETIAYTGQVKQVKALGIMALLDEGETDWKVIIDINDPLAKLNDIEDVEKYFPGLLRTNEWFRIYKIPDG
KPENQFAFSGEAKNKKYALDIKETHDSWKQLIAGKSSDSKGIDLTNVTLPTDPTYSKAASDAIPPASLKADAPIDKSIDKWFFISG

>d1qeza_b.40.5.1 (A:) Inorganic pyrophosphatase {Archaeon Sulfolobus acidocaldarius}
KLSPGKNAPDVNVNLVEIPQGSNIYEYDDEEGVIKVDRLVLYTSMNYPFNYGFIPGTLEEDGDPLDVLTNYQLYPGSVIEVRPIGILYMKDEEGEDAK
IVAVPKDKTDPSFSNIKDINDLPQATKNKIVHFFEHYKELEPGKYVKISGWGSATEAKNRRIQLAIKRVSG

>d1i40a_b.40.5.1 (A:) Inorganic pyrophosphatase {Escherichia coli}
SLLNVPGKDPDLYVIEIPANADPKYEIDKESGALFVDRFMSTAMYPCNYGYINHTSLDGDPLDVLPVPLQPGSVTRCRPVGVLMKTDEA
GEDAKLVAVPHSKLSKEYDHKDNDLPELLKAQIAHFFEHYKDEKGKWWKVEGWENAEAAKAEIVASFERAKNK

>d2prd_b.40.5.1 (-) Inorganic pyrophosphatase {Thermus thermophilus}
ANLKSLPGDKAPEVVHMVIEVPRGSGNKYEYDPDLGAIKLDRLVPLGAQFYPGDYGFIPSTLAEDGDPLDGLVLSTYPLPGVVVEVRVVGLLMED
KGDAKIVGVVAEDQRLDHIQDGDVPEGVKQEIQHFETYKALEAKKGKWWKVTGWRDRKAALEEVRACIARYKG

>d1fr3a_b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {Sporomusa ovata}
MKISGRNKLREATVKEIVKGTVMAKIVMDYKGTELVAITIDSVALDLVPGDKVTALVKATEMEVLK

>d1guta_b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {Clostridium pasteurianum, MOP II}
SISARNQLKGKVVGLKKGVVTAEVVLEIAGGNKITSIISLDSVEELGVKEGAELTAVVKSTDMILA

>d1h9ma1_b.40.6.2 (A:1-73) Cytoplasmic molybdate-binding protein ModG {Azotobacter vinelandii}
MKISARNVFKGTVSALKGAVNAEVDIRLGGDKLAAVVTLESARSLQLAGKEVVAVKAPWVLLMTDSSGY

>d1h9ma2_b.40.6.2 (A:74-141) Cytoplasmic molybdate-binding protein ModG {Azotobacter vinelandii}
RLSARNILTGTVKTIETGAVNAEVTALQQGTEITSMVTKEAELGLKPGASASAVIKASNVLGV
P>d1h9ra1_b.40.6.2 (A:123-199) C-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}
MQTSARNQWFGTITARDHDDVQQHVVDLLADGKTRLKVAITAQSGARGLGDEGKEVLILLKAPWVGITQDEAVAQNA

>d1h9ra2_b.40.6.2 (A:200-261) C-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}
DNQLPGIIISHIERGAEQCEVLMALPDGQTLCATVPVNEATSLQQGQNVAYFNADSVIATL

>d1g2913_b.40.6.3 (1:241-301) Maltose transport protein MalK, C-terminal domain {Archaeon Thermococcus litoralis}
GSPPMNFLDAIVTEDGFVDFGEFLKLLPDQFEVLGEGLGYVGREVIFGIRPEDLYDAMFAQ

>d1g2914_b.40.6.3 (1:302-372) Maltose transport protein MalK, C-terminal domain {Archaeon Thermococcus litoralis}
VRVPGENLVRADVVEIVENLGSERIVRLRVGGVTFGSFRSERVREGVEVVFDMMKKIHIFDKTTGKAIF

>d1b3qa2_b.40.7.1 (A:540-671) Histidine kinase CheA, C-terminal domain {Thermotoga maritima}
TLAIICALLVKNNLVYAIPIANIQTILSISKEDIQRVQDRDVIRGEVIPVYRLWEVLQIEHKEELEEMEAVIRVGNRKYGVVDDLLGQDDIVKSLGK

VFSEVKEFSGAAILGDGSIALIINVSGIV

>d1k0sa_b.40.7.1 (A:) Chemotaxis protein CheW {Thermotoga maritima}

MKTLADALKEFEVLSFEIDEQALFDVNIEVMIEKSDITPVPKSRHFVEGVINLRGRIIPVVNLAKILGISFDEQKMKSIIVARTKDVEVGFLDRVLGV
LRITENQLDLTNVSDKFGKKSKGLVKTDGRLIIYLDIDKIIIEITVKEGV

>d1dxrh1 b.41.1.1 (H:37-258) Photosynthetic reaction centre {Rhodopseudomonas viridis}

RREGYPLVEPLGLVKLAPEDGQVYELPYPKTFVLPHGGTVPRRRPETRELKLAQTDGFEGAPLQPTGNPLVDAVPASYAERAEVVDATVDGKAKI
VPLRVATDFSIAEGDVDPRLGPVVAADGVEAGTVTDLWVRSEHYFRYLELSVAGSARTALIPLGFCDVKKDKIVVTSILSEQFANVPRLQSRDQITLRE
EDKVSAYYAGGLLYATPERAESLL

>d1qovh1 b.41.1.1 (H:36-250) Photosynthetic reaction centre {Rhodobacter sphaeroides}

MREGYPLENEDGTPAANQGPFLPKPKTFLPHGRGTLTVPGPESEDRIALARTAVSEGFPHAPTGDPMKDGVPGPASWVARRDLPEDGHGNKI
KPMKAAAGFHVSAGKNPILGPLVRGCDELIAKGKVVDIWVDIPEQMARFLEVELKDGSTRLLPMQMVKVQSNRVHVNALSSDLFAGIPTIKSPTEVLL
EEDKICGYVAGGLMYAAPKRKS

>d1eysh1 b.41.1.1 (H:59-259) Photosynthetic reaction centre {Thermochromatium tepidum}

PDLPDPKTFVLPHNGGTVVAPRVEAPVAVNATPFSPAGSPLVPNGDPMLSGFGPAASPDRPKHCDLTFEGLPKIVPMRVAKEFSIAEGDPDPRGM
TVVGLDGEVAGTVSDVVVDRSEPQIRYLEVEAANKKVLLPIGFSRFDKKARKVKVDAIKAAHFANVPTLSNPDQVTLYEEDKVCAYYAGGKLYATA
ERAGPLL

>d1bfg__ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}

DPKRLYCKNGFFLRIHPDGRVVGREKSDPHIKLQLQAEERGVSIKVSANRYLAMKEDGRLLASKSVTDECFFERLESNNYNTYRSRKYTSWYV
ALKRTGQQYKLGSKTGPGQKAILFLPMSA

>d1bla__ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}

MAEGEITTLPALPEDGGSGAFPPGHFKDPKRLYCKNGFFLRIHPDGRVVGREKSDPHIKLQLQAEERGVSIKVSANRYLAMKEDGRLLASKSV
TDECFFERLESNNYNTYRSRKYTSWYVALKRTGQQYKLGSKTGPGQKAILFLPMSAKS

>d1bara_ b.42.1.1 (A:) Acidic FGF (FGF1) {Cow (Bos taurus)}

PKLLYCSNGGYFLRILPDGTVDGKDRSDQHQIQLQLAAE SIGEVYIKSTETGQFLAMDTGLLYGSQTPNEECLFLERLEENGNTYISKKHAEKHWFV
GLKKNGRSKLGPRTHFGQKAILFLPLPV

>d1jqza_ b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}

HHHHFNLPNGNYKKPKLlyCSNGGHFLRILPDGTVDGTRDRSDQHQIQLQLSAESVGEVYIKSTETGQYLAMDTGLLYGSQTPNEECLFLERLEENHY
NTYISKKHAEKNWVGLKKNGSCKRGPRTHYQKAILFLPLPV

>d2afga_ b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}

KPKLLYCSNGGYFLRIFPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSTETGQYLAMDSDGQLYASQSPSEECLFLERLEENHYNTYISKKHAENWF
VGLKKNGSCKRGPRTHYQKAILFLPLPV

>d1fmms_ b.42.1.1 (S:) Acidic FGF (FGF1) {Eastern newt (Notophthalmus viridescens)}

QKPKLLYCSNGGYFLRIFPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSTETGQYLAMDSDGQLYASQSPSEECLFLERLEENHYNTYISKVHADKD
WFVGIKKNGKTKPGSRTHFGQKAILFLPLPVSSD

>d1ijta_ b.42.1.1 (A:) Fibroblast growth factor 4 (FGF4) {Human (Homo sapiens)}

GIKRLRRLYCNVIGFHLQALPDGRIGGAHADTRDSLLELSPVERGVVSIFGVASRFFVAMSSKGKLYGSPFFTDECTFKEILLPNNNAYESYKPGMFI
ALGKNGKTKKGNRVSPTMKVTHFLPRL

>d1qqka_ b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus norvegicus)}

DIRVRLFCRTQWYLRIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIKGVSEYYLAMNKEGKLYAKKECNECDNFKEILLENHYNTYASAKWTHSG
GEMFVALNQKGLPVKGKTKKEQKTAHFLPMAIT

>d1qqla_ b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus norvegicus)}

DIRVRLFCRTQWYLRIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIKGVSEYYLAMNKEGKLYAKQTPNEECLFLERLEENHYNTYISKKHAENKN
WFVGLKKNGSCKRGPRTHYQKAILFLPLPVSS

>d1ihka_ b.42.1.1 (A:) Fibroblast growth factor 9, FGF9 {Human (Homo sapiens)}

TDLDHLKGILRRRQLYCRTGFHLEIFPNTGTRIQGTRKDHSRGILEFISIAVGLVSIRGVDSGLYLGGMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNL
YKHVDTGRYYVALNKDGTPREGTRTKRHQKFTHFLPRPVDPDKVPELYKDILSQS
>d1i1b__ b.42.1.2 (-) Interleukin-1beta {Human (Homo sapiens)}
VRSLNCLRDSQQKSLVMSGPYELKALHLQGQDMEQQVFSMSFVQGEESNDKIPVALGLKEKNLYLSCVLKDDKPTLQLESVDPKYPKKKMEKR
FVFN KIEINN KLEFESA QFPN WYI STSQA EN MPV FGGT KGGQ DITDFT MQFVSS
>d8i1b__ b.42.1.2 (-) Interleukin-1beta {Mouse (Mus musculus)}
QLHYRLRDEQQKSLVLSDPYELKALHLNGQNINQQVIFSMSFVQGEPSNDKIPVALGLKGKNLYLSCVMKDGPTLQLESVDPKQYPKKKMEKFV
NKIEVKSKVEFESA EFPN WYI STSQA EH KPV FGLNN SGQD II DFT MESV
>d1ilr1_ b.42.1.2 (1:) Interleukin-1 receptor antagonist protein {Human (Homo sapiens)}
SKMQAFRIWDVNQKTFYLRNNQLVAGYLQGPVNLEEKIDVVPIEPHALFLGIHGGKMCLSCVKSGDETRLQLEAVNITDLSENRKQDKRFAFIRSD
SGPTTSFESAACPGWFLCTAMEADQPVS LT NMPDEGV MVTKFYFQED E
>d2ila__ b.42.1.2 (-) Interleukin-1alpha {Human (Homo sapiens)}
NVKYNFMRII KYE FILN DALN QSI I RANA QYL TAA ALHN LDE AVKF DMGAY KSS KDDA KIT VIL RISK TQLY VTA QDED QP VLL KEM P EIPK TIT GSET NL
LFFWETHGT KNYFTSVAHPNLFATKQDYWVCLAGGPPSITDFQILE
>d2aaib1 b.42.2.1 (B:1-135) Plant cytotoxin B-chain (lectin) {Castor bean (Ricinus communis), Ricin}
ADVCMDPEPIV RIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTYGYSPGVYMIYDCNTAATDATRWQIWD
NGTIINPRSSLVLAATSGNSGTTLVQTNIYAVSQGWLPNT
>d2aaib2 b.42.2.1 (B:136-262) Plant cytotoxin B-chain (lectin) {Castor bean (Ricinus communis), Ricin}
NTQP FVTIV GLYGLC LQANSGQV WIEDCSSEKA EQQQW ALYADGSIRPQQNRDNCLSDSNI RETV V KILSCGPASSGQRWMFKNDGTI LNLYSGLV
LDVRASDPSLKQJILYPLHGDPNQIWLP LF
>d1abrb1 b.42.2.1 (B:1-140) Plant cytotoxin B-chain (lectin) {Abrus precatorius}
IVEKSKICSSRYEPTVRIGGRDGM CVDVYDNGYHNGNRIIMWCKDRLEENQLWTLKSDKTIRSNGKCLTYGYAPGSYVMIYDCTS AVEAT YWEI
WDNGTIINPKSALVLSAESSSMGGTLTVQTNEYLMRQGWRTGN
>d1abrb2 b.42.2.1 (B:141-267) Plant cytotoxin B-chain (lectin) {Abrus precatorius}
NTSPFVTSISGYSDLCM QAQGS NVWMADCDSN KKEQQW ALYTDGSIRSVQNTNNCLTSKDHKG STILLMGCSNGWASQRWVFKNDG SIYSLY
DDMVMDVKGS DPSL KQII LW PYTG KPNQ IWL TL F
>d1ce7b1 b.42.2.1 (B:1-133) Plant cytotoxin B-chain (lectin) {European mistletoe (Viscum album)}
CSA EPTV RIVGRNGM VN D VR DDDFHD G NQIQLWPSKS NNDP NQLWTIK RDGT IR S NGK CLTYGYTAGV YMI FDCATA VGEATV WQI WGN GT
IIN PRS NLV LAASSG IKGTT LTV QTLDY TLQ GWL AG ND
>d1ce7b2 b.42.2.1 (B:134-255) Plant cytotoxin B-chain (lectin) {European mistletoe (Viscum album)}
TAPRE VTIV GFN DLCM ESGG SVT VET CSG KADK WALY GDG SIRPEQ NQA QCL TSGG DS VAG V NIVCS G AAS G QRW VFTNEG AILNLK NGL AM
DVANPGGGRII YPATG KPNQ MW LPV F
>d1hwmb1 b.42.2.1 (B:3-135) Plant cytotoxin B-chain (lectin) {Sambucus ebulus, ebulin}
ETCAI PAPFTRRIVGRD GLCVD VRNGYDT DGTP IQLWPCGTQRNQ QWTFYNDK TIRSMGK CMTANGL NSGSYIMI DCSTA E DATKWEV LID GSII
NPSSGLV MTA PGS AS RT LL ENNI HAAS SQG WTV SN
>d1hwmb2 b.42.2.1 (B:136-266) Plant cytotoxin B-chain (lectin) {Sambucus ebulus, ebulin}
DVQPIATLIVGYNEMCLQANGENN NVW MEDCDV TSVQQW ALFD DR TIRV NN SRL C VTSNGYVSKDLIVIRKCQGLATQRWFFNSDGS VV NLK
STRVMDVKESD VSLQEVII FPATG NPNQ QWRT QVPQI
>d1xyfa1 b.42.2.1 (A:313-436) Endo-1,4-beta-xylanase C-terminal domain {Streptomyces olivaceoviridis}
GQIKGVGSGR CLDVPN ASTTDGTQVQLYDCHSATNQQW TYTDAGE LRVYGD KCLDAAGT GNGT KVQIYSCWG GDNQ KW RLNSD GSIVGVQS GL
CLDAVGGGTANGTLIQLYSCNGSNQRWTRT
>d1dqga_ b.42.2.2 (A:) Mannose receptor {Mouse (Mus musculus)}
DARQFLIY NEDHKRCV DALS AISV QTATCNP EAESQKFRW VSDS QIM SVA FKLC LVGP SKTD WASV TLYACDSK SEYQ KWECKNDT LFGIKG TELY FN
YGNRQEKNIKLYKGSGLWSR WKVY GTT DDLC SRGYE

>d1jlx1 b.42.3.1 (A:1-153) Agglutinin {Love-lies-bleeding (*Amaranthus caudatus*)}
AGLPVIMCLSKNNHQYLRQSDNIQQYGLLQFSADKILDPLAQFEVEPSKTYDGLVHIKSRYTNKYLVRWSPNHYWITASANEPDENKSNWACTLF
KPLYVEEGNMKKVRLHVQLGHYTQNYTGGSFVSYLFQAESSQIDTGSKDVFHVID

>d1jlx2 b.42.3.1 (A:154-299) Agglutinin {Love-lies-bleeding (*Amaranthus caudatus*)}
WKSIFQFPKGYVTFKGNNGKYLGVITINQLPCLQFGYDNLNPKVAHQMFVTSNGTICIKSNYMNKFWRSLSTDDWILVDGNDPRETNEAAALFRSD
VHDFNVISLLNMQKTWFIRFTSGKPGFINCMAATQNVDETAILEIIEL

>d1wba__ b.42.4.1 (-) Winged bean albumin 1 {Goa bean (*Psophocarpus tetragonolobus*)}
DDPVYDAEGNKLVRNGKYTIASFSDGAGIDVVATGNENPEDPLSIVKSTRNIMYATSISSEDKTPPQPRNILENMRLKINFATDPHKGDVWSVDFQP
DGQQLKLAGRPNQVKGAFTIQKGSNTPRTYKLLFCPVGSPCKNIGISTDPEGKKRLVSYQSDPLVVKFHRH

>d1tie__ b.42.4.1 (-) Erythrina cafra trypsin inhibitor {*Erythrina caffra*}
VLLDGNGEVVQNGGYLLPQVWAQGGGVQLAKTGEETCPLTVQSPNELDGKPIRIESRLRSAFIPDDDVKRIGFAYAPKCAPSPWWTVVEDEQ
EGLSVKLSEDESTQFDYPFKFEQVSDQLHSYKLLYCEGKHEKCASIGINRDQKGYRRLVVTEDYPLTVVLKKDE

>d1eyla_ b.42.4.1 (A:) chymotrypsin inhibitor WCI {Winged bean (*Psophocarpus tetragonolobus*)}
EFDDDLVDAEGNLVENGGTYLLPHIWAHGGIETAKTGNEPCPLTVVRSPNEVSKGEPIRISSQFLSFLPRGSLVALGFANPPSCAASPWWTVVDS
QGPRAVQLSQQKLPDKDILVFKFEKVSHNIIHVYKLLYCEGKHEKCASIGINRDQKGYRRLVVTEDYPLTVVLKKDE

>d1avwb_ b.42.4.1 (B:) Soybean trypsin inhibitor {Soybean (*Glycine max*)}
DFVLDNEGNPLENGGTYYILSDITAFGGIRAAPTGNERCPLTVQSRNELDKGIGTISSPYRIRFIAEGHPLSLKFDSFAVIMLCVGIPTEWSVVEDLPEG
PAVKIGENKDAMDGWFRLERVSEFNNYKLVFCPQDKCGDIGISIDHDDGTRRLVSKNKPVLVQFQKLD

>d1avac_ b.42.4.1 (C:) Amylase/subtilisin inhibitor {Barley (*Hordeum vulgare*), seed}
ADPPPWHDTDGHELRADANYVLSANRAHGGGLTMAPGHHGRHCPLFVSDQPNQHDGFPRITPYGVAPSDFKIRLSTDVRISFRAYTTCLQSTEW
HIDSELAAGRRHVITGPVKDPSPSGRENAFRIEKYSGAEVHEYKLMSCGDWCQDLGVFRDLKGGAWFGLATEPYHVVFKKAPPA

>d1a8d_2 b.42.4.2 (248-452) Tetanus neurotoxin {*Clostridium tetani*}
ITFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYMILTNAPSNTNGKLNYYRRLYNGLFIKRYTPNNEIDSFKSGDFIKLYVSYNNNEHIVGYP
KDGNNAFNLDRLRVGYNAPGIPLYKKMEAVKRLDLKTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNWYFNHLKDKILGCDWYFVPTD
EGWTND

>d3btaa2 b.42.4.2 (A:1079-1295) Botulinum neurotoxin {*Clostridium botulinum*, serotype A}
NEKEIKDLYDNQSNSGILKDFWGDYLQYDKPYMLNLYDPNKYVDVNNVGIRGYMYLKGRGSVMTTNIYLNSSLRGTIFIKKYASGNKDNIVRN
NDRVYINVVKNKEYRLATNASQAGVEKILSALEIPDVGNLSQVVVMKSNDQGITNKCKMNLQDNNNGNDIGFIGFHQFNNIAKLVASNWYNRQI
ERSSRTLGCSEFIPVDDGWGERPL

>d1epwa2 b.42.4.2 (A:1080-1290) Botulinum neurotoxin {*Clostridium botulinum*, serotype B}
SEYLKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKNQNSKYINYRDLYIGEKFIRRKSNSQSINDDIVRKEDYIYLDFFLNQEW
VYTYKYFKKEEKLFLAPISDSDEFYNTIQKEYDEQPTYSQCLFFKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYLKEVKRKPYNLKGNCNWQF
IPKDEGWTE

>d1dfca1 b.42.5.1 (A:1008-1140) Fascin {Human (*Homo sapiens*)}
EAVQIQFGLINCGNKYLTAEAFGFVNASSLKKQIWTLLEQPPDEAGSAAVCLRSHLGRYLAADKDGNCEREVPGPDCRFIVAHDDGRWSLQ
SEAHRRYFGGTEDRLSCFAQTVPSPAEKWSVHIAHMHP

>d1dfca2 b.42.5.1 (A:1141-1259) Fascin {Human (*Homo sapiens*)}

QVNIYSVTRKRYAHLSPADEIAVDRDVPWGVDLSLTLAFQDQRYSVQTADHFLRHDGRLVARPEPATGYTLEFRSGKVAFRDCEGRYLAPSGPSG
TLKAGKATKVGKDEFALEQS

>d1dfca3 b.42.5.1 (A:1260-1382) Fascin {Human (*Homo sapiens*)}
CAQVVLQAANERNVSTRQGMDSLANSQDEETDQETFQLEIDRDTKKCAFRTHTGKYWLTATGGVQSTASSKNASCYF DIEWRDRRITLARASNGKFV
TSKKNGQLAASVETAGDSELFLMKLIN

>d1dfca4 b.42.5.1 (A:1383-1493) Fascin {Human (*Homo sapiens*)}
RPIIVFRGEHGFIGCRKVGTLDANRSSYDVFQLEFDGAYNIKDISTGKYWTVGSDAVTSSGDTPVDFFFEFCDYNKVAIKVGGRLKGDHAGVLKA

SAETVDPASLWEY

>d1hcd__ b.42.5.2 (-) Histidine-rich actin-binding protein (hisactophilin) {Dictyostelium discoideum}
MGNRAFKSHHGHFLSAEGEAVKTHGHHDHHFHVHENGGKVALKTHCGKYLIGDHKQVYLSHHLGDHSLFHLEHHGGKVSIKGHHHHYIS
ADHHGHVSTKEHHDHDTTFEEIII
>d1i8da1 b.43.4.3 (A:1-93) Riboflavin synthase {Escherichia coli}
MFTGIVQGTAKLVSIDEKPNFRTHVVELPDHMLDGETGASVAHNGCCLTVTEINGNHVSFDLMKETLRITNLGDLKVGDWVNVERAAKSDE
>d1i8da2 b.43.4.3 (A:94-206) Riboflavin synthase {Escherichia coli}
IGGHLMMSGHIMTTAEVAKILTSENNRQIWFKVQDSQLMKYILYKFIGIDGISLTVEVTPTRFCVHLIPETLERTLGKKLGARVNIEIDPQTQAVVD
TVERVLAARENAM
>d1fnc_1 b.43.4.2 (19-154) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Spinach (Spinacia oleracea)}
HSKKMEEGITVNKFKPCKTPYVGRCLLNTKITGDDAPGETWHMVFSHEGEIPYREGQSVGVIPDGEDKNGKPHKLRLYSIASSALGDFGDAKSVC
KRLIYTNDAGETIKGVCSNFLCDLKPGAEVKLTGPVGKE
>d1qfza1 b.43.4.2 (A:1-153) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Garden pea (Pisum sativum)}
QVTTEAPAKVVKHSKKQDENIVNKFKPCKEPYVGRCLLNTKITGDDAPGETWHMFSTEGEREGQSIVIPDGIDKNGKPHKLRLYSIASSAIGD
FGDSKTVSLCVKRLVYTNDAGEVVKGVCNSNFLCDLKPGADVKTGPVGKEMLMPK
>d1fb3a1 b.43.4.2 (A:67-207) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Paprika (Capsicum annuum)}
ISKKQDEGVVVNKFRPCKEPYIGRCLLNKITGDDAPGETWHMFSTEGEREGQSIVIADGVDANGKPHKLRLYSIASSALGDFGDSKTVSLCVKR
LVYTNDKGEEVKGVCSNFLCDLKPGADVKTGPVGKEMLMPK
>d1gawa1 b.43.4.2 (A:11-156) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Maize (Zea mays), leaf isoform}
PATAKAKKESKKQEEGVVTNLYKPKEPYVGRCLLNTKITGDDAPGETWHMFSTEGEREGQSIVIADGVDKNGKPHKVRLYSIASSAIGDFGDS
KTVSLCVKRLIYTNDAGEIVKGVCNSNFLCDLQPGDNVQITGPVGKEML
>d1jb9a1 b.43.4.2 (A:6-162) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Maize (Zea mays), root isoform}
SRSKVSVAPLHLESAKEPPLNTYKPKEPFTATIVSVELVGPKAPGETCHIVIDHGGNVPYWEGQSYGVIPPGENPKPGAPQNVRLYSIASTRYGDNF
DGRTGSLCVRRAYYDPETGKEDPSKNGVCSNFLCNSKPGDKIQLTGPGSGKIMLLPEE
>d1que_1 b.43.4.2 (1-141) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Cyanobacterium (Anabaena sp.), pcc
7119}
TQAKAKHADVPVNLYRPNAPFIGKVISNEPLVKEGGIGIVQHIKFDTGGNLKYIEGQSIGIIPPGVVDKNGKPEKLRLYSIASTRHGDDVDDKTISLCVRQ
LEYKHPESGETVYGVCSYSTLTHIEPGSEVKITGPVGKEML
>d1fdr_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Escherichia coli}
ADWVTGKVTQNWTDSLTVHAPVLPTAGQFTKLGLEIDGERVQRAYSIVNSPDNPDEFYLVTVPDGKLSPLRAALKPGDEVQVSEAAGF
FVL
>d1a8p_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Azotobacter vinelandii}
SNLNVERVLSVHHWNDSLFSKTRNPSLRFENGQFVMIGLEVDRPLMRAYSIASPNYEEHLEFFSIKVQNGPLTSRLQHLKEGDELMVSRKPTGTL
V
>d1qfja1 b.43.4.2 (A:1-97) NAD(P)H:flavin oxidoreductase {Escherichia coli}
TTLSCKVTSVEAITDTVYRVRIVPDAAFSFRAGQYLMVVMDERDKRPFMSMASTPDEKGFIELHIGASEINLYAKAVMDRILDHQIVVDIPHGEAWL
>d2cnd_1 b.43.4.2 (11-124) Nitrate reductase core domain {Corn (Zea mays)}
GRIHCRLVAKKELSRDVRFLRFSPDQVLGLPIGKHIFVCATIEGKLCMRAYPTSMVDEIGHFDLLKVFNEHPKFPNGGLMTQYLDLSPVGSYI
DVKGPLGHVEYTGR
>d1ndh_1 b.43.4.2 (3-125) cytochrome b5 reductase {Pig (Sus scrofa), liver}
PAITLENPDIKYPLRLIDKEVVNHDRTRRFRALPSPEHILGLPVGQHIYLSARIDGNLVRPYTPVSSDDKGFDLVIKVYFKDTHPKFPAGGKMSQYLE
SMKIGDTIEFRGPNGLLVYQGK
>d1i7pa1 b.43.4.2 (A:29-153) cytochrome b5 reductase {Rat (Rattus norvegicus)}
HHHMITLENPDIKYPLRLIDKEILSHDTRRFRALPSHQHILGLPIGQHIYLSTRIDGNLVRPYTPVSSDDKGFDLVIKVYFKETHPKFPAGGKMSQY

LENMNINGDTIEFRGPNGLLVYQGK

>d2pia_1 b.43.4.2 (1-103) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}

TTPQEDGFLRLKIASKEIARDIWSFELTDQPGAPLPPFEAGANLTAVPNGSRRTYSLCNDSQERNRYIAVKRDSNGGGSIFDDTSEGDAEVSLPRN

>d1ep3b1 b.43.4.2 (B:2-102) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}

SQLQEMMTVVSQREVAYNIFEMVLKGTLVDEM DLPGQFLHLAVPNGAMLLRRPISISSWDKRAKTCTILYRIGDETTGTYKLSKLESGAKVDVMGPLGNFG

>d1cqxa2 b.43.4.2 (A:151-261) Flavohemoglobin, central domain {Alcaligenes eutrophus}

WKGRWRTFVIREKRKPESDVITSFILEPADGGPVVNFE PGQYTSAIDVPALGLQQIRQYSLSDMPNGRTYRISVKREGGGPQPPGYVSNLHDHVNVGDQVKLAAPYGSFHI

>d1ja1a1 b.43.4.1 (A:240-518) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}

SSIRQYELVWHEDMDVAKVTGEMGRLKSYENQKPPFDAKNPFLAAVTANRKLNQGTERHLMHLELDISDSKIRYESGDHVAVYPANDSALVNQIGEILGADLDVIMSLNNLDEESNKKHPFPCPTTYRTALTYLDITNPPTRNVLYELAQYASEPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDYPSSLRPPIDHLCELLPRLQARYYIASSSKVHPNSVHICAVAVEYEAKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQF

>d1ddga1 b.43.4.1 (A:226-446) Sulfite reductase flavoprotein {Escherichia coli}

IHTSPYSKDAPLVASLVNQKITYGRNSEKDRHIEDLGDSLRYQPGDALGVWYQNDPALVKELVELWLKGDEPVTVEGKTLPLNEALQWHFELTVNTANIVENYATLRTSETLLPLVGDKAKLQHYATTPIVDMVRFSPAQLDAEALINLLRPLTPLYIASSQAEVENEVHTVGVVRYDVEGRARAGGASSFLADRVEEEGEVRVFIEHDNDNR

>d1f20a1 b.43.4.1 (A:963-1232) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat (Rattus norvegicus)}

SWKRKNKFRLTYVAEAPDLTQGLSNVHKKRVSAARLLSRQNQLQSPKSSRSTIFVRLHTNGNQELQYQPGDHLGVFPGNHNEDLVNALIERLEDAPPANHVVKVEMLEERNTALGVISNWKDESRLPPCTIFQAFKYLDITPPPTPLQLQQFASLATNEKEKQRLLVLSKGLQEYEEWKWGKNPMTMVEVLEEFPSIQMPATLLLQLSLLQPRYYISSSPDMPYDPEVHLTVAIVSYHTRDGEGPVHHGVCSSWLNRIQADDVVPFCVRGAP

>d1fua1 b.43.2.1 (A:356-591) L-fucose isomerase, C-terminal domain {Escherichia coli}

AQVFADVRVYWSPEAIEVRTGHKLDGLAEHIIHLINSGSAALDGSCQKRDSEGNPTMKPHWEISQEAACLAATEWCPAHEYFRGGYSSRFLT EGGVPFTMTRVNIIKGLGPVLQIAEGWSVELPKDVHDILNKRTNSTWPTTWFAPRLTGKGPTDVSYVMANWGANHGVLIGHVGADFITLASML RIPVCMHNVEETKVRPSSAWAAHGM DIEGQDYRACQNYGPLYKR

>d1efca1 b.43.3.1 (A:205-296) Elongation factor Tu (EF-Tu), domain 2 {Escherichia coli}

AIDKPFLPIEDVFSISGRGTVVTGRVERGIKVGEEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGKIKREEIERGQVLAKPG

>d1exma1 b.43.3.1 (A:213-312) Elongation factor Tu (EF-Tu), domain 2 {Thermus thermophilus}

PVRDVDPKFLMPVEDVFTITGRGTATGRIERGKVKVGDEVEIVGLAPETRKTVTGVEMHRKTLQEGIAGDNVGVLRRGVSVREEVERGQVLAKPGSITP

>d1d2ea1 b.43.3.1 (A:251-348) Elongation factor Tu (EF-Tu), domain 2 {Cow (Bos taurus), mitochondrial}

TRDLEKPFLPVESVYSIPGRGTVVTGTLERGILKKGDECEFLGHSKNIRT VVTGIEMFHKS LDR AEAGDNL GALV RGL KREDL RRG LVMAKPGSIQP

>d1f60a1 b.43.3.1 (A:241-334) Elongation factor eEF-1alpha, domain 2 {Baker's yeast (Saccharomyces cerevisiae)}

DKPLRLPLQDVYKIGGIGTVPGVGRVETGVKPGMVVTFAPAGVTTEVKSVEMHHEQLEQGVPGDNVGFNVKNVSVKEIRGNVCGDAKNDPKKG

>d1jnya1 b.43.3.1 (A:228-322) Elongation factor eEF-1alpha, domain 2 {Archaeon Sulfolobus solfataricus}

PVDKPLRIPIQDVYSISGVGTVPGRVESGVLKVGDKIVFMPAGKVG EVRSIETHHTKMDKAEPGDNIGFNVRGVEKKDIKRGDVVGHPNNPPTV

>d1dar_1 b.43.3.1 (283-400) Elongation factor G (EF-G), domain II {Thermus thermophilus}

PLDIPPIKGTPEGEVVEIHDPNGPLAALAFKIMADPYVGRLTFIRVYSGTLTSGSYVYNTTKGRKERVARLLRMHANHREEVEELKAGDLGAVVGLK ETITGDTLVGEDAPR VILE

>d1g7sa1 b.43.3.1 (A:228-328) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

EDSPARGTILEVKEETGLGMTIDA VYDGLILRKDDTIAMMTSKDVISTRIRSLKPRPLEMRESRKKFQKVDEVAAAGIKIVAPGIDDVMAGSPLRVVTT

>d1g7sa2 b.43.3.1 (A:460-587) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

IIPASIRLIPKLFRQSKPAIGGVELTGVIRQGYPLMNDGETVGTVESMQDKGENLKSASRGQKVAMAIKDAVGKTIHEGDTLYVDIPENHYHILK
EQLSGDLTDEELDLMKDIAEIKRKKNPD

>d1d1na_ b.43.3.1 (A:) Initiation factor IF2/eIF5b, domains 2 and 4 {Bacillus stearothermophilus}

YEEKVIGQAERQTFKVKVGTIAGCYVTDGKITRDSVKRLIRQGIVVYEGEIDSCHKYKDDVREVAQGYECGLTICKNFNDIKEGDVIEAYVMQEVARA

>d1jj2b_ b.43.3.2 (B:) Ribosomal protein L3 {Archaeon Haloarcula marismortui}

PQPSRPRKGSLGFGRKRSTSETPRFNSWPSDDGQPGVQGFAGYKAGMTHVVLNDEPNSPREGMEETPVTVIETPPMRAVALRAYEDTPYQQ
RPLTEVWTDEFHSELDRTLDVPEDHPDAAEEQIRDAHEAGDLGDLRLITHTVPDAVPSPKKPDMETRVGGGSVSDRLHALDIVEDGGEHA
MNDIFRAGEYADVAGVTKGKGTQGPVKRWGVQKRKGKHARQGWRRIGNLGPWNPSRVSTVPQQGQTGHQRTELNRKLIDIGEGDEPTVD
GGFVNNGEVDPYTLVKGSVPGPDKRLVRFRPAVRPNQPRLDPEVRYVSNESNQG

>d1efca2 b.44.1.1 (A:297-393) Elongation factor Tu (EF-Tu) {Escherichia coli}

TIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTTIELPEGVEMVMPGDNIMKVVTLIHIPIAMDDGLRAIREGGRTVGAGVVAKVL

>d1exma2 b.44.1.1 (A:313-405) Elongation factor Tu (EF-Tu) {Thermus thermophilus}

HTKFEASVYVLKKEEGGRHTGFFSGYRPQFYFRTTDVTGVVQLPPGVEMVMPGDNVFTVELIKPVALEEGLRAIREGGRTVGAGVVTKILE

>d1d2ea2 b.44.1.1 (A:349-451) Elongation factor Tu (EF-Tu) {Cow (Bos taurus), mitochondrial}

HQKVEAQVYILTKEEGGRHKPVSHMPVMSLTWDMACRIILPPGKELAMPGEDLKLTLRQPMILEKGQRFTRDGNRTIGTGLVTDPAMTEE
DKNIKW

>d1f60a2 b.44.1.1 (A:335-441) Elongation factor eEF-1alpha, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

CASFNATVVLNHPGQISAGYSPVLDCHTAICRFDELLEKNDRRSRKLEDHPKFLKSGDAALVKFVPSKPMCVEAFSEYPPPLGRFAVRDMRQTV
VGVIKSVDK

>d1jnya2 b.44.1.1 (A:323-429) Elongation factor eEF-1alpha, C-terminal domain {Archaeon Sulfolobus solfataricus}

ADEFTARIIVVWHPTALANGTPVHLVHTASVACRSELVKLDPRTGQEAENPQFLKQGDVAIVKFKPIKPLCVEKYNEFPPLGRFAVRDMGKTV
GVGIIVDVVKP

>d1flma_ b.45.1.1 (A:) FMN-binding protein {Desulfovibrio vulgaris, strain Miyazaki F}

MLPGTFFEVLKNEGVVIAITQGEDGPHLNTWNSYLKVLDGNRIVVPGGMHKTEANVARDERVLMTLSRKVAGRNGPGTFLRGSAAFRTD
GPEFEAIARFKWARAALVITVVAEQTL

>d1ci0a_ b.45.1.1 (A:) Pyridoxine 5'-phoshate oxidase (PNP oxidase) {Baker's yeast (Saccharomyces cerevisiae)}

FTLNEKQLTDDPIDLFTKWFNEAKEDPRETLPEAITFSSAELPSGRVSSRILLFKELDHRGFTIYSNWGTSRKAHDIAITNPNAIVFFWKLQRQVRVEG
ITEHVNRRETSEYFKTRPRGSKIGAWASRQSDVIKNREELDELTQKNTFRKDAEDIPCPDYWGGLRIVPLEIEFWQGRPSRLHDRFVYRRKTENDPW
KVVRLAP

>d1dnla_ b.45.1.1 (A:) Pyridoxine 5'-phoshate oxidase (PNP oxidase) {Escherichia coli}

GGLRRRDLPADPLTLFERWLSQACEAKLADPTAMVVATVDEHGQPYQRIVLLKHYDEKGMVFYTNLGSRKAHQIENNPRVSLFPWHTLERQVMVI
GKAERLSTLEVMKYFHSRPRDSQIGAWVSKQSSRISARGILESKFELKQKQQGEVPLPSFWGGFRVSLEQIEFWQGGEHRLHDRFLYQRENDAW
KIDRLAP

>d1ejea_ b.45.1.2 (A:) FMN-binding protein MTH152 {Archaeon Methanobacterium thermoautotrophicum}

GSQAAHMMSMDFEDFPVESAHRILTPRPTVMVTTVDEEGNINAAPFSFTMPVSIDPPVAFASAPDHHTARNIESTHEFINITPADIERMWVTAR
DIPAGENELEAAGLAWTSSRRVKPPRIVEAPGHLECELLRMFEVGDHNLTGSVSVSASVRSGAVKEGLLDVESVKPVLVHGGNKFVVGHDHVRHVE

>d1i0ra_ b.45.1.2 (A:) Ferric reductase {Archaeon Archaeoglobus fulgidus}

MDVEAFYKISYGLYIVTSESNGRKGQIANTVFQLTSKPVQIAVCLNKENDTHNAVKESGAFGVSVLELETPMEFIGRGFRKSSEFEKFDGVEYKTGK
TGVPLVTQHAVAVIEAKVVKEDC�VGTHTLFVGEAVDAEVLKDAEVLYADYHLMKKGKTPRT

>d1k28d1 b.106.1.1 (D:4-200) Baseplate structural protein gp27 {Bacteriophage T4}

LQRPGYPNLSQLKLFDSYDAWSNNRFV рлаатитLTMRDСLуGRNEGMLQFYDSKNIHTKMDGNEIIQISVANANDINNVKTRIYGCKHFSV рDSKG
DNIIAIELGTIHSIENLKFGFРFFPDAGESIKEMLGVYQDRTLTPAINAINAYVPDIPWTSTFENYLSVREVALVGSDKFVFWQDIMGVNMMDF

>d1k28d2 b.106.1.1 (D:201-376) Baseplate structural protein gp27 {Bacteriophage T4}

DMMINQEPMIVGEPSLIGQFIQELKPLAYDFVWLTKSNPHKRDPMKNAТИYAHSLDSSIPMITTGKGENSIVV рSGAYSEMTYRNGYEEAIRL

QTMAQYDGYAKCSTIGNFNLTGPKIIFNDSKNQFKTEFYVDEVIHELSNNNSVTHLYMFTNATKLETIDPVKVKEF
>d1fmta1 b.46.1.1 (A:207-314) Methionyl-tRNAfmet formyltransferase, C-terminal domain {Escherichia coli}
LSKEEARIDWLSAAQLERCIRAFNPWPMSWLEIEGQPVKVWKASVIDTNAAPGTILEANKQGIQVATGDILNLSSQAGKAMSAQDLLNSR
REWFPGNRLV
>d1ewna_b.46.1.2 (A:) 3-methyladenine DNA glycosylase (AAG, ANPG, MPG) {Human (Homo sapiens)}
HLTRLGLEFFDQPAVPLARAFLGQVLVRRLPNGTELGRIVETQAYLGPEDEAAHSRGGRQTPRNRMFMKPGTLYVIIYGMYFCMNISSQGDGA
CVLLRALEPLEGETMRQLRSLRKGTASRVLKDRELCGPSKLCQALAINKSFDQRDLAQDEAVWLERGPLEPSEPAVVAARVGVGHAGEWARKP
LRFYVRGSPWVSVDRVAEQD
>d1arb__ b.47.1.1 (-) Achromobacter protease {Achromobacter lyticus, strain m497-1}
GVSGSCNIDVVCPCEGDGRRIIRAVGAYSKSGTLACTGSLVNNTANDRKMYFLTAHHCGMTASTAASIIVYWNYQNSTCRAPNTPASGANGDGS
MSQTQSGSTVKATYATSDTLELNNAANPAFNLFWAGWDRRDQNYPGAIHHPNVAEKRISNSTPSFVAWGGGAGTTHLNVQWQPSGGVT
EPGSSGSPPIYSPEKRVLGQLHGGPSSCATGNTNRSDQYGRVFTSWTGGAAASRLSDWLDPASTGAQFIDGLDS
>d1qq4a_b.47.1.1 (A:) alpha-Lytic protease {Lysobacter enzymogenes, 495}
ANIVGGIEYSINNASLCSVGSVTRGATKGFVTAGHCGTVNATARIGGAVVGTFAARVFPGNDRAWVSLSAQTLPRVANGSSFTVRGSTEAAVG
AAVCHSRTTGTYQCGTITAKNVTANYAEGAVRGLTQSACMRGDSGGSWITSAGQAQGVMSGNNVQSNGNNCIPASQRSSLERLQPILSQY
GLSLVTG
>d2sga__ b.47.1.1 (-) Protease A {Streptomyces griseus, strain k1}
IAGGEAITTGGSRCISLGFNVSVNGVAHALTAGHCTNISASWSIGSTRGTSFPNNNDYGIIRHSNPAADGRVYLYNGSYQDITAGNAFGQAVQRSG
STTGLRSGSVTGLNATVNYGSSGIVYGMIIQTNVCAQPGDGGSLFAGSTALGLTSGGSGNCRTGGTTFYQPVTEALSAYGATVL
>d1hpga__ b.47.1.1 (A:) Glutamic acid-specific protease {Streptomyces griseus}
VLGGGAIYGGGSRCSAFNVTKGARYFVTAGHCTNISANWSASSGGSVVGVRGTSFPNDYGIIVRTDGSSPAGTVVDLYNGSTDISSAANAVV
GQAIKKSGSTTKVTSGTVTAVNVTVNYGDGPVYNMVRTTACSAGGDGGAHFAGSVALGIHSGSSGCSGTAGSAIHQPVTEALSAYGVTY
>d1sgt__ b.47.1.1 (-) Trypsin {Streptomyces griseus, strain k1}
VVGGRGTRAAQGEFPFMVRSLSMGCGGALYAQDIVLTAACVSGSGNNNTITATGGVVDLQSGAAVKVRSTKVLQAPGYNGTGKDWAliklaqpinqp
TLKIATTAYNQGTFVAGWGANREGGSQQRYLLKANVPVSDAACRSAYGNELVANEEICAGYPDTGGVDTQGDSSGPMFRKDNADEWIQVGI
VSWGYGCARPGYPGVYEVSTFASAIASAARTL
>d2sfa__ b.47.1.1 (-) Serine proteinase {Streptomyces fradiae}
IAGGEAIYAAGGGRCISLGFNVRSSSGATYALTAGHCTEIASTWYTNSGQTSLLGTRAGTSFPNDYGLIRHSNASAADGRVYLYNGSYRDITGAGNAY
VGQTVQRSGSTTGLHSGRVTGLNATVNYGGDIVSGLIQTNVCAEPGDSGGALFAGSTALGLTSGGSGNCRTGGTTFFQPVTEALSAYGVSIL
>d1sgpe__ b.47.1.1 (E:) Protease B {Streptomyces griseus, strain k1}
ISGGDAIYSSTGRCSLGFNVRSGSTYYFLTGHCTDGATTWWANSARTVLTGTTGSSFPNDYGIIVRTNTTIPKDGTVGGQDITSAANATVGMAY
TRRGSTTGTHGSVTALNATVNYGGDVVYGMIRTNVCAEPGDSGGPLYSGTRAIGLTSGGSGNCSSGGTFFQPVTEALVAYGVSVY
>d1agja__ b.47.1.1 (A:) Epidermolytic (exfoliative) toxin A {Staphylococcus aureus}
EVSAEEIKKHEEKWNKYYGVNAFLPKELFSKVDEKDRQKPYNTIGNVFVKQTSATGVLIGKNTVLTNRHIAKFANGDPSKVSFRPSINTDDNGNT
ETPYGEYEVKEILQEPFGAGVDLALIRLKPDQNGVSLGDKISPAKIGTSNDLKDGDKLEIGYPFDHKVNQMHRSEIELTLSRGLRYGYFTVPGNSGSG
IFNSNGELVGIHSSKVSHLDREHQINYGVGIGNYVKRIINEKNE
>d1qtfa__ b.47.1.1 (A:) Exfoliative toxin B {Staphylococcus aureus}
KEYSAEEIRKLKQKFEVPPTDKELYTHITDNARSPYNSVGTVPKGSTLATGVLIGKNTIVTNHVAREAKNPSNIIFTPQANRDAEKNEFPTPYKFEA
EEIKESPYGQQLDLAIILKPKNEKGESAGDLIQPANIPDHIDIAKGDKYSLLGYPYNSAYSLSYQSQIEMFNDSDQYFGYTEVGNNSGSGIFNLKGELIGIHSG
KGGQHNLPIGVFFNRKISSLYSDNTFGDTLGNDLKKRAKLDK
>d1ezxc__ b.47.1.2 (C:) Trypsin(ogen) {Cow (Bos taurus)}
CGGSLINSQWVVAACYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSYNSNTLNNDIMILKSAASLNSRVASISLPTSCASAGTQCLISGWGN
TKSSGTSPDVLKCLKAPILDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGDGGPVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQT
ASN

>d1hj9a_b.47.1.2 (A:) Trypsin(ogen) {Cow (Bos taurus)}

IVGGYTCGANTVPYQVSLNSGYHFCGGLSINSQWVSAAHCYKSGIQVRLGEDNINVVEGNEQFISASKSIVHPSYNNTLNDIMILKLKAASLNS
RVASISLPTSCASAGTQCLISWGNGTKSSGTSPDVLKCLKAPILSDSSCKSAYPGQITSNMFCAGYLEGGKDSCQGDGGPVVCSKLQGIVSWGSG
CAQKNKPGVYTKVCNYVSWIKQTIAAS

>d1mcta_b.47.1.2 (A:) Trypsin(ogen) {Pig (Sus scrofa)}

IVGGYTCAAANSIPYQVSLNSGSHTFCGGLSINSQWVSAAHCYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPNFNGNTLDNDIMILKLSSPATLNSR
VATVSLPRSCAAAGTECLISWGNGTKSSGTSPSLLQCLAKPVLNSSSCKSSPGQITGNMICVGFLQGGKDSCQGDGGPVVCNGQLQGIVSWG
GCAQKNKPGVYTKVCNYVNWIQQTIAAN

>d1f7za_b.47.1.2 (A:) Trypsin(ogen) {Rat (Rattus norvegicus)}

IVGGYTCQENSVPYQVSLNSGYHFCGGLSINDQWVSAAHCYKSRIQVRLGEHNINVLEGNEQFINAAKIIRHPQYDRKTLNNDIMILKLSSPVKLN
ARVATVALPSSCAPAGTQCLISWGNGNTLSSGVNEPDLLQCLADPLPQADCEASYPGKITDNMVCVGFLEGGKDSCQGDGGPVVCNGQLQGIVSWG
WGYZCALPDNPVGVTKVCNYVDWIQDTIAAN

>d1trna_b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens)}

IVGGYNCEENSPVYQVSLNSGYHFCGGLINEQWVVSAGHCYKSRIQVRLGEHNIEVLEGNEQFINAAKIIRHPQYDRKTLNNDIMILKLSSRAVINAR
VSTISLPTAPPATGTKCLISWGNGNTASSGADYPDELQCLADPVLQAECKASYPGKITSNMFCVGFLEGGKDSCQGDGGPVVCNGQLQGIVSWG
GCAQKNKPGVYTKVYNYVKWIKNTIAANS

>d1h4wa_b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens), trypsin IV (brain isoform)}

IVGGYTCEENSLPYQVSLNSGSHTFCGGLISEQWVSAAHCYKTRIQRVLEHNIVLEGNEQFINAVKIIRHPKYNRDTLDNDIMILKLSSPAVINARV
STISLPTAPPAGTECLISWGNGNTLSFGADYPDELKCLADPVLQAECKASYPGKITSNMFCVGFLEGGKDSCQGDGGPVVCNGQLQGIVSWG
CAWKNRPGVYTKVYNYWDWIKDTIAANS

>d1a0ja_b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo salar)}

IVGGYECKNSASYQASLQSGYHFCGGLSISSTWVSAAHCYKTRIQRVLEHNIAVNEGTEQFIDSVKVIMHPSYNRSRNLDNDIMILKLSPASLNSY
VSTVALPSCASSGTRCLVSGWGNLGSNSNYPDTLRLDPLILSSSCNSAYPGQITSNMFCAGFMEGGKDSCQGDGGPVVCNGQLQGIVSWG
YGCAQRNKPVGVTKVCNYRWSISSTMSSN

>d1hj8a_b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo salar)}

IVGGYECKASQPHQVSLNSGYHFCGGLVNENWVSAAHCYKSRVEVRVLEHNIVTEGSEQFISSSRVIRHPNYSSYNIDNDIMILKLSPATLNTY
VQPVALPTSCAPAGTMCTVSGWGNMSSADSNKLQCLNIPILSYDCNNSYPGMITNAMFCAGYLEGGKDSCQGDGGPVVCNGELQGIVSWG
GYGCAEPGNPGVYAKVICIFNDWLTSTMASY

>d1gdna_b.47.1.2 (A:) Trypsin(ogen) {Mold (Fusarium oxysporum)}

IVGGTSASAGDFPIVSISSRNGGPWCGGSLNANTVLTAAHCVSGYACQSGFQIRAGSLSRSGITSSLSRVHPSYSNNNDLAILKLSTSIPSGGNI
GYARLAASGSDPVAGSSATVAGWGATSEGGSTPVNLKVTPIVSRATCRAQYGTSAITNQMFCAGVSSGGKDSCQGDGGPVIDSSNTLIGAVS
WGNGCARPNYSGVYASVGALRSFIDTYA

>d1pytd_b.47.1.2 (D:) (alpha,gamma)-chymotrypsin(ogen) {Cow (Bos taurus)}

CGAPIFPQNLSSARVVGGEADAIPHSPWPWQISLQLQYLRDNTWRHTCGGTITPNHVLTAAHCISNTLTYRVALGKNNLEVEDEAGSLYVGVDTIFVHEKW
NSFLVRNDIALIKLAETVELGDTIQVACLSEGSLLPQDYPCFVTGWGRLYTNGPIAAELQQGLQPVVDYATCSQRDWVGTTVKETMVCAGGDGV
SACNGDSGGPLNCQADQWVDRGIVSFGLSLCNTFKKPTVFRVSAYIDWINQKLQ

>g1gg6.1 b.47.1.2 (A;B;C;) (alpha,gamma)-chymotrypsin(ogen) {Cow (Bos taurus)}

CGVPAIQPVXLIVNGEEAVPGSPWVQVSLQDKTGFHFCGGLINENWVTAACVGTTSVVAGEFDQGSSEKIQKLKIAKVFKN SKYNSLTIN
NDITLLKSLTAASFQTSVAVCLPSASDDFAAGTTCTTGWLTRYXANTPDRLOQQASLPLSNTNCKKYWGTKIKDAMICAGASGVSSCMGDGGP
LVCKKNGAWTLGIVSWGSSCTSTPGVYARVTAJVNWWQQLAAN

>d1eq9a_b.47.1.2 (A:) (alpha,gamma)-chymotrypsin(ogen) {Red fire ant (Solenopsis invicta)}

IVGGKDAPVGKYPYQVSLRLSGSHRCGASILDNNNVLTAAHCVDGLSMLNRLKVHVGTYLSESGDVYDVEDAVVNKNYDDFLRNNDVALVHLTNPI
KFNDLVQPIKLNDELDLESNPCTLTGWGSTRLLGGNTPNALQEIELIVHPQKQCERDQWRVIDSHICLTKRGEGACHGDSGGPLVANGAQIGIVSF
GSPCALGEPDVYTRVSSFVSWINANLK

>d1npma_b.47.1.2 (A:) Neuropsin {Mouse (*Mus musculus*)}
ILEGRECIPHSQPWQAALFQGERLICGGVLVGDRWVLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQVAQSIQHPCYNNNSNPEDHSHDIMLIRLQN
SANLGDKVKPVQLANLCPKVQKCIISGWGTVTSPQENFPNTLNCAEVKIYSQNKCERAYPGKITEGMVCAGSSNGADTCQGDGGPLVCDGMLQ
GITSWGSDPCGKPEKPGVYTICKRYTTWIKKTMD

>d1azza_b.47.1.2 (A:) Crab collagenase {Atlantic sand fiddler crab (*Uca pugilator*)}
IVGGVEAVPNSWPHQAALFIDDMYFCGGSLISPEWILTAAHCMDAGFVDVVLGAHNIREDEATQVTIQSTDFTVHENYNSFVISNDIAVIRLPV
TLTAAIATVGLPSTDVGVGTVPTGWLPSDSLALGSDVLRQVDVPIMSNADCDAVYGIWTGNICIDSTGGKGTNGDSGGPLNYGLTYGITSFG
AAAGCEAGYPDAFRVTFLDWIQTQGTP

>d2hlca_b.47.1.2 (A:) HL collagenase {Common cattle grub (*Hypoderma lineatum*)}
IINGYEAYTGLFPYQAGLDITLQDQRRWCAGGLDINWKWILTAACVHDASVVYLGSAVQYEAEVVNSERIISHSMFNPDTYLNDVALIKIPHVEY
TDNIQPIRLPSGEELNNKFENIWTAVSGWGQSNTDTVILQYTYNLVIDNDRCAQEYPPGIVESTICGDTSDGKSPCFGSQGPFLSDKNLLIGVVFS
VSGAGCESGKPVGFSRVTSYMDWIQQNTGIKF

>g1h8d.1 b.47.1.2 (L;H:) Thrombin {Human (*Homo sapiens*)}
EADCGLRPLFEKKSLLEDKTERELLESIXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTR
YERNIEKISMLEKIYIHPRYNWRENLDRDIALMLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETGQPSVLQVVNLPIVERPVCKD
STRIRITDNMFACAGYKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRGKYGFYTHVFRKKWIQKVIDQFGCSSVLIVVC

>g1jou.1 b.47.1.2 (A;B:) Thrombin {Human (*Homo sapiens*)}
SEYQTFNFNRTFGSGEADCGLRPLFEKKSLLEDKTERELLESYIDGXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKN
FTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLDRDIALMLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWTAN
VGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFACAGYKPDEGKRGDACEGDAAGGPVFMKSPFNNRWYQMGIVSWGEGCDRGKYGFYTHV
RLKKWIQKVIDQFGE

>g1vr1.1 b.47.1.2 (L;H:) Thrombin {Human (*Homo sapiens*)}
ADCGLRPLFEKKSLLEDKTERELLESIXIVEGSDAEIGMSPWQVMLFAKHRRSPGERFLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHS
RTRYERNIEKISMLEKIYIHPRYNWRENLDRDIALMLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVGKGQPSVLQVV
LPIVERPVCKDSTRIRITDNMFACAGYKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRGKYGFYTHVFRKKWIQKVIDQ

>g2hnt.1 b.47.1.2 (L;C;E;F;) Thrombin {Human (*Homo sapiens*)}
ADCGLRPLFEKKSLLEDKTERELLESYDXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSXEKI
SMLEKIYIHPRYNWRENLDRDIALMLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGXPSVLQVVNLPIVERPVCKDSTRIRITDNMFAC
YKPDEGKRGDACEGDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRGKYGFYTHVFRKKWIQKVIDQ

>g1etr.1 b.47.1.2 (L;H:) Thrombin {Cow (*Bos taurus*)}
TFGAGEADCGLRPLFEKKQVQDQTEKELFESYIEGRXIVEGQDAEVGLSPWQVMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTVDDLL
VRIGKHSRTRYERKVEKISMLEDKIYIHPRYNWKENLDRDIALKLKRPIELSDYIHPVCLPDKQTAAKLLHAGFKGRVTGWGNRRETWTTVAEVQPSV
LQVVNLPLVERPVCKASTRIRITDNMFACAGYKPGEKRGDACEGDSGGPFVMKSPYNNRWYQMGIVSWGEGCDRGKYGFYTHVFRKKWIQK
VIDRLGS

>d1fona_b.47.1.2 (A:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (*Bos taurus*)}
SWSWQVSLQYEKDGAFHHTCGGLIAPDWVVTAGHCISTSRTYQVVLGEYDRSVLEGSEQVIPINAGDLFVHPLWNSNCVACGNDIALVLSRSAQ
LGDKVQLANLPPAGDILPNEAPCYISGWGRLYTGGPLDKLQQALLPTVDYEHCSQWDWWGITVKKTMVCAGGDTRSGCNGDSGGPLNCPAAD
GSWQVHGVTFSVSAFGCNTIKKPTVFTRVSAFIDWIDETIASN

>d1ptyc_b.47.1.2 (C:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (*Bos taurus*)}
SRPSSRVVNGEDAVPYWSWQVSLQYEKDGAFHHTCGGLIAPDWVVTAGHCISTSRTYQVVLGEYDRSVLQGSEQVIPINAGDLFVHPLWNSNC
VACGNDIALVLSRSAQLGDKVQLANLPPAGDILPNEAPCYISGWGRLYTGGPLDKLQEALLPVVDYEHCSQYDWWGITVKKTMVCAGGDTRSGC
DGDGGPLNCPAAGDSWQVHGVTFSVSAFGCNTIKKPTVFTRVSAFIDWINETIASN

>d1ppfe_b.47.1.2 (E:) Elastase {Human (*Homo sapiens*)}
IVGGRRARPHAWPFMVSQQLRGHHFCATLIAPNFVMSAACVANVNRAVRVVLGAHNLRSREPTRQVFAQRIFENGYDPVNLLNDIVILQLN

GSATINANVQVAQLPAQGRRRLGNGVQCLAMGWGLLGRNRGIASVLQELNVTVTSLCRSSNVCTLVRGRQAGVCFGDSGPLVCNGLIHGIAFV
RGGCASGLYPDAFAPVAQFVNWIDSIIQ

>d1brup_b.47.1.2 (P:) Elastase {Pig (Sus scrofa)}

VVGGEDARPNSWPWQVSLQYDSSGQWRHTCGGTLDQSWVLTAAHCISSSRTYRVVLGRHSLSTNEPGSLAVKVKLVVHQDWNSNQLSNGND
IALLKLASPVLTDKIQLGCLPAAGTILPNNYCYVTGWLRTNGASPDILQQGQLLVVDYATCSKPGWWGSTVKTNMICAGGDGISSCNGDSGG
PLNCQGANGQWQVHGIVSGSSLGCNYYHKPSVFRVSNYIDWINSVIANN

>d1qnja_b.47.1.2 (A:) Elastase {Pig (Sus scrofa)}

VVGGEAQRNSWPSQISLQYRSGSSWAHTCGTLIRQNWWMTAAHCVDRELTFRVVGEHNLNQNDTEQYVGQKIVVHPYWNTDDVAAGY
DIALRLAQSVTLNSYVQLGVLPRAVTILANNSPCYITGWLRTNGQLAQTLQQAYLPTVDYACSSSYWGSTVKNSMVCAAGGDGVRSQCGDGS
GGPLHCLVNGQYAVHGVTFSVRLGCNVTRKPTVFTRVSAYISWINNVIASN

>d1elt_b.47.1.2 (-) Elastase {Salmon (Salmo salar)}

VVGGRVAQPNSWPWQISLQYKSGSSYYHTCGSLIRQGWVMTAAHCVDARTWRVVLGEHNLNTNEGKEQIMTVNSVFIHSGWNNSDDVAGGY
DIALRLNTQASLNSAVQLAALPPSNQILPNNPCYITGWLRTGGPLSDLKQAWLPSVDHATCSSGWWGSTVKTTMVCAGGGANGCNGD
SGGPLNQCNGSYVHGVTFSVSSGCNASKPTVFRVSAYISWMNGIM

>d1ekbb_b.47.1.2 (B:) Enteropeptidase (enterokinase light chain) {Cow (Bos taurus)}

IVGGSDSREGAWPWWVVALYFDDQQVCGASLVSRDWLVAACVYGRNMEPSKWKAVALGLHMASNLSPQIETRLIDQIVINPHYNKRRKNNIA
MMHLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGALIYQGSTADVLQEADVPLSNEKCQQQMPEYNITENMVCAGYEAGGVDSQGDGS
GPLMCQENNWRLLAGVTSFGYQCALPNRPGVYARVPRFTEWIQSFLH

>d1a7s_b.47.1.2 (-) Heparin binding protein, HBp {Human (Homo sapiens)}

IVGGRKARPRQFPFLASIQNQGRHFCCGALIHFARVMTAACFPGVSTVVLGAYDLRRRERQSRQTSFISSMSENGYDPQQNLNDLMLQLDREAN
LTSSVTILPLPLQNATVEAGTRCQVAGWGSQRSGGRISRFPRFVNVTVPEDQCRPNNVCTGVLRGGICNGDGTPLVCEGLAHGVASFSLGPC
GRGPDFTRVALFRDWIDGVLNNGPGP
G>d1a0la_b.47.1.2 (A:) beta-Tryptase {Human (Homo sapiens)}

IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSILHPQWVLTAAHCVGPDVKDLAALRVQLREQHLYQDQLLPVSRIIVHPQFYTAQIGADIALL
ELEEPVKVSSHVHTVTLPPASETFPPGMPCWVGTGWDVDNDERLPPPFLKQVKVPMENHICDAKYHLGAYTGDDVIRDDMLCAGNRRDSC
QGDSSGPGVCKVNGTWLQAGVVSWGECAQPNRPGIYTRVYYLDWIHHYVPKK

>d1cgha_b.47.1.2 (A:) Cathepsin G {Human (Homo sapiens)}

IIGGRESRPHSRPYMAYLQIQSPAGQSRCGGFLVREDFLVTAACWGSNINVTLGAHNQRRRENTQQHITARRAIRHPQYNQRTIQNDIMLLQLSRR
VRRRNRVNPVALPRAQEGLRPGTLCTVAGWGRVSMRRGDTLREVQLRVQRDRQCLRFIGSYDPRRQICVGDRRERKAFAFKGDGGPLLNNVA
HGIVSYGKSSGVPEVFTRSSFLPWIRTTMRS

>d1danh_b.47.1.2 (H:) Coagulation factor VIIa {Human (Homo sapiens)}

IVGGKVKCPKGECPWQVLLVNGAQLCGGTINTIWVSAAHCFDKIKNWRNLIAVLGEHDLSHQDEQSRRVAQVIIIPSTYVPGTTNHDIALRLH
QPVVLTDHVPLCLPERTFSERTLAFVRFSLVSGWGQLLDRGATALELMVLNVPRLMTQDCLQQRKVGDSPNITEYMFCAVYSDGSKDSCKGDG
GPHATHYRGWTYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP

>d3rp2a_b.47.1.2 (A:) Chymase (Proteinase II) {Rat (Rattus rattus)}

IIGGVESIPHSPYMAHLIDIVTEKGLRIVCGGLISRQFLVTAACKGREITVILGAHDVRKRESTQQKIKVEKQIIESYNNSVNLHDIMLLKLEKKVELTP
AVNVVPLPSPDFIHPGAMCWAAGWGKTGVRDPTSYTREVELRIMDEKACVDYRYYEYKFQCVGSPTLRAAFMGDSGGPLLCAVAGVHSY
GHPDAKPPAIFTRVSTYVWPWINAVIN

>d1klt_b.47.1.2 (-) Chymase (Proteinase II) {Human (Homo sapiens)}

IIGGTESKPHSRPYMAYLEVTSNGPSKFCGGFLIRRNFVLTAAHCAGRISITVTLGAHNITEEEDTWQKLEVQFRHPKYNTSTLHHDIMLLKEKASL
TLAVGTLPPSQFNFPVPPGRMCRVAGWGRGTVLKPGSDTLQEVKLRLMDPQACSHFRDFDHNLQLCVGNPRKTKSAFKGDGGPLLCAVAGVHQ
VSYGRSDAKPPAVFTRISHYRPWINQILQAN

>g2pka_1 b.47.1.2 (A;B:) Kallikrein A {Pig (Sus scrofa)}

IIGGRECEKNSHPWQVAIHYSSFCGGVLVNPWKVLTAAHKNDNYEVWLGRHNLFENENTAQFFVTADFPHPGFNLXADGKDYSHDLMLR

LQSPAKITDAVKVLELPTQEPELGSTCEASGWGSIEPGPDDFEFPDEIQCVQLTLLQNTFCADAHPDKVTESMLCAGYLPGGKDTCMDSGGPLICN
GMWQGITSWGHTPCGSANKPSIYTKLIFYLDWIDDTITENP

>d1ton__ b.47.1.2 (-) Tonin {Rattus rattus}

IVGGYKCEKNSQPWQAVINEYLCGGVLIDPSWVITAACYSNNYQVLLGRNNLFKDEPFAQRRLVRQSFRHPDYIPLIVTNDTEQPVHDHSNDLML
LHLSEPADITGGVKVIDLPTKEPKVGSTCLASGWGSTNPSEMVVSHDLQCVNIHLLSNEKCIETYKDNTDVMLCAGEMEGGKDTAGDSGGPLIC
DGVLQGITSGGATPCA PKTPAIYAKLIKFTSWIKKVMKENP

>d1sgfa_ b.47.1.2 (A:) 7S NGF protease subunits {Mouse (Mus musculus)}

NSQPWHAVYRFNKYQCGGVLLDRNWLTAAHCYNDKYQVWLGNNEFEDPSDQHRLVSKAIPHDFNMSLLNEHTPQPEDDYSNDMLRL
SKPADITDVVKPITLPTEEPKLGSTCLASGWGSTTPIKYPPDLQCVNLKLLPNEDCDKAHEMKVTDAMLCAGEMDGGSYTCEHDSSGPLICDGILQG
ITSWGPEPCGEPEPSVYTKLIKFTSWIRETMANNP

>d1sgfg_ b.47.1.2 (G:) 7S NGF protease subunits {Mouse (Mus musculus)}

IVGGFKCEKNSQPWHAVYRYTQYLCGGVLLDPNWLTAAHCYDDNYKVWLGNLFKDEPSAQHRFVSKAIPHPGFNMSLMRFLEYDYSNDLM
LLRLSKPADITDTVKPITLPTEEPKLGSTCLASGWGSITPTKFQFTDDLYCVNLKLLPNEDCAKAHIEKVTDAMLCAGEMDGGKDTCKGDSSGPLICDG
VLQGITSWGHTPCGEPDMPGVYTKLNKFTSWIKDTMAKNP

>d1dele_ b.47.1.2 (A:) Factor B {Human (Homo sapiens)}

ADPDESQSLSCGMVWEHRKGTDYHKQPWQAKISIRPSKGHESCMGAVVSEYFVLTAAHCFTVDDKEHSIKVSVGGEKRDLIEEVVLFHPNYNIN
GKKEAGIPEFYDYDVALIKLNKLKYGQTIRPICLPCTEGTTAALRLLPPTTCQQQKEELLPAQDIKALFVSEEEKKLTRKEVYIKNGDKKGSCERDAQYA
PGYDKVKDISEVVTPRFLCTGGVSPYADPNTCRGDSGGPLIVHKRSRFIQVGVISWGVV DVCKNQKRQKQVPAHARDFHINLFQVLPWLKEKLQDE
DLGFL

>d1bio__ b.47.1.2 (-) Factor D {Human (Homo sapiens)}

ILGGREAEAHARPYMASVQLNGAHLGGVLVAEQWVLSAACHEADA DGKVQVLLGAHSLSQPEPSKRLYDVLRAVPHPDSQPD TIDHDLLLQLS
EKATLGPAVRPLPWQRVDRDVAPGTLCDVAGWGIVNHAGRRPDSLQHVLLPVLDRATCNRRTHHDGAITERLMCAESNRRDSCKGDSGGPLVC
GVLEGVVTSGSRVCGNRKPGIYTRVASYAAWIDSVA

>g1rtf.1 b.47.1.2 (A;B;) Two-chain tissue plasminogen activator (TC)-T-PA {Human (Homo sapiens)}

TCGLRQYSIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAHCFQERFPPHHLTVILGRTYRVVPGEEEQKFEVEKYIVHKEFDDD
TYDNDIALLQLKSDSSRCAQE SSSVVRTVCLPPADLQLPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVDNMLCAGDTRSG
GPQANLHDACQGDSGGPLVCLNDGRMTLVGIISWGLCGQKDVPGVYTKVTNYLDWIRDNMRP

>d1a5ia_ b.47.1.2 (A:) Single chain tissue plasminogen activator {Vampire bat (Desmodus rotundus)}

TCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAQNRRSSGERFLCGGILISSCWVLTAAHCFCQESYLPDQLKVVLGRTYRVKPGEEEQTFVKVKKYIVHK
EFDDDTYNNDIALLQLKSDSPQCAQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSPFYSEQLKEGHVRLYPSSRCAPKFLNKTVTNNMLCAG
DTRSGEIYPNVHDACQGDSGGPLVCMNDNHMTLLGIISWGVGC GEKDVPGVYTKVTNYLGWIRDNMHL

>d1bqya_ b.47.1.2 (A:) Plasminogen activator from snake venom, TSV-PA {Chinese green tree viper (Trimeresurus stejnegeri)}

VFGGDECNINEHRSLLVLFNSNGFLCGGTLINQDWVVTAAHCDSNNFQLLFGVHSKKILNEDEQTRDPKEKFFCPNRKKDDEVDKDIMALIKLDSSVS
NSEHIAPLSLPSSPPSVGSVCRIMGWGTKIPTKEIYPDVPHCANINILDHAVCRTAYSRQVANTTLAGILQGGRDTCHFDSSGPLICNGIFQGIVS
WGGHPCGQPGE PGVYTKVFDYLDWIKSIIAGNKDATCPP

>d1ao5a_ b.47.1.2 (A:) Kallikrein-13 {Mouse (Mus musculus)}

VVGGFNCEKNSQPWQAVYYQKEHICGGVLLDRNWLTAAHCYDQYEVWLGNKLQEEPSAQHRLVSKSFPHGFNMSLLMLQTIPPGADFS
DDMLLRLSKPADITDVVKPIALPTKEPKPGSKCLASGWGSITPTRWQKPDDLQCVFITLLPNENCAKVLQKVTDVMLCAGEMGGGKDTCRDDSG
GPLICDGILQGTTSYGPVPCGKPGVPAIYTNIKFN SWIKDTMMKNA

>d1pxc_ b.47.1.2 (C:) Coagulation factor IXa, protease domain {Pig (Sus scrofa)}

IVGGENAKPGQFPWQVLLNGKIDAFCGGSIINEKWVTAACIEPGVKITVVA GEYNT ETEPTEQRRNVIRAI PHHSYNATVNKYSHDIALLELDEPL
TLNSYVTPICADIKEYTNIFLKFGSGYVSGWGRVFNRGRSATILQYLVPLVDRATCLRSTKFTIYSNMFCAGFHEGGKDCQGDSSGGPHVTEVEGTSF
LTGII SWGEECAVKGKYGIYTKVSRYVNWIKEKTKLT

>d1rfna_ b.47.1.2 (A:) Coagulation factor IXa, protease domain {Human (Homo sapiens)}

VVGGEDAKPGQFPWQVVLNGKVDACCGGSIVNEKWIVTAAHCVETGVKITVVAEGHNIETEHTEQKRNVRIPHHNNAIAINKYNHDIALLEDE
PLVLNSYVTPICIADKEYTNIFLKGSGYVSGWGRVFHKGRSALVLQYLRVPLVDRATCLRSTKFTIYNNMFCAGFHEGGRDSCQGDSGGPHVTEVEG
TSFLTGIISWGEECAMKGKYGYITKVSRYVNWIKEKTLT

>d1fjsa_b.47.1.2 (A:) Coagulation factor Xa (Chrismas factor), protease domain {Human (Homo sapiens)}

IVGGQECKDGECPWQALLINEENEGFCGGTILSEFYVLTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVRLKTPITF
RMNVAPACLPERDWAESTLMTQKTGIVSGFGRTHEKGRQSTRLKMLEVPYVDRNSCLSSFIITQNMFCAGYDTKQEDACQGDSGGPHVTRFKD
TYFVTGIVSWGEGCARKGKYGYITKVTAFKLWIDRSMKT

>d1kigh_b.47.1.2 (H:) Coagulation factor Xa (Chrismas factor), protease domain {Cow (Bos taurus)}

IVGGRDCAEGECPWQALLNEENEGFCGGTILSEFYVLTAAHCLHQAKRFKVRVGDRNTEQEEGNEAMAHEVEMTVKHSRFVKETYDFDIAVRLK
PIFRRNVAPACLPKDWAETLMTQKTGIVSGFGRTHEKGRLSSTLKMLEVPYVDRSTCKLSSFTITPNMFCAGYDTQPEDACQGDSGGPHVTRF
KDTYFVTGIVSWGEGCARKGKGFGVYTKVSNFLKIDKIMKARAGAAGS

>d1fxya_b.47.1.2 (A:) Coagulation factor Xa-trypsin chimera {Synthetic, based on Homo sapiens sequence}

IVGGYNCKDGECPWQALLINEENEGFCGGTILSEFYVLTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVIKHNRFTKETYDFDIAVRLKTPITF
RMNVAPASLPTAPPATGKCLISGWGNTASSGADYPDELQCLAPVLSQAKCEASYPGKITSNMFCVGFLEGGKDSCQGDSGGPVVCNGQLQGVV
SWGDGCAQKNKPGVYTKVNYVWKWIKNTIAANS

>d1elva1_b.47.1.2 (A:410-668) Complement C1S protease, catalytic domain {Human (Homo sapiens)}

CGVPREPFEKQRIIGGSDADIKNFPWQVFFDNPWAGGALINEYWLTAHVVEGNREPTMYVGSTSQTSLAKSKMLTPEHVFHPGWKLLAV
PEGRTNFDNDIALVRLKDVKMGPTVSPICLPGTSSDYNLMGDLGLISWGWRTEKRDRAVRLKAARLPVAPLRKCDEVKVEKPTADAEEAYVFTPNM
ICAGGEKGMDCKGDGGFAVQDPNDKTFYAAGLVSWPQCGTYGLYTRVKNYVDWIMKTMQENS

>d1autc_b.47.1.2 (C:) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}

LIDGKMTRRGDSPWQVVLLSKKLACGAVALIHPSWLTAHCMDESKLLVRLGEYDLRRWEKWEVDLDIKEVFVHPNYSKTTDNDIALLHLAQ
PATLSQTIVPCLPDGSLAERELNQAGQETLVGWWYHSSREKEAKRNRTFVLNFIIKIPVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSG
GPMVASFHGTWFLVGLWSWGEKGCLLHNHYGVYTKVSRYLDWIHGHIRD

>d1fuja_b.47.1.2 (A:) Myeloblastin, PR3 {Human (Homo sapiens)}

IVGGHEAQPHSRPYMASLQMQRGNPGSHFCGGTLIHPSFVLTAAHCLRDIPQRLNVVLAHNVRTQEPQQHFSVAQVFLNNYDAENKLNDILLQ
LSSPANLSASAVTVQLPQQDQPVPHGTQCLAMGWGRVGAHDPPAQVLQELNVTVTFCRPHNICTFVPRRKAGICFGDSGGPLICDGIQGIDS
VIWGCATRLFPDFTRVALYVDWIRSTLR

>g1c5y.1_b.47.1.2 (A;B;) Urokinase-type plasminogen activator (LMW U-PA), catalytic domain {Human (Homo sapiens)}

LKFQCGQKTXIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGGSLMSPCWVISATHCFIDYPKKEDYIVYLGRSRLNSNTQGEMKFEVENLILHKDYSA
DTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCIEITGFGKEASTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADP
QWKTDSCQGDSGGPLVCSLQGRMTLTGIVSWGRGALKDKPGVYTRVSHFLPWIRSHTKEE

>d1ddja_b.47.1.2 (A:) Plasmin(ogen), catalytic domain {Human (Homo sapiens)}

SFDGKPKQVEPKKCPGRVVGCVAHPHSWPWQVSLTRFGMHFCGGTLISPEWVLTAAHCLEKSPRPSSYKVLGAHQEVNLEPHVQEIEVSRFL
EPTRKDIALLKLSAPPVTDKVIPACLPSPNYYVADRTECFITGWGETQGTFGAGLLKEAQLPVIENKVCNRYEFNLRVQSTELCAGHLAGGTDSCQG
DAGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRSRFTWIEGVMRNN

>d1fi8a_b.47.1.2 (A:) Granzyme B {Rat (Rattus norvegicus)}

IIGGHEAKPHSRPYMAYLQIMDEYSGSKKCGFLIREDFVLTAAHCSGSKIQVTLGAHNIKEQEKMQQIIPVVKIIPHPAYNSKTISNDIMLLKSKAKR
SSAVKPLNLPRRNKVKGPGDVCYVAGWGKLGPMGKYSDTLQEVETVQEDQKCESYLNKFYDKANEICAGDPKIKRASFRGDSGGPLVCKVVAAGI
VSYGQNDGSTPRAFTKVSTFLSWIKKTMKK

>d1iaua_b.47.1.2 (A:) Granzyme B {Human (Homo sapiens)}

IIGGHEAKPHSRPYMAYLMIWDQKSLKRCGGFLIRDDVLTAAHCWGSINVTLAGHNIKEQEPTQQFIPVKRPIPHPAYNPKNFSNDIMLLQLERKA
KRTRAVQPLRLPSNKAQVKPGQTCVAGWGQTAGPLGKHSHTLQEVKMTVQEDRKCESDLRHYYDSTIELCGDPEIKKTSFKGDGGPLVCNKVAQ
GIVSYGRNNGMPPRACTKVSSFVHWIKKTMKR

>d1eufa_b.47.1.2 (A:) Duodenase {Cow (Bos taurus)}

IIGGHEAKPHSRPYMAFLFKTSGKSHICGGFLVREDFVLTAHCLGSSINVTLGAHNIMERERTQQVIPVRPIPBDYNDETLANDIMLLKLTRKADI
TDKVSPINLPRSLAEVKPGMMCSVAGWGRGLVNMPSTDQLQEVDLEVQSEEKCIARFKNYIPFTQICAGDPSKRKNFSFGDSGGPLCNGVAQGIV
SYGRNDGTTPDVYTRISSFLSWIHSTM

>g1fiw.1 b.47.1.2 (L;A:) Beta-acrosin {Sheep (Ovis aries)}

TCDCPCGVFRQNIXIIGGQDAAHGAWPVMVSLQIFTYHNNRRYHCGGSSLNSQWLTAACFRIKKVTDWRLIFGAKEVEWGTNKPVKPPL
QERYVEKIIIEHKYSASSEANDIALMKITPPVTCGHFIGPGCLPQFRAGPPRVPQTCWAGWGFLQENARRTSPMLQEAVDIDLGLCNSTRWYNG
RIRSTNVCAKYPEGKIDTCQGDGGPLMCKDSAENSYVVVGITSWVGVCARA KPGVYTSTWSYLNWIASKIGSTAVHMIQLPT

>g1fiz.1 b.47.1.2 (L;A:) Beta-acrosin {Pig (Sus scrofa)}

ATCDGPCGLRFRQXVVGMSAEPGAWPVMVSLQIFTYHNNRRYHTCGGILLNSHWLTAACFKNKKVTDWRLIFGANEVVWGSNKPVKPP
LQERFVEEIIIHEKYVSGLEINDIALKITPPVPCGPFIGPGCLPQFKAGPPRAPQTCWVTGWGLKEKGRTSPTLQEAVRALIDLELCNSTRWYNGRIR
STNVCAKYPRGKIDTCQGDGGPLMCRDRAENTFVVVGITSWVGVCARA KPGVYTSTWPYLNWIASKIGSNALQMVLQGTTPR

>d1eaxa_b.47.1.2 (A:) Matriptase MTSP1 {Human (Homo sapiens)}

VVGGETADEGEWPWQVSLHALGQGHICASLISPWNLSAAHCYIDDRGFRTSDPTQWTAFGLHDQSQRSAVGQERRLKRIISHPFFNDFTFD
YDIALLELEKPAEYSSMVRPICLPDASHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCENLPPQQITPRMMCVCVGFLSGGVDSQGDSG
GPLSSVEADGRIFQAGVVSVGDGCAQRNKPGVYTRLPLFRDWIKENTGV

>d1svpa_b.47.1.3 (A:) Viral capsid protein {Sindbis virus}

ALKLEADRLFDVKNEGDGVIGHALAMEGKVMKPLHVKGTDIDHPVLSKLKFTKSSAYDMEFAQLPVNMRSEAFYTSEHPEGFYNWHGAVQYSGG
RFTIPRGVGRGDAGRPMIDNSGRVVAIVLGGADEGTRTALS VVTWNSKGKTIKTTPEGTEEWSA

>d1vcpa_b.47.1.3 (A:) Viral capsid protein {Semliki forest virus}

CIFEVKHEGVTKGYACLVGDKVMKPAHVKGVIDNADLA LAKFKKSSYDLECAQIPVHMRSDASKYTHEKPEGHYNWHGAVQYSGGRTIPTGAG
KPGDSGRPIFDNKGRVVAIVLGGANEGR TALS VVTWNKDMVTRVTPEGSEEW

>d1a1qa_b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

PITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTYHGAGSKTLAGPKGPIQMYTNVDQDLVGWQAPPGARSLSLPC
TCGSSDLYLVTRHADVIPVRRRGDSRGSSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRSVPF

>d1cu1a1 b.47.1.3 (A:705-720,A:3-186) NS3 protease {Human hepatitis C virus (HCV), different isolates}

GSVIVGRIILSGSGSXITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTYHGAGSKTLAGPKGPIQMYTNVDQDLV
GWQAPPGARSLSLPCCGSSDLYLVTRHADVIPVRRRGDSRGSSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTM
SPVFTD

>d1dxwa_b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

TGRDKNQVEGEVQVSTATQSFLATCVNGVCWTYHGAGSKTLAGPKGPIQMYTNVDQDLVGWQAPPGARSLSLPCCGSSDLYLVTRHADVIPV
RRRGDSRGSSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFVPVESMETTMRSASKKKK

>g1a1r.1 b.47.1.3 (A;C;) NS3 protease {Human hepatitis C virus (HCV), different isolates}

VEGEVQIVSTATQTFLATCINGVCWTYHGAGTRTIASP KGPVIQMYTNVDQDLVGW PAPQGSRSLSLPCCGSSDLYLVTRHADVIPVRRRGDSRG
SSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMRXGSVIVGRIVLSGKPA

>g1a1r.2 b.47.1.3 (B;D;) NS3 protease {Human hepatitis C virus (HCV), different isolates}

PITAYAQQTTRGLLGCIITS LTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTYHGAGTRTIASP KGPVIQMYTNVDQDLVGW PAPQGSRSLSLPC
CGSSDLYLVTRHADVIPVRRRGDSRGSSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMRXGSVIVGRIVLSGKPAII
PK

>g1dy9.1 b.47.1.3 (A;C;) NS3 protease {Human hepatitis C virus (HCV), different isolates}

APITAYSQQTRGLLGCIITS LTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTYHGAGSKTLAGPKGPIQMYTNVDQDLVGW PAPPGARSMT
CTCGSSDLYLVTRHADVIPVRRRGDSRGSSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMRXGSVIVGRIVLSGKPA

>g1ns3.1 b.47.1.3 (A;C;) NS3 protease {Human hepatitis C virus (HCV), different isolates}

ITAYSQQTRGLLGCIITS LTGRDKNQVEGEVQVSTATQSFLATCVNGVCWTYHGAGSKTLAGPKGPIQMYTNVDQDLVGW QAPPGARSLSLPC
CGSSDLYLVTRHADVIPVRRRGDSRGSSLLSPRPVSYLGSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVDFIPVENLETTMRXGSVIVGRIVLSGKPA

>d1befa_b.47.1.3 (A:) NS3 protease {Dengue virus serotype 2}
WDVPSPPVGKAELEDGAYRIKQKGILGYSQIGAGVYKEGTFTMWHVTRGAVLMHGKRIEPSWADVKKDLVSCGGGWKLEG EWKEGEEVQL
ALEPGKNPRAVQTCKPLFKTNAGTIGAVSLSDFSPGTSGSPIIDKKGVVGIYGNGVTRSGAYSAIAQTEKSIEDNPEIEDD

>d1cqqa_b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human rhinovirus type 2}
GPEEEFGMSLKHNSCVITTENGKFTGLGVYDRFVVVPTHADPGKEIQVDGITTKVIDSYDLYNKNGIKLEITVLKLDNEKF RDIRRIPNNEDDYPNC
NLALLANQPEPTIINVGDVSYGNILLSGNQTARMLKSYPTKSGYCGGVLYKIGQVLGIHVGGNGRDGFSAMLLRSYFT

>d1hava_b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human hepatitis A virus}
STLEIAGLVRKNLVQFGVGEKNGSVRWWVNALGVKDDWLLVPSHAYKFEKDYEEMMEFYFNRRGGTYYISAGNVVIQSLDVG FQDV VLMKVPTIPK
FRDITQHFIIKKGDVPRALNRLATLTTVNGTPMLISEGPLKMEEKATYVHKKNDGTTV DLTVDQAWRGKGEGLPGMC GGGALVSSNQSIQNAILGIH
VAGGNSILVAKLVTQEMFQNI DKKI

>d2hrva_b.47.1.4 (A:) 2A cysteine proteinase {Human rhinovirus 2}
GPSDMYVHVGNLIYRNHLFNFNSEMHEISLVS YSSD LIIYRTNTVGDDYIPSCDCTQATYYCKHKNRYFPITVTS HDWYEIQESEYYPKHIQY NLLIGEGP
CEPGDCGGKLLCKHG VIGIVTAGGDNHVAFIDL RHFHC A

>d1bco_1 b.48.1.1 (481-560) mu transposase, C-terminal domain {Bacteriophage mu}
TEEQKRMLLPAEA NVSRKG EFTLKVGSSLGAKNVYNNM ALMNA GVKKV VRDPQQLH STV CYTL DGRFICEAECL

>d1e79a2 b.49.1.1 (A:19-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}
ADTSVDLEETGRVLSIGDGIARVHGLRVNQAEMVEFSSGLKGMSLNLEPDNVGVVVF GNDKLIK EGDIVKRTGAI

>d1e79d2 b.49.1.1 (D:9-81) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}
TTGRIVAVIGAVV DVQFDEGLPPI LNALEVQGRETRLVLEVAQHLGESTV RTIAMDGTEGLVRGQKVLD SGAP

>d1maba2 b.49.1.1 (A:10-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (Rattus norvegicus)}
SSILEERILGADTSVDLEETGRVLSIGDGIARVHGLRVNQAEMVEFSSGLKGMSLNLEPDNVGVVVF GNDKLIK EGDIVKRTGAI

>d1mabb2 b.49.1.1 (B:1-81) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (Rattus norvegicus)}
SAAPKAGTATGQIVAVIGAVV DVQFDEGLPPI LNALEVQGRETRLVLEVAQHLGESTV RTIAMDGTEGLVRGQKVLD SGAP

>d1skyb2 b.49.1.1 (B:21-95) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}
SQIQVSDVGTVIQVGDIARAHGLDNVMSGEAVEFANA VMGMALNLEENN VGIVILGPYTGIKEGDEV RRTGRIM

>d1skye2 b.49.1.1 (E:1-82) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}
MTRGRV I QVMGPV DVFKFENGHLPAIYNALKIQHKARNENEVDIDL TLEVALH LGDDTV RTIAMASTDGLIRGM EVIDT GAP

>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}
NLGRIAQIIGPV LNVAFPPGKMP NIYNALIVKGRDTAGQPMN VTCEVQQLGNN RVRAVAMSATDGLTRGMEVIDT GAP

>d1bd0a1 b.49.2.1 (A:2-11,A:245-382) Alanine racemase {Bacillus stearothermophilus}
NDFHRDTWAEXFSLHSRLVHVKKLQPGEK VSYGATYTAQTEEWIGTIPIGYADGWLRRLQHFHVLDGQKAPIVGRICMDQCMIRLPGPLVGT KV
TLIGRQGDEVISIDDVARHLETINYEVPC TISYRVPRIF FRHKRIMEV RNAIG

>d1d7ka1 b.49.2.1 (A:7-43,A:284-427) Eukaryotic ornithine decarboxylase {Human (Homo sapiens)}
EEFDCHFLDEGFTAKDILDQKINEVSSDDKDAFYVAXFTLAVNIIAKKVLKEQTGS DDEDESSEQTFMYYVNDGVYGSFNCILYDH AHVKPLLQKR PK
PDERYYSSSIWGPTCDGLRIVERCDLPEMHVG DWMLFENMGAYTVAA ASTFNGFQRPTIYVMSGPAWQLMQQFQNPDFPP

>d7odca1 b.49.2.1 (A:2-43,A:284-418) Eukaryotic ornithine decarboxylase {Mouse (Mus musculus)}
SSFTKDEF DCHILDEGFTAKDILDQKINEVSSDDKDAFYVAXFTLAVNIIAKKTVWKEQPGS DDEDESNEQTFMYYVNDGVYGSFNCILYDH AHVK
LLQKRPKPDEKYYSSSIWGPTCDGLRIVERCNLPEMHVG DWMLFENMGAYTVAA ASTFNGFQRPNI YYVMSRP MWQLMK

>d1f3ta1 b.49.2.1 (A:14-43,A:284-422) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}
RFLEGFNTRDALCKKISMNT CDEGDPFFVAXFTLAVNVI AKKVT PGVQTDV GAHAESNAQSF MYYVNDGVYGSFNCILYDH AVVRPLPQREP IPNEK

LYPSSVVGPTCDGLDQIVERYYLPEMQVGEWLLFEDMGAYTVVGTSFNGFQSPTIYVVSGLPDHVVRELKS
>d2toda1 b.49.2.1 (A:37-43,A:284-410) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}
GDPFFVAXFTLAVNVIACKVTGPGVQTGVGAHAESNAQSFMYVNDGVYGSFNCLYDHAVRPLPQREPNEKLYPSSVVGPTCDGLDQIVERYYL
PEMQVGEWLLFEDMGAYTVVGTSFNGFQSPTIYVV
>d1b6la_b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWKRPLVTIRIGGQLKEALLDTGADDTVIEEMNLPGKWPCKMIGGIGGFIKVRQYDQIPVEIXGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
>d1bdqa_b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWQRPLVTIKIGGQLKEALLDTGADDSIVAGIELPGRWKPKMVGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
>d1c6ya_b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWQRPVVTIKIGGQLMEALDTGADDTVLEEMDLPGRWKPKIIGGIGGFVKVRQYDQIPIEICGHKVIGTVLVGPTPTNIIGRNLLTQIGCTLNF
>d1dazc_b.50.1.1 (C:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWKRPLVTIKIGGQLKEALLDTGADDTVIEEMSLPGRWKPKMIGGIGGFIKVRQYDQIIIEAGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
>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}
PQITLWQRPLVTIRIGGQLKEALLDTGADDTVLEEMNLPGKWPCKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
GSSGPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCT
LNF
>d1idaa_b.50.1.1 (A:) Human immunodeficiency virus type 2 (HIV-2) protease {Human immunodeficiency virus type 2}
PQFSLWKRPLVTAIEGQPVEVLLDTGADDSIVAGIELGNNSPKIVGGIGGFINTKEYKNVEIEVLKKVRATIMTGDTPINIFGRNILTALGMSLN
>d1az5_b.50.1.1 (-) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}
PQFHHLWKRPLVTAIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVEEVLGKRIKGTIMTGDTPINIFGRNLLTALGMSLN
>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}
PQFSLWRRPVTAIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVIEVLGKRIKGTIMTGDTPINIFGRNLLTALGMSLN
>d4fiv_b.50.1.1 (-) Feline immunodeficiency virus (FIV) protease {Feline immunodeficiency virus}
VGTTTLEKRPEIIFVNYPKFLLDTGADITILNRRDFQVKNSIENGQRQNMIGVGGGKRGTNYINVHLEIDENYKTQCIFGNVCVLEDNSLIQPLL
RDNMFIKFNIRLVM
>d1baia_b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}
LAMTMEEHKDRPLVRVILNTGSHPVKQRSVYITALDTGADDTVISEEDWPTDWPVMEAANPQIHGGGIPVRKSRDMIELGVINRDGSLERPLLL
FPLVAMTPVNIILGRDCLQGLGLRLTNL
>d2rspa_b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}
LAMTMEEHKDRPLVRVILNTGSHPVKQRSVYITALDSGADITIISEEDWPTDWPVMEAANPQIHGGGIPMRKSRDMIELGVINRDGSLERPLLF
PAVAMVRGSILGRDCLQGLGLRLTNL
>d1fmb_b.50.1.1 (-) EIAV protease {Equine infectious anemia virus}
VTYNLEKRPTTIVLINDTPLNVLLDTGADTSVLTAAHYNRLKYRGRKYQGTGIGGVGGNVETFSTPVTIKKGRHIKTRMLVADIPVTILGRDILQDLGA
KLVL
>d2er7e_b.50.1.2 (E:) Endothiapepsin {Chestnut blight fungus (Endothia parasitica)}
STGSATTPIDSDDAYITPVQIGTPAQTLNLDFTGSSDLWVFSSETTASEVDGQTIYTPSKTTAKLLSGATWSISYGDSSSSGDVYDTVSVGGLTV
TGQAVESAKVSSFTEDSTIDGLLAFSTLNTVSPTQQKTFDNAKASLDSPVFTADLGYHAPGTYNFGFIDTTAYTSITYAVSTKQGFWEWTST
GYAVGSGTFKSTSIDGIADTGTLLYLPATVVSAYWAQVSGAKSSSVGGYVFPCSATLPSFTFGVGSARIVPGDYIDFGPISTGSSCFGGIQSSAGIGI
NIFGDVALKAFAVFVNGATTPTLGFASK
>d1bxoa_b.50.1.2 (A:) Acid protease {Fungus (Penicillium janthinellum), penicillopepsin}

AASGVATNPTANDEEYITPVТИGTTLNLFDTGSADLWVFSLELPASQQSGHSVYNPSATGKELSGYTWSISYGDGSSASGNVFTDSVTGGVTA
HGQAVQAQQQISAQFQQDTNNGLLAFSSINTVQPQSQTFFDTVKSSLAQPLFAVALKHQQPGVYDFGFIDSSKYTGSLTGVDNSQGFWSF
NVDSYTAGSQSGDGFSGIADTGTLLLDSSVSVQYSQVSGAQQDSNAGGYVFDCSTNLPDFSVSISGYTATVPGSLINYGPSGDGSTCLGGIQSNS
GIGFSIFGDIFLKSQYVVFSDGPQLGFAPQA

>d1ibqa_b.50.1.2 (A:) Acid protease {Fungus (*Aspergillus phoenicis*), aspergilopepsin}

SKGSAVTPQNNDEEYLTPVTVGKSTLHLDFTGSADLWVFSDELPSEQTGHDLYTPSSATKLSGYSWDISYGDGSSASGDVYRDTVTGGVTTNK
QAVERAASKISSEFVQDTANDGLLGAFSSINTVQPKAQTTFDTVKSQLDPLFAVQLKHDAPGVYDFGYIDDSKYTGSITYTDADSSQGYWGFSTDG
YSIGDGSSSSSGFSIAADTGTLLILLDEIVSAYEQVSGAQESYEAGGYVFSCSTDLPDFTVIGDYKAVVPGKYINYAPVSTGSSTCYGGIQSNSGLGS
ILGDFVFLKSQYVVFNFSEGPKLGFAAQAA

>d2apr__ b.50.1.2 (-) Acid protease {Bread mold (*Rhizopus chinensis*)}

AGVGTVPMTDYGNIDIEYYGQVTIGTPGKKFNLDFTGSSDLWIASTLCTNCGSQTKYDPNQSSTYQADGRTWSISYGDGSSASGILA KDNVNLLGG
LLIKGQTIELAKREAASFASGPNDGLLGFDITTVRGVKTMDNLISQGLISRPIFGVYLGKAKNGGGYEIFFGYDSTKFKGSLTTVIDNSRGWW
GITVDRATVGTSTVASSFDGILDGTLLIPNNIAASVARAYGASDNGDGTYTISCDTSAFKPLVFSINGASFQVSPDSLVEEFQGQCIAGFGYGNWG
FAIIGDTFLKNYYVVFNQGVPEVQIAPVAE

>d2asi__ b.50.1.2 (-) Acid protease {Rhizomucor miehei}

GSVDTPGYYDFDLEEEYAI PVSIGTPGQDFLFDTGSSDTWPHKGCKTSEGCVGSRFFDPSASSTFKATNYNLNITYGTGANGLYFEDSIAIGDITVTK
QILAYVDNRGPTAEQSPNADIFDGLFGAAYPDNTAMEAEYGSTYNTVHVNLKQGLISSPLFSVYMNTNSGTGEVVFGVNNTLLGGDIAYTDV
MSRYGGYYFWDAPVTGITVDGSAAVRFSRPQAFTIDTGTNFFIMPSSAAASKIVKAALPDATETQQGWVVP CASYQNSKSTISIVMQKGSSSDTIEIS
VPVSKMLLPVQDQSNETCMFIILPDGGNNQYIVGNLFLRFFVNVDGNNRIGFAPLASAYENE

>d1eaga_b.50.1.2 (A:) Acid protease {Yeast (*Candida albicans*)}

QAVPVTLHNEQVTYAADITVGSNNQKLNVIDTGSSDLWVPDVNVDCQVTSQDQTAFCQKQTYDPGSSASQDLNTPFKIGYGDGSSSQGTLYK
DTVGFGGSVIKNQVLADV DSTS IDQGILGVYKTN EAGGSYDNPVTLKKQGVIKNASYLNSPDAATGQIIFGGVDNAKYSGSLIALPVTSDRELR
ISLG SVEVSGKTINTDNVDVLLSGTTITYLQQDLADQIKA FNGKLTQDSNGNSFYEVDCNLSGDVVFNFSKNAKISVPAEFAASLQGDDGQPYDK
CQLLFDVN DANILGDNFLRSAYIVYD LDDNE ISLAQVKY TSASSISALT

>d1j71a_b.50.1.2 (A:) Acid protease {Yeast (*Candida tropicalis*)}

SDVPTTLINEGPSYAADIVVGSNNQKQTVVDTGSSDLWVVDTDAECQVTSQGQTNFCKQEGTFDPSSSAQNLNQDFSIEYGD LSSQGSFYKD
TVFGGGISIKNQQFADVTTSVDQGIMGIFTADEAGYNYLDNPVTLKKQGIIKNASYLNSEDASTGKII FGGVDNAKYTGTLTALPVTSV ERL
HLGSINF DGT SVSTNADV VLD SGTTIYFSQ STADK FARIVGAT WDSR NEIYRLPSCDLSGDAVNFQDQGVKITVPLSEI LK DSSIC YFG ISRN DANI
LGDNFLRRAYIVYD LDDKTISLAQVKY TSSSD ISAL

>d1dpja_b.50.1.2 (A:) Acid protease {Baker's yeast (*Saccharomyces cerevisiae*), proteinase A}

GGHDVPLNYLNAQYYTDTLGTTPQNFKVILDGSSNLWVPSNECGSLACFLHSKYDHEASSYKANGTEFAIQYGTGSLEGYISQDTLSIGDLTIPKQ
DFAEATSEPLGTFAGKFDGILGLGYDTISV DKV VPPFYNAIQQ DLLDEKRF AFY LGDTSKDTENGGEATFGGIDESFKG DITWLPVRRKAYWEVKFE
GIGLGDEYAELES HGAIA DTG SLTLP SGLAEMINA EIGAKKGWTGQYTLDCNTRDNLPD LIFNFNGYNFTIGPYD TLEVSGSCISAITPMDFPEPVG
PLAIVGDAFLRKYYSIYDLGNNAVGLAKAI

>g1b5f.1 b.50.1.2 (A;B:) Plant acid proteinase, phytepsin {*Cynara cardunculus*}

GS AVV ALT NDR DTSYFGEIGIGTPPQKFTVIFDTGSSNLWVPSAKCINSKACRAHSMYESSDSSTYKENGTFGAIYGTGSITGFFS QDSVTIGDLVVKEQ
DFIEATDEADNVFLHRLFDGILGLSFQTISV PVWY NMLNQGLVKERRFSFWLNRN VDEE EGGELVFGGLDPNHF RDHTYVPTVQYYWQFGIGDV
LIGDKSTGFCAPGCQAFADSGTSLLSGPTAIVTQINHAIGANXEELQVDCNTLSSMPNVSFTIGGKKFGLTPEQYILKVGKGEATQCISGFTAM DATLLG
PLWI LGDV FM RP YHTVFDYGNLLVGFAEAA

>d1qdma2 b.50.1.2 (A:2-247,A:248-338) Plant acid proteinase, phytepsin {Barley (*Hordeum vulgare*)}

EEEGDIVALKNYMNAQYFGEIGVGTPPQKFTVIFDTGSSNLWVPSAKCYSIACYLHSRYKAGASSTYKKNKGKPAAIQYGTGSIAGYFSED SVT GDLV
VKDQE FIEATKEPGITFLVAKFDGILGLGFKEISVGKAVPVWYK MIEQGLVSDPVFSFWLNRHVDEGEGGEIIFGGMDPKHYVGEHTYVPTQKGW
QFDMDGVLVGGKSTGFCAGGCAAIA DSGTSLLAGPTAITEINEKIGAAGXSPMGE SAVDCGSLGSMPDIEFTIGGKKFALKPEEYILKVGEGAAAQC
SGFTAMDIPPRGPLWILGDVFMGPYHTVFDYGKL RIGFAKAA

>d3psg__ b.50.1.2 (-) Pepsin(ogen) {Pig (Sus scrofa)}

LVKVPLVRKKSLRQNLIKDGKLFKLTHKHNPASKYFPEAAALIGDEPLENYLDTEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDSSSTFEATSQEELSITYGTGSMGTILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISASGATPVFDNLWDQGLVSQDLSFSVYLSNDDSGSVVLLGGIDSSYYTGSLNWVVPVSVEGYWQITLDSITMDGETIACSGGCQAIVDTGTSLLGPTSAIANIQSDIGASENSDGEMVISCSSIDSPLDIVFTIDGVQYPLSPSAYILQDDDSCTSGFEGMDVPTSSGELWALGDVFIRQYYTFDRANNKVGLAPVA

>d4pep__ b.50.1.2 (-) Pepsin(ogen) {Pig (Sus scrofa)}

IGDEPLENYLDTEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDSSSTFEATSQEELSITYGTGSMGTILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISASGATPVFDNLWDQGLVSQDLSFSVYLSNDDSGSVVLLGGIDSSYYTGSLNWVVPVSVEGYWQITLDSITMDGETIACSGGCQAIVDTGTSLLGPTSAIANIQSDIGASENSDGEMVISCSSIDSPLDIVFTIDGVQYPLSPSAYILQDDDSCTSGFEGMDVPTSSGELWALGDVFIRQYYTFDRANNKVGLAPVA

>d1psoe_ b.50.1.2 (E:) Pepsin(ogen) {Human (Homo sapiens), 3A}

VDEQPLENYLDMEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACTNHNRNFNPEDSSTYQSTSETVSITYGTGSMGTILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISASGATPVFDNLWDQGLVSQDLSFSVYLSADDQGSVVIFFGIDSSYYTGSLNWVVPVTVEGYWQITVDSITMNGEAIACAEGCQAIVDTGTSLLGPTSPIANIQS DIGASENSDGDMVVSCAISLSDP DIVFTINGVQYPVPPSAYILQSEGSCISGFQGMNLPTESGELWILGDVFIRQYYTFDRANNKVGLAPVA

>g1htr.1 b.50.1.2 (P;B;) Pepsin(ogen) {Human (Homo sapiens), progastricsin (pepsinogen C)}

AVVKVPLKKFSIRETMKEKGLGEFLRTHKYDPAWKYRGDLXSVTYEPMAYMDAAYFGEISIGTPQNFNLVFDTGSSNLWVPSVYCSQACTSHSRFNPSESSTYTNQQTFLSQYQSGSLTGFYDTLTQSIQVNPNEQFGLSENEPGTNFVYAQFDGIMGLAYPALSVDEATTAMQGMVQEGALTSPFVSVYLSNQQGSSGAFFGGVDSSLYTQIYWAPVTQELYWQIGIEFLIGGQASGWCEGCQAIVDTGTSLLTVQPQYMSALLOQATGAQEDEYQGFVN CNSIQNLPSLTFIINGVEFPLPSSYIISNNNGYCTVGEPTYLSSQNGQPLWILGDVFLRSYYSYDLGNRRVGATAA

>d1am5__ b.50.1.2 (-) Pepsin(ogen) {Atlantic cod (Gadus morhua)}

RVTEQMKNADTEYYGVISIGTPPESFKVIFDTGSSNLWVSSHCSAQACSNHNKFPRQSSSTYETGKTVDLTYGTGGMRGBILQDTSVVGGSDPNQELGESQTEPGPFQAAAPFDGILGLAYPSIAAGAVPVFDNMGSQSLVEKDLFSFYLSGGGANGSEVMLGGVDNSHTGSIHWIPVTAEKYWQVALDGITVNGQTAACEGCGQAIVDTGTSKIVAPVSALANIMKDIGASENCQGEMMGNCASVQLPDITFTINGVKQPLPPSAYIEGDQAFCTSGLGSSGPNSNTSELWIFGDVFLRNEYTIYDRTNNKVGFAA

>d1mpp__ b.50.1.2 (-) Pepsin {Mucor pusillus}

GSDVTPGLYDFDLEEYAIPIVSIGTPGQDFYLLFDTGSSDTWVPHKGCDNSEGCVGKRFFDPSSSTFKETDYNLNITYGTGGANGIYFRDSITVGGATVKQQTLAYVDNVSGPTAEQSPDSELFLDGIGFGAAYPDNTAMEAEYGDYNTVHVNLKYQGLISSPFSVYMNTNDGGQVVFGGVNNTLLGGDIQYTDVLKSRGGYFFWDAPVTGVKIDGSDAVSFDAQAFTIDGTNFIAPSSFAEKVKAALPDATESQQGYTVPCSKYQDSKTTFSLVLQKGSSSDTIDVSVPISKMLLPVDKSGETCMFIVLPDGGNQFIVGNLFLRFFVNVDGKRNIGFAPLASGYEND

>g1lyb.1 b.50.1.2 (A;B;) Cathepsin D {Human (Homo sapiens)}

GPIPEVLKNYMDAQYYGEIGIGTPPQCFTVFDTGSSNLWVPSIHCCKLIDACWIHHKYNSDKSSTYKNGTSFDIHGSGSLSGYLSQDTVSPCQXGGVKVERQVFGEATKQPGITFIAAKFDGILGMAYPRISVNNVLPVFDNLMQQKLVDQNISSFYLSRDPDAQPGGELMLGGTDSKYKGSLSYLNTRKAYWQVHLDQVEVASGLTLCKEGCEAIVDTGTSLMVGPVDEVRELQKAIGAVPLIQGEYMIPCEKVSTLPAITLKGKGYKLSPEDYTLKVSQAGKTLCLSGFMGMDIPPPSGPLWILGDVFIGRYYTFDRDNRRVGFAA

>d3cms__ b.50.1.2 (-) Chymosin (synonim: renin) {Cow (Bos taurus)}

GEVASVPLNYLDSQYFGKIYLGTPPQEFTVLFDTGSSDFWVPSIYCKSNACKNHQRFDPRKSSTFQNLGKPLSIHYGTGSMQGILGYDTVTSNIVDIQQTVGLSTQEPGDFTYAEFDGILGMAYPSLASEYSIPVFDNMNNRHLVAQDLSFSVYMDRNGQESMLTGAIDPSYYTGSLLHWVPPVTVQQYWQFTVDSVTISGVVVAEEGCCQAILDTGTSKLVGPSSDILNIQQAIGATQNQYGEFDIDCDNLSYMPTVFEINGKMYPLTPSAYTSQDQGFCTSGFQSENHSQKWILGDVFIREFYYSVDRANNLVGLAKAI

>d1hrna_ b.50.1.2 (A:) Chymosin (synonim: renin) {Human (Homo sapiens)}

GNTTSSVILTNYMDTQYYGEIGIGTPPQTFKVVFDTGSSNVWVPSKCSRLYTCVYHKLFDASDSSSYKHNGTELTLYSTGTVSGFLSQDIITVGGITVTQMFGEVTEMPALPFMЛАЕFDGVVGGMGFIЕQAIGRVTIFDNIISQGVLKEDVFSFYNNRDSENSQSLGGQIVLGGDPQHYEGNFHYINLIKTVWQIQMKGVSVGSSTLLCEDGCLALVDTGASYISGSTSSIEKLMEALGAKKRLFDVVKCNEGPTLFDISFHLLGKEYTLSADYVFQESYSSKKLCTLA

HAMDIPPTGPTWALGATFIRKFYTEFDRRNNRIGFALAR

>d1smra_b.50.1.2 (A:) Chymosin (synonym: renin) {Mouse (*Mus musculus*)}

TDLISPVVLNTYLNQYGEIGITPPQTFKVIFDTGSANLWVPSTKCSRILACGIHSLYESSDSSYMENGDDFTIHGSGRVKGFLSQDSVTVGGITV
TQTFGEVTQLPLIPFMLAQFDGVLMGMGPAQAVGGTPVFDHILSGVLKEKVFSVYYNRGPHLGGEVVLGGSDPQHYQGDFHYVLSKTDWSQ
ITMKGVSVGSSTLLCEEGCEVVDTGSSFISAPSSLKLIMQALGAKEKRRLHEYVVSCSQVTPLDISFNLLGRAYTLSSTDYLQYPNRRDKLCTVALH
AMDIPIPPTGPVWVLGATFIRKFYTEFDRHNNRIGFALAR

>d1fkna_b.50.1.2 (A:) beta-secretase (memapsin) {Human (*Homo sapiens*)}

RRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFAVGAAPHFPLHRYYQRQLSSTYDLRKGVVPTYQGKWEGLGTDLVSIPH
PNVTVRANIAITESDKFFINGSNWEGLAYAEIARPDDSLEPFDSLKVQTHVNPNLFLQLCAGFPQNLQSEVLA
S VGGSMIIGGIDHSLYTGSWY
TPIREWYYEVIVRVEINGQDLKMDCKEYD
KSIVD
SGTTNLRPKVFEAAV
KSI
AASSTE
KFPDGFWLGEQLVCWQAGTPWN
IFPVISLYLM
GEVTNQSFRITILPQQYLRPVEDVATSQDDCYKFAISQS
STGTVMGAVIMEGFYVV
FDRARKRIGFAVSACHV
DEFRTAAVEGPFV
TLD
MEDCGYN

>d1pfza_b.50.1.2 (A:) Plasmeprin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}

HLTIGFKVENAHDRIKTIKHLKNYIKESVN
FLNSGLTKTN
LGSSNDNIELVDFQ
NIMFYGDAEV
GDNQ
PFT
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TSANLW
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KCTAGCLT
KHLYDSS
KSRTY
EKG
DKV
EMNY
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>d1smea_b.50.1.2 (A:) Plasmeprin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}

SSNDNIELVDFQ
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>d1qs8a_b.50.1.2 (A:) Plasmeprin ii (a hemoglobin-degrading enzyme) {Plasmodium vivax}

SENDVIELDDVANIMFYGE
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>d1ile_2 b.51.1.1 (198-386) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}

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>d1ffya2 b.51.1.1 (A:201-394) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

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>d1gaxa2 b.51.1.1 (A:190-342) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}

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>d1gmua1 b.107.1.1 (A:1-70) Urease metallochaperone UreE, N-terminal domain {Klebsiella aerogenes}

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>d1eara1 b.107.1.1 (A:1-74) Urease metallochaperone UreE, N-terminal domain {Bacillus pasteurii}

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>d2eng_b.52.1.1 (-) Endogucanase V {Humicola insolens}

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>d1bw3_b.52.1.2 (-) Barwin {Barley (*Hordeum vulgare*)}

EQANDVRATYHYYRPAQNNWDLGAPAVSAYCATWDASKPLSWRSKYGTAFCGPAGPRGQAACGKCLRVTNPATGAQITARIVDQCANGGLID
WDTVFTKIDTNGIGYQQGHLNVNYQFVDCRD

>g1aw8.1 b.52.2.1 (A;B:) Pyruvoyl dependent aspartate decarboxylase, ADC {Escherichia coli}

MIRTMILQGKLHRVKVTHADLHYEGXCAIDQDFLDAAGILENEAIDIWNVNTNGKRFSTYIAAERGSRIISVN GAAAHCASVGDIVIIASFVTMPDEE
ARTWRPNVAYFEGDNEMIK

>d1eu1a1 b.52.2.2 (A:626-780) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter sphaeroides}

ERLGGAGAKYPLHVVASHPKSRLHSQNLNTSLRDLYAVAGHEPCLINPADAARGIADGDVLRVFNDRGQILVGAKVSDAVMPGAIQIYEGGWYDP
LDPSEEGTLDKYGDVNVLSDLVGTSLAQGNCGQTILADVEKYAGAPVTVTVFDTPKGA

>d1dmr_1 b.52.2.2 (626-781) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter capsulatus}

ERLDGPGAKYPLHIAASHPFNRLHSQNLNTLVREGYAVQGHEPCLMHPPDAAARGIADGDVVRVHNDRGQILGVKVTDAVMKGVIQIYEGGWY
DPSDVTEPGTLDKYGDVNVLSDLVGTSLAQGNCGQTVAEVEKYGPAVTLTGFVAPKAAE

>d1aa6_1 b.52.2.2 (565-715) Formate dehydrogenase H {Escherichia coli}

PIDKLTDEYPMVLSRVREVGHYSCRSMGNCAALALA DEPGYA QINTEDAKRLGIEDEALVVWHSRKGIITRAQVSDRPNKGAIYMTYQWWIGA
CNELVTENLSPITKTPYEKYCAVRVEPIADQRAAEQYVIDEYNKLKTRLREAALA

>d1tmo_1 b.52.2.2 (632-798) Trimethylamine N-oxide reductase {Shewanella massilia}

ERSHGGPGSDKHPIWLQSCHPDKRLHSQMCSREYRETYAVNGREPVYISPVDAKARGIKDGDIVRFNDRGQLLAGAVVSDNFPKGIVRIHEGAW
YGPVGKDGSTEAGVGALCSYGDPNTLTDIGTSKLAQACSAYTCLVEFEKYQGKVPKVSSFDGPIEVI

>d1g8ka1 b.52.2.2 (A:683-825) Arsenite oxidase large subunit {Alcaligenes faecalis}

LPATVQQQDKYRFWLNNGRNNEVWQTAYHDQNSLMQERYPMAYIEMNPDDCKQLDVTGGDIVEVYNDFGSTFAMVYPVAEIKRGQTFMLF
GYVNGIQGDVTTDWTDIIPYYKGTWGDIRKVGSMSEFKRTVSFKSRRFG

>d2napa1 b.52.2.2 (A:601-723) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}

AAEEDPAEYPLYLTSMRVIDHWHTATMTGKPELQKANPIAFVEINEEDAARTGIKHGDSVIVETRRDAMELPARVSDVCRPLIAVFFDPKKLVNK
LFLDATDPVSREPEYKICAARVRKA

>d1qcsa1 b.52.2.3 (A:0-85) N-terminal domain of NSF-N, NSF-Nn {Hamster (Cricetulus griseus)}

NMAGRSMQAARCPTDELNSNCAVVSEKDYQSGQHVIRTPNHYIFTLTHPSVPGSVAFLPQRKWAGLSIGQEVALYSF

>d1cr5a1 b.52.2.3 (A:26-107) N-terminal domain of NSF-N, NSF-Nn {Baker's yeast (Saccharomyces cerevisiae), sec18p}

TRHLKVSNCPPNSYALANVAAVSPNDFPNNIYIIIDNLVFTTRHSNDIPP GTIGFNGNQRTWGGWSLNQDVQAKAFDLFKY

>d1cz4a1 b.52.2.3 (A:1-91) N-terminal domain of VAT-N, VAT-Nn {Archaeon Thermoplasma acidophilum}

MESNNNGIILRVAEANSTDPGMSRVRLESSLRLDAEIGDVVEIEKVRKTVGRVYRARPEDENKGIVRIDSVMRNNCGASIGDKVKVRKVR

>d1e32a1 b.52.2.3 (A:21-106) Membrane fusion atpase p97 N-terminal domain , P97-Nn {Mouse (Mus musculus)}

NRPNRILIVEAINEDNSVVSLSQPKMDELQLFRGDTVLLKGKKRREAVCIVLSDDTCSDEKIRMNRVVRNNLRVRLGDVISIQPCP

>d1dfup_ b.53.1.1 (P;) Ribosomal protein L25 {Escherichia coli}

MFTINAVERKEQGKGASRRLRAANKFPAAIYGGKEAPLAIELDHDKVMNMQAKAEFYSEVLTIVDGKEIKVKAQDVQRHPYKPKLQLQHIDFVRA

>d1feua_ b.53.1.1 (A;) Ribosomal protein TL5 (general stress protein CTC) {Thermus thermophilus}

MEYRLKAYYREGEKPSALRRAAGKLPGLMYNRHLNRKVYVDLVEFDKVFRQASIHIVLELPDGQSLPLVRQVNLDKRRRPEHVDFVLSDEPVE
MYVPLRFVGTAGVRAGGVQLQEIHDLVKVSPRNIPEFIEVDVSGLEIGDSLHASDLKLPPGVELASPEETIAAVVPPPEDVEKLAE

>d1gtra1 b.53.1.2 (A:339-547) Glu-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain {Escherichia coli}

APRAMAVIDPVKLVIENYQGECEMVMPNHPNPKPEMGSRQVPFSGEWIDRADFREEANKQYKRLVLGKEVRLRNAYVIKAERVEKAEGNITTIF
CTYDADTLSKDPADGRKVKGVIHWVSAAHALPVEIRLYDRLFSVPNPGAADDFLSVINPESLVIKQGFAEPSLKDAVAGKAFQFEREGYFCLDSRHSTA
EKPVFNRTVGLRDT

>d1h9db_ b.54.1.1 (B;) Core binding factor beta, CBF {Human (Homo sapiens)}

PRVVPDQRSKFENEFFRQLSRECEIKYTGFRDRPHEERQARFQNACRDRSEIAVATGTNLSQFFPASWQGEQRQTPSREYVDLEREAGKVLKA
PMILNGVCVIWKGWIDLQRDGMGCLEFDEERAQQE

>d1mai__ b.55.1.1 (-) Phospholipase C delta-1 {Rat (Rattus norvegicus)}

GLQDDPDLQALLKGSQLKVKSSEWRRERFYKLQEDCKTIWQESRKVMRSPESQLFSIEDIQEVRMGRTEGLEKFARDIPEDRCFSIVFKDQRNTLD
LIAPSPADAQHWVQGLRIIH

>d1btn__ b.55.1.1 (-) beta-spectrin {Mouse (Mus musculus), brain}

MEGFLNRKHEWEAHNKASSRSWHNVYCVINNQEMGFYKDAKSAASGIPYHSEVPVSLKEAICEVALDYKKKKHVFKLRLSDGNEYLFQAQKDDEE
MNTWIQAISSA

>d1dro__ b.55.1.1 (-) beta-spectrin {Fruit fly (Drosophila melanogaster)}

GSGTGAGEGHGYVTRKHEWDSTTKASNRSWDKVYMAAKAGRISFYKDQKGYSNPELTFRGEPSYDLQNAIAEIASDYTKKHVLRVKLANGAL
FLLQAHDDTEMSQWVTSLKAQSDSTA

>d1dyna_ b.55.1.1 (A:) Dynamin {Human (Homo sapiens)}

ILVIRKGWLTIINIGIMKGGSKEYWFVLTAEENLSWYKDDEEKKYMLSVNDNLKLRDVEKGMSSKHIFALFNTEQRNVYKDYRQLELACETQEEVDS
WKASFLRAGVYPERV

>d1btk_ b.55.1.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}

AAVILEISFLKRSQQKKKTSPLNFKCLFLTVHKLSYYEYDFERGRGSKGSIDVEKITCETVVPEKNPPPERQIPRRGEESSEMEQISIIERFPYPFQV
VYDEGPLYVFSPTTEELRKRWIHLQKNVIRYNSDLVQKYHPCFWIDGQYLCCSQTAKNAMGCQILEN

>d1pls__ b.55.1.1 (-) Pleckstrin, N-terminal domain {Human (Homo sapiens)}

MEPKRIREGYLVKKGSVFNTWKPMWVVLLEDGIEFYKKSDNSPKGMIPLKGSTLTSPCQDFGKRMFVKITTKQQDHFFQAAFLEERDAWVRDI
NKAICIEGLEHHHHHH

>d1dbha2 b.55.1.1 (A:418-550) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}

AIKKMNEIQKNIDGWEGKDIGHGCCNEFIMEGTLTRVGAKHERHIFLDGLMICCKSNHGQPRLP GASNAEYRLKEKFFMRKVQJNDKDDTNEYKHA
FEIILKDENSVISAKSAAEKNNWMAALISLQYRSTL

>d1foea2 b.55.1.1 (A:1240-1401) GEF of TIAM1 (T-Lymphoma invasion and metastasis inducing protein 1) {Mouse (Mus musculus)}

EFGAVFDQLIAEQTGEKKEVADLSMGDLLHTSVIWLNPASLGWKKEPELAASFVFTAVVLVYKDGSQKQKKLVGSHRLSIYEWDPFRFRHMIPT
EALQVRALPSADAEEANAVCEIVHVKSESEGRPERVFHLCCSPESRKDFLKSVHSILRDKHRRQ

>d1bak__ b.55.1.1 (-) G-protein coupled receptor kinase 2 (beta-adrenergic receptor kinase 1) {Human (Homo sapiens)}

GSHMGKDCIMHGYSMSKMGNPFLTQWQRRYFYLFPNRLEWRGEAPEQSLLTMEEIQSVEETQIKERKCLL KirGGKQFILQCDSDPELVQWKEL
RDAYREAQQLVQRVPKMKKNKPRS

>d1faoa_ b.55.1.1 (A:) Dual adaptor of phosphotyrosine and 3-phosphoinositides DAPP1/PHISH {Human (Homo sapiens)}

PSLGTKEGYLTQKQGLVKTWKTRWFTLHRNELKYFKDQMSPEPIRILDTECSAVQFDYSQERVNCFCLVFPFRTFYLCAKTGVEADEWIKILRWKLSQ
I

>d1fgya_ b.55.1.1 (A:) Grp1 {Mouse (Mus musculus)}

TFFPNDREGWLLKLGGRVKTWKRWFILTDNCLYYFEYTTDKEPRGIIPLENLSIREVLDPRKPNCFELYNPShKGQVIACKTEADGRVVEGNHVY
RISAPSPEEKEWMKSIKASISRDPFYDM

>d1fhoa_ b.55.1.1 (A:) UNC-89 {Nematode (Caenorhabditis elegans)}

MGDTGKLGRRIRHDAFQVWEGDEPPKLYVFLFRNKIMFTEQDASTSPSYTHYSSIRLDKYNIRQHTTDEDTIVLQPQEGLPSFRIKPDKFETSEYV
RKAWL RDIAEEQEKYAAERD

>d1aqca_ b.55.1.2 (A:) X11 {Human (Homo sapiens)}

MEDLIDGIIFAANYLGSTQLLSDKTPSKNVRMMQAQEAVSRIKMAQKLAKSRKKAPEGESQPMTEVDLFILTQRIKVLNADTQETMMDHPLRTISYI
ADIGNIVVLMARRIPRNSQENVEASHPSQDGKRQYKMICHVFESEDAQLIAQSIGQAFSVAYQEFLR

>d1qqga1 b.55.1.2 (A:12-114) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

DVRKVGYLRPKSMHKRFFVLRASEAGGPARLEYYENEKKWRHKSSAPKRSIPLSCFNINKRADSKNHLVALYTRDEHFAIAADSEAEQDSWYQ
ALLQLH

>d1qqga2 b.55.1.2 (A:159-262) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

AFKEVWQVILPKGLGQTKNLIGIYRLCLTSKTISFVKLNSEAAAVVLQLMNI RRGHSENFFFIEVGRSAVTGPGEFWMQVDDSVVAQNMHETILEA
MRAMSD

>d1shca_b.55.1.2 (A:) Shc adaptor protein {Human (Homo sapiens)}

GSHMGQLGGEWTRHGSFVNKPTRGWLPNDKVMGPGVSYLVRYMGCVEVLQSMRALDFNRTQVTREASLVCEAVPGAKGATRRKPCSRP
LSSILGRSNLKAGMPITLTNSTSLNLMAADCKQIIANHHMQSISFASGGDPDTAEYVAYVAKDPVNQRACHILECPLELAQDVISTIGQAFELRFKQY
LR

>d1ddma_b.55.1.2 (A:) Numb {Fruit fly (Drosophila melanogaster)}

HQWQADEEAVRSATCSFSVKYLGCVEVFESRGMQVCEALKVLRQSRRPVRGLLHVSGDGLRVVDDETKGLIVDQTIKVSFCAPDRNHERGFSYI
CRDGTTRRWMCHGFLACKDSGERLSHAVGCAFAVCLER

>d1rrpb_b.55.1.3 (B:) Nuclear pore complex protein Nup358 {Human (Homo sapiens)}

HFEPVVPLPDKIEVKTGEDEEEFFCNRAKLFRFDVESKEWKERGIGNVKILRHKTSGKIRLLMRREQVLKICANHYISPDMKLTPNAGSDRSFWHA
LDYADELPKPEQLAIRFKTPEEAALFKCKFEEAQSI

>d1k5db_b.55.1.3 (B:) Ran-binding protein 1, Ranbp1 {Human (Homo sapiens)}

NHDPQFEPIVSLPQEIKTLEEDEEELFKMRAKLFRAFENDLPEWKERGTGDVKLLKHKEKGAIIRLLMRRDKTLKICANHYITPMMEALKPNAGSDRA
WWWNTHADFADECPKPELLAIRFLNAENAQKFKTFEECRKEIEEREK

>d1evha_b.55.1.4 (A:) Enabled {Mouse (Mus musculus)}

SEQSICQARAAVMVYDDANKWVPGGSTGFSRVHIYHHTGNNTFRVGRKIQDHQVVINCAIPKGLKYNQATQTFHQWRDARQVYGLNFGSKE
DANVFASAMMHALEVLN

>d1qc6a_b.55.1.4 (A:) Ena/vasp-like protein {Mouse (Mus musculus)}

MSEQSICQARASVMVYDDTSKKWVPIKPGQQGFSRINIYHNTASSTFRVVGVLQDQQVVINYSIVKGLKYNQATPTFHQWRDARQVYGLNFGSKE
EEATTFSNAMLFALNIMN

>d1egxa_b.55.1.4 (A:) Vasodilator-stimulated phosphoprotein (VASP) {Human (Homo sapiens)}

MSETVICSSRATVMLYDDGNKRWLPGTPQAFSRVQIYHNPTANSFRVGRKMQPDQQVVINCAIVRGVKYNQATPNFHQWRDARQVWGLN
FGSKEDAAQFAAGMASALEALEG

>d1ddwa_b.55.1.4 (A:) Homer {Rat (Rattus norvegicus)}

MGEQPQFSTRAHVFQIDPNTKKNWVPTSKHAVTVSYFYDSTRNVYRIISLDGSKAIINSTPNMTFTKTSQKFGQWADSRANTVYGLFSSEHLSK
FAEKFQEKFKEAR

>d1i7aa_b.55.1.4 (A:) Homer {Mouse (Mus musculus), 2b/vesl 2}

EQPIFTTRAHVFQIDPSTKKNWVPAKQAVTVSYFYDVTNSYRIISVDGAKVIINSTTPNMTFTKTSQKFGQWADSRANTVYGLFSSELQLTKFAE
KFQEVRREAAR

>d1e5wa2_b.55.1.5 (A:199-346) Moesin {Human (Homo sapiens)}

EMYGVNYFSIKNKKGSELWLGVDALGLNIYEQNDRTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVYAPRLRINKRILALCMGNHELYMRRRK
DTIEVQQMKAQAREEKHQKQMERAMILENEKKREMAEKEKEKIEREKEE

>d1ef1a2_b.55.1.5 (A:199-297) Moesin {Human (Homo sapiens)}

EMYGVNYFSIKNKKGTELWLGVDALGLNIYEHDDKLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVYAPRLRINKRILALCMGNHELYMRRRK
>d1gc7a2_b.55.1.5 (A:199-297) Radixin {Mouse (Mus musculus)}

EMYGVNYFEIKNKKGTELWLGVDALGLNIYEHDDKLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVYAPRLRINKRILALCMGNHELYMRRRK
>d1gg3a2_b.55.1.5 (A:188-279) Erythroid membrane protein 4.1R {Human (Homo sapiens)}

GVDLHKAKDLEGVDIILGVCSSGLLVYKDCLRINRFPWPVKVLKISYKRSSFFIKIRPGEQEQQESTIGFKLPSYRAAKKLWKCVEHHTFFR
>d1h4ra2_b.55.1.5 (A:215-313) Merlin {Human (Homo sapiens)}

EMYGVNYFAIRNKKGTELLLGVDALGLHIYDPENRLTPKISFPWNEIRNISYSDKEFTIKPLDKKIDVFKFNSSKLRVNKLILQLCIGNHDLMRRKA
>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)}

NTQSMLTVKGNLDTYGFCCDDVWTFIVKNCQVTVEDSHRDASQNGSGDSQSVISVDKLRIVACNSK
>d1iega_b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}

QAVAPVYVGGLARYDQSPDEAELLLPRDVVEHWLHAQQGQGPQLSVALPLNINHDDTAVVGHVAAMQSVRDGLFCLGCVTSRFLIEVRRASEKS
ELVSRGPVSPLOPDKVVEFLGSYAGLSLASRRCDDEQATSLSGSETTPKAVALCSVGRGGTLAVYGRDPEWVTQRFPDLTAADRDGLRAQWQR
CGSTAVDASGDPFRSDSYGLLGNVDALYIRERLPKLRYDKQLGVTERESYKA

>d1jq6a_b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}

VAPVYVGGLARYDQSPDEAELLLPRDVVEHWLHAQQGQGPQLSVALPLNINHDDTAVVGHVAAMQSVRDGLFCLGCVTSRFLIEVRRASEKSEL
VSRGPVSPLOPDKVVEFLGSYAGLSLSSRCCDDEQATSLSGSETTPKAVALCSVGRGGTLAVYGRDPEWVTQRFPDLTAADRDGLRAQWQRC
GSTAVDASGDPFRSDSYGLLGNVDALYIRERLPKLRYDKQLGVTERESYKA

>d1at3a_b.57.1.1 (A:) HSV-2 protease {Herpes simplex virus type 2}

RAVPIYVAGFLALYDSGDPGELALDPDTVRAALPPENPLPINVDHRARCEVGRVLAVVNDPRGPFFVGLIACVQLERVLETAASAAIFERRGPALSREE
RLLYLITNYLPSVSLSTKRGDEVPPDRTLFAHVALCAIGRRGTIVTYDTSLAAIAFRHLDPATREGVRREAAEALAGRTWAPGVEALTHTLST
AVNNMMLDRWSLVAERRRQAGIAGHTYLQA

>d1fl1a_b.57.1.1 (A:) KSHV protease {Kaposi's sarcoma-associated herpes virus}

AQGLYVGGLFDVVSCPYLEQEYLDPDQVTDYLPVTEPLPITIEHPETEVGWTGLFQVSHGIFCTGAITSPAFLERASRLADTSVARAPVKNLPKEP
LLEILHTWLPGSLSSIHPRELSQTSGPVFQHVSLCALGRRGTAVYGHDAEWVVSFSSVSKSERAHILQHVSSCRELDLSTPNFVSPLETLMAKAI
DAGFIRDRLLLKTDRGVASILSPVYLKA

>d1vzv_b.57.1.1 (-) VZV protease {Varicella-Zoster virus}

EALYVAGYLALYSKDEGELINITPEIVRSALPPTSKIPINIDHRKDCVVGEVIAIIEDIRGPFFLGIVRCPQLHAVLFEEAHNSFFGNRDSVSLPLERALYLVTN
YLPSVSLSSKRLFTHVALCVVGRVGTVVNYDCTPESSIEPFRVLSMESKARLLSLVKDYAGLNKVWKVSEDKLAKVLLSTAVNNMLLDRWDVVAKR
RREAGIMGH

>d1a49a1_b.58.1.1 (A:116-217) Pyruvate kinase (PK) {Rabbit (*Oryctolagus cuniculus*)}

PEIRTGLIKSGTAEVELKKGATLKITLEDNAYMEKCDENILWLDYKNICKVVDVGSKVVDDGLISLQVKQKGPDFLVTEVENGGFLGSKKGVNLPGAA
VDL

>d1pkm_1_b.58.1.1 (116-217) Pyruvate kinase (PK) {Cat (*Felis domestica*)}

PEIRTGLIKSGTAEVELKKGATLKITLEDNAYMEKCDENILWLDYKNICKVVEVGSKVVDDGLISLLVKEKGADFLVTEVENGGSLGSKKGVNLPGAA
VDL

>d1pkla1_b.58.1.1 (A:88-186) Pyruvate kinase (PK) {Leishmania mexicana}

EIRTGQFVGDAVMERGATCYVTTDPAFADKGTKDKFYIDYQNLSKVVRPGNYIYIDDGILILQVQSHEDEQTLECTVNSHTISDRRGVNLPGCDVD
L

>d1a3wa1_b.58.1.1 (A:88-188) Pyruvate kinase (PK) {Baker's yeast (*Saccharomyces cerevisiae*)}

PEIRTGTTNDVDYPIPPNHEMIFTDDKYAKACDDKIMVYDYNITKVISAGRIYVDDGVLQVLEVVDDKTLVKALNAGKICSHKGVNLPGTDV
DL

>d1e0ta1_b.58.1.1 (A:70-167) Pyruvate kinase (PK) {Escherichia coli}

PEIRTMKLEGGNDVSLKAGQTFTTDXVGNSEMVAVTYEGFTTLSVGNTVLVDDGLIGMEVTAIEGNVICKVLNNGDLGENKGVNLPGVIA
L

>d1g8fa1_b.58.1.2 (A:2-168) ATP sulfurylase N-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}

PAPHGGILQDILIARDALKKNESEAQSSDILVWNLTQRLCDIELILNGGFSPLETGFLNENDYSSVVTDSRLADGTLWITIPITLVDDEAFANQIKPDTRI
ALFQDDEIPIAILTVQDVYKPNKTIEAERVFRGDPEHPAISYLFNVAGDYYVGGSLEAIQLPQHYD

>d1i2da1_b.58.1.2 (A:2-170) ATP sulfurylase N-terminal domain {Fungus (*Penicillium chrysogenum*)}

ANAPHGGVLKDLLARDAPRQAEAAEESLPAVTLTERQLCDLELIMNGGFSPLEGFMNQADYDRVCEDNRLADGNVFSMPITLDASQEVIDEKKL
QAGSRITLRDFRDRRNLAILTDDIYRPDKTKEAKLVFGGDPEHPAIVYLNNTVKEFYIGGKIEAVNKLHNHY

>d1jhda1_b.58.1.2 (A:1-173) ATP sulfurylase N-terminal domain {unnamed symbiont of Riftia pachyptila}

MIKPVGSDELKPLFVYDPEEEHKLSHEAESLPSVISSQAAGNA/MMGAGYFSPLQGMNVADAMGAAEKMTLSGSFFPVVLCLLENTDAIGD
AKRIALRDPNVEGNPVLAVMDIEAIEEVSDEQMAVMTDKVYRTTDMHDIGVTFNSQGRVAVGPIQVLNFSYFQADF

>d1ik9a1_b.59.1.1 (A:1-117) XRCC4, N-terminal domain {Human (*Homo sapiens*)}

MERKISRIHLVSEPSITHFLQVSWEKTLESGFVITLDGHSAWTGTVSESEISQEADDMAMEKGKYVGELRKALLSGAGPADVYTFNFSKESAYFFFEK
NLKDVSFRIGSFNLEKVE

>d1hbq__ b.60.1.1 (-) Retinol binding protein {Cow (Bos taurus)}

ERDCRVSSFRVKENFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGQMSATAKGRVRLNNWDVCADMVGFTDTEPAFKMKYWG
VASFLQKGNNDDHWIIDTDYETFAVQYSCRLLNLDGTCADSYFVFARDPSGSPEVKIVRQRQEELCLARQYRLIPHNGYCNGK

>d1aqb__ b.60.1.1 (-) Retinol binding protein {Pig (Sus scrofa domestica)}

ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDENGHMSATAKGRVRLNNWDVCADMVGFTDTEPAFKMKYWG
ASFLQKGNNDDHWIIDTDYAVQYSCRLLNLDGTCADSYFVFARDPHGSPEVKIVRQRQEELCLARQYRIITHNGYCD

>d1rbp__ b.60.1.1 (-) Retinol binding protein {Human (Homo sapiens)}

ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDETQMSATAKGRVRLNNWDVCADMVGFTDTEPAFKMKYWG
ASFLQKGNNDDHWIIDTDYAVQYSCRLLNLDGTCADSYFVFSDPGLPPEAQKIVRQRQEELCLARQYRLIVHNGYCD

>d1iua__ b.60.1.1 (A:) Retinol binding protein {Chicken (Gallus gallus), plasma isoform}

MDCRVSSFKVKENFDKKNRYSGTWYAMAKKDPEGLFLQDNVAQFTDENGQMSATAKGRVRLNNWDVCADMIGSFTDTEPAFKMKYWG
VASFLQKGNNDDHWVVDTDYDTYALHYSCRELNEDGTACDSYFVFSRDPKGGLPPEAQKIVRQRQIDLCMDRKYRVIVHNGFCS

>d1hn2a__ b.60.1.1 (A:) Odorant-binding protein {Cow (Bos taurus)}

AQEEEAEQNLSELSPWRTVYIGSTNPEKIQENGPFRTYFRELVFDDEKGTVDFYFSVKRDGKWNVHVAKTQDDGYVADYEGQNVFKIVSLSRT
HLVAHNINVVKHGQTTELTEFVKLNVEDEDLEKFWKLTEDKGIDKKNNVNFLLENENHPHE

>d1dzka__ b.60.1.1 (A:) Odorant-binding protein {Pig (Sus scrofa)}

FELSGKWKITSYIGSSDLEKIGENAPFQVFMRSLFDDKESKVYLNFFSKENGICEEFLIGTKQEGNTYDVNYAGNNKFVSYASETALIISNINVDEEGD
KTIMTGLGKGTIEDQDLEKFKEVTRNGIPEENIVNIERDDCPA

>d1bj7__ b.60.1.1 (-) Lipocalin allergen {Cow (Bos taurus), bos d 2}

IDPSKIPGEWRIIYAADNNDKIVEGGPLRNYYRRIECINDCESLISITFYLKQDGTCLLTEVAKRQEGYVVLEFYGTNTLEVHVSENMLVTYVENYDG
ERITKMTEGLAKGTSFTPEELEYQQQLNSERGVNPENIENLIKTDNCPP

>d1ew3a__ b.60.1.1 (A:) Lipocalin allergen {Horse (Equus caballus), equ c 1}

VAIRNFDISKISGEWYSIFLASDVKEKIEENGSMRVFVDVIRALDNSSLAYEQTKVNGETEFPMVFDKTEEDGVYSLNYDGVNVFRISEFENDEHIILY
LVNFDKDRPFQLFEFYAREPDVSPEIKEEFVKIVQKRGIVKENIIDLTKIDRCFQLRG

>d1e5pa__ b.60.1.1 (A:) Aphrodisin, a sex pheromone {Golden hamster (Mesocricetus auratus)}

FAELQGKWTYTIVIAADNLKEIEEGGPLRFYFRHIDCYKNCSEMEITFYVITNNQCSKTTVIGYLKNGNTYETQFEGNNIFQPLYITSKIFFTNKNMDRA
GQETNMIVVAGKGNALTPEENEILVQFAHEKKIPVENILNILATDTCPE

>d1beba__ b.60.1.1 (A:) beta-Lactoglobulin {Cow (Bos taurus)}

QTMKGLDIQKVAGTWYSLAMAASDISLDAQSAPLRYVEELKPTPEGDLEILLQKWEENGCAQKKIIAEKTKIPAVFKIDALNENKVVLTDYKKYL
LFCMENSAEPEQSLVCQCCLVRTPEVDDEALEKFDKALKALPMHIRLSFNPTQLEEQC

>d1exsa__ b.60.1.1 (A:) beta-Lactoglobulin {Pig (Sus scrofa)}

VEVTPIMTELDTQKVAGTWHTVAMAVSDVSLDAKSSPLKAYVEGLKPTPEGDLEILLQKRENDKCAQEVLAKTDIPAVFKINALDENQLFLTDY
DSHLLCMENSASPEHSLVCQSLARTLEVDDQIREKFEDALKTLSVPMRILPAQLEEQCRV

>d1epba__ b.60.1.1 (A:) Retinoic acid-binding protein {Rat (Rattus norvegicus), albino}

VKDFDISKFLGFWYEIAFASKMGTPGLAHKEEKMGAMVVELKENLLALTTYYSEDHCVLEKVTATEGDGPAKFQVTRLSGKKEVVVEATDYLTYAIID
ITSLVAGAVHRTMKLYRSRSLDDNGEALYNFRKITSDHGFSETDLYILKHDLTCVKVLQSA

>d1jv4a__ b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Mouse (Mus musculus)}

EEASSTGRNFNVEKINGEWTIILASDKREKIEDNGNFRLFLEQIHVLEKSLVLFHTVRDEECSELSMVADKTEKAGEYSVTYDGFNTFTIPKTDYDNF
LMAHLINEKDGETFQLMGLYGREPDLSIDIKERFAQLCEEHGILRENIIDLSNANRC

>d2a2ua__ b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Rat (Rattus norvegicus)}

EEASSTRGNLDVAKLNGDWFSIVVASNKREKIEENGSMRVFMQHIDVLENSLGFKFRIKENGECRELYLVAYKTPEDGEYFVEYDGGNTFTILKTDY
RYVMFHILFKNGETFQLMVLYGRTKDLSIDEKFAKLCEAHGITRDNIIIDLTKTDRCI

>d1qqs_a_b.60.1.1 (A:) Neutrophil gelatinase-associated lipocalin (NGAL) {Human (Homo sapiens)}

TSDLIPAPPLSKVPLQQNFQDNQFQGKWYVVLAGNAILREDKDPQKMYATIYEKEADSYNTSLFRKKCDYAIRTFVPGCQPGEFTLGNIKSYP
GLTSYLVRRVSTNYNQHAMVFFKVSQNREYFKITLYGRTKELTSELKNNFIRFSKSLGLPENHIVFPVPIDQCID

>d1bbpa_b.60.1.1 (A:) Bilin-binding protein {Cabbage butterfly (Pieris brassicae)}

NVYHDGACPEVKPVDFDWSNYHGKWWEVAKYPSNSVEKYKGKCGWALEYPEGKSVKVSNYHVIHGKEYFIEGTAYPGDSKIGKIHKLTYGGVTK
ENVFNVLSTDNKNYIIGYYCKYDEDKKGHQDFVWLSRSKVLTGEAKTAVENYLIGSPVVDSQKLVYSDSEAACKVN

>d1i4ua_b.60.1.1 (A:) Alpha-crustacyanin {European lobster (Homarus gammarus)}

DKIPDFVPGKASVDRNKLWAEQTPNRNSYAGVWYQFALTNNPYQLIEKCVRNEYSFDGKQFVIESTGIAVDGNNLLRNGKLYPNPFGEPHLSIDYE
NSFAAPLVILETDYSNYACLYSCIDYNFGYHSDFSIFSRSANLADQYVKKCEAAFKNINVDTTRFVKTQGSSCPYDTQKTL

>d1qfta_b.60.1.1 (A:) Histamine binding protein {Brown ear tick (Rhipicephalus appendiculatus)}

NQPDWADEAANGAHQDAWKSLLKADVENVYVMVATYKNDPVWGNDFTCVGMANDVNEDEKSQAEFLFMNNADTNMQFATEKVAVKM
YGYNRENAFRYETEDGQVFTDVIAYSDDNCDVYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLEIAAA

>d1np1a_b.60.1.1 (A:) Nitrophorin 1 {Rhodnius prolixus}

KCTKNALAQTGFNPKDQYFNGDVWYVTDYLDLEPDDVPKRYCAALAAGTAGSKLKEALYHYDPKTQDTFYDVSELQEESPGKYTANFKKVEKNGNVK
VDVTSGNYYTFTVMYADDSSALIHTCLHKGNDLGLDLYAVLNRNKDAGDKVKGAVTAASLKFSDFISTKDNKCEYDNVSLKSLTK

>d1euoa_b.60.1.1 (A:) Nitrophorin 2 (prolixin-s) {Rhodnius prolixus}

MDCSTNISPQQLDKAKYFSGKWWVTHFLDKDPQVTDQYCSSFTPRESDTVKEALYHYNANKTSFYNIGEKLESSGLQYTAKYKTVDKKKAVLKE
ADEKNSYTLTVLEADDSSALVHICLREGSKDLGDLTVLHQDKDAEPSAKVSAVTQAGLQLSQFVGTKDLCQYDDQFTSL

>d1koia_b.60.1.1 (A:) Nitrophorin 4 {Rhodnius prolixus}

ACTKNIAQQTGFNPKDQYFNGDVWYVTDYLDLEPDDVPKRYCAALAAGTAGSKLKEALYHYDPKTQDTFYDVSELQVESLGKYTANFKKVDKNGNVK
VAVTAGNYYTFTVMYADDSSALIHTCLHKGNDLGLDLYAVLNRNKDAAAGDKVKSASAATLEFSKFISTKENNCAYDNDLSKSLTK

>d1hms_b.60.1.2 (-) Muscle fatty acid binding protein (m-fabp) {Human (Homo sapiens)}

VDAFLGTWKLVDSKNFDDYMKSLGVGFATRQVASMTKPTTIIKNGDILTLKTHSTFKNTEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHLQKWD
GQETTLVREIDGKLILTHTGTAVCTRTEKE

>d1bwya_b.60.1.2 (A:) Muscle fatty acid binding protein (m-fabp) {Cow (Bos taurus)}

VDAFVGTVKLVDSKNFDDYMKSLGVGFATRQVGNTMKTIIEVNGDTVIIKTQSTFKNTEISFKLGVEFDETTADDRKVKSIVTLDGGKLVHVQKW
NGQETSLVREMVDGKLILTHTGTAVCTRTEKEQA

>d1a57_b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}

AFDGTWKVDRNENYSGAHDNLKLTITQEGNKFTVKESSNFRNIDVVFELGVDFAYSLADGTELGTWTMEGNKLVGFKRVDNGKELIAVREISGNE
LIQTYTYEGVEAKRIFKKE

>d1ifc_b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}

AFDGTWKVDRNENYEKFMEKMGINVVKRKLGHDNLKLTITQEGNKFTVKESSNFRNIDVVFELGVDFAYSLADGTELGTWTMEGNKLVGFKRV
VDNGKELIAVREISGNELIQTYTYEGVEAKRIFKKE

>d3ifba_b.60.1.2 (A:) Intestinal fatty acid binding protein {Human (Homo sapiens)}

AFDSTWKVDRSENYDKFMEKMGVNIVRKLAHDNLKLTITQEGNKFTVKESSAFRNIEVVFELGVTNFYNLADGTELRTGSLEGNKLIKFKRTD
NGNELNTVREIIGDELVQTYYEGVEAKRIFKKD

>d1fdqa_b.60.1.2 (A:) Brain fatty acid binding protein {Human (Homo sapiens)}

VEAFCATWKLTNSQNFDEYMKALGVGFATRQVGNTKPTVIISQEGDKVVIRTLSTFKNTEISFQLGEEFDETTADDRNCKSVVSLGDKLVHIQKW
DGKETNFVREIKDGKVMVMTFGDVVAVRHYEKA

>d1b56_b.60.1.2 (-) Epidermal fatty acid binding protein {Human (Homo sapiens)}

TVQQLEGRWRLVDSKGFDGYMKELGVGIALRKGAMAKPDCIITCDGKNLTIKTESTLKTQFSCTLGEKEFTTADGRKTQTCVNFDTGALVQHQEW
WDGKESTITRKLKDGMVMTFGDVVAVRHYEKA

>d1lid_b.60.1.2 (-) Adipocyte lipid-binding protein, ALBP {Mouse (Mus musculus)}

CDAFVGTVKLVSSENFDDYMKEVGVGFATRKVAGMAKPNMIISVNGDLVTIRSESTFKNTEISFKLGVEFDEITADDRKVKSIITLDGGALVQVQKWD

GKSTTIKRKRDGDKLVVECMKGVTSTRVYERA

>d1mdc__ b.60.1.2 (-) Fatty acid-binding protein {Tobacco hornworm (*Manduca sexta*)}

SYLGKVYSLVKQENFDGFLKSAGLSDDKIQALVSDKPTQKMEANGDSYSNTSTGGGAKTVSFKSGVFDDVIGAGDSVKSMYTVDGNVVTHVVK
GDAGVATFKKEYNGDDLVITSSNWDGVARRYYKA

>d1ftpa_ b.60.1.2 (A:) Fatty acid-binding protein {Desert locust (*Schistocerca gregaria*)}

VKEFAGIKYKLDSQTNFEEYMAIGVGAIERKAGLALSPVIELEILDGDKFKLTSKTAKNTEFTFKLGEEFDEETLDGRKVKSTITQDGPNKLVHEQKGD
HPTIIREFSKEQCVITIKLGLDVATRIYKAQ

>d1cbs__ b.60.1.2 (-) Cellular retinoic-acid-binding protein (CRABP) {Human (*Homo sapiens*), CRABP-II}

PNFSGNWIKIRSENFEELLKVLGVNVMLRKIAVAASKPAVEIKQEGDTFYIKTSTTVRTTEINFKVGEFFEEQTVDGRPKCSLVWESENKMVCEQKL
LKGEGPKTSTRELTNDGELILTMTADDVVCTRYYVRE

>d1cbia_ b.60.1.2 (A:) Cellular retinoic-acid-binding protein (CRABP) {Cow and mouse (*Bos taurus*) and (*Mus musculus*), CRABP-I, identical sequences}

PNFAGTWKMRSSENFDELLKALGVNAMLRKVAVAAASKPHVEIRQDGDQFYIKTSTTVRTTEINFVGEGFEEETVDGRKCRSLPTWENENKIHT
QTLLEGDPKTYWTRELANDELILTFGADDVVCTRYYVRE

>d1crb__ b.60.1.2 (-) Cellular retinol-binding protein II (CRBP) {Rat (*Rattus norvegicus*)}

PVDFNGYWKMISNENFEELYRLADVNVALRKIANLLKPDKEIVQDGDHMIIRTLSTFRNYIMDFQVGKEFEEDLTGIDDRKCMTTVSWDGDKLQCV
QKGEKEGRGWTQWIEGDELHLEMRAEGVTCKQVFKKVH

>d1opaa_ b.60.1.2 (A:) Cellular retinol-binding protein II (CRBP) {Rat (*Rattus norvegicus*)}

TKDQNGTWEMESNENFEGYMKALDIDFATRKIAVRLTQTKIIVQDGDNFKTKTNSTFRNYDLDFTVGVEFDEHTKGLDGRNVKTLVTWEGNTLVCV
QKGEKENRGWKQWVEGDKLYLETCGDDQVCRQVFKKK

>d1gbla_ b.60.1.2 (A:) Cellular retinol-binding protein III {Human (*Homo sapiens*)}

PPNLGTGYRFVSQLNEDYLQALNISLAVRKIALLLLKDKEVHQGNHMTVRTLSTFRNYTVQFDVGVEFEEDLRSVDGRKCQTVTWEHHLCVQ
KGEVPNRGWRHWLEGEMIYLELTARDAVCEQVFRKVH

>d1lfo__ b.60.1.2 (-) Liver fatty acid binding protein {Rat (*Rattus norvegicus*)}

MNFSGKYQVQSQENFEPFMKAMGLPEDLIQKGKDIKGVSEIVHEGKKVKLITYGSKVIHNEFTLGEECELETMTGEVKAVVKMEGDNKMVTTFK
GIKSUTEFNGDTITNTMTLGDIVYKRVSKR

>d1pmpa_ b.60.1.2 (A:) P2 myelin protein {Cow (*Bos taurus*), caudal spinal root myelin}

SNKFLGTWKLVSSENFDEYMKALGVGLTRKLGNLAKPRVIISKKGDIITRTESPFKNTEISFKLGQEEFTTADNRKTSTVTLARGSLNQVQKWNG
NETTIKRKLVDGKMWVECKMKDVKVCTRYYEKV

>d1eal__ b.60.1.2 (-) Ileal lipid binding protein {Pig (*Sus scrofa*)}

AFTGKYIESEKNYDEFMKRLALPSDAIKDARNLKIISEVKQDGQNFTWSQQYPGGHSITNTFTIGKECDIETIGGKKFATVQMEGGKVVVNSPNYH
HTAEIVDGKLVEVSTVGGVSYERVERSKLA

>d1avg_i_ b.60.1.3 (I:) Thrombin inhibitor {Triatomine bug (*Triatoma pallidipennis*)}

AEGDDCSIEKAMGDFKPPEEFFNGTWYLAHGPVTSPAVCQKFTTSGSKGFTQIVEIGYNKFESNVKFQCNQVDNKNGEQYSFKCKSSDNTEFEADF
TFISVSYDNFALVCRSITFTSQPKEDRYLFERTKSDTDPAKEIC

>d1swga_ b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}

SRYVLTGRYDSAPATDGSgtALGWTVAWKNNYRNAHSATTWSGQYVGGEARINTQWLTSgtTEANAWKSTLVGHDTFTKVKPSAASGGSAE
AGITGTWYNQLGSTFIVTAGADGALTGTYESA

>d1swua_ b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}

GITGTWYNQLGSTFIVTAGADGALTGTYESA
GITGTWYNQLGSTFIVTAGADGALTGTYESA
TSGTTEANAWKSTLVGHDTFTKVKP

>d1ij8a_ b.61.1.1 (A:) Avidin {Chicken (*Gallus gallus*)}

KCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYTTAVTATSNEIKESPLHGHTENTINKRTQPTFGFTVNWKFSESTTVFTGQCFIDRNGKEVLKTMWLL
RSSVNDIGDDWKATRVRGINIFTRL

>d1smpi_b.61.2.1 (I:) Metalloprotease inhibitor {Erwinia chrysanthemi}
SSLRLPSAELSGQWVLSGAEQHCDIRLNTDVLGTTWKLADTAACLQKLLPEAPVGWRPTPDGLTLTQADGSAAFFSRNRDRYEHKLVGSVRT
LKKK

>d1jiwi_b.61.2.1 (I:) Metalloprotease inhibitor {Pseudomonas aeruginosa, aprin}
SSLLSASLAGQWTLQQDEAPAICHLELRDSEVAEASGYDLGGDTACLRWLSEPRAWRPTPAGIALLERGGTLMLGRQGEGDYRVQKGDG
QLVLRRAT

>d1ei5a1 b.61.3.1 (A:336-417) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum anthropi}
EVSRVEADSAWFGSWLDDETGLVLSLEDAGHGRMKARFGTSPEMMDVVSANEARSAVTIRRGETIELVRASENLRLSMKR

>d1ei5a2 b.61.3.1 (A:418-520) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum anthropi}
VKGEAKHDIIGRYHSDELDADLLVSEGGAIFYGAFEGFLGKSDMYPLYSVGSBVWLLPVQRSMADSPGEWKVFRDDKGEITGLSVCWLARGV
EYRRVQP

>d1jjua5 b.61.4.1 (A:166-273) Quinohemoprotein amine dehydrogenase A chain, domain 3 {Paracoccus denitrificans}
PDAYADDASGAYVLAGRQPGRGDYTGRLVKKAGEDYEVTMTLDFADGSRSFGTGRILGAGEWRATLSDGTVTIRQIFALQDGRFSGRWHADSD
VIGGRLAAVKAD

>d1jmxa5 b.61.4.1 (A:163-281) Quinohemoprotein amine dehydrogenase A chain, domain 3 {Pseudomonas putida}
ESAAWAEWQKARPKADALPGQWAFSGHMLAKGDVRGVMSVTPDQGDTFKVEVKGAYADGTPNGSGSAILYNGEWRGNVKVDANLRQVF
AALDGEMKGRMFEAEHDERGLDFTAVKE

>d2cpl_b.62.1.1 (-) Cyclophilin (eukaryotic) {Human (Homo sapiens), variant A}
VNPTVFFDIAVDGEPLGRVSFELFADKVPKTAENRALSTGEKGFGYKGSCFHRIIPGFMCQGGDFTRHNGTGGKSIYGEKFEDENFILKHTGPGILSM
ANAGPNTNGSQFFICTAKTEWLDGKHVVFGKVEGMNIVEAMERFGSRNGKTSKKTIADCGQLE

>d1cyna_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens), variant B}
GPKTVTVYFDLRLIGDEDVGRVIFGLFGKTVPKTVDNFVALATGEKGFGYKGSCFHRIKDFMIQGGDFTRDGTGGKSIYGERFPDENFKLHYGP
GWVSMANAGKDTNGSQFFITTVKTAWLDGKHVVFGKLEGMEVVRKVESTKTDSDRKPLKDVIIADCGKIEVEKPFIAKE

>d1qoia_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens), U4/U6 snRNP-specific cyclophilin snucyp-20}
NSSPVNPVVFDDVSIGGQEVRGMKI ELFADVVPKTAENFRQFC TGEFRKDGVPIGYKGSTFHRVIKDFMIQGGDFVNGDGTGVASIYRGPFADENFK
LRHSAPGLLSMANSGPSTNGCQFFITCSKCDWLDGKHVVFGKIIDGLLVMRKIENVPGNPKLPVISQCGEM

>d2rmca_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Mouse (Mus musculus), variant C}
KRGPSVTDKVFFDVRIGDKDVGRI VIGLFGNVVPKTVENFVALATGEKGFGYKGSCFHRIKDFMIQGGDFTRDGTGGMSIYGETFPDENFKLHYG
IGWVSMANAGPDTNGSQFFITLTKPTWLDGKHVVFGKLDGMTVVHSIELQATDGHDRPLTDCTIVNSKIDVKTPTFVVEVPDW

>d1a33_b.62.1.1 (-) Cyclophilin (eukaryotic) {Nematode (Brugia malayi)}
KDRRRVFLDTIDGNLAGRIVMELYNDIAPRTCNNFLMLCTGMAGTGKISGKPLHYKGSTFHRVIKNFMIQGGDFTRDGTGGESIYGGMFDEEF
VMKHDEPVVSMANKGPNTNGSQFFITTPAPHLNNIHVFGKVVSGQEVVTKIEYLKTNKNRPLADVILNCGELV

>d1dywa_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Caenorhabditis elegans, isoform 3}
MSRSKVFFDITIGGKASGRIVMELYDDVVPKTAGNFRA LCTGENGIGKSGKPLHFKGSKFHRIIPNFM IQGGDFTRGNGTGGESIYGEKFPDENFKEK
HTGPGVLSMANAGPNTNGSQFFLCTVKT EWLDGKHVVFGRVVEGLDVVKAVESNGSQSGKPVKDCMIADCGQLK

>d1qnga_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Plasmodium falciparum}
SKRSKVFFDISIDNSNAGRIIFELFSITPRTCENFRA LCTGEKIGSRGKNLHYKNSIFHRIIPQFM CQGGDITNGNGSGGESIYGRSFTDENFNMKHDQ
PGLLS MANAGPNTNSSQFFITLVPCPWLDGKHVVFGK VIEGMNVREMEKEGAKSGYV KRSV VITDCGEL

>d1ihga2_b.62.1.1 (A:2-196) Cyclophilin 40 isomerase domain {Cow (Bos taurus)}
SHPSPQA KPSNPSNPRVFFDVGGERVGRIVLELFADIVPKTAENFRA LCTGEKGIGPTTGKPLHF KGCPFHRIKKFMIQGGDFSNQNGTGGESIYG
EKFEDENFHYKHDKEGLLSMANAGSNTNGSQFFITVPTPHLDGKHVVFGQVIKG MGVA KILENVEVKGEPAKLCVIAECGELKEGDDWGIFPKD

>d1clh_b.62.1.1 (-) Bacterial cyclophilin {Escherichia coli}
AKGDPHVLLTTSAGNIELEDKQKAPVSVQNFVDYVNSGFYNNTFH RVIPGFMIQGGGGTEQMQQKKPNPIKNEADNGLRNTRGTIAMARTAD
KDSATSQFFINVADNAFLDHGQRDFGYAVFGKVVKGMDVADKISQVPTHDVGPYQNPSKPVVI SAKVLP

>d1lopa_b.62.1.1 (A:) Bacterial cyclophilin {Escherichia coli}
MVTFHNTNGDIVIKTFDDKAPETVKNFLDYCREGFYNNTIFHRVINGFMIQGGGFEPGMKQKATKEPIKNEANGLKNTRGTLAMARTQAPHSAT
AQFFINVVDNDFLNFGESLQGWGYCVFAEVVDMGEVDKIKGVATGRSGMHQDVPKEDVIIESVTSE

>d1jsg__ b.63.1.1 (-) p14-TCL1 {Human (Homo sapiens)}
CPTLGEAVTDHPDRLWAWEKFVYLDKQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMPTQIGPSLLPIMWQLYPDGRYRSSDSSFWRLVYHIKID
GVEDMLLELLPDD

>d1jnpa_b.63.1.1 (A:) p14-TCL1 {Mouse (Mus musculus)}
RAETPAHPNRLWIWEKHVLDEFRRSWLPVVIKSNEKFQVILRQEDVTLGEAMSPSQLVYELPLMWQLYPKDRYRSADSMYWQIYHIKFRDVED
MLLEL

>d1a1x__ b.63.1.1 (-) p13-MTCP1 {Human (Homo sapiens)}
AGEDVGAPPDHLWVHQEGIYRDEYQRTWAVVVEETSFLRARVQQIQVPLGDAARPSHLLTSQPLMWQLYPEERYMDNNSRWLWQIQHHLMVR
GVQELLLKLLPDD

>d1jaa_b.100.1.1 (A:) Sortase {Staphylococcus aureus}
MQAKPQIPKDKSKVAGYIEPDADIKEPVYPGPATPEQLNRGVSAEENESLDDQNISIAGHTFIDRPNYQFTNLKAACKGSMVYFKVGNETRKYKMT
SIRDVKPTDVGVLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEVK

>d1c39a_b.64.1.1 (A:) Cation-dependent mannose 6-phosphate receptor, extracytoplasmic domain {Cow (Bos taurus)}
EKTCDLVGEKGKESEKELALLKRLTPLFQKSFESTVGQSPDMYSVFRVCREAGQHSSGAGLVQIQKSNGKETVVGRFNETQIFQGSNWIMLIYKGGD
EYDNHCGREQRRAVVMISCRNHTLADNFNPVSEERGVQDCFYLFEMDSSLACS

>d1e6fa_b.64.1.1 (A:) Cation-independent mannose-6-phosphate receptor (MIR-receptor) {Human (Homo sapiens)}
DDCQVTNPSTGHLFDLSSLSGRAGFTAAYSEKGLVYMSICGENENCPPGVACFGQTRISVGKANKRLRYVDQVLQLVYKDGS PCPSKSGLSYKSVIS
FVCRPEAGPTNRPMLISLDKQTCTLFFSWHTPLACE

>d1f3ua_b.65.1.1 (A:) TFIIF beta subunit, Rap30 {Human (Homo sapiens)}
AERGELDTGAKQNTGVVLVKPKYLSQQWAKASGRGEVGKLRIAKTQGRTEVSFTLNEDLANIHDIGGKPASVSAPREHPFVLQS VGGQTLTVFTE
SSSDKLSLEGIVVQRAECRPA

>d1f3ub_b.65.1.1 (B:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}
GPSSQNVTEYVVRVPKNTKKYNIMAFNAADKVNFATWNQARLERDLNSNKKIYQEEEMPESGAGSEFNRLREEARRKKYGI VLKEFRPEDQPWLL
RVNGKSGRKFKGIKKGGVTENTSYIFTQCPDGAFEAFPVHNWYNFTPLARHR

>d1f3ud_b.65.1.1 (D:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}
SSQNVTEYVVRVPKNTKKYNIMAFNAADKVNFATWNQARLERDLNSNKKIYQEEEMPESGAGSEFNRLREEARRKKYGI VLKEFRPEDQPWLLRV
NGKSGRKFKGIKKGGVTENTSYIFTQCPDGAFEAFPVHNWYNFTPLARHRTAEEEAEWWERRN

>d1hxn__ b.66.1.1 (-) Hemopexin {Rabbit (Oryctolagus cuniculus)}
ESTRCDPDLVLSAMVSDNHGATYFSGSHYWRDLTNRDGWHSWPIAHQWPQGPSTVDAAFSWEDKLYLIQDTKVYVFLTKGGYTLVNGYPRKLE
KELGSPVISLEAVDAAFVCPGSSRLHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKPLGPNSCTSGPNLYLIHGPNLYCYRHVDKL
NAAKNLPQPQRVSRLLGTH

>d1qhua1 b.66.1.1 (A:24-215) Hemopexin {Rabbit (Oryctolagus cuniculus)}
IEQCSDGWSFADTTLDDNGTMILFFKDEFVWKSHRGIRELISERWKNFIGPVDAAFRHGHTSVYLIKGDKVWVYTSEKNEKVYPKSLQDEFPGPFL
DAAVECHRGEQCQDEGILFFQGNRKWFWDLTTGTKKERSWPAVGNCTSALRWLGRYYCFQGNQFLRFNPVS GEVPPGYPLDVRDYFLSCPGRGHS
S

>d1gen__ b.66.1.1 (-) Gelatinase A (MMP-2), C-terminal domain {Human (Homo sapiens)}
LGPVTPEICKQDIVFDGIAQIRGEIFFFKDRFIWRTVTPRDKPMGPPLLWATFWPELPEKIDAVYEAPQEEKAVFFAGNEYWIYASASTLERGYPKPLTSGL
PPDVQRVDAAFNWSKNKKTYIFAGDKFWRYNEVKKKMDPGFPKLIADAWNAIPDNLDLVQGGGHSYFFKGAYYLKLENQSLKSVKFGSIKSD
WLGC

>d1fbl_1 b.66.1.1 (272-466) Collagenase, C-terminal domain {Pig (Sus scrofa)}
PQTPQVCDSKLTFDAITLREGELMFFKDRFYMRNSFYPEVELNFISVFWPQVPNGLQAAYEIADRDEVRFKGNKYWA VRGQDVLYGYPKDIHRSF

GFPSTVKNIDAAVFEEDTGKTYFFVAHECWRYDEYKQSMDTGYPKMAEEFPGIGNKVDAVFQKDGFLYFFHGTRQYQDFKTKRILTLQKANSWF
NC

>d1pex__ b.66.1.1 (-) Collagenase-3 (MMP-13), C-terminal domain {Human (Homo sapiens)}

TPDKCDPSLSDAITSLRGETMIFKDRFFWRLHPQQVDAELFLTSFWPELPNRIDAAYEHPSHDLIFIFRGRKF WALNGYDILEGPKKISELGLPKEVK
KISAAVHFEDTGKTLFSGNQVWRYDDTNHIMDKDYPRLIEEDFGIGDKVDAVYEKNGYIYFFNGPIQFEYSIWSNRIVRVMPANSILWC

>d1tl2a__ b.67.1.1 (A:) Tachylectin-2 {Japanese horseshoe crab (Tachypleus tridentatus)}

GGESMLRGVYQDKFYQGTYQPQNKNNDNLARATLIGKGGWSNFKFLSPGGELYGVLDNKIYKGTPPTHDNDNWGRACKIGNGGWNQFQFL
FFDPNGLYAVSKDKLYASPPQSRTDNWIARATEVGSGGWSGFKFLFPNGYLYAVHGQQFYKALPPVSNQDNWLARATKIGQGGWDTFKFLF
FSSVGTFLGVQGGKFYEDYPPSYAYDNWLARAKLIGNGGWDDFRFLF

>d3sil__ b.68.1.1 (-) Salmonella sialidase {Salmonella typhimurium, strain lt2}

EKSVVFKAEGEHFTDQKGNTIVGSGSGGTTKYFRIPAMCTTSKGTIVFADARHNTASDQSFDITAAARSTDGGKTWNKKIAINYDRVNSKLSRVMD
PTCIVANIQGRETILVMVGKWNNNDKTWGAYRDKAPDTDWDLVLYKSTDDGVTFSKVETNIHDIVTKNGTISAMILGGVGSGLQLNDGKLVFPVQ
MVRTKNITTVLNTSFYSTDGITWSPSGYCEFGSENNIIEFNASLVNNIRNSLRRSFETKDFGKWTTEFPPMDKKVDNRNHHVGQGSTITPSGNKL
VAAHSSAQNKNNDYTRSDISLYAHNLYSGEVKLIDDFYFVKVGNASGAGYSCLSYRKNVDKETLYVVEANGSIEFQDLSRHLPVIKSYN

>d1f8ea__ b.68.1.1 (A:) Influenza neuraminidase {Influenza A virus, different strains}

RDFNNLTKGTLTINSWHYGDNAVRIGEDSDVLVTREPYVSCDPDECRFYALSQGTTIRGKHSNGTIHRSQYRALISWPLSSPTVYNSRVECIGWS
STSCHDGKTRMSICISGPNNNASAVIWNRRPVTETINTWARNLRTQESECVCCHNGVCPVVFDTGSATGPAETRIYYFKEGKILKWEPLAGTAKHIEE
CSCYGERAEITCTCRDNWQGSNRPVIRDPVAMHTSQYICSPVLTNDNPRNDPTVGKCNPDYPGPNNNNGVKGSYLDGVNTWLGRTISIASRSGY
EMLKVPNALDDSKPTQGQTIVLNTDWSGSGSFMDYWAEGECYRACYVELIRGRPVEDKVVWTSNSIVSMCSSTEFLGQWDWPDGAKIEYF
L

>d2bat__ b.68.1.1 (-) Influenza neuraminidase {Influenza A virus, different strains}

VEYRNWNSKPQCQITGFAPFSKDNSIRSLAGGDIWVTRPYVSCDPVKCYQFALGQGTTLDNKHSNDTVDHRPHRTLLMNELGVPFHGTRQV р
WSSSSCHDGKAWLHVСITGDDKNATASIYDGRLVDSIGSWSQNILRTQESECVСINGTCTVMTDGSASGRADTRILFIEEGKIVHISPLAGSAQHV
ЕЕССҮРҮРҮВСТРСИСГРННСАВИWYNNRРVTEINTWARNLRTQESECVCCHNGVCPVVFDTGSATGPAETRIYYFKEGKILKWEPLAGTAKHIEE
DLRSGYETFKVIGGWSTPNSKSQINRQVIVDSDNRSGYSGIFSVEGKSCINRCFYVELIRGRKQETRVWWTSNSIVFCGTSGTYGTGSWPDGANINF
MPI

>d1inv__ b.68.1.1 (-) Influenza neuraminidase {Influenza B virus, different strains}

EPEWTPRSLCQGSTFQKALLSPHRFGEIKGNSAPLIIREPVACGPKECRHFALTHYAAQPGGYYNGTRKDRNKLRLHSVKLGKIPTVENSIFHMA
AWSGSACHDGREWTYIGVDGPNDALVKIKYGEAYTDYHSYAHNILRTQESACNCIGGDCYLMITDGSASGISKCRFLKIREGRIIKEILPTGRVEHTE
ECTCFGASNKTIECACRDNSYTAKRPFVKNVETDTAEIRLMCTYLDTPRPPDDGSIAGPCESNGDKWLGGIKGGFVHQRMASKIGRWYSRTMSKT
NRMGMELYVRYDGPWTSDALTLGVMVSIEPGWYSFGFEIKDKKCDVPCIGIEMVHDGGKDTWHSATAIYCLMGSQQLWDTVTGVDM
L

>d1nsca__ b.68.1.1 (A:) Influenza neuraminidase {Influenza B virus, different strains}

EPEWTPRSLCQGSTFQKALLSPHRFGEARGNSAPLIIREPVACGPKECKHFALTHYAAQPGGYYNGTREDRNKLRLHSVKLGKIPTVENSIFHMAA
WSGSACHDGREWTYIGVDGPDSNALIKIKYGEAYTDYHSYANNILRTQESACNCIGGDCYLMITDGSASGISKCRFLKIREGRIIKEIFPTGRVEHTEE
CTCGFASNKTIECACRDNSYTAKRPFVKNVETDTAEIRLMCTYLDTPRPPDDGSIAGPCESNGDKGRGGIKGGFVHQRMASKIGRWYSRTMSKT
RMGMELYVRYDGPWTSDALAHSGVMVSMKEPGWYSFGFEIKDKKCDVPCIGIEMVHDGGKDTWHSATAIYCLMGSQQLWDTVTGVDM
AL

>d1e8ua__ b.68.1.1 (A:) Paramyxovirus hemagglutinin-neuraminidase head domain {Newcastle disease virus}

GAPIHDPDFIGGIGKELIVDNAASDVTFSYPSAFQEHLNFIPAPTTGSGCTRIPSFDMSATHCYTHNVLSGCRDHSHHQYLAQVLRTTATGRIFFSTL
RSISLDDTQNRKSCSVSATPLGCDMLCSKVTEEEEDYNSAVPTLMAHGRGLFDGQYHEKLDVTTLFEDWVANYPGVGGGSIDGRVWFSVYGGL
KPNPSDTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKPGRGFGKRIQQAISIKVSTLGEDPVLTPPNTVTLMAEGRILTVGTSFLYQRGSS
YFSPALLYPMVTNSNKTATLHSPTYTFNAFRPGSIPQASARCPNSCTGVYTDYPLIFYRNHTLGVFGTMLDSEQARLNPSAVFDSTSRSRITRVSS
SSTKAAYTTSTCFKVVTKNTKTYCLSIAEISNTLGEFRIVPLLVEILKND

>d1eur__ b.68.1.1 (-) Micromonospora sialidase, N-terminal domain {Micromonospora viridifaciens}

GEPLYTEQDLAVNGREGFPNYRIPALTVPDG DLLASYDGRPTGIDAPGPNSILQRRSTDGGRTWGEQQVVSAGQTAPIKGFS DPSYLV DRETGTIF
NFH VYSQRQGFAGSRPGTDPADPNVLHANVATSTDGLTWSHRTITADTPDGPWRSRFAASGEIGIQLRYGPHAGR LIQQTII NAAGAFQAVSVY
SDDHGRTRAGEAVVGMDENKTV ELSDRVLLNSRDSARSGYRKAVSTDGGHSYGPV TIDRLPDPTNNASIIRAFPDAPAGSARAKVLLFSNA
ASQTSRSQGTIRMSCDDQTWPVSKVFPQGSMSYLTALPDGYGLLYEPGTGIRYANFNLAWLGGICAP

>d2sli_2 b.68.1.1 (277-759) Leech intramolecular trans-sialidase, C-terminal domain {North american leech (Macrobdella decora)}

GENIFYAGDVTESNYFRIPSLLTSTGTVISAADARYGGTHDSKSKINIAFAKSTDGGNTWSEPLPLKFDDYIAKNIDWPRDSVGKNVQIQGSASYIDP
VLLEDKLTKRIFLFADLMPAGIGSSNASVGSGFKEVNGKKYLKLRWHKDAGR AYDTIREKGVIYNDATNQPTEFRDGEYNLYQHDTNLCKQYDYN
FSGNNLIESKTDVDVNMMNIFYKNSVFKAFPTNYLAMRYS DDE GASWSLDIVSSFKPEVSKFLVVGPGIGKQISTGENA RLLVPLYSKSSAELGF MYS
DDHGDNW TYVEADNLGGATAEAQIVEMP DGS LKTYLRTGSNCIAEVTSIDGGETWSDRVPLQGISTTSYGTQLSVINYSPIDGKPAA ILLSPNATN
GRKNGKI WIGL VN DGTGNTGIDKSYE VEWKSYA VDTPQMGYSCLAEPLDQGVGLLYEKYD SWSRNELHLKDI KFEKYSI ELTGQA

>d1kit_3 b.68.1.1 (217-346,544-781) Vibrio cholerae sialidase {Vibrio cholerae}

VIFRGPD RIPSIVASSVTPGVVTAF AEKRVGGGD PGALS NTNDIITR TS RDGGITW DTEL NLTE QIN VSDEF DFSD PRPI YDPSSNTV LV SYARWPTDAA
QNGDRIKPWMPNGIFYSYDVASGNWQAPIXVNPGPGH GITL TRQQNISGSQNGRLIYPAIVLDRFFLN VMSIYSDGGSNWQTGSTLPI F RWK
SSSI LETPE SEADM VELQ NGD LLLTAR LD FNQIVNG VNSP RQQFLSK DGGITW SLE ANNAN VFSN I STGT VDAS IT RFE QSDG SHF LLFT NPQGN
PAGTNGRQNLGLWFSFDEGV TWKGPIQLVNGASAYSDIYQLDSENAIVIVETD NSNM RLM PITT LKQKL TLSQN

>d1crua_b.68.2.1 (A:) Soluble quinoprotein glucose dehydrogenase {Acinetobacter calcoaceticus}

DVPLTPSQFAKSENFDKKVILSNLNPKHALLWGP DNQIWLTERATGK ILRVNPESGSVKTVFQVPEIVNDAGQNGLLGFAFHPDFKNNP YIISG
TFKNPKSTDKE LPN QTII RRTY NKSTD TLEKPVDLLAGLPSSKDHQS GR L VIGPDQK IYYTIGDQGRNQ LAYL FLPNQ A QHTPTQQE LNGK DYHTYM
GKV LRLNLDGSIPKDNPSFNGVV SHI TLGH RNPQ GLAFTPNGKLLQSEQGPNSD DE INLIVKGG NYGP NVAGYK DSGYAYA NYSA AANKS IKDL
AQNGVKVAAGV PVTK ESEWTG KNFV PPLK TLYTV QD TYN NDPT CGEM TYIC WPTV APSSAYV YKGGKA ITGW ENTL VPSL KR GVIF RI KLD PTY
STYDDA VPMFKS NN RYD VIAS PDGNV LYV L TDAGNV QKDDG SVNT LENPGS LIKFT

>d1h6la_b.68.3.1 (A:) Thermostable phytase (3-phytase) {Bacillus amyloliquefaciens}

KLSDPYHFTV NAAA ETEPV DTAGDA ADDP AIWL DP KPNP QNSK LIT TNK SG LAVS L EKGML HS YHTG KLN NVDI RYDF PLNG KK VDIAA SNRSEG
KNTIEIYAIDGKNGTLQSITDPN RPI ASAI DEVYGF SLYHSQKTGKY AMVTGKE GEFEQ YELNADKNGYISGKKVRA FK MNSQ TEGMA ADDEY GS LYI
AEEDEAIWKFSAEPDGG SNGT VIDRADGRH LT P DIEGLT IYYA DKG KYLL ASQGN SSYAIYERQGQNK YVADF QITD GPETD GTSDT D GIDV LGFG
LGPEYPFGLFVAQNGENIDHGQKANQNF KM VPWE RIADKIGFHPQVN KQV DPKM TDRS

>d1crza1 b.68.4.1 (A:141-409) TolB, C-terminal domain {Escherichia coli}

AFRTRIAYV VQTNGGQFPYELRVSDYDGYNQFV VHRSPQPLM SPAWSPD GS KLAYVTFESGRS ALV I QTLANGA VRQV ASF PRH NGAP AFSPD GS K
LA FALS KTGS LNL VMDL ASG QIRQ VTD GR SNN TEPTW FP DSQ NLA FTSDQ AGRP QVY KV VING GAP QR ITWE GS QN QDAD VSS DGK FMV MVS
SNGG QQHIA KQD LATGGV QV LSST FLD ETPS LAPNGT MVIYSS SQGM GS VLN L VSTD GRF KARL PA TDG QV KFP AWSPYI

>d1ijqa1 b.68.5.1 (A:377-642) Low density lipoprotein (LDL) reseptor YWTD domain {Human (Homo sapiens)}

IAYLFTNRHEVRKMTLDRSEYTS LIPN LRNV VALD TEV ASN R IYWS DLS QR M IC ST QL DR AHGV SSY DT V ISR DIQAPD GLA VDW IHS NIY WT DSV
GTV SADT KG VKR KTL FREN GSK PRA IVV DPV HGF MYW TDW GTP A KIK GGL NGV D IYSL VTEN I QW PNG I TLD L SGR LYW VDS K LHS ISS IDV NG
GNR KTI LEDE KRLA HPF SLAV FED KVF WTD I INE A IF SAN RLT GSD VNL A ENL SPED M VL FH NL TQ PRG

>d1e1aa_b.68.6.1 (A:) Diisopropylfluorophosphatase (phosphotriesterase, DFP) {Squid (Loligo vulgaris)}

IPVIEPLFTK VTEDIPGAEGPV FDNGDFYIVAPEVEVNGK PAGEI L RIDL KTG KKT VICK PEVNGYGGIPAGCQC DRD ANQLF VADM RL GLLV QT DG
T FEEIAKKDSEGR RMQG CND CAFDYEGNLW ITA PAG EVA PAD YTRSM QK FG SIYCF TTDG QM IQV DTA FQF PNG IAV RH MN DGP YQL V AET PT
KKLW SYDI KGP AKIEN KVV GHIP GTHEGGAD GMDF DEDN NLL VAWG SSHIEVFGPD GGQPKM RICP FEKPS NLHF K PQT K TIFV TEHEN NAV
WK FEW QRNG KKQYCETLKFGIF

>d1k32a2 b.68.7.1 (A:39-319) Tricorn protease N-terminal domain {Archaeon Thermoplasma acidophilum}

MPNLLNPD IHG DRII FVCC DLLWEHDLKSGSTRKIVSNLGVINN ARFFPD GRKIA RV/MRGSS LNTADLYFYNGEN GEIKRITYFSGKSTGRRMFTDV
AGFDPDG NLI ISTDAM QPFSSMT CLYR VENDG INFVPLNLG PATHI LFAD GRV IRG RNTFEL PHW KGYRG GTRG KI WIEVNSGAFKKIVDMSTHVSS
PVIVGHR IYFITD IDGFGQIYST DLDG KDLR KHTSFTD YYPRH LNTD GRR I LFSKGG SIYIFNP DTEKIEKIEIGD LESP DRII

>d1k3ia3 b.69.1.1 (A:151-537) Galactose oxidase, central domain {Fungi (Fusarium spp)}

YTAPQPGLRGWPTIDLPVAAAIEPTSGRVLMWSSYRNDAGGSPGGITLSSWPSTGIVSDRTVTVKHDMFCPGISMDGNGQIVVTGGND
DAKTSLYDSSSDSWIPGPDMQMVGARYQSSATMSDGRVFTIGGSWSGGVFEKNGEVYSPSSKTWTSLPNAKVNPMLTADKQGLYRSDNHAWLFG
WKKGSVFQAGPSTAMNWYYTSGSGDVKSAGKRQSNRGVADAMCGNAVMYDAVKGILTFGGSPDYQDSATTNAIIITLGEPGTSPNTVFASN
GLYFARTFHHTSVVLPGSTFITGGQRGIPFEDSTPVFTPEIYVPEQDTFYKQNPNSIVRYHSISLLPDGRVFNGGGLCGDCTTNHFDAQIFTPNYL
YNSN

>d1mdah_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}

EKSKVAGSAAAASAAAASDGSSCDHGPAGAISRRSHITLPAYFAGTTENWVSCAGCGVTLGHSLGAFLSLAVAGHSGSDFALASTSFARSAGKRTDYY
EVFDPTVFLPIADIELPDAPRFSVGPVRVHIGNCASSAACLLFLFGSSAAGLSVPAGSDDQLTKSASCFIHPGAAATHYLGSCPASLAASDLAAAPAA
AGIVGAQCTGAQNCSQAAQANYPGMILWAVASSILQGDIPAAGATMKAIDGNESGRKADNFRSAGFQMVAKLKNTDGIMILTVEHSRSCLAA
AENTSSVTAVGQTSGPISNGHDSDAIIAQDGASDNYANSAGTEVLDIYDAASDQQSSVELKGPELSVQNEA

>d2bbkh_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}

DEPRILEAPAPDARRVYVNDPAHFAAVTQQFVIDGEAGRIGMIDGGFLPNPVVADDGSFIAHASTVFSRIARGERTDYVEVFDPVTLPTADIELPD
APRFLVGTYPWMITSLPDGKTLFYQFSPAPAVGVVDLEGKAKFKRMLDVPDCYHIFPTAPDTFFMHCRDGLSLAKVAFGTETGPTEITHTEVFHPEDEF
INHPAYSQKAGRLVWPTYTGKIHQIDLSSGDAKFLPAVEALTEAERADGWRPGGWQQVAYHRA LDRIYLLV DQRDEWRHTASRFVVLDAKTGER
LAKFEMGHEIDSINVSQDEKPLLYALSTGDKTLYIHDAESEGEELRSVNQLGHGPQVITTADMG

>d2madh_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Gram negative methylotrophic bacteria (Thiobacillus versutus)}

SSASAAAAAAAALAAAGAADGPTNDEAPGADGRRSYINLPAHHSAIIQQWVLDAGGSGSILGHVNGGFLPNPVAHSGSEFALASTSFRIAKGKRT
DYVEVFDPVFLPIADIELPDAPRFDVGPYSWMNANTPNNA D L F Q F A A G P A V G L V V Q G G S S D D Q L L S P T C Y H I H P G A P S T F Y L L C A Q G G L A K T D
HAGGAAGAGLVGAMILTAQNL T Q P A Q K N G S R I V W P V Y S G K I L Q A D I S A A G A T N K A P I D A L S G G R K A D T W R P G G W Q Q V A Y L K S S D G I Y L L T S E Q
SAWKLHAAAKEVTSVTGLVGQTSSQISLGHVDVAISVAQDGDPDLYALSAGTEVLHIYDAGAGDQDQSTVELGSGPQVLSVMNEA

>d1jjub_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Paracoccus denitrificans}

RDYILAPARPDKLVVIDTEKMA/DKVITIADAGPTPMVPMVAPGGRIAYATVNKSESLVKIDLVTGETLGRIDLSTPEERVKSLFGAALSPDGKTLAIYES
PVRLELTHFEVQPTRVALYDAE TL SRRKAFEAPRQITMLAWARDGSKLYGLGRDLHVMDPEAGT L V E D K P I Q S W E A T Y A Q P D V L A V W N Q H E S S G V
MATPFYTARKDIDPADPTAYRTGLTM DLETGEMAMREVRIMDVYFSTA V NPAKTRAFGAYNVLESFDLEKNASIKRVPPLPHSY SVNVSTDGSTV
WLGGALGDLAAYDAETLEKKGQV D L P G N A S M S L A S V R L F T R D E

>d1jmxb_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Pseudomonas putida}

GPALKAGHEYMIVTNYPNNLHVVDVASDTVYKSCVMPDKFGPGTAMMAPDNR TAYVLNNHYGDIYKIDLTCKNTFHANLSSVPGEVGRSMYSF
AISP DGKEVYATVNPTQRLNDHYVVKPPRLEV F STADGLEAKPV RTFPMPRQVYLMRAADDGSLYVAGPDIYKMDVKTGKYTV ALPLRNWNRKGYS
APDVLYFWPHQSPRHEFSMLYTIARFKDDKQDPATADLLYGYLSVDLKTGKHTQEFA DL T E Y FTGLRSPKDPNQIYGVNRLAKYDLKQRKLIKAANL
DHTYYCVAFDKKGDKLYLGGTFNDLAVFNPDTLEKVKNIKLPGGDMSTTPQVFIR

>d1qnia2 b.69.3.1 (A:10-450) Nitrous oxide reductase, N-terminal domain {Pseudomonas nautica}

AHVAPGELDEYYGFWSGGHQGEVRVLGVPSMRELMRIPVFNVDSATGWGITNESKEILGGDQQYLN G DCHH PHISMTDGRYDGKYLINDKANT
RVARI RL DIMKTDKITHIPNVQAIHGLRLQKVPKTNYFCNAEFVIPQPN D GTDFSLD NSYTMFTAIDAETMDVAWQVIVDGNLDNTDAD YTGKYAT
STCYNSERA V DLAGTMRNDRD W V V FNVERIAAAV KAGNF K TIGDSKVPV DGRGESEFTRYIPVPKNPHGLNTSPDGKYFIANGKLSPTV S VIAID
KLDDLFEDKIELRDTIVAEPELGLGPLHTTFDGRGNAYTTLFIDSQVCKWNIA DA IKHYGDRV NYIRQKLDVQYQPGHNHASL TESRDADGKWL V VL
SKFSKDRFLPVGPLHPENDQLIDISGEEMKLVHDGPTYAEPHD CILVRRDQIKTK

>d1fwxa2 b.69.3.1 (A:8-451) Nitrous oxide reductase, N-terminal domain {Paracoccus denitrificans}

ADGSVAPGQLDDYYGFWSGGQSGEMRILGIPSMRELMRVPVFNRC SATGWGQTNESVR IHERTMSERTKKFLAANGKRIHDNGDLHHVHMSFT
EGKYDGRFLFMNDKANTRVARVRC DVMKCD AILEIPNAKG I HGLRPQK WPRS NYVFCNGEDETPLVNDGTN MEDVANYVN VFTAVDADKWEVA
WQVLVSGNLDNCADYEGKWA FSTS YNSEKGM TLPEM TAAE MDHIVVFNIAEIEKAIAAGD YQELNGVKVVDGRKEASSLTRYIPIANNPHGCN
MAPDKKHLVAGKLSPTVLDVTRFDAVYENADPRSAVVAEPELGLGPLHTAFDGRGNAYTSFLDSQVVKWNIEDAIRAYAGEKVDPIKD KLDV
HYQPGHHLKTVMGETLDA TDNDWL VCLSKFSKDRFLNVGPLKPENDQLIDISGDKMVLHDGPTFAEPHD AIAVHPSILSDIK

>d1tbga_ b.69.4.1 (A:) beta1-subunit of the signal-transducing G protein heterotrimer {Cow (Bos taurus)}

MSELDQLRQEAEQLKNQIRDARKACADATLSQTNNIDPVGRIQMRTRTLGHHLAKIYAMHWGTDSSLVSASQDGKLIWDSYTTNKVHAIPRS
SWVMTCAVAPSGNYVACGGLDNICSINYLNKREGNVRVSRELAGHTGYLSCRFDDNQIVTSSGDTTCALWDIETGQQTTFTGHTGDVMSLSA
PDTRLFVSGACDASAKLWDVREGMCQFTGHESDINAICFFPNGNAFATGSDDATCRFLRADQELMTYSHDNIICGITSFSKSGRLLAGYDD
FNCNVWDALKADRGVLAGHDNRVSLGVTDGMAVATGSWDSFLKIWN

>d1erja_b.69.4.1 (A:) Tup1, C-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}

HYLVPYNQRANHSKPIPPFLDLDSQSVPDALKKQTNDYYILYNPALPREIDVELHKSLDHTSVVCCVKFSNDGEYLATGCNKTQVYRVDGSLVARLS
DDSAANKDPENLNTSSPSSDLYIRSVCFSPDGKFLTAGEDRLIRIWDIENRKIVMILQHGHEQDIYSLDFPSGDKLVSGSGDRTVRIWDLRTGQCSLT
LSIEDGVTTAVSPGDGKYIAAGSLDRAVRVWDSETGFLVERLDSENESTGHKDSVSVVFTRDGQS VSGSLRSVKLWNLNQNANNKSDSKTPN
SGTCEVTYIGHKDFVLSVATTQNDEYILSGSKDRGVLFWDKKGPNPLMLQGHHRNSVISVAVANGSSLGPEYNVFATGSGDCKARIWKYKKI

>d1k8kc_b.69.4.1 (C:) Arp2/3 complex 41 kDa subunit ARPC1 {Cow (*Bos taurus*)}

AYHSFLVEPISCHAWNKDRTQIAICPNHHEVHIYEKSGNKWVQVHELKEHNGQVTGVDWAPDSNRIVTCGDRNAYVWTLGRTWKPTLVIRINR
AACRCVRWAPNEKKFAVGGSRVISICYFEQENDWWVCKHICKPIRSTVSLDWHPNSVLAAGSCDFKCRIFSAYIKEVEERPAPTPWGSKMPFGE
MFESSSSCGWVHGVCFSANGSRVAWVSHDSTVCLADADKMAVATLASETLPLLAVTFITESSLVAAGHDCFVLFYDSAAGKLSFGGRLDVPKQS
SQRGLTARERFQNLDKKASSEGSAAGAGLDSLHKNSVSQISVLSGGAKCSQFC TTGMDGGMSIWDRSLESALKDLKIV

>d1a12a_b.69.5.1 (A:) Regulator of chromosome condensation RCC1 {Human (*Homo sapiens*)}

KKVKVSHRHSHSTEPGLVLTGQGDVGQLGLGENVMERKKPALVSI PEDVVQAEAGGMHTVCLSKSGQVSYFGCNDEGALGRDT SVEGSEMVPKV
ELQEKKVQVSAGDSHTAA LTDDGRVFLWGSFRDNNGVIGLLEPMKKS M VPVQVQLDVPVV KVASGNDHLVMLTADGDLYTLGCGEQGQLGRVPE
LFANRRGGRQGLERLLPKCVMILKSRGSRGHVRFQDAFCGAYFTFAISHEGHVYGFGLSNYHQLGTPGTESCFIPQNLTSFKNSTKSWVGFSQQHHT
VCMDSEGKAYSLGRAEYGRGLGEGAEEKSIPTLISRLPAVSSVACGASVGYAVTKDGRVFAWGMGTNYQLGTGQDED AWPVEMMGKQLENRV
VLSVSSGGQHTVLLVKDKEQS

>d1jtdb_b.69.5.2 (B:) of beta-lactamase inhibitor protein-II, BLIP-II {*Streptomyces exfoliatus*}

VAATSVVAWGNNNDWGEATVPAEAQSGVDAIAGGYFHGLALKGGKVLGWGANLNQLTMAATQSGVDAIAAGNYHSLALKDGEVIAWGGNE
DGQTTVPAEARSGVDAIAAGAWASYALKDGKVI AWGDDSDGQTTVPAEAQSGVTALDGGVYTALAVKNGGVI AWGDNYFGQTTVPAEAQSGVD
DVAGGIFHSLALKDGKVI AWGDNRYKQTTVPEALSGVSAIASGEWYSLAKNGKVI AWGSSRTAPSSVQSGVSSIEAGPNAAYALKG

>d1c9la2_b.69.6.1 (A:3-330) Clathrin heavy-chain terminal domain {Rat (*Rattus norvegicus*)}

QILPIRFQEHLQLQNLGINPANIGFSTLTMESDKFICIREKVGEQAQVVIIDMN D PNSPIR PISADS AIMNPASKVIALKAGKTLQIFNIE MKSKMKAH
TMTDDVTFWKWI SLNTVALTDNAV YHWSMEGESQPVKMFDRHSSLAGCQIINYRTDAKQKWLLTGISAQQNRVVGAMQLYSVDRKVSPQIEG
HAASFAQFKMEGNAEESTLFCFAVRGQAGGKLHII EVGTPPTGNQFPKKAVDVF PPEAQNDFPVAMQISEKHDVFLITKYGYIHLYDLETGTCIY
MN RISGETIFVTAPHEATAGIIGVNRKGQVLSVCVE

>d1jv2a4_b.69.8.1 (A:1-438) Integrin alpha N-terminal domain {Human (*Homo sapiens*)}

FNLDVDSPEYSGPEGSYFGAVDFVPSASSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRRCQPIEF DATG NR DYAKDDPLEFKSHQWFGA
SVRSKQDKLACAPLYHWRTEMKQEREPVGTCLQDGTKTVEYAPCRSQDIDADGQGFCQGGFSIDFTKADR VLLGGPGSFYWQGQLISDQVAEIV
SKYDPNVSYIKYNNQLATRTAQAFDDSYLGYSVAVGDFNGDGIDDFVSGV PRAARTLG MVYIYDGKNMSSLYNFTGEQMAAYFGSVAATDINGD
DYADVFIGAPLFMDRGS D GK LQEVGQVSVSLQRASGDFQTTKLNGFEV FARFGSIAIPLG DLDQDG FNDIAIAAPYGGEDKKGIVYIFNGRSTGLNA
VPSQILEGQWAARS MPPSF GYSMKGAT DIDKNGYPDLIVGAFGVDRAILYRAR

>d1qfma1_b.69.7.1 (A:1-430) Prolyl oligopeptidase, N-terminal domain {Pig (*Sus scrofa*)}

MLS FQY PDV YR DETA I QDY HGH KVCD PYA WLED P DSE QT KAF VEA QNK IT VP FLE QCP IR GLY KER MTE LYD P KYS CH FK KG KRY FYF Y NT GLQ NQ
RVL VY QD SLEG A R VFL DP NIL SDD GTV AL RGY AF S E DGE Y FAY GLS AS GSD WVT KF MKV DGA KEL PDV LER VKF SCMA WTH DG KG MF YN AY PQ
QDG KSD GT ET ST NLH QK LY HVL GTD QSE DIL CAE FP D E P KWM GG A ELS DD GR YV LL SIREG CDP VN RLW Y CDL QQ E NG IT G IL KW V KL IDN FEG
EY DY VT NE GTV FT FK TNR HSP NY RL NI DFTD PE E SKW VL VPE HEK DV LEW VAC VR S N F L CYL HDV K N T L Q L H D L AT G ALL K IF P LEV GS VVG Y SG
QKK DTE IF Y QFT SFLSPG IY HCD LT KEE E L PR V F REV TV KGI

>d1k32a3_b.69.9.1 (A:320-679) Tricorn protease N-terminal domain {Archaeon *Thermoplasma acidophilum*}

SIPS KFA ED FS PLD GD LIA F VS RG QAF I QDV SG TYV LK VPE PLR I RY V R RGG DT K VAF IH G T REG DF LGI YD Y RT GKA EK FEE NL GN V F AM G V DR NG K F
AVV AND R FE IM T VD LET G K PT V IERS REAM T DFT ISD NSR F I AY GF PL KH GET DGY VM QAIH VY DM ER K I FA ATT EN SHD Y A PA FD AD SKN LY LS Y

RSLDPSPDRVVLNFSFEVVSKPFVPLIPGSPNPTKLVRSPMTSEAGEYDLNDMYKRSSPINVDPGDYRMIIPLESSILYSPVHGEFAAYYQGAPEKGV
LLKYDVKTRKVTEVKNNLTLRLSADRKTVMVRKDDGIYTFPLEKPEDERTVETDKRPLV

>d1g72a_b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylophilus methylotrophus, w3a1}

DADLDKQVNNTAGAWPIATGGYYSQHNSPLAQINKSVKNVKAWSFSTGVNGHEGAPLVGDMMVHSAPNNTYALNLNDPGKIVWQHKPK
QDASTKAVMCCDVDRGLAYGAGQIVKKQANGHLLADAKTGKINWEVEVCDPKVGSTLTQAPFVAKDTVLMGCGAELGVRAVNAFDLKTGE
LKWRRAFATGSDDSVRLAKDFNSANPHYGQFLGTWTWEGDAWKIGGGTNWGWWYADPKLNLFYGGNPAPWNETMRPGDNKWTMTIWGR
DLDTGMAKGWYQKTPHDEWDFAVNQMVLDQPVNGKMTPLSHIDRNGILYTLNRENGNLIVAEKDPAVNVFKVDLKTGTPVDRPEFATR
MDHKGTNICPSAMGFHNQGVDSYDPESRTLYAGLNHICMDWEPMPLPYRAGQFFVGATLAMYPPNGPTKEMGQIRAFDLTTGAKWTKWE
KFAAWGGTLYTKGLVWYATLDGYLKALDNKDGKELWNFKMPGSGIYGSPMTYSFKGKQYIGSMYGVGGWPGVGLVFDLTDPSAGLGAVGAFREL
QNHTQMGGGLMVFSL

>d1h4ia_b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylobacterium extorquens}

NDKVELSKSDDNWVMPGKNYDSNNFSDLQINKGNVKQLRPAWTSTGLNGHEGAPLVVDGKMYIHTSFPNNTFALGLDDPGTILWQDKPKQ
NPAARAVACCDLVNRGLAYWPGDGKTPALIKTQLDGNVAALNAETGETVWKVENSDIKVGSTLTAPIVVKDKVIIGSSGAELGVRGYLTDVKTG
EQVWRAYATGPDKDILLASDFNIKNPHGQKGLGTWTWEGDAWKIGGGTNWGWWYADPGTNLIYFGTGNPAPWNETMRPGDNKWTMTIFGR
DADTGEAKFGYQKTPHDEWDYAGVNVMMLSEQKDKDGKARKLLTHPDRNGIVYTLDRDGALVSANKLDDTVNFKSVDLKGQPVDRPEYGR
MDHLAKDICPSAMGYHNQGHDSYDPKRELFFMGINHICMDWEPMPLPYRAGQFFVGATLNMYPPGKGRQNYEGLGQIKAYNAITGDYKWEK
MERFAVWGGTMATAGDLVYGTLDGYLKARDSDTGDLLWKFKIPSGAIGYPMTYTHKGTQYVAIYYGVGGWPGVGLVFDLADPTAGLGAVGAFKK
LANYTQMGGGVVVFSLDGKGPYDDPNVGEWK

>d1flga_b.70.1.1 (A:) Ethanol dehydrogenase {Pseudomonas aeruginosa}

KDVTWEDIANDDKTTGDLVQYGMGTHAQRWSPLKQVNADNVFKLTPAWSYSFGDEKQRQESQAIVSDGVIYTASYSRLFADAKTGKRLWTY
NHRLPDIRPCCDVVNRGAAIYGDKVFFGTLASVVALNKNTGKVVWKKFADHGAGYMTGAPTIVKDGKTGKLLIHGSSGDEFGVVGRFLFAR
DPDTGEEIWMRPFVEGHMGRNGKDSTVTGDKAPSWPDDRNSPTGKVESWSHGGAPWQSASFDAETNTIIVGAGNPGPWNTWARTAKGG
NPHDYDSLTSQGVGDPSSGEVKWFYQHTPNDAWDFSGNNELVLDYKAKDGKIVKATAHADRNFFYVDRSNGLQNAFPFVDNITWASHI
DLKTGRVEREGQRPLPEPGQKHGKAVEVSPPFLLGKWNWPMAYSQDTGLFYVPAHWKEDYWTEEVSYTKGSAYLGMGFRKRYDDHVGS
LRAMDPVSGKVVWEHKEHLPLWAGVLATAGNLVFTGTDGYFKAFDAKSGKELWKQTGSGIVSPPIWEQDGEQYLGTVGYGGAVPLWGGD
MADLTRPVQAQGSFWVFKLPSW

>d1kb0a2_b.70.1.1 (A:1-573) Quinoprotein alcohol dehydrogenase, N-terminal domain {Comamonas testosteroni}

TGPAAQAAAQVRVGDGFIRANAARTPDWPTIGVYDYEATRYSRLDQINAANVKDLGLAWSYNLESTRGVEATPVVVDGIMYVSASWSVVHAIDTR
TGNRIWTYDPQIDRSTGFKGCCDVNRGVALWKGKVYVGAWDGRLLAATGKEVWHQNTFEGQKGSLTITGAPRVFKGVIIINGGAEYGR
YITAYDAETGERKWRWFSPVPGDPSPKFEDESMKRAARTWDPSGKWEAGGGGTMWDSMTDAELNTMYVGTNGSPWSHKVRSPKGDDNL
YLASIVALDPDTGKYKWHYQETPGDNWDTSTQPMILADIKIAGKPRKVILHAPKNGFFFVLDRTNGKFISAKNFVPNWASGYDKHGKPIGIAAR
DGSKPQDAVPGPYGAHNWHPMFSNPQTGLVLPQAQNVPVNLMDKKWEFNQAGPGKPQSGTGWNATAFFNAEPPSKPFGRLAWDPVAQK
AAWSVEHVSPWNGGTTAGNVVFQGTADGRLVAYHAATGEKLWEAPTGTGVVAAPSTYMDGRQYVSAVGWGGVYGLAARATERQGPGTV
YTFVVGKARMPE

>d1nira2_b.70.2.1 (A:118-543) C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase {Pseudomonas aeruginosa}

EWGMPEMRESWKVLVKPEDRKKQLNLDLPLNLSVTLRDAGQIALVDGDSKKIVKVIDTGYAVHISRMSASGRYLLVGRDARIDMIDLWAKEPTK
VAEIKIGIEARSVESSKFKGYEDRYTIAGAYWPPQFAIMDGETLEPKQIVSTRGMTVDTQTYHPEPRVAAIIASHEHPEFIVNKETGKVLVNYKDIDN
LTVTSIGAAPFLHDGGWDSSHRYFMTAANNNSNKVAVIDSKDRRLSALDVGKTPHPGRGANFVHPKYGTVVWSTSHLDGSIISLIGTDPKHNHPQYA
WKKVAELQGQGGGSLFIKTHPKSSHLYVDTTFNPDRARISQSVAVFDLKNLDAKYQVLPIAEWADLGEAKRVAQPEYNKRGDEVWFSVWNGKND
SSALVVVDDKTLKLAJVVKDPRLITPTGKFNVYNTQHDVV

>d1qksa2_b.70.2.1 (A:136-567) C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase {Paracoccus denitrificans}

EFGMKEMRESWKVHVAPEDRPTQQMNDWDLENLFSVTLRDAGQIALIDGSTYEIKTVDLDTGYAVHISRLSASGRYLFVIGRDGKVNIDLWMKEP
TTVAEIKIGSEARSIESTSMEGWEDKYIAAGAYWPPQYVIMDGETLEPKKIQSTRGMTYDEQEYHPEPRVAAILASHYRPEFIVNVKETGKILLVDYTDL
NNLKTEISAERFLHDGGLDGSHYFITAANARNKLVIDTKEGKLVAIEDTGGQTPHPGRGANFVHPTFGPVWATSHMGDDSVALIGTDPGEHDP

NAWKILDSPALGGGSLFIKTHPNSQYLYVATLNPEAEISGSVAVFDIKAMTGDGSDPEFKTLPIAEWAGITEGQPRVVQGEFNKDGTEVWFSVWN
GKDQESALVVDDKTLELKHKVIKDERLVTPTGKFNVNTMTDTY
>d1e43a1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus licheniformis}
YAYGAQHDYFDHHDIVGWTRREGSSVANGLAALITDGPAGKRMVGRQNAGETWHDTGNRSEPVINSEGWGEFHNGGSVSIYVQR
>d1g94a1 b.71.1.1 (A:355-448) Bacterial alpha-Amylase {Pseudoalteromonas haloplancis (Alteromonas haloplancis)}
NWAUTNWWDNTNNQISFGRGSSGHMAINKESTLTATVQTDMASGQYCNCVLKGELSADAKSCSGEVITVNSDGTINLNIGAWDAMAIHKNAKL
N
>d1bag_1 b.71.1.1 (348-425) Bacterial alpha-Amylase {Bacillus subtilis}
QPEELSNPNGNNQIFMNQRGSHGVLANAGSSSVSINTATKLPDGRYDNKAGAGSFQVNDGKLTGTINARSAVLYPD
>d1hvxa1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus stearothermophilus}
YAYGTQHDYLDHSIDIIGWTRREGVTEKPGSGLAALITDGPAGGSKWMYVGKQHAGKVFYDLTGNRSDTVINSWGWFVKNGGSVSVWVPR
>d1gjwa1 b.71.1.1 (A:573-636) Maltosyltransferase {Thermotoga maritima}
GKFENLTTKDLVMYSYEKNGQKIVIAANVGKEPKEITGGRVWNGKWSDEEKVVLKPYLEALVQ
>d1cgt_3 b.71.1.1 (407-494) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}
GSTQQRWINNDVYVYERKFGKSVAVVAVNRLSTSASITGLSTSPLTGSYTDVLGGVLNGNNITSTNGSINNFTLAAGATAVWQYTTA
>d1kla3 b.71.1.1 (A:407-495) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}
GSTQERWINNDVLIYERKFGSNVAVVAVNRNLNAPASISGLVTSLPQGSYNDVLGGLLNGNTLSVGSGGAASNFTLAAGGTAVWQYTA
>d1cyg_3 b.71.1.1 (403-491) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus}
GDTEQRWINGDVYVYERQFGKDVVLAVANRNSSSNSITGLFTALPAGTYTDQLGGLLDGNTIQVGSNGSVNAFDLGPGEVGWVWAYSAT
>d1qho4 b.71.1.1 (A:408-495) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}
GTTTQRWINNDVYIYERKFFNDVVLVAINRNTQSSYSISGLQTALPAGSYADYLSGLLGGNGISVSNGSVASFTLAPGAVSVWQYSTS
>d1pama3 b.71.1.1 (A:407-496) Cyclodextrin glycosyltransferase {Bacillus sp., strain 1011}
GSTHERWINNDVYIYERKFGNNVAVVAINRNMNTPASITGLVSLPRGSYNDVLGGILNGNTLVGAGGAASNFTLAPGGTAVWQYTTA
>d1ciu_3 b.71.1.1 (407-495) Cyclodextrin glycosyltransferase {Thermoanaerobacterium thermosulfurigenes, EM1}
GTTQQRWINNDVYIYERKFGNNVALVAINRNLSTSNTGLYTAALPAGTYTDVLGGLLNGNSISVADGSVTPFTLSAGEVAVWQYVSS
>d1hx0a1 b.71.1.1 (A:404-496) Animal alpha-amylase {Pig (Sus scrofa)}
QPFANWWNDNGSNQVAFGRGNRGFIVFNNDDWQLSSTLQTGLPGGYCDVISGDKVGNCTGIKVYSSDGTAAQFSISNSAEDPFIAIHAESKL
>d1smd_1 b.71.1.1 (404-496) Animal alpha-amylase {Human (Homo sapiens)}
QPFNTNWYDNGSNQVAFGRGNRGFIVFNNDDWTFSLTQLTGLPAGTYCDVISGDKINGNCTGIKIYSSDGKAHFSISNSAEDPFIAIHAESKL
>d1jae_1 b.71.1.1 (379-471) Animal alpha-amylase {Yellow mealworm (Tenebrio molitor), larva}
GTQVENWWNSNDNQIAFSRGSQGFVAFTNGGDLNQNLTGLPAGTYCDVISGELSGGSGCTGKSVVDNGSADISLGSAEDDGVLAHVNAKL
>d2aaa_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus niger, acid amylase}
YANDAFYTDSNTIAMAKGTSQSQVITVLSNKGGSSYTLTSGSGYTSGTKLIEAYTCTSVTVDSGGDIPVPMASGLPRLVLPASVVDSSLCG
>d2taaa1 b.71.1.1 (A:382-478) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}
YKNPYIKDDTTIAMRKGTDSQIVTILSNKGASGDSYTLSGASASYTAGQQQLTEVIGCTTVGSDGNVPVPMAGGLPRLVLPTEKLAGSKICSDSS
>d7taa_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}
YKNWPIYKDDTTIAMRKGTDSQIVTILSNKGASGDSYTLSGAGYTAGQQQLTEVIGCTTVGSDGNVPVPMAGGLPRLVLPTEKLAGSKICS
>d1smaa2 b.71.1.1 (A:506-588) Maltogenic amylase {Thermus sp.}
GDVAFLTADDEVNHLVYAKTDGNETVMIINRSNEAAEIPMPIDARGKWLVLNLLGERFAAEATLCVSLPPYGFVLYAVESW
>d1bvza2 b.71.1.1 (A:503-585) Maltogenic amylase {Thermoactinomyces vulgaris, TVAII}
GNVRSWHADKQANLYAFVRTVQDQHVGVLNNRGEKQTVLLQVPESGGKTWLDCLTGEEVHGKQGQLKLTLPYQGMILWNGR
>d1eh9a2 b.71.1.1 (A:491-557) Glycosyltrehalose trehalose trehalohydrolase {Archaeon Sulfolobus solfataricus, km1}
CDRRVNVVNGENWLIIKGREYFSLYVFSKSSIEVKYSGTLLSSNNSPHQHIEEGKYEFDKGFALYK
>d1bf2_2 b.71.1.1 (638-750) Isoamylase {Pseudomonas amylofera}

YSGSQLTWYQPSGAVADSNYWNNNTSNYIAYAINGPSLGSNSIYVAYNGWSSVTFTLPAPPSTGTQWYRVTDTCDWNDGASTFVAPGSETLIGGA
GTTYGQCGQSLLLISK
>d1gcya1 b.71.1.1 (A:358-418) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase) {Pseudomonas stutzeri}
RADSAISFHSGYGLVATVSGSQTLVVALNSDLGNPGQVASGSFSEAVNASNGQVRVWRS
>d1avaa1 b.71.1.1 (A:347-403) Plant alpha-amylase {Barley (*Hordeum vulgare*), seeds, AMY2 isozyme}
HNESKLQIIEADADLYAEIDGKIVKLGPRYDVGNLIPGGFKVAHGNDYAVWEKI
>d1uok_1 b.71.1.1 (480-558) Oligo-1,6-glucosidase {Bacillus cereus}
GSYDLILENNPSIFAYVRTYGVKEKLLVIANFTAEECIFELPEDISYSEVELLIHNYDVENGPIENITLRPYEAMVFKLK
>d1g5aa1 b.71.1.1 (A:555-628) Amylosucrase {Neisseria polysaccharea}
RLVTFTNNKHIIGYIRNNALLAFGNFSEYPQTVAHTLQAMPKAHDLLIGGKTVSLNQDLTLQPYQVMWLEIA
>d1f8ab1 b.72.1.1 (B:1-42) Mitotic rotamase PIN1 {Human (*Homo sapiens*)}
GSHGMADEEKLPPGWEKRMSRSGRYYYFNHITNASQWERPS
>d1i8hb_ b.72.1.1 (B:) Mitotic rotamase PIN1 {Human (*Homo sapiens*)}
KLPPGWEKRMSRSGRYYYFNHITNASQWERPSGNSSG
>d1pina1 b.72.1.1 (A:6-39) Mitotic rotamase PIN1 {Human (*Homo sapiens*)}
KLPPGWEKRMSRSGRYYYFNHITNASQWERPSG
>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*)}
PASQHFLSTSVQGPWERAISPKNVPYYINHETQTTCW
>d1i5hw_ b.72.1.1 (W:) Ubiquitin ligase NEDD4 WWIII domain {Rat (*Rattus norvegicus*)}
GSPVDSNDLGPLPPGWEERTHTDGRVFFINHNICKTQWEDPRMQNVAITG
>d1e0na_ b.72.1.1 (A:) Hypothetical protein Yjq8 (Set2p) {Baker's yeast (*Saccharomyces cerevisiae*)}
PGWEIIHENGRLPLYNAEQKTKLHYPP
>d1jmqa_ b.72.1.1 (A:) Yap65 ww domain {Human (*Homo sapiens*)}
FEIPDDVPLPAGWEMAKTSSGQRYFKNHIDQTTWQDPRKAMLSQM
>d1k9ra_ b.72.1.1 (A:) Yap65 ww domain {Human (*Homo sapiens*)}
FEIPDDVPLPAGWEMAKTSSGQRYFLNHIDQTTWQDPRK
>d1aiw__ b.72.2.1 (-) Cellulose-binding domain of endoglucanase Z {Erwinia chrysanthemi}
MGDCANANVYPNWVSKDWAGQQPTHNEAGQSIVYKGNLYTANWYTASVPGSDSSWTQVGSCN
>d1ed7a_ b.72.2.1 (A:) Chitin-binding domain of chitinase A1 {Bacillus circulans}
AWQVNATAGQLVTNGKTYKCLQPHTSLAGWEPSNVPALWQLQ
>d1goia1 b.72.2.1 (A:447-498) Chitinase B, C-terminal domain {Serratia marcescens}
NLPIIMTAPAYVPGTTYAQGALVSQGYVWQTKWGYITSAPGSDSAWLKVGRV
>d1dkga1 b.73.1.1 (A:139-197) Head domain of nucleotide exchange factor GrpE {Escherichia coli}
VEVIAETNPVLDPNVHQIAMVESDDVAPGNVLGIMQKGYTLNGRTIRAAMVTAKAKA
>d1e44b_ b.101.1.1 (B:) Ribonuclease domain of colicin E3 {Escherichia coli}
GFKDYGHDYHPAPKTENIKGLGDLKPGIPKTPKQNGGGKRKRWTGDKRKYEWDSQHGELEGYRASDGQHLGSFPKTGNQLKGPDPKRNICKY
L
>d1hcb__ b.74.1.1 (-) Carbonic anhydrase {Human (*Homo sapiens*), erythrocytes, isozyme I}
PDWGYDDKNGPEQWSKLYPIANGNNQSPVDIKTSETKHDTSLKPISVSYNPATAKEIINVGHSHVNFDNDNRSLKGPFSDSYRLFQFHWG
STNEHGSEHTVDGVKYSaelVHAHWNSAKYSSLAEAASKADGLAVIGVLMKVGLEANPKLQVKLDQAIKTKGKRAPFTNFDPLPSSLDFWTYP
GSLTHPPLYEVSTWIICKESISVSSEQLAQFRSLLSNVEGDNAVPMQHNNRPTQPLKGRTVRASF
>d2cba__ b.74.1.1 (-) Carbonic anhydrase {Human (*Homo sapiens*), erythrocytes, isozyme II}

HHWGYGKHNGPEHWHKDFPIAKGERQSPVDIDTHTAKYDPSLKPLSVSYDQATSLRILNNGHAFNVEFDDSQDKAVLKGGLDGTYRLIQFHFHW
GSLDGQGSEHTVKKKYAAELHLVHWNTKYGDFGKAVQQPDGLAVLGIFLKVGSAKPGLQKVVDLSDIKTKGSADFTNFDPRGLLPESLDYWWTY
PGSLTTPPLLECVTIVLKEPISVSEQVLKFRKLNFGEGEPEELMVNDNRPAQPLKNRQIKASFK
>d1flja_b.74.1.1 (A:) Carbonic anhydrase {Rat (*Rattus norvegicus*), isozyme III}
AKEWGYASHNGPEHWHELYPIAKGDQNQSPIELHTKDIRHDPSLQPWSVYDPGSAKTLNNNGKTCRVVFDDTFDRSMLRGGPLSGPYRLRQFH
WGSSDDHGSEHTVDGVKYAAELHLVHWNPKYNTFGEALKQPDGIAVVGIFLKIGREKGEFQIILDAKTIKTKGEAPFNHFDPSCLPACRDYWTY
HGSFTTPCEECIVWLKEPMVSSDQMAKLRSLFASAENEPPVPLVGNWRPPQPKGRVVASFK
>d1znca_b.74.1.1 (A:) Carbonic anhydrase {Human (*Homo sapiens*), isozyme IV}
WCYEVQAESSNNYPCLPVKWGGNCQKDRQSPINVTAKVAKVDKLGRRFFSGYDKQQTWTVQNNHSVMMILLENKASISGGGLPAPYQAKQLHL
HWSDLPYKGSEHSLDGEHFAMEMHIVHEKEGTNSRNKEAQDPEDEIAVLAFLVEAGTQVNEGFQPLVEALSNIPKPEMSTMAESSLLDLPKEEK
LRHYFRYLGSLTPTCDEKVVWTVFREPIQLHREQILAFSQKLYYDKEQTVMKDNVRPLQQLGQRTVIKS
>d2znc_b.74.1.1 (-) Carbonic anhydrase {Mouse (*Mus musculus*), isozyme IV}
WCYEIQTEDPRSSCLGPEKWPAGACKENQQSPINVTARTKVNPRLTPFILVGYDQKQQWPINKNNQHTVEMTLGGACIIGGDLPARYEAVQLHLHW
SNGNDNGSEHSIDGRHFAMEMHIVHKKLTSSKEDSKDKFAVLAFMIEVGDKVNKGQFQPLVEALPSISKPHSTSTVRESSLQDMLPSTKMYTYFRYN
GSLTPNCDETIVWTVYKQPKIHKNQFLEFSKNLYDEDQKLNMKDNVRPLQPLGKRQVFKSHA
>d1dmxa_b.74.1.1 (A:) Carbonic anhydrase {Mouse (*Mus musculus*), liver, isozyme V}
GTRQSPINIOWKDSVYDPQLAPLRVSYDAASCYLVNTGYFFQVEFDDSCEDSGISGGPLGNHYRLKQFHFHWGATDEWGSEHAVDGHTYPEAELH
LVHNWNSTKYENYKKASVGENGALIVGFLKLGAAHQALQKLVDVLPVVRHKDTQVAMGPFDPSCLMPACRDYWTYPSLTTPLAESVTWIVQKT
PVEVSPSQLSMFRLLSGRGEEDVMVNYYRPLQPLRDRKLRSSFR
>d1jd0a_b.74.1.1 (A:) Carbonic anhydrase {Human (*Homo sapiens*), isozyme XII}
KWTYFGPDGENSWSKYPSCCGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLTNNGHSVKLNLPDMHIQGLQSRYSATQLHLHWGNPN
DPHGSEHTVSGQHFAELHIVHYNSDLYPDASTASNKSEGLAVLAVLIEMGSFNPSYDKIFSHLQHVVKYKGQEAEPVPGNIEELLPERTAEYYRYRGSLT
TPPCNPTVLWTVFRNPVQISQEQLLAETALYCTHMDDPSPREMINNFRQVQKFDERLVTSFS
>d1kopa_b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}
HTHWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPKVNPKPSMVVDENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFHVPS
NQIKGRTFPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVMPMTAGVKLNQPFDASTLLPKRLKYYRFAGSLTTPPCTEGVSWLVLKTYDH
IDQAQAEKFTRAVGSENNRPVQPLNARVIE
>d1koqa_b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}
THWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPKVNPKPSMVVDENNGHTIQVNYPEGGNTLTVNGRTYTLKQFHFHVNGRT
YTLKQFHFHVPSENQIKGRTFPMEAHFVHLDENKQPLVLAVLYEAGKTNGRLSSIWNVMPMTAGVKLNQPFDASTLLPKRL
KYYRFAGSLTTPPCTEGVSWLVLKTYDHIDQAQAEKFTRAVGSENNRPVQPLNARVIE
>d4bcl_b.75.1.1 (-) Bacteriochlorophyll A protein {Prosthecochloris aestuarii, strain 2k}
TTAHSDYIEIILEGGSSSWGQVKGRAKVNVPAAIPLLPTDCNIRIDAKPLDAQKGVRFTKIESVDSVKNTLNVEVDIANETKDRRIAVGEGSLVG
DFSHSFSFEGSVVNMYYRSDAVRRNIPNPIYMQRQFHILMKVPLDNNDLVTWEGFQQSISGGGANFGDWIREFWFIGPAFAAINEGGQRIS
PIVVNSSNVEGGEKGPGVGVTRWKFSHAGSGVVDISRWTELPVEQLNKPASIEGGFRSDSQGIEVKVDGNLPGVSRDAGGLRRILNHPLIPLVHH
GMVGKFNDFTVDTQLKIVLPKGYKIRYAAPQFRSQNLEEYRWSGGAYARWVEHVCKGGTGQFEIYAQ
>d1ksaa_b.75.1.1 (A:) Bacteriochlorophyll A protein {Green sulfur bacterium (*Chlorobium tepidum*)}
TTAHSDYIEIILEGGSSSWGQVKGRAKVNAPPASPLPADCDVKNVKPLDPAKGFVRISAVFESIVDSTKNKLTIEADIANETKERRISVGEGMVSGD
FSHTFSFEGSVVNLFYRSDAVRRNVPNPIYMQRQFHILMKVPLDNNDLDTWEGFQQSISGGGANFGDWIREFWFIGPAFTALNEGGQRISRIEV
NGLNTESGPKGPVGVSRRWRFSHGGSGMVDSISRWAELPSDKLNRAQVEAGFRSDSQGIEVKVDGEFPGVSVDAGGLRRILNHPLIPLVHHGM
VGKFNNFNVDQLKVVLPKGYKIRYAAPQYRSQNLEEYRWSGGAYARWVEHVCKGGVGQFEIYAQ
>d1ospo_b.76.1.1 (O:) Outer surface protein A {Lyme disease spirochete (*Borrelia burgdorferi*)}
SLDEKNSVSDLPGEMKVLVSKENKDGYDLIATVDKLEKGTSDKNNGSGVLEGVKADKCKVKTISDDLQTTLEVFKEDGKTLVSKVTSKDKSS
TEEKFNEKGEVSEKIITRADGTRLEYTGKSDGSGKAEVLKGYVLEGTLAETKTLVVKEGTVTLSKNISKSGEVSVELNDSSAATKTAAWNNSGTST

LTITVNSKKTKDLVFTKENTITVQQYDSNGTKLEGSAVEITKLDEIKNALK
>d1vmoa_ b.77.1.1 (A:) Vitelline membrane outer protein-I (VMO-I) {Hen (Gallus gallus)}
RTREYTSVITVPNGGHWGKWGIRQFCHSGYANGFALKVEPSQFRDOTALNGIRLRCLDGSVIESLVGKWTWTSFLVCPTGYLVFSLRSEKSQGG
GDDTAANNIQFRCSDAEVLVGDGLSWGRFGPWSKRCKICGLQTKVESPOGLRDTALNNVRFFCCK
>d1dlc_2 b.77.2.1 (290-499) delta-Endotoxin (insecticide), middle domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}
LYPKEVKTELTRDVLTDPIVGVNRLRGYGTTSNIENYIRKPHLFYLHRIQFHTRFQPGYYGNDSFNYWSGNVSTRPSIGSNDIITSPFYGNKSEPV
QNLEFNGEKVYRAVANTNLAVWPSAVYSGVTKVEFSQYNDQTDEASTQTYSKRNNGHVAWSIDQLPPTTDEPLEKGYSHQLNYVMCFLMQG
SRGTIPVLTWTHKSVD
>d1ji6a2 b.77.2.1 (A:291-502) delta-Endotoxin (insecticide), middle domain {Bacillus thuringiensis, CRY3bb1}
LYSKGVKTELTRDIFTDPISLNTLQEYGPTFLSIENSIRKPHLFYDYLQGIEFHTRLQPGYFGKDSFNYWSGNVETRPSIGSSKTITSPFYGDKSTEPVQKL
SFDGQKVYRTIANTDVAAPNGKVYLGVTKVDFSQYDDQKNETSTQTYDSKRNNGHVAQDSIDQLPPTTDEPLEKAYSHQLNYAECLMQRRT
GTIPFFTWTHERSV
>d1ciy_2 b.77.2.1 (256-461) delta-Endotoxin (insecticide), middle domain {Bacillus thuringiensis, CRYIA (A)}
PIRTVSQTLREIYTNPVLENFDGSFRGMAQRIEQNRQPHLMDILNSITIYDVRHGFNYWSGHQITASPVGFSGPEAFPLFGNAGNAAPPVLVSLTG
LGIFRTLSSPLYRRIILGSGPNNQELFVLGTEFSFASLTTLNPSTIYRQRTVDSLVDIPPQDNVPRAFGSHRLSHVTMLSQAAGAVYTLRAPTFSW
QHRSAEF
>d1i5pa2 b.77.2.1 (A:264-472) delta-Endotoxin (insecticide), middle domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}
YQSLMVSSGANLYASGSGPQQTQSFTAQNWPFLYSLFQVNSNYILSGISGTRLSITFPNIGGLPGSTTHSLNSARVNYSGGVSSGLIGATNLHNHFNC
STVLPPPLSTPFVRSWLDSGTDRAVGATSTNWQTESFQTTLSLRCGAFSARGNSNYFPDYFIRNISGVPLVIRNEDLTRLHYNQIRNIESPSGTPGGAR
AYLVSVHNRKN
>g1jac.5 b.77.3.1 (B;A:) Jacalin {Jackfruit (*Artocarpus integrifolia*)}
SGKSQTVIVGSWGAKGAKAFDDGAFTGIREINLSYNKETAIGDFQVYDNGSPYVGQNHKSFITGFTPVKISLDFPSEYIMEVSGYTGNVSGYVVVR
SLTFKTNKTYGPYGVTSGTPFNLPPIENGLVGFKGSIGYWLDFSMYLSL
>g1jot.2 b.77.3.1 (B;A:) Lectin MPA {Osage orange (*Maclura pomifera*)}
RNGKSQSIIVGPWGDRXGVTFDDGAYTGIREINFEYNSETAIGGLRVTYDLNGMPVAEDHKSFITGFKPVKISLEFPSEYIVEVSGYVGKVEGYTVIRS
LTFTKTNKTYGPYGVTVNGTPFSLPIENGLVGFKGSIGYWLDFSIYLSL
>d1c3ma_ b.77.3.1 (A:) Heltuba lectin {Jerusalem artishoke (*Helianthus tuberosus*)}
ASDIAVQAGPWGGNGGKRWLQTAHGGKITSIIKGTCIFSICQFVYKDDNIEYHSGKFGVLGDKAETITFAEDEDITASGTFGAYYHMTVVTSLTFQT
NKKVYGPFGTVASSFSLPLTKGKFAGFFGNNSGDVLDSIGGVVV
>d1jpc_ b.78.1.1 (-) Lectin (agglutinin) {Snowdrop (*Galanthus nivalis*)}
DNILYSGETLSTGEFLNYGSFVFIMQEDCNLVLYDHSTAVWSSNTDIPGKKGCKAVLQSDGNFVVYDAEGRSLWASHSVRGNGNYVILQKDRNVV
VIYRSDIWST
>d1bwua_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (*Allium sativum*)}
RNILRNDEGLYGGQSLDVNPYHFMQEDCNLVLYDHSTAVWSSNTDIPGKKGCKAVLQSDGNFVVYDAEGRSLWASHSVRGNGNYVILQEDGNV
VIYRSDIWST
>d1bwud_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (*Allium sativum*)}
RNILTNEGLYGGQSLDVNPYHLMQEDCNLVLYDHSTAVWSSNTDIPGKKGCKAVLQSDGNFVVYDAEGRSLWASHSVRGNGNYVILQEDGNV
VIYRSDIWSTNTYR
>d1kj1a_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (*Allium sativum*)}
RNLLTNDEGLYAGQSLDVEPYHFMQEDCNLVLYDHSTAVWTTNTDIPGKKGCKAVLQSDGNFVVYDAEGRSLWASHSVRGNGNYVILQEDGNV
VIYGSDIWSTGTYK
>d1kj1d_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (*Allium sativum*)}
RNILMNDEGLYAGQSLDVEPYHLMQEDCNLVLYDHSTAVWTTNTDIPGKKGCKAVLQSDGNFVVYDAEGRSLWASHSVRGNGNYVILQEDGNV
VIYGSDIWSTNTYK

>d1npla_b.78.1.1 (A:) Lectin (agglutinin) {Daffodil (*Narcissus pseudonarcissus*)}

DNILYSGETLSPGEFLNNGRYFIMQEDCNLVLYDKPIWATNTGGLRRCIHSMSQSDGNLVYSPRNNPIWASNTGGENGNYCVLQKDRNVV
IYGTARWATGTNIH

>d1b2pa_b.78.1.1 (A:) Lectin (agglutinin) {Bluebell (*Scilla campanulata*)}

NNIIFSKQPPDNHPQILHATESLEIFGTHVYRFIMQTDCNLVYDNNNPWATNTGGLGNGCRAVLQPDGVLVITNENVTWQSPVAGKAGHYV
LVLPDPNVVIYGDALWATQTVR

>d1d1pa1 b.78.1.1 (A:1-115) Fetuin-binding protein Scafet precursor {Bluebell (*Scilla campanulata*)}

NNILFGLSHEGSHPQLHAAQSLELSSFRFTMQSDCNLVFDSDVRVWASNTAGATGCRAVLQSDGLLVITAQNTIRWSSGTKGSGNYVVLQPDR
TVTIYGPLWDSGTSNK

>d1d1pa2 b.78.1.1 (A:116-235) Fetuin-binding protein Scafet precursor {Bluebell (*Scilla campanulata*)}

GSVVVANNNSILYSTQGNDNHPQLHATQLQLSPYRLSMETDCNLVFDRDRVWSTNTAGKGTGCRRAVLQPNGRMDVLTNQNIAVWTSGNS
RSAGRYVFVLPQDRNLAIYGGALWTT

>d1kapp1 b.79.1.1 (P:247-470) Metalloprotease, C-terminal domain {*Pseudomonas aeruginosa*, alkaline protease}

GANLTTRTGDTVYGFNSNTERDFYSATSSSKLVFSVWDAGGNDLDFSGFSQNQKINLNKEKALSDVGLKGNVIAAGVTVENAIGGGSIDLIGN
DVANVLKGGAGNDILYGGLGADQLWGGAGADTFVYGDIAESSAAAPDTLRFVSGQDKIDLSGLDAFVNGGLVLQYVDAFAGKAGQAILSVDAA
KAGSLAIDFSGDAHADFAINLIGQATQADIVV

>d1sat_1 b.79.1.1 (247-471) Metalloprotease, C-terminal domain {*Serratia marcescens*}

GANLSTRGDTVYGFNSNTGRDFLSTSNSQKVIFAAWDAGGNDTDFSGYTANQRINLNEKSFDVGLKGNVIAAGVTENAIAGGSGNDVIVG
NAANNVLKGGAGNDLFGGGGADELWGGAGKDIFVSAASDASPASDWIRDFQKGIDKIDLSFFDKEANSSFIHFVDFSGTAGEALLSYNASS
NVTDSLNVNIGGHAAPDFLVKIVGQVVDVATDFIV

>d1air__ b.80.1.1 (-) Pectate lyase {*Erwinia chrysanthemi*, type C}

ATDTGGYAATAGGNVTGAVSKTATSMQDIVIIAARLDANGKKVGGAYPLVITYGNEDSLINAAAANICQWQSKDPRGVEIKEFTKGITIIGANG
SSANFGIWIKSSDVVVQNMRIGYLPGGAKDGDMIRVDDSPNVVDHNELFAANHECDGTPNDTTFESAVDIKGAANTVTSYNYIHGVKKVG
LDGSSSSDTGRNITYHHNNYNDVNARLPLQRGGGLVHAYNNLYTNITGSGLNVRQNGQALIENNWFKEAINPVTSRDGKNFGTWVLGNNTKPA
DFSTYSITWTADTKPYVNADSWTSTGTFPTVAYNYPVSAQCVKDKLPGYAGVGKNLATLTSTAC

>d1pcl__ b.80.1.1 (-) Pectate lyase {*Erwinia chrysanthemi*, type E}

AVETDAATTGWATQNGGTTGAKAAKAVEVKNISDFKKALNGTDSSAKIIVTGPIDISGGKAYTSFDDQKARSQISIPSNTIIGVGSNGKFTNGSLVI
KGVKVNLIRNLNLYIETPVDPAPHYESGDPGWNAEWDAAVIDNSTNVWDHVTSIDGFTDDKYTTKDGKEVYQHDGALDIKKGSDYVTISRFELHD
KTILIGHSDSNGSQDSGKLRVTFHNNVFDRVTERAPRVRGSIHAYNNVYLDVKHSVYPLYSFGLGTSGILSESNFTSLNLKSIDGKNPECSIVKQF
NSKVFSDKGSLVNGSTTKLDTCLGTYKPTLPYKSAQTMSSLATSIINNNAGYGKL

>d1bn8a_b.80.1.1 (A:) Pectate lyase {*Bacillus subtilis*}

ADLGHQTLGSNDGWAYSTGTTGGSKASSNVYTVSNRNQLVSALGKETNTTPKIIYIKGTIDMNVDDNLKPLGLNDYKDPEYDLDKYLKAYDPSTW
GKKEPSGTQEEARARSQKNQKARVMVDIPANTTIVGSGTNAKVGGSFQIKSDNVIRNIEFQDAYDYFPQWDPTDGSSGNWSQYDNITINGGT
HIWIDHCTFNDGSPRDSTPKYYGRKYQHHDGQTDASNGANYITMSYYHDHKSSIFGSSDSKTSDDGKLKTLHHNRYKNIVQRAPRVRFGQV
HVYNNYYEGSTSSSYPSYAWGIGKSSKIYAQNNVIDVPGLSAAKTISVFSGGTALYDSTLLNGTQINASAANGLSSVGWTPSLHGSIDASANVKS
NVINQAGAGKLN

>d1ee6a_b.80.1.1 (A:) Pectate lyase {*Bacillus* sp., strain ksmp15}

APTVVHETIRVPAGQTFDGKGQTYVANPNTLGDGSQAENQKPIFRLEAGASLKNVVGAPAADGVHCGDCTITNVIWEDVGEDALTLKSSGTVNIS
GGAAYKAYDKVFQINAAGTINIRNFRAADDIGKLVRQNGGTTVKVMNVENCNISRVKDAILRTDSSTGRIVNTRYSVPTLFKGFKSGNTTASGNT
QY

>d1idk__ b.80.1.2 (-) Pectin lyase {*Aspergillus niger*, type A}

VGVSGSAEGFAKGVTGGSATPVYPTIDELSYLGDDEARIVLTKTFDFTDSEGTTGTGCAPWTASACQVAIDQDDWCENYEPDAPSVSVEYY
NAGTLGITVTSNKSILIGEGRSGAIKGKGLRIVSGAENIIQNIATDINPKYVWGGDAITLDDCDLVWIDHVTARIGRQHYVLGTSADNRVSLNNYID
GVSDYSATCDGYHYWAIYLDGDAVLTMKGNYIYHTSGRSPKVQDNTLLHAVNNYWDISGHAFIEGEGGYVLAEGNWFQNVDTVLETYEGEAFT

VPSSTAGEVCSTYLRDCVINGFGSSGTFSEDSTSFLSDFEGKNIASASAYTSVASRVVANAGQGNL

>d1qcx_a_b.80.1.2 (A:) Pectin lyase {Aspergillus niger, type B}

AGVVGAAEFAHGVGGGSASPVPPTTDELVSYLDNEPRVIILDQTFDFTGTEGTETTGACPGTASQCQVAINLHSWCDNYQASAPKSVTY
DKAGILPITVNSNKSIVGQGTKVIGKGLRVSGAKNVIQNIAVTDINPKYVWGGDAITVDDSDLVWIDHVTARIGRQHIVLGTSAADNRVTISYLI
DGRSDYSATCNGHHYWGIVLDGSNDMVLKGNYFYNLSGRMPKVQGNTLLHAVNNLFHNFDGHAFEGTGGYVIAEGNVFQDVNVVETPISG
QLFSSPDANTNQQCASVGRSCQLNAFGNSGMSGSDTSIISKFAGKTIAAHPPGAIAQWTMKNAQGK

>d1rmg__ b.80.1.3 (-) Rhamnogalacturonase A {Aspergillus aculeatus}

QLSGSGVPLTSASTKGATKTCNILSYGAVADNSTDVGPAITSAWAACSGGLVYIPSGNYALNTWVLTGGSATAIQLDGIYRTGTASGNMIAVTDT
DFELFSSTSKGAVQGFYVYHAEGTYGARILRDTDVTHFSVHDILVDAPAFHFTMDTCSDGEVYNMAIRGGNEGGLGIDVWGSNIWHDVEVTN
KDECVTVKSPANNILVESIYCNWSGGCAMGSLGADTDVTDIVRNVTWSSNQMYMIKSNGSGTVSNVLENFIGHGNAYSIDLIDGYWSSMTAV
AGDGVQLNNITVKNWKGTEANGATRPPIRVVCSDTAPCTDLTLEDIAIWTEGSSELYCRSAYGSGYCLKDSSHTSYTTSTVTAAPSGYATTMAA
DLATAFGLTASIPIPTIPTSFYPGLTPYALAG

>d1bhe__ b.80.1.3 (-) Polygalacturonase {Erwinia carotovora, subsp. carotovora}

SDSRTVSEPKTPSSCTTLKADSSTATSTIQKALNNCDQKGAVRLSAGSTSFLSGPLSLPGVSLLIDKGVTLRAVNNAKSFENAPSSCGVVDKNGKGC
DAFITAVTTNSGIYGPGLDGQGGVKLQDKKVSWWELAADAKVKKLKQNTPLRIQINKSKNFTLYNVSILNSPNFHVVFSDDGFTAWKTTIKTPST
ARNTDGDPMSSKNITIAYNSIATGDDNVAIKAYKGRAETRNLISLHNDFTGTHGMSIGSETMGVNVTVDDLMNGTTNGLRIKSDKSAAGVVNG
VRYSNVVMKNAKPIVIDTVYEKKEGSNPWDWSITFKDVTSETKGVVVLNGENAKPIEVTMKNVKLTSDSTWQIKNVNVKK

>d1ia5_a_b.80.1.3 (A:) Polygalacturonase {Fungus (Aspergillus aculeatus)}

ATTCTFSGSNGASSASKTSCSTIVLSNAVPSGTTDLTKLNDGTHVIFSGETTFGYKEWSGPLISVSGSDLITGASGHSINGDGSRWWDGEGGN
GGKTKPKFAAHSLTNVISGLKIVNVPVQVFSVAGSDYLTLDKIDTIDNSDGDDNGHNTDAFDIGTSTVYTISGATVYNQDDCVAVNSGENIYFSGGY
CSGGHGLSIGSVGRSDNTVKNVTFVDTIINSNDNGVRIKTNIDTTGSVDVTYKDTILTSIAKYGIVVQQNYGDTSSPTTGPITDFVLDNVHGSVVS
SGTNILISCGSGSCSDWTWDDVSVGGKSSCTNVPSGASC

>d1czfa_ b.80.1.3 (A:) Polygalacturonase {Fungus (Aspergillus niger), endo-polygalacturonase II}

DSCTFTAAAKAGKAKCSTITNNIEVPAGTTLTGLTSGTKVIFEGTTFQYEEWAGPLISMGEHITVTGASGHLINCDGARWWDGKGTSKKK
PKFFYAHGLDSSITGLNIKNTPLMAFSVQANDITFTDVTINNADGDTQGGHNTDAFDVGNSVGVNIIKPWVHNQDDCLAVNSGENIWFTEGGTCI
GGHGLSIGSVGDRSNNVVKNVTIEHSTVNSENAVRIKTISGATGSVSEITYSNIVMSGISDYGVVIQQDYEDGKPTGKPTNGVTIQDVKLESVTGSVD
SGATEIYLLCGSGSCSDWTWDDVKTGGKSTACKNFPVASC

>d1hg8_a_b.80.1.3 (A:) Polygalacturonase {Fusarium moniliforme}

DPCSVTEYGLATAVSSCKNIVLNGFQVPTGKQLDLSSLQNDSTVTFKGTTFATTADNDNFPIVISGSNITITGASGHVIDGNGQAYWDGKGSNSNS
NQKPDHFIVVQKTTGNSKTNLNQIQNWPVHCFDITGSSQLTISGLIILDNRAGDKPNAKSGSLPAAHNTDGFDISSDHVTLDNNHVYNQDDCVAVTS
GTNIVVSNMYCSGGHGLSIGSVGGKSDNVVGQFLSQVVSQNSQNCRIKSNSGATGTINNVTVYQNIALTNIYSTGVDVQQDYLNGGPTGKPTNG
VKISNIKFIKVTGTVASSAQDWFILCGDGSFCFTSGNAITGGGKTSSCNYPTNTCP

>d1dbga_ b.80.1.4 (A:) Chondroitinase B {Flavobacterium heparinum}

QVVASNETLYQVKEVKPGGLVQIADGTYKDVQLIVSNSGKGLPITIKALNPGKVFTGDAKVELRGEHLILEGIWFKDGNAIQAWKSHGPGLVIA
YGSYNRITACVFDCFDEANSAYITSLTEDGKVPQHCRIDHCSFTDKITFDQVINLNNTARAIDGSVGGPGMYHRVDHCFSNPQKPGNAGGGIRIG
YYRNDIGRCLVDSNLFMQRDSEAEIITSKSQENVYGYNTLNCQGTMNFRHGDHQVAINNFYIGNDQRFGYGGMFVWGSRHVIACNYFELSETIKS
RGNAALYLNPGAMASEHALAFDMIANNAFINVNGYAIHFNLDERKEYCAANRLKFETPHQLMLKGMLFFKDKPVYVPPFKDDYFIAGKNSWTG
NVALGVEKGPVNISANRSAYKPVKIKDIQPIEGIALNLALISKIGTGPMLKGNLFFKDKPVYVPPFKDDYFIAGKNSWTG

>d1h80_a_b.80.1.8 (A:) iota-carrageenase {Alteromonas sp., atcc 43554}

VSPKTYKDADFYVAPTQQDVNYDLVDDFGANGNDTSDDSNAQRRAINAIISRKPNGGTLIPNGTYHFLGIQMKSNVHIRVESDVIKPTWNGDGKN
HRLFEVGVNNIVRNFSFQGLGNGFLVDFKDSRDKNLAVFKLGDRVNYKISNFTIDDNKTFASILVDVTTERNGLHWRSRNGIIERIKQNNALFGYGLI
TYGADNLFRNLHSEGGIALRMETDNLLMKNYKQGGIRNIFADNIRCSKGLAAVMFGPHFMKNGDVQVTNVSSVSCGSAVRSDSGFVELFSPTDEV
HTRQSWKQAVESKLGRGCAQTPYARGNGGTRWAARVTQKDACLKAKLEYGIEPGSFGTVKVFDTARFGYNADLKQDQLDYFSTSNPCKRC
LPTKEQWSKQGQIYIGPSLAVIDTTPETSKYDYDVKTFNVRINFPVNHSKTIIDTNTESSRCVYYGMSECSSSRWER

>d1qjva_b.80.1.5 (A:) Pectin methylesterase PemA {Erwinia chrysanthemi}

ATTYNAVVKSSSDGKTFKTIADAIASAPAGSTPFVILIKNGVYNERLITRNNLHLKGESRNGAVIAATAAGTLKSDGSKWGTAGSSTITISAKDFSAQ
SLTIRNDFDPANQAKSDSSKIKDTQAVALYVTKGDRAYFKDVSLVGYQDLYVSGGRSFFSDCRISGTVDIFGDGTALFNNCDLVSRYRADVKG
NVSGYLATPSTNINQKYGLVITNSRVIRESDSVPAKSYGLRPWHPTTFSDRYADPNAIGQTFLNTSMNDNHIYGWDKMSGKDKNGNTIWFNP
DSRFFEYKSYGAGAAVSKDRLQLTDAQAAEYTQSKVLGDWTPLP

>d1qq1a_b.80.1.6 (A:) P22 tailspike protein {Salmonella phage P22}

YSIEADKKFKYSVKLDYPTLQDAASAADVAGLLIDRDYNFYGGETVDFGGKVLTIECKAKFIGDGNLIFTKLGKGSRIAGVFMESTTPWVIKPWTDDN
QWLTDAAAVVATLKQSCTDGYQPTVSDYVKFGIETLLPPNAKGQNITSTLEIRECIGVEVHRASGLMAGFLFRGCHFCMVVDANNPSGGKDGIITFE
NLSGDWGKGNVYIGGRTSYGSVSSAQFLRNNGGFERDGGVIGFTSYRAGSGGVKTWQGTVGSTSRNYNLQFRDSVVIYPVWDGFDLGADTDM
NPELDRPGDYPITQYPLHQLPLNHLDNLLVRGALGVGFMDGKGMVVSNTVEDCAGSGAYLLTHESVFTNIAIDINTKDFQANQIYISGACRVNG
LRLIGIRSTDGQLTIDAPNSTVSGITGMVDPSPRINVANLAEGLGNIRANSFGYDSAAIKLRIHKLSDLGALYSHINGGAGSGSAYTQLTAISGSPD
AVSLKVNHKDCRGAEIPFPVDIASDDFIKDDSCFLPYWENNSSLKALVKKPNGELVRLTLATL

>d1daba_b.80.1.7 (A:) Virulence factor P.69 pertactin {Bordetella pertussis}

DWNNQSIVKTGERQHGIHQGSDPGGVRTASGTTIKVSGRQAQGILLENPAELQFRNGSVTSSGQLSDDGIRRLGTVTVKAGKLVADHATLANV
GDTWDDGIALYVAGEQAQASIADSTLQGAGGVQIERGANVTQRSIAVQGLHIGALQSLQPEDLPPSRVVLRTNVTAVPASGAPAAVSLGAS
ELTLDGGHHTGGRAGVAAMQGAVVHQLRATIRRGDALAGGAvggavpggavpgggfgpVLDGWYGVDSVSGSSVELAQSIVEAPELGA
AIRVGRGARVTVPGGSLSAPHGNVIETGGARRFAPQAAPSLTLOQAGHAQGKALLYRVLPEPVKLTGGAQGDIVATELPSIPGTSGPLDVALA
SQARWTGATRAVDSLISDNATWVMTDNNVNGALRLASDGSVDFQQPAEAGRKFVLTNTLAGSGLFRMNVFADLGLSDKLVMQDASGQHRLW
VRNSGSEPARANTLLVQTPLGSAATFTLANKDGVDIGTYRYLAANGNGQWSLVGAKAPP

>d1ezga_b.80.2.1 (A:) Insect cysteine-rich antifreeze protein {Yellow mealworm (*Tenebrio molitor*)}

QCTGGADCTSCTGACTGCGNCPCNAVTCTNSQHCVKANTCTGSTDNTAQCTNSKDCFEANTCTDSTNCYKATACTNSSGCP

>d1hf2a1_b.80.3.1 (A:100-206) Cell-division inhibitor MinC, C-terminal domain {Thermotoga maritima}

TGKVIKRNIRSGQTVVHSGDViVFGNVNKGAElLAGGSVVVFGKAQGNIRAGLNEGGQAVVAALDLQTSLIQIAGFITHSKGEENVPSIAHVKGNI
IEPFDKVFS

>d1ea0a1_b.80.4.1 (A:1203-1472) Alpha subunit of glutamate synthase, C-terminal domain {Azospirillum brasilense}

GRNEVPDTLDARIVADARPLFEEGEKMQLAYNARNTQRAIGTRLSSMVTRKFGMFLQPGHITIRLRTAGQSLGAFAVQGKLEVMDANDYVG
KGLSGGTIVVRPTTSSPLETNKNTIIGNTVLYGATAGKLFAAGQAGERFAVRNSGATVVVEGCGSNGCEYMTGGTAVILGRVGDNFAGMTGGMAY
VYDLDDSLPLYINDESVIFQRIEVGHYESQLKHLLIEEHVTETQSRFAAEILNDWAREVTKFWQVVPKEMLNRLEVPHL

>d1kq5a_b.80.5.1 (A:) C-terminal domain of adenylylcyclase associated protein {Baker's yeast (*Saccharomyces cerevisiae*)}

MPPRKELVGNKWFENYENETESLVIDANKDESIFIGKCQVLVQIKGVNAISLSETESCSVLDSSISGMDVIKSNKFGIQVNHSLPQSIDKSDGGNI
YLSKESLNTEIYTCSTAINVNLPIGEDDDYVEFPISEQMKHSFADGKFKSAVFE

>d1lx_a_b.81.1.1 (-) UDP N-acetylglucosamine acyltransferase {Escherichia coli, gene ipxA}

MIDKSAFVHPTAIVEEGASIGANAHGPFICIVGPHVEIGEGTVLKSHVVNGHTKIGRDNEIYQFASIGEVNQDLKYAGEPTRVEIGDRNRIRESVTIHR
GTVQGGGLTKVGSDNLLMINAHIAHDCTVGNRCLANNATLAGHSVDDFAIIGGMTAVHQFCIIGAHMVVGCGSVAQDVPPVIAQGNHATPF
GVNIEGLKRRGFSREAITAIRNAYKLIYRSGKTLDEVKPEIAELAETYPEVKAFTDFRSTRGLIR

>d3tdt_b.81.1.2 (-) Tetrahydrodipicolinate-N-succinyltransferase, THDP-succinyltransferase, DapD {Mycobacterium bovis}

MQQLQNVIESAFERRADITPANVDTVTREAVNQVIGLLSDGALRVAEKIDGQWVTHQWLKAVLLSFRINDNKVMDGAETRYDKVPMKFADYD
EARFKQEGFRVVPATVRQGAFIARNTVLMPSYVNIGAVYDEGTMVDTWATVGSCAQCIGKVNHLGGVGGVLEPLQANPTIEDNCFIGARSE
VEGVIVEEGSVISMGVYLGQSTRIYDRETGEIHYGRVPAGSVVSGNLPSKDGSSLYCAVIVKKVDAKTRGVGINELLRTID

>d1xat_b.81.1.3 (-) Xenobiotic acetyltransferase {Pseudomonas aeruginosa}

NYFESPFRGKLLSEQVSNPNIKVGRYSYYGHHFDDCARYLMPDRDDVDKLVIGSFCSIGSGAAFIMAGNQGHRAEWASTFPFHFMHEEPAF
AGAVNGYQPAGDTLIGHEVWIGTEAMFMPGVRVGHGAIGSRALVTGDVEPYAIVGGNPARTIRKRFSDGDIQNLLMAWWWDWPLADIEAAMPL
LCTGDIPALYQHWKQRQA

>d1kk6a_b.81.1.3 (A:) Xenobiotic acetyltransferase {Enterococcus faecium, VAT(D)}

MGPNPMKMYPIEGNKSQFIKPILEKLENVEVGEYSYDSKNGETFDKQILYHYPILNDKLKIGKFCISPGVTIIMNGANHRMDGSTYPFNLFGNG
WEKHMPKLDQLPIKGDTIIGNDVWIKDVFIMPVKIGDGAIAVANSVVVKDIAPYMLAGGNPANEIKQRFDQDTINQLLDIKWWNPIDIINEN
IDKILDNSIIREVIW
>d1fxja1 b.81.1.4 (A:252-329) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Escherichia coli}
VMLRDPARFDLRLGTLHGRDVEIDTNVIIEGNTLGHRVKIGTGCIVKNSVIGDDCEISPYTVVEDANLAACTIGPFARLRGAELLEGAHVGNFVE
>d1hv9a1 b.81.1.4 (A:252-452) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Escherichia coli}
VMLRDPARFDLRLGTLHGRDVEIDTNVIIEGNTLGHRVKIGTGCIVKNSVIGDDCEISPYTVVEDANLAACTIGPFARLRGAELLEGAHVGNFVE
MKKARLGKGSKAGHLTYLGDAEIGDNVNIGAGTITCNYDGANKFKTIIGDDVFGSDTQLVAPVTVGKGATIAAGTTVTRNVGENALAIRVPQTQK
EGWRRP
>d1hm9a1 b.81.1.4 (A:252-459) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, C-terminal domain {Streptococcus pneumoniae}
VSFVNPEATYIDIDVIAPEVQJEANVILKGQTKIGAETVLNTGTYVVDSTIGAGAVITNSMIEESSVADGVTGVPYAHIRPNSSLGAQVHIGNFVEVK
SSIGENTKAGHLTYIGNCEVGSNVNFAGGTITVNYDGKNKYKTVIGDNVFVGSNSTIIAPVELGDNLSVGAGSTITKDVPADAIAIGRGRQINKDEYAT
RLPHHPKNQ
>d1qrea_ b.81.1.5 (A:) Carbonic anhydrase {Archaeon Methanoscincus thermophila}
TVDEFSNIRENPVTPWNPEPSAPVIDPTAYIDPQASVIGEVITIGANVMVSPMASIRSDEGMPIFVGDRSNVQDGVVLAETINEEGEPIEDNIVEVD
GKEYAVYIGNNVSLAHQSQVHGPAVGDDTFIGMQAFVFKSKVGNNCVLEPRSAIGVTIPDGRYIPAGMVVTSQAEADKLPEVTDDYASHTNEA
VVVNVVHLAEGYKETS
>d1ewwa_ b.81.2.1 (A:) An insect antifreeze protein {Spruce budworm (Choristoneura fumiferana)}
DGSCTNTNSQLSANSKCEKSTLTNCYVDKSEVYGTCTGSRFDGVTITSTSTGSRISPGCCKISTCIITGGVPAPSAACKISGCTFSAN
>d1dzra_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC {Salmonella typhimurium}
MMIVIKTAIPDVLLIEPKVFGDERGFFFESYNQQTFEELIGRKVTVQDNHSKSKNNVLRGLHFQRGENAQGKLVRCAVGEVFDAVDIRKESPTFGQ
WVGVNLSAENKRQLWIPEGFAHGFVTLSEYAEEFLYKATNYYSPSSEGSILWNDEAIGIEWPFSQLPELSAKDAAAPLLDQALLTE
>d1ep0a_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC {Archaeon Methanobacterium thermoautotrophicum}
EFRFIKTSLDGAIIEPEVYTDERGYFMETFNEAIFQENGLEVRFVQDNESMSVRGVRLGLHFQREKPQGKLVIRGEIFDVAVDLRKNSDTYGEWTG
VRLSDENRREFFIPEGFAHGFALSLDECIVNYKCTELYHPEYDSGPWDDPDIGIDWPLEMVDDLIISEKDRNWKPLRENPVYL
>d1fi2a_ b.82.1.2 (A:) Germin {Barley (Hordeum vulgare)}
TDPDPLQDFCVADLDGKAVSVNGHCKPMSEAGDDFLSSKLTKAGNTSTPNGSAVTELDAEWPGNTLGVSMMNRDFAPGGTNPPHIHPRATE
IGMVMKGELLVGILGSLDSGNKLYSRVRAGETFVIPRGLMFQFNVGKTEAYMVVSFNSQNPGIVFVPLTFGSDPPIPTPVLTALKRVEAGVVELLK
SKFAGGS
>d2phla1 b.82.1.2 (A:11-210) Seed storage 7S protein {French bean (Phaseolus vulgaris), phaseolin}
DNPFYFNSDNSWNTLFKNQYGHIRVLQRFDQQSKRQLQNLLEDYRLVEFRSKPETLLPQQADAELLLVVRSGSAILVLVKPDDRREYFFLTSNDNPIFSDH
QKIPAGTIFYLVNPDPKEDLRIIQLAMPVNNPQIHEFFLSSTEAQQSYLEFSKHILEASFNSKFEIINRVLFEEGQQEGVIVNIDSEQIKELSKHAKSS
>d2phla2 b.82.1.2 (A:220-381) Seed storage 7S protein {French bean (Phaseolus vulgaris), phaseolin}
NTIGNEFGNLTERTDNSLNVLISIEMEEGALFVPHYSKAIVILVNEGEAHVELVGPKNKETLEYSYRAELSKDDVFVIPAAYPVAIKATSNVNFTG
FGINANNNNRNLLLAGTKTDNVVISSIGRALDGKDVGLTFSGSGDEVMKLINKQSGSYFVDAH
>d1dgwa_ b.82.1.2 (A:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}
NNPYLFRSNKFLTFKNQHGSRLLQRNFEDTEKLENLRDYRVLEYCSKPNTLLPHSDSDLVLVLEGQAILVLVNPDGRDTYKLDQGDAIKIQAGTP
FYLINPDNNQNLRILKFAITFRRPGTVEDFFLSSTKRLPSYLSAFSKNFLEASYDSPYDEIEQTLLQEEQEGVIVKMP
>g1dgr.3 b.82.1.2 (M;N:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}
QLRRYAATLSEGDIIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQVSDLTFPMSGEEVEELLENQKESYFVDGQPXDKPFNL
RSRDPIYSNNYGKLYEITPEKNSQLRDLDILLNCLQMNEGALFVPHNSRATVILVANEGRAEVELVPLEXQLRYAATLSEGDIIPSSFPVAL
>g1dgw.1 b.82.1.2 (X;Y:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}
DKPFNLRSLRDPYISNNYGKLYEITPEKNSQLRDLDILLNCLQMNEGALFVPHNSRATVILVANEGRAEVELVPLEXQLRYAATLSEGDIIPSSFPVAL

KAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQVS DLTFGSGEEVEELLENQKESYFVDGQP

>d1fxza1 b.82.1.2 (A:10-248) Seed storage 7S protein {Soybean (Glycine max), proglycinin}

NECQIQKLNALKPDNRRIESEGGLEIWTNPNNKPFQCAGVALSRCTLRNRLNARLRRPSYTNGPQEYIYQQGKGIFGMYPGCPSTFEPPQQPQQRGQSSRPQDRHQKIYNFREGDLIAVPTGVAWWMYNNEDTPVVAWSIITNSLENQLDQMPPRFYLAGNQEFLKYQQEQGGHQSQKGKHQQEEENEGGSILSGFTLEHAFSDKIAKNLQGENEGEDKGAIKVKGGLSVIKP

>d1fxza2 b.82.1.2 (A:297-470) Seed storage 7S protein {Soybean (Glycine max), proglycinin}

ICTMRLRHNIQGTSSPDYNNPQAGSVTTSLDFPALSWRLSAEFGSLRKNAMEFVPHYNLNANSIIYALNGRALIQVNCNGERVFDGELQEGRVLI VPQNFVVAARSQSDNFEYVSFKTNTPMI GTLAGANSLNALPEEVIQHTFNLKSQQARQIKNNNPFKFLVPPQES

>d1pmi_ b.82.1.3 (-) Phosphomannose isomerase {Yeast (Candida albicans)}

SSEKLFRICQCGYQNYDWGKIGSSAVAQFVHNSDPSITIDETKPYAELWMGTHPSVPSKAIDLNNQTLDLVTAKPQEYLGESIITKFGSSKELPLFKVL SIEKVLISQAHPDKKLGAQHLAADPKNYPDDNHKPEMAIAVTDFFEGFCGFPLQLAKTLATVPELNEIIIGQELVDEFISGIKLPAEVGSQDDVNNRKL LQKVFGLKLMNTDDDVIKQQTAKLLERTDREPQVFKDIDSRLPELIQRNLQFPNDIGLCGCLLNHVGLNKGEAMFLQAKDPHAYISGDIIECMAAS DNVVRAGFTPKFKDVKNLVEMLTYYESVEKQKMLQEFPRSKGDAVKSVLYDPPIAFSVLQTIFDKSKGGKQVIEGLNGPSIVATNGKTIQITGDD STKQKIDTGYVFFVAPGSSIETADSANQDQDFTTYRAFVEA

>d1eyba_ b.82.1.4 (A:) Homogentisate dioxygenase {Human (Homo sapiens)}

AELKYISGFGNCESSEDPRCPGSLPEGQNNPQVCPYNYAEQLSGSAFTCPRSTNKRSLWYRILPSVSHKFESIDEGHVTHNWDEVDPDPNQLRWK PFEIPKASQKKVDFVSGLHTLCGAGDIKSNNGLAIHIFLCNTSMENRCFYNNSDGDFLIVPQKGNNLIIYTEFGKMLVQPNEICVIQRGMRSIDVFEETR GYILEVYGVHFELPDGLPIGANLANPRDFLPIAWYEDRQVPGGYTVINQYQGKLFAAKQDVSPFNVAWHGNYTPYKYNLKNFMVINSVAFDHA DPSIFTVLTAKSVRPGVIAIDFVIFPPRGVADKTFRPPYYHRNCMSEFMGLIRGHYEAKQGGFLPGGGSLHSTMTPHGPADC FEKASKVKLAPER IADGTMFMFESSLSLAVTKWGLKASRCLDENYHKCWEPLKSHFTPNRSN

>d1qjea_ b.82.2.1 (A:) Isopenicillin N synthase {Emericella nidulans}

SKANVPKIDVSPLFGDDQAAKMRVAQQIDAASRDTGFFYAVNHGINVQLSQKTKEFHMSITPEEKWDLAIRAYKEHQDQVRAGYYLSIPGKKAV ESFCYLNPNFTPDPHPRIQAKPTHEVNWPDET KHPGFQDFAEQYYWDVFGLSSALLKGYALALGKEENFFARHFKPDDTLASVVLIRPYLDPYPEA AIKTAADGKLSFEWHEDVSLITVLYQSNVQNQVTAAGYQDIEADDTGYLINC SYMAHLTNNYYKAPIHRV/KWVNAERQSLPFFVNLGYDSVID PFDPREPNGKSDREPLSYGDYLQNGLVSINKNGQT

>d1dcs_ b.82.2.1 (-) Deacetoxycephalosporin C synthase {Streptomyces clavuligerus}

MDTTVPTFSLAEQQGLHQDEFRRCLRDKGFLYLTDCGLTDTELKSAKDLVIDFFEHGSEA EKRAVTSPVPTMRRGFTGLEESTAQITNTGSYSYDYSM CYSMGTADNLFP SGD FERIWTQYFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLFRFYFPQVPEHRSAAEQPLRMAPHYDLSMVTLIQQTP CANGFVSLQAEVGGAFTDLPYRPDAVLVFCGAIATLVTGGQVKAPRHVAAPRRDQIAGSSRTSSVFLRPNADFTFSVPLARECGFDVSLDGETATF QDWIGGNYVNIRRTSKA

>d1gp6a_ b.82.2.1 (A:) Anthocyanidin synthase {Mouse-ear cress (Arabidopsis thaliana)}

VAVERVESLAKSGIISIPKEYIRPKEELESINDV FLEEKKEDGPQVPTIDLNKIESDDEKIRENCEIELKKASLDWGVMHLINHGIPADLMERVKKAGEEFF SLSVEEKEKYANDQATGKIQGYGSKLANNASGQLEWEDYFFHAYPEEKRDLSIWPKTPSDYIEATSEYAKCLRLLATKVFKALSVGLGLEPDRLEKEVG GLEELLLQMKINYPKCPQPELALGV EAHTDVSALTFLHNMVPGQLFYEGK WVTAKCVPDSIVMHIGDTLEILSNGKYKSILHRLGVNKEKVRISWA VFCEPPDKDVKLPLPEMVSVESPAKFPPRTFAQHIEHKLFGKEQEEL

>d1ds1a_ b.82.2.2 (A:) Clavaminate synthase {Streptomyces clavuligerus}

TSVDCTAYGPELRALAARLPRTPRADLYAFLDAAHTAAASLPGALATALDTFNAEGSEDGHLLRGLPVEADADLPTPSSTPAPEDRSLLTMEAMLGL VGRRRLGLHTGYREL RSGTVYHDVYPSGAAHHSSETSETLEFHTEMAYHRLQPNYVMLACSRADHERTAATL VASVRKALPLLDERTRARLLDRRM PCCVDVAFRGGVDDPGAIQVKPLYGDADDPFLGYDRELLAPEDPADKEAVAALSKALDEVTEAVYLEPGD LIVDNFR TT HARTPFS PRWDGKDR WLHRVYIRTDRNGQLSGGERAGDVVAFTPRG

>d1jr7a_ b.82.2.3 (A:) Gab protein (hypothetical protein YgaT) {Escherichia coli}

GQDYSGF TLPSAQSPRLLELTFTEQTTKQFLEQVAEWPVQALEYKSFLRFRVAKI LDDCANQLQPLLKTLNRAEGALLINA VGVDDVKQADEMV KLATAV AHLIGRSNFDAMSGQYYARFVVKNVDNSDSYLRQPHRMELHNDGTYVEEITDYVLM MKIDEQNMQGGNSLLHLDWEHLDNYFRH PLARRPMRFA APPSKNVSKDVFHPVFDV DQQGRPV MRYIDQFVQPKDFEEGVWL SELSDAIETSKGILSVPVPGKFLINNLFWLHGRDRFTP HP

DLRRELMRQRGYFAYASNHYQTHQ

>d1e5sa_b.82.2.4 (A:) Type II Proline 3-hydroxylase (proline oxidase) {Streptomyces sp.}

MRSHILGKIELDQTRALPDLAYLAAPVTEEEYDEFSNGFWKHVPLWNASGDSEDRLKDAAAQPTAHVEHVPYLKEIVTTVFDGTHLQMARS
RNLKNAIVIPHDFVELDREVDRYFRTFMVLEDSPLAFHSNEDTVIHM RPGEIWFLDAATVHSAVNFSEISRQLCVDFAFDGFDEKEIFADATLYAP
GSTPDLPEERRPFTAHEHRRRLSLGQVIERENFRDILFLSKVHYKYDVHPSETYDWLIEISKQAGDEKMVVKAEQIRDFAVEARALSERFSLTSW

>d1ft9a2 b.82.3.1 (A:2-133) CO-sensing protein CooA, N-terminal domain {Rhodospirillum rubrum}

PPRFNIANVLLSPDGETFFRGFRSKIHAKGSLVCTGEVDENGVVVVGRLRVYLVGEEREISLFYLTSGDMFCMHSGCLVEATERTEVRFADIRTFEQ
KLQTCPSMAWGLIAILGRALTSCMRTIEDLMFH

>d1hw5a2 b.82.3.2 (A:1-137) Catabolite gene activator protein, N-terminal domain {Escherichia coli}

VLGKPQTDPTEWFLSHCHIHKYPSKSTLIHQGEKAETLYIVKGSAVLIKDEEGKEMILSYLNQGDFIGELGLFEEGQERSAWVRAKTACEVAEISYKK
FRQLIQVNPDILMRLSAQMARRLQLVLAEVGNLAF

>d1rgs_1 b.82.3.2 (113-244) Regulatory subunit of Protein kinase A {Cow (Bos taurus)}

RKVIPKDYKTMAALAKAIEKNVLFSHLDDNERSDIFDAMFPVSFIAGETVIQQGDEGDNFYVIDQGEMDVVVNEWATSVGEGGSFGE LALIYGTPR
AATVKAKTNVKLWGIDRDSYRILMGSTLRKRKMY

>d1rgs_2 b.82.3.2 (245-376) Regulatory subunit of Protein kinase A {Cow (Bos taurus)}

EEFLSKVSI LESLDKWERLTVADALEPVQFEDGQKIVVQGEPGDEFFIILEGSAAVLQRRSENEEFVEVGRLGPSDYFGEIALLMNRPRAATVVAR GPLK
CVKLDRPRFERVLGPCSDILKRNIQQYNSFVS

>d1cx4a1 b.82.3.2 (A:130-265) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}

RIIHPKTDDQRNRQLQEACKDILLFKNLPEQMSQVLDAMFEKLVKEGEHVIDQGDDDNFYVIDRGTDFDIYKCDGVGRCVGNYDNRGSFGE LAL
MYNTPRAATITATSPGALWGLDRVTFRIIIVKNNNAKKRKM Y

>d1cx4a2 b.82.3.2 (A:266-412) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}

ESFIESLPFLKSLEV SERLKVV D VIGTKVYNDGEQIIAQGSDADS FIVESGEV RITMKRKGS DIEENG AV E IARCLRGQYFG E LALV TNK PRA ASAHAI
GTVKCLAMDVQA FERLLG PCMEIM KRNIA TYEEQLV ALFGTNMDIV

>d2arca_b.82.4.1 (A:) Regulatory protein AraC {Escherichia coli}

DPLLPGYSFNAHLVAGLPIEANGYLDFFIDRPLGMKG YILNL TIRGQGVV KNQGREFVCRPGDILLFPPGEIH YGRHPEAREWYHQWVYFRPRAY
WHEWLNWPSI FANTGFFRPDEAHQPHFSDFLFGQIINAGQGEGRYSELLAINLLEQLLRRM EAI

>d1ig3a1 b.82.6.1 (A:179-263) Thiamin pyrophosphokinase, substrate-binding domain {Mouse (Mus musculus)}

DSLIYLLQPGKHLHVDTGMEGSWCGLIPVGQPCNQVTTGLKWNLNDV LGFTLV STSNTYDG SGLVT VETDHPLLWT MAIKS

>d1ig0a1 b.82.6.1 (A:224-319) Thiamin pyrophosphokinase, substrate-binding domain {Baker's yeast (Saccharomyces cerevisiae)}

TDLFLIKKNGT LIEYDPQFRNT CIGNCG LPIGEATLV KETRGLKWDVKNWPTS VVTGRVSSNRFVG DNCCFIDTKDDIILNVEIFV DKLIDFL

>d1wapa_b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP) {Bacillus subtilis}

DFVVIAVEDGVNVIGL TRGADTRFHSEKLDKGEVIIAQFTEHTSAIKVRGKAYI QTRHGVIESEGK

>d1c9sa_b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP) {Bacillus stearothermophilus}

SDFVVIKALEDGVNVIGL TRGADTRFHSEKLDKGEVIIAQFTEHTSAIKVRGKAYI QTRHGVIESEGK

>g1h6w.1 b.108.1.1 (A:,B:) Heat- and protease-stable fragment of the short fibre {Bacteriophage T4}

TGATLNGRGS TTS MRGVV KLT TAGS QSGG DASSA LAWN ADVI HQRGG QT INGTLR INN NTI ASGG ANIT GTV NM TGGY IQG KRV VTQ NEID RTI
PVG AIMM WAADSLPSD AWRF CHGG TVS ASDC PLY ASRIG TRY GSSN PGL PDM RXS LNY II KVKE

>d1k28a2 b.108.1.2 (A:362-584) Tail-associated lysozyme gp5, C-terminal domain {Bacteriophage T4}

DPADPP IPNDSR ILFKEPVSSYKGEYPVHTMETESGH IQEFDDTPGQERY RLVHPTGTYEEVSPSGRTRKTV DNLYD ITNADGNFLVAGDKK TNVG
GSEI YYNM DRNLH QIDG SNTI FVRGDET KTVEG NGTILVKG NVTII VEGN ADITVKG DATT LVE GNQ NT VNGN LS WKVAGTV DW DVGG DW TEK
MASM SSISSG QYT IDG SR IDIG SV DHHHHHH

>d1qiu a2 b.83.1.1 (A:319-395) Adenovirus {Human adenovirus type 2}

VSIKKSSGLNFDNTAIAINAGKLEFDNTSES PDI NPIKTKIGSGIDYNENGAMITKLGAGLSFDNSGAITIGNKN

>d1kkea2 b.83.1.2 (A:313-455) Reovirus attachment protein sigma 1 {Reovirus}

YRFRQSMWIGIVSYSGGLNWRVQVNNSDIFIVDDYIHICLPAFDGFSIADGGDLSNFVTGLPPLTGDTPEAFHNDVVTYGAQTVAILSSGGAPQ
YMSKNLWVEQWQDGVLRLRVEGGGSITHNSNKWPAMTVSYPRSFT
>d1h8ga__ b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}
TDGNWYWFDNSGEMATGWKKIADKWYYFNEEGAMKTGWVKYKDTWYYLDAKEGAMVSNAFIQSADGTGWYYLKPDGLADRPEFTVEPDGL
ITVK
>d1hcxa__ b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}
GSYPKDKFEKINGTWYYFDSGYMLADRWRKHTDGNWYWFDNSGEMATGWKKIADKWYYFNEEGAMKTGWVKYKDTWYYLDAKEGAMVSN
AFIQSADGTGWYYLKPDGLADRPEFTVEPDGLITVK
>d1bdo__ b.84.1.1 (-) Biotinyl domain of acetyl-CoA carboxylase {Escherichia coli}
EISGHIVRSPMVGTFYRTPSDAKAFIEVGQKVNVGDTLCIVEAMKMMNQIEADKSGTVKAILVESGQPVEFDEPLVVIE
>d1dd2a__ b.84.1.1 (A:) Biotin carboxyl carrier domain of transcarboxylase (TC 1.3S) {Propionibacterium freudenreichii, subsp. shermanii}
AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQQLIKIG
>d1htp__ b.84.1.1 (-) Protein H of glycine cleavage system {Pea (Pisum sativum)}
SNVLDGLKYAPSHEWVKHEGSVATIGITDHAQDHLGEVVVFVELPEPGVSVTKKGKFGAVESVKATSVDVNSPISGEVIEVNTGLTGKPLINSSPYEDG
WMIKIKPTSPDELESLLGAKEYTKFCEEDAAH
>d1lac__ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Bacillus stearothermophilus}
AEFKFLPDIGEGIHEGEIVKWFVKPGDEVNEDDVLCVEQNDAKVEEIPSPVKGKVLEILVPEGTVATVGQTLITLDAPGY
>d1iyu__ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Azotobacter vinelandii}
SEIIIRVPDGGDGEVIELLVKTGDLIEVEQGLVVLESAKASMEVPSPKAGVVKSNSVKGDKLKEGDAIILEPAAGAR
>d1qja__ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Escherichia coli}
MVKEVNVPDGGDEVEVTEVMVKVGDKVAEEQSLITVEGDKASMEVPAPFAGVVKELKVNVDKVKTGSIMIFEVEGAA
>d1gjxa__ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Neisseria meningitidis}
ALVELKVPDIGHENVDIAVEVNNGDTIAVDDTLITLETDKATMDVPAEVAGVVKEVKVKVGDKISEGGGLIVVVEAEGTA
>d1fyc__ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Human (Homo sapiens)}
GSNMSYPPHMQVLLPALSTMTMGTQQRWEKKVGEKLSEGDLLEIETDKATIGFEVQEETYLAKEVPEGTRDVPLGTLCLIIVEKAADISAFADYRP
TEVTDLK
>d1ghk__ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Azotobacter vinelandii}
AIDIKAPTFPESIADGTATWHKKPGEAVKRDELIVDIETDKVVMVEVLAEDGVIAEIVKNEGDTVLSGELLGKLTEGG
>d1pmr__ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Escherichia coli}
SSVDILVPDLPESVADATVATWHKKPGDAVRDEVLVEIETDKVLEVVASADGILDAVLEDEGTTTSRQILGRLREGN
>d1k8ma__ b.84.1.1 (A:) Lipoyl domain of the mitochondrial branched-chain alpha-ketoacid dehydrogenase {Human (Homo sapiens)}
MGQVVQFKLDIGEGIRETVKEWYVKEGDTVSQFDSICEVQSDKASVTITSRYDGVIKKLYNNLDDIAYVGKPLVDIETEALKDLE
>d1dv1a1 b.84.2.1 (A:331-446) Biotin carboxylase subunit of acetyl-CoA carboxylase, C-terminal domain {Escherichia coli}
RGHAVECRINAEDPNTFLPSPGKIRTFHAPGGFGRWESHIYAGYTVPYYDSMIGKLICYGENRDVAIARMKNALQELIIDGIKTNVDLQIRIMNDE
NFQHGGTNIHYLEKKLGL
>d1gsoa1 b.84.2.1 (A:328-426) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}
ERASLGVVMAAGGYPGYRTGDIHGLPLEEVAGGKVFHAGTKLADDEQVVTNGGRVLCVTALGHTVAEAQKRAYALMTDIHWDDCFRKDIGH
RAIER
>d1b6ra1 b.84.2.1 (A:277-355) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}
NNPSVMINLIGSDVNYDWLKLPLVHLHWYDKEVRPGRKVGHNLTDSDTSRLTATLEALIPLLPEYASGVIWAQSKFG
>d1eyza1 b.84.2.1 (A:319-392) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}
GPAASAVILPQLTSQNVTFDNVQNAVGAIDLQIRLFGKPEIDGSRRGLVALATAESVVDAIERAKHAAGQVKVQG

>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}
TIYNASAAGKIVAITALSEKKGGFEVSIKANGEVVVDKIPAGPDLIVKEGQTVQADQPLTNNP

>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}
EPLQNEIGEEVFVSPITGEIHPITDVPDQVFSGKMMGDGFALPSEGIVVSPVRGKILNVFPTKHAIGLQSDGGREILIHFGIDTVSLKGEGFTSFVSEGDRVEPGQKLLEVLDLAVKPNNVPSLMPIVFTNLAEGETVSIKASGSVNREQEDIVKIE

>d2gpr__ b.84.3.1 (-) Glucose permease IIA domain, IIA-glc {Mycoplasma capricolum}
MWFFNKNLKVLAPCDGTIITLDEVEDEVFKERMLGDFAINPKSNDHFAPVSGKLVTAPTKHAFGIQTSGVEILLHIGLDTVSLDGNGFESFVTQDQEVNAGDKLVTLKSVAKKVPISIPIFTNNNGKTLEIVKMGEVKQGDVVAILK

>d1glaf_b.84.3.1 (F:) Glucose-specific factor III (glsIII) {Escherichia coli}
GLFDKLKSLVSDDKKDTGTIEIIAPLSGEIVNIEDVDPVVFAEKIVGDGIAIKPTGNKMVAPVDTGKIFETNHAFSIESDSGVLFVHFGIDTVELKGEGFKRIAEEGQRVKVGDVIEFDPLLEEKAKSTLTPVVISNMDEIKELIKLSGSVTVGETPVIRIKK

>d2f3ga_b.84.3.1 (A:) Glucose-specific factor III (glsIII) {Escherichia coli}
TIEIIAPLSGEIVNIEDVDPVVFAEKIVGDGIAIKPTGNKMVAPVDTGKIFETNHAFSIESDSGVLFVHFGIDTVELKGEGFKRIAEEGQRVKVGDVIEFDPLLEEKAKSTLTPVVISNMDEIKELIKLSGSVTVGETPVIRIKK

>d1hg7a_b.85.1.1 (A:) Type III antifreeze protein {Ocean pout (*Macrozoarces americanus*), different isoforms}
MNQASVANQLIPINTALTLVMMRSEVVTVPVGIPADEIPRLVSMQVNRAVPLGTTLMPDMVKGYAA

>d1ops__ b.85.1.1 (-) Type III antifreeze protein {Ocean pout (*Macrozoarces americanus*), different isoforms}
SQSVVATQLIPMTALTPAMMEGKVTPNIPGIPFAEMSQLVKGQVNTPVAKGQTLMPNMVKTYAA

>d1c8aa2 b.85.1.1 (A:69-134) Type III antifreeze protein {Antarctic eel pout (*Austrolycichthys brachycephalus*) and (*Lycodichthys dearborni*)}
SPGLKSVVANQLIPINTALTLVMMKAEEVSPKGIPSEEISKLVMQVNRAVPLGTTLMPDMVKNYE

>d3rdn__ b.85.1.1 (-) Type III antifreeze protein {Antarctic eel pout (*Austrolycichthys brachycephalus*) and (*Lycodichthys dearborni*)}
NKASVANQLIPINTALTLIMMKAEVTPMGIPAAEIPNLVGMQVNRAVPLGTTLMPDMVKNYE

>d1c5ea_b.85.2.1 (A:) Head decoration protein D (gpD, major capsid protein D) {Bacteriophage lambda}
SDPAHTATAPGGLSAKAPMTPLMLDTSSRKLVADGTTDGAAGVILAQAADQTSTLTIFYKSGTFRYEDVLWPEAASDETKKRTAFAGTAISIV

>d1ejrb_b.85.3.1 (B:) Urease, beta-subunit {Klebsiella aerogenes}
MIPGEYHVKGQIALNTGRATCRVVENHGDRPIQVGSHYHFAEVNPALKFDRQQAGYRLNIPAGTAVRFEPGKREVELVAFAGHRAVFGFRGEVMGPL

>d4ubpb_b.85.3.1 (B:) Urease, beta-subunit {Bacillus pasteurii}
NYIVPGEYRVAEGEIEINAGREKTTIRVSNTGDRPIQVGSHIHFVEVNKEFLFDRAEGIGRRLNIPSGTAARFEPGEEMEVELTELGGNREVFGISDLNGSVDNKELILQRAKELGYKGVE

>d1e9ya1 b.85.3.1 (A:106-238) Urease, beta-subunit {Helicobacter pylori}
LVPGEFLKNEDITNEGKKAVSVKVNKGDRPVQIGSHFFVNRCDFRDREKTFGKRLDIAAGTAVRFEPGEEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGFHGAKSDDNNYVKTKE

>d1g8la1 b.85.6.1 (A:327-409) Molybdenum cofactor biosynthesis protein MoeA, C-terminal domain {Escherichia coli}
LPARQRVRTASRLKKTPGRLDFQRGVQLQRNADGELEVTTGHQGSHIFSSFSLGNCFIVLERDRGNVEGEWVEVEPFNALFG

>d1euwa_b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Escherichia coli}
MMKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIADPSLAAMMLPRSGLGHKGIVLGNLVLGIDLSDYQGQLMISVWNRGQDSFTIQPGERIAQMIFVPPVQAEFNLVEDF

>d1f7da_b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline immunodeficiency virus}
MIIEGDGILDKRSEDAGYDLLAAKEIHLPGEVKVIPTGVKLMPLPKGYZGLIGKSSIGSKGLDVGGVIDEGYRGEIGVIMINVSRSITLMEQKIAQLI
ILPKCKHEVLEQQGVMM
>d1f7ra_b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline immunodeficiency virus}
MIIEGDGILDKRSEDAGYDLLAAKEIHLPGEVKVIPTGVKLMPLPKGYZGLIGKSSIGSKGLDVGGVIDEGYRGEIGVIMINVSRSITLMEQKIAQLI
ILPKCKHEVLEQQGVMM
>d1dun__b.85.4.1 (-) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Equine infectious anemia virus}
MLAYQGTQIKEKRDEDAGFDLCVPYDIMIPVSDTKIPTDVKIQVPPNSFGWVTGKSSMAKQGLLINGGIIDEGYTGEIQVICTNIGKSNIKIEGQKFA
QLIILQHHSNSRQPWDENKI
>d1tul__b.85.5.1 (-) ACMPNP telokin-like protein {Baculovirus (*Autographa californica*), nuclear polyhedrosis virus}
GTPDIIVNAQINSEDENVLDFIIDEYYLKKRGVGAHIKVASSPQLRLYKNAYSTVSCGNYGVLNLVQNGEYDLNAIMFNCAEIKLNKGQMLFQTKI
WR
>d1at0__b.86.1.1 (-) Hedgehog {Fruit fly (*Drosophila melanogaster*)}
CFTPESTALLESGVRKPLGEISIGDRVLSMTANGQAVYSEVLFMDRNLEQMGNFVQLHTDGGAVLTVPAHLVSVWQPESQKLTFFADRIEKNQ
VLVRDVETGELRPQRVVKGSRSGVVAPlTREGTIVVNSVAASCY
>d1dfa1_b.86.1.2 (A:1-180,A:416-454) PI-Sce1 intein {Baker's yeast (*Saccharomyces cerevisiae*)}
CFAKGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKPRGRETMSVVKQSQHRAHKSDSSREVPELLKFTCNATHELVVRTPRSVRLSRTIKG
VEYFEVITFEMGQKKAPDGRIVELKEVSKSYPSEGPERANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAXCRGFYFELQELKEDDY
GITLSDDSDHQFLLANQVVHN
>d1dq3a1_b.86.1.2 (A:1-128,A:415-454) PI-Pfu1 intein {Archaeon *Pyrococcus furiosus*}
CIDGKAKIIFENEGEREEHLLTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPESKRVVKGVNVWVYELGKDVTKEYIITNKGTKILTSPWH
PFFVLTPDFKIVEKRADELKEGDILIGGMXGLEVVRHITTNEPRTFYDLTVENYQNYLAGENGMIHVHN
>d1am2__b.86.1.2 (-) GyrA intein {Mycobacterium xenopi}
ASITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDLHRGNPVLADRLFHSGEHPVYAVRTVEGLRVGTANHPLLCLVDVAGVPTLLWKLIDEIK
PGDYAVIQRSAFSVDCAGFARGKPEFAPTTYTVGVPGLRFLEAHHRDPDAKIADELTGFRYYAKVASVTDAGVQPVSLVDTADHAFITNGFVS
HN
>d1umua_b.87.1.1 (A:) UmuD' {Escherichia coli}
DYVEQRIDLNQLIQHPSATYFKASGDSMIDGGISDGDLIVDSAITHGDIVIAAVDGEFTVKKLQLRPTVQLIPMNSAYSPIISSEDTLVFGVVI
HVVK
>d1jhfa2_b.87.1.1 (A:73-198) LexA C-terminal domain {Escherichia coli}
EEGLPLVGRVAADEPLLAQQHIEGHYQVDPSSLFKPNADFLRVSGMSMKDIGIMDGDLAVHKTQDVRNGQVVVARIDDETVKRLKKQGNKVEL
LPENSEFKPIVVDLRQQSFTIEGLAVGVIRN
>d1f39a_b.87.1.1 (A:) Lambda repressor C-terminal domain {Bacteriophage lambda virus}
ASASAFWLEVEGNSMTAPTGSKPSFPDGMLILVDPEQAVEPGDFCIARLGGDEFTFKKLRDGGQVFLQPLNPQYPMIPCNCSCVVGKVIASQWPE
ETFG
>d1b12a_b.87.1.2 (A:) Type 1 signal peptidase {Escherichia coli}
RSFIYEPFQIPSGSMMPTLLIGDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSQQACEN
ALPVTVSNVEPSDFVQTFSRRNGGEATSGFFEVPKNETKENGILSERKETLGDVTHRILTVPIAQDQVGMYYQQPGQQLATWIVPPGQYFMMGD
NRDNSADSRYWGFVPEANLVGRATAIWMSFDKQEGETPGLRLSRIGGIH
>d1jcha2_b.110.1.1 (A:84-315) Colicin E3 translocation domain {Escherichia coli}
VAAPVAFGFPALSTPGAGGLAVSISAGALSAIADIMAALKGPFKGLWGVALYGVLPQIAKDDPNMMSKIVTSLPADDITESPVSSLPLDKATVNV
NVRVVDDVKDERQNISVSGVPMSPVVDAKPTERPGVFTASIPGAPVLNISVNNSTPAVQLSPGVTNNTDKDVRPAFGTQGGNTRDAVIRFPKD
SGHNAVYVSVSDVLSPDQVKQRQDEENRRQQEWDAH
>d1hxra_b.88.1.1 (A:) RabGEF Mss4 {Rat (*Rattus norvegicus*)}

ELVAEGRNRKAVLCQRCGSRVLQPGTALFSRRQLFLPSMRKKPDLVDSNPDGDVLEEHVLVNDMFIFENVGFTKDVGNIKFVCADCEIGPIGW
HCLDDKNSFYVALERSHE
>d1fwqa_b.88.1.1 (A:) RabGEF Mss4 {Human (Homo sapiens)}
ELVAEGRNRKAVLCQRCGSRVLQPGTALFSRRQLFLPSMRKKPALS DGSNP DGDLLQEHWLVEDMFIFENVGFTKDVGNIKFV CADCEIGPIGW
HCLDDKNSFYVALERSHE
>d1h6qa_b.88.1.2 (A:) Translationally controlled tumor-associated protein tctp, p23fyp {Fission yeast (Schizosaccharomyces pombe)}
MLLYKDVISGDELVDAYDLKEVDDIVYEADCQMVTVKQGGDVDIGANPSAEDAEEAEEGTETVNNLVYSFRSPTSF DKKSYMSYIKGYMKA
IKA RLQESNPERVPVFEKNAIGFVKKILANFKDYDFYIGESMDPDAMVVL MNYREDGITPYMIFFKDG LVSEKF
>d3ezma_b.89.1.1 (A:) Cyanovirin-N {Cyanobacterium (Nostoc ellipsosporum)}
LGKFSQTCYNSAIQGSVLTSTCERTNGGYNTSSIDLNSVIENVDGSLKWQPSNFIETCRNTQLAGSSELAAECKTRAQQFVSTKINLDDHIANIDGTLKY
E
>d1fjra_b.102.1.1 (A:) Methuselah ectodomain {Fruit fly (Drosophila melanogaster)}
DILECDYFD TVDISAAQKLQNGSYLFEGLLVPAILTGEYDFRILPDDSKQKV ARH IRGC VCKLPC VR FCCPHIMDNGVCYDNMSDEELAELDPFLN
VTLDGSVSR HFKNELIVQWDLPMPCDMFYLQDNREEQDKYTLFENGTF FRHDFR VTLR KREYCLQH LT FADGNAT SIRIAPHNCLIV
>d1lkta_b.90.1.1 (A:) Head-binding domain of phage P22 tailspike protein {Salmonella bacteriophage P22}
ANVVSNPRP IFTESRSFKAVANGKIYIGQIDTPVNPANQIPVYIENEDGSHVQITQPLIINAAGKIVYNGQLVKIVTVQGHSMAIYDANGSQVDYIA
NVLKY
>d1qqha_b.91.1.1 (A:) E2 regulatory, transactivation domain {Human papillomavirus type 18}
KSKAHKAI ELQMA LQGLAQSAYKTEDWTLQDTCEELWNTEPTHCFKKGQTVQVYFDGNKDCMTVVA WDSVYYMT DAGTW DKTATCVSHRG
LYYVKEGYNTFYIEFKSECEKYGNTGTWEVHFGNNVIDCNDSCMCSTSDDTVS
>d1dtoa_b.91.1.1 (A:) E2 regulatory, transactivation domain {Human papillomavirus type 16}
HMETLCQLNV CQDKILTHYENDSTDLRDHIDYWKHMRLECAI YYKAREMGFKHINHQV VPTLA VSKN KALQ AIELQLT LETI YNSQYSNEKWT LQD
VSLEVYLTAPTGC IKKHGYTVEVQFDGDICNTM HYTNW THIYICEEAS TVV EGQV DYY GLYY HEGIR TYFVQFK DDAEK YSKN KVWEV HAGG QV
I LCPT SVFS
>d1g8la2 b.103.1.1 (A:7-177) Molybdenum cofactor biosynthesis protein MoeA, N-terminal and linker domains {Escherichia coli}
LMSLD TALNEMLS RVTPLAQETLPLVQCFGRILASDVSP LDV PGFD NSAMD GYAVRLADI ASGQPLVAGK SFAG QPYH GEWPAGTCIRIMT GAP
VPEGCEAVVMQEQTEQM DNGVRFTA EVRSGQNIRRG EDISAGAVVFPAGTRLTTAELPVIASL GIAEV P VIRK
>d1k6wa1 b.92.1.2 (A:4-55,A:376-426) Cytosine deaminase {Escherichia coli}
ALQTII NARLPGE EGLWQIHLQDGKISAIDAQSGVMPITENSLDAEQGLVIPXLI LPAENGFD ALRRQV PVRY SVRG GKVI ASTQPAQTTV YLEQPEAI
DYKR
>d1ejrc1 b.92.1.1 (C:1002-1129,C:1423-1475) alpha-Subunit of urease {Klebsiella aerogenes}
SNISRQAYADMFGPTVGDKVRLADTELWIEVEDLTYGEEVKFGGGK VIRDGMGQGQMLAADCVDL VLTNA LIVDHGIVKADIGVKDGRIFAIG
KAGNPDIQPNTIPIGAATEVIAAEKGIVTAGXSIEVGK LADL VVW SPAFFGVKPATVI KGGMIAIAPMDINASIPTPQPVHYRP
>d4ubpc1 b.92.1.1 (C:1-131,C:435-483) alpha-Subunit of urease {Bacillus pasteurii}
MKINRQQYAESYGP TGVG DDEV RLAD TLWIEV EKDY TTGDEV NF GGGK VLR EGMG ENGT YTRTEN VL DLLT NA LILD YTG IYKADIGVKDGYIVGIG
KG GNP DIMDGVTP NMIV GTATEVIAAEKGIVTAXLVLWEPKFFGVKAD RVIKGGIIAYAQIGDPSASIPTPQPVGMRR MYGT
>d1e9yb1 b.92.1.1 (B:1-131,B:432-480) alpha-Subunit of urease {Helicobacter pylori}
M KKISRKEYVSMYGP TTGDKVRLGDTLIAEVEHDYTIYGEELKFGGGK TLREGMSQSNNPSKEELD LIITNA LIVD YTG IYKADIGIKDGKIAIGIGKGG
NKDMQDGVKNNLSVG PATEA LAGEGLIVTAGXADLVLWSPAFFGVKP NMII KGGFIALSQMGD ANASIPTPQPVY REMFA
>d1aqt_2 b.93.1.1 (2-86) Epsilon subunit of F1FO-ATP synthase N-terminal domain {Escherichia coli}
STYHLDVVSAEQQMFSGLVEKIQVTGSEGELGIYPGHAPLLTAIKPGMIRIVKQHGHEEYI LSGG ILEVQPGN VTVLADTAIRG
>d1e79h2 b.93.1.1 (H:15-100) Epsilon subunit of F1FO-ATP synthase N-terminal domain {Cow (Bos taurus)}
QMSFTFASPTQVFFNSANVRQVDVPTQTGAFGILAHHVPTLQVLRPGLVVHAEDGTT SKYFVSSG S VTVNADSSVQLAEEAVTL

>d1hhna_ b.104.1.1 (A:) Calreticulin {Rat (*Rattus norvegicus*)}
SKKIKDPDAAKPEDWDERAKIDDPTDSKPEDWDKPEHIPDPAKKPEDWDEEMDGEWEPPVIQNPEYKGEWKPRQIDNPDYKGTWIHPEIDNPE
YSPDANI

>d1jhna3 b.104.1.1 (A:270-411) Calnexin {Dog (*Canis familiaris*)}
PVNPSREIEDPEDQKPEDWDERPKIPDPDAVKPDDWNEDAPAKIPDEEATKPDGWLDEPEYVPDPDAEKPEDWDEDMDGEWEAPQIANPKCE
SAPCGVWQRPMIDNPNEYKGKWKPPMIDNPNEYQGIWKPRKIPNPDFED

>d1tph1_c.1.1.1 (1:) Triosephosphate isomerase {Chicken (*Gallus gallus*)}
RKFFVGGNWKMNGDKSLGELIHTLNGAKLSADTEVVCAGPSIYLDFARQKLDKIGVAACQNCYKVPKGAFTGEISPAMIKDIGAAWVILGHSERH
VFGESDELIGQKVAHALAEGLVIACTGEKLDEREAGITEKVVFQTKVIAADNVKDWSKVVAYEPVWAIGTGTATPQQAQEVHEKLRGWLKTHVS
DAVAQSTRIYGGSVTGGNCHELASQHDVDFLVGGASLKPEFVDIINAKH

>d1htia_c.1.1.1 (A:) Triosephosphate isomerase {Human (*Homo sapiens*)}
APSRKFFVGGNWKMNGRKQSLGELIHTLNAAKVPADTEVVCAPPTAIDFARQKLDKPIAAACQNCYKVTNGAFTGEISPAGMIKDCGATWVLGH
ERRHVFGESDELIGQKVAHALAEGLVIACTGEKLDEREAGITEKVVFQTKVIAADNVKDWSKVVAYEPVWAIGTGTATPQQAQEVHEKLRGWLK
SNVSDAVAQSTRIYGGSVTGATCKELASQPDVDFLVGGASLKPEFVDIINAKQ

>d1i45a_c.1.1.1 (A:) Triosephosphate isomerase {Baker's yeast (*Saccharomyces cerevisiae*)}
ARTFFVGGNFKLNGSKQSKEVERLNTASIPENVEVICPPATYLDYSVSLKKPQVTVGAAQNAYLKGSAFTGENSVQIKDVGAKYVILGHSERSY
FHEDDKFIADKTFALGQGVGVLICGETLEEKAGKTLVVERQLNAVLEEVKDFTNVVAYEPVWAIGTGLAATPEDAQDIHASIRKFLASKLGDKA
ASELRILYGGSANGSNAVTFKDKADVDGLVGGASLKPEFVDIINSRN

>d1ttj_c.1.1.1 (-) Triosephosphate isomerase {*Trypanosoma brucei*}
SKPQPIAAANWKCNGSQSLSELIDLNSTSINHDVQCVVASTSSHLMATKERLSPKFVIAACQNAGNADALASLKDFGVNWIVLGHSERAYGET
NEIVADKVAAVAVASGMVIACIGETLQERESGRTAVVLTQIAAIAKKKADWAKVVIAYEPVWAIGTGVATPQQAQEAHALIRSWVSSKIGADVA
GELRILYGGSVNGKNARTLYQQRDVNGFLVGGASLKPEFVDIICKATQ

>d5tima_c.1.1.1 (A:) Triosephosphate isomerase {*Trypanosoma brucei*}
SKPQPIAAANWKCNGSQSLSELIDLNSTSINHDVQCVVASTFVHLAMTKERLSPKFVIAACQNAAKSGAFTGEVSLPILKDFGVNWIVLGHSER
AYYGETNEIVADKVAAVAVASGMVIACIGETLQERESGRTAVVLTQIAAIAKKKADWAKVVIAYEPVWAIGTGVATPQQAQEAHALIRSWVSSKI
GADVAGELRILYGGSVNGKNARTLYQQRDVNGFLVGGASLKPEFVDIICKATQ

>d1tcda_c.1.1.1 (A:) Triosephosphate isomerase {*Trypanosoma cruzi*}
KPQPIAAANWKCNGSESLLVPLIETLNAAFTDHVDVQCVVAPTFHLIPMTKARLTNPKFQIAACQNAITRSGAFTGEVSLQILKDYGISWWLGHSER
YGETNEIVAEKVAQACAAGFHIVCVGETNEEREAGRRTAAVLTQLAAVAQQLSKEAWSRVVIAYEPVWAIGTGVATPQQAQEVHELLRRWVRSK
LGTDIAAQLRILYGGSVTAKNARTLYQMRDINGFLVGGASLKPEFVEIIETAK

>d1ydfa_c.1.1.1 (A:) Triosephosphate isomerase {*Plasmodium falciparum*}
RKYFVAANWKCNGTLESIKSLNSFNNLDFPSKLDVVVFPSVSYHDTRKLLQSKFSTGIQNVSKFGNGSYTGEVSAEIAKDLNIEYVIIGHFERRKF
HETDEDVREKLQASLKNNLKAVVCFGESLEQREQNKTIETVKQVKAFVLDIDNFNDNVILVYEPLWAIGTGTATPQQAQEVHLLRKW
NQIRILYGGSVNTENCSSLIQQEDIDGFLVGNASLKESFVDIICKSAM

>d1amk_c.1.1.1 (-) Triosephosphate isomerase {*Leishmania mexicana*}
SAKPQPIAAANWKCNGTTASIEKLVQVFNEHTISHDQCVVAPTFVHPLVQAKLRNPKYVISAENAIAKSGAFTGEVSMPLKDIGVHWVILGHSER
RTYYGETDEIVAQKVSEACKQGFVIACIGETLQQREANQTAKVVLSQLTSIAAKLTDWANQVVLAYEPVWAIGTGVATPQQAQEVHLLRKW
SENIGTDVAAKLRILYGGSVNAANAATLYAKPDINGFLVGGASLKPEFRDIIDATR

>d1tre_c.1.1.1 (A:) Triosephosphate isomerase {*Escherichia coli*}
MRHPLVMGNWKMNGLNGSRHMVHELVSNLRKELAGVAGCAVIAAPPMEYIDMAKREAEGSHIMLGAQNVNLNLGAFTGETSAAMILDICAQYIIG
HSERRTYHKESDELIakkFAVLKEQGLTPVLCIGETEAENEAGKTEEVCARQIDAVLKTQGAAAFEGAVIAYEPVWAIGTGSATPAQQAQAVHKFIRDHI
AKVDANIAEQVIIQYGGSVNASNAAELFAQPDIIDGALVGGASLKADAFAVIVKAAEAAKQA

>d2btma_c.1.1.1 (A:) Triosephosphate isomerase {*Bacillus stearothermophilus*}
RKPIIAGNWKMNGTLAEAVQFVEDVKGHVPPADEVISVVCAPFLFLDRLVQAADGTDLKIGAQTMHFADQGAYTGEVSPVMLKDLGVTVILGHSE

RRQMFAETDETVNKKVLAATRGLIPIICCGESLEEREAGQTNAVVASQVEKALAGLTPEQVKQAVIAYEPIWAIGTGKSSTPEDANSVCGHIRSVSR
LFGPEAAEAIQYGGSVKPDNI RDFLAQQQIDGALVGASLEPASFLQLVEAGRH

>d1aw1a_c.1.1.1 (A:) Triosephosphate isomerase {Vibrio marinus}

RHPVVMGNWKLNGSKEMVV DLLNGLNAELEGVTGV DVAVAPPALFV DLAERTLTEAGSAIILGAQNTDLNNSGAFTGDMSPAMLKEFGATHIIIG
HSERREYHAESDEFVAKKAFLKENG LTPVLCIGESDAQNEAGETMAVCARQLDAVINTQGV EALEGAIAYEPIWAIGTGKAATAEDAQRHQAQIRA
HIAEKSEAVAKNVVIQYGGSVKPENAAAYFAQPDIDGALVGA ALDAKSFAAIAKAAAEEAKA

>d1b9ba_c.1.1.1 (A:) Triosephosphate isomerase {Thermotoga maritima}

TRKLILAGNWKMHTISEAKKFVSLLVNEHDVKEFEIVC PPF TALSEVGEILSGRN KLG A QNVFYEDQGAFTGEISPLMLQEIGVEYVIVGHSERRRI
FKEDDEFINRKVKAVL EKG MTPILCVGETLEEREKGLTFCV VEV KQVREGFYGLDKEEAKRVVIA YEPVVAIGTGRVATPQQAQEVHAFIRKL SEMYDE
ETAGSIRILYGGSIKPDNFGLLIVQKDIDGGLVGGASLKESFIELARIMRGV

>d1hg3a_c.1.1.1 (A:) Triosephosphate isomerase {Archaeon Pyrococcus woesei}

AKLKEPIIAINFKTYIEATGKRALEIAKAAEKVYKETGVTIVAPQLVDRMIAESVEIPVFAQHIDPIKPGSHTGHVLPEAVKEAGAVGTLLNHSENRMIL
ADLEAAIRRAEEVGLMTMVCNNPAVSAAVAALNPDYVAVEPPELIGTGPVSKAKPEVITNTVELVKVNPEVKVLCAGISTGEDVKKIAELGTGVG
LLASGVTKAKDPEKAIWDLVSGI

>d1qo2a_c.1.2.1 (A:) Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase HisA {Thermotoga maritima}

MLVVPAILFRGKVARMIKRKENTIFYE KDPV EKVLIEEGFTLHVVDLSNAIENSGENLPVLEKLSEFAEHIQIGGGIRSLDYAEKLRLKGYRRQIVSS
KVLEDPSFLKSLREIDV EPVFS LDTRGGRVAFKGWLAEEEIDPV SLLKRLKEYGLEEVHTEIEKDGT LQEHDFSLTKKIAIEAEVKVLAAGGI SSEN SLKTA
QKVHTETNGLKGIVGRAFLEGILTVE VMKRYAR

>d1thfd_c.1.2.1 (D:) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}

MLAKRIIA CLDV KDGRV VKGSNFENLRD SGDP VELGKF YSEIG IDELV FLDITAS V EKRKT MLE LVE KVA EQJDIPFTV GGGI HD FETASE LILRGAD KV SI
NTAAVENPSLITQIAQTFGSQAVVVAIDAKRV DGE FMVFTYSGKKNTGILLRDWV VVEKRGAGEILLTSIDRDTKSGYDTEMIRFVRPLTTLPIIASG
GAGKMEHF HLEA FLAGADA ALA ASV FH FREIDV RELKEYLK KHGV NVRLE GL

>d1jvna1_c.1.2.1 (A:230-552) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}

DYSNYGLTRRIIACLDVRTNDQGDLVVTKG DQYDVREKSDGKGVRNLGKP VQLAQKYYQQGADEV TFLNITSFRDCPLKDTPMLEV LKQAAKTVFV
PLT VGGGIKDIVDVGDKIPALEV ASVLYFRSGADKV SIGTD AVYAAE KYYELGNRGDGTSPIETISKAYGAQAVV ISVDPKRVYVNSQADTKNKVFETEY
PGPN GEKYCWYQCTIKGGRESRDLGVW ELTRACEALGAGEILLNCIDKDGNSNSGYDLELIEHV KDAV KIPVIASSGAGVPEH FEE AFLK TRADACLGA
GMFHRGEFTVNDVKEYLLEHGLKVRMDEE

>d1h5ya_c.1.2.1 (A:) Cyclase subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Archaeon Pyrobaculum aerophilum}

HMALRIIPCLIDGGAKVVVKGVNFQGIREVGDPVEMA VRYEEGADEIAILDITAAP EGRATFIDS V K R VAEAVSIPV LVGGVRSLEDATT LFRAGA
DKV SVNTA VRNPQLV ALLAREFGSQ STVVAIDAKWN G EYEVYVKG GREATGLDAV KWAKE VEELGAGEILLTSIDRDTG LGYDVELIRR VADS VR
IPVIA SGAGRVE HFYEA AAAGADAVLAASLFHFRVLSIAQVKRYLK ERGV E V RI

>d1rpxa_c.1.2.2 (A:) D-ribulose-5-phosphate 3-epimerase {Potato (Solanum tuberosum)}

SRVDKFSKSDIIVSPSILSANFSKLGEQVKAI EQAGCDWIHV DVM DGRFVPN ITIGPLV DSLRPITDPLDV HLMIVEPDQRVPDFIKAGADIVS VHCE
QSSTIHLHRTINQIKSLGAKAGVVLNP GTPLTAIEVYVLDV LVLIMS VNP GFGQSFIESQVKKISDLRKICAERGLNP WIE DGGVGPKNAYK VIEAG
ANALVAGSAVFGAPD YEAIA KGIKTSKRPE

>d1dbta_c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Bacillus subtilis}

MKNNLPII ALDFASAETLAFLAPFQQEPLFVKVGMELFYQEGPSIVKQLKERNCELF LDLKLHDIP TVNKAMKRLASLGVDLV NV HAAGGKKMMQ
AALEGLEEGTPAGKKRPSLIAVTQLSTSEQIMKDELLIEKSLIDTVVHYSQAEESGLDGV CSVHEAKAIYQAVSPSFLT VPGIRMSEDAANDQVRV
ATPAIAREKGSSAIVVGRSITKAEDPVKAYKAVRLEWEGI

>d1eixa_c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Escherichia coli}

VTNSP VVALDYHNRDDA LFV DKIDPRDCRLKVGKEMFTLFGPQFVRELQQRGF DIFL DLK FHDIPNTAAHAVA AAAA DLGVW MVNV HASGGAR
MMTAAREALV PFGKDAPL LIAV T L TSMEASD VL DLM TLSPAD YEA RL A ALT QK CGL DG VVCSAQ EAVRFKQVFGQEFKL VTPG IRP QG SEAGDQR

RIMTPEQALSAGVDYMIIGRPVTQSVDPQTLKAINASLQ

>d1dvja_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Archaeon Methanobacterium thermoautotrophicum}

MDVMNRLILAMDLNRDDALRTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRGCRRIADFKVADIPETNEKICRATFKAGADAIIVHGFPGADSVRACLNA
ACLNVAEEMGREVFLTEMSPGAEMFIQGADEIARMGVLDLGKNYVGSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSI
YLADNPAAAAGIIESIKDLLIPEDPAANKARKEAELAAATA

>d1dvjb_ c.1.2.3 (B:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Archaeon Methanobacterium thermoautotrophicum}

RLILAMDLNRDDALRTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRGCRRIADFKVADIPETNEKICRATFKAGADAIIVHGFPGADSVRACLNA
EEMGREVFLTEMSPGAEMFIQGADEIARMGVLDLGKNYVGSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSI
YLADNPAAAAGIIESIKD

>d1dqwa_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Baker's yeast (Saccharomyces cerevisiae)}

MHKATYKERAATHPSPVAAKLFNIMHEKQTNLCASLDVRTKELLELVEALGPKICLLKTHVDILDFSMEGTVKPLKALSAKYNFLLFEDRKFADIGN
VKLQYSAGVVYRIAWEADITNAHGVVGPGIVSGLKQAAEEVTKEPRGLLMLAELSCKGSLSTGEYTKGTVDIAKSDKDFVIGFIAQRDMGRDEGYD
WLIMTPGVGLDDKGDALGQQYRTVDDVVSTGSDIIIVGRGLFAKGRDAKVEGERYRAGWEAYLRCGQQD

>d1pii_2 c.1.2.4 (255-452) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Escherichia coli}

GENKVCGLTRGQDAKAYDAGAIYGLLFVATSPRCVNVEQAQEVMAAAPLQYVGFRNHDIADVVDKAKVLSLAQLHGNEEQLYIDTLREALP
AHVAIWKALSVGETLPAREFQHVLDKYVLDNGQGGSGQRFDWSLLNGQSLGNVLLAGGLGADNCVEAAQTGCAGLDFNSAVESQPGIKDARLLAS
VFQTLRAY

>d1nsj_ c.1.2.4 (-) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Thermotoga maritima}

MVRVKICGITNLEDALFSVESGADAVGFVFYPKSKRYISPEDARRISVELPPFVFRGVFVNEEPEKILDVASVYQLNAVQLHGEEPIELCRKIAERILVIK
AVGVSNERDMERALNYREFILLDTKPEYGGSGKTFDWLSLILPYRDRFRYLVLSGGLNPNENVRSайдVVRPAVDVSSGVEAFPGKKDHDSIKMF
NAKGL

>d1pii_1 c.1.2.4 (1-254) Indole-3-glycerophosphate synthase, IPGS {Escherichia coli}

MQTVLAKIVADKAIWVEARKQQQPLASFQNEVQPSTRHFYDALQGARTAFILECKKAPSKGIVRDDFDPARIAAIYKHYASAISVLTDEKYFQGSFNF
LPIVSQIAPQPILKDFIIDPYQIYLARYYQADACLLMLSVLDDDQYRQLAAVHSLEMGVLTEVSNEEEQERAIALGAKVVGINNRDLRDLSIDLNRT
ELAPKLGHNVTVISESGINTYAQVRELHFANGFLIGSALMAHDDLHAAVRRVLL

>d1a53_ c.1.2.4 (-) Indole-3-glycerophosphate synthase, IPGS {Archaeon Sulfolobus solfataricus}

PRYLGWKLKVQLSLSRRPSFRASRQRPISLNERILEFNKRNTIAAIEYKRKSPSGLDVERDPIEYSKFMERYAVGLSILTEEKYFNGSYETLRKIASSV
PILMKDFIVKESQIDDAYNLGADTVLLIVKILTERELESLEYARSYGMEMPIEINDENDLIALRIGARFIGINSRDLETLEINKENQRKLISMIPSNVVKA
ESGISERNEIEELRKLGVNAFLIGSSLMRNPEIKEFIL

>d1qopa_ c.1.2.4 (A:) Trp synthase alpha-subunit {Salmonella typhimurium}

MERYENLAQLNDRREGAFPVFTLGDPGIEQSLKIIDTLIDAGADALELGVPFSDPLADGPTIQNANLRAFAAGVTPAQCFCMELAIIREKHPTIPIGLL
MYANLVFNNGIDAFYARCEQVGVDSDLVADVPVEESAPFRQAAALRHNIAPIFICPPNADDLLRQVASYGRGYTYLLSRSGVTGAENRGALPLHHIE
KLKEYHAAPALQGFGISSIONPEQVSAAVRAGAAGAISGSAIVKIIKNLASKPKQMLAELRSFVSAMKAASR

>d1geqa_ c.1.2.4 (A:) Trp synthase alpha-subunit {Archaeon Pyrococcus furiosus}

MFKDGSLIPLYLTAGDPDKQSTLNFLALDEYAGAIELGIPFSDFPDIADGKTIQESHYRALKNGFKLREAFWIVKEFRRHSSTPIVLMTTYNPIYRAGVRNFL
AEAKASGVGILVVDLPVHAKEFTIAREEGIKTVFLAAPNTPDERLKVIDDMTTGFVYLVSLYGGTAREEIPKTAYDLRRAKRICRNKVAVGFGVSK
REHVVSLLEGANGVVVGSALVKIIGEKCREATEFLKKVEELLGI

>d2tpsa_ c.1.3.1 (A:) Thiamin phosphate synthase {Bacillus subtilis}

HGIRMTRISREMMKELLSVYFIMGSNNKADPVTVVQKALKGGATLYQFREKGGDALTGEARIKFAEKQAACREAGVPIVNDVVELALNLKADGI
HIGQEDANAKEVRAAIGDMILGVSAAHTMSEVKQAEEDGADYVGLGPIYPTETKKDTRAQGVSLIEAVRRQGISIPIVGIGGITIDNAAPVIQAGADG
VSMISAISQAEDPESAARKFREEIQTQYKTGR

>d1ho1a_c.1.24.1 (A:) Pyridoxine 5'-phosphate synthase {Escherichia coli}

AELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRILRQLDTRMNLEMAVTEEMLAIAVETKPHFCCLVPEKRQ
EVTEGGGLDVAGQRDKMRDACKRLADAGIQVSLFIDAEEQKAAAEGVAPFIEHTGCYADAKTDAEQAQELARIAKAATFAASLGLKVAGHGLT
YHNVKAIAAIPEMHELNIGHAIIGRAVMTGLKDAVAEMKRLMLEARG

>d2dora_c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme A}

MNNTTFANAKFANPFMNASGVHCMTIEDLEELKASQAGAYITSSTLEKREGNPLPRYVDLELGSINSMLPNLGFDYLDYVLKNQKENAQEGPIF
FSIAGMSAAENIAMLKQIRESDFSGITELNLSCPVPKGPKQLAYDFEATEKLLKEVFTFTKPLGVKLPPYFDLVHFIDIMAEILNQFPLTYVNSVSIGNG
LFIDPEAESVVIKPDKDGFGGIGGAYIKPTALANVRAFYTRLKPEIQIIGTGGIETQDAFEHLLCGATMLQIGTALHKEGPAIFDRIIKELEEIMNQKGYQSI
ADFHKLKS

>d1ep3a_c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme B}

MTENNRLSVKLPGLDLKNPIIPASGCFGGEYAKYYDLNKLGSIMVKATTLHPRFGNTPRVAETASGMLNAIGLQNPGLEVIMTEKLPWLNFPE
LPIIANVAGSEEADYVAVCAKIGDAANVKAELNISCPNVKHGGQAFGTDEPEAAALVKACKAVSKVPLVVKLSPNVTDIVPIAKAVEAAGADGLTMIN
TLMGVRFDLKTRQPILANGLSGPAIKPVALKLIHQVAQDVDIPIIGMGGVANAQDVLEMYMAGASAVAVGTANFADPFVCPKIIDLKPELMDQY
RIESLESLIQEVKEGKK

>d1d3ga_c.1.4.1 (A:) Dihydroorotate dehydrogenase {Human (Homo sapiens)}

MATGDERFYAEHLMPTLQGLLDPEAHRLAVRFTSLGLPRARFQDSDMILEVRVLGHKFNRNPVGIAAGFDKHGEAVDGLYKMGFFVEIGSVTPKP
QEGRNPRPRVFRLPEDQAVINRYGFNSHGLSVVEHRLRARQQKQAKLTEDGLPLGVNLGKNTSVDAADYAEGVRVLGPLADYLVVNVSSPNTAGL
RSIQKAEIERRLLTKVLRQERDGLRRVHRPAVLVKAIPDLTSQDKEDIASVVKELGIDGLVTNTTCSRPLQGALRSETGGLSGKPLRDLSTQTIREMY
ALTQGRVPIIIVGGVSSGQDALEKIRAGASLVQLYTALTFWGPPVVGKVKRELEALLKEQGFGGVTDAGDHRR

>d1oyb_c.1.4.1 (-) Old yellow enzyme (OYE) {Brewer's yeast (Saccharomyces carlsbergensis)}

SFKDFKPQALGDTNLKPIKIGNNELLHRAVIPPTRMRALHPGNIPNRDWAVEYYTQRAQRPGTMIITEGRFQAGGYDNAPGVWSEEQMVE
WTKIFNAIHEKKSFWVQQLWVLGWAAPDNLARDGLRYDSASDNVFMDAEQEAKAKKANNPQHSLTKDEIKQYIKEYVQAANSIAAGADGVEIH
SANGYLLNQFLDHSNRTDEYGGSIENRARFTLEVVDALVEAIGHEKVGLRLSPYGVNSMSGGAETGIVAQYAYVAGELEKRAKAGKRALFVHLVE
PRVTNPFLTEGEYEYEGGSNDFVSYIWGPVIRAGNFAHPEVVREEVKDKRTLIGYGRFFISNPDLRLEKGLPLNKYDRDTFYQMSAHGYIDYPTY
EEALKLGWDKK

>d1icpa_c.1.4.1 (A:) 12-oxophytidienoate reductase 1 (OYE homolog) {Tomato (Lycopersicon esculentum)}

QVDKIPLMSPKCMGKFELCHRVLAPLTRQRSYGYIPQPHAILHYSQRSTNGGLIGEATVISETGIGYKDVTKEQVEAWKPIVDAVHAKGIIFF
CQIWHVGRVSNKDFQPNGEDPISCTDRGLTPQIMSNGIDIAHFRPRRLTTDEIPQIVNEFRVAARNAIEAGFDGVEIHGAHYLIDQFMKDQVND
RSDKYGGSLENRCRFALEIVEAVANEIGSDRVGIRISPFAHYNEAGDTNPTALGLYMVESLNKYDLAYCHVVEPRMKTAWEKICTESLPMRKAYKGT
FIVAGGYDREDGNRALIEDRADLVAYGRLFISNPDLPKRFELNAPLNKYNRDTFTSDPIVGYTDYPFLE

>d1gox_c.1.4.1 (-) Glycolate oxidase {Spinach (Spinacia oleracea)}

MEITNVNEYEAIAKQKLPKMVYDYASGAEDQWTLAENRNRASRILFRPRILIDVTNIDMTTILGFKISMPIMIAPTAMQKMAHPEGEYATARAASA
AGTIMTSSWATSSVEEVASTGPGIRFFQLYVYKDRNVVAQLVRAERAGFKAIALTVDTPRLRREADIKNRFLPPFLTNFEGIDLGKMDKANDS
GLSSYVAGQIDRSLSWKDVAWLQQTISLPLVKGVITAEDARLAQVHGAAGIIVSNHGARQLDYVPATIMALEEVVKAAQGRIPVFLDGGVRRGTDVF
KALALGAAGVFIGRPVVFSLAEGEAGVKKVLQMMRDEFELTMALSGCRSLKEISRSHIAADWD

>d1huva_c.1.4.1 (A:) Membrane-associated (S)-mandelate dehydrogenase {Pseudomonas putida}

NLFNVEDYRKLAQKRLPKMVYDYLEGGADEYGVKHNRDVQQWRFPKRLVDVSRRSLQAEVLGKRQSMPLLIGPTGLNGALWPKGDLALARA
ATKAGIPFVLSTASNMSIEDLARQCDGDLWFQLYVHREIAQGMVLKALHTGYTTLVTTDVAVNGYRERDLHNRFKIPPFLTKNFEGIDLGKMDKA
NLEMQAALMSRQMDASFNWEALRWLRDLWPHKLVKGLLSAEDADRCIAEGADGVILSNHGRQLDCaisPMEVLAQSVAKTGPVLIDSGFRR
GSDIVKALGAEAVLLGRATLYGLAARGETGVDEVTLKADIDRTLAQIGCPDITSLSPDYLQNE

>d1h61a_c.1.4.1 (A:) Pentaerythritol tetranirate reductase {Enterobacter cloacae}

SAEKLFTPLVKVGAUTAPNRVFMAPLTRLRSIEPGDIPTPLMGEYYRQRASAGLISEATQISAQAKGYAGAPGLHSPEQIAAWKKITAGVHAEDGRIAV
QLWHTGRISHSSIQPGQCAPVSASALNANTRTSLRDENGNAIRVDTTPRALELDEIPGIVNDFRQAVANAREAGFDLVELHSAGYLLHQFLSPSS
NQRTDQYGGSVENRARLLEVDAVCNEWSADRIGIRVSPIGTFQNVDNGPNEEADALYIEELAKRGIAYLHMSETDLAGGKPYSEAFRKVRF

HGVIIAGAGAYTAEKAEDLIGKGLIDAVAFGRDYIANPDLVRLQKKAELNPQRPESFYGGGAEGYTDYPSL

>d1djna1 c.1.4.1 (A:1-340) Trimethylamine dehydrogenase, N-terminal domain {Methylophilus methylotrophus, w3a1}
ARDPKHDILFEPICQGPCKTLRNRFYQVPHCIGAGSDKPGFQSAHRSVKAEGGWALNTEYCSINPESDDTHRLSARIWDEGDVRNLKAMTDEVHKY
GALAGVELWYGGAHAPNMESRATPRGPSQYASEFETLSYCKEMDLSIAQVQQFYVDAAKRSRADGFDIVVYGAHSYPLQFLNPYYNKRTDKYG
GSLENRARFWLETLEVKVHAVGSDCAITRFGVDTVYPGQIEAEVDGQKFVEMADSLVDMWDITIGDIAEWGEDAGPSRFYQQGHTIPWVKLVK
QVSKKPVLGVGRYTDPEKMIEIVTKGYADIIGCARPSIADPFLPKVEQGRYD

>d1ltda1 c.1.4.1 (A:98-511) Flavocytochrome b2, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
APGETKEDIRKEQLKSLLPLDNIIINLYDFEYLASQTLTKQAWAYSSGANDEVTHRENHNAYHRIFFKPKILDVDRKVDISTDMILGSHVDVPFYVSAT
ALCKLGNPLEGEKDVARCGCGQGVTKVPPQMISTLASCSPEEIAPSDKQIQWYQLVNSDRKITDDLKNVKEKLGVKALFVTVDAPSLGQREKDMK
LKFSNTKAGPKAMKKTNEESQGASRALSKFIDPSLTWKDIEELKKTKLPVIKGVQRTEDVIKAAEIGVSGVVLNSNHGRQLDFSRAPIEVLATMPI
LEQRNLKDKLEVFDGGVRRGTDVLKALCLGAKVGVLGRPFLYANSCYGRNGVEKAIEILRDEIEMSMRLLGVTSAIELKPDLLSTLKARTVGVPND
VLYNEVYEGPTLTFEDA

>d1h7wa2 c.1.4.1 (A:533-844) Dihydropyrimidine dehydrogenase, domain 4 {Pig (Sus scrofa)}
ISVEMAGLKFINPFGLASAAPTTSSSMIRRAFEAGWGFAKTFSLKDINTNVSPRIVRGTTSGPMYGPQSSFLNIELISEKTAAYWCQSVELKADF
PDNVIASIMCSYNKNDWMELSRKAEASGADALENLSCPBMGERGMGLACGQDPFLVRNICRWWRQAVQIPFFAKLTPNVTDIVSIARAKEG
GADGVTATNTVSLMGLKADGTPWPAGKRTTYGGVSGTAIRPIALRAVTTIARALPGFPILATGGIDSAESGLQFLHSGASVLQVCSAVQNQDF
TVIQDYCTGLKALLYLKSIE

>d1ea0a2 c.1.4.1 (A:423-1193) Alpha subunit of glutamate synthase, central and FMN domains {Azospirillum brasiliense}
TTHLDELVKTASLKGEPSDMKAEIIRRQQAFGLTMEDMELILHPMVEDGKEAIGSMGDDSPIAVLSDKYRGLHHFFRQNFSQVTNPPIDSLRR
VMSLKTRLGNLGNILDEDETQTRLLQLESPLVLTAEFRAMRDYMGDTAAEIDATFPVDGGPEALRDLRRIQETEADAVRGGATHVILTDEAMGPAR
AAIPAILATGAVHTHLIRSNLRTFTSLNVRTAEGLDTHYFAVLIGVATTNAYLAQEAIERHRRGLFGSMPLKG MANYKKAIDDGLLKIMSKMGIS
VISSYRGGGNFIAIGLSRALVAEHFPAMVSRISSGIGLNGIQKKVLEQHATAYNEEVVALPVGGYFRKSGDRHGWEGBVIHTLQQAVTNDSYTFKK
YSEQVNKRPPMQLDLLELRSTKAPPVDEVESITAIRKRFITPGMSMGALSPEAHGTLNVAMNRIGAKSDSGEGGEDPARFRPDKNGDNWNSAIK
QVASGRFGVTAEYLNCRELEIKAQGAKPGEQQQLPGFKVTEMIARLRHSTPGVMLISPPP HDIYSIEDLAQLIYDLKQINPDAKVTVKLVSRSIG
TIAAGVAKANADIISGNSGGTGASPQTSIKFAGLPWEMGLSEVHQVLTNRLRHRVRLTDGGLKTGRDIVIAAMLGAEEFGIGTASLIAMGCIMV
RQCHSNCPVGVCVQDDKLRLQFKVGTPEKVVNLFTAEEVREILAGLFRSLNEIGRTDLLHQVSRAEHLDLDPNRLAQVDPG

>d1eepa_c.1.5.1 (A:) Inosine monophosphate dehydrogenase (IMPDH) {Lyme disease spirochete (Borrelia burgdorferi)}
NKitKEALTFFDVSLLPRKSSVLPSEVSLKTLTKNISLNIPFLSSAMDVTESQMAIAIAKEGGIGIHHKMSIEAQRKEIEVKTYKFQKTINTNGDTNE
QKPEIFTAKQHLEKSDAYKNAEHKEDFPNACKDLNNKLRVGAASIDIDTIERVEELVKAHDILVIDSAHGHSTRIEELKKIKTKYPNLDIAGNIVTKEA
ALDLISVGADCLKVIGPGSICTRIVAGVGPQITAICDVYEACNNTNIIADGGIRFSGDVKAIAAGADSVMIGNLFAGTKESPSEEIYNGKKFSY
VGMGSISAMKRGSKSRYFQLENNEPKKLVPEGIEGMVPSGKLKDILTQLKGGLMSGMGMGYLGAATISDLKINSKFKVSHS

>d1zfja1 c.1.5.1 (A:2-94,A:221-492) Inosine monophosphate dehydrogenase (IMPDH) {Streptococcus pyogenes}
SNWDTKFLKKGYTFDDVLLIPAESHVLPNEVDLTKLADNLTLNIPITAAMDTVTGSKMAIAIARAGGLGVIHKNMSITEQAEEVRKVKRSEXGRLLV
AAAAGVTSDFTERAELFEAGADAIVIDTAHGSAGVLRKIAEIRAHFPNRTLIAGNIATAEGARALYDAGVDDVVKVGI PGSICTR VAGVGPQVT
AIYDAAAVAREYGTIIADGGIKYSGDIVKALAAGGNAVMGSMFAGTDEAPGETEIQYQGRKYKTYRGMGIAAMKKGSSDRYFQGSVNEANKLVP
EGIEGRVAYKGAAASDIVFQMLGGIRSGMGYVGAGDIQELHENAAQFVEMSGAGLIESPHDVQITNEAPNYSV

>d1ak5_1 c.1.5.1 (2-101,222-483) Inosine monophosphate dehydrogenase (IMPDH) {Tritrichomonas foetus}
AKYYNEPCHTFNEYLLIPGLSTVDCIPSNVNLSTPLVKFQKGQQSEINLKIPLVS AIMQSVS GEKMAIA LAREGGISFIFGSQSIESQAAMVHAVKNFKA
XHNELVDSQKRYLVGAGINTRDFRERVPALVEAGADVLCIDSSDG FSEWQKITIGWIREKYGDVKVGAGNIVDGEFGRYLA DAGADFIKIGIGGGSI
CITREQKGIGRGQATAVIDVAERNKYFEETGIYIPVCS DGGIVYDYHMTLALAMGADFIMLGRYFARFEESPTRKV TINGSVMKEYWGE GSSRARN
WQRYDLGGKQKLSFEEGVDSYV PYAGKLKDNEASLNKV KSTMNCNGALTIPQLQSKAKITLVSSVI

>d1jr1a1 c.1.5.1 (A:17-112,A:233-514) Inosine monophosphate dehydrogenase (IMPDH) {Chinese hamster (Cricetulus griseus)}
GLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKITLKPLVSSPMDTVTEAGMAIA MALTGGIFIHNCNTPEFQANEVRVKKKYEQXYP
LASKDAKKQLLCGAAIGTHEDDKYRLLLALAGVDDVVLDSSSQGNSIFQINMIKYMKEKPNLQVIGGNVVTAAQAKNLIDAGVDA RVMGCGSI

CITQEVLACGRPQATAVYKVSEYARRFGVPVIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKRYRGMSLDAMDKHLSSQ
NRYFSEADKIKVAQGVSGAVQDKGSIHKFV рули IQHSCQDIGAKSLTQVRAMMYSГЕLKEKRTSSAQVEGGVHSLHSYEKRLF
>d1bd0a2 c.1.6.1 (A:12-244) Alanine racemase {Bacillus stearothermophilus}
VDLDAlYDNVENLRRLLPDDTHIMAVV рули KANAYGHGDVQVARTALEAGASRLAVAFLDEALALREKGIEAPIVLGASRPADAALAAQQRIALTVFRSD
WLEEASALYSGPFPIHFHLKMDTGMGRIGV рули KDEEETKRIVALIERHPHFVLEGLYTHFATADEVNTDYFSYQYTRFLHMLEWPSRPLVHCANSAA
LRFPDRTFNMVRFGIAMYGLAPSPGIKPLPYPLKEA
>d1d7ka2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Human (Homo sapiens)}
DLGDILKKHLRWЛKALPRVTPFYAVKCNDSKAIVKTLAATGTGFDCASKTEIQLVQSLGVPPERIIYANPCKQVSQIKYAANNGVQMMTFDSEVELMK
VARAHPKAKLVLRIATDDSKAVCRLSVKFGATLRTSRLLERAKELNIDVVGVSFHVGSCTDPETFVQAISDARCVFDMGAEVGFSMYLLDIGGGFP
GSEDVKLKFEITGVINPALDKYFPSDSGVRIIAEPGRYYVASA
>d7odca2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Mouse (Mus musculus)}
DLGDILKKHLRWЛKALPRVTPFYAVKCNDNSRAIVSTLAAIGTGFDCASKTEIQLVQGLGVPAERVIYANPCKQVSQIKYAASNGVQMMTFDSEIELMK
VARAHPKAKLVLRIATDDSKAVCRLSVKFGATLRTSRLLERAKELNIDVVGVSFHVGSCTDPETFVQAISDARCVFDMATEVGFSMHLLDIGGGFP
GSEDTKLKFEITSVINPALDKYFPSDSGVRIIAEPGRYYVASA
>d2toda2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}
DLGDIVRKHETWKKCLPRVTPFYAVACNDDWRVLGTLAALGTGFDCASNTEIQRVRGIGVPPEKIIYANPCKQISHIRYARDSGV рули VMTFDCVDELEK
VAKTHPKAKMVLRISTDLSLARCRSLVKFGAKVEDCRFILEQAKKLNIDVTGVSFHVGSCTDASTFAQAISDSRFVFDMGTELGFNMHILDIGGGFP
GTRDAPLKFEEITSVINPALDKYFPSDSGVRIIAEPGRYYVASA
>d1ct5a_ c.1.6.2 (A:) "Hypothetical" protein ybl036c {Baker's yeast (Saccharomyces cerevisiae)}
TGITYDEDRKTQLIAQYESREVVNAEAKNVHNENASNKILLV рули VSKLKPASDIQILYDHGVREFGENYVQELIEKAKLLPDIKWHFIGGLQTNKCKDL
AKVPNLYSVETIDSLKKAKLNESRAKFQPDNCNIPILCNV рули QINTSHEDQKSGLNNEAEIFEVIDFFLSEECKYIKLNGLMТИGSWNVSHEDSKENRDFATL
VEWKKKIDAKFGTSKLSMGMSADFREAIRQGTAEVRIGHTIFG
>d1frb__ c.1.7.1 (-) FR-1 (fibroblast growth factor-induced) protein {Mouse (Mus musculus)}
ATFVELSTKAKMPIVGLTWKSPPNQVKEAVKAIAIDAGYRHIDCAYACNEENEVGEAIQEKEIKEAKVQREDLFIVSKLWPTCFEKLLKEAFQKTLTDLK
LDYLDLYLIHWPKQGLQPGKEFPKDDQGRILTSKTTFLEAWEGMEELVDQGLVKALGVSNFNHFQIERLLNKPLKHKPVTNQVECHPYLTQEKLQY
CHSKGISVTASYPLGSPDRPSAKPEDPSLLEDPKIKEIAAKHEKTSAQV рули LIRFHIQRNVV рули IPKSVTPSRIQENIQVFDFQLSDEEMATILSFNRNWRACL
LPETVNMEEYPYDAEY
>d1exba_ c.1.7.1 (A:) Voltage-dependent K+ channel beta subunit {Rat (Rattus norvegicus)}
LQFYRNILGSGLRV рули SCLGLTWVTFGQQITDEMAEHLMLAYDNGINLFDTAEV рули YAAGKAEV рули VLGNIIKKGVRRSSLV рули ITKIFWGKAETERGLSR
KHII EGLKASLERLQLEYDV рули VFV рули FANRPDPNTPMEETV рули RAMTHV рули INQGMAMYWGTSRWSSMEIMEAYSVARQFNLIPPICEQAЕYHMФQREKVEV
QLPELFHKIGVGAMTWSPLAGIVSGKYDSGIPPSRASLKGYQWLKDКILSEEGRQQAKLKELQ рули AERLGCTLPLQ рули LAI рули WCLRNEGVS рули VLLGAS
NAEQLMENIGAIQVLPKЛSSIVHEIDSILGNKPYS
>d1ads__ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (Homo sapiens)}
ASRLLLNNAGAKMPILGLTWKSPPGQVTEAVKVAIDV рули GYRHIDCAH рули VYQNENEVGV рули VAIQEKLREQV рули VKREELFIVSKLWCTYHEKGLVKGACQKTLS
DLKLDYLDLYLIHWPTGKPGKEFPKLDENGNV рули VPSDTNILDTWAAMEELVDEGLVKAIGISNFNHLQV рули MILNKPLKYKPAVNQIECHPYLTQEKL
QYCQS рули KGIVV рули TAYPLGSPDRPWAKPEDPSLLEDPRKIAIAAKHNKTTAQV рули LIRFPMQRNLV рули IPKSVT PERIAENFKV рули FDFLSSQDMTLLSYNRNW
RVCALLSCTSHKDYPFHEEF
>d2alr__ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (Homo sapiens)}
AASCVLLHTGQKMPILGLTWKSPPGQV рули KAAV рули KYALSVG рули YRHIDCAH рули VYQNENEVGV рули VAIQEKLREQV рули VKREELFIVSKLWNTKHHПEDVEPALRKT
LADLQLEYLDLYLMHW рули PYAFERGDNPFPKNAДGTCYDSTHYKETW рули KALEALV рули AKGLV рули QALGLSNFSNRQIDDI рули LSVASVRPAVLQVECHPYLAQNEL
IAHCQARGLEV рули TAYPLGSSDRAW рули RDPDEPV рули LLEPV рули VLAЕKYGRSPAQILRW рули VQQRKVICIPKSITPSRILQNIKVFDFTFSPPEEMKQLNALNKN
WRYIVPMILTVDGKRVPRDAGHРЛPFNDPY
>d1ah4__ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Pig (Sus scrofa)}
ASHLVLYTGAKMPILGLTWKSPPGKVTEAVKVAIDLGYRHIDCAH рули VYQNENEVGV рули GLQKЛQGVV рули KREDLFIVSKLWCTDHEKNLVKGACQTTLR

DLKLDYDLYLIHWPTGFKPGKDPFLDGDGNVPDESDFVETWEAMEELVDEGLVKAIGVSFNHLQVEKILNKPGLKVKPAVNQIEVHPYLTKQL
IEYCKSKGIVVTAYSPGLSPDRPWAKPEDPSLLEDPRIKAIAKYNKTTAQVLIRFPMQRNLIVIPKSVTPERIAENFQVFDFELSPDMNTLLSYNRNW
RVCALMScASHKDYPFHEEY
>d1hqta_c.1.7.1 (A:) Aldose reductase (aldehyde reductase) {Pig (Sus scrofa)}
AASCVLLHTGQKMPLIGLGTWKSEPGQVKAIIKYALTGYRHIDCAAIFGNELEIGEALQETVPGKAVPREELFVTSKLWNTKHHPEDVEPALRKT
ADLQLEYLDLYLMHWPYAFERGDNPFPKNADGTIRYDATHYKDTWKALEALVAKGLVRALGLSNFSSRQIDDVLSVASVRPAVLQVECHPYLAQNELI
AHQCARGLEVTAYSPGLSSDRAWRDPNPEVPLLEEVQVQALAEKYNRSPAQILLRWQVQRKVICIPKSVTSPSIPQNIQVFDFTFSPEEMKQLDALNKN
LRFIVPMILTVDGKRVPRDAGHPLYPFNDPY
>d1afsa_c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Rat (Rattus norvegicus)}
MDSISLRVALNDGNFIPVLGFHTVPEVKAVDEVIKATKIAIDNGFRHFDSAYLYEVEEVGQAIRSKIEDGTVKREDIFYTSKLWSTFHRELVRTCLEKT
LKSTQLDYVDLYIIHFPMLQPGDFIFPRDEHGKLLFETVDCDTWEAMEKCKDAGLAKSIGVSNFCRQLERILNKPGLKVKPVCNQVECHLYLNQS
MLDYCKSKDIIIVSYCTLGSSRDWTVDQKSPVLLDDPVLCIAKKYKQTPALVALRYQLQRGVVPLRSFNAKRIKELTQVFSQLASEDMKALDGLNR
NFRYNNNAKYFDDHPNHPF
>d1ihia_c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Human (Homo sapiens), type III}
SKYQCVKLNDGHFMPVLFQFTYAPAEVPKSKALEAVKLAIEAGFHHIDSAYVNNNEEQVGLAIRSKIADGSVKREDIFYTSKLWSNSHRPELVRPALE
SLKNLQLDYVDLYIIHFPVSVKPGEEVIPKDENGKILFDVTLCATWEAMEKCKDAGLAKSIGVSNFNHRLLEMILNKPGLKVKPVCNQVECHPYFNQ
RKLLDFCKSKDIVLVAYSALGSHREEPWVDPNNSPVLLLEDPVLCALAKHKRTPALIALRYQLQRGVVVLAKSYNEQRIRQNVQVFSQLTSEEMKAIDG
LNRRNVRVLTLDIFAGPPNYPFSDE
>d1c9wa_c.1.7.1 (A:) CHO reductase {Chinese hampster (Cricetulus griseus)}
STFVELSTAKMPIVGLGTWQSPPGQVKEAVKVAIDAGYRHIDCAYAYNEHEVGEAIQEIKEAKVRRDELFIWSKLWPTCFERKLLKEAFQKTLTDLK
LDYLDLYLIHWQPGLQPGKELFPKDDQGNVLTSKITFLDAWEVMEELVDEGLVKALGVSNFNHFQIERILNKPGLKHKPVTNQVECHPYLTQEKLIEYC
HSKGITVTAYSPGLSPNRPWAKPEDPSLLEDPKIKEIAAKHKKTSQAQVLIRFHIQRNVVVIPKSVTPARIHENFQVFDFQLSQEMATILGFNRNWRC
LLPETVNMEYYPYDAEY
>d1hw6a_c.1.7.1 (A:) 2,5-diketo-D-gluconic acid reductase A {Corynebacterium sp.}
TVPSIVLNDGNSIPQLGYGVFKVPPADTQRAVEEALEVGYRHIDTAIYGNEEGVGAIAASGIARDLIFTKLWNRHDGDEPAAIAESLAKLAD
QVDLYLVHWPTPAADNYVHAWEKMIELRAAGLRTSIGVSNHLVPHLERIVAATGVPPAVNQIELHPAYQQREITDWAAAHDVKIESWGPLGQGKYD
LFGAEPVTAAAAAGKTPAQAVLRWHLQKGFFVFPKSVRERLEENLDVFDFDLTDTEIAIDAMDP
>d1bli_2 c.1.8.1 (3-393) Bacterial alpha-amylase {Bacillus licheniformis}
LNGTLMQYFEWYMPNDGQHWKRLQND SAYLAEHGITAVWIPPAYKGT SQADVG YGAYDLYDLGEFHQKGTVRTKYGTKGELQSAIKSLHSRDINV
YGDVVINHKGGADATEDVTAVEVDPADRN RVISGEHLIKAWTHFHPGRG STYSDFKWHYHFDGT DWDES RKL NRIYK FQG KAWDWEVSNEF
GNYDYL MYADIDYDH PDVAAEIK RWG T WYANE L QLDG FR LDAV K HIK FSFL RDW V NHV REKT G KEM FTVA EYW SYD LG A E NYLN K TNF NSV
D VPLHYQFHAA STQGGGYDMRKL L NGTVVSKHPLK SVR ERLEEN LDV FDF DLT DTEIA IDAM DP
KKIEPILKARKQ
>d1e43a2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus amyloliquefaciens/Bacillus licheniformis chimera}
VNGTLMQYFEWYTPNDGQHWKRLQND AEHLS DIGITAVWIPPAYKGLSQSDNGYGPYDLYDLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNQV
YGDVVLNHKAGADATEDVTAVEVNPANRNQETSEYYQIKAWTDFRPGRGNTYSDFKWHYHFDGADWDES RKL NRIYK FQG KAWDWEVS
ENGNYDYL MYADVDYDH PDVVAETKKW GIWY ANEL SL DG FR IDA AKH IK FSFL RDW V QAVR QAT G KEM FTVA EYW QNNAGKLEN YLN K TSF NQ
SVFDVPLHFNLQASSQGGGYDMRKL L NGTVVSKHPLK SVR ERLEEN LDV FDF DLT DTEIA IDAM DP
PALKH KIEPILKARKQ
>d1g94a2 c.1.8.1 (A:1-354) Bacterial alpha-amylase {Pseudoalteromonas haloplancis (Alteromonas haloplancis)}
TPTTFVHLFEWNWQDVAQECEQYLGPKGYAAVQVSPPNEHITGSQWWTRYQPVSYELQSRGGNRAQFIDMVNRCSAAGVDIYVDTLINHMAAG
SGTGTAGNSFGNKSFPISPQDFHESCTINNSDYGNDRYRVQNCELVGLADLDTASNYVQNTIAAYINDLQAIKGFRFDASKHVAASDIQSLMAK
VNGSPVVFQEVIDQGGEAVGASEYLSTGLVTEFKYSTELGNTFRNGSLAWLSNFGEWGFMPS SAVVFDNHDNQRGHGGAGNVITFEDGR
DLANVFMLAPYGYPKVMSSYDFHGDTDAGGPNVPVHINNGNLECFASNWKCEHRWYIAGGVDFRNNTAD

>d1bag_2 c.1.8.1 (1-347) Bacterial alpha-amylase {Bacillus subtilis}

LTAPSIKSGTILHAWNWSFNTLKHNMKDIHDAGYTAIQTSPINQVKEGNQGDKSMSNWYWLQPTSYQIGNRYLGTEQEKFEMCAAAEYGIKVIVDAVINHTFDYAAISNEVKSPNWTHGNTQIKNWSRWDVTQNSLLGLYDWNTQNTQVQSYLKRFRLERALNDGADGFRFDAAKHIELPDDGSYGSQFWPNITNTSAEFQYQGQLQDSASRDAAYANYMDVTASNYGHISRALKRNRLGVSNISHYASDVSADKLTVWVESHTYANDDEESTWMSDDIRLGWAVIASRGSTPLFFSRPEGGGNGVRFPGKSQIGDRGSALFDAQITAVNRFHNVMAG

>d1hvxa2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus stearothermophilus}

AAFPNGTMMQYFEWYLPDDGTLWTKVANEANNLSSGLITALWPPAKGTSRSDVGYGVYDLYDLGEFNQKGAVRTKYGTKAQYLQAIQAAHAAGMQVYADVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNTYSSFKWRWYHFDGVWDERSRKLRIYKFRGIGKAWDWEVDTENGNYDYLMYADLDMDHPPEVVTTELKSWGKWWVNTTNIDGFRDAVKHIFKSFPPDWSYVRSQTGKPLFTVGEYWSYDINKLHNHYIMKTNGTMSLFAPLHNKFYTAKSGTFDMRTLMTNTLMKDQPTLAFTFDVNHDEPGQALQSWVDPWFKPLAYAFILTRQEGYPVCVFYGDYYGIPQYNIPSLKSKIDPLLIARRD

>d1gjwa2 c.1.8.1 (A:1-572) Maltosyltransferase {Thermotoga maritima}

MLLRREINRYCKEKATGKRIYAVPKLWIPGFFKKFDEKSGRCFVDPYELGAEITDWILNQSREWDSQPLSFLKGEKTPDWIKRSVVGSLPRTTAAYNKGSGYYEENDVLGFREAGTFFKMMMLLPFKVSLGADAIYLLPVSRMSDLFKKGADSPYSVKNPMELDERYHDPILLEPFKDEEFKAFVEACHILGIRVILDIFPRATAARDSDLIREHPDWFYWIKEVELADYTPPRAEELPKVPDEDELEIIYNKENVKRHLKKTFPPNLIDPKWEEKIKREEGNILELIVKEFGIITPGFSDLINDPQPTWDDVTFLRLYLDHPEASKRFLDPNPQPPYVLYDVIKASKFPGKEPNRELWEYLAGVIPHYQKKGIDGARLDMGHALPKELLDLIIKNVKEYDPAFVMIAEELDMEKDJKASKEAGYDVILGSSWYFAGRVEEIGKLPIAEEELVLPFLASVETPDTPRIATRKYASKMKKLPFTYFLPNSIPYVNTGQEIGEKQPMNLGLTDPNLRKVLSPTEFFGKLAFFDHVHLWDSPDRGVLFNFIKKLIKVRHEFLDFVLN

>d1cgt_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

DPDTAVTNKQSFSTDVIYQVFTDRFLDGNNPNTGAAYDATCSNLKLYCGGDWQGLINKINDNYFSDLGVTALWISQPVENIFATINYSGVTNTAYHGYWARDFKKTNPYFGTMADFQNLTAAHAKGKIVIDFAPNHTSPAMETDTSFAENGRYDNGTLVGGYTNDTNGYFHNGGSDFSSLNGIYKNLYDLADFNHNNTATDKYFKDAIKLWLDGMVGDIRDAVKHMPLGWQKSMSSIAHKPVFTFGEWFLGASAASDADNTDFANKSGMSLDFRFNSAVRNVFRDNTSNMYALDSMINSTATDYNQVNDQVTIDNHDMDRFKTSAVNNRRLEQALATLTSRGVPAIYYGTEQYLTGNGDPDNRAKMPFSKSTTAFNVISKLAPLRKSNPAIAY

>d1kcla4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

APDTSVSNKQNFSTDVIYQIFDRFSDGNPANNPTGAFFGTCTNLRLYCGGDWQGIINKINDGYLTGMGVTAIWISQPVENIYISINYSGVNNTAYHGYWARDFKKTNPAYGTIADFQNLIAAAHHAKNIKVIIDFAPNHTSPASSDQPSFAENGRYDNGTLLGGYTNDTQNLFHNLGDFSTTENGIYKNLYDLADLNHNNTVDVYLKDAIKMWLDLGIDGIRMDAVKHMPFGWQKSFMAAVNNYKPVFTFGEWFLGVNEVSPENHKFANESGMSLDFRFQKVHQVFRDNTDNMYGLKAMLEGSAADYAQVDDQVTIDNHDMERFHASNANRRKLEQALATLTSRGVPAIYYGTEQYMSGGTDPDNRARIPSSTS TTAYQVIQKLAPLRKCNPAIAY

>d1cyg_4 c.1.8.1 (1-402) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus}

AGNLNKVNFTSDVYQIVVDRFDGNTSNPNSGALFSSGCTNLRKYCGGDWQGIINKINDGYLTGMGVTAIWISQPVENFSVMNDASGSASYHGYWARDFKKPNPFFGTLDFQRLVDAAHAKGKIVIDFAPNHTSPASETNPSYMENGRYDNGTLLGGYTNDANMYFHNGGTTFSSLEDGIYRNLFDLADLNHQNPVIDRYLKDAVKMWIDMGIDGIRMDAVKHMPFGWQKSLMDEIDNYRPVFTFGEWFLSENEVDANNHYFANESGMSLDFRFQGKLRQVLRNNSDNWYGFNQMIQDTASAYDEVLDQVTIDNHDMDRFMIDGGDPRKVDMALAVLLTSRGVPNIYYGTEQYMTGNGDPNNRKMMSSFNKNTRAYQVIQKLSSLRRNNPALAY

>d1qhoa4 c.1.8.1 (A:1-407) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}

SSASVKGDIYQIIDRFYDGTNTNNNPAKSYGLYDPTSKWKMYWGGDLEGVRQKLPYKQLGVTIWLSPVLDNLDLAGTDNTGYHGYWTRDFKQIEEHFGNWTTFTLVNDAHQNGIKIVDFVPNHSTPFKANDSTFAEGGALYNNGTYMGNYFDDATKGYFHNGDISNWDDRYEAQWKNFTDPAGFSLADLSQENGIAQYLTDAAVQLVAHGDGLRIDAVKHFNNSGFSKSLADKLYQKKDIFLVEWYGGDPGTANHLEKVRYANNSGVNVLDFTLNTVIRNVFGTFTQTMYDLNNMVNQTGNEYKYKENLITFIDNHDMSRFLSVNSNKANLHQALAFILTSRGTPSIYYGTEQYMAGGNDPYNRGMMPAFDTTTAFKEVSTLAGLRRNNAAIQY

>d1pama4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Alkalophilic bacillus sp., strain 1011}

APDTSVSNKQNFSTDVIYQIFDRFSDGNPANNPTGAFFGSCTNLRLYCGGDWQGIINKINDGYLTGMGVTAIWISQPVENIYISVINYSGVNNTAYH

GYWARDFKKTNPAYGTMQDFKNLIDTAHANIKVIIDFAPNHTSPASSDDPSFAENGRLYDNGNLLGGYTNDTQNLFHHYGGTDFSTIENGIYKNLY
DLADLNHNNSSVLVLDLGVDGIRDAVKHMPFGWQKSFMATINNYKPVFTGEWFLGVNEISPEYHQFANESEGMSSLDFRFAQKA
RQVFRDNTDNMYGLKAMLEGSEVDYAQVNDQVTIDNHDMERFHTSNGDRRKLEQALATLSRGVPAIYYGSEQYMSGNDPDNRARLPSFT
TTTAYQVIQKLAPLRKSNPAIAY

>d1ciu_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Thermoanaerobacterium thermosulfurigenes, EM1}

ASDTAVSNVVNSTDVIYQIVTDRFVDGNTSNNPTGDLYDPHTSLKKYFGGDWQGIINKINDGYLTGMGVTAIWISQPVENIYAVLPSTFGGSTY
HGYWARDFKRTPYFGSRTDFQNLINTAHANIKVIIDFAPNHTSPASETDPTYAENGRLYDNGTLLGGYTNDTNGYFHGGTDFSSYEDGIYRNLF
DLADLNQQNSTIDSYLKSAIKVWLDMGIDGIRLDAVKHMPFGWQKNFMDISLYRPVFTGEWFLGTNEIDVNNTYFANESEGMSSLDFRSQKVR
QVFRDNTDMYGLDSMIQSTASDYNFINDMVTIDNHDMDRFYNGGSTRPVEQALATLTSRGVPAIYYGTEQYMTGNGDPYNRAMMTSFNTST
TAYNVVIKKLAPLRKSNPAIAY

>d1hx0a2 c.1.8.1 (A:1-403) Animal alpha-amylase {Pig (Sus scrofa)}

EYAPQTSGRTSIVHLFEWRWVVDIALECERYLGPKGFGGVQVSPPNENIVVTNPSRPWWERYQPVSYKLCTRSGNENEFRDMVTRCENNNGVRIYV
DAVINHMCGSGAAAGTGTCGSYCNPGRNREFPAPVYSAWFNDGKCKTASGGIESYNDPYQVRDCQLVGLLDLAKEKDYVRSMIADYLNKLIDIGV
AGFRIDASKHMHWPDIKAVLDKLHNLNNTNWFPAGSRPFIFQEVIDLGGEAIKSEYFGNGRVTEFKYGAALKGTVVRKWSGEKMSYLNWGEWG
FMPSDRAVLVFDNHNDNQRGHGAGGSSILTFWDARLYKIAVGFMLAHPYGFTRVMSSYRWARNFVNGEDVNDWIGPPNNNGVIKEVTINADTT
GNDWVCEHRWREIRNMVWFRNVVVDG

>d1smd_2 c.1.8.1 (1-403) Animal alpha-amylase {Human (Homo sapiens)}

EYSSNTQQGRTSIVHLFEWRWVVDIALECERYLAPKGFGGVQVSPPNENVAIHNPFRPWWERYQPVSYKLCTRSGNENEFRNMVTRCENNNGVRIYV
DAVINHMCGNAVASGTSSTCGSYFNPGSRDFPAVYSGWDNFNDGKCKTSGDIENYNDATQVRDCRLSGLDDALGKDYVRSKIAEYMNHLIDIGV
AGFRIDASKHMHWPDIKAILDKLHNLNNSWFPEGSKPIFYQEVIDLGGEPIKSSDYFGNGRVTEFKYGAALKGTVIRKWNGEKMSYLNWGEWG
MPSDRAVLVFDNHNDNQRGHGAGGASILTFWDARLYKMAVGFMLAHPYGFTRVMSSYRWPRYFENGKDNDWVGPPNDNGVTKEVTINPD
CGNDWVCEHRWREIRNMVWFRNVVVDG

>d1jae_2 c.1.8.1 (1-378) Animal alpha-amylase {Yellow mealworm (Tenebrio molitor), larva}

EKDANFASGRNSIVHLFEWKNDIACDECERFLQPQGFGGVQJSPPNEYLVADGRPWVERYQPVSYIINTRSGDESAFTDMTRRNDAVGVRIVDA
VINHMTGMNGVGTSGSSADHDGMNYPAPVYGSDFHSPCEVNNYQDADNVRNCELVGLRDLNQGSDYVRGLIDYMNHMIDLGVAGFRDA
AKHMSPGDLSVFSGLKNLNTDYGFADGARPFYQEVIDLGGEAIKNEYTGFVCVLEFQFGVSLGNAFQGGNQLKNLANWGPEWGLLEGDAVVF
VDNHDNQRTGGSQILTYKNPKPYKMAIAFMLAHPYGTTRIMSSFDFTNDQGPPQDGSGNLISPGINDDNTCSNGYVCEHRWRQVYGMVGFRN
AVE

>d2aaa_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus niger, acid amylase}

LSAASWRTQSIYFLLTDRFGRDNSTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAIWISPITEQLPQDTADGEAYHGYWQQKIYDVNSNFTAD
NLKSLSDLHARGMYLMVDVVDHMGYAGNGNDVDYSVFDPFDSYYFHPYCLITWDNLTMVEDCWEGDTIVSLPDLTTAVRTIWYDWV
ADLVSNSVSDGLRIDSVLEVQPDFFPGYNKASGVYCVGIEDNGNPASDCPYQKVLDGVLYNPIYWQLLYAFESSGSISNLYNMIKSVASDCSDPTLLG
NFIENHDNPRFAKYTSYDQSAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAEYTWIATTNAIRKLAIAADSAYIT

>d7taa_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus oryzae, Taka-amylase}

ATPADWRSQSIYFLLTDRFARTDGTTATCNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWITPVTQALPQTTAYGDAYHGYWQQDIYSLNENYGTA
DDLKALSSALHERGMYLMVDVVANHMGYDGAGSS/DYSVFKPFSSQDYFHPFCFIQNYEDQTQVEDCWLGNDNTVSLPDLTTKDVVKNEWYDW
VGSLVSNSYIDGLRIDTVKHVKQDFWPGYNKAAGVYCGIVEVLGDPAYTCPYQNVMDGVLYNPIYYPLNNAFKSTSGSMDDLYNMINTVKSDCPDS
TLLGTFVENHDNPRFASYTNIDIALAKNVAIFIILNDGIPIVYAGQEQHYAGGNDPANREATWLSGYPTDSELYKLIASANAIRNYAISKDTGFVT

>d1smaa3 c.1.8.1 (A:124-505) Maltogenic amylase, central domain {Thermus sp.}

DLFQAPDWVKDTVWYQIFPERFANGNPAISPKGARPWGSEDPTPTSFVGGDLQGIIDHLDYIADLGITGIYLTPIFRAPSNHKYDTADYFEIDPHFGD
KETLKTLVKRCKEKGIRVMIDAVFNHCYEFAPFQDVLKNGAASRYKDWFHIREFPLQTEPRPNYDTFAVPHMPKLNTAHPEVKRYLLDVATYWIR
EFDIDGWRLDVAEIDHQFWREFRQAVKALKPDVYILGEIWHDAMPWLRGDQFDAVMNYPLADAALRFFAKEDMSASEFADRLMHVLHSYPKQ
VNEAAFNLLGSHDTPRLLTVCGGDVRKVKLLFLQLTFTGSPCIYYGDEIGMTGGNDPECRKCMVWDPEKQNKELYEHVKQLIALRKQYRALRR

>d1bvza3 c.1.8.1 (A:121-502) Maltogenic amylase, central domain {Thermoactinomyces vulgaris, TVAII}

VFTTPEWAKEAVIYQIFPERFANGDPSNDPPGTEQWAKDARPRHDSFYGGDLKGVIDRLPYLEELGVITALYFTPIFASPSHHKYDTADYLAIIDPQFGDL
PTFRRILVDEAHRRGIKIILDAVFNHAGDQFFAFRDVLQKGEOQSRYKDWFIEDFPVSCTSRTNYETFAVQVPAMPKLRLENPEVKYLFDFVARFWME
QGIDGWRLDVANEVDHFWRFRRLVKSLSNPDALIVEIWHASGWLMDQFDVMNYLFRESVIRFFATGEIHAERFDAELTRARMILYPEQAA
QGLWNLLSDSHTERFLTSCGGNEAKFRLAVLFQMITYLGTLIYYGDEIGMAGATDPDCRRPMIWEKEQNRLFFEFYKELIRLRHRLASLTR
>d1eh9a3 c.1.8.1 (A:91-490) Glycosyltrehalose trehalohydrolase, central domain {Archaeon Sulfolobus solfataricus, km1}
FNNETFLKKEDLIYEIHVGFTPEGTFEGVIRKLDYLKDLGITAEIMPIAQFPGKRDWGYDGVLVYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYN
HVGPEGNYMVKLPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVNEYWIKEYNVDGFRDAVHAIIDTSPKHILEEIADVHHKYNRIVIAESDLNDP
RVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYYTDFGNLDDIVKSYKDVFVYDGKYSNFRKTHGEPVGELDCNFVVIQNHQDQVGNRGK
GERIIKLVDRSHEYKIAAAALYLLSPYIPMFMGEEYGEENPFFSDSKLIQGVREGRKKENGQDTPQDESTFNASKLSWKIDEEIFSFKILKMRKE
LSIA
>d1bf2_3 c.1.8.1 (163-637) Isoamylase, central domain {Pseudomonas amylofera}

PSTQSTGTKPTRAQKDDVIYEHVVRGFTEQDTSIPAQRGTYYAGLKASYLASLGVTAVEFLPVQETQNDANDVVPNSDANQNYWGYMTENYFS
PDRRYAYNKAAGGPTAEFQAMVQAFHNAGIKVYMDVYVNHATAEGGTWTSSDPTTATIYSWRGLDNATYYELTSGNQYFYDNTGIGANFNTYNTV
AQNLIVDSLWANTMGVDGFRFDLASVGNCLNGAYTASAPNCPNGYNFDAADSVAIRLREFTVRAAGGSDLFAEPWAIGGNSYQL
GGFPQGWSEWNGLFRDSLROAQNELGSMTIYVTQDANDFGSSNLFQSSGRSPWNSINFIDVHDGMTLKVYSCNGANNSQAWPYGPSDGGT
STNYSWDQGMSAGTGAAVDQRRAARTGMAFEMISAGTPLMQGGDEYLRTLQCNNAYNLDSSANWLTSWTTDQSNFTFAQRLIAFRKAHP
ALRPSSW
>d1gcy2 c.1.8.1 (A:1-357) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase) {Pseudomonas stutzeri}
DQAGKSPNAVRYHGGDEIILQGFHWNVVREAPNDWYNILRQQATIAADGFSAIWMPVPWRDFSSWSDGSKSGGGEGYFWHDFNKNGRYGS
DAQLRQAASALGGAGVKLYDVVPNHNMRGYPDKEINLPAGQGFWRNDCADPGNYPNDCDDGDRFIGGDADLNTGHPQVYGMFRDEFTNLRS
QYGAGGFRDFVRYAPERVNSWMTSDADNSFCVGELWKGPEYPNWDWRNTASWQQIKDWSRAKCPVFDFALKERMQNGSIADWKHGL
NGNPDPWRWREVAVTFVDNHDTGYSPGQNGGQHHWALQDGLIRQAYAILTSPGTPVYWDHMYDWGYGDFIRQLIQVRRAAGV
>d1avaa2 c.1.8.1 (A:1-346) Plant alpha-amylase {Barley (*Hordeum vulgare*), seeds, AMY2 isozyme}
QVLFQGFNWESWKHNGGWYNFLMGKVDDIAAGITHVWLPPASQVAEQGQMPGRYLDLASKYGNKAQLSLIGALHGKGVKAIADIVINHRT
AEHKDGRGIYCIFEGGTPDARLDWGPHMICRDDRPyADGTGPNPTGADFGAAPDIDHNLRLVQKELVEWLNLKADIGFDGWRDFAKGYSADV
AKIYIDRSEPSFAVEIWTSLAYGGDGKPNLNQDQRQELVNWDVKVGGKGPATTFDFTKGILNVAVEGELWRLRGTDGKAPGMIGWWPAKAVT
FVDNHDTGSTQHMWPFPNSDRVMQGYAYILTHPGTPCIFYDHFFDWGLKEEIDRLSVRTRHGI
>d1uok_2 c.1.8.1 (1-479) Oligo-1,6, glucosidase {Bacillus cereus}
MEKQWWKESVVYQIYPRSFMDNSGDGIGDLRGIIKLDYLKELGIDVIWLSPEVYESPNDDNGYDISDYCKIMNEFGTMEDWDELLHEMHERNMKL
MMDLVNVNHTSDEHNWFIESRKSKDNYKRDYYIWRPGKEGKEPNNWGAAGSGSAWQYDEMTDEYLYHLFSKKQPDLNWDNEKVRQDVYEMMK
FWLEKGIDGFRMDVINFISKEEGLPTVETEEGYVSGHKHFMNGPNIIKYLHEMNEEVLSHYDIMTVGEMPGVTTEEAKLYTGEERKELOQMVFQFE
HMQLDSGEGGKWDVVKPCSLTLKENLTWKQKALEHTGWNSLYWNNHDQPRVVSFRGNDGMYRIESAKMLATVLHMMKGTPYIYQGEEIGMTN
VRFESIDEYRDIETLNMYKEKVMERGEDIEKVMQSIYIKGRDNARTPMQWDDQNHAFFTGEPWITVNPNEYKEINVKQAIQNKSIFYYYKKLIELR
KNNEIVVY
>d1g5aa2 c.1.8.1 (A:1-554) Amylosucrase {Neisseria polysaccharea}
SPNSQYLKTRILDIYTPEQRAGIEKSEDWRQFSRRMDTHFPKLMNELDHSVGNNEALLPMLEMILLAQAWQSYQRNSSLKDIDIARENNDWILSN
KQVGGVCYVDLFAGDLGKLDKIPYFQELGLTYLHLMPLFKCPEGKSDGGYAVSSYRDVNPALGTIGDLREVIALHEAGISAVVDFIFNHTSNEHEWA
QRCAAGDPLFDNFYYIFPDRRMPDQYDRTLREIFPDQHPGGFSQLEDGRVVWTTFSFQWDLNYSNPWVFRAMAGEMLFLANLGVDILRMDA
VAFIWQMGTSCENLPOQAHALIRAFNAVMRIAAPAVFKSEAIVHPDQVQVYIGQDECQIGYNPLQMAXLWNTLATREVNLLHQALTYRHNLPEHT
AWVNYVRSHDDIGWTFADEADAAYLGISGYDHRQFLNRFFVNRFDGSFARGVPFQYNPSTGDCRVSGTAAALVGLAQQDDPHAVDRKLSSIALSTG
GLPLIYLGDEVGTLNDDWSQDSNKSDDSRWAHRPRYNEALYAQRNDPSTAAGQIYQDLRHMIAVRQSNPRFDGG
>d1eswa_c.1.8.1 (A:) Amylomaltase MalQ {Thermus aquaticus}
MELPRAFGLLLHPTSLPGPYGVGVLGREARDFLRLKEAGGRYWQVPLGPTGYGDSPYQSFSAFAGNPYLIIDLRPLAERGYVRLEDPGFPQGRVDF
GLLYAWKWPALKEAERGFKEKASPEEREAFAREREAWWLEDYALFMALKGAGGLPWRPLRKREEKALREAKSALAEVAFAHTQWLF

FRQWGALKAEAEALGIRIIGDMPIFVAEDSAEVWAHPEWFHLDEEGRPTVAGVPPDYFSETGQRWGNPLRYWDVLEREGFSWIRRLEKALELFH
LVRIDHFRGFEAYWEIPASCPAVEGRWKAPGEKLQKIQEVFGEPVLAEDLGVTPEVEALRDRGLPGMKVLQAFDDGMENPFLPHNYPAHG
RVVVYTGTHDNDTTLGWYRTATPHEAKFMARYLADWGITFREEEEVPWALMHLGMKSVARLAVPVQDVLAGSEARMNYPGRPSGNWAWRL
LPGELSPEH GARL RAMA EATERL

>d1byb__ c.1.8.2 (-) beta-Amylase {Soybean (Glycine max)}

SNMLLNYPVYVMLPLGVNVNDNVFEDPDGLKEQLLQLRAAGVDGMVVDVWWGIIELGPKQYDWRAYRSFLQLVQECGLTLQAIMSFHQCGG
NVGDIVNIPIPQWVLDIGESNHDIFYTNRSGTRNKEYLTVGVDNEPIFHGRTAIEIYSDYMSFRENMSDFLESGLIIDIEVGLGPAGELRYPSPQSQG
WEFPRIGEFQCYDKYLKADFKAavaraghPEWLPDDAGKYNDVPESTGFFKSNGTYVTEKGKFFLTWYSNKLLNHGDQILDEANKAFLGCKVKLAI
KVSGIHWWYKVENHAAELTAGYYNLNDRDGYRPIARMLSRHHAILNFTCLEMRDSEQPSDAKSGPQELVQQVLSGGWREDIRVAGENALPRYDAT
AYNQIILNAKPQGVNNNGPPKLSMFGVTYRLSDDLLQKSNFNIFKKFVLKMADQDYCANPQKYNHAITPLKPSAPKIPIEVLEATKPTLPFWLP
ETDMKVDG

>d1b1ya__ c.1.8.2 (A:) beta-Amylase {Barley (Hordeum vulgare)}

MKGNYVQVYVMLPLDAVSVNNRFEKGDELRAQLRKLVAGVDGMVVDVWWGLVEKGPKAYDWSAYKQLFELVQKAGLKQAIMSFHQCGG
VGDAVNIPIPQWVRDVGTRPDIFYTDGHGTRNIEYLTGVDNQPLFHGRSAVQMYADYMTSFRENMKDFLDAGVIVDIEVGLGPAGELRYPSPQ
SHGWSFPGIGEFICYDKYLQADFKAaaaAVGHPEWFPNDAGQYNDTPERTQFFRDNQTYLSEKGRFFLAWYSNNLKHGDRILDEANKVFLGYKV
QLAIKIAGHWYVYKVPShAAELTAGYYNLHDRVGYRTIARMLKRHRASINFCAEMRDSEQPPDAMSAPEELVQQVLSAGWREGLNVSCENALP
RYDPTAYNTILRNARPHGINQSGPPEHKLFGFTYRLSNQLVEGQNYVNFKTFVDRMHANLPRDPYVDPMAPLPRSGPEISIEMILQAAQPKIQPFP
FQEHTDLPVGPTGGMGGQAEGPTCG

>d1fa2a__ c.1.8.2 (A:) beta-Amylase {Sweet potato (Ipomoea batatas)}

APIPGVMPIGNYVSLYVMLPLGVVNADNVFPDKEKVEDELKQVKAGGCDGMVVDVWWGIIAKGPQYDWSAYREFQLVKKGLKIQAIMSFH
QCGGNVGDADVFIPIPQWILQIGDKNPDIFYTNRAGNRNQEYLSGVDNQRLFQGRTALEMYRDFMESFRDNMADFLKAGDIVDIEVCGAAGELR
YPSYPETQGWVFPGIGEFQCYDKYMADWKEAVKQAGNADWEMPGKAGTYNDTPDKTEFFRPNGTYKTDMGKFFLTWYSNKLIHGDRQVLEE
ANKVFGLRVNIAAKVSGIHWWYVNVSHAAELTAGFYNVAGRDIYRPIARMLARHHATLNFTCLEMRDSEQPAEAKSAPQELVQQVLSGGWKEYI
DVAGENALPRYDATAVNQCMLLKLRPNGVNLNGPPKLMMSGTLYRLSDDLLQTDNFELKKFVKKMHADLDPSPNAISPAVLERNSAITDELMEAT
KGSRPFPWYDVTDMPVDGSNPF

>d1b9za2 c.1.8.2 (A:1-417) Bacterial beta-amylase, catalytic domain {Bacillus cereus}

AVNGKGMPDYKAYLMAPLKKIPEVTNWTFENDLRWAKQNGFYAITVDFWWGDMEKNGDQQFDSYAQRFQSVKNAGMKMIPISTHQCG
GNVGDCCNVPIPSWWNQKSDDSYLFKSETGTVNKTLNPLASDVIRKEYGELYTAFAAAAMPKVDIAKIYLSGGPAGELRYPSTTSQDTGYPYRG
KFQAYTEFAKSFKRLWVLNKY GSLNEVNKA WGTKLISELAI LPPSDGEQFLMNGYLSMYGDYLEWYQGILENHTKLIGELAHNAFDTTFQVPIGAKI
AGVHWQYNNPTIPHGAEPKAGYNDYSHLLAFKSAKLDVFTCLEMDKGSPYEYSMPKTLVQNIATLANEKGIVLNGENALSIGNEEYKRAEMA
FNYNFAGFTLLRYQDVMYNNSLMGKFKDLLGV

>d1xyza__ c.1.8.3 (A:) Xylanase {Clostridium thermocellum, XynZ}

NALRDYAEARGIKIGTCVNYPFYNNSDPTYNSILQREFSMVVCENEMKFDALQPRQNVFDFSKGDQLLAERNGMQMRGHTLIWHNQNPSWLT
NGNWNRDSLAVMKNHITTVMTHYKGKIVEWDVANECEMDDSGNGLRSSIWRNVQGDYLDYAFRYAREADPDALLFYNDYNIEDLGPKSNAVF
MIKSMKERGVPIDGVGFQCHFINGMSPEYLASIDQNIKRYAEIGVIVSFTEDIRIPQSENPATAFQVQANNYKELMKICLANPNCNTFVMWGFTDKY
TWIPGTFPGYGNPLIYDSNNYNPKPAYNAIKEALM

>d1hiza__ c.1.8.3 (A:) Xylanase {Bacillus stearothermophilus, Xt6}

SYAKKPHISALNAPQLDQRKYNEFTIGAAVEPYQLQNEKDVQMLKRHFNSIVAENVMKPISIQPEEGKFNFQADRVKFAKANGMDIRFHTLVWHS
QVPQWFFLDKEGKPMVNEDPVPKREQNKQLLKRLETHIKTIVERYKDDIKYWDVNEVGDDGKLRNSPQYQJAGIDYIKVAFQAARKYGGDN
LYMNDYNTVEPKRTALYNLVQLKEEGVPIDGIGHQSHIQGWPSEAEIEKTINMFAALGLDNQITELDVSMYGWPPRAYPTYDAIPKQKFLDQAAR
YDRLFKLYEKLSDKISNVTFWGIADNHTWLDSRADVYYDANGNVVDPNAPYAKVEKGKGKDAPFVFGPDYKVKPAYWAIIDHK

>d1bg4__ c.1.8.3 (-) Xylanase {Penicillium simplicissimum}

EASVSIDAKFKAHGKKYLIGDQYTLTKNTKNPAAIKADFGQLTPENSMKWDATEPNRGQFTFSGSDYLVNFAQSNGKLIRGHTLVWHSQPGW
SITDKNTLISVLKNHITTVMTRYKGKIYAWDVLNEIFNEDGSLRNSVFYNVIGEDYVRIAFETARSVDNAKLYINDNLDAGYSKVNGMVSHVKKWL

AAGIPIDGIGSQTHLGAGAGSAVAGALNALASAGTKEIAITELDIAGASSTDYVVNVNACLNQAKCVGITVWGVADPDSWRSSSPLFDGNYNPKA

AYNAIANAL

>d1edg__ c.1.8.3 (-) Endoglucanase CelA {Clostridium cellulolyticum}

MYDASLIPNLQIPQKNIPNNNDGMNFVKGLRGWNLGNTFDAFNGTNITNELDYETWSGIKTTKQMIDAIKQKGNTVRIPVSWHPHVSGSDYKIS
DVWMNRVQEVVNYCIDNKMYVILNTHHDVDKVKGYFPSSQYMASSKKYITSVWAQIAARFANYDEHLEFGMNEPRLVGHANEWWPELNSDV
VDSINCINQLNQDFVNTRATGGKNASRYLMCPGYVASPDGATNDYFRMPNDISGNNNKIIIVSVHAYCPWNFLAGAMADGGTNAWNINDSKQ
SEVTWFMDNIYNKYTSRGIPVIIGECGAVDKNNLKTRVEYMSYYVAQAKARGILCILWDNNNFSGTGEFFDRSCQFKFPEIIDGMVKAFLIN

>d1ceo__ c.1.8.3 (-) Endoglucanase CelC {Clostridium thermocellum}

MVSFKAGINLGGWISQYQVFSKEHFDTFITEKDIETIAEAGFDHVRLPDFDPIIESDDNVGEYKEDGLSYIDRCLEWCKYKLNGLVLDMHAPGYRFQ
DFKTSTLFEDPNQQKRFVDIWRFLAKRYINEREHIAFELLNQVVEPDSTRWNKLMLECIKAIREIDSTMWLIGGNNYNSPDELKNLADIDDDYIVYN
HFYFNPFHTHQKAHWSAMAYNRTVKYPGQYEGIEEFVKNNPKYSFMMELNNLKLNLKELLRKDLKPAIEFREKKCKLYCGEFGVIAADLESRIK
WHEDYISLEEVYDIGGAVVNYKKMDFEIYNEDRKPVSQELVNILAR

>d1cz1a_c.1.8.3 (A:) Exo-beta-(1,3)-glucanase {Yeast (Candida albicans)}

AWDYDNNVIRGVNLGGWFVLEPYMTPSLFEPFQNGNDQSGVPVDEYHWTQTLGKEAALRILOKHWSTWITEQDFKQISNLGLNFVRIPIGYWAF
QLLDNDPYVQGQVQYLEKALGWARKNNIRVWIDLHGAPGSQNGFDNSGLRDSYNFQNGDNTQVTNLVNTIFKKYGGNEYSDVVGIELLNEPLG
PVLNMDKLKQFFLDGYNSLRQTGSVTPVIIHDAFQVFQVFGWNNFLTVAEQGQWNVVDDHHHYQVFSGGELSRNINDHISVACNWGDAKKESHW
NVAGEWSAALTDCAKWLNQVNREGARYEGADNAPYIGSCQPLDISQWSDEHTDTRRYIEAQLDAFEYTGGWVFWSWKTEAPEWSFQTLTY
NGLFPQPVTDRQFPNQCGFH

>d1ece_a_c.1.8.3 (A:) Endocellulase E1 {Acidothermus cellulolyticus}

AGGGYWHTSGREILDANNVPVRIAGINWFGFTCNYVHGLWSRDYRSMLDQIKSLGYNTIRLPYSSDILKPGTMPPNSINFYQMNQDLQGLTLSQ
VMDKIVAYAGQIGLIILDRHRPDCSGQSALWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEPHDPACWGCGDPSIDWRLAAERAGNAVLS
VNPNLLIFVEGVQSYNGDSYWWGGNLQGAGQYPVVLNPNRVYSAHDYATSVYQPTWFSDPFPNNMPGIWNKNWGYLFNQNIAPVWLGEF
GTTLQSTTDQTWLKTLVQYLRTAQYGADSFQWTFWSWPDSGDTGGILKDDWQTVDTVKDGYLAPIKSSIFDPV

>d7a3ha_c.1.8.3 (A:) Endoglucanase Cel5a {Bacillus agaradhaerens}

SVVEEHGQLSISNGELVNERGEQVQLGMSSHGLQWYQFVNYESMKWLRDDWGINFRAAMYTSSGGYIDDPVKEKVKEAVEAAIDLDIYVII
DWHILSDNDPNIYKEEAKDFFDEMSELYGDYPNVIYEIANEPNGSDVTWGNQIKPYAEVPIIRNNDPNNIIIVGTGTWSQDVHHAADNQLADPN
VMYAFHFYAGTHGQNLRDQVYALDQGAAIFVSEWGTSAATGDGGVFLDEAQVWIDFMDERNLSWANWSLHKDESSAALMPGANPTGGWT
EAELSPSGTFVREKIRES

>d1egza_c.1.8.3 (A:) Endoglucanase Cel5a {Erwinia chrysanthemi}

SVEPLSVNGNKIYAGEKAKSFAGNSLFWSNNGWGEKFYADTVASLKKDWKSSIVRAAMGVQESGGYLQDPAGNIKAKVERVDAAIANDMYAII
GWHSHSAENNREAIRFFQEMARKYGNKPNVIYEIYNEPLQVWSNTIKPYAEAVISAIRAIIDPDNLIVGTPSWSQNVDEASRDPINAKNIAYLHFY
AGTHGESLRNKRQALNNINGIALFTEWGTVNADGNGGVNQTETDAWVTFMRDNNISNANWALNDKNEGASTYYPDSKNLTESGKKVKSIIQSW
PYKA

>d1g0ca_c.1.8.3 (A:) Alkaline cellulase K catalytic domain {Bacillus sp.}

PAGMQAVKSPSEAGALQLVELNGQLTLAGEDGTPVQLRGMSTHGLQWFGEIVNENAFVALSNDWGSNMIRLAMYIGENGYATNPEVKDLVYEGI
ELAFEHDMYVIVDWHVHAPGDPRADVSGAYDFFEEIADHYKDHPKHNHYIIWELANEPEPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGD
NMILVGNPNWSQRPDLSADNPIDAENIMYSVHFYTGSHGASHIGYPEGTSSERSNVMANVRYALDNGVAVFATEWGTQSANGDGGPYFDEAD
VWLNFLNKHNIWANWSLTNKNEISGAFTPFLGRDTDLDPGANQVWAEELSLSGEYVRARIKGIEYTPIDRTK

>d1bqca_c.1.8.3 (A:) Beta-mannanase {Thermomonospora fusca}

ATGLHVKNGRILYEANGQEIFIIRGVSHPHNWYPQHTQAFADIKSHTGANTVRVVLNGVRWSKNGPSDVANVISLCKQNRLICMLEVHDTTGGEQS
GASTLDQAVDYWIELKSVLQGEEDYVLINIGNEPYGNDSATVAAWATDTSAIQLRRAAGFEHTLVVDAPNWGQDWNTMRNNADQVYASDPT
GNTVFSIHMYGVYVQCASTSITYLEHFVNAGLPLIIGEFGHDHSMDNPDEDTIMAEAERLKLGYIGWSWSNGGGVEYLMVYNFDGDNLSPWGER
IFYGPNGIASTAKEAVIFG

>d1qnra_c.1.8.3 (A:) Beta-mannanase {Trichoderma reesei}

ASSFTISGTQFNIDGKVGYFAGTN CYWCSFLTNHADVDSTFSIHSSGLKVVRVWFNDVNTQPSPQIWFQKLSATGSTINTGADGLQTLDYVV
QSAEQHNKLIIIPVNNWSDYGGINAYVNAFGGNATTWYTNTAAQTQYRKYVQAVVSRYANSTAIFAWELGNEPRCNGCSTDVIVQWATSVSQYV
KSLSDNHLVTLGDEGLSTGDGAPTYGEGTDFAKNVQIKSLDFTFHLYPDSWGTNTWGNGWIQTHAAACLAAGKPCVFEEYGAQQNPCTN
EAPWQTTSLTRGMGGDMFWQWQGDTFANGAQNSNDPYTVWYNSSNWQCLVKNHVDAIN

>d1j9ya_c.1.8.3 (A:) Mannanase 26A {*Pseudomonas fluorescens*, subsp. *cellulosa*}

PTVVLVDSQATMETRSLFAFMQEQRHSIMFGHQHETTQGLTIRTDGTQSDTFNAVGDFAAVYGDTLSIVAPKAEGDIVAQVKKAYARGGIITV
SSHFDNPKTDTQKGVWPVGTSWDQTPAVVDSLPGGAYNPVNLNGYLDQVAEWANNLKEQGRILPIFRLYHENGTGSFWWWGDKQSTPEQYKQL
FRYSVEYL RDVKGVRFYAYSPNNFWDVTEANYLERYPGDEWVVLGFDTYGPVADNADWFRNVVANAALVARMAEARGKIPVISEIGIRAPDIE
AGLYDNQWYRKLSIGLKADPDAREIAFLVWRNAPQGVPGPNTQVPHWVPA NR PENINNGTLEDFQAFYADEFTA FN RDIEQVYQRPT

>d1ghsa_c.1.8.3 (A:) Plant beta-glucanases {*Barley (Hordeum vulgare)*, 1,3-beta-glucanase}

IGVCYGVIGNNLPSRSDDVQLYRSKGINGMRIYFADGQALSALRN SIGLILDIGNDQLANIAASTSNAASWVQNNVRPYYPAVNIKYIAAGNEVQG
GATQSILPAMRNLAALSAAGLGAIKVTSIRFDEVANSFPPSAGVFKNAYMTDVALLASTGAPLLANVVPYFAYRDNGPSISLN YATFQPGTTVRD
QNNGLTYSLF DAMVDAVYAALEKAGAPAVKVVSESGWPSAGGFAASAGNARTYNQGLINHVG GTPKKREALETYIFAMFNENQKTG D ATERS
FGLNPDKSPAYNIQF

>d1aq0a_c.1.8.3 (A:) Plant beta-glucanases {*Barley (Hordeum vulgare)*, 1,3-1,4-beta-glucanase}

IGVCYGM SANNLPAASTVSMFKSNGIKSMRLYAPNQAA LQAVGGTINVVVGAPNDVLSNLAAS PAAA ASWVKSNIQAYPKV SF RY VCGNEVA
GGATRNLV PAMKNVHG ALVAAGLGHIKVTTSVSQAILGVFSPPSAGSFTGEAA FMGPV VQFL ARTNAPLMANIYPYLA WAYNPSAMD MGYALF
NAS GTVVRD GAYQYQNLFDTTVDAFY TAMGKHGGSSV KLV VSE SGWPSGGTAAT PANARFYNQH LINHVG RT PRHPGAIETYIFAMFNENQK
DSGVEQN WGLF YPNMQHVYPINF

>d1jz8a5_c.1.8.3 (A:334-625) beta-Galactosidase, domain 3 {*Escherichia coli*}

EVRIENGLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRCSHYPNPLWYTLCDRYGLYVVDEANIETHGMVPMNRLT
DDPRWL PAMSERVTRMVQRDRNHP SIIWLSGNES GHGANHDALYR WIKS VDPSRPVQYEGGADTTATDIICPMYARVDEDQPFPAVPKWSIK
KWLSLPGETRPLILCQYAHAMGN SLGGFAKYWQAFRQYPRLOQGFVWDWV DQSLIKYDEN GPW SAYGGDFGDT PNDRQFCMNGLV FADRTP
HPALTEAKHQ QQ

>d1bhga3_c.1.8.3 (A:329-632) beta-Glucuronidase, domain 3 {*Human (Homo sapiens)*}

VAVTKSQFLINGKPFYFHGVNKHEDADIRGKGF DWPLLV KDFNLLRW LGANA FR TS HYPYAE EVMQM CDRY GIVV IDECPGV GLAL PQFFNNVSLH
HHMQVME EVVRRDKNHPAV VMWSVANE PASHLESAGY YLKM VIA HTKSLDPSRPVTFVS NSNYA ADKGAP YVDV ICLNSYY SWYHDY GHLEIQL
QLATQFENWYKKYQKPIQSE YGAETIAGFH QDPPLMFTEEYQKS LEQYH LGDQ KRR KYV VGE LIWN FADFM TEQSPTRVL GNKK GIFT RQPK
SAAFL RERYW KIANE

>d1e0wa_c.1.8.3 (A:) Xylanase A, catalytic core {*Streptomyces lividans*}

AESTLGAAA AQS GRYFG TAIAS GR LS DSTY TSIA GREF NMVTA ENEM KIDATE PQR GQNF SSADR VY NWAV QNG KQ VRG HTL AW HSQQ PGWM
QSLSGS ALRQ AMIDH INGVM AHYKG KIVQ WD VV NEA FDG SSGARR DS NLQR SGND WIEA FR TARA ADPSA KLCY NDY N VEN WT WAKT QAM
YNMVRDFK QRG VP IDC VGF QSH FN SGSPY NSN FRT LQ NF AALG DV AITE LDI QG A PAST YAN VT ND CLA VS RCL GIT VV GVRD SD SWR SE QTPL
LFN ND GS KKA YT AV L D AL NG

>d1clxa_c.1.8.3 (A:) Xylanase A, catalytic core {*Pseudomonas fluorescens*}

GLASLADFP IGVAVA ASGGNAD IF TSS ARQ NIVRAE FN QITA ENIM KMSYM SGNS FTNS DR LV SWAA QNG QTV HG HALVW HPSY QLP NWAS
DSN ANFR QDFAR HIDT VAA HFAG QV KS WDV VNE ALFD SADD PDGR GSANG YR QSVF YR QFGG PEYIDEA RR RAA ADPTA ELYY NDFN TE ENGA
KTT ALVN LVQ RL NNNG VP IDGV GFQ MVM ND YPSI AN IRQ AM QK IVAL SPTL KIKI TE LDV RL NN PYDG NSS ND YTR RN DC AVSCA GLDR QKARYK
EIV QAY LEV VPPG RRG GITV VV GIAD PDSW LYTHQ NLPD WPLL FND NLQ PKP AYQ GV VE ALS

>d1fxma_c.1.8.3 (A:) Xylanase A, catalytic core {*Thermoascus aurantiacus*}

QAAQSV DQLIK ARGK VYFG VATD QNRL TTGK NAA II QAD FGQ VTPEN SMK WDATE PSQ GN FNF AGAD YLV NW AQQ NGK LIRG HTL VWH SQLPS
WV SSI TD KNTL NV MKN HITT LMTRY KG KIR AW DV VNE AFN EDG S L RQ TVFL N VIG EYIPIA F QTARA ADP NAK LYI NDY N L DSAS YPK TQA IV NR
VKQW RAAG VPI D GIG SQ THLS AGQ GAG VL QAL PLLA SAGT P EVA IT EL DVAG ASPTD YV NVV NA CLNV QSC VGI TVW GVA DPDS WRAS TPL LF
GNF NP KPA YNA I VQDLQ

>d1tux__ c.1.8.3 (-) Xylanase A, catalytic core {Thermoascus aurantiacus}

AAAQSVDQLIDARGKVFVATDQNRLTGKNAAIIQADFGQVTPENS MKWDATEPSQGNFNAGADYL VNWAQQNGKLIRGHTLVWHSQLPS
WVVSITDKNTLNVMKNHITTIMTRYIGKIRAWDVVNEAFNEDGSLRQTVFNNVIGEDIPIA FR TARAADPNAKLYINDYNLDSASKPKTSAIVKRV
KKWRAAGVPIDGIGSQTHLSAGQQGASIDAALPNLASAGTPEVAITELDIAGATSTDYDVVNACLDVDCIGITVVGVADPDSWRASTTPLFDGNF
NPKPAYNAIVQLL

>d1xyfa2 c.1.8.3 (A:1-303) Xylanase A, catalytic core {Streptomyces olivaceoviridis}

AESTLGAAAQS GR YFGTAIASGKLGDSAYTTIASREFNMVTAENEMKIDATEPQRGQFNFSAGDRV YNWA VQNGKQVRGHTLAWHSQQPGW
MQSLSGSTLRQAMIDHINGVMGHYKGKIAQWDVVNEAFSDDGSGRRDSNLQRTGNDWIEVAFR TARAADPAAKLCYNDYNIENWTWAKTQG
VYNMVRDFKQRGVPI D C VGFQSHFNNSGP YNSNFRTTLQNFAALGV DVAITELDI QGASSSTYAA VTNDCLAVSRCLGITVWGVRDTSWRSGDTP
LLFNGDGSKKAAYTAVLNALNGG

>d1fh9a_ c.1.8.3 (A:) Xylanase A, catalytic core {Cellulomonas fimi}

ATTLK EADGAGRDFGFLDPNRLSEAQYKAIADSEFNLVVAENAMKW DATEPSQNSFSFGAGDRV ASYAADTGKELYGHTLVWHSQLPDWAKNL
NGSAFESAMVN HVTKVADHFEGKVASWDVVNEAFADGGGRQDSAFQQKLNGNYIETAFRAARAADPTAKLCINDYNVEGINAKNSLYDLVKDF
KARGVPLDCVGFQSHLIVGQVPGDFRQNLQRFADLGVDVRITELDIRMRTPSDATKL ATQAADYKKV VQACMVTRCQGVTVWGITDKYSWVPD
VFPGE GAALVW DASYAKPKAYA VMEAF

>d1e4mm_ c.1.8.4 (M:) Plant beta-glucosidase (myrosinase) {White mustard (Sinapis alba)}

EITCQENLPFTCGNTDALSSSFSSDFIFGVASSAYQIEGTIGRGLNIW DG FTH RYPNKGSPDH GNGDTCDFSYWQKDIDVLDELNATGYRFSIAW
SRIIPRGKRSRGNVEKGIDYYHGLISGLIKKGITPFVTLFHWDLPQTLQDYEFGFLDPQI DDFKD YADLCFEFGDSV KYWLTI NQLYSPTRGYSALD
APGRCSPTVDPSCYAGNSSTEPYIAHHQLLAHAKVVDLYRKNYTHQGGKIGPTMITRWFLPYNDTRHSIAATERMKEFFLGWMGPLNTGTYPQ
IMIDTVGERLPSFSPEE SNLVKGSDFLGLNYYFTQYAQPSPNPVN STNHTAMMDAGAKLT INASGHYIGPLFEKDKADSTDNI YYYYPKGIYSVMDYF
KNKYYNPLIYTENGISTPGDENRNQSMLDYTRIDYLC SHLCFLNKVIKEKD VNVKG YLA WALGD NYEFNKGFTVRG LSYIDWNNVTDRDLKSGQ
WYQSFISP

>d1cbg_ c.1.8.4 (-) Plant beta-glucosidase (myrosinase) {Creeping white clover (Trifolium repens)}

FKPLPISFDDFSDLNRSCFAPGV FGTASSAFQYEGA AFEDGKGPSI WDTFTH KYPEKIKD RTNGDVA IDEYHRYKEDIGIMKDMNLDAYRFSISWPRV
LPKGKLSGGVNREGINYNNLINEVLANGM QPYVTLFHW DVPQALEDEYRGFLGRNIVDDFRDYAE LCFKEFGDRV KH WITLNEPWGVSMNAYAY
GTFAPGRCS DWLKLNC TGGDSGREPYLA AHYQLLA AAAAR LYKTKYQASQNGIIGITLVSHWFEPASKEKADVDAKRG LD FMLGWF MHPLTKG
RYPESMRYLVRKRLPKFSTEESKELTGSFDFLGLNYYSSYYAKA PRIPNARPAIQTD SLINATFEHNGKPLGPMAASSWLCIYPQGIRKLLYVKNHY
NPVIIYITENG RNEFDPTLSLQESLLDTPRIDYYRHLYYVLT AIGDGVNVKG YFAWSLFDNMEWDSGYTVRFG LVFDKNNLKRHPKLSAHWFKS
LKK

>d1e55a_ c.1.8.4 (A:) Plant beta-glucosidase (myrosinase) {Maize (Zea mays), zmg lu1}

VQMLSPSEIPQRDWFPS DFTFGAAT SAYQIEGA WNEDGKGESNWDHFCHNHPERILDGSNSD I GANSYHMYKTDVRLKEMGM DAYRFSISWPR
ILPKGTKEGGINPDG IKYRN LINLLENGIEPYVTIFHW DVPQALEEKYGGFLDKSHKSIVEDYTFAKVCFDNFGDKVKNWLTFNDPQTFSY GTG
VFAPGRCS PGLCAYPTGNSLVEPYTAGHNILLAHAEAVDLYNKHYK RDDTRIGLA FDMGRV PYG TSFLDKQAEERSWDINLGWFLEPVVRGDYPF
SMRS LARERLPFFKDEQKEKLAGSYNMLGNYY TSFS KNIDIS PNYS PVLNT DDAYASQEVNGPDG KPIGPPMGNPWIY MPEGLK DLMIMK NK
YGNPPIYITENGIGDVDTKETPLPMEA ALNDYKRLD YIQRHIA TLKESIDL GS NVQGYFAWSL DNFEW FAGFTERYGIVYVDRNNNCTRYM KESAK
WLKEFNTA

>d1pbga_ c.1.8.4 (A:) 6-phospho-beta-D-galactosidase, PGAL {Lactococcus lactis}

MTKTLKDFIFGGATAAYQAE GATHDGKGPV AW DKYLED NYWYTAEPASDFYHK YPV DLEA EYGVNGIRISIAWSRIFPTGYGEVNEKGVEFYHK
LFAECHKRHVEPFVTLHHFDTPEALHSNGDFLNRENIEHFIDYAAFC FEEFPEV NYWTTFNEIGPIGDQYLVGF PPPGIKYDLAKVFO SHHNMMV
HARAVKLYKDKGYKGEIGVVHALPTKPYDPENP ADVRAAELEDIIH NKFI DAT LGHYS DKTMEGVN HILAENG GEL DRDEF QALDA AKD LND
LGINYYMSDW MQAFDGETEIIHNGKGEKGSSKYQIKGVGR RVAPD YV PRTD WD WIYPEG LYDQIMRVKNDY PNYKKIYITEN GLGYKDEF DVNT
YDDGRIDYVQKHL E VLS DAIADGANVKG YFIW SLM DFV FS WSNG YEK RYGLF VDF DTQ ERYPK KSAH WYKK LAET QVIE

>d1e4ia_ c.1.8.4 (A:) Beta-glucosidase A {Bacillus polymyxa}

TIFQFPQDFMWG TATAAYQIEGAYQEDGRGLSIWDTFAHTPGKV FNGDNGNVACDSYHRYEEDIRLMKELGIR TYRFSV SWPRIFPNGDGEV NQK

GLDYYHRVVDLLNDNGIEPFCTLYHWDLQPALQDAGGWGNRRTIQAFVQFAETMFREFHGKIQHWLTFNEPWCIASLSNMLGVHAPGLTNLQTAIDVGHHLLVAHGLSVRRFRELGTSGQIGIAPNVSAVPYSTSEEDKAACARTISLHSDWFLQPIYQGSYPQFLWDFAEQGATVPIQDGDMIDIIGEPIDMIGINYYSMSVNRFNPEAGFLQSEEINMGLPVTIDGPVESPRLYEVHLQKYGNIDYITENGACINDEVNGKVQDDRRISYMQQHLVQVHRTIHDLHVKGYMAWSLLDNFEWAEGYNMRFGMIHVDFRTQVRTPKQSYYWYRNVVSNNWLETR

>d1qoxa_c.1.8.4 (A:) Beta-glucosidase A {Bacillus circulans, subsp. alkalophilus}

SIHMFPSDFKWGVATAAYQIEGAYNEDGRGMSIWDTFAHTPGKVNGDNGNVACDSYHRVEEDVQLKDLGVKVYRFSISWPRVLPGTGEVNRAGLDYYHRLVDELLANGIEPFCTLYHWDLQPALQDQGGWGSRITDAFAEYAEALMFKELGKIKQWITFNEPWCMALSNYLGVHAPGNKDLQLADVSHHLLVAHGRAVTLFRELGISGEIGIAPNTSWAVPYRTKEDMEACLRVNGWSGDWYLDPIYFGEYPKFMLDWYENLGYKPPIVGDMELIHQPIDFIGINYTTSSMNRYNPGEAGGMLSSEAISMGAPEKTDIGWEIYAEGLYDLLRTADKYGNPTLYITENGACYNDGLSLGRIHDQRRIDYLAHQLIASRAIEDGINLKGYMEWSLMDNFEWAEGYGMRFGLVHDYDTLVRTPKDSFYWKVVISRGWLDL

>d1gowa_c.1.8.4 (A:) beta-Glycosidase {Archaeon Sulfolobus solfataricus}

MYSPFPNSFRFGWSQAGFQSEMGTGSEDPTNDWYKVVHDPEVMAAGLVSGLPENGPYWNQYKTFHDNAQKMGLKIAIRLNSEWSRQFPNPLPRPQNFDISKDQDVTEVEINENELKRLDEYANKDALNHYREIFKDLKSRGLYFIQNMYHWPLPLWLHDPIRVRRGDFTGPSGLSTRTVYEFARFSAYTAWKFDDLVDESTMNEPNVVGGLGYVGKSGFPPGYLSFELSRRAMYNIIQAHARAYDGKSVSKPVGIIYANSSFQPLTDKDMEAVERMAENDNRWWFFDAIRGEITRGNEKIVRDDLKGRLDWIGVNYYTRTVKRTEKGYVSLGGYGHGCERNVSLAGLPTSDFGEFFPEGLYDVLTKYWNRYHLYMYVTENGIADDADYQRPYYLVSHVYQVHRAINSGADVRGYLHWSLADNYEWASGFSMRGFLKVDYNTKRLYWRPSALVYREIATNGAITDEIEHLNSVPPVKPLRH

>d1qvba_c.1.8.4 (A:) beta-Glycosidase {Archaeon Thermosphaera aggregans}

MKFPKDFMIGYSSPFQFEAGIPGSEDPTNSDWVWVWHDPEVTAAGLVSGLPENGPYWNLNQNDHDLAEKLGVNTIRVGVEWSRIFPKPTFNVKVPVERDENGSIVHVDVDDKAVERDELANEVNHVEMYKDWVERGRKLILNLHWPLPLWLHNPIVMRRMPDRAPSGWLNEESVVEFAKYAAIYIAWKGELPVMWSTMNEPNVVEQGYMFVKGGFPYLSLEAADKARRNMQIQAHAZADNIKRSKKPVGLIYAFQWFELLEGPAEVDFKFKSSKLYYFTDIVSKGSSIINVEYRRLANRLDWLGVNYYSLRVYKIVDDKPIILHGFLCPTGGISPANPCSDFGWEVYPEGLYLLKELYNRYGVDLIVTENGVSDSRDALRPAYLVS HVYVSVWKAANEGIPVKGVLHWSLTDNYEWAQGFRQKFGLVMVDFKTKKRYLRPSALVREIATHNGIPDELQHLTI

Q

>d2hvm_c.1.8.5 (-) Hevamine A (chitinase/lysozyme) {Para rubber tree (*Hevea brasiliensis*)}

GGIAIYWGQNGNEGTLTCSTRKSYVNVIAFLNKFGNGQTPQINLAGHCNPAAAGGCTIVSNGIRSCQIQGKVMILSLLGGGIGSYTLASQADAKNVADYLWNNFLGGKSSRPLGDAVLGIDFDEHGSTLYWDDLARYLSAYSQGKKVYLTAAPQCPFDRLGTALNTGLFDYVWVQFYNNPPCQYSSGNINNIINSWRWTT SINAGKIFLGLPAAPEAAGSGYVPPDVLSRILPEIKKSPKGVGGVMLWSKFYDDKNGYSSILDSV

>d1nar_c.1.8.5 (-) Seed storage protein {*Vicia narbonensis*, Narbonin}

PKP1FREYIGVKPNSTTLHDFPTEINTTLEFHYILGFIAIESYYESGKGKGTFFEWVDFELFGPEVKVNLKRRHPEVKVVISIGGRGVNTPFDPAEENVWVSNAKESLKLIIQKYSDDSGNLIDGIDIHYEHIRSDEPFATLMQLITEKKDDDLNINVVIAPSENNSHYQKLYNAKKDYINWVDYQFSNQQKPVSTDADFVEIFKSLEKDYHPHKVLPFGSTDPLDTKHKNKITRDIFIGGCTRLVQTFSLPGVFFWNANDSVIPKRDGDKPFIVELTQQLAA

>d1cnv_c.1.8.5 (-) Seed storage protein {Jack bean (*Canavalia ensiformis*), Concanavalin B}

DISSTEIAVYWGQREDGLLRLDTCKTNNYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPCSFLESQIKECRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVALDGIHFIDIQKPVDELNWDNLLEELYQIKDVFQSTFLSAAPGCLSPDEYLDNAIQTRHFDYIFVRFYNDRSCQYSTGNIQRIRNAWLTSWTKSVYPRDKNLFLELPASQATAPGGGYIPPSALIGQVLPYLPDLQTRYAGIALWNRQADKETGYSTNIIRYL

>d2ebn_c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {*Flavobacterium meningosepticum*, endoglycosidase F1}

TTKANIKLFSFTEVNDTNPNNLNFTLKNNSGKPLVDMVVLFSANINYDAANDKVFVSNNPNVQHLLNRAKYLKPLQDKGKIVLSQLNIDDDVSWQSSKPGGFASAA GSYDLATNYPGLAKSGMVMSQEFNQGRYATAQALRNIVTKGYGGHMFAMDPNRSNFTSGQLPALKIAKELYGDELVYSNTPYSKDW

>d1eoka_c.1.8.5 (A:) Endo-beta-N-acetylglucosaminidase {*Flavobacterium meningosepticum*, endoglycosidase F3}

NGVCIAYITDGRNPTFKLKDIPDKVDMVILFGKYWSLQDTTKLPGGTGMMGSFKSYKDLDTQIRSLQSRGIVKLQNIQDDVSWQSSKPGGFASAA AYGDAIKSIVDKWKLKGISLDIEHSGAKPNPIPTFGYATGYNGWYSGSMAATPAFLNVISELTKYFGTTAPNNKQLQIASGIDVYAWN KIMENFRNFNFIQLQSYGANVSRTQLMMNYATGTNKIPASKMVFAYAEGGTNQANDVEVAKWTPTQGAKGGMMIYTNSNVSYANAVRDAV

>d1edt__ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {Streptomyces plicatus, endoglycosidase H}
KQGPTSVAYVEVNNNSMLNVKYTLADGGGNAFDVAVIFAANINYDTGKTAYLHFNEVQRVLDNAVTQIRPLQQGIKVLLSVLGNHQGAGFA
NFPSSQAAASFAKQLSDAVAKYGLDGVDFDDEYAEGNNNTAQPNDSSFVHLVTALRANMPDKIISLYNGPAASRLSYGGVDVSDKFDYAWNPPY
GTWQVPGIALPKAQLSPAEEIGRTSRSTVADLARRTVDEGYGVLYTNLDGGRTADVSATRELYGSEAVRT

>d1edqa2 c.1.8.5 (A:133-443,A:517-563) Chitinase A, catalytic domain {Serratia marcescens}
TDGSHLAPLKEPLLEKNKPYKQNSGKVGSYFVEWGIVGRNFTVKIPAQNLTHLLYGFIPICGGNGINDSLKEIEGSFQALQRSCQGREDFKVSIHDP
FAALQKAQKGTAWDDPYKGNGFQLMALKQAHPDLKLPSIGGWTLSDPFFMGDKVKRDRFVGSKVEFLQTWKFFGVDIDWEFGGKGANP
NLGSPQDGTYVLLMKELRAMLDQLSVETGRKYELTS AISAGKDIDKVAVNVAQNSMDHIFLMSYDFYGAFLKNLGHQTALNAPAWKPDAYTT
VNGVNALLAQGVKPGKIVVGTAMXDAR SVQAKGKVLDKQLGLFSWEIDADNGDILNSMNASLGN SAGVQ

>d1goia2 c.1.8.5 (A:3-291,A:380-446) Chitinase B, catalytic domain {Serratia marcescens}
TRKAVIGYYFIPTNQINNYTETDTSVVPFPVSNITPAKAKQLTHINFSLDINSNLECAWDPATNDAKARDVVNRILTALKAHNPSLRIMFSIGGWWYNS
DLGVSHANYVNAVTPASRAKFAQSCVRIMKDYGFDGVNI DWEYPQAAEVDFGIAALQEIRTLNNQQTIDGRQALPYQLTIAGAGGAFFLSRYYSK
LAQIVAPLDYINLMTYDLAGPWEKVTNHQAALFGDAAGPTFYNALREANLGWSWEELTRA FSPFSLTVDAAVQQHLMMEGVPSAKIVMGVPFX
DDAESFKYKAKYIKQQQLGGVMFWHLGQDNRNGDLAALDRYFNAADYDDSQLDMGTGLRYTGPG
>d1d2ka1 c.1.8.5 (A:36-292,A:355-427) Chitinase 1 {Fungus (Coccidioides immitis)}
GGFRSVVYFVNWAIYGRGHNPQLKADQFTHILYAFANIRPSGEVYLSDTWADTDKHYPGDKWDEPGNNVYGC IKQMYLLKKNNRNLTLLSIGG
WTYSPNFKTPASTEEGRKKFADTSKLMKDLGFDGIDIDWEYPEDEKQANDFVLLKACREALDAYS AKHPNGKKFLTIASPAGPQNYNKLKLAEM
DKYLFWNLMAYDFSGSWDKVSGHMSNVFPSTTKPESTPFSSDKAVKD YIKAGVPANKIVLGMP LXDTV KIAGKKA EYITKNGMGGGMWWE SSS
DKTGNESLVGTVVNGGGTGKLEQRENELSYPESVYDNLKNGMPS

>d1e9la1 c.1.8.5 (A:22-266,A:337-393) Chitinase-like lectin ym1, saccharide binding domain {Mouse (Mus musculus)}
YQLMCYT SWAKDRPIEGSFKPGNIDPCLCTHILYAFAGMQNNEITYTHEQDLRDYEALNGLDKNT ELKTLLAIGGWKF G PAPFSAMVSTPQNRQI
FIQS VIRFLRQYNFDGLNL DWQY PGSRGSPPKDKHLFSVLKEMRKAFEEVES K DIPRLLLSTGAGI IDVIKSGYKIP ELSQSLDYIQVMTYDLHD PKD
GYTGENSP LYKSPY DIGKSADLN VDSIIS YWKDHGAASEK LIVGFPAXDNVR SFKLKAQWLKDNNL GGAVV WPLDMDDFSGSFCHQRHFPLSTLK
GDLN IHSAS

>d1jfxa_ c.1.8.8 (A:) Streptomyces lysozyme {Streptomyces coelicolor, "mueller" dsm3030}
DTSGVQGIDVSHWQGSINWSSVKSAGMSFAYIKATEG TNYKDDR FSANYTNAYNAGI IRGAYHFARPNASS GTAQADYFASNGGGWS RDNRTLPG
VLDIEHNPSGAMCYGLSTTQMRTWINDFHARYKARTTRDVVIYTTASWWNTCTGSWNGMAAKSPFWVAHWGVSA PTVPSGFPTWTFWQYSA
TRGVGGVSGD VDRNKFNGSAARLLALANNTA

>d1qba_3 c.1.8.6 (338-780) Bacterial chitobiase (beta-N-acetylhexosaminidase) {Serratia marcescens}
FPYRGIFLDVARNFHKKDAVLRLDQMAAYKLNKFHFHLSDDEGWR IEIPGLP E LTEL VGGQRCHDLSETTCLLPQYQGQPDVYGGFSRQDYIDIIKYA
QARQIEVIEIDMPA HARA AVVS M EARYKKLHAAGKEQEANE FRLV DPTDT SNTT SVQFFNRQSYLNPC LDSSQRF DVK VIGEIAQMHEAGQPIK
TWHFGGDEAKNIRLGAGYTDKAKPEPGKIIDQGNEDKPWAKSQVC QTMIKEG KVADMEH LPSYFG QEVSKLVKAHGIDRMQAWQDGLKDAES
SKAFATS RGVNFWD TLYWGGFDSVNDWANKGYEVV VSNP DYVYMDFPYEVNPDERGYYWGTRFS DERKVF SFAPDNMPQNAETSV DRDGNH
FNAKSDKPWP GAYGLSAQ LWSETQRTDPQMEYMFPR AL SVAERSWHRAGWEQDYRAGREYKG

>d1jaka1 c.1.8.6 (A:151-506) beta-N-acetylhexosaminidase {Streptomyces plicatus}
YAWRSAMLDVSRHFFGVDEVKRYIDRVARYKYNKLHLHSDDQGWR IAIDSWP RLAT YGGSTE VGGGPGG YYT KAEYKEIVRYAASRHLEV VPEID
MPGHTNAALASYAELNC DGVA PPLY GTKVGFS SLCDV KDV TYDFV DDVIGELA ALTPGRYLHIGGDEAH STPKADF VAFM KRVQPIV AKY GKT VVG
WHQLAGAEP VEGALQWY WLDRGDAEKA EVA EA ARNGT GLLSPAD RTY LDM KYT KDT PLG LSWAGY VEV QR SYD WDPAGY LGP GAPAD A VRG
VEAPLWTETL SDPDQ LDYMAF PRL PGVAELG WSPAST HDW DTY KVRLA A QAP YWEA GIDF YRSPQ VPWT

>d1iexa1 c.1.8.7 (A:1-388) Beta-D-glucan exohydrolase, N-terminal domain {Barley (Hordeum vulgare)}
DYVLYKDATKPVEDRVADLLGRMT LAEKIGQMTQIERLVATPDVLRDNFIGSLLSGGGSVPRKGATA KEWQDMV DGFQKACMSTR LGIP MIY GIDA
VHGQNNVYGATIFPHNVGLGATRDPYLVKRIGEATA LEV RATG I QYAFPCIA CRDPRW GRC YES ED RRI VQSMTE LIPGLQGDV PKDFTSGMPF
VAGKNKVAACAKHFVG DGGTV DGINEN NTI INREG L MNHIMPAYKNAMDKV STV M ISSS WNGVK MHAN QDL VTG YLKD TLK FG FV ISD WE
GIDR ITT PAGSDY SVKASILA GLD MIMV PNK YQQFIS ILTGHVNGG VIPMSR DDAVTR LRV KFTM GLFEN PYADPAMA EQLG KQE HRD LARE AA

RKS

>d1fcqa_c.1.8.9 (A:) Bee venom hyaluronidase {Honeybee (*Apis mellifera*)}

EFNVYWNVPTFMCHKYGLRFEVSEKYGILQNWMKDGRGEIAILYDPPGMFPALLKDPNGNVVARNGGPQLGNLTKHLQVFRDHЛИNQIPDKSF
PGVGVIDFESWRPIFRQNWASLPYKKLSVEVVRREHPFWDDQRVEQEAKRFEKYGQLFMEETLKAAKRMRPAANWGYAYPYCYNLTPNQPS
AQCEATTMQENDKMSWLFESEDVLLPSVYLRWNLTSGERVGLVGGRVKEALRIARQMTTSRKVLPPYYWYKYQDRRDTDLRADLEATLRKITDLG
ADGFIIWGSSDDINTKAKCLQFREYLNNELGPAVKR

>d1a4ma_c.1.9.1 (A:) Adenosine deaminase (ADA) {Mouse (*Mus musculus*)}

TPAFNPKVKELHVHLDGAIKPETIYFGKKRGIALPADTVEELRNIIGMKDPLSLPGFLAKFDYYMPVIAGCREAIKRIAYEVEMKAEGVVYEVRYSP
HLLANSKVDPMPWNQTEGDVTDPDDVVNLVNQGLQEQAQFGIKVRSILCCMRHQPSWSLEVLELKCKYNQKTVVAMDLAGDETIEGSSLFPGHV
EAYEGAVKNGIHTRVHAGEVGSPEVVREADILKTERVGHGYHTIDEALYNRLKENMHFEVCPWSSYLTGAWDPKTHAVVRFKNDKANYSLNT
DDPLIFKSTLDTDYQMTKKDMGFTEEEFKRLNINAACKSSLPEEEKKELLERYREYQ

>d1j79a_c.1.9.4 (A:) Dihydroorotase {Escherichia coli}

SQVLKIRRPDDWHLHLRDGMLKTVVPTSEIYGRAIVMPNLAPPVTTVEAAVAYRQRIADAVPAPHDFTPLMTCYLTDSDLPELERGFNEGIFTA
AKLYPANATTNSHGVTSVDIMPVLERMEKIGMPLLHVGEVTHADIDFDRARFIESVMEPLRQRLTALKVVFHITTKDAADYVRDGNERLAATIT
PQHLMFNRNHMLVGGVRPHLYCLPLIKRNHIIHQQLRELVASGFQRVFLGTDSSAPHARHRKESCGCAGCFNAPTAALGSYATVFEEMNALQHFEAFC
SVNGPQFYGLPVNDTFIELVREEQQVAESIALDDTLVPLFLAGETVRWSVK

>d1k6wa2_c.1.9.5 (A:56-375) Cytosine deaminase catalytic domain {Escherichia coli}

PFVEPHIHLDTTQTAGQPWNQSGTLFEGIERWAERKALLTHDDVKQRAWQTLKWQIANGIQHVRTHDVSDATLITALKAMLEVQEVAPWIDL
QIVAFPQEGILSYPNGEALLEEARLGADVVGAIPIHFETREYGVESLHKTFAHQYDRLIDVHCDIEIDDEQSFRFETVAALAHHEGMGARVTASHTT
AMHSYNGAYTSRLFRLLKMSGINFVANPLVNIHLQGRFTYPKRRGITRVKEMLESGINVCFGHDDVFDPWYPLGTANMLQVHMLHVQCLMG
YQQINDGLNLITHHSARTLNLDYQIAAGNSAN

>d1ejrc2_c.1.9.2 (C:1130-1422,C:1476-1567) alpha-subunit of urease, catalytic domain {Klebsiella aerogenes}

GIDTHIHWCPOQQAEALVSGVTTMVGGGTGPAAAGTHATTCTPGPWYISRMLQAADSLPVNIGLLGKGNVSQPDALREQVAAGVIGLKIHAWGA
TPAAIDCALTVADEMDIQVALHSDTLNESGFVEDTLAAIGGRTIHTFHTEGAGGGHAPDIITACAHPNLPSSTNPRLPTLNTIDEHLDMLMVCHHL
DPDIAEDVAFAESRIRRETIAAEDVLHDLGAFSLTSSDSQAMGRVGEVILRTWQVAHRMKVQRGALAEETGDNDNFRVKRYIAKYTINPALTHGIAHE
VGXMFAGLSARHHCRITFLSQAAAANGVAERLNRSIAIVVKGCRTVQKADMVHNSLQPNITVDAQTYEVRDGELETSEPADVLPMAQRYFLF

>d4ubpc2_c.1.9.2 (C:132-434,C:484-570) alpha-subunit of urease, catalytic domain {Bacillus pasteurii}

GGIDTHVHFINPDQDVVALANGITTLFGGGTGPAGSKATTVPGPWNIEKMLKSTEGLPINVGILKGKGSSAPIEQIDAGAAGLKIHEDWGAT
PASIDRSLTVADEADVQVAIHSCTLNEAGFLEDTLRAINGRVIHSFVEGAGGGHAPDIMAMAGHPNVLPSSTNPTRPFTVNTIDEHLDMLMVCHH
LKQNIPEVDVAFADSRSRIPETIAAEDILHDLGIISMMSTDALMGRAGEMLVRTWQTAQDKMKKQRGPLAEEKNGSDNFRVKRYVSKYTINPAIAQGIA
HEVGSIEEGKFADXGDLIHDNTNITFMSKSSIQQGVPAKGLKRRIGTVKNCRNIKGKDMWKNDVTTDIDINPETYEVKVDGEVLTCEPVKELPMAQR
YFLF

>d1e9yb2_c.1.9.2 (B:132-431,B:481-569) alpha-subunit of urease, catalytic domain {Helicobacter pylori}

GIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRRNLKWLRAAEYEYSMNLGFLAKGNASNDAQIEAGAIGFKIHEDWGTTP
SAINHALDVADKYDVQVAIHTDLNEAGCVENTMAAIAGRTMHTFHTEGAGGGHAPDIIVAGEHNILPASTNPFTVNTAEHMDMLMVCHH
LDKSIKEDVQFADSRSRIPETIAAEDILHDLGIISMMSTDALMGRAGEMLVRTWQTAQDKMKKQRGPLAEEKNGSDNFRVKRYVSKYTINPAIAQGIEY
VGSVEVGKXHHGAKYDANITFVSQAAYDKGIKEELGLERQVLPVKNCRNVTKKDMQFNNTTAHIEVNPETYHVFVDGKEVTSKPANKVSLAQLF
SIF

>d1i0da_c.1.9.3 (A:) Phosphotriesterase {Pseudomonas diminuta}

DRINTVRGPITISEAGFTLTHEHICSSAGFLRAWPEFFGSRKALAEKAVRGLRARAAGVRTIVDVSTFDIGRDVSLLAEVSRAADVHIVAATGLWFD
PPLSMRLRSVEELTQFFLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGEQQAAIFSEGLSPSRVCIGHSDDT
DDLSYLTALAARGYLIGLDHIPHSAGLEDNASASALLGIRSWQTRALLIKALIDQGYMKQILVSNDLWFGFSSYVTNIMDVMDRVNPDGMAFIPLRVI
PFLREKGVPQETLAGITVTNPARFLSPTLRS

>d1bf6a_c.1.9.3 (A:) Phosphotriesterase homology protein {Escherichia coli}

SDPTGT LAHEHL HIDSGFKNNVDCRLDQYAFICQE MNDLMTRGV RVNIE MTNR YMR RNAQ FM LDVM RETG IN VVACT GYY QDAFF P EHV AT
RSVQELAQEMVDEIEQGIDGTELKAGIIAEIGTSEGKITPLEEKVFIAAALAHNQTGRPISTHTSFSTMGLEQLALLQAHGV DLSRVTVGHCDLKNDNL
NILKMIDLGA YVQFD TIGKNSYY PDEKRIAMLHALDRG L NRVMLSMDITRRSHLKANGGYGDYLTTFIPQLRQSGFSQADVDMLRENP SQFF
Q

>d1jcla_c.1.10.1 (A:) Deoxyribose-phosphate aldolase DeoC {Escherichia coli}

HMTDLKASSRLALKMDLTLNDDDTDEKVIALCHQAKTPVGNATAICIPRFIPIAKRTLKEQGTPEIRIATVNFPHGNDIDIAETRAAIAYGAD
EVDVVFVPRYRALMAGNEQVGFDLVKACKEACAAANVLLKVIETGELKDEALIRKASEISIKAGADFIKTSTGKVAVNATPESARIMMEVIRDMGVKTV
GFKPAGGVRTAEDAQKYLAIADELFGADWADARHYRFGASSLLASLLKALGHG

>d1nal1_c.1.10.1 (1:) N-acetylneuraminate lyase {Escherichia coli}

NLRGVMAALLTPFDQQQALDKASLRRLVQFNQQGIDGLYVGGSTGEAFVQSLSEREQVLEIVAEGKGKIKLIAHVGCVTTAESQQLAAASKRYGFD
AVSAVTPFYYPFSFEEHCDHYRAIIDSADGLPMVVNIPALSGVKLTLDQINTLVTLPVGALKQTSGDLYQMEQIRREHPDLVLYNGYDEIFASGLLAG
ADGGIGSTYNTIMGWRYQGIVKALKEGDIQTAQKLQTECNKVIDLILITGVFRGLKTVLHYMDVVSVPLCRKPFGPVDEKYQPELKALAAQQLMQ

>d1f74a_c.1.10.1 (A:) N-acetylneuraminic acid lyase {Haemophilus influenzae}

MRDLKGIFSALLSVFNEGDGTINEKGLRQIIRHNIDKMKVGDGLYVGGSTGENFMLSSTEKKIEFRIAKDEAKDQIALIAQVGSVNLKEAVELGKYATELG
DCLSAVTPFYKFSFPEIKHYDTIIAETGSNMIVSYIPFLGVNMGIEQFGELYKNPKVLGVKFTAGDFYLLERLKKAYPNHLIWAGFDEMMLPAASLG
VDGAIGSTFNVNGVRARQIFELTKAGKLKEALEIQHVTNDLIEGILANGLYLTICKELLKLEGVDAGYCREPMTSKATAEQVAKAKDLKAFLS

>diampa_c.1.10.1 (A.) Dihydrodipicolinate synthase [Escherichia coli]

MFTGSIVAVTPMDERGNVCRASLKKLDYHVASGTSIAVSVGTIGESATLNHDEADVVMIMTLDLADGRPVIAGTGANATAEAISLTQRFNDSGV
GCLTVTPYYNRPSQEGLYQHFKAIAEHTDLPQIYNVPSRTGCDLLPETVGRLAKVKNIIGIKEATGNLTRVNQIKELVSDDFVLLSGDDASALDFMQLG
GHGVISVTANVAARDMAQMCKLAAEGHFAEARVINQRLMPLHNKLFVEPNPIPVKWACKELGLVATDLRLPMTITDSGRETVAALKHAGLL

>d1qo5b_c.1.10.1 (B:) Fructose-1,6-bisphosphate aldolase {Human (Homo sapiens), liver isozyme}

AHRFPALTQEQQKKESEIAQSIVANGKGLAADESVGTMGNRLQRKVNTEENRRQFREILF-SVDSSINQSIGGVLFHETLYQKDSQGKLFRNILKEKG
IVVGIKLDQGGAPLAGTNKETTIQQLDGLSERCAQYKKDGVDFGKWRVLRIADQCPSLAIQENANALARYASICCQQNGLVPIVEPEVIPDGDHD
EHCQYVTEKVLAAYKALNDHHVYLEGTLKPNVTAGHACTKKYTPEQVAMATVTALHRTVPAAVPGICFLSGGMSEEDATLNNA
WKLSFSYGRALQASALAAWGGKAANKEATQEAFMFKRAMANCQAAGKQYVHTGSS

>d1adoa_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (*Oryctolagus cuniculus*), muscle isozyme}

PHSHPALTPEQKKELSDIAHIRIVAPKGKILADESTGSIAKRLQSIGTENTEENRFYRQLLTADDRVNPICGGVLFHETLYQKADDGRFPQVKSKG
GVVGIVKVDGVVPLAGTNGETTQGLDLSERCAQYKKDGADFAKWRVCVLKIGEHTPSALAIMENANVLARYASICQQNQGIVPIVEPEIPLPDGHDL
KRCQYVTEKVLAAYKALSDHHIYLEGTLKPNMVTGHACTQKYSHEEIAMATVTLRRTVPPAVTGVTFLSGGQSEEASINLNAINKCPLLKPWA
LTFSYGRALQASALKAWGGKKENLKAQQEYVKRALANSACQGKYTSSGQAGAAASESLFISNHAY

>d1fdja_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (*Oryctolagus cuniculus*), liver isozyme}

AHRFPALTPEQKKELSDIAQRIVANGKGILAADESVGTMGNRLQRIKVENSEENRRQFREILFTVDNSINQSIGGVLFHETLYQKDSQGKLFRNLKEKGIVVGIKLDQGGAPLAGTNKETTIQGLDGLSERCAQYKKDGVDFGKWRAVLRIADQCPSLAIQEENANTLARYASICQCNGLPIVEPEVIPDGDHDELEHCQYVTEKVLAAVYKALNDHHVYLEGTLKPNMVTAGHACTKKYTPEQVAMATVTLHRTVAAVPGICFLSGGMSEEDATLNLNAINLCPLPKPKWKLSFSYGRALQASALAAWGGKAENKKATQEAFMKRAVVNCQAQKGQYVHTGSSGAASTQSLFTASYTY

>d1fbaa_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Drosophila melanogaster}

TTYFNPSKELQDELREIAQKIVAPGKGILAADSGPTMGKRLQDVGVENTEDNRNRRAYRQLLFSTDPKLAENISGVILFHETLYQKADDGTPFAEILKKK
GIIIGIKVDKGVVPLFGSEDEVTTQGLDDLAARCAQYKKDGCFDFAKWRCVLKIGKNTPSYSILEANVLARYASICQSQRIVPIVEVLPGDHDLD
RAQKVTEVLAavyKALSDHHVYLEGTLKPNMVTAGQSAKKNTPEEIALATVQALRRTVPAAVTGVTLSGGQSEEATVNLSAINNVPLIRPWALT
FSYGRALQASVLRAWAGKKENIAAGQNELLKRAKANGDAAQGKYVAGSAGAGGSGLFVANHAY

>d1a5ca_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Plasmodium falciparum}

LPADVAEELATTAQKLVQAGKGLADESTQTIKKRFDNKLIENTIENRASYRDLFGTKGLGKFISGAILFEETLFQKNEAGVPMVNLLHNENIIPGIV
DKGLVNIPICTDEEKSTQGLDGLAERCKEYYKAGARFAKWRTVLVIDTAKGKPTDLSIHETAWGLARYASICQQNRLVPIVEPEILADGPHSIEVC
AVVTQKVLSCVFKAHQENGVLLEGALLKPNNMTAGYECTAKTTQDVGLTVRTLRRTPALPGVVFLSGGQSEEASVNLNSINALGPHPWALTFSYGRAL

QASVLNTWQGKKENVAKAREVLLQRAEANSLATYGYKGGAGG

>d1epxa_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (*Leishmania mexicana*)}

MSRVTVLQLSQLPAYNRLKTPYESELIATVKKLTTPGKGLLADESIGSCTKRFQPIGLSNTEEHRRQYRALMLEAEGFEQYISGVILHDETVGQKASNG
QTFPEYLARGVVPGIKTDMGLCPLEGAEGEQMTEGLDGYVKRASAYYKKGCRFCWRNVYKIQNGTVSEAVRFNAETLARYAILSQMSGLVPIV
EPEVMIDGKHIDTCQRVSEHVWREVVAAQLRHGVIEGCLLPNGVAESGKTAAPEQVAHYTVMLTARTMPALPGVMFLSGGLSEVQ
ASEYLNAINNSPLPRYFLFSYARALQSSALKAWGGKESGLAAGRRAFLHRARMNSMAQLGKYKRSDD

>d1f2ja_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (*Trypanosoma brucei*)}

SKRVEVLLTQLPAYNRLKTPYEAEELIETAKKMTAPGKGLLADESTGSCSKRFAGIGLSNTAEHRRQYRALMLECEGFEQYISGVILHDETVYQAKTGE
TFPQYLRGGVVPGIKTDGLEPLVEGAKGEQMTAGLDGYIKRACKYYAMGCRFCWRNVYKIQNGTVSEAVVRFNAETLARYAILSQCGLVPIVEP
EVMIDGTHDIETCQRVSQHVWSEVVSALRHGVVWEGLLPNMVPGAESGLKGHAEQVAEYTVKTLARVIPPALPGVTFLSGGLSEVMASEYL
NAMNNCPLPRPWKLTSYARALQSSAIKWGGKESGVAGRRAFMHRAKMNSLAQLGKYNRADD

>d1euua_c.1.10.1 (A:) KDPG aldolase {Escherichia coli}

MKNWKTSAESILTTGPVPPVIVVKLEHAVPMAKALVAGGRVRLVTLTECAVDAIRIAKEVPEAIVGAGTVLNPQLAEVTEAGAQFAISPGLTE
PLLKAATEGTIPLIPGISTVSELMLGMDYGLKEFKFFPAEANGGVKALQAIAGPFSQVRFCPTGGISPANYRDYLALKSVCIGGSWLVPADALEAGDYD
RITKLAREAVEGAKL

>d1qfea_c.1.10.1 (A:) Type I 3-dehydroquinate dehydratase {Salmonella typhi}

MKTVTVKNLIIIGEGMPKIVSLMGRDINSVKAECALAYREATFDILEWRVDHFMDIASTQSVLTAARVIRDAMPDIPLFTFRSAKEGGEQTITTQHYLTL
NRRAIDSGLVDMDLLELFTGDADVKATVDYAHANVVVMSNHDFHQTPSAEMVSRLRMQALGADIPKIAVMPQSCHKDVLTLLTATLEMQQH
YADRPVITMSMAKEGVISRLAGEVFGSAATFGAVKQASAPGQIAVNDLRSVLMILHNA

>d1i2oa_c.1.10.1 (A:) Transaldolase {Escherichia coli}

TDKLTSLRQYTTVADTGIAAMKLYQPQDATTNPSLILNAAQIPEYRKLIIDDAWAKQQSNDRQQIVDATDKLAVNIGLEILKLPGRISTAVDAR
LSYDTEASIAKAKRLLKLYNDAGISNDRILIKLASTWQGIRAAEQLKEGINCNLTLLSFAQARACAEAGVFLISPFGVGRILDWYKANTDKKEYAPAEDP
GVVSVSEIYQYYKEHGYETVVMGASFRNIGEILELAGCDRLTIAPALLKELAESGAIERKLSYTGEVKARPARITESFLWQHNQDPMADVDKLAEHIRK
FAIDQEKEKLMIGDLL

>d1f05a_c.1.10.1 (A:) Transaldolase {Human (*Homo sapiens*)}

MESALDQLKQFTTVADTGFHAIDEYKPQDATTNPSLILAAAQMAYQELVEEAIAYGRKLGGSQEDQIKNAIDKLFVLFGEAEILKKIPGRVSTEVA
RLSFDKDAMVARARRLIELYKEAGISKDRILIKLSSTWEQIAGKELEEQHGIHCNMTLLSFAQAVACAEAGVTLISPFGVGRILDWHVANTDKSYEPL
EDPGVKSVTKIYNYKKFSYKTIVMGASFRNTGEIKALAGCDFLTISPKLGEELLQDNALKLPVLSAKAAQASDLEKIHLDKESFRWLHNEDQMAVEKL
SDGIRKFAADAVKLERMLTERMFN

>d1dosa_c.1.10.2 (A:) Fructose-bisphosphate aldolase {Escherichia coli}

SKIFDFVKPGVITGDDVQVFQVAKENNFAFPNVNCVGTDSINAVLEAAVKVAPVIVQFSNGGASFIAGKGVKSDVPQGAAILGAISGAHHVHQMA
EHYGVVILHTDHCAKKLWPIDGLLAGEKHFATGKPLFSSHMDLSEESLQENIEICSKYLERMSKIGMTLEIELGCTGGEEDGVNDNSHMDASALY
TQPEDVDYAYTELISKISPRFTIAASFGNVHGVKAGNVVLTPTILRDSQEYVSKKHNLPNSLNFVHGGSGSTAQEIKDSVSYGVVKMNIDTDQWA
TWEGVLYNKANEAYLQGQLGNPKGEDQPNKKYYDPRVWLRAGQTSMIARLEKAFQELNAIDL

>d1h7na_c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Baker's yeast (*Saccharomyces cerevisiae*)}
MHTAEFLETEPTEISSVLAGGYNHPLLQWQSERQLTKNMLIFPLFISDNPDFTEIDSLPNINRIGVNRLKDYLKPLVAKGLRSVILFGVPLIPGKDPV
GTAADDPAGPVIQGIKFIREYFPELYIICDVCLEYTSGHCHGVLYDDGTINRERSVSRLAAVAVNYAKAGAHCVAPSDMIDGRIRDIKRGLINANLAHK
TFVLSYAAKFSGNLYGPFRDAACSAPSNGDRKCYQLPPAGRGLARRALERDMSEGADGIIVKPSTFYLDIMRDASEICKDLPICAYHVSGEYAMLHAA
AEKGVVDLKTIAFESHQGFLRAGARLIITYLAPEFLDWLDE

>d1e51a_c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Human (*Homo sapiens*)}

MQPQSVLHSGYFHPLLRAWQTATTLNASNLIVYPIFVTDPDDIQPITSPLGVARYGVKRLEEMLRPLVEEGLRCVLIFGVPSRVPKDERGSAADSEES
PAIEAIHLLRKTFPNLLVACDVCLCPYTSRGHCGLLSENGAFRAEESRQLRAEVALAYAKAGCQVVAPSDDMMGRVEAIKEALMAHGLGNRVSVMS
YSAKFASCYGPFRDAAKSSPAFGDRRCYQLPPGARGLALRAVDRDVGREGADMVKGPMYLDIVREVKDKHPDPLAVYHVSGEFAMILWGA

QAGAFDLKAAVLEAMTAFRRA GADII YYTPQLLQWLK

>d1b4ka_c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Pseudomonas aeruginosa}
YPYTRLRRNRRDDFSRRLVRENVLTVDDILPVFVLGVNQRESIPSPMPGVERLSIDQLLIEAEWVALGIPALALFPVTPEKKSLAAEAYNPEGIAQRATRALRERFPELGII TDVALDPFTTHGQDGILDDDGYVLNDVSIDVLVRQALSHAEAGAQVVAPSDMMDGRIGAIREALESA GHNTVRIMAYSAKYASAYGGPF RDAVG SASNLGKGNKATYQMDPANSDEALHEVAADLAEGADMVMVKPGMPYLDIVRRVKDEFRAPTFVYQVSGEYAMHMGAIQN
GWLAESVILESLTAFKRAGADGILTYFAKQAAEQLRR

>d1b4ea_c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Escherichia coli}
TDLSQRPRRLRKSPALRAMFEETTLSNLDLVLPIFVEEEIDDYKAVEAMPGVMRIPEKHLAREIERIANAGIRSVMTFGISHHTDETGSDAWREDGLVARMRSICKQTVP E MIVMSDTCFCEYTSHGCVLKEHGVDNATLENLGQAVVAAAAGADFIAPS AAMDGVQVQAIRQALDAAGFKDTAIMSYTKFASSFYGP FREAAGSALKDRKSYQMNP MNRREAIRESLLDEAQGADCLMVKPAGAYLDIVREL RERTE LPIGAYQVSGEYAMIKFAALAGAIDEEK
VVLESLGSIKRAGADLIFSYFALDLAEKKILR

>d1gg1a_c.1.10.4 (A:) 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (DAHP synthase, AroG) {Escherichia coli}
DLRIKEIKELLPPVALLEKFPATENAANTVAHARKAIHKILKGND DRLLVIGPCSIHD PVAKEYATRLLA REELKDELEIVMRVYFEK PRTT VGW KGLIN DPHMDNSFQINDGLIARKLLL DINDS GLPAAGEFLDMITPQYLADLMSWGAIGARTTESQVHRELASGLSCPVGFKNGTDGTIKVAIDAINAAG
APHCFLSVTKWGHSAIVNTSGNGDCHI LRGKKEPNYSAKHVAEVKEGLNKAGLPAQVMIDFSHANSSKQFKQMDVCADVCQQIAGGEKAIIGV
MVESH LVEGNQSLES GEPLAYGKSITDACIGWEDTDALLRQLANAVKARR

>d1d9ea_c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P synthase) {Escherichia coli}
MKQKVVSIGD INVANDLPFLVFGGMNVLESRDLAMRICEHYVTVTQKLGI PVYFKASF D KANRSSIHSYRGPGLEEGM KIFQELK QTFGVKIITDVHE
PSQAQPVADVV DVIVQLPAFLARQTDLV EAMAKTGAVINVKKPQFVSPGQMG NIVDKFKEGGNEKVILCDRGANFGYDNLV DMLGFSIMKKVGS
NSPVIFDV THALQCRDPFGAASGG RRAQVAELARAGMAVGLAGLFIEAHPDPEHAKCDGPSALPLAKEPFLKQMKAI DDLVKGFEELDTSK

>d1jcx a_c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P synthase) {Aquifex aeolicus}
EKFLVIAGPCAIESEELLKV GEEIKRLSEKFKEV EFVFKSSFDKANRSSIHSFRGH GLEYGVKALRKVKEEFGLKITT DIESWQAE PVAEVADIIQIPAFLC
RQTDLLAAAKTGRAVN VKKGQFLAPWDTKNV VEKLFGGAK EYLTERGTTFGYNNLVDFRS LPI MKQWAKV IYDATHS VQLPGGLGDKSGGM
REFIFPLIRAAV AVGCDGVFMETHPEPEKALSDASTQLPLSQLEGII EAILEIREVASKYYETI

>d1onea1 c.1.11.1 (A:142-436) Enolase {Baker's yeast (Saccharomyces cerevisiae)}
SPYVLPVPFLNVNGGSHAG GALALQEFMIAPTGA KTFAE ALRIGSEV YHNLKSLT KRY GASAG NVDEGG VAPNI QTAE EALD LIVDAI KAAGHD
KVKIGLDCASSEFFKD GK YD LDFK NPN SDK SKWLT GPQLAD LYH SLMK RYPIV SIEDPFAE DDWE AW SHFFTAG IQIV ADDL TVTNPKRIATAIEKK
AD ALLL KV NQIG TLSE SIKA QDS FAAG WGV MVSH RSG ETD TFIADLV GLRTG QIKT GPARSER LA LNQ LLRIEE ELGD NAVF AGEN FH HGDKL
>d1pdz_1 c.1.11.1 (140-433) Enolase {Lobster (Homarus vulgaris)}

DEVILPVPA FN VINGGSHAG NKLAMQEFM ILPTGAT SFT EAM RGM TEVY HHLKAVIKAR FG LDATAVG DEGG FAPN ILNNK DAL DLIQ EA IKKAG YT
GKIEIGMDV AASEF YKQNNIYD LDFKTAN NDG SQKIS GDQL RD M YM FCKDFPIV SIEDPFDQDDWETWSKMTSGTTIQIVGDDLT VTNPKR ITTA
VEKKACKCLL KV NQIG SVTESIDA HLLAKKNGW GTM VSH RSG ETE DCFIADLV GLCTG QIKT GAP CR SERLAK YNQ ILR IEE ELGSGAKFAG KNF RA
PS

>d1e9ia1 c.1.11.1 (A:140-430) Enolase {Escherichia coli}
PGKYSMPVPM MN IINGGE HADNNV DIQEFM IQPV GAKT VKEA IR MGSE VFH LAK VL KAGM NT AV D EGG YAP NL GS NAE ALA VIA EAV KAA
GYELGKD ITL AMDCA ASEF YKDG KYVL AGE G NKA FTSE EFTH FLEEL TKQY PIV SIED GLD ESD WDGF AYQT KV LG DKI QLV GDD LFV NT KILKE IEK
GIAN Sili k FNQIGSLT ET LAAIKMAK DAGY TA VISH RSG ETE DATI ADL AVG TA AGQIKT GMS RSD RVAK YNQ LIR IEE ALGE KAP YN GRKE IKG Q

>d1bqg_1 c.1.11.2 (144-422) D-glucarate dehydratase {Pseudomonas putida}
EGQQQRDAV EMLGYLFYVGDRNKTDLGYRSEHEADNEWFRLRNKEALTPESVVALA EAYDRYGF KDFKLKG GVLRGEDEIAVTALSERFPDARITL
DPNGAWSLK EAVALCRDQHHV LAYAEDPCGAENG YSGREVMAE FRRSTGLRTATNMIA TDWRQMGHAIQLQSVDIPLADPHFW TMQGS VRVA
QMCNEWGLTWGSHSN NHFDISLAMFTH VAAAPGNITA IDTH WIWQDGQRLTKEPLQIKGGLVEV PKKPGLGVELDWDALMKAHEVYKSM

>d1ec7a1 c.1.11.2 (A:138-446) D-glucarate dehydratase {Escherichia coli}
DGQQRSEV EMLGYLFVGNR KATPLPYQS QP DSCD WYRLRHEAMTPDAV VRLAE AAYE KYG NDFKLKG GVLA GEE EAESI VALA QRFP QAR IT
LD PNGA WSLNEA KIGK YLKG SLAYAEDPCGA E QG FSG REVMAE FRRAT GLPT ATNMIA TDWRQMGH TLSQ SVDIPLADPHFW TMQGS VRVAQ

MCHEGLTWGSNSNNHFDISLAMFTHAAAAPGKITAIDTHWIWQEGNQRLTKEPFEIKGLVQVPEKPGLGVEIDMDQVMKAHELYQKHGLGA
RDDAMGMQYLIPGWTFDNKRPCMVR

>d1fhua1 c.1.11.2 (A:100-320) O-succinylbenzoate synthase {Escherichia coli}

QAANYRAAPLCNGDPDDLILKLADMPGEKAVKVGLYEAVRDGMVVNLLEAPDLHLRLDANRAWTPLKGQQFAKYVNPDYRDRIAFLEEPCKT
RDDSRAFARETGIAIWDESLEPDFAFVAEEGVRAVVIKPTLTGSLEKVRREQVQAAHALGLTAVISSISSLGLTQLARIAAWLTPDTIPGLDTLDLMQ
AQQVRRWPGSTLPVVEVDALERLL

>d1muca1 c.1.11.2 (A:131-372) Muconate-lactonizing enzyme {Pseudomonas putida}

RVRDSLEVATLASGDTARDIAEARHMLEIRRHRVFKLKIGANPVEQDLKHVTIKRELGDSASRVDVNVQYWDSEQAIRACQVLGNDNGIDLIEQPI
SRINRGQVRLNRQRTPAPIMADESIESVEDAFLSLAADGAASIFALKIAKNGGPRAVLRTAQIAEAAGIGLYGGTMLEGSIGTLASAHAFLTLRQLTWGT
ELFGPLLLTEEVNEPPQYRDFQLHIPRTPLGLTLDEQRALARFAR

>d2mnr_1 c.1.11.2 (133-359) Mandelate racemase {Pseudomonas putida}

PVQAYDSHSLDGVKLATERAVTAELGFRAVTKIGYPALDQDLAVRSIRQAVGDDFGIMVDYNQSLDVPAAIKRSQALQQEGVTWIEEPTLQHDY
EGHQRIQSCLNVPVQMGGENWLGPPEMFKALSIGACRALAMPDAMKIGGVTGWIRASALAQQFGIPMSSHLFQEISAHLLAATPTAHWLERLDAVG
SVIEPTLTATEGGNAVIPDPLPGVGIWREKEIGKYLV

>d2chr_1 c.1.11.2 (127-370) Chlormuconate cycloisomerase {Alcaligenes eutrophus}

PLRSAIPIAWTASGDTKRDLDSAVEMIERRHNRFKVKGFRSPQDDLIHMEALSNLSKAYLRDVDNQAWDEQVASVYIPELEALGVELIEQPVG
RENTQALRRLSDNNRVAIMADESLSTLASAFDLARDRSVDVFSLKLCNMGGVSATQKIAAAEASGIASYGGTMLDSTIGTSVALQLYSTVPSLPGCE
LIGPFVLADETLHSHEPLEIRDYELQVPTGVGHGMTLDEDKVRQYARVS

>d1jpdx1 c.1.11.2 (X:114-321) L-Ala-D/L-Glu epimerase {Escherichia coli}

TLPETVITAQTVVIGTPDQMANSASTLWQAGAKLLVKVLDNHILSERMVAIRTAVIDANESWRAEGLAARCQLLADLGVAMLEQPLPAQD
DAALENFIHPLPICADESCHTRSNLKALKGRYEMVNICKLDTGGLTEALALATEARAQGFSMLGCMILCTSRAISAALPLVPQVFADLDGPTWLAVD
VEPALQFTTGEHLH

>d1jpma1 c.1.11.2 (A:126-359) L-Ala-D/L-Glu epimerase {Bacillus subtilis}

YRDTLETDYTVSNSPEEMAADAENYLKQGFQTLKIKVGKDDIATDIARIQEIRKRVGSAVLRDLDANQGWRPKEAVTAIRKMEDAGLGIELVEQPVH
KDDLAGLKKVTDATDTPIMADESVFTPQAFEVLQTRSADLINIKLMKAGGISGAEKINAMAECGVEMVGSMIETKLGITAAHFAASKRNITRF
DFDAPMLKTDVFNGGITYSGSTISMGPKGPKGLGIAGAAL

>d1kcza1 c.1.11.2 (A:161-413) beta-Methylaspartase {Clostridium tetanomorphum}

GAEINAVPVFAQSGDDRYDNVDKMIKEADVLPHALINNVEEKGLGKGEKLLEYVKWLDRRIKLRVREDYAPIFHIDVYGTIGAAFVDV рикамадио
TLEAAKPFHLRIEGPMV рикамадио DEDRQKQMEAMRDLRAELDGRGVDAELVADEWCNTVEDVKFTDNKAGHMV рикамадио QIKTPDLGGVNNIADAIMYCKANG
MGAYCGGTCTNETNRSAEVTNIGMACGARQV рикамадио LAKPGMGVDEGMMIVKNEMNRV рикамадио LALVGRRK

>d1kko1 c.1.11.2 (A:161-411) beta-Methylaspartase {Citrobacter amalonaticus}

PCVPEAIPFGQSGDDRYIAVDKMLKGVDLPHALINNVEEKGLGKGEKLREYVRWLSDRILSRSSPRYHPTLHIDVYGTIGAAFVDV рикамадио EYIASL
EKEAQGLPLYIEGPVDAGNKPDQIRMLTAITKELTRLGSGVKIVADEWCNTYQDIVDFTDAGSCHMV рикамадио QIKTPDLGGIHNIVDAV рикамадио LYCNKHGMEAYQG
GTCNETEISARTCVHV рикамадио ALAARP MRM LIKPGM GFDEGLNIVFNEMNR TIALLQT

>d1a49a2 c.1.12.1 (A:12-115,A:218-395) Pyruvate kinase, N-terminal domain {Rabbit (Oryctolagus cuniculus)}

IQTQLHAAMADTFLEHMCRLDIDSAPITARNTGICTIGPASRSVETLKEMIKSGMNVARMFNSHGHTHEYHAETIKNVRTATESFASDPILYRPAVA
LDTKGXPAVSEKDIQDLKFGVEQDVDMVFASFIRKAADVHEVRKILGEKGKNIKIISKIENHEGVRRFDEILEASDGIMVARGDLGIEIPAЕKVFIAQKM
IIIGRCNRAGKPVICATQMLESMIKKPRPTRAEGSDVANAVLDGADCIMLSGETAKGDYPLEAVRMQHЛИAREAEAAMFHRKLFE

>d1pkla2 c.1.12.1 (A:1-87,A:187-357) Pyruvate kinase, N-terminal domain {Leishmania mexicana}

SQLAHNLTLSIFDPVANYRAARIICTIGPSTQSVEALKGLIQSGMSVARMFNSHGSHSHEYHQTINVRQAAELGVNIAIALDTKGXPAVSAKDRV
QFGVEQGVDMIFASFIRSAEQVGDVRKALGPGRDIMIICKIENHQGVQNIDSIEESDGIMVARGDLGVEIPAЕKVVVAQKILSKCNVAGKPVICAT
QMLESMTYNPRPTRAEVSDVANAVFNGADCVMLSGETAKGKYPNEVVQYMARICLEAQSL

>d1a3wa2 c.1.12.1 (A:2-87,A:189-366) Pyruvate kinase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

SRLERLTSN VAGSDLRRTSIIGTIGPKTNNPETLVALRKAGLNIVRMNFSGHSYEYHKSVIDNARKSEELYPGRPLAIALDTKGXPALSEKDKE
DLRGF

VKNGVHMVFASFIRTANDVLTIREVLGEQGKDVKIIVKIENQQGVNNFDEILKVTDGMVARGDLGIEIPAPEVLAVQKKLIAKSNLAGKPVICATQM
LESMTYNPRPTRAEVSDVGNAILGADCVMISGETAKGNYPINAVTTMAETAIAEQAIAYLPNYD

>d1e0ta2 c.1.12.1 (A:1-69,A:168-344) Pyruvate kinase, N-terminal domain {Escherichia coli}

MKTKTIVCTIGPKTESEEMLAKM DALGMNVMRNLNFSGHDYAEHGQRQIQLRNVMSKGKTAIILDTKGXPALAEKDQDIFGCEQGVDFVAAS
FIRKRSVDVIEIREHLKAHGGENIHIISKIENQEGLNNFDEILEASDGIMVARGDLGVEIPVEEFAQKMMIEKCIRARKVVITATMMLDSMIKNPRPTD
AEAGDVANAILDGTDAVMLSgesAKGKYPLEAVSIMATICERTDRVVMNSRLE

>d1kbla1 c.1.12.2 (A:510-873) Pyruvate phosphate dikinase, C-terminal domain {Clostridium symbiosum}

IETQEASVSGSFERIMVWADKFRTLKVRTNA DTPEDTLNAVKGAEIGILCRTEHMFFEADRMKIRKMLSDSVEAREEALNEIPFQKGDFKAMYK
ALEGRPMVTYRLDPPLHEFVPHTEEQAELAKNMGLTAEVKAKVDELHEFNPMMGHRGCRLAVTYPEIAKMQTRAVMEA AIEVKEETGIDIVPEI
MIPLVGEKKELKFV KDV VVEVAEQVKKEKGSDMQYHIGTMIEIPRAALTADAIAEEAEFFSGTN DLQMTFGSRDDAGKFLDSYYKAKIYESDPFAR
LDQTGVGQLVEMAVKKGRQTRPLCGICGEHGGDPSSVEFCHVGLNYVSCSPFRVPIARAAAQALNN

>d1fiy__ c.1.12.3 (-) Phosphoenolpyruvate carboxylase {Escherichia coli}

QYSALRSNVSMLGVLGETIKDALGEHILERVETIRKLSSRAGNDANRQELLTLQNLSDELLVARAFSQFLNLANTAEQYHSISPKGEAASNPEV
IARTLRKLKNQPELSEDTIKKAVESLSLELVTAHPTEIRRTLH KMVEVNACLQLDNKDIADYEHNQLMRRRLQLIAQS WHTDEIRKL RPSPVDEAK
WGF AVVENS L WQGPVNYLRELNEQLEENLGYKLPVEFVPRFTSWMGGDRDGNPNVTADIRHVLLSRWKATD LFKDIQV LVS ELMV EATPEL
LALVGEEGAEPYRYLMKNLRSRLMATQAWLEARLGEE LPKPEG L TQNEELWEPLYACYQSLQAC GMIIANGD LDT LRRV KCFGVPLVRIDIRQ
ESTRHT EAL GELTRYLGIGDYESWSEADKQ AFLIRELNSKRPLLPRNWQPSAETREV LDT CQVIAEAPQGSIAAYVISM AKTPSDV LAV HLL KEAGIGF
AMPVAPLFETL D LNN N ANDV M T Q L N I D W Y R G L I Q G K Q M V M I G Y S D S A K D A G V M A A S W A Q Y Q A Q D A L I K T C E K A G I E L T F H G R G G S I G R G G A
PAHA ALLS Q PPG S L K G G L R V T E Q G E M I R F K Y G L P E I T V S S L S Y T G A I L E A N L L P P E P K E S W R R I M D E L S V I C D V Y R G Y V R E N K D F V P Y F R S A T P E Q E L
GKLPLGSRAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWL GAGT ALQKVVEDGKQSE LEAMCRDWPF FSTR LG MLEM VFAKADLWLA EYYDQR
LVDKALWPLGKE RL NLQ EEDI KV VL AI AND SHL MAD LPWIAEISIQLRN ITDPLNVLQAELLHRSRQAEKEGQEPDPRV EQALMVTIAGIAAGMRNT
G

>d1pyma_ c.1.12.4 (A:) Phosphoenolpyruvate mutase {Blue mussel (Mytilus edulis)}

VKKTTQLKQMLNSK DLE FIMEAHNGLSARIVQEAGFKIWGSGLSVSAQLGVRDSNEASWTQVVEVLEFMSDASDVPILLADTG YGNFNNARRL
VRKLEDRGVAGAC LEDKLFPKTNSLHDGRAQPLADIEEFALKIKACKDSQTDPDFCIVARVEAFIAGWG LDEALKRAEAYRNAGADAILMHSKKADPS
DIEAFMKAWNNQGPVVIVPTKYYKPTDHFRDMGVSMVIWANHNL RASVSAIQ QTTKQIYDDQSLVNVEDKIVSVKEIFRLQRDDELVQAEDKYLP
KN

>d1dx ea_ c.1.12.5 (A:) 2-dehydro-3-deoxy-galactarate aldolase {Escherichia coli}

DVFPNKFKAALA AKQVQIGCWSALS NPISTEVLGLAGFDWLVL DGEHAPN DISTFIPQLMALK GSASAPV VRVPTNEPVII KRL DIFYN FLIPF VETK
EEAELAVASTRYPPEGIRGVSVSHRANMFGTVADYFAQCSNKNITILVQIESQQGVDNVDAIAATEGV DGFIVG PSDLA ALGH LGNASHPDVQKAIQ
HIFNRASA HGKPSG ILAPV EADARRY LEWGATF V AVGSDLGVFRSATQKLADTFKK

>d1dqua_ c.1.12.6 (A:) Isocitrate lyase {Aspergillus nidulans}

SYIEEDQRYWDEVAVKNWWKDSRWYTKRPTAEQIVAKRGNLKIEYPSNVQAKLW GILER NFKNKEASFTY GCLDPTMVTQMAKYLDTVYV
SGWQSSSTAS STDEPSPD LADY PMNTV PNK VNH LWMA QLF HDRK QREER MTTPKD QRH KVANV DYL RIPIADADTGH GGLT AV MKL TKL FVERG
AAGIHIEDQAPGT KKG H MAGKVLVPISEH INRL VAI RAQAD IMG TDLL A I ARTD SE AAT LIT STID HRDHPFIIGSTNP DIQPLN DLMV MAE QAG KN
GAE LQAI EDEW LAKA GLK LF ND AVV DAIN NSPL PNK KAA IE KYLT QSK GKS NLEA RAI AKEI AGTDIY FDWEAPRT REG YYR YQGGT QC AIN RAV AYA
PFADLIW MESKL PDYK QAKEF ADGV HAVW PEQKL AY NLSP SFN WKK AM PRD EQ ETYI KRL GAL GYAW QF ITLAG LHTT ALIS DTF AKAYA KQGM RA
Y GELVQEPEMANGDV VTHQKWS GANYV DNML KMIT GG

>d1f8ma_ c.1.12.6 (A:) Isocitrate lyase {Mycobacterium tuberculosis}

ASVVGTPKSAE QI QQEW DTNPRW KDV TRT YSAEDV VAL QGS VVEHTLARRGA EVLWEQLHDLEW VN ALGALT GNMAVQQV RAGLKAIYLSGW
QVAGDANL SGHT P DQSL P ANS VPQ VRR INN AL QRAD QIA KIEG DTS VEN WL API VAD GEAG FGG AL NVY ELQ KALIA AGVAG SHW EDQ LASE
KKCGH LGG KV LIPT Q QH IR TLTSARLA ADV ADV PTV I ART DAE AAT LIT SDV DER DQPF ITGER TREG Y RTK NGIE PCI ARA KAYA PFADL IWMET GT
PDLEARQFSEAVKA EYPDQMLAYNCSPSFNWKH LDDA TI AKF QKELA AMG FK QF ITLAG FHAL NYS MF D LAY GYA QNQ MSAY VELQ EREF AA
E ERGY TAT KH Q REV GAG Y FDRI ATT V DPNS TT ALT GSTE EGQ F

>d1igwa_c.1.12.6 (A:) Isocitrate lyase {Escherichia coli}

KTRTQQIEELQKEWTQPRWEGITRPYSAEDVVKLRGSVNPECTLAQLGAAKMWRLLHGESKKGYINSLGALTGGQALQQAKAGIEAVYLSGWQVA
ADANLAASMPDQSLSYPANSVPAVVERINNTFRRADQIQWSAGIEPGDPRYVDYFLPIVADAEGFGGVLNAFELMKAMIEAGAAAVHFEDQLAS
VKKCGHMGKGVLVPTQEAIQKLVAAARLCADVTGVPTLVARTDADAADLITSDCDPYDFSEFITGERTSEGFFRTHAGIEQAISRLAYAPYADLVWCET
STPDLELARRFAAQAIHKAYPGKLLAYNCSPSFNWQNKNLDDKTIASFQQQLSDMGYKFQFIFTLAGIHSMWFNMFDLANAYAQGEGMKHYVEKVQQ
PEFAAAKDGTYFVSHQQEVGTGYFDKVTTIIGQ

>d1d8ca_c.1.13.1 (A:) Malate synthase G {Escherichia coli}

QTITQSRLRIDANFKRFVDEEVLPGTGLDAAFWRNFDEIVHDLAPENRQLLAERDRIQAALDEWHRSNPGPVKDAAKSFLRELGYLVPQPERVT
VETTGIDSEITSQAGPQLVVPAMNARYALNAANARWGSYDALYGSIDIIPQEGAMVSGYDPQRGEQVIAVVRRFLDESLPLENSYQDVVFVAKVVD
KQLRIQLKNGKETTLRTPAQFVGVRGDAAPTCILLKNNGLHIELQIDANGRIGKDDPAHINDVIVEAAISTILDCEDSVAAVDAEDKILLYRNLLGLMQ
GTLQEKMENGRQIVRKLNDDRHYAADGSEISLHGRSLLFIRNVGHLMITPVWDSSEGNEIPEGILDGVMTGAIYDLKVQKNSRTGSVYIVPKPM
HGPQEVAFANKLFTRIETMLGMAPNTLKGIMDEERRTSNLRSICIAQARNRVAFINITGFLRTGDEMHSVMEAGPMLRKNMKSTPWIKAYER
NNVLSGLFCGLRGKAQIGKGMWAMPDLMADMYSQKGDQLRAGANTAWVPSPTAATLHALHYHQTNVQSVQANIAQTEFNAEFEPLDDLLTIP
VAENANWSAQEIQQELDNNVQGILGYVVRWVEQGIGCSKVPDIHNVALMEDRATLRISSQHIANWLRHGILTKEQVQASLENMAKVVDQQNAG
DPAYRPMAGNFANSCAFKAASDLIFLGVKQPNGYTEPLLHAWRLREKES

>d3rbl1 c.1.14.1 (L:148-467) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (*Nicotiana tabacum*), variant turkish samsun}

FQGPPHGIQVERDKLNKYGRPLLGCCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLCAEALYKAQAETGEIKGHYNATA
GTCEEMIKRAVFARELGVPIVMHDYLTTGGFTANTS LAHYCRDNGLLLHIIH RAMHAVIDRQKNHGIHFRVLAKALRMSGGDHIHSGTVVGKLEGERD
ITLGFVDLLRDDFVEQDRSRGIYFTQDWVSLPGVLVASGGIHVWHMPALTEIFGDDSVLQFGGMTLGH PWGNAPGA VANRV ALEACVKARNEG
RDLAQEGNEIIREACKWSPELAAACEVWKEIVF

>d1bura1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (*Spinacia oleracea*)}

FQGPPHGIQVERDKLNKYGRPLLGCCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLCAEALYKAQAETGEIKGHYNATA
GTCEDEMMKRAVFARELGVPIVMHDYLTTGGFTANTS LAHYCRDNGLLLHIIH RAMHAVIDRQKNHGIHFRVLAKALRMSGGDHIHSGTVVGKLEGERD
ITLGFVDLLRDDFVEKDRSRGIYFTQSWVSTPGVLVASGGIHVWHMPALTEIFGDDSVLQFGGMTLGH PWGNAPGA VANRV ALEACVQARNEG
RD LAREGNTIIREAKTWSPELAAACEVWKEIKFEFPAMDTV

>d1bwva1 c.1.14.1 (A:150-478) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

GPATGVILERERLDKFGRPLLGCCTTKPKLGLSGKNYGRVYEA LGKGLDFVKDDENINSQPFMRWRDRFLTMEAVNKASAATGEV/KGHYNVTAAT
MEEMYARANFAKELGSVIIIDL VIGYTAI QTMAKWARDNDMILHLHRAGNSTYSRQKNHGMNFRICKWMRMAGVDHIIAGTVVGKLEGDPII
TRGFYKTL LPKLERNLQEGLFFDMEWASLRK VMPV ASGGIHAGQM HQLI HLG EDV VLQ FGG GTL GH PWGNAPGA ANRV ALEACM IARNEN RD
YLT EGPEI LREA AKTC GAL RT AL DLW K DIT FN YT ST DT SD FV

>d1gk8a1 c.1.14.1 (A:150-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}

GPPHGIQVERDKLNKYGRPLLGCCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLVAEAIYKAQAETGEVKGHYNATAG
TCEEMMKRAVCAKE LGVPII MHDYL TTGGFTANTS LAI YCRDNGLLLHIIH RAMHAVIDRQRNHGIHFRVLAKALRMSGGDHLHS GTVVGKLEG EREV
TLGFVDLMRDDYVEKDRSRGIYFTQDWCSMPGVMPV ASGGIHAGQM HQLI HLG EDV VLQ FGG GTL GH PWGNAPGA ANRV ALEACTQARNE
GRDLAREGGDVIRSACKWSPELAAACEVWKEIKFEFDTIDKL

>d1bxna1 c.1.14.1 (A:151-467) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}

FAGPSTGIIVERERLDKFGRPLLGATTPKPKLGLSGRNYGRVYEGLKGGDFMKDDENINSQPFMRWRDRFLFVMDAVNKASAATGEVKGSYLNVT
AGTMEEMYRRAEFAKSLGSVIIIMVDLIVGWTCIQSMSNWCRQNDMILHLHRAGHGTYTRQKNHGV SFRVIAKWLRLAGVDHMHTGTA VGKLEG
DPLTVQGYYNVCRDAYTQDLTRGLFFDDQDWASLRK VMPV ASGGIHAGQM HQLI HLG EDV VLQ FGG GTL GH PWGNAPGA ANRV ALEAM VLR
NEG RDILNEGPEI RDAARWCGPLRAALDTWGDI

>d1rbla1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}

FQGPPHGIQVERDLLNKYGRPMLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENINSQPFQRWRDRFLVADAIIKSQAETGEIKGHYNVTA
TCEEMMKRAEFAKELGMPIMHDFTAGFTANTTLAKWCRDNGVLLHIIH RAMHAVIDRQRNHGIHFRVLAKCLRLSGGDHLHS GTVVGKLEGDK

ASTLGFVDSLREDHIEADRSRGVFFTQDWASMPGLPVASGGIHVWHMPALVEIFGDDSVLQFGGGTLGHPWGNAPGATANRVALEACVQARN
EGRDLYREGGDILREAGKWSPELAALDWKEIKFEFETMDKL

>d5ruba1 c.1.14.1 (A:138-457) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Rhodospirillum rubrum}

GPSVNISALWKVLGRPEVDGGLVVTIIPKPLRPKFAEACHAFWLGGDFIKNDEPQGNQPFAPLRDTIALVADAMRRAQDETGEAKLFSANITA
DDPFEIIARGEYVLETFGENASHVALLVDGYVAGAAIAITARRFPDNFLHYHRAGHGAVTSPQSCKRGYTAVFHCKMARLQGASGIHTGTMGFGKM
EGESSDRAIAYMLTQDEAQGPFYRQSWGGMKACTPIISGGMNALRMPGFFNLGNANVILTAGGGAFGHIDGPVAGARSLRQAWQAWRDGV
VLDYAREHKELARAFESFPGDADQIYPGWRKALGV

>d1geha1 c.1.14.1 (A:137-443) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Archaeon Thermococcus kodakaraensis}

DGPAFGIEGVRKMILEIKDRPIYGVPKPKVGYSPEEFKLAYDLLSNGADYMKDDENLTSPWYNRFEERAEMAKIIDKVENETGEKKTWFANITADL
LEMEQRLEVLAQGLKHAMVDVVITGWGALRYIRDALADYGLAIHGHRAMHAAFTRNPYHGISMFVLAKLYRLIGIDQLHVGTAGAGKLEGGKWD
VIQNARILRESHYKPDENDVFHLEQKFYSIAAFPTSSGGLHPGNIQPVIEALGTDIVLQLGGGTGHPDGPAAGARAVRQAIDAIMQGIPDEYAKT
HKELARALEKWGHVTP

>d1qtwa_c.1.15.1 (A:) Endonuclease IV {Escherichia coli}

MKYIGAHVSAAGGLANAIRAAEIDATAFALFTKNQRQWRAAPLTTQTIDEKAACEKYHYTSAQILPHDSYLINLGHPVTEALEKSRAFIDEMQRC
EQLGLSLNFNHPGSHLMQISEEDCLARIAESINIALDKTQGVAVIENTAGQGSNLGFKEHLAAIIDGVEDKSRVGVCIDTCHAFAGYDLRTPAECEK
TFADFARTVGFKYLRGMHLNDAKSTFGSRVDRHSLGEGNIGHDAFRWIMQDDRFDGIPLILETINPDIWAEEIAWLKAQQTEKAVA

>d1d8wa_c.1.15.2 (A:) L-rhamnose isomerase {Escherichia coli}

TQLEQAWELAKQRFAAVGIDVEEALRQLDRLPVSMHCWQGDDVSGFENPEGSLTGGIQATGNPGKARNASELRADLEQAMRLIPGPKRNLHAI
YLESDTDPSRDQIKPEHFKNWVEWAKANQLGLDFNPSCFSHPLSADGFTLSHADDISRQFWIDHCKASRRVSAYFGEQLGTPSVMNIWIPDGMKDI
TVDR LAPRQRLLAALDEVISEKLNPAHHIDAVESKLFIGAESYTGSNEFYMGYATSRQTA CLDAGHFHPTEVISDKISAAMLYVPQLLHVSRPVR
WDSDHVVLLDDETQAIASEIVRHDLFDRVHIGLDFDASINRIA AWVIGTRNMKKALLRALLEPTAELRKLEAPGDYTLRALLEEQKSLPWQAVWE
MYCQRHDTDPAGSEWLESVRAYEKEISRR

>d1dxia_c.1.15.3 (A:) D-xylose isomerase {Streptomyces murinus}

MSFQPTPEDRFTFGLWTGVWQGRDPFGDATRPA LD P VETVQRLAELGAYGVTFHDDDLIPFGSSDTERESHIKRFRQAL DATGMTVPMATTNLFT
HPVFKDGGFTANDRDVRRYALRK TIGNIDLAAELGAKTYVAWGREGAESGGAKDVRDALDRMKEAFD LGEYVTAQGYDLRFAIEPKPNEPRGD
LLPTVGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVLDLLETAGYEGPRHFD
FKPPRTEDFDGVWASAAGCMRNYLILKDR AAFRADPEVQE ALRAARLDQLAQPTAADGLD ALLADRAAFEDFDVAAAARGMAFEHLDQLAM
DHLLGARG

>d2gyia_c.1.15.3 (A:) D-xylose isomerase {Streptomyces olivochromogenes}

YQPTPEDRFTFGLWTGVWQGRDPFGDATRPA LD P VETVQRLAELGAYGVTFHDDDLIPFGSSDTERESHIKRFRQAL DATGMTVPMATTNLFT
VFKDGGFTANDRDVRRYALRK TIRNI DL AVELGAETYVAWGREGAESGGAKDVRVALDRMKEAFD LGEYVTSQGYDIRFAIEPKPNEPRGD
TVGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVLDLLESAGYEGPRHFD
PRTEDIDGVWASAAGCMRNYLILKDR AAFRADPEVQE ALRASRL DELA QPTAADGVQELLADRTA FEDFDVAAAARGMAFERLDQLAMD
GAR

>d1xis_c.1.15.3 (-) D-xylose isomerase {Streptomyces rubiginosus}

NYQPTPEDRFTFGLWTGVWQGRDPFGDATRPA LD P VETVQRLAELGAYGVTFHDDDLIPFGSSD SEREEHV K RFRQAL DDTGMK VPMATTNLFT
HPVFKDGGFTANDRDVRRYALRK TIRNI DL AVELGAETYVAWGREGAESGGAKDVRVALDRMKEAFD LGEYVTSQGYDIRFAIEPKPNEPRGD
LPTVGHALAFIERLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVLDLLESAGYEGPRH
KPPRTEDFDGVWASAAGCMRNYLILKDR AAFRADPEVQE ALRASRL DELA QPTAADGLQAL LDRSAFEEFDVAAAARGMAFERLDQLAMD
LLGARG

>d1qt1a_c.1.15.3 (A:) D-xylose isomerase {Streptomyces diastaticus, M1033}

SYQPTPEDKFTFGLWTGVWQGRDPFGDATRGALDPAESVRLAELGAYGVTFHDDDLIPFGATD SERA EHI K RFRQGLDETGMK VPMATTNLFT
PVFKDGGFTANDRDVRRYALRK TIRNI DL AVELGAQTYVAWGREGAESGGAKDVRVALDRMKEAFD LGEYVTSQGYDTPFAIEPKPNEPRGD
PTIGHALAFIDGLERPELYGVNPEVGHEQMAGLNFPHGIAQALWAGKLFHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVLDLLESAGYEGPRH
DFK

PPRTEDFDGVWASAAGCMRNYLILKERAFAFRADPEVQEALRAARLDELAQPTAGDGLQALLPDRSAFEDFPDAAAARGMAFERLDQLAMDHL
LGARG

>d4xiao_c.1.15.3 (A:) D-xylose isomerase {Arthrobacter, strain b3728}

VQPTPADHFTFLWTVGWTGDPFGVATRANLDPVEAVHKLAELGAYGITFHNDNLIPFDATAAEREKILGDFNQALADTGLKVPMTTNLFHPV
FKDGGFTSNDRSIRRFALAKVLHNIDLAAEMGAETFVMWGGREGSEYDGSKDLAALDRMREGVDTAAGYIKDKGYNLRIALEPKPNEPRGDIFLP
TVGHGLAFIEQLEHGDIVGLNPETGHEQMAGLNFTHGINAQALWAELFHIDNGQRGIKYDQDLVFGHDLTSAFFTVDLLENGFPNGGPKYTGPR
HFDYKPSRTDGYDGVWDSAKANMSMYLLKERALAFRADPEVQEAMKTSGVFELGETTLAGESAADMNDSASFAGFDAEAAAERNFAIRLN
QLAIEHLLGSR

>d1xima_c.1.15.3 (A:) D-xylose isomerase {Actinoplanes missouriensis}

VQATREDKFSFLWTVGWQARDAGDATRTALDPVEAVHKLAEGAYGITFHDDLVPGSDAQTRDGIAGFKKALDETGLIVPMVTTNLFTPV
KDGGFTSNDRSRRYAIRKVLRQMDLGAELGAKTFLVWGGREGAEYDSAKDVSAALDRYREALNLLAQYSEDRGYGLRFAIEPKPNEPRGDILLTAG
HAIAFVQELEPFLGGINPETGHEQMSNLNTQGIAQALWHKKLFHIDNGQHGPFDQDLVFGHDLNAFLSLVDLLENGPDGAPAYDGPRHF
KPSRTEDYDGVWESAKANIRMYLLKERAKAFRADPEVQEALASKVAELKPTLNPGEGYAELLADRSAFEDYDADAVGAKGFGFVKNQLAIEHLL
GAR

>d1a0ca_c.1.15.3 (A:) D-xylose isomerase {Clostridium thermosulfurogenes, also known as Thermoanaerobacter thermosulfurigenes}

NKYFENVSKIKYEGPKSNPYSFKFYNPEEVIDGKTMEEHLRFSIAYWHTFTADGTDQFGKATMQRPNHYTDPMDIAKARVEAAFFDKINAPY
FCFHDRDIAPEGDTLRETNKNLDTIVAMIKDYLKTSKTKVLWGTANLFSNPRFVHGASTSCNADVFAWSAAQVKKALEITKELGGENYVFWGGREGY
ETLLNTDMEFELDNFARFLHMAVDYAKEIGFEGQFLIEPKPKEPTKHQYDFDVANVLAFLRKYDLDKYFKVNIEANHATLAFHDFQHELRYARINGVL
GSIDANTGDMILLGWDTDQFPTDIRMTTLMAMYEVIKMGGFDKGGLNFDAKVRASFEPEDLFLGHIAGMDAFAKGFVAYKLVKDRVFDKFIEERYA
SYKDYGIGADIVSGKADFRSLEYALERSQIVNKSGRQELLESILNQYLFA

>d1a0da_c.1.15.3 (A:) D-xylose isomerase {Bacillus stearothermophilus}

PYFDNISTIAYEGPASKNPLAKFYNPEEKVGDKTMEEHLRFSVAYWHTFTGDGSDPGAGNMIRPNKYSGMDLAKARVEAAFFEKLNIPFCF
HDVDIAPEGTLKETYKNLDIIVDMIEEYMKTSKTKLWNTANLFTHPRFVHGAATSCNADVFAAAAKVKKGLEIAKRLGAENYVFWGGREGYETLL
NTDMKLELDNLARFLHMAVDYAKEIGFDGQFLIEPKPKEPTKHQYDFDVATALAFLQTYGLKDYFKFNIEANHATLAGHTFEHELRVARIHGMLGSVD
ANQGDMILLGWDTDQFPTLAMYEILKNGGLGRGLNFDAKVRGSFEPEDLFYAHAGMDSAVGLVAHRLIEDRVDEFIEERYKSYTEGI
GREIVEGTADFHKLEAHALQLGEIQNQSGRQERLKTLNNQYLLEV

>d1a0ea_c.1.15.3 (A:) D-xylose isomerase {Thermotoga neapolitana}

AEFFPEIPKVQFEGKESTNPLAKFYDPEEIIDGKPLKDHLKFSVAFWHTVNEGRDPFGPTADRPWNRYTDPMDKAFARVDALFECEKLNIEYFC
FHDRDIAPEGKTLRETNKLDKVVVERIKERMKDSNVKLLWGTANLFSHPRYMHGAATTCSADVFAAAQVKKALEITKELGGEGYVFWGGREGYET
LLNTDLGFELENLARFLRMAVDYAKRIGFTGQFLIEPKPKEPTKHQYDFDVATAYAFLKSHGLDEYFKFNIEANHATLAGHTFQHELRMARILGKLSID
ANQGDMILLGWDTDQFPTLAMYEILKNGGLGRGLNFDAKVRGSFEPEDLFYAHAGMDSAVGLVAHRLIEDRVDEFIEERYKSYTEGI
IGRDIVEGKVDFEKKLEIYIIDKETIELPSGKQEYLESLINSYIVKTILER

>d1bxca_c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp. Caldophilus}

MYEPKPEHRFTFLWTVGNGRDPFGDAVRERLDPVYVGHKLAELGVHGVNLHDEDLIPRGTTPQERDQIVRRFKRALDETGLKVPMTGNLFSD
PGFKDGGFTSRDPWVRAYAERKSLETMDLGAELGAEIYVWPGREGAEVEATGKARKVWDWVREPLNFMAAYAEDQGYGYRFALEPKPNEPRG
DIYFATVGSMILALIHTLERPERFGLNPEFAHETMAGLNFVHAVAQALDAGKLLHIDNGQRMNRFDQDLRGSENLKAAFLVLLESSGYQGPRHF
DAHALRTEDEEGVWAFARGCMRTYLILKERAFAFREDPEVKELLAAYYQEDPAALPLMDPYSHEKAELKRAELPLEAKRHRGYALERLDQLAVEYLL
GVRG

>d1bxba_c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp. Thermophilus}

MYEPKPEHRFTFLWTVGNGRDPFGDAVRERLDPVYVGHKLAELGVHGVNLHDEDLIPRGTTPQERDQIVRRFKALDETGLKVPMTANLFSDP
AFKDGAFTSPDPWVRAYAERKSLETMDLGAELGAEIYVWPGREGAEVEATGKARKVWDWVREALNFMAAYAEDQGYGYRFALEPKPNEPRGD
YFATVGSMILAFIHTLDRPERFGLNPEFAHETMAGLNFVHAVAQALDAGKLFHIDLNDQRMSRFDQDLRGSENLKAAFLVLLESSGYQGPRHF
AHALRTEDEEGVWAFARGCMRTYLILKERAFAFREDPEVKELLAAYYQEDPAALLGPYSREKAELKRAELPLEAKRHRGYALERLDQLAVEYLL
GVRG

RG

>d1luca_c.1.16.1 (A:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}
MKFGNFLTYQPPELSQTENVKRLVNLGKASECGCFDTVWLLHHFTFGLLNPYAAAHLGATELVGTAAIVLPTAHPVRQAEDVNLLDQM
SKGRFRFGICRGLYDKDFRVFGTMDNSRALMDCWYDLMKEGFNEGTYIAADNEHIKFPKIQLNPSATQGGAPVVVAESASTTEWAERGLPMI
LSWIINTHEKKAQLDLYNEVATEHGYDVTKIDHCLSYITSVDHSNRACKDICRNFLGHWYDSVNTAKIFDDSDQTKGYDFNKQWRFVLKGHKDT
NRRIDYSYEINPVGTPEECIAIIQQDIDATGIDNICCGFEANGSEEIIASMKLFQSDVMPYLKEKQ

>d1lucb_c.1.16.1 (B:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}
MKFGLFLNFMNSKRSSDQVIEEMLDTAHYVDQLKFDTLAVYENHSNNGVVGAPLTAVGFLGMKNAKVASLNHVITTHPVRVAEEACLLDQ
MSEGRFAFGFSCEKSADMRFNRPRTDSQFQLFSECHKIINDAFTTYCHPNNDYFSFPKISVNPHTEGGPQAQFVNATSKEVVEAAKLGPLVF
RWDDSNQRKEYAGLYHEVAQAHGVDSQVRHKLTLVNVNQVDGEAARAEARVYLEEFVRESYSNTDFEQKMGEILLENAIGTYEESTQAARVAIE
CCGAADLLMSFESMEDKAQQRAVIDVVNNANIV

>d1nfp_c.1.16.2 (-) Non-fluorescent flavoprotein (luxF, FP390) {Photobacterium leiognathi}
MTKWNYGVFFLNFYHVGQQEPSTMSNALETLRIIDEDTSIYDVAFSEHHIDKSYNDETKLAPFVSLGKQIHVLATSPETVVKAACYGMPLFKWDD
SQQKRIELLNHQAAAQFNVDIANVRHRLMLFVNVDNPTQAKAELSIYLEDYLSYTQAETSIDEIINSNAAGNFDTCLHHVAEMAQGLNNKVDFL
FCFESMKDQENKKSLMINFDKRVINYRKEHNLN

>d1fvp_a_c.1.16.2 (A:) Non-fluorescent flavoprotein (luxF, FP390) {Photobacterium phosphoreum}
MNWKWNYGVFFVNFYNKQQQEPSTMNNALETLRIIDEDTSIYDVINIDDHYLVKKDSEDKKLAPFITLGEKLYVLATSENTVDIAAKYALPLVKWDDI
NEERLKLLSFYNASASKYNKNIDLVRHQMLHVNVNEAETVAKERLKYIENYVACTQPSNFNGSIDSIIQSNTGSYKDLSYVANLAGKFDNTVDLL
CFESMQDQNKKKSVMIDLNNQVIKFRODNNLI

>d1ezwa_c.1.16.3 (A:) Coenzyme F420 dependent tetrahydromethanopterin reductase {Archaeon Methanopyrus kandleri}
AEVSFGIELLPDDKPTKIAHLIKVAEDNGFEYAWICDHYNNSYMGVLAAVITSKIKLPGITNPYTRHPLITASNIATLDWISGGRAIGMGPDKAT
FDKMGMLPFPCKIPIWNPAAEDEVGPATAIREVKEVIYQYLEGGPVEYEGKVKTGADVKARSIQGSDFYMGAAQGPIMLKTAGEIANGVLVNASNP
KDFEVAVPKIEGAKEAGRSLDEIDVAAYTCFSIDKDEDKIAEATKIVVAFIVMGSPDVVLERHGIDTEKAEQIAEAIGKGDFGTAIGLVDEDMIEAFSIA
GDPDTVVVKIEELLKAGVTQVVVGSPIGPDKEKAIELVGQEVIPHFK

>d1f07a_c.1.16.3 (A:) Coenzyme F420 dependent tetrahydromethanopterin reductase {Archaeon Methanobacterium thermoautotrophicum}
MKFGIEFPNEPIEKIVKLVKLAEDVGFEYAWTDHYNNKNVYETLALIAEGTETIKLPGVTNPYVRSPAITSIAITALDELSNGRATLGIGPGDKATFD
ALGIEWVKPVSTIRDAIAMMRTLLAGEKTESGAQLMGVKAVQEKIPIYMGAAQGPMMKLKAGEISDGALINASNPKDFEAAPVLIKEGAEAAGKSIA
DIDVAAYTCCSIDEDAAAAANAAKIVVAFIAAGSPPPVERHGLPADTGKKFELLKGDFGGAIGAVDDALMEAFSVVGTDEFIPKIEALGEMGVT
QYVAGSPIGPDKEKSILGEVIASF

>d1qapa1_c.1.17.1 (A:130-296) Quinolinic acid phosphoribosyltransferase, C-terminal domain {Salmonella typhimurium}
VASEVRRYVGLLAGTQTQLLDRKTLPLGLRALQYAVRTGGGVNHRGLGDAALIKDNHVAAAGSVVDAVRNAAPDLPCVEVDSLEQLDAVLP
GADIIMLDNFNTDQMREAVKRVNGQARLEVSGNVTAEYLREFAETGVDFISVGALTKHVRALDSMRFC

>d1qpoa1_c.1.17.1 (A:117-285) Quinolinic acid phosphoribosyltransferase, C-terminal domain {Mycobacterium tuberculosis}
IATATAAWVDAVRGTTKAKIRDTRKTLPLGLRALQYAVRTGGGVNHRGLGDAALIKDNHVAAAGSVVDAVRNAAPDLPCVEVDSLEQLDAVLP
EKPELILLDNFAVWQTQTAQVRRDSRAPTVMLLESSGGLSLQTAATYAEYGVDYLAvgalthsvrvldigldm

>d1qasa3_c.1.18.1 (A:299-625) Phospholipase C isozyme D1 (PLC-D1) {Rat (Rattus norvegicus)}
DQPLSHYLVSSSHNTYLEDQLTGPSSTEAYIRALCKGCRCLEDCWDGPQEPYIYHGTYFTSKILFCVLRPAIRDYAFKASPYPVILSLENHCSLEQQRV
MARHLRAILGPILLDQPLDGVTTSLPSPEQLKGKILLKGKLLGGLLPAGGENGSEATDVSDEVEAAEMEDEAVRSQVQHCKPKEDKLKLVPELSDMIIYC
KSVHFGGFSSPGTSGQAFYEMASFSESRALLLQESNGFVRHNVSCLSRIYPAGWRTDSSNYSPVEMWNGGCQIVALNFQTPGPEMDVYLGCFQ
DNGGCGYVLKPAFLRDPNTTFNSRALTQGPW

>d2ptd_c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Bacillus cereus}
ASSVNELENWSKWMQPIDSIPALARISIPGTHDSGTFKLQNPKQVWGMTQEYDFRYQMDHGRARIFDIRGRLTDDNTIVLHHGPLYLYVTLHEFINE
AKQFLKDNPSETIIMSLKEYEDMKGAEFSSTFEKKYFVDPIFLKTEGNIKLGDARGKIVLLKRYSGSNEPGGYNFVWPNETFTTVNQNANVT

VQEKYKVSYDEKVKSICDKTMDETMNNSEDLNHLYINFTSLSSGGTAWNSPYYASYINPEIANYIKQKNPARVGWVIQDYINEKWSPLLYQEVRANK

SLI

>d2plc__ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Listeria monocytogenes}

VTTKQWMSALPDNTNLAAALSIPGTHDTSYNGDITWTLKPLAQQTMSLYQQLEAGIRYIDIRAKDNLNIYHGPFLNASLSGVLETITQFLKNPKETIIMRLKDEQNSNDSFDYRQPLNIYKDIFYTTPRTDTSNKIPTLKDRGKILLSENHTKKPLVINSRKFGMFGAPNQVIQDDYNGPSVTKFKEIV

QTAYQASKADNKLFLNHISATSLTFTPRQYAAALNNKVEQFVLNLSEKVRGLGILIMDFPEKQTIKNIKNNKF

>d7reqa1 c.1.19.1 (A:4-560) Methylmalonyl-CoA mutase, alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

LPRFDSVDLGNAPVPADAARRFEELAKAGTGEAWETAEQIPVGTLFNEDVYKDMDWLDTYAGIPPFVHGPYATMYAFRPWTIRQYAGFSTAKESNAFYRRNLAAGQKGLSVAFLPLTHRGYDSNDNPRVAGDVGMAVGVAIDSIDIYDMRELFAPILDQMSVSMTMNGAVLPILALYVTAEEQGVKPEQLAGTIQNDILKEFMVRNTYIYPQPQPSMRUISEIFAYTSANMPKWNSISIGYHMQEAGATADIEMAYTLADGVYDAGESVGLNVDFQFAPRLSFFWGIGMNNFFMEVAKLRAARMLWAKLVHQFGPKNPKSMSLRTHSQTSQWSLTQDVYNNVVRCIEAMAATQGHTQLSHTNSLDEAIALPTDFSARIARNTQLFLQQESGTTTRVIDPWGSAYVEELTWDLARKAWGHIQEVEKGMAKIEKGIPKMRIEEEAAARTQARIDSGRQPLIGVNKYLHEPPLDVLKVDNSTVLAEQKAKLVLKRAERDPEKVKAAALKITWAAGNPDDKDPDRNLLKLCIDAGRAMATVGEMSDALEKVFGRYT

>d7reqb1 c.1.19.1 (B:16-475) Methylmalonyl-CoA mutase, alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

LTPTTLSLAGDFPKATEEQWEREVEKVLNRGRPPEQLTAECLKRLTVHTVDGIDIVPMYRPKDAPKKLGYPGVAPFTRGTTVRNGDMAWDVRA LHEDPDEKFRKAILEGLERGVTSSLRVDPDAIAPEHLDEVLSVLEMTKVEVFSRYDQGAAAELSVYERSDKPAKDLALNLGLDPIGFAALQGTEPDLTVDWVRRRLAKFSPDSRAVTIDANIYHNAGAGDVAELAWALATGAEVRALVEQGFTATEAFDTINFRVTATHDQFTIARLRLREAWARIGEVFGVDEDKRGARQNAITSWRELTDPPVNLRGSIATFSASVGGAESITTLPTQALGLPEDDFPLRIARNTGIVLAEEVNIGRVNDPAGGSYYVESLRTSLADAAWKEFQEVEKLGGMASKAVMTEHVTKVL DACNAERA KRLRKQPITAVSEFPMIGARSIE

>d1ccwb__ c.1.19.2 (B:) Glutamate mutase, large subunit {Clostridium cochlearium}

MELKNKKWTDEFHKQREEVLQQWPTGKEVDLQEAVDYLKKIPAENKAELVLAKKGITMAQPRAGVALDEHIELRLQDEGGADFLPSTIDA YTRQNRYDECENGKESEKGRSLLNGFPGVNFVGKCRKVLEAVNLPQLQARHGTPDSRLLAEIIHAGGWTSNEGGGISYNVPYAKNVTIEKSLLDW QYCDRLVGFYEEQGVHINREPFGPLTGTIVPPSMSNAV GITEALLAAEQGVKNITVGYGECGNMIQDIAALRCLEEQTNEYLKAYGYNDVFVTTVHQWMGGFPQDESKAFGVIVTATTIALAGATKVIVKTPHEAIGPTKEANAAGIKATKMLNMLEGQRPMMSKELETEM AVIKAETKICLDMFELKGDLAIGTVKAFETGVMDIPFGPSKYNAGKMM PVRDNLGCVRYLEFGNVPFTEEIKNYNRERLQERAKFEGRDVSFQMVIDDIFAVGKGRRLIGRPE

>d1eexa__ c.1.19.3 (A:) Diol dehydratase, alpha subunit {Klebsiella oxytoca}

MRSKRFEALAKRPVNQDFVKEWIEEGFIAMESPNPKPSIKIVNGAVTELDGKPVSDFDLIDHFIARYGINLNRAEV MAMDSVKLANMLCDPNV KRSEIVPLTTAMTPAKIVEVVSHMNVVEEMMMAMQKMRARRTPSQAHVTVKDNPVQIAADAAEGA WRGFDEQETTVAVARYAPFNAIALLVGSQVGRPGVLTQSLEEATELKGMLGHTCYAETISVYGETPVFTDGD DTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMILYLEARCIYITKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSL DLECASSNDQFTHSMDMRRTARLLMQFLPGTDFISSGYSAVPNYDNMFAGSNEDAED FDDYNVIQRDLKVDGGLRPVREEDVIAIRNKAARALQAVFAGMGLPITDEEVAATYAHGSKDM PERNIVEDIKFAQEIINKRNNGLEVVKALAQGGFTDVAQDMLNIQKAKLTDYHTSIIIVGDGQVLSA VNDVNDYAGPATGYRLQGERWEEIKNIPGALDPN

>d1f3ea__ c.1.20.1 (A:) tRNA-guanine transglycosylase {Zymomonas mobilis}

RPRFSFSIAAREGKARTGTIEMKRGVIRTPAFMPVGTAATVAKLPETVRATGADI LGNTYHMLRPG AERIAK LGGHSFM GWDRPI L DS GGGYQVMSLSSLTQKSEEGVTFKSHLDGSRHMLSPERSIEQHLLGSDIVMAFDCTPYPATPSRAASSMERSMRWAKRSRDA FDSRKEQAENAALFGIQQGS VFENLRQQSADALAEIGFDGYAVGGLAGVGEQDEMFRVLD FSVPMLPDDKPHYL MGVGK PDDIVGAVERGIDMFDCLV PTRS GRNGQAFTWDG PINIRNARFSEDLKPLDSECHACVCKW SRAYIHHLIRAGEILGAMLMT EHNIAYQQLMQKIRDSISEGRFSQFAQDFRARYF

>d1aj2__ c.1.21.1 (-) Dihydropteroate synthetase {Escherichia coli}

MKLFAQGTSLDLSPHVMGILNVTPDSFSDGGTHNSLIDAVKHANLMINAGATI IDVGGESTRPGAAEVSV EELQRVIPVVEAIAQRFEVWISV DTS KPEVIRESAKVG AHIINDIRSLSEPGALEAAAETGLPVCLMHMQGNPKTMQEAPK YDDVFAEVNRYFIEQIARCEQAGIAKEKLLDPGF GFGK NLSH NYSLLARLAEFH HFNLPLLVGMSRKS MIGQLLN VGP SERL SGLACAVIAAMQGAH IRVHDV KETVEAMRV VEATLSAKENKRYE

>d1ad1a__ c.1.21.1 (A:) Dihydropteroate synthetase {Staphylococcus aureus}

TKTKIMGILNVTDPDSFDGGKFNNVESAVTRVKAMMDEGADIIDVGGVSTRPGHEMITVEEELNRVLPVVEAIVGFDVKISVDTFRSEVAEACLKG
VDIINDQWAGLYDHRMFQVAKYDAEIVMHNGNGRDEPVVEEMLTSLLAQAHQAKIAGIPSNIWLDPGIGFAKTRNEEAEVMARLDELVATE
YPVLLATSRKRFTKEMMGYDTPVERDEVATAATTAYGIMKGVRRAVHNVELNAKLAKGIDFLKENENARHN

>d1eye_a_c.1.21.1 (A:) Dihydropteroate synthetase {Mycobacterium tuberculosis}

PVQVMGVNLNTDDSFSDGGCYLDLDDAVKHGLAMAAAGAGIVDVGESSRPGATRVPAPVETSRVIPVVKELAACQGITSIDTMRADVARAALQ
NGAQMVNDVSGGRADPAMGPLAEADPVWLMHWRAVSADTPHPVRYGNVVAEVRA DLLASVADAAGVDPARLVLDPGLGFAKTAQHN
WAILHALPELVATGIPVLGASRKRLGALLAGPDGVMRPTDGRDTATAVSALAALHGA WGVRVHDVRASVDAIKVVEAWMGAE

>d1f6ya_c.1.21.2 (A:) Methyltetrahydrofolate: corrinoid/iron-sulfur protein methyltransferase MetR {Moorella thermoacetica}

MLIIGERINGMFGDIKRAIQERDPAPVQEWA RQEEGGARALDLNVGPVQDKV SAMEWLVEVTQEVSNLTLCSTDSTNIKAIEAGLKKKNRAMIN
STNAEREKVEKLFPLAVEHGAALIGLTMNKTGIPKDS DTRLAFAME LVA ADEFGLPMEDLYIDPLIL PANVAQDH APEVLKTLQQIKMLADPAKTV
LGLSNVSQNCQRPLINRTFLAMAMACGLMSIA DACDELIETAATAEILLNQTVYCDSFVKMFKTR

>d1uroa_c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Human (Homo sapiens)}

GFPELKNDTFLRAWGEETDYTPVWCMRQAGRYLPFRETRAQDFFSTCRSPEACCELTQPLRRPLDAIIIFSDILVVPQALGMEVTMVPKG
SFPEPLREEQDLERLRDPEVVA SELGYVFQAITL RQRLAGR VPLIGFAGAPWTLTYMVEGGGSSTM A QAKRWLYQRPQASHQLR I LDALPVY
VGQVVAGAQALQLFESHAGH LGPQLFNKFALPYIRDVA KVQ KARL REAGLAPVPM II FAKDGHFA EELA QAGYEVV GLDW TVAPK KARECV GKT
TLQGNLDPCALYASEEEIGQLVKQM LDDFGPHRYIANLGHGLYPDMDE HVGAFVDAVHKHSRLLRQ

>d1j93a_c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Tobacco (Nicotiana tabacum), UROD-III}

TQPLLDAVRGKEVERPPVLMRQAGRYMKSYQLLCEKYPLFRDRSENV DLVVEISLQPWKVFRPDGVILFS DILPLSGM NI PFDI IKGKGPVIFDPL
RTAADVEKVREFIPEKS PVYVG EAL TIRKEV NNQ AAVL GFVGAPFT LAS YVVEGGSSK NFTKIKRLAFAEPKVLH ALLQKFAT SMAK YIRY QADSGAQ
AVQJFD SWATE LSPVDFEEFSLPYLKQIV DSVKLTHPNL LILYAS GS GGLL ERPLTGVDV VSLDWT VMADG RRR LGP NVAI QGNVDPGVLF GS KEF
ITNRINDTVKKAGKGKHILNLGHGIKVG TPEENFAHFFEIA KGLR Y

>d1b5ta_c.1.23.1 (A:) Methylenetetrahydrofolate reductase {Escherichia coli}

GQINVSEFFPPRTSEMEQTLWNSIDRLSSLKP KFVSVTYGANS GERDRTHSIKGIKDRTGLEAAPH LT CIDATP DELRTIARDYWNNGIRHIVALRG
LPPGSGKPEMYASDLV TLKEVADFDISVAAYPEVHPEAKSAQADL NLK R KV DAGAN RAI TQFFF DVEYSLR FRDRC VSAGID V EIIPG ILP VSN FKQA
KKFADMTNVRIPAWMAQM FDGL DDDAETR KL VG AN IAM DMV K ILS REGV K DFH FYTLN RAE MSY AICHTL GVRPA

>d1heta2_c.2.1.1 (A:175-324) Alcohol dehydrogenase {Horse (Equus caballus)}

GFSTGYGS AVK VAK VTQGSTCAV FGLGGVGLS VIMGCKAAGAARIIGVDINKDKFAKAKEVGATEC VNPQDYKKPIQEV LTEM SNGGV DFS FEVIGR
LDTM VTA LSCC QEA YGV SIV GVPP DSQNL S MNPMLL SGRTWKG AIFGGF K

>d1d1ta2_c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

GFSTGYGA AV/KTGKVPG STCAV FGLGGVGLS VIMGCKAAGAARIIAV DINKDKFAKAK ELGATEC INPQDYKKPIQEV LKEMTDGGV DFS FEVIG
TMID ALAS CH MN YGT SVV VGVPPSA KML TYD PMI LLFT GR TWKG CVFG GLK S

>d1ht0a2_c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

GFSTGYGS AVK VAK VTPG STCAV FGLGGVGLS VIMGCKAAGAARIIAV DINKDKFAKAK ELGATEC INPQDYKKPIQEV LKEMTDGGV DFS FEVIG
DTMM ASLLC C H EAC GT S VIV GVPP DSQNL SINPMLL TGR TWKG AIFGGF K

>d1teha2_c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

GISTGYGA AVNTAKLEPGSVC AV FGLGGVGLA VIMGCKAAGAARIIAV DINKDKFAKAK ELGATEC INPQDYKKPIQEV LIEMTDGGV DFS FECIGNV
VMRAA LEACH KG WG VSVV VGV AAS GEEI ATRP FQL VGT RTWKG TA FGGW KS

>d1e3ia2_c.2.1.1 (A:175-324) Alcohol dehydrogenase {Mouse (Mus musculus), class II}

LICCGFSSGYGA INTAKVTPG STCAV FGLGC VGLS AII GCKIAGASRIIAID INGEKFPKA KALG ATDCLN PRELDKPVQDV IT ELAGG VDYS FLC
AGT AQ TLKA A VDCT VLWG WS CT VVG AKVDEM TIPT DVIL GR SING TFFGGW

>d1cdoa2_c.2.1.1 (A:176-324) Alcohol dehydrogenase {Cod (Gadus callarias)}

GVSTGFGA VNTAKV EPG STCAV FGLG AVGLA VMGCH SAGA KRIIAV DLNP DKF EAKV FGAT DFVN PNDH SEP ISQ VLS KMT NGG VDFS LEC
CV NVG VMR NALES CLKG WG VSVL VGW TD LH DVAT RP IQ LIAG RTWKG SMF GGFK G

>d1keva2_c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase {Clostridium beijerinckii}

MMTTGFHGAELADIQMGSVVVIGAVGLMGIAGAKLRGAGRIIVGSRPICVEAAKFYGATDILNYKNGHIVDQVMKLTNGKGVDRVIMAGGG
SETLSQAVSMVKPGGIISNINYHGSGDALLIPRVEWCGMAHKTIKGGLCPGGLRAEMLRDMVVYNRV
>d1ykfa2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase {Thermoanaerobacter brockii}
MMTTGFHGAELADIELGATVAVLGIGPVGLMAVAGAKLRGAGRIIAVGSRPVCVDAAKYYGATDIVNKDGPIESQIMNLTEGKGVDAIIAGGNAD
IMATAVKIVKPGGTIANVNYYFGEGEVLPVPRLEWGCGMAHKTIKGGLCPGGLRMRERLIDLVFYKRV
>d1e3ja2 c.2.1.1 (A:151-313) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}
LEPLSVGVHACRRAGVQLGTTVLVIGAGPIGLVSAAKAYGAFVVCTSPRRLLEVAKNCGADVTLVDPKAEEESSIIRSAIGDLPNTIDCSGNE
KCITIGINITRTGGTMLVGMGSQMVTPLVNACAREIDIKSFRYCNDPIALEMVASGRC
>d1qora2 c.2.1.1 (A:136-265) Quinone oxidoreductase {Escherichia coli}
YEIKPDEQFLFHAAAGGVGLIACQWAKALGAKLIGTVGTAQKAQSALKAGAWQVINYREEDLVERLKEITGGKKVRRVYDSVGRDTWERSLDCLQR
RGLMVSFGNSSGAVTGVNLGILNQKSLYVTRPS
>d1udc_c.2.1.2 (-) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase) {Escherichia coli}
MRVLVTGGSGYIGSHTCVQLLQNQHVDIILDNLCNSKRSPVIERLGGKHPTFVEGDIRNEALMTEILHDHAIDTVIHAGLKAVGESVQKPLEYYDN
NVNGTLRLISAMRAANVKNFIFSSSATVYGDQPKIPYVESFTGTPQSPYQSKLMVEQILTDLQKAQPDWSIALLRYFNPVGAHPSGDMGEDPQGI
PNNLMPYIAQVAVGRDRSLAIFGNDYPTEDGTGVRDYIHVMDLADGHVVAMEKLANKPGVHIYNLGAGVGNSLVDVNAFSKACGKPVNYHFAP
RREGDLPAYWADASKADRELNWVTRTLDEMAQDTWHWQSRHPQGYPD
>d1ek6a_c.2.1.2 (A:) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase) {Human (Homo sapiens)}
MAEKVLTGGAGYIGSHTVLELEAGLYLPVIDNFHNAFRGGGLSPESLRRVQELTGRSVEFEEMDILDQGALQRLFKKYSFMAVIHFAGLKAVGESV
QKPLDYYRVNLGTIQLLEIMKAHGVKNLFSSSATVYGNPQYLPLDEAHPTGGCTNPYQSKFFIEEMIRDLQCADKTWNNAVLLRYFNPTGAHASG
CIGEDPQGPQIPNNLMPYVSQVAIGRREALNVFGNDYTEDGTGVRDYIHVVDLAKGHIAALRKLKEQCGCRIYNLGTGTGYSVLQMVQAMEKASGK
KIPYKVVARREGDVAACYANPSLAQEELGWTAALGLDRMCEDLWRWQKQNPSFGFT
>d1bxka_c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Escherichia coli}
MRKILITGGAGFIGSALVRYIINETSDAVVVVDKLTYAGNLMMSLAPVAQSERFAFEKVDICDRAELARVFTEHQPDVMHLAAESHVDRSIDGPAAFIE
TNIVGTYTLEEARAYNALTEDKKSAFRFHISTDEVYGDLLHSTDFFETTPYAPSSPYASKASSDHVRAWLRTYGLPTLITNCNNYGPYHFPEK
LIPLMILNALAGKSLPVYGNQQIRDWLVEDHARALYCVATTGKVGETYNIGGHNERKNLDVVTICELLEELAPNPKPHGVAHYRDLITFVADRGH
DLRYAIDASKIARELGCVPQETFESGMRKTVQWYLANESWWKQVQDGSYQGER
>d1kepa_c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Streptococcus suis, serotype 2}
QFKNIIVTGGAGFIGSNFVHYVYNNHPDVHVTLDKLTYAGNKRNLAEAILGDRVELVVDIADAELVDKLAAKADAIVHYAAESHNDNSLNDPSFIH
TNFIGTYTLEARKYDIRFHHVSTDEVYGDPLREDLPGHGEGPGEKFTAETNYPSSPYASKASSDHVRAWRRTYGLPTIVTCNNYGPYQHIE
KFIPRQITNLAGIKPKLYGEGKVNDRWIHTNDHSTGVWAILTKGRMGETYIGADGEKNNKEVLELILEKMGQPKDAYDHTDRAGHDLRYAIDASK
LRDELGWPQFTDFSEGLEETIQWYTDNQDWKAEKEAVEANYAKTQEVIK
>d1kewa_c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Streptococcus suis, serotype 2}
MKILITGGAGFIGSAVRHIINKNTQDTVNNIDKLTYAGNLESLSIDESNRYNFEHADICDSAEITRIFEQYQPDAMHLLAAESHVDRSITGPAIFIETNIV
GTYALLEVARKYWSALGEDKKNNFRFHISTDEVYGDLPHPDEVENSTLPLFTETTAYAPSSPYASKASSDHVRAWRRTYGLPTIVTCNNYGPY
HFPEKLIPLVILNALEGKPLIYGKGDQIRDWLVEDHARALHMVTEGKAGETYNIGGHNEKKNLDVFTICDLDEIVPKATSREQITYVADRGH
DRRYAIADAGKISRELGWKPLETEFESGIRKTVEWYLANQTQWVNNVKSGAYQSWIEQNYEGRQ
>d1e6ua_c.2.1.2 (A:) GDP-4-keto-6-deoxy-d-mannose epimerase/reductase (GDP-fucose synthetase) {Escherichia coli}
AKQRVFIAGHGRMVGSAIRRQLEQRGDVELVLRTRDELNLLSDRAVHDFFASERIDQVYLAACKVGGIVANNTYPADFIYQNMIMIESNIIHAHQN
DVNKLLFLGSSCIYPKLAKQPMMAESELLQGTLEPTNEPYIAKIAGIKLCESYNRQYGRDYRSVMPNLVYQPHDNFHPNSHVIPALLRFHEATAQKAP
DVVVWGSQTPMREFLHVDDMAASIHMELAHEVWLNTQPMPLSHINVGTGVDCIRELAQTIKVVGYKGRVVFDAKPDGTPRKLLDVTRLH
QLGWWYHEISLEAGLASTYQWFLENQ
>d1db3a_c.2.1.2 (A:) GDP-mannose 4,6-dehydratase {Escherichia coli}
SKVALITGVGQDGSLAEFLLEKGYEVHGIKRRASSFNTERVDHIYQDPHTCNPKFHLHYGDLSDTSNLTRILREVQPDEVNLGAMSHVAVSFESPE
YTADVDMGTRLLEAIRFLGLEKKTRFYQASTSELYGLVQEIPQKETTPFYPRSPYAVAKLYAYWITVNYRESYGMYACNGILFNHESPRRGETFVTRKI

TRAIANIAQGLESCLYLGNMDSLRDWGHAKDYVKMQWMMLQQEQPEDFVIATGVQYSVRQFVEMAAAQLGIKLRFEGTVEEKGIVSVTGH
APGVKPGDVIIAVDPRYFRPAEVETLLGDPTKAHEKLGWKPEITLREMVSEMVANDLEAKKHS

>d1eq2a_c.2.1.2 (A:) ADP-L-glycero-D-mannoheptose 6-epimerase {Escherichia coli}

MIIVTGGAGFIGSNIVKALNDKGITDILVVVDNLKDGTKFVNVLVDLNIAIDYMDKEDFLIQIMAGEEFGDVEAIFHEGACSTTEWDGKYMMMDNNYQY
SKELLHYCLEREIPFLYASSAATYGGRTSDFIESREYEKPLNVGYSKLFDEYVRQILPEANSQIVGFRYFNVYGPREGHKGSMASVAFLNTQLNNGES
PKLFEGSENFKRDFVYVGADVNLWFLENGVSGIFNLGTGRAESFQAVADATLAYHKKQIEYIPFPDKLKGRYQAFTQADLTNLRAAGYDKPFKTV
AEGVTEYMAWLN

>d1qrra_c.2.1.2 (A:) Sulfolipid biosynthesis protein SQD1 {Thale cress (Arabidopsis thaliana)}

KRVMVIGGDGYCGWATALHLSKKNYEVICVDNLVRRLFDHQLGLESLTIASIHDRISRWKALTGKSIELYVGDICDFEFLAESFKSFEPDSVVFHGEQR
SAPYSMIDRSRAVYTQHNNVIGTLNVLFIAKEFGECHVLKLTGMEYGTNPIDIEGYITITHNGRTDLPYPKQASSFYHLSKVHDHNIAFTCKAW
GIRATDLNQGVVYGVKTDETEMHEELRNRLDYDAVFGTALNRFCVQAAVGHPLTVYGKGGQTRGYLDIRDTVCQCVEIAIANPAKAGEFRVFNQFT
QFSVNELASLVTAGSKLGLDVKKMTVPNPRVEAEEHHYNAKHTKLMELGLEPHYLSDSLDSLLNFAVQFKDRVDTQIMPSSWKKIGVKT
>d1k6xa_c.2.1.2 (A:) Negative transcriptional regulator NmrA {Aspergillus nidulans}

QQKKTIAVNVNATGRQAASLIRVAAAVGHHVRAQVHSLKGLIAEELQAIPNVTLFQGPLLNNVPLMDTLPFEGAHLAFINTTSQAGDEIAIGKDLADAA
KRAGTIQHYIYSSMPDHSLYGPWPAPMVWAKPFTVENYVRQLGLPSTFYAGIYNNNFTSLPYPLFQMELMPDGTFEWHPFDPIPLPWLD
DVGPELLQIFKDPGPQKWNGHRIALTFTLSPVQVCAAFSRALNRRVTVQVPKVEIKVNIPVGYREQLAEIEVVFGEHKAPYFPLPEFSRPAAGSPKGL
GPANGKGAGAGMMQGPGGVISQRTDEARKLWSGRWDMEYAREVPIEEEANGLDWML

>d1cyda_c.2.1.2 (A:) Carbonyl reductase {Mouse (Mus musculus)}

LNFSGLRALVTGAGKGIGRDTVKALHASGAKVVAVRTNTSDLVSLAKECPGIEPVCVDLGDWDATEKALGGIGPVDLLVNAALVIMQPFL
DRSFVNLRSVQFQSVQMVARDMINRGVPGSIVNVSSMVAHVTPNLTYSSTKGAMTMLTKAMAMELGPHKIRVNSVNPTVV/LTDMGKKVSADP
EFARKLKERHPLRKFAEVEDVVNSILFLLSDRSASTSGGGILVDAGYL
>d1oaa_c.2.1.2 (-) Sepiapterin reductase {Mouse (Mus musculus)}

ADGLGCAVCVLTGASRGFGRALAPQLARLLSPGSVMLVSARSESMLRQLKEELGAQQPDLKV/LAAADLGTEAGVORLLSAVRELPRPEGLQRLLL
NNAATLGDVSKGFLNVNDLAEVNNYWLNLTSMLCLTSGTLNAFQDSPGLSKTVVNISSLCALQPYKGWGLYCAGKAARDMLYQVLAEEPSVRL
SYAPGPLDNDMQQLARETSKDPPELRSKLQKLKSDGALVDCGTSAQKLLQQKDTFQSGAHVDFYD

>d1hdr_c.2.1.2 (-) Dihydropteridin reductase (pteridine reductase) {Human (Homo sapiens)}

EARRVLVYGGRGALGSRCVQAFRARNWWVASVDVENEASASIIVKMTDSFTEQADQVTAEVGKLLGEEKVDAILCVAGGWAGGN
KAKSLSFKNC
CDLMWKQSIWTSTISSHLATKHLKEGGLLAGAKAALDGTGPMIGYGMAGKAVHQLCQSLAGKN
NSGMPPGAAIAVLPV
TLDPMNRKS
MPEA
DFSSWTPL
EFLVETFHDWITGKNRPS
GS
LIQV
VTT
EGRT
ELTPAY
>d1e7wa_c.2.1.2 (A:) Dihydropteridin reductase (pteridine reductase) {Leishmania major}

TV
PVALVTGAAKRLGRSIAEGLHAEGYAVCLHYHR
SAAEANALSATLNARRPNSAITVQADLSNV
ATAPVSGADGS
APV
TLF
TRCA
ELV
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>d1fds_c.2.1.2 (-) Human estrogenic 17beta-hydroxysteroid dehydrogenase {Human (Homo sapiens)}

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>d1fmca_c.2.1.2 (A:) 7-alpha-hydroxysteroid dehydrogenase {Escherichia coli}

MFNSDNLRDGKCAITGAGAGIGKEIAITFATAGASVV
VSDINADAANHV
VDEIQLGGQAFACRCDITSEQELS
ALADFAISKLGKV
DILVNNAGGG
GPKPF
DMP
MAD
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>d1hdca_c.2.1.2 (A:) 3-alpha,20-beta-hydroxysteroid dehydrogenase {Streptomyces hydrogenans}

NDLSGKTVIITGGARGAEARQAVAAGARVV
LADVLDEEGAATARELGDAARYQHLD
VTIEDW
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RQGEGNYPNTPMGRVGEPEIAGAVVLLSDTSSYVTGAELAVDGGWTTGPTVKYVMQ

>d1fjha_c.2.1.2 (A:) 3-alpha-hydroxysteroid dehydrogenase {Comamonas testosteroni}

MSIIVISGCATGIGAATRKVLEAGHQIVGIDIRDAEVIADLSTAEGRKQAIADVLAKCSKGMDGLVCAGLGPQTVKLGNNVSVNYFGATELMDAFLP
ALKKGHQPAAVVISSVASAHAFDKNPLALALEAGEEAKARAIIVEHAGEQGGNLAYAGSKNALTVAVRKRAAAWGEAGVRLNTIAPGATEPLLQAG
LQDPRYGESIAKFVPPMGRRAEPSEMASVIAFLMSPAASYVHGAQIVIDGGIDAVMRPTQF

>d1bdb_c.2.1.2 (-) Cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase {Pseudomonas sp., lb400}

MKLGEAVLITGGASGLRALVDRFAEGAKVAVLDKAERLAELETDHGDNVLGIVGDVRSLEDQKQAASRCVARFGKIDTLIPNAGIWYSTALVD
LPEESLDAAFDEVFHINVKYIHAVKACLPALVASRGNVIFTISAGFYPNGGGPLYTAAKHAIVGLVRELAFELAPYVRVNGVGSGGINSDLRGPSLLG
MGSKAISTVPLADMLKSVPPIGRMPEVEEYTGAYVFFATRGDAAPATGALLNYDGGLGVRFSGAGGNNDLLEQLNIH

>d1b16a_c.2.1.2 (A:) Drosophila alcohol dehydrogenase {Fruit fly (Drosophila lebanonensis)}

MDLTNKVIFVAALGGIGLDTSRLEVCRNLKNFVILDRVENPTALAEKAINPKVNITFHTYDVTVPVAESKKLLKIFDQLKTVIDLINGAGILDDHQIE
RTIAINFGLVNTTAAILDFWDKRKGPGGIIANICSVTGFNAIHQPVYSAKAAVSVFTNSLAKLAPITGVTAYSINPGITRPLVHTFNSWLDVEPRV
AEULLSHPTQTSEQCGQNFVKAIEANKNGAIWKLDLGTEAIEWTKHWDShI

>d1gcoa_c.2.1.2 (A:) Glucose dehydrogenase {Bacillus megaterium}

MYKDLEGKVVITGSSTGLKSMAIRFATEKAKVVVNRSKEDAEANSVLEEIKVGGEIAVKGDVTESDVINLVQSAIKEFGKLDVMINNAGLENP
VSSHESMSLDWNKVIDTNLTGAFLGSREAIKYFVENDIKGTVINMSSVHEKIPWPLFVHYAASKGGMCLMTETLALEYAPKGIRVNNIGPGAINTPIN
AEKFADPEQRADVESMIPMGYIGEPEEIAAVAWLASSEASYYTGITLFADGGMTQYPSFQAGRG

>d1gega_c.2.1.2 (A:) meso-2,3-butanediol dehydrogenase {Klebsiella pneumoniae}

KKVALVTGAGQQIGKIALRLVKDGFAVAIADYNDATAKAVASEINQAGGHAVAVKVDVSDRDQVFAAVEQARKTLGGFDVIVNNAGVAPSTPIESIT
PEIVDKVYININVKGVIWGIQAAVEAFKKEGHGGKIINACSQAGHVGNPPELAYSSSKFAVRGLTQTAARDLAPLGITVNGYCPGIVKTPMWAEIDRQ
VSEAAGKPLGYGTAEFAKRITLGRLESEPEDVAACSYLASPDSDYMTGQSLLIDGGMVFN

>d1h5qa_c.2.1.2 (A:) Mannitol dehydrogenase {Mushroom (Agaricus bisporus)}

PGFTISFVNKTIVTGGNRIGLAFTRAAAAGANVAVIYRSAADAVEVTEKGKEFGVKTAKYQCDVSNTDIVTKTIQQIDADLGPIGLIANAGVSVV
KPATELTHEDFAFYDVNVFGVFNTCRAVAKLWLQKQQKGSIVVTSSMSSQIINQSSLNGSLTQVFYNSSKAACSNLVKGLAAEWASAGIRVNALSPG
YVNTDQTAHMDKKIRDHQASNIPLNRFAQPEEMTGQAILLSDHATYMTGGEYFIDGGQLIW

>d1edo_a_c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Oil seed rape (Brassica napus)}

SPVVVTGASRGIGKIALSLGKAGCKVLNYARSAAEEVSKQIEAYGGQAITFGGDVSKEADVEAMMKTADAWGTIDVVNNAGITRDTLLIR
MKKSQWDEVIDLNLTGVFLCTQAATKIMMKRKGRRIINIASVVGIGNIGQANYAAKAGVIGFSKTAAREGASRNINVNVCVPGFIASDMTAKLGE
DMEKKILGTIPLGRTGQPENVAGLVEFLSPAASYITGQAFTIDGGIA

>d1i01a_c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Escherichia coli}

MNFEKGKIALVTGASRGIGRAIAETLAARGAKVIGTATSENGAQASDYLGANGKGLMLNVTDPASIESVLEKIRAEFGEVDIILVNNAGITRDNLLMRM
KDEEWNDIETNLSSVFRLSKAVMRAMMKRKGRRIITGSVVGTMGNNGQANYAAKAGLIGFSKSLAREVASRGITNVVAPGFIETDMTRALSD
DQRAGILAQPAGRLGGAQEIANAVAFLASDEAAYITGETLHVNGGM

>d1eno_c.2.1.2 (-) Enoyl-ACP reductase {Oil seed rape (Brassica napus)}

LPIDLRLGKRAFIAGIADDNGYWAVAKSLAAGAEILVGTWVPALNIFETSLRRGKFDQSRVLPDSLIMEIKKVYPLDAVFDPEDVPEDVKANKRYA
GSSNWTVQEAAECVRQDFGSIDILVHSLANGPEVSKPLLETSRKGYLAISASSYSFVSLSHFLPIMNPGGASISLTLYIASERIIPGYGGGMSSAKAALE
SDTRVLAFEAAGRKQNIRVNTISAGPLGSRAAKAIGFIDTMIEYSNNAPIQKLTADEVGNAAFLVPLASAITGATIYVDNGLNSMGVALDSPVK

>d1eny_c.2.1.2 (-) Enoyl-ACP reductase {Mycobacterium tuberculosis, TB, gene InhA}

AGLLDGKRLVSGIITDSSIAFIHARVAQEQAQLVLTGFDRRLIQRITDRLPAKAPLLELDVQNEEHLASLAGRVTEAIGAGNKLGVVHSIGFMPQT
GMGINPFFDAPYADVSKGHIHISAYSYASMAKALLPIMPGGSIVGMDFDPSRAMPAYNWMTVAKSALESVNRVAREAGKYGVRSNLVAAGPIRTL
AMSAIVGGALGEEAGAQIQLLEEGWDQRAPIGWNMKDATPVAKTCALLSDWLPATTGDIYADGGAHTQLL

>d1qg6a_c.2.1.2 (A:) Enoyl-ACP reductase {Escherichia coli}

GFLSGKRILVTVASKLSIAYGIAQAMHREGAELAFTYQNDKLGRVEEFAAQLGSDIVLQCDVAEDASIDTMFAELGKVWPKFDFVHSIGFAPGDQ
LDGDYVNAVTRGFKIAHDISYSFVAMAKACRSMLNPGSALLTLSYLGAEAIPNVMGLAKASLEANVRYMANAMGPEGVRVNAISAGPIRTL

AASGIKDFRKMLAHCEAVPIRRTVIEDVGNSAFLCSDLASAGISGEVVHVDGGFSIAAMNE

>d1ae1a_c.2.1.2 (A:) Tropinone reductase {Jimsonweed (*Datura stramonium*), I}

RWSLKGTTLATVGGSKIGGYAIVELAGL GARVYTCRSNEKELEDECLEIWREKG LNEVEG S VCDLLS TERD KLMQTV AHVFDG KLNILVNNAGVVIHK
EAKDFTEKDYNII MGTNF EAAYHLSQIAYPLLK ASQNGN VIFLSSIA GFSALPSV SLYSASKGAINQMT KSLACEWAKDNIRVNSVAPGVILTPLVETAIK
KNPHQKEEIDNFIVKTPMGRAGKPQEVS ALIAFLC FPAASYITGQIIWADGGFTANGGF

>d2ae2a_c.2.1.2 (A:) Tropinone reductase {Jimsonweed (*Datura stramonium*), II}

AGRWNLEGCTALTVGGSRIGGYGIVEELASLGASVYTCRSRNQKELNDCLTQWRSKGKFVEASVCDLSSR SERQELMNTVANFHGKLNILVNNAGIV
IYKEAKDYTVEDYSLIMSINFEAAYHLSVLAHPFLKASERGNVVFISSSVSGALAVPYEA VY GATKGAMDQLTRCLAFEWAKDNIRVNGVPGVIA TSLV
EMTIQDPEQKENLNKLIDRCALRRMGEPKELAAMVAFLCFPAASYVTGQIYV DGGLMANC GF

>d1g0oa_c.2.1.2 (A:) 1,3,8-trihydroxynaphthalene reductase (THNR, naphtol reductase) {Rice blast fungus (*Magnaporthe grisea*)}
KYDAIPGPLGPQSASLEGKVALVTGAGRGIGREMAMELGRRGCKVIVNYANSTESAEEVVAIKKNGSDAACVKANVGVVEDIVMFEEAVKIFGKL
DIVCSNSGVVSGHVKDVTPPEFDRVFTINTRGQFFVAREAYKHEIGGRLILMGSITGQAKAVPKHAVYSGSKGAIETFARCMAIDMADKKITVNVV
APGGIKTD MYH AVCREYIPNGENLSNEEVDEYAAVQWSPLRRVGLPIDIARVVCF CLASNDGGWVTGKVIGIDGGACM

>d1ja9a_c.2.1.2 (A:) 1,3,6,8-tetrahydroxynaphthalene reductase {Rice blast fungus (*Magnaporthe grisea*)}

SKPLAGKVALTTGAGRGIGRIAIELGRGASVVNVYNGSSKAAEEVVAELKKLGAQGVAIQADISKPSEVVALFDKAVSHFGGLDFVMSNSGM EVW
CDELEV TQELFDKVFNLNTRGQFFVAQQGLKHCRGGRIILTSSIAAVMTGIPNH AYAGSKAAVEGFCRAFAVDCGAKGTVNCIAPGGVKTDMFD
ENSWHYAPGGYKGMPQEKIDEGLANMNPLKRIGYPADIGRAVSALCQE ESEWINGQVI LTGGGI

>d1hdoa_c.2.1.2 (A:) Biliverdin IX beta reductase {Human (*Homo sapiens*)}
MAVKKIAIFGATGQTGLT LAQAVQAGYEVTLVRDSSRLPSEGPRPAHVVG DV LQAADVDKTVAGQDAVIVLLGTRNDLSP TVMSEGARNIVA
AMKAHGV DVKVVACTSAFLWDP TKVPP RLQAVTDDHIRMHKVLRES GLKYVAVM PPHIGDQPLTGAYTVTLDRGRPSRVISKHDLGHFMLRCLTT
DEYDGHSTYPSHQY

>d1e6wa_c.2.1.2 (A:) 3-hydroxyacyl-CoA dehydrogenase {Rat (*Rattus norvegicus*)}
SVKGLAVITGGASGLSTAKRLVGQGATAVLLDVPNSEGETEAKKLGGNCIFAPANVTSEKEVQAALT LAKEKFGRIDVA NCAGIAV AIKTYHEKKN
QVHTLED FQRVINVN LIGTFN VIRL VAGVMGQNEPDQGGQRGV INTAS VAA FEGQV GQAA YASKGGIVG MTLPIARDL APIRV VTIAPGLFATP
LTLPDKVRNFLASQVFPFSRLGDPAEYAH LVQM VIENPFLN GEVIR LDGAI RMQP

>d1hu4a_c.2.1.2 (A:) Carbonyl reductase/20beta-hydroxysteroid dehydrogenase {Pig (*Sus scrofa*)}
SSNTRVALVTGANKGIGFAIVRDLCRQFAGDVLTARDVARGQAAVKQLQAEGLSPRFHQLDIIDLQ SIRALCDFLRKEYGGLDV VNNAIAFQLDN
PTPFHIQAE LTMKT NFMGTRNVCTELLPLIKPQGRV NVSSTEGVR ALNECSPELQQKF SETITEELV GLMNKF VEDTKNGVHRKEG WSD STYGV
TKIGVSLSRIYARKLREQ RAGDKILLNACCPGWVRTDMGGPKAPSPEVGAETPVYALLPSDAEGPHQFVTDK VVEWGVPPE SYPWVNA

>d1gad01 c.2.1.3 (O:0-148,O:313-330) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Escherichia coli}
TIKVGINGFGRIGRIVFRAAQKRS DIEIVAIN DLDADYMAYMLKYD STHGRFDGT VEVDGHLIVNGKKIRVTAERDPANLK WDEVGV DVA EATGL
FLTDETARKHITAGAKKVVMTGPSKDNTPMFVKGANFD KYAGQD IVSNASXNETGYSNKVLDLIA HISK

>d1gd1o1 c.2.1.3 (O:0-148,O:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Bacillus stearothermophilus, nca 1503}
AVKVGINGFGRIGRNVFRAALKNP DIEVVAVNDLT DANTLAHLLKYDSVHGR LDAEV SVNGNNLVVNGKEIIVKAERDPENL AWGEIGV DIVV ESTG
RFTKREDAAKHLEAGAKKVIISAPAKNEDITIVMGVNQDKYDPKAH HVISNASXNETGYSNRV DLA YIAS KGL

>d1cer01 c.2.1.3 (O:1-148,O:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermus aquaticus}
MKVGINGFGRIGRQVFRILHSRGVEVALINDTDNKT LAHLLKYDSIYH RFPGEV AYDDQYLYV DGKAIRATAV KDPK EIPWAEAGVGV VIESTGVFTD
ADKAKAHLEGGAKKVIITAPAKG EDITIVMGVNHEADPSRHHIISNASXNEWGYANR VADL VELV LRKG V

>d1hdgo1 c.2.1.3 (O:1-148,O:313-331) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermotoga maritima}
ARVAINGFGRIGRLVYRIIYERKNP DIEVVAINDL TD TKT LAHLLKYDSVHKKFPGKVEY TENS LIVDGKEIKVFAEPDPSKLPW KDLGVDFVIESTGVFR
NREKAELH LQAGAKKVIITAPAKG EDITIVV IGCNEDQLKPEHTIISCASXNEYGYSNRV DLELLK M

>d1b7go1 c.2.1.3 (O:1-138,O:301-340) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Sulfolobus solfataricus}
MVNVAVNGYGTIGKRVADAIKQPDMKLVGVAKTSPN YEA FIAHRRGIRIYV PQQS IKKFEES GIPVAGT VEDLIK TS DIVVDTT PNGVGA QYKPIY LQL

QRNAIFQGGEKAEVADISFSALCNYNEALGKKYIRVVSXESIVVPENIDAIRASMKLMSAEDSMRITNESLGILKGYLI
>d1cf2o1 c.2.1.3 (O:1-138,O:304-336) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Methanothermus fervidus}
MKAVAINGYGTVGKRVADAIAAQQDDMKVIGVSKTRPDEARMALKGYDLYVAIPERVKLFKAGIEVAGTVDDMLDEADIVIDCTPEGIGAKNLK
MYKEKGIAIFQGGEKHEDIGLSFNSLNYESYGKDYTRVVXIVPENVDAVRAILEMEEDKYKSINKTNKAMNIL
>d1gaa1 c.2.1.3 (A:1-164,A:334-358) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Trypanosoma brucei brucei, glyosome}
TIKVGINGFGRIGRMVFQALCDDGLLNEIDVVAVVDMNTDARYFAYQMKYDSVHGKFHSVSTTSKPSVAKDDTLVVNGHRLCVKAQRNPADL
PWGKLGVEYVIESTGLFTVKSAAEGLRGGARKVVISAPASGGAKTFVMGVNVHNYYNPREQHVSNASXNEWGYSHRVVDLVRHMAARDRAAK
L
>d1i32a1 c.2.1.3 (A:1-165,A:335-358) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Leishmania mexicana}
APIVGINGFGRIGRMVFQACDQGLIGTEIDVVAVVDMSTNAEYFAYQMKHDTVHGRPKYTVEAVKSSPSVETADLVVNGHRIKCVKAQRNPAD
LPWGKLGVDYVIESTGLFTDKLKAEGHIKGAKKVVISAPASGGAKTIVMGVNQHEYSPASHHVVSNASXNEWAYSHRVVDLVRYMAAKDAASS
>d1dssg1 c.2.1.3 (G:1-148,G:313-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Lobster (*Palinurus versicolor*)}
SKIGINGFGRIGRLVRAALEMGAQVAVNDPFIALEYMVYMFYDSTHGMFKGEVKAEDGALVVDGKKTIVFNEMIKPENIPWSKAGAEYIESTG
VFTTIEKASAHKGGAKKVIISAPSADAPMFVCGVNLEKYSKDMKVVSNASXNEFGYSQRVIDLIKHMHQVDSA
>d3gpdg1 c.2.1.3 (G:1-150,G:315-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Human (*Homo sapiens*)}
GKVKGVDGFGRIGRLVTRAFAFNNSGKVDIVAINDPFIDLHYMVMFQYDSTHGKHFHTVKAEDGKLVIDGKAITFQERDPENIKWGDAGTAYV
TGVFTTMEKAGAHLKGGAKRIVISAPSADAPMFVMGVNHFKYANSLKIISNASXNEFGYSERVVVLMAHMASKE
>d1jn0a1 c.2.1.3 (A:0-148,A:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Spinach (*Spinacia oleracea*)}
KLKVAINGFGRIGRNFLRCWHGKDSPLDVVINDTGGVKQASHLLKYDSILGTFDADVKTAGDSAISVGKVIKVVSDRNPVNLPWGDMGIDLVIEGT
GVFVDRDGAGKHLQAGAKKVLTAPGKDIPTYVVGVNEEGYTHADTIIISNASXNEWGYSRVVDLADIVANKWQ
>d1g3a1 c.2.1.3 (A:1-133,A:355-367) Aspartate beta-semialdehyde dehydrogenase {Escherichia coli}
MKNVFIGWRGMVGSVLMQRMVEERDFDAIRPVFFSTSQLGQAAPSFGGTTGLQADFLEALKALDIITCQGGDYTNEIYPKLRESGWQGYW
IDAASSLRMKDDAIILDVPNQDVITDGLNNGIRTFGGXAAEPLRRMLRQLA
>d1ebfa1 c.2.1.3 (A:2-150,A:341-359) Homoserine dehydrogenase {Baker's yeast (*Saccharomyces cerevisiae*)}
STKVVNVAVIGAGVVGSAFLDQLLAMKSTITYNLVLLAEAERSLISKDFSPNVGSWDKAALAASTTKTPLDDLIAHLKTPKPVILVDNTSSAYIAGFY
TKFVENGISATPNKKAFSSDLATWKALFSNKPTNGFVYHEATVGAGLXAAVTAAGVGLGVKIAQRL
>d1e5qa1 c.2.1.3 (A:2-124,A:392-450) Saccharopine reductase {Rice blast fungus (*Magnaporthe grisea*)}
ATKSVLMILGSGFVTRPLDVLTDGKVTACRTLESACKLSAGVQHSTPISDLVNDDAALDAEVAKHDVLVISLIPYTFHATVIKSAIRQKKHV
PAMMELDQAQKDAGITVMNEIGXYSAMAKLGVGPCAVAVKFVLDTISDRGV/LAPMNSKINDPLMKEKYGIECKEKVVA
>d1f06a1 c.2.1.3 (A:1-118,A:269-320) Diaminopimelic acid dehydrogenase (DAPDH) {Corynebacterium glutamicum}
MTNIRVAIVGYGNLGRSVEKLIAKQPDMDLVGIFSRATLDTKTPVFDADVDKHADDVDVLFCMGSATDIPEQAPKFAQFACTVDTYDNHRDIPR
HRQVMNEATAAGNVALVSTGXRNPDFTASSQIAFGRAAHRMKQQGQSGAFTVLEVAPYLLSPENLDDLIARDV
>d1dih_1 c.2.1.3 (2-130,241-273) Dihydrodipicolinate reductase {Escherichia coli}
HDANIRVAIAGAGGRMGRQLIQAALALEGVQLGAALEREGRSSLLGSDAGELAGAGKTVQSSLDAVKDDFDVFIDFTRPEGLNHLAFCRQHGK
GMVIGTTGFDEAGKQAIRDAADIAIVFAANFSXMTFANGAVRSALWSKGESGLFDMRDVLDLNNL
>d1k5ha2 c.2.1.3 (A:1-125,A:275-300) 1-deoxy-D-xylulose-5-phosphate reductoisomerase {Escherichia coli}
MKQLTILGSTGSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLEFSPRYAVMDDEASAKLLKTMILQQQGSRT
EVLSGQQAACDMALEDVD
QVMAAIVGAAGLLPTLAIRAGKTILLANKXDMRTPIAHTMAWPNRVNSGVKPLDFC
>d1gcua1 c.2.1.3 (A:1-128,A:247-292) Biliverdin reductase {Rat (*Rattus norvegicus*)}
MDAEPKRKFGVVVVGVRAGSVRLRDLKDPRSAFLNLIBFVSRRELGSDEVQRQISLEDALRSQEIDVAYICSESSHEDYIRQFLQAGKHL
VEYPM
TLSFAAAQELWELAAQKGRVLHEEHVELLXKNIFLKDQDIFVQKLLDQVSAEDLAAEKKRIMHCLGLASDIQKLCH
>d1evja1 c.2.1.3 (A:30-160,A:323-381) Glucose-fructose oxidoreductase, N-terminal domain {Zymomonas mobilis}

RRFGYAIVGLKYALNQILPGFAGCQHSRIEALVDGNAEKAKIVAAEYGVDPRKIYDYSNFDKIAKDPKIDAVYIILPNSLHAEFAIRAFKAGKHVMCEK
PMATSVADCQRMIDAAKAANKLMIGYRCHYXNQFSACQLDHAEAVINNKPVRSPEGMCDVRLIQAIYEARTGRPVNTDWGYVRQGGY
>d1h6da1 c.2.1.3 (A:51-212,A:375-433) Glucose-fructose oxidoreductase, N-terminal domain {Zymomonas mobilis}
QAATLPAGASQVPTTPAGRPMYAIRPMPEDRRFGYAIVGLKYALNQILPGFAGCQHSRIEALVSGNAEKAKIVAAEYGVDPRKIYDYSNFDKIAK
PKIDAVYIILPNSLHAEFAIRAFKAGKHVMCEKPMATSVADCQRMIDAAKAANKLMIGYRCHYXNQFSACQLDHAEAVINNKPVRSPEGMCDV
RLIQAIYEARTGRPVNTDWGYVRQGGY
>d1dpga1 c.2.1.3 (A:1-181,A:413-426) Glucose 6-phosphate dehydrogenase, N-terminal domain {Leuconostoc mesenteroides}
VSEIKTLVTFFGGTDLAKRKLYPSVFNLKKGYLKHFIAVGTAQRQALNDDEFKQLVRDCIKDFTDDQAQAEAFIEHFSYRAHDVTDAASYAVLKEAIE
EAADKFIDGNRIFYMSVAPRFFGTIAKYLKSEGGLADTGYNRLMIEKPGFTSYDTAAELQNDLENAFDDNQLFRIDHLYLGXEPMIHDTMNGD
>d1qkia1 c.2.1.3 (A:12-199,A:435-449) Glucose 6-phosphate dehydrogenase, N-terminal domain {Human (Homo sapiens)}
VCGILREELFQGDAFHQSDFHIFIIMGASGDLAKKKIPTYWWLFRDGLLPENTFIVGYARSRLTADIRKQSEPFKATPEEKLKLEDFFARNNSVAGQY
DDAASYQRQLNSHNMNALHLGSQANRLFYALPPPTVYEAVTKNIHESCMSQIGWNRIIVEKPFGRDLQSSDRLSNHISLFREDQIYRIXDAYERLILDVF
CGSQ
>d2naca1 c.2.1.4 (A:148-335) Formate dehydrogenase {Pseudomonas sp., strain 101}
ISVAEHVMMILSLVRNYLPSHEWARKGGWNIACVSHAYDEAMHVGTVAAAGRIGLAVLRLAPFDVHLHYTDRHRLPESVEKELNLTWHATRE
DMYPVCDVVTLNCLPLPETEHMINDETLKLFKRGAYIVNTARGKLCRDAVARALESGRLAGYAGDVWFQPQAPKDPWRTMPYNGMTPHISG
>d1qp8a1 c.2.1.4 (A:83-263) Putative formate dehydrogenase {Archaeon Pyrobaculum aerophilum}
ADAVAEEFALALLAPYKRIQYGEKMKGDYGRDVEIPLIQGEKVAVLGLGEIGTRVGKILAALGAQVRGFSRTPKEGPWRFTNSLEALREARAACVA
LPLNKHTRGLVKYQHLAGMAEDAVFNVGRAEVLDRDGVLRILKERPQFIFASDVWWGRNDFAKDAEFFSLPNVVATPWVAG
>d1dxy_1 c.2.1.4 (101-299) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}
SPAIAEFALTDLYLLRNMGKVQAQLQAGDYEKAGTFIGKELGQQTVGVMGTGHIGQVAIKLFKGFGAKVIADPYPMKGDHPDFDYVSLEDLFKQ
SDVIDLHVPGIEQNTHIINEAFNLMKPGAIINTARPNLIDTQAMLSNLKSGKLAGVGIDTYEYETEDLLNLAKHGSFKDPLWDELLGMPNVVLSPHI
AYY
>d1gdha1 c.2.1.4 (A:101-291) D-glycerate dehydrogenase {Hyphomicrobium methylovorum}
VTVATAEIAMLLLGSARRAGEGEKMRTRSWPGWEPLEVGEKLDNKTLCIYGFSGIQQALAKRAQGFDMIDYFDTHRASSSDEASYQATFHDSL
DSLLSVSQFFSLNAPSTPETRYFFNKAТИKSLPQGAIVVNTARGDLVDNELVVALEAGRLAYAGFDVFAGEPNINEGYYDLPNTFLPHIGSA
>d1psda1 c.2.1.4 (A:108-295) Phosphoglycerate dehydrogenase {Escherichia coli}
NTRSVAELVIGLLLLRGVPEANAKAHRGVWNKLAAGSFEARAKKLGIIGYGHIGTQLGILAESLGMVYFYDIENKLPLGNATQVQHLSDLLNMSD
VVSLHVPENPSTKNMMGAKESLMKPGSLLINASRTVVDIPALCDALASKHLAGAAIDVFPTEPATNSDPFTSPLCEFDNVLLTPHIGG
>d2ldda1 c.2.1.4 (A:104-300) D-lactate dehydrogenase {Lactobacillus helveticus}
PNAIAEHAAIQARVLRQDKRMDEKMAKDLRWAPTIIGREVRDQVVGVTGHIGQVFMRIMEGFGAKVIADIFKNPELEKKGYVDSLDDLYK
QADVISLHVPDVPANVHMINDKSIAEMKDGVIVNCSRGLVDTAIVRLDSKIFGFVMDTYEDEVGVFNKDWEKGKEFPDKRLADLDRPNVLV
TPHTAF
>d1pjca1 c.2.1.4 (A:136-303) L-alanine dehydrogenase {Phormidium lapideum}
AGRLSVQFGARFLERQQGRGVLLGGVPGVKPGKVVILGGVVGTAAKMAVGLGAQVQIFDINVERLSYLETLFGSRVELLYNSAEIETAVAЕADL
LIGAVLPGRRAPILVPASLVEQMRTGSIVDVAVDQGGCVTLHPTSHTQPTYEVFGVVHYGVPNMPGA
>d1f8ga1 c.2.1.4 (A:144-326) Nicotinamide nucleotide transhydrogenase dI component {Rhodospirillum rubrum}
AGYRAVIDGAYEFARAFPMMMTAAGTVPPARVLVFGVGAGLQAIATAKRLGAVVMATDVRATKEQVESLGGKFTVVDDEAMKTAETAGGYAKE
MGEEFRKKQAEAVLKEVLKTDIAITTLIPGKPKAPVLITEEMVTMKPGSVIIDLAVEAGGNCPLEPGKIVVKHGVKIVGHTNVPSR
>d1b3ra1 c.2.1.4 (A:190-352) S-adenosylhomocysteine hydrolase {Rat (Rattus norvegicus)}
NLYGCRESLIDGIKRATDVMAGKVAVVAGYGDVGKGCAQALRGFGARVIITEIDPINALQAAMEGYEVTTMDEACKEGNIFVTTGCVDIILGRHFE
QMCKDDAIVCNIGHFDVEIDVKWLNEAVEKVNIKPQVDRYLLKNGHRIILLAEGRLVNLGCAMGH
>d1gpja2 c.2.1.10 (A:144-302) Glutamyl tRNA-reductase middle domain {Archaeon Methanopyrus kandleri}
SEGAWSIGSAAVELAERELGSLHDKTVLVVGAGEMGKTVAKSLVDRGVRAVLVANRTYERAVELARDLGGEAVRFDELVDHLARSDDVVSATAAPH

VIHVDDVREALRKDRRSPILIIDIANPRDVEEGVENIEDVEVRTIDDLRVIARENLERRK
>d1mlda1 c.2.1.5 (A:1-144) Malate dehydrogenase {Pig (Sus scrofa)}
AKVALVGASGGIGQPLSLLKNNSPVLRSRLLYDIAHTPGVAADLSHETRATVKYLGPEQLPDKLKGCDVVVIPAGVPRKPGMTRDDLFNTNATIVATL
TAACAQHCPDAMICIISNPVNSTIPITAEVFKKHGKVYNPNKIFG
>d5mdha1 c.2.1.5 (A:1-154) Malate dehydrogenase {Pig (Sus scrofa)}
SEPIRVLTGAAGQIAYSLYSIGNGSVFGKDQPIIILVLDITPMGMVLDGVLMELQDCALPLLKDIATDKEEIAFKLDLVAILVGSMPRRDGMERKDL
LKANVKIFKCQGAALDKYAKKSVKIVVGNPANTNCLTASKSAPSIPKENFSCL
>d7mdha1 c.2.1.5 (A:23-197) Malate dehydrogenase {Sorghum (Sorghum vulgare), chloroplast}
DCFGVFCTTYDLKAEDTKSWKKLVNIAVSGAAGMISNHLLFKLASGEVFGQDQPIALKLLGERSFQALEGVAMELEDSLYPLLREVSIGIDPYEVFE
DVDWALLIGAKPRPGMERAALLDINGQIFADQGKALNAVASKNVKLVGNPCNTNALICLNAPDIPAKNFHAL
>d1civa1 c.2.1.5 (A:12-193) Malate dehydrogenase {Flaveria bidentis, chloroplast}
LPAKQKPECFGVFCLTYDLKAEETKSWKKIINVAVSGAAGMISNHLLFKLASGEVFGPDQPISLKLLGERSFAALEGVAMELEDSLYPLLQVSIGIDP
YEIFQDAEWALLIGAKPRPGMERAADLLDINGQIFAEQGKALNAVASPNVKVMVGNPCNTNALICLNAPNIPPKNFHAL
>d2cmd_1 c.2.1.5 (1-145) Malate dehydrogenase {Escherichia coli}
MKVALGAAAGGIGQALALLKTQLPSGSELSDYDIAPVTGVAVDLSHIPTAVKIKGFSGEDATPALEGADVVLSAGVRRKPGMDRSDFNVNAGIVK
NLVQQVAKTCPKACIGIITNPVNTTVIAAAEVKKAGVYDKNKLFG
>d1bdma1 c.2.1.5 (A:0-154) Malate dehydrogenase {Thermus flavus}
MKAPVRVAVTGAAGQIGQSYLLFRIAAGEMLGKDQPVILQLLEIPQAMKALEGVVMELEDCAFPLLAGLEATDDPDVAFKDADYALLVGAAPRKAGM
ERRDLLQVNGKIFTEQGRALAEVAKKDVKVLVGNPANTNALIAYKNAPGLNPRNFTAM
>d2h1pa1 c.2.1.5 (A:22-162) Malate dehydrogenase {Archaeon Haloarcula marismortui}
TKVSVVGAAGTVGAAAGYNIALRDIADEVVFDIPDKEDDTVGQAADTNHGIYDSNTRVRQGGYEDTAGSDVVVITAGIPRQPGQTRIDLADNA
PIMEDIQSSLDEHNDDYISLTSNPVDLNRHLYEAGDRSREQVIG
>d1b8pa1 c.2.1.5 (A:3-158) Malate dehydrogenase {Aquaspirillum arcticum}
KTPMRVAVTGAAGQICYSLLFRIAANGDMLGKDQPVILQLLEIPNEKAQKALQGVMMEEIDDCAFPLLAGMTAHADPMATAFKDADVALLV GARPRGP
GMERKDLLEANAQIFTVQGKAIADAVERNIKVLVGNPANTNAYIAMKSAPSLPAKNFTAM
>d1guya1 c.2.1.5 (A:1-143) Malate dehydrogenase {Chloroflexus aurantiacus}
MRKKISIIGAGFVGSTTAHWLAKELGDIVLLDIVEGVPQGKALDLYEASPIEGFDVRTGTNNYADTANSDIVVITSGAPRKPGMSREDLIKVNADIT
RACISQAAPLSPNAVIIMVNNPLDAMTYLAAEVSGFPKERVIGQ
>d1gv0a1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium tepidum}
MKITVIGAGNVGATTAFRLAEKQLARELVLDDVEGIPQGKALDMYESGPVGLFDTKVTGSNDYADTANSDIVVITAGLPRKPGMTREDLLSMNAGI
VREVTGRIMEHSKNPIIVVSNPLDIMTHVAWQKSLPKERVIGM
>d1guza1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium vibrioforme}
MKITVIGAGNVGATTAFRLAEKQLARELVLDDVEGIPQGKALDMYESGPVGLFDTKVTGSNDYADTANSDIVVITAGLPRKPGMTREDLLMKNAGIV
KEVTDNIMKHSKNPIIVVSNPLDIMTHVAWVRSGLPKERVIGM
>d1hyha1 c.2.1.5 (A:21-166) L-2-hydroxyisocapronate dehydrogenase, L-HICDH {Lactobacillus confusus}
ARKIGIIGLGNVGAAVAHLIAQGVADDYVFIDANEAKVKADQIDFQDAMANLEAHGNIVINDWAALADADVVISTLGNIKLQDNPTGDRFAELK
FTSSMVQSVGTNLKESGFHGVLVVISNPDVITALFQHVTGFPKAHKVIGT
>d5ldh_1 c.2.1.5 (1-162) Lactate dehydrogenase {Pig (Sus scrofa)}
ATLKEKLIAPVAQQETTIPDNKITVVGVGQVGMACAIISLGKSLTDELALDVLEDKLKGEMMDLQH GSLFLQTPKIVANKDYSVTANSKIVVVTAGVR
QQEGESRLNLVQRNVNVFKFIIPQIVKYSPPNCIIIVVSNPVDILTYVAWKLGLPKHRVIG
>d9ldta1 c.2.1.5 (A:1-162) Lactate dehydrogenase {Pig (Sus scrofa)}
ATLK DQLIHNLKEEHVPHNKITVVGVGAVGMACAIISLMKELADEIALDVMEDKLKGEMMDLQH GSLFLRTPKIVSGKDYNVTANSRLVVITAGA
RQQEGESRLNLVQRNVNIFKFIIPNIVKYSPPNCIIIVVSNPVDILTYVAWKLGLPKHRVIG
>d1i0za1 c.2.1.5 (A:1-160) Lactate dehydrogenase {Human (Homo sapiens), heart isoform (H chain)}

ATLKEKLIAPVAEEATVPNNKITVVGQVGMACAIISLGKSLADELALVDVLEDKLKGEMMDLQHGSFLQTPKIVADKDYSVTANSKIVVVTAGVR
QQEGESRLNLVQRNVNVFKFIIPQIVKYSQDCIIIVSNPVDILTYVTWKLGLPKHRVIG
>d1i10a1 c.2.1.5 (A:1-159) Lactate dehydrogenase {Human (Homo sapiens), muscle isoform (M chain)}
ATLKDQLIYNLLKEEQTPQNKITVVGAVGMACAISILMKDLADELALVDVIEDKLKGEMMDLQHGSFLRTPKIVSGKDYNVTANSKLVITAGARQ
QEGESRLNLVQRNVNIFKIFIIPNVVKYSPNCKLIVSNPVDILTYVAWKISGFPKNRVIG
>d2Idx_1 c.2.1.5 (1-159) Lactate dehydrogenase {Mouse (Mus musculus)}
STVKEQLIQNLVPEDKLSRCKITVVGAVGMACAISILKGLADELALVDVADTDKLGEALDLQHGSFLSTPKIVFGKDYNVSANSKLVITAGARMV
SGQTRLDLQRNVAIMKAIVPGVIQNSPDCIIIVTNPVDILTYVWKISGFPVGRVIG
>d1ldm_1 c.2.1.5 (1-160) Lactate dehydrogenase {Dogfish (Squalus acanthias)}
ATLKDKLIGHLATSQEPRSYNKITVVGAVGMACAISILMKDLADEVALDVMDKLKGEMMDLQHGSFLHTAKIVSGKDYSVSAGSKLVITAGA
RQQEGESRLNLVQRNVNIFKIFIIPNIVKHSPDCIIILVSNPVDVLTVVAWLGLPMHRIIG
>d1ceqa1 c.2.1.5 (A:19-163) Lactate dehydrogenase {Malaria parasite (Plasmodium falciparum)}
PKAKIVLVGSGMIGGVMATLIVQKNLGDVLFIDVKNMPHGKALDTSHTNVMAYSNCKVSGSNTYDDLGSVDVIVTAGFTKAPGKSDKEWNRD
DLLPLNNKIMIEIGGHIKKNCPNAFIIIVTNPVDVMVQLHQHSGVPKNKIIGL
>d1ldna1 c.2.1.5 (A:15-162) Lactate dehydrogenase {Bacillus stearothermophilus}
MKNNGGARVVVIGAGFVGASYVFALMNQGIADEIVLIDANESKAIGDAMDFNHGKVFAFPVDIWHGDDCRDADLVVICAGANQKPGETRL
DLVDKNIAIFRSIVESVMASGFQGLFLVATNPVDILTYATWKFSGLPHERVIGSG
>d1lc_1 c.2.1.5 (13-164) Lactate dehydrogenase {Lactobacillus casei}
ASITDKDHQKVILVGDGAVGSSYAFAMVLQGIAQEIGIVDIFKDGTKGDAIDLNSNALPFTSPKKIYSAEYSDAKDADLVITAGAPKQPGETRLDLVNKN
LKILKSIVDPVIDSGFNLFIVAAANPVVDILTYATWKSGFPKNRVVGSG
>d1ez4a1 c.2.1.5 (A:16-162) Lactate dehydrogenase {Lactobacillus pentosus}
SMPNHQQVKVLVGDGAVGSSYAFAMAQQGIAEEFVIVDVVKDRTKGDALDLEDAQAFATPKKIYSGEYSDCKDADLVITAGAPKQPGESRLDLVNK
NLNLSSIVKPVVDSGFQGLFLVAAANPVVDILTYATWKFSGLPKERVGSG
>d1llda1 c.2.1.5 (A:7-149) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}
PTKLAVIGAGAVGSTLAFAAAQRGIAREIVLEDIAKERVEAEVLDMQHSSFYPTVSIDGSDDEICRDADMVVITAGPRQKPGQSRELVGATVNILK
AIMPNLVKVAPNAYIYMLITNPVDIATHVAQKLTGLPENQIFGSG
>d1a5z_1 c.2.1.5 (22-163) Lactate dehydrogenase {Thermotoga maritima}
MKIGIVGLGRVGSSATAALLMKGFAREMVLIDVDKKRAEGDALDLIHGTPFTRRANIYAGDYADLKGSDDVVVAAGVPQKPGETRLQLLGRNARVMK
EIARNVSKYAPDSIVIVTNPVDVLTYFFLKGMDPRKVFGS
>d1hyea1 c.2.1.5 (A:1-145) MJ0490, lactate/malate dehydrogenase {Archaeon Methanococcus jannaschii}
MKVTIIGASGRVGSATALLAKEPFMVKDLVLIGREHSINKLEGREDIYDALAGTRSDANIYVESDENLRIIDESDVVIITSGVPRKEGMSRMDLAKTNA
KIVGKYAKKIAEICDTKIFVITNPVDVMTYKALVDSKFERNQVFG
>d1qmga2 c.2.1.6 (A:82-307) Acetohydroxy acid isomeroreductase, ketoacid reductoisomerase (KARI) {Spinach (Spinacia oleracea)}
SATTDFDSSVFKEKVTLSGHDEYIVRGGRNLPLLPAFKGKQIVGIGWGSQAPAQAQNLKDSLTEAKSDVVVKGRLKGSNSFAEARAAGFSEEN
GTLGDMWETISGSDLVLLISDSAQADNYEKVFShMKPNSILGSHGFLLQLQSLQDFPKNISIVAVCPKGMGPSVRRLYVGKEVNGAGINSSFA
VHQDVDRATDVALGWSIALGSPFTFATT
>d2pgd_2 c.2.1.6 (1-176) 6-phosphogluconate dehydrogenase {Sheep (Ovis orientalis aries)}
AQADIALIGLAVMGQNLINNMNDHGFVVCAFNRVSKVDDFLANEAKGTKVLAHSLEEMVSKLKKPRRIILVKGQAVDNFIEKLVPLLDIGDIID
GGNSEYRTMRRCRDLKDKGILFGSGVSGGEDGARYGPSLMPGGNKEAWPHIKAIFQGIAAKVGTGEPCCDWVGDD
>d1pgja2 c.2.1.6 (A:1-178) 6-phosphogluconate dehydrogenase {Trypanosoma brucei}
SMDVGVVGLVMGANLALNIAEKGFKVAVFNRTYSKSEEFMKANASAPFAGNLKAFETMEAFAASLKKPRKALILVQAGAATDSTIEQLKKVFEKGD
ILVDTGNAHFKDQGRRAQQLEAAGLRFMGISGEGEARGKGPaffPGGTLSVWEIRPIVEAAAACKADDGRPCVTMNGSG
>d1f0ya2 c.2.1.6 (A:12-203) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (Homo sapiens)}

KIIVKHVTIGGGLMAGIAQVAAATGHTVVLDQTEDILAKSKKGIEESLRVAKKKFAENPKAGDEFVEKTLTIATSTDAASVHSTDLVVEAIVEN
LKVKNELFKRLDKFAAEHTIFASNTSSLQITSIANATTRQDRFAGLHFFNPVPVMKLVEIKTPMTSQKTFESLVDFSKALGKHPVSCKDTP
>d1dija2 c.2.1.6 (A:1-196) UDP-glucose dehydrogenase (UDPGDH) {Streptococcus pyogenes}
MKIAVAGSGYVGLSLVLLSLQNEVTIVDILPSVKDKINNGLSPIQDEYEYLYKSQLSIKATLDSKAAYKEAELVIIATPTNYNSRINYFTQHVETVIKE
VLSVNASHATLIKSTIPGFITEMRQKFQTDRIIFSPEFLRESKALYDNLYPSRIIVSCEENDSPVKVAKADAEKFALLKSAAKNNVPVLIMG
>d1bg6_2 c.2.1.6 (4-187) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}
SKTYAVLGLGNMGHAFAYALAKGQSVLAWDIDAQRIKEIQDGRGAIIAEGPGLAGTAHPDLLTSDIGLAVKDADVLIVVPAIHASIAANIASYISEGQLI
ILNPGATGGALEFRKILRENGAPEVTIGETSSMLFTCRSERPGQVTVNAIKGAMDFACLPAAKAGWALEQIGSVPQYVAVE
>d1evya2 c.2.1.6 (A:9-188) Glycerol-3-phosphate dehydrogenase {Trypanosome (Leishmania mexicana)}
KDELLYLNKAVVFGSGAFGTALAMVLSKKCREVCVWHMNEEVRLVNEKRENVFLKGVQLASNITFTSDVEKAYNGAEIILFVIPTQFLRGFFEKGSG
NLIAYAKEKQVPLVCTKGIERSTLKFPAEIIGEFLPSPLSVLAGPSFAIEVATGVFTCVSIASADINVARRLQRIMSTG
>d1ks9a2 c.2.1.6 (A:1-167) Ketopantoate reductase PanE {Escherichia coli}
MKITVLGCGALGQLWLTLCKQGHEVQGWLRVPQPYCSVNLVETDGSIFNESLTANDPDFLATSDLLVTLKAWQVSDAVKSLASTLPVTPILLIHNG
MGTEELQNIQQPLLMGTTTHAARRDGTVIIVANGITHIGPARQQDGDSYLAQILQTVLPDVAWHN
>d1jaya_c.2.1.6 (A:) Coenzyme F420H2:NADP+ oxidoreductase (FNO) {Archaeon Archaeoglobus fulgidus}
MRVALLGGTGNLGKGLALRLATLGHEIVVGSREEKAEEAKAAEYRRAGDASITGMKNEDAAEACDIAVLTIPWEHAIDTARDLKNILREKIVVSPVLP
VSRGAKGFTYSSERSAAEVAELESEKVVSLHTIPAARFANLDEKFDWDVPCVGDDDESKKVVMLSIEIDGLRPLDAGPLNSRLVESLTPLILNIM
RFNGMGELGIKFL
>d1bgva1 c.2.1.7 (A:195-449) Glutamate dehydrogenase {Clostridium symbiosum}
KARSFGGSLVRPEATGYGSVYYVEAVMKHENDTLVGKTVLAGFGNVAVGAAKKLAELGAKAVTLSGPDGYIYDPGETTEEKINYMLEMRASGRN
KVQDYADKFGVQFFPGEKPWGQKVDDIIMPCATQNDVDLEQAKKIVANNVKYYIEVANMPTTNEALRFLMQQPNMVVAPSKAVNAGGVLVSGFE
MSQNSERLSWTAEEVDSKLHQVMTDIHDGSAAAERYGLGYNLVAGANIVGFQKIADAMMAQGIAW
>d1gtma1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}
GGSLGRIEATARGASYTIREAAKVLGWDLTKGKTIAIQGYGNAGYYLAKIMSEDGMKVVAVSDSKGGIYNPDGLNADEVLKWKNEHGSVKDFPGA
TNITNEELLELEVDTVLAPEAAIEEVITKKNADNIKAKIVAEVANGPVTPEADEILFEKGILQIPDFLCNAGGTVTSYFEWVQNITGYWTIEEVRELDKK
MTKAFYDVYNIKEAKNIHMRDAAVVAQRVYQAMKDRGVVKH
>d1euza1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Thermococcus profundus}
IGGSLGRGTATAQGAIFTIREAAKALGIDLKGKKIAVQGYGNAGYYTAKLAKEQLGMMTVAVSDSRGGIYNPDGLNADEVLKWKREHGSVKDFPGAT
NITNEELLELEVDTVLAPEAAIEEVITEKNADNIKAKIVAEVANGPVTPEAADDILREKGILQIPDFLCNAGGTVTSYFEWVQNINGYYWTEEVRELDKK
MTKAFWEVYNTHKDKNIHMRDAAVVAQAMKDRGVVKH
>d1bvua1 c.2.1.7 (A:181-418) Glutamate dehydrogenase {Archaeon Thermococcus litoralis}
GGIVARMDATARGASYTIREAAKALGMDLKGKTIAIQGYGNAGYYMAKIMSEEYGMKVVAVSDTKGGIYNPDGLNADEVLAWKKKTGSVKDFPG
ATNITNEELLELEVDTVLAPEAAIEEVITKKNADNIKAKIVAEELANGPTTPEADEILYEGKILQIPDFLCNAGGTVTSYFEWVQNITGDYWTVEETRAKLDKK
MTKAFWDVYNTKEDKNIHMRDAAVVAQAMKDRGVVKH
>d1b26a1 c.2.1.7 (A:179-412) Glutamate dehydrogenase {Thermotoga maritima}
GGSKGGREEATGRGVVKCAGLAMDVLGIDPKKATVAVQGFGNVGQFAALLISQELGSKVVAVSDSRGGIYNPEGFDVEELIRYKKEHGTVVTPKG
TNEELLELDVDILVPAALEGAIHAGNAERIKAKAVVEGANPPTPEADEILSRRGILVVPDILANAGGTVTSYFEWVQDLQSFWLDQVRNALEKM
MKGAFNDVMVKEKYNVDMRTAACYIALIDRVAYATKKRG
>d1hwxa1 c.2.1.7 (A:209-501) Glutamate dehydrogenase (Cow (Bos taurus))
HGRISATGRGVFHGIENFIENASYMSILGMPGFDKTFAVQGFGNVGLHSMRYLHRFGAKCVAVGESDGSIWNPDGIDPKELEDFKLQHGTLGFP
KAKIYEGSILEVDCDILIPAASEKQLTKSNAPRVKAKIIAEGANGPTTPQADKIFERNIMVIPDLYLNAGGTVTSYFQILKNLNHVSYGRFTKYERDSNY
HLLMSVQESLERKFGKHGGTIPVPTAEFQDRISGASEKDIVHSGLAYTMERSARQIMRTAMKYNLGLDLRTAAYVNAIEKVFVRYNEAGVTFT
>d1leha1 c.2.1.7 (A:135-364) Leucine dehydrogenase {Bacillus sphaericus}
GISPAFGSSGNPSPVTAYGVYRGMKAAAKEAFGSDSLEGLAVSVQGLGNVAKALCKKLNTEGAALKVVTDVNKAAVSAAVAEGADAVAPNAIYGVTC

DIFAPCALGAVLNDFTIPQLKAKVIAGSADNQLKDPRHGKYLHELGIVYAPDYVINAGGVINVADELYGYNRTRAMKRVVDGIYDSIEKIFAISKRDGVPS
YVAADRMAEERIAKVAKARSQFLQDQRNILNGR

>d1c1da1 c.2.1.7 (A:149-349) Phenylalanine dehydrogenase {Rhodococcus sp., M4}

SAFTTAVGVFEAMKATVAHRLGSLDGLTVLQGLGAVGGSLASLAAEAGAQLVADTDTERVAHALGHTAVALEDVLSTPCDFAPCAMGGVIT
TEVARLDCSVVAGAANNVIADEAASDILHARGILYAPDFVANAGGAIHLVGREVLGWSESVHERAVAGDTLNQVFEISDNDGVTPDEARTLAG
RRAREAS

>d1a4ia1 c.2.1.7 (A:127-296) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Human (Homo sapiens)}

LTSINAGRLARGDLNDCFICPKGCLELIKETGVPIAGRHAVVGRSKIVGAPMHDLLWNNTVTCHSKTAHLDEEVNKGDILVVATGQPEMVKG
EWIKPGAIVIDCGINYVPDDKKPKNGRKVVGDVYDEAKERASFITPVPGVGPMVTAVMLMQSTVESAKRFLE

>d1b0aa1 c.2.1.7 (A:123-288) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Escherichia coli}

FHPNVNGRLCQRAPRLPCTPRGIVTLLERYNIDTFGLNAVIGASNIVGRPMSSMELLAGCTTVTHRFTKLRHHVENADLLIVAVGKPGFIPGDW
IKEGAIVIDVGVINRLENGKVVGDVVFEDAARKASYITPVPGVGPMVTATLIENTLQACVEYHDPQDE

>d1edza1 c.2.1.7 (A:149-319) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}

PCTPLAIVKILEFLKIYNNLLPEGNRLYGKKCIVNRSEIVGRPLAALLANDGATVYSVDVNNIQKFTRGESLKNKHHVEDLGEYSEDLLKKCSLDSDVVI
TGVPSENYKFPTYEIKEGAVCINFACKNFNSDDVKEKASLYVPMTGKVTIAMLLRNMLRLVRNVELSKE

>d1do8a1 c.2.1.7 (A:280-573) Mitochondrial NAD(P)-dependent malic enzyme {Human (Homo sapiens)}

IQGTAVALAGLAAQKVISKPISEHKILFLGAGEAALGIANLIVMSMVENGLSEQEAQKKIWMFDKYGLVKGRKAKIDSYQEPFTHSAPESIPDTFED
AVNLKPKSTIIGVAGAGRLFTPVDVIRAMASINERPVIFALSNTAQAEACTEEAYLTTEGRCLFASGSPFGPVKLTDGRVFPTPGQGNVYIFPGVALAVIL
CNTRHISDSVFLEAAKALTSQLTDEELAQGRLYPPLANIQEVSINIAIKVTEYLYANKMAFRYPEPEDKAKYVKERTWRSEYDSLLPDVYEW

>d1id1a_ c.2.1.9 (A:) Rck domain from putative potassium channel Kch {Escherichia coli}

HRKDHFIVCGHSILAINTILQLNQRGQNVTISNLPDEDIKQLEQRLGDNADVIPGDSNDSSVLKKAGIDRCRAILALSDNDADNAFVLSAKDMSSD
VKTVLAVSDSKNLNIKMKVHPDIILSPQLFGSEILARVLNGEEINNDMLVSMLLN

>d1jkja1 c.2.1.8 (A:1-121) Succinyl-CoA synthetase, alpha-chain, N-terminal (CoA-binding) domain {Escherichia coli}

SILIDKNTKVICQGFTGSQGTFHSEQIAYGTKMVGGVTPGKGGTTHLGLPVFNTVREAVAATGATASVIYVPAPFKDSILEAIDAGIKLIITITEGIPTLD
MLTVKVKLDEAGVRMIGP

>d1euca1 c.2.1.8 (A:1-130) Succinyl-CoA synthetase, alpha-chain, N-terminal (CoA-binding) domain {Pig (Sus scrofa)}

CSYTSRKHLVYDKNTKVICQGFTGKQGTFSQQALEYGTNLVGGTPGKGGTTHLGLPVFNTVKEAKEQTGATASVIYVPPPFAAAINEAIDAEVP
LVVCITEGIPQQDMVRVKHRLLRQGKTRLIGP

>d1djna2 c.3.1.1 (A:490-645) Trimethylamine dehydrogenase, C-terminal domain {Methylophilus methylotrophus, w3a1}

RWNTDGTNCLTHDPGADASLPDQLTPEQVMDGKKKIGKRVVILNADTYFMAPSLAEKLATAGHEVTIVSGVHLANYMHTLEYPNMMLRRHEL
HVEELGDHFCSRIEPMRMEIYNIWGDGSKRTYRGPGVSPRDANTSHRWIEFDLSLVLTGRH

>d1cjca1 c.3.1.1 (A:107-331) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos taurus)}

HQALDIPGEELPGVFSARAFVGWYNGLLENRELADPLSCDTCVILGQGNVALDVARILLTPPDHLEKTDITEAALGALRQSRVKTWIVGRRGPLQVA
FTIKELREMIQLPGTRPMLDPADFLGLQDRIKEARPRKRLMELLRTATEKPGVEEAARRASASRAWGLRFFRSPQQVLPSPDGRRAGIRLAVTRL
EGIGEATRAVPTGDVEDLPCGLVLSSIGY

>d1h7wa3 c.3.1.1 (A:288-440) Dihydropyrimidine dehydrogenase, domain 3 {Pig (Sus scrofa)}

PKTDDIFQGLTQDGQFYTSKDFLPLVAKSSKAGMCACHSPLPSIRGAVIVLGAGDTAFDCATSALRCGARRVFLFRKGVNIRAVPEEVELAKEEKCEF
LPFLSPRKVIVKGGRIVAVQFV RTEQDETGKWNEDEDQIVHLKADVVISAFGS

>d1coy_1 c.3.1.2 (4-318,451-506) Cholesterol oxidase {Brevibacterium sterolicum}

RTLADGDRVPALVIGSGYGGAVAALRLTQAGIPTQIVEMGRSWDTPGSDGKIFCMLNPDKRSMWLADKTDQPVSNFMFGINKSIDRYVGVLDS
ERFSGIKVYQGRGVGGGSLVNGGMAVTPKRNYFEEILPSVDSNEMYNYFPRAINTGLGVNNIDQAWFESTEWYKARTGRKTAQRSGFTTAFVPN
VYDFEYMKKEAGQVTKSGLGGEVYGNNAAGKKSLSKTYLAQAAATGKLTITLHRVTKVAPATGSGYSVTMEQIDEQGNVVATKVVADRFFAAG
SVGTSKLLVSMKAQGHLPNLSSQVGEWXGVLLNKATDNFGRLPYEPGLYVVDGSLVPGNVGVNPFTITALAERNMDKISSL

>d1ijha1 c.3.1.2 (A:9-318,A:451-506) Cholesterol oxidase {Streptomyces sp.}

GYVPAVVGTYGAAVSALRGEAGVQTLMLEMQLWNQPGPDGNIFCGMLNPDKRSSWFKNRTEAPLGSFLWLDVNRNIIDPYAGVLRVNY
DQMSVYVGRGVGGSLVNGGMAVEPKRSYFEEILPRVDSSEMYDRYFPRANSMLRVNHIDTKWFEDTEWYKCARVSREQAGKAGLGTVFVNPVY
DFGYMQREAAGEVPKSALATEVIYGNHKGQSLDKTYAAALGTGKVTIQTLHQVKTRQTKDGGYALTVEQKDGDKLATKEISCRYLFLGAGSLG
STELLVRARDTGTPLNLNSEVAGWXGCVLGKATDDYGRVAGYKNLYTDGSLIPGSVGLPFTITALAERNVERIICKDV

>d1k0ia1 c.3.1.2 (A:1-173,A:276-394) p-Hydroxybenzoate hydroxylase, PHBH {Pseudomonas aeruginosa}

MKTQVAIIAGPSGLLQLHKAGIDNVILERQTPDYVLGRIRAGVLEQGMV DLLREAGVDRRMARDGLVHEGVIAFAGQRRRIDLKRLSGGKTV
TVYGQTEVTRDLMEAREACGATTVYQAAEVRHLHDLQGERPYVTFERDGERLRLDCDYIAGCDGFHGISRQSIPAERXMQHGRFLAGDAAHIVPPT
GAKGLNLAASDVSTLYRLLKAYREGRGELLERYSAICLRIWKAERFSWWMTSVLHRFPDTDAFSQRQQTELEYLGSEAGLATIAENYVGLPYIEE

>d1el8a1 c.3.1.2 (A:1-217,A:322-385) Sarcosine oxidase {Bacillus sp., strain b0618}

STHFDVIVVAGSMGMAAGYQLAKQGVKTLVDAFDPPHTNGSHGDTRIIRHAYGEGREYVPLALRSQELWYELEKETHHKIFTKTGVLVFGPKGE
SAFAETMEAKEHSLTVLLEGDEINKRWPGITV PENYNAIFEPNSGVLFSENCIRAYRELAEARGAKVLTHTRVEDFDISPSVKETANGSYTADKL
IVSMGAWNSKLLSKLNLDIPXDEHFIDLHPEHSNVVIAAGFSGHGFKFSSGVGEVLSQLALTGKTEHDISFSINRPALKESLQ

>d1foha5 c.3.1.2 (A:1-240,A:342-461) Phenol hydroxylase {Soil-living yeast (Trichosporon cutaneum)}

TKYSESYCDVLIVGAGPAGLMAARVLSEYVRQKPDLKVRIIDKRSTKVYNGQADGLQCRTLESKLNGLADKILSEANDMSTIALYNPDENGHIRRTDR
IPDTLPGISRYHQVVLHQGRIERHILDSIAEISDTRIKVERPLIKEPKMEIDSSKAEDPEAYPTMTLRYMSDHESTPLQFGHKTENSLFHSNLQTQEEEDA
NYRLPEGKEAGEIETVHCKYVIGCDGGHSWVRRTLGFEMIXVTEKFSKDERVFIAGDACHTHSPKAGQGMNTSMMDTYNLGWKLGLVLTGRAKR
DILKYEERHAFAQALIDFDHQFSRLFSGRPAKDVADEMGSMDVFKEAVKGNEFASGTAINYDE

>d1cf3a1 c.3.1.2 (A:3-324,A:521-583) Glucose oxidase {Aspergillus niger}

GIEASLLTDPDKVSGRTVDIAGGGLTGTTAARLTENPNISVLVIESGSYESDRGPIIEDLNAYGdifGSSVDHAYETVELATNNQTALIRSGNGLGGSTL
VNGGTWTRPHKAQVDSWETVFGNEGWNWDNVAAYSLQAERARAPNAQIAAGHYFNASCHGVNGTVHAGPRDTGDDYSPIVKALMSAVEDR
GVPTKKDFCGDPHGVSMPNTHEDQVRSDAAREWLLPNYQRPNLQVLTGQYVGKVLLSQNQTTPRAVGVFGTHKGNTHNVYAKHEVLLAA
GSAVSPITLEYSGIGMKSILEPLGIDTVV DLPVGLXCSMMPKEMGGVV DNAARVYGVQGLRIDGSIPPTQMSSHVMVTFYAMALKISDAILEDYAS
MQ.

>d1gpea1 c.3.1.2 (A:1-328,A:525-587) Glucose oxidase {Penicillium amagasakiense}

YLPAQQIDVQSSLSDPSKVAGKTYDIAGGGLTGTTAARLTENPNISVLVIESGSYESDRGPIIEDLNAYGdifGSSVDHAYETVELATNNQTALIRSGNGLGGSTL
GLGGSTLINGDSWTRPDKVQIDSWEKVFMEGWNWDNMFEYMKKAEAARTPTAAQLAAGHSFNATCHGTNGTVQSGARDNGQPWSPIMKA
LMNTVSALGPVQVQDFLCGHPRGVSMIMNNLENQVRDAARAWLLPNYQRNSNLEITGQMVGVKLFQKQTASGPQAVGVNFGTNKAVNFDVFA
KHEVLLAAGSAISPLILEYSIGLKSVDQANVTQLLDLPGIXCSMMSRELGGVV DATAK VYGTQGLRIDGSIPPTQVSSHVMVTFYAMALKISDAILEDYAS
LDDYAKSA

>d1b5qa1 c.3.1.2 (A:5-293,A:406-463) Polyamine oxidase {Maize (Zea mays)}

PRIVVGAGMSGISAARKLSEAGITDILLIEATDHIGGRMHKTNFAGINVELGANWVEGVNGGKMNPWIWPIVNSTLKLRNFRSDFDYLAQNRYKED
GGVYDEDYVQKRIELADSVEEMGEKLSATLHASGRDDMSILAMQRLNEHQPNGPATPVDMVV DYYKFDYFAEPPRVTSQNTVPLATFSDFGDD
VYFVADQRGYEA VVYLAGQYKLTDKSKGKIVDPRQLNKVVREIKYSPGGVTVKTEDNSVSYADYVMSASLGVLQSDLIQFKPKLPTWKVRAIYQ
FXWPVGVNRYEYDQLRAPVGRVYFTGEHTSEHYNGVHGAYLSGIDSAEILINCAQKKMC

>d1f8ra1 c.3.1.2 (A:4-319,A:433-486) L-amino acid oxidase {Malayan pit viper (Calloselasma rhodostoma)}

RNPLAECFQENDYEEFLEIARNGLKATSNPKHVVIVGAGMAGLSAAYVLAGAGHQVTLEASERPGGRVRTYRNEEAGWYANLGPMRLPEKHRIV
REYIRKFDLRLNEFSQENDNAWYFIKNIKKVGEVKKDPLKYPVKPSEAGKSAGQLYEESLGKVVEELKRTNCSYILNKYDTYSTKEYIKEGLDSPA
VDMIGDLLNEDSGYYVSFIESLKDDIFAYEKRFDEIVDGMDFKLPTAMYRDIQDKVHFNAQVIKIQQNDQKVTVVYETLSKETPSVTADYVIVCTTSR
AVRLIKFNPLPKKAHALRSVXFTPYQFQHFSPLTASQGRIFYPAGEYTAQAHGWIDSTIKSGLRAARDVNLASEN

>d1gosa1 c.3.1.2 (A:4-289,A:402-500) Monoamine oxidase B {Human (Homo sapiens)}

KCDVVVGGISGMAAKLLHDSGLNVVLEARDRVGGRTYTLRNQKVYV D LGGSYVGPTQNRIILAKELGLETYKVNEVERLIHHVKGKSPFR
GPFPPVWNPITYLDHNNFWRTMDDMGR EIPS DAPWKA PLAEEDNMTMKE LLKLCW TESAKQLATL FVNLCVTAETH VESALWFLWYVKQC
GGTTRIISTTNGGQERKFVGSGQV SERIMD LLLGDRV KLERPV YIDQ TREN VL VETLN HEME YAKV VISA PPTL GMKI HF NPLPM MRN QM IT RV

XFPPGILTQYGRVLRQPVDRIYFAGTETATHWSGYMEGAVEAGERAAREILHAMGKIPEDEIWQSEPESDVPAQPTTFLERHLPSVPGLLRLIGLT

T

>d1d5ta1 c.3.1.3 (A:-2-291,A:389-431) Guanine nucleotide dissoiation inhibitor, GDI {Cow (Bos taurus)}

HHMDEEYDVIVLGTGLTECILSGIMSVNGKKVLHMDRNPYGGESSITPLEELYKRFQLLEGPPETMGRGRDWNVDLIPKFLMANGQLVKMLLYTE
VTRYLDFKVVVEGSFVYKGKGIYKPVSTETEALASNLMGMFEKRRFRKFVANFDENDPKTFEGVDPQNTSMRDVYRKFDLGQDVIDFTGHALALY
RTDDYLDQPCLETINRIKLYSES LARYGKSPYLYPLYGLGELPQGFARLSAIYGGTYMLNKPVDIIMENGKVVGKSEGEVARCKQLICDPSYVPDRVX
PIDDGSESQVFCS CSYDATTHFETTCNDIKDIYKRMAGSAFDF

>d1chua2 c.3.1.4 (A:2-237,A:354-422) L-aspartate oxidase {Escherichia coli}

NTLPEHSCDVLII GSGAAGLSSLALR LADQHQVIVLSKGPVTEGSTFYAQGGIAAVFDETDSIDSHVEDTLIAGAGICDRHAVEFVASNARSCVQWLIDQ
GVLFDTHIQPNGEESYHLTREGGHSHRRILHAADATGREVETTL SKALNHPNIRV LERTNAVDLIVSDKI GLPGTRRVGA WVN RNKETVETCHA
KAVV LATGGASKVYQYTTPDISSGDG IAMAW RAGCRVAN XCGGV MVDDHGR TDVEGL YAI GEVS YTGL HG ANRM ASNSL LECLV YGWS AEDI
TRR MPYAH D I STL P PP W

>d1fuma2 c.3.1.4 (A:1-225,A:358-442) Fumarate reductase flavoprotein subunit {Escherichia coli}

QTFQADLAIVGAGGAGLRAAIAAAQANPNAKIALISKVYPMRSHTVAEEGSAAVAQDHDSFEYHFHD TVAGGDWLCEQDVVDYFVHHCPTEMT
QLELWGCPWSR P DGS VNR RFGGM KIERTWFAADKTGFHMLHTLFQTS LQFPQIQR FDEHFVLDI VDDGHVRGLVAMNMMEGTLVQIRANA
VVMATGGAGR VYRYNTNGGIVTGDGMGMALSHGVPLRDXMGGIETDQNCETRIKGLFAVGECSSVGLHG ANRLGSNSLAELVVFGRLAGEQATE
RAATAGNGNEAAIEAQAGVEQRLKDLV NQ

>d1qlaa2 c.3.1.4 (A:1-250,A:372-457) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}

MKVQYCD S L V I G G G L A G L R A A V T Q Q K G L S T I V L S I P V K R S H S A A A Q G G M Q A S L G N S K M S D G D N E D L H F M D T V K G S D W G C D Q K V A R M F V N T A
PKAIRELA AWGVPWTRIHKGDRMAIINAQKTTITEEDFRHGLIHSRDFGGT KK WRT CYTADATGHTMLFAVANECL LGV SI QDRKEA I ALI HQDGK
CYGAVV RDLVTGDIIAYVAKT LIATGGYGRYKNTTNAV VCEGTGTAIA LETGIAQLGNXMGGIRT DYRGEAKLKG LFSAGEAACWDMHGFNRLGG
NSVSEAVVAGMIVGEYFAEH CANTQV DLET K TLEK FVKG QEA YM KS L VES

>d1e39a2 c.3.1.4 (A:103-359,A:506-568) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

PTIAELAKDKSERQ A LASAPHD T DV V V V GSGGAGFS AASATD SGAKV ILIEKEPVIGGNAKLAAGGMNAAWTDQQKAKK I TDSP ELMF EDT MK
GGQNINDPALVKV LSSHS KDSV DWMTAMGADLTDVGMMGGASVNRAHRPTGGAGVGAHV VQVLYDNAV KRNI DLR MNTRGIEVLKDDKGTV
KGILVKGMYKYYWVKA DAVI LATGGFAKN NERVAKL DPLSK LGFISTNQPGAVGDGLDVAENAGGALKDMXTMGGVMI DTKAEV MNAKKQVIPG
LYGAGEV TGGVHG A N RL GGNAISDIITFGRLAGEEAKYS

>d1qo8a2 c.3.1.4 (A:103-359,A:506-565) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

DGWDQDKI QK AIAAGPSETT QV LV V GAGSAG FN ASLA KKAGA N VIL DKAPFSGG NSM ISAG GMNA V GTK Q QT AH GVED K VEW FIED AMKGG
RQQNDIKLVTI LAE QSAD QV W LES LGANL DDLKRSGG ARV DRTHRPHGGKSSGPEI IDL RKA AKE QGID TRLS RVV KLV V N DDH SVV GAVV HG
KHTGYYMIGAKSVVLATGGYGMNKEMIAYYRPTMKDMTSSNNITATGDGV L MAKEIGASMT DIDWVQAXAINTTASVLDLQSKPIDGLFAAGEV T
GGVHGYNRLGGNAIADTVFVFGRIAGDNAAKHALD

>d1d4ca2 c.3.1.4 (A:103-359,A:506-570) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella putrefaciens}

KFVPVDADKA AAGV KETTDVVI GSGGAGLAAASARDAGAKVILLEKEPIPGGNTKLAAGGMNAETKPQAKLGIEDKKQIMIDDTMKG
GRNINDPELVKVL ANN SS DIDL TSMGADM TDV GRMGGASVN RSHRPTGGAGVGAHVAQV LWDNAV KRGTDIRLNSRV RILEDAS GKV TV
LVKGEYTGYYV KADAVVIAAGGFAKN NERVSKYDPLKGF KATNHPGATGDGLDVALQAGAATR DLEMGGV IDT KAEV KSEKTGK P ITGLY AAGE
VTGGVHG A N RL GGNAISDIV TYGRIAGASA AKFAKD

>d1jnra2 c.3.1.4 (A:2-256,A:402-502) Adenylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

VYYPKKYELYKADEVPTEV VETDILI IGGG FSGCGAAYEAAYWAKLGGLKVTLVEKA AV ERS GAVA QGL SAINTYIDL TGR SERQ NTLEDYVRYV TL DM
MGLAREDLVADYARHVDGTVHLFEKWL P IWKTPDGK YVREGQWQIMIHGESYKPIIAAEAKM AVEGEENIYERVFIFELLKDNN DPNAVAGAVGFS
VREP KFYVFKAKA VILATGGATLLFRPRSTGEAAGRTWY AIFDTGSGY YMGLKAGAMLTQXAGFWVCGP E DLMPEEYAKL FPLKYNRM TTVKGLFAI
GDCAGANPHKFSSGSFTEGRIA AAKA AVFILEQKPNPEIDD AVEELKKK YAPMER FMQYKDL S

>d3grs_1 c.3.1.5 (18-165,291-363) Glutathione reductase {Human (Homo sapiens)}

VASYDYL VIGGGSGGLASARRAELGARA AVVESHKLGGTCVN VGC VP KKV MWNTAVHSEFMHDHADYGFPSCEGKF NWRV I KEK RDAY VS RL N

AIYQNNLTSHIEIIRGHAFTSDPKPTIEVSGKKYTAPHILATGGMPSTPHEXRVPNTKDSLNLGIQTDDKGHIIVDEFQNTNVKGIVAVGDVCGKA
LLTPVAIAAGRKLAHRLFEYKEDSKLD

>d3grs_2 c.3.1.5 (166-290) Glutathione reductase {Human (Homo sapiens)}

SQIPGASLGITSDGFFQLEELPGRSVIVGAGYIAVEMAGILSALGSKTSLMIRHDKVLSFDSMISTNCTELENAGVEVLKFSQVKEVKKTLSGLEVSM
VTAVPGRLPVMTMIPDVDCCLWAIG

>d1gera2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}

DIPGVEYGIDS DGFALPALPERVAVVAGGYIAVELAGVINGLGAKTHLFVRKHAPLRSFDPMISETLVEVMNAEGPQLHTNAIPKAVVKNDGSLTE
LEDGRSETVDCLIWAIG

>d1gesa1 c.3.1.5 (A:3-146,A:263-335) Glutathione reductase {Escherichia coli}

KHYDYIAIGGGSGGIASINRAAMYGQKCALIEAKELGGTCVNVCVPKKVMWAAQIREAIHMYGPDYGFDTTINKFNWETLIASRTAYIDRIHTSYE
NVLGKNNVDVIKG FARFVDAKTLEVGETITADHILIATGGRPSHPXREPANDNINLEAAGVKTNEKG YIVVDKYQNTNIEGIYAVGDNTGAVELPVA
VAAGRRLSERLFNNKPDEHLD

>d1gesa2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}

DIPGVEYGIDS DGFALPALPERVAVVAGGYIGVELGGVINGLGAKTHLFEMFDAPLPSFDPMISETLVEVMNAEGPQLHTNAIPKAVVKNDGSLT
ELEDGRSETVDCLIWAIG

>d1fea1 c.3.1.5 (A:1-169,A:287-357) Trypanothione reductase {Crithidia fasciculata}

SRAYDLVVIGAGSGGLEAGWNAASLHKKRVAVIDLQKHHGPPHYAALGGTCVNVCVPKKLMVTGAN YM D T I R E S A G F G W E L D R E S V R P N W K A L
IAAKNKAVSGINDSYEGMFADTEGLTFHQFGALQDNHTLVRESADPNSA VLETLDTEYILLATGSWPQHLGIEXVPRSQTLOLEKAGVEVAKNGAI
KVDAYSKTVDNIYAIGDVTDRVMLTPVAINEGA AFVDTV FANKPRATD

>d1fea2 c.3.1.5 (A:170-286) Trypanothione reductase {Crithidia fasciculata}

GDDLCITSNEAFYLDEAPKR ALCVGGGYISIEFAGIFNAYKARGGQV D L A Y R G D M I L R G F D S E L R K Q L T E Q L R A N G I N V R T H E N P A K V T K N A D G T R H V
VFESGAEADYDVVMLAIGR

>d1aoga1 c.3.1.5 (A:3-169,A:287-357) Trypanothione reductase {Trypanosoma cruzi}

SKIFDLVVIGAGSGGLEAAWNAATLYKKRVAVIDVQM VHGPPFFSALGGTCVNVCVPKKLMVTGAQYMEHLRESAGFGWEFDR TTLRAEWKNLI
AVKDEAVLNINKSYDEMFRDTEGLEFLWGGSLESKNVVNVRESADPASAVKERLETEHILLASGSWPHMPNXGRSPRTKDLQLQNAGVMIKNGG
VQVDEYSRTNVSNIYAIGDVTNRVMLTPVAINEEAAALVDTVFGTTPRKT

>d1aoga2 c.3.1.5 (A:170-286) Trypanothione reductase {Trypanosoma cruzi}

IPGIEHCISSEAFYLPEPPRRVLTVG GGFISVEFAGIFNAYKPKDQGVTL CYRG E M I L R G F D H T L R E E L T K Q L T A N G I Q I L T K E N P A K V E L N A D G S K S V T F
ESGKKMDFDLVMMAI

>d1h6va1 c.3.1.5 (A:10-170,A:293-366) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}

SYDFDLIIIGGGSGGLAAA KEAAKFDKKVMVLDFTPTPLGTNWGLGGTCVNVC CIPKKLMHQA ALLGQALKD S RNYGWKLED TVKHDWEKMTE
SVQN HIGSLN WGYRVALREKKV VENAYGKFIGPHKIMATNNKGKEV YSAERFLIATGERPRYLGIXRDSCTR TIGLETVGVKINEKTGKIPVTDEEQT
NVPYIYAI GDILEGKLELTPV AIQAGRLLAQR LYGGSTVKCD

>d1h6va2 c.3.1.5 (A:171-292) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}

PGDKEYCISSSDLFSLPYCPGKTLVVGAS YVALE CAGFLAGI GLDVTM VRSILLRGFDQDMANKIGEHMEEHGIKFIRQFVPTKIEQIEAGTPGRLKV
TAKSTNSEETIEDEFNTVLLAVG

>d1trb_1 c.3.1.5 (1-118,245-316) Thioredoxin reductase {Escherichia coli}

GTKHKS KL LILGSGPAGYTA AVY AARANLQPVLITGM EKGQLTTTEVENWPGDPNDLTGPLL MERMHEHATKFETEII FDHINKV DLQNRPFRLN
GDNGEYTC DALI IATGASARYXHSPNTAIFEGQLE ENGYIKVQSGI HGNAT QTSIPGVFAAGDVM DHYRQAITSAGTGCM AALDAERYLDGL

>d1trb_2 c.3.1.5 (119-244) Thioredoxin reductase {Escherichia coli}

LGLPSEE AFKGRGV SACATSDGFFYRNQKVAVIGGGNTAVEEALYLSNIA SEVHLI HRRDG FRAEKILIKR LMDK VENG NIILHTNRT LEE VTGDQM GV
TGVRLR DTQNSDNIESLDVAGLFVAIG

>d1vdc_1 c.3.1.5 (1-117,244-316) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}

LETHNTRL CIVGSGPAAHTAAIY AARA ELKPLL FEGWM ANDIAPGGQLTTTD VENFP GFPEG ILGV E L TD KFRK QSERFGTTIFTETVTKVDFSSKPKF

LFTDSKAILADAVILAIGAVAKXGHEPATKFLDGGVELSDGYVVTKGTTQTSVPGVFAAGDVQDKYRQAITAAGTCMAALDAEHYLQEI
>d1vdc_2 c.3.1.5 (118-243) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}
RLSFVGSGEVLGGFWNRGISACAVCDGAAPIFRNKPLAVIGGGDSAMEEANFLTKYGSKVYIIHRRDAFRASKIMQQRALSNPKIDVIWNSSVVEAY
GDGERDVLLGLKVKNVVTGVDSDLKVSGLFFAI
>d1hyua1 c.3.1.5 (A:199-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Salmonella typhimurium}
AEKRAAEALNKRDAYDVLIVGSGPAGAAAAYSARKGIRTGLMGERFGGQVLDVDIENYISVPKTEGQKLAGALKAHVSDYDWDVIDSQSASKLVP
AATEGGLHQIETASGAVLKARSIIIATGAKXLPNTHWLEGALERNRMGEIIDAKCETSVKGVFAAGDCTTVPYKQIIIATGEGAKASLSAFDYLIRTKIA
>d1fl2a1 c.3.1.5 (A:212-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Escherichia coli}
AYDVLIVGSGPAGAAAAYSARKGIRTGLMGERFGGQILDVDIENYISVPKTEGQKLAGALKHVDEYDWDVIDSQSASKLIPAAVEGGLHQIETASG
AVLKARSIIIATGAKXLPNTHWLEGALERNRMGEIIDAKCETSVKGVFAAGDCTTVPYKQIIIATGEGAKASLSAFDYLIRTKTA
>d1fl2a2 c.3.1.5 (A:326-451) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Escherichia coli}
WRNMNVPGEDQYRTKGVTVYCPHCDGPLFKGKRVAVIGGGNSGVEAAIDLADGIVEHVTLEFAPEMKADQVLQDKLRLSLKNVDIILNAQTTEVKGD
GSKVVGLEYRDRVSGDIHNIELAGIFVQIGL
>d1nhp_1 c.3.1.5 (1-119,243-321) NADH peroxidase {Enterococcus faecalis}
MKVIVLGSSHGGYEAVEEELNLHPDAEIQWYEKGDFISLASMQLYLEGVKDVSRYMTGEKMESRGVNVFSNTEITAIQPKEHQVTVKDLVSG
EERVERNYDKLIISPGAVPFELDXGVRPNTAWLKTLEHPNGLIKTDYMRTEYSEPDVFAVGDATLIKYNPADTEVNIALATNARKQGRFAVKNLEEVVK
PFP
>d1nhp_2 c.3.1.5 (120-242) NADH peroxidase {Enterococcus faecalis}
IPGKLDNIYLMRGRQWAIKLKQKTVDPPEVNNVVVIGSGYIGIEAAEAFAKAGKKVTIDILRPLGVYLDKEFTDVLTEEMEANNINITATGETVERYE
GDGRVQKVTDKNAYDADLVVVAV
>d1d7ya1 c.3.1.5 (A:5-115,A:237-308) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}
ALKAPVVVLGAGLASVSFAELRQAGYQGLITVVGDEAERPVDPPLSKDFMAHGAEKIRLDCKRAPEVEWLLGVTAQSFDPQAHTVALSDGRTL
PYGTLVLTGAAPRAXVLANDALARAGLACDDGIFVDAYGRTPDVTALGDVTRQRNPLSGRFERIETWSNAQNQGIAVARHLVDP
>d1d7ya2 c.3.1.5 (A:116-236) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}
LPTLQGATMPVHTLRTLEDARRIQAGLRPQSRLLIVGGGVIGLELAATARTAGVHSVSLVETQPRPLMSRAAPATLADFVARYHAAQGVDLRFERSVTGS
VDGVVLLDDGTRIAADMVVVGIG
>d1lv_1 c.3.1.5 (1-150,266-335) Dihydrolipoamide dehydrogenase {Pseudomonas putida}
QQTIQTTLLIIGGGPGGYVAAIRAGQLGIPTVLVEGQALGGTCLNIGCIPSALKIHVAEQFHQASRFTEPSPLGISVASPRLDIGQSVAWKDGIVDRLLT
GVAALLKKHGKVVHGWAKVLDGKQVEDGQRIQCEHLLATGSSVELPXRRPRTKGFNLECLDLKMNGAAIAIDERCQTSMHNVWAIGDVAGE
PMLAHRAMAQGEMVAEIIAGKARRFE
>d1lv_2 c.3.1.5 (151-265) Dihydrolipoamide dehydrogenase {Pseudomonas putida}
MLPLGGPVISSTEALAPKALPQHLVVGGGYIGLELGIAZRKLGAQVSVEARERILPTYDSELTAPVAESLKKLGINHLGHSVEGYENGCLLANDGKG
GQLRLEADRVLVAVG
>d1lpfa1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}
SQKFDVVIAGPGGGVAAIRAAQLGLKTACIEKYIGKEGKVALGGTCLNVGCIPSALKLDSSYKYHEAKEAFKVHGIKEAKVTIDVPAMVARKANIVK
NLGGIATLFKANGVTSFEGHGKLLANKQVEVTGLDGKTQVLEAENVIIASGSRPVEIPXRRPVTDLAADSGVTDERFIYVDDHCKTSVPGVFAI
GDVVRGAMLAHKASEEGVMVAERIAGHKAQMN
>d1lpfa2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}
PAPLSDDIIVDSTGALEFQAVPKKLGVIGAGVIGLELGSVWARLGAEVTVLEALDKFLPAADEQIAKEALKVLTQGLNIRL GARVTASEVKKQVTVF
TDANGEQKETFDKLIVAVG
>d3lada1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}
SQKFDVVIAGPGGGVAAIKSAQLGLKTALIEKYKGKEGKVALGGTCLNVGCIPSALKLDSSYKFHEAHESFKLHGISTGEVAIDVPTMIARKDQIVRNL
TGGVASLIKANGVTLFEGHGKLLAGKKVEFTAAGSSQVLDTENVILASGSKPVEIPXRRPVTDLAADSGVTDERFIYVDDYCATSPGVYAIJD

VVRGAMLAHKASEEGVVAERIAGHKAQMN

>d3lada2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}

PAPVDQDVIVDSTGALDFQNPGKLGVIAGVGIGLELGSVWARLGAETVLEAMDKFLPAVDEQVAKEAQKILTKQGLKILLGARVTGTEVKNKQVT
VKFVDAEGERKSQAFDKLIVAVG

>d1ebda1 c.3.1.5 (A:7-154,A:272-346) Dihydrolipoamide dehydrogenase {Bacillus stearothermophilus}

AIETETLVGAGPGGYVAAIRAAQLGQKVTEKGNGVCLNGCIPSKALISASHRYEQAKHSEEMGIKAENVTDFAKVQEWKASVVKKLTGGVE
GLLGNKVEIVKGEAYFVDANTVRVNGDSAQTYTFKNAAITGSRPIELXVGRPNTELGLEQIGIKMTNRGLIEVDQQCRTSVPNIFAIGDIVPGPA
LAHKASYEGKVAEEAIAGHPSAVDYV

>d1ebda2 c.3.1.5 (A:155-271) Dihydrolipoamide dehydrogenase {Bacillus stearothermophilus}

PNFKFSNRILDSTGALNLGEVPKSLVVGIGGYIGIELGTAYANFGTKVILEGAGEILSGFEKQMAIIKKRLKKKGVEVVTNALAKGAEREDGVTVTYE
ANGETKTIDADYVLVT

>d1ojt_1 c.3.1.5 (117-275,401-470) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

GSADAEDVVVLGGPGGGYSAFAAADEGLKVAIVERYKTLGGVCLNVGCIPSKALLHNAAVIDEVRLAANGIKYPEPELDIDMLRAYKDGVVSRLT
GLLAGMAKSRSRKVDVIQGDGQFLDPHHLEVSLTAGDAYEQAAAPTGEKKIAFKNCIIAGSRXAPNGKLISAEKAGVATDRGFIEVDKQMRTNVPHI
YAIGDIVGQPMLAHKAVHEGHVAAENCAGHKAYFD

>d1ojt_2 c.3.1.5 (276-400) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

VTKLPIPEDPRIIDSSGALALKEVPGKLIIGGGIIGLEMGTVSTLGSRLDVEMMDGLMQGADRDLVWQKQNEYRFDNIMVNKTVAVEPK
DGYYVTATEGANAPKEPQRYDAVLVAAGR

>d1jeha1 c.3.1.5 (A:1-160,A:283-355) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

TINKSHDVIIIGGGPAGYVAAKAAQLGFNTACVEKRGKLGTCNVGCIPSKALLNNSHLFHQMHTEAQKRGIDVNGDIKINVANFQAKDDAVKQ
LTGGIELLFKKNKVTYYKGNGSFEDETKIRVTPVDLEGTVKEDHILDVKNIIIVATGSEVTPFXVGRPYIAGLGAEKIGLEVDKRGRLVDDQFNSKFPHI
KVVGDVTFGPMLAHKAECEEIAVEMLKTGHGHVH

>d1jeha2 c.3.1.5 (A:161-282) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

PGIEIDEKKIVSSTGALSLKEIPKRLTIIGGGIIGLEMGSVYRLGSKVTVVFQPOQIGASMDGEVAKATQKFLKKQGLDFKLSTKVISAKRNDDKNVVEIV
VEDTCKTNQENLEAEVLLVA

>d1dxla1 c.3.1.5 (A:4-152,A:276-347) Dihydrolipoamide dehydrogenase {Garden pea (*Pisum sativum*)}

SDENDVVIIGGGPGGYVAAKAAQLGFKTTIEKRGALGGTCLNVGCIPSKALLHSSHYHEAKHSFANHGVKVSNEIDLAMMGQKDKAVSNLT
RGIEGLFKKNKVTYVKGKGKVFSPSEISVDTIEGENTVVKKGKIIIATGSDVXGRTPFTSGLNLDKIGVETDKLGRILVNERFSTNVSGVYAIQDVIPGP
MLAHKAEEDGVACVEYLAGKVGHD

>d1dxla2 c.3.1.5 (A:153-275) Dihydrolipoamide dehydrogenase {Garden pea (*Pisum sativum*)}

SLPGVTIDEKKIVSSTGALALSEIPKKLVVIGAGYIGLEMGSVWGRIGSEVTVEFASEIVPTMDAEIRKQFQRSLEKQGMFKLTKVVGVDTSGDGV
KLTVEPSAGGEQTIIADEVVLVA

>d1fcda1 c.3.1.5 (A:1-114,A:256-327) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (*Chromatium vinosum*)}

AGRKVVVVGTTGGATAAKYIKLADPSIEVTIEPNTDYTCYLSNEVIGGDRKLESIKHGVDGLRAHGIQVHDSATGIDPDKKLVTAGGAEFGYDR
CVVAPGIELIYDKIEXQRAGKIAQIAGLNDAGWCPVDIKTFESSIHKGIVGDASIANPMPKSGYSANSQGKAAAAAVVLLKGEI

>d1fcda2 c.3.1.5 (A:115-255) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (*Chromatium vinosum*)}

GYSEEAAAKLPHAWKAGEQTAILRKQLEDMADEGGTVVIAPP AAPFRCPGPYERASQVAYYLKAHKPMMSKVIILDSSQTSKQSFSKGWERLYGFG
TENAMIEWHPGDSAVVKVDDGEMMVETAFGDEFKADVNLIPP

>d1djna3 c.4.1.1 (A:341-489,A:646-729) Trimethylamine dehydrogenase, middle domain {Methylophilus methylotrophus, w3a1}

DIRVCIGCNVCISRWEIGGPPMICTQNATAGEEYRRGWHPEKFRQTKNKDSVLIVGAGPSGSEAARVLMESGYTVHLTDAAEKGHLNQVAALPGL
GEWSYHRDYRETQITKLLKNKESQLALGQKPMTADDVLQYGADKVIIATGAXSECTLWNELKARESEWAENDIKGIYLIGDAEAPRIADATFTGHR
VAREIEEANPQIAIPYKRETIAWGTPHMPGGNFKIEYKV

>d1cjca2 c.4.1.1 (A:6-106,A:332-460) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos taurus)}

TPQICVVGSGPAGFYTAQHLLKHSRAHVDIYEKQLVPFLVRFGVAPDHPEVKNVINTFTQTARSDRCAFYGNVEGRDVTVQELQDAYHAVVLSY
GAEDXKSRPIDPSVPFDPKLGVVPNMEGRVVDVPGLYCSGWVRKGPTVITTTMTDSFLTGQILLQDLKAGHLPSGPRPGSAFIKALLDSRGVWPVS
FSDWEKLDAEEVSRGQASGKPREKLLDPQEMLRLLGH

>d1h7wa4 c.4.1.1 (A:184-287,A:441-532) Dihydropyrimidine dehydrogenase, domain 2 {Pig (Sus scrofa)}

EAYSAKIALLGAGPASISCASFRLGYSGITIFEKQEYVGLSTSEIPQFRLPYDVNFIELMKDLGVKIICGKSLSENEITLNLKEEGYKAFIGIGLPEX
VLRDPKVKEALSPIKFNRWDLPEVDPETMQTSEPVVFAGGDIVGMANTTVESVNDGKQASWYIHKYIQAQYGSVASAKPELPLFYTPVLDLV

>d1an9a1 c.4.1.2 (A:1-194,A:288-340) D-amino acid oxidase, N-terminal domain {Pig (Sus scrofa)}

MRVVVIGAVIGLSTALCIHERYHSVLQPLDVKVYADRFTPFTTDVAAGLWQPYTSEPSNPQEANWNQQTFNYLLSHIGSPNAANMGLTPVSGYN
LFREAVPDYWKDMVLGFRKLTPRELDMPDYRYGWFNNTSILEGRKYLQWLTERLTERGVKFFLRKVESFEEVARGGADVIICTGVWAGVLQPDP
LXQVRLEREQLRGSSNTVEIHNYGHGGYGLTIHWGCALEVAKLFGKVLEERNLL

>d1c0pa1 c.4.1.2 (A:999-1193,A:1289-1361) D-amino acid oxidase, N-terminal domain {Yeast (Rhodotorula gracilis)}

LMMHSQKRVVVLGSGVIGLSSALILARKGSVHILARDLPEDVSSQTFASPWAGANWTPFMTLTDGPRQAKWEESTFKWVELPTGHAMWLKG
TRRFAQNEDGLLGHWYKDITPNYRPLPSSECPPGAIGVTYDTLSVHAPKCYCQLARELQKLGATFERRTVTSLEQAFDGADLVVNATGLGAKSIAGID
DQAXRGGPRVEAERIVLPLDRTKSPLSLGRGSARAACEKEVTLVHAYGFSSAGYQQSWGAEDVAQLVDEAFQRYHG

>d1i8ta1 c.4.1.3 (A:1-244,A:314-367) UDP-galactopyranose mutase, N-terminal domain {Escherichia coli}

MYDYIIVGSGLFGAVCANELKKLNKKVLVIEKRNHIGGNAYTEDCEGIQIHKYGAHIFHTNDKYIWDDYVNDLVEFNRTNSPLAIYDKLFNLPMNT
FHQMWGKVDPQEAQNIIAQKKYGDVKPENLEEQAISLVGEDLYQALIKGYTEKQWGRSAKELPAIIKRIPIRFTFDNNYFSDRYQGIPVGGYTKL
IEKMLEGVDVKLGIDFLKDSDLASKAHRIYTGPIDQYDFYRGALXNDNMELFKKYRELASREDKVIFFGRLAEYKYYDMHQVISAALYQVKNIM
STD

>d2uaga1 c.5.1.1 (A:1-93) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD, N-terminal domain {Escherichia coli}

ADYQGKNNVIIIGLGLTGLSCVDFFLARGVTPRVMMDTRMTPGGLDKLPEAVERHTGSLNDEWLMAADLIVASPGIALAHPSLSAAADAGIEIVG

>d1tml__ c.6.1.1 (-) Cellulase E2 {Thermomonospora fusca, strain yx}

NDSPFYVNPNMSSAEWRNNPNDPRTVIRDRIASVPPQGTWFAHHNPGQITGQVDALMSAAQAGKIPILVYNAPGRDCGNHSSGGAPSHSA
YRSWIDEFAAGLKNRPAYIIVEPDLSLMSSCMQHVQQEVLETMAYAGKALKAGSSQARIYFDAGHSAWHSPAQMASWLQQADISNSAHGIANTS
NYRWTADEVAYAKAVLSAIGNPSLRAVIDTSRNGNGPAGNEWCDPSGRAIGTPSTNTGDPMIDAFLWIKLPGEADGCIAGAGQFVPOAAYPEMAI
AA

>d1qjwa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Trichoderma reesei, Cel6a}

ATYSGNPFVGTPWANAYYASEVSSLAIPS LTGAMATAAAVAKVPSFMWLDTLDKPLMEQTLADIRTANKNGGNYAGQFVVFDPDRCAALA
SNGEYIADGGVAKYKNYIDTRIQIVVEYSDIRTLVIEPDSLNLVTNLGTPKCANAQSAYLECINYATQLNLPNVAMYLDAGHAGWLGPANQDP
AAQLFANVYKNASSPRLGLATNVANYNGWNITSPPSYTQGNAVYNEKLYIHAIGPLLANHGWSNAFFITDQGRSGKQPTGQQQWDWCNVIG
TGFGIRPSANTGDSLLDSFWVVKPGGECDGTSDDSSAPRFDSHCALPQAPQAGAWFQAYFVQLLTANPNSFL

>d2bvwa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6a}

NGNPFEVGQLWANNYRSEVHTLAIQPQITDPALRAAASAVAEVPSFWLDRNVTDTLLVQTLSEIREANQAGANPQYAAQIVVYDLPDRDCAAAA
SNGEWAIAANGVNNYKAYINRIREILISFDRVTLVIEPDSLAMVTNMNVPKCGAASTYRELTIYALKQLDLPHVAMYDAGHAGWLGPANI
QPAAEFLAKIYEDAGKPRAVRGLATNVANYNAWSVSSPPYTSPNPNEYDEKHYIEAFRPLLEARGFPAQFIVDQGRSGKQPTGQKEWGHWCNAIGT
GFGMRPTANTGHQYVDAFWVKPGGECDGTSDDTAARYDYHCGLEDALKPAPEAGQWFNEYFQLRNANPPF

>d1dysa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6b}

GNPFSGRTLLVNSDSSKLDQTRQAFLSRGDQTNAAKVKYVQEKGTFWISNIFLLRDIDVAIQNARAACKARGENPIVGLVLYNLPDRDCSAGESSG
ELKLSQNLNRYKNEYVNPFAQKLKAASDVQFAVILEPDAIGNMVTGTSACFCRNARGPQQEAIGYAISQLQASHIHLYLDVANGGWLWADKLEPT
AQEVATILQKAGNNAKIRGFSSNVSNYPSTSNNPPYTSGSPSPDESRYATNIANAMRQRGLPTQFIIDQSRVALSGARSEWGQWCNVNPAGFGQ
PFTTNTNNPNVDAIVWVKPGGESDGQCGMGGAPAAGMWFDAYAQMLTQNAHDEIA

>d1cm5a_ c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}

SELNEKLATAWEGFTKGDWQNEVNVRDFIQKNYTPYEGDESFLAGATEATTLWDKVMEGVKLENRTHAPVDFDTAVASTITSHDAGYINKQLEKIV

GLQTEAPLKRALIPFGGIKMIEGSCKAYNRELDPMIKKIFTEYRKTHNQGVFDVYTPDILRCRKSGVLGPDAYGRGRIIGDYRRVALYIDYLMKDKL
AQFTSLQADLEGNVNLEQTIRLREEIAEQHRALGQMKEAMAKEYGYDISGPATNAQEAIQWTYFGYLAAVKSQNGAAMSFGRTSTFLDVIERDLKA
GKITEQEAEQEMVHDHVMKLRMVRFLRTPEYDELFSGDPWATESIGGMGLDGRVTKNSFRFLNTLYTMGPSPEPNMTILWSEKLPLNFKKFAAKV
SIDTSSLQYENDLMPDFNNDDYIAAAVSPMIVGKQMQFFGARANLAKTMLYAINGVDEKLKMVQVGPSEPIKGDVLYDEVMERMDHFM
DWLAKQYITALIIHYMHDKSYEASLMAHLHRDVIRTMACGIAGLSVAADSLSAIKYAKVPIRDEDGLAIDFEIEGEYPQFGNNPDRVDDLAVIDLV
ERFMKKIQKLHTYRDAIPTQSVLTTSNVVYGGKTGNTPDGRAGAPFGPGANPMHGRDQKGAVASLTSVAKLPFAYAKDGISYTFISVNPNALGDDE
VRKTNLAGLMDGYFHHEASIEGGQHNVNVNMREMLLDAMENPEKYPQLTIRVSGYAVRFNSLTKEQQQDVITRTFTQSM

>d1qhma_c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}

NEKLATAWEGFTKGDWQNEVNVRDFIQKNYTPYEGDESFLAGATEATTLWDKVMEGVKLENRTHAPVDFDTAVASTITS HDAGYINKQLEKIVGL
QTEAPLKRALIPFGGIKMIEGSCKAYNRELDPMIKKIFTEYRKTHNQGVFDVYTPDILRCRKSGVLGPDAYGRGRIIGDYRRVALYIDYLMKDKL
FTSLQADLEGNVNLEQTIRLREEIAEQHRALGQMKEAMAKEYGYDISGPATNAQEAIQWTYFGYLAAVKSQNGAAMSFGRTSTFLDVIERDLKA
GKITEQEAEQEMVHDHVMKLRMVRFLRTPEYDELFSGDPWATESIGGMGLDGRVTKNSFRFLNTLYTMGPSPEPNMTILWSEKLPLNFKKFAAKV
SIDTSSLQYENDLMPDFNNDDYIAACCSPMIVGKQMQFFGARANLAKTMLYAINGVDEKLKMVQVGPSEPIKGDVLYDEVMERMDHFM
LAKQYITALIIHYMHDKSYEASLMAHLHRDVIRTMACGIAGLSVAADSLSAIKYAKVPIRDEDGLAIDFEIEGEYPQFGNNPDRVDDLAVIDLVERF
MKKIQKLHTYRDAIPTQSVLTTSNVVYGGK

>d1rlr_2 c.7.1.2 (222-748) R1 subunit of ribonucleotide reductase, C-terminal domain {Escherichia coli}

FSSCVLIECGDSLDSINATSSAIVKYVSQRAGIGINAGRIRALGSPRGGEAFHTGCIPFYKHFQTAVKSCSQGGVRGAATLFYPMWHVESLLVKN
NRGVEGNRVRHMGYGVQINKLMYTRLLKGEDITLFSVDPSDVPGLYDAFFADQEEFERLYTKYEKDDSIRKQRVKAVELFSLMMQERASTGRIYIQNVD
HCNTHSPFDPAIAPVRQSNLCLEIALPTKPLNDVNDENGEIALTLSAFNLGAINNLDELDELAILAVRALDALLDYQDYPIAAKRGAMGRRTLIGVI
NFAYYLAKHGKRYSDGSANNLTHKTFEAIQYLLKASNELAKEQGACPWFNETTYAKGILPIDTYKKDLTIANEPLHYDWEALRESIKTHGLRNSTLSA
LMPSETSSQISNATNGIEPPRGYVSIKASKDGILRQVVPDYELHDAYELLWEMPGNDGYLQLVGIMQFIDQISANTNYDPSRFPMSGKVPMQQLL
KDLLTAYKFGVKTLYYQNTRDDDDLSNFQL

>d1b8ba_c.7.1.3 (A:) Class III anaerobic ribonucleotide triphosphate reductase NRDD subunit {Bacteriophage T4}

SRVFPTQRDLMAGIVSKHIAKNCMVPSFIMKAHESGIIHVHDIDYSPALPFTNCCLVLDKGMLENGFKLGNQIETPKSIGVATAIMAQITAQVASHQY
GGTTFANVDKVLSPYVKRTYAKHIEDAEKWQIADALNYAQSKEKDVFYDAFQAYEYEVNTLFSSNGQTPVTLFTGTGTDWTERMIQKAILKNRIKGL
GRDGITPIFPKLVMFVEEGVNLYKDDDPYDIKQLALECASKRMYPDIISAKNNKAITGSSVPVSPMGCRSFLSVWKDSTGNEILDGRNNNLGVVTLNLP
RIALDSYIGTQFNEQKFVELFNERMDLCFEALMCRISSLKGVKATVAPILYQEGAFGVRLKPDDIIELFKNGRSSVSLGYIGIHELNILVGRDIGREILTK
MNAHLKQWTERTGFASFSLYSTPAENLCYRFCKLDETEKYGSVKDVTKGWYTNFSVSEENITPFEKISREAPYHFIATGGHISYVELPMKNNLKG
EAVWDYAAQHLDYFGVNMPVDKCFTCGSTHEMPTENGVCSCICGETDPKKMNTIRRTCAVLGNPNERG

>d1kbla2 c.8.1.1 (A:377-509) Pyruvate phosphate dikinase, central domain {Clostridium symbiosum}

LHPTFNPAALKAGEVIGSALPASPAGAAAGKVYFTADEAKAAHEKGERVILVRLTSPEDIEGMHAAEGILTVRGGMTSHAAVARGMGTCCVSGCGE
IKINEEAKTFELGGHTFAEGDYISLDGSTKYGKD

>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}

SGILASPGIAFGKALLKEXKIIDLSAIQDEVILVAADLTPSETAQLNLKKVLFITDAGGRTSHTSIMARSLELPAIVGTGSVTSQVKNDDYLILDAVNNQ
VYVNPTNEVIDKMRRAVQEQQVASE

>d1aco_1 c.8.2.1 (529-754) Aconitase, C-terminal domain {Cow (Bos taurus)}

VDVSPTSQRQLLEPFKDWDGKDLEDLQLIKVKGKCTTDHISAAGPWLKFRGHLNDISNNNLIGAINSENRKANSVRNAVTFEGPV PDTARYYKQH
GIRWVVGDENYGEGRSREHSALEPRFLGGRAITKSFARIHETNLKKQGLLPLTFADPADYNKIHVDKLTIQGLKDFAPGKPLTCIHKPNTQETILLN
HTFNETQIEWFRAGSALNRMKELQQK

>d1a9xb1 c.8.3.1 (B:1502-1652) Carbamoyl phosphate synthetase, small subunit N-terminal domain {Escherichia coli}

IKSALLVLEDGTQFHGRAIGATGSAVGEVVFNNTSMTGYQEILDPYSRQIVTLTYPHIGNVGTNDADEESSQVHAQGLVIRDPLIASNFRNTEDLSSY
LKRHNIVAIADIDTRKLTRLREKGQAQNGCIIAGDNPDAALEKARAFPG

>d1de4c2 c.8.4.1 (C:190-382) Transferrin receptor ectodomain, apical domain {Human (Homo sapiens)}

IQVKDSAQNQNSVIVDKNGRLVYLVENPGGYVAYSKAATVTGKLVHANFGTKDFEDLYTPVNGSIVVRAGKITFAEKVANAESLNAIGVLIYMDQTKFP
IVNAELSFFGHAHLTGDPYTPGFPFNHTQFPPSRSSGLPNIPQTISRAAEKLFGNMEGDCPSDWKTDCRMVTSESKNVKLTNSNVLK
>d1dk7a_c.8.5.1 (A:) GroEL {Escherichia coli}
EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVEAVAKAGKPLIIAEDVEGEALATLVNTMRGIVKVAAVKAPGFGDRRKAML
QDIATLTGGTVISEEIGMELEKATLEDLGQAKRVEINKDTTIIDGV
>d1kid__ c.8.5.1 (-) GroEL {Escherichia coli}
GLVPRGSEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVEAVAKAGKPLIIAEDVEGEALATLVNTMRGIVKVAAVKAPGFGD
RRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVEINKDTTIIDGVGEEAAIQGRVAQIRQQIEATSDYDREKLQERVAKLAGGV
>d1oela2 c.8.5.1 (A:191-366) GroEL {Escherichia coli}
EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVEAVAKAGKPLIIAEDVEGEALATAVVNTIRGIVKVAAVKAPGFGD
RRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVEINKDTTIIDGVGEEAAIQGRVAQIRQQIEATSDYDREKLQ
>d1ioka2 c.8.5.1 (A:191-366) GroEL {Paracoccus denitrificans}
EGMQFDRGYLSPYFVTNADKMIAELEDAYILLHEKKLSSLQPMVPILLESVIQSQKPLLLVAEDVEGEALATLVNKLRGGKIAAVKAPGFGD
RRKAMLQDIATLTGGQVISEDLMKLENVTIDMLGRAKKVSINKDNTTIVDGAGEKAEIEARVSQIRQQIEETTSYDREKLQ
>d1srva_c.8.5.1 (A:) GroEL {Thermus thermophilus}
GYQFDKGYISPYFVTNPETMEAVLEDAFILIVEKKVSNVRELLPILEQVAQTGKPLIIAEDVEGEALATLVNKLRGTLVAEVKAPGFGD
RRKEMLKDI
AAVTGGTVISEELGFKLENATLSMLGRAEVRTKDETTIVGGK
>d1a6db2 c.8.5.2 (B:216-367) Thermosome {Archaeon Thermoplasma acidophilum}
GIIVDKEKVHPGMPDVVKDAKIALLDAPLEIKKPEFTNLRIEDPSMIQKFLAQEEENMLREMVDKIKSVGANVVITQKGIDDMAQHYLSRAGIYAVR
VKKSDMDKLAKATGASIVSTIDEISSSDLGTAERVEQVKVGEDYMTFVTGCKNP
>d1ass__ c.8.5.2 (-) Thermosome {Archaeon Thermoplasma acidophilum}
MSGVIDKEVKHSKMPDVVKNAKIALIDSALALEKKTEIAKVKQJSDPSKIQDFLNQETNTFKQMVEKIKSGANVVLQKGIDVAQHYLAKEGIYAVR
RVKKSDMELAKATGAKIVTDLDDLTSPVLEGAETVEERKIGDDRMTFVMGCK
>d1ay7b_c.9.1.1 (B:) Barstar (barnase inhibitor) {Bacillus amyloliquefaciens}
KKAVINGEQIRSISDLHQTLKELALPEYYGENLDALWDCLTWVVEYPLVLEWRQFEQSQQLTENGAESVLQVFREAKAEGCDITIILS
>d1jj2x_c.9.2.1 (X:) Ribosomal protein L32e {Archaeon Haloarcula marismortui}
TELQARGLTEKTPDLSDEDARLLTQRHRVGKPQFNQRDHKKKRVSTWRKPRGQLSKQRRGIKGKDVT
EAGFRSPTAVRGKHPSGFEEVRVHN
DDLEGVDGDETEAVRIASKVGARKRERIEEEAADAGIRVLNPPTYEV
>d1e8ca1 c.98.1.1 (A:3-87) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}
RNLRDLLAPWVVDAPSRALREMTLDSRVAAGDLFVAVVGHQADGRRYIPQIAQGVAAIIAEAKDEATDG
EIREMHGVPIYLS
>d1gg4a3 c.98.1.1 (A:1-81) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}
MISVTLSQLTDILNGEIQGADITLDAVTTDTRKLTPGCLFVALKGERFDAHDFA
DQAKAGGAGALLSRPLDIDLPQLIVK
>d2bnh__ c.10.1.1 (-) Ribonuclease inhibitor {Pig (Sus scrofa)}
MNLDIHCEQLSDARWTELLPLLQQYEVRLDDCGLTEHCKD
IGSALRANPSLTELCLRTNELGDAGVHLVQQLQSP
TCIQLKSLQNC
SLTEAGCG
VLPSTLRSLPTLRELHSDNPLGDAGLRLCEGLDPQCH
LEKQLLEYCR
LTAASCEPLASV
LRA
TRALKELTV
SNNDIGEAG
ARVLQ
GQGLADSAC
QLET
RLEN
CGLT
PANC
KDL
C
GIV
ASQ
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RELD
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>d1a4ya_c.10.1.1 (A:) Ribonuclease inhibitor {Human (Homo sapiens)}
SLDIQSLDIQCEELSDARWAELLPLLQQCQVVR
LDDCGLTE
ARCKDI
SSALR
VNP
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>d1yrga_c.10.1.2 (A:) Rna1p (RanGAP1), N-terminal domain {Fission yeast (Schizosaccharomyces pombe)}

ARFSIEGKSLKLDAITTEDEKSVFAVLLEDDSVKEIVLSGNITIGTEARWLSENIASKDLEIAEFSIDFTGRVKDEIPEALRLLQALLKCPKLHTVRLSDN
AFGPTAQEPLIDFLSKHPTLEHLYLHNNGLPQAGAKIARALQELAVNKKAKNAPPLRSIICGRNRLENGSMKEWAKTFQSHRLHTVKMVQNGIRP
EGIEHLLLEGAYCQELKVLDLQDNTFTHLGSSALAIALKSWPNLRELGLNDCLLSARGAAAVVDAFSKLENIGLQLTRLQYNEIELDAVRTLKTVIDEK
MPDLLFLENGNRFSEEDDVVDEIREVFSTRGRGELDELDDME

>d1fqva2 c.10.1.3 (A:146-431) Cyclin A/CDK2-associated p19, Skp2 {Human (Homo sapiens)}

ESLWQTLDLTGKNLHPDVTGRLLSQGVIAFCRPRSFMDQPLAEHFSPFRVQHMDLSNSVIEVSTLHGILSQCSKLQNLISLEGRLSDPIVNTLAKNSNL
VRLNLSGCSGFSEFALQTLSSCSRDELNLSCDFTEKHVQVAHVSETITQLNLGYRKNLQKSDLSTLVRCNPVLHDLSDSVMLKNDCFQE
FQLNYLQHLSLSRCYDIIPETLLELGEIPTLKLQLQVFGIVPDGTQLLKEALPHLQINCSHFTTiarptignkknqeiwgikcrltlq
>d1fs2a2 c.10.1.3 (A:146-401) Cyclin A/CDK2-associated p19, Skp2 {Human (Homo sapiens)}

ESLWQTLDDEFRVQHMDLSNSVIEVSTLHGILSQCSKLQNLISLEGRLSDPIVNTLAKNSNLVRLNLSGCSGFSEFALQTLSSCSRDELNLSCDFTE
KHVQVAHVSETITQLNLGYRKNLQKSDLSTLVRCNPVLHDLSDSVMLKNDCFQEFFQLNYLQHLSLSRCYDIIPETLLELGEIPTLKLQLQVFGIVP
DGTLQLLKEALPHLQIN

>d1h6ta2 c.10.2.1 (A:31-240) Internalin B {Listeria monocytogenes}

GPLGSETITVPTPIKQIFSDAFAETIKDNLKKSVTDAVTQNELNSIDQIIANNSDIKSVQGIQYLPNVTKLFNGNKLTIDKPLANLKNLGWLFDENK
VKDLSSLKDLKKLKSLSLEHNGISDINGLVHLPQLESYLGNNKITDTVLSRLTKLDTLSEDNQISDIVPLAGLTKLQNLYSKNHISDLRALAGLKNLDVL
ELFSQ

>d1h6ua2 c.10.2.1 (A:36-262) Internalin H {Listeria monocytogenes}

GSITQPTAINVIFPDPALANAIIKIAAGKSNTDVTQADLDGITLASFGTGVTIEGVQYLNNLIGLELKDNQITDLAPLKNLTKitELELSGNPLKNVSA
IAGLQSIKTLDLTSTQJTDVTPLAGLSNLQVLYLDLNQITNISPLAGLTNLQYLSIGNAQVSDLTPANLSKLTTLKADDNKISDISPLSPNLI
EVHLKNNQISDVSPLANTSNLFI
LTQNQ

>d1ji5a_c.10.2.6 (A:) Leucine rich effector protein YopM {Yersinia pestis}

KSKTEYYNAWSEVERNAPPNGEQREMAVSRLRDCLDQAHELENNLGLSSPELPPHESLVASCNSLTTELPELPQSLKSLLV
DNNNLKALSDLPP
LLEYLGVSNNQLEKLPQELQNSFLKIIDVDNNNSLKKLPDLPPLSLEFIAAGNNQLEELPELQNLQFLTAIYADNNSLKKLPDPLSLESIVAGNNILEELPELQ
NLPFLTTIYADNNLLKTLPLDPLPSLEALNVRDNYLTDLPELPQSLTFLDVSENIFSGLSELPPNLYLNASSNEIRSLCDLPPSLEELNVSNNKLI
ELPALPPR
LERLIASFNHHLAEVPELPQNLKQLHV
EYNPLREFPDIPESVEDLRMNS

>d1dcea3 c.10.2.2 (A:444-567) Rab geranylgeranyltransferase alpha-subunit, C-terminal domain {Rat (Rattus norvegicus)}

RVLHLAHKDLTVLCHLEQLLVTLDLSHNRRLALPPALAALRCLEV
LQASDNALENVDGVANLPRLQELLCNNRLLQSAAIQPLV
SCPRIVLNNLQG
NSLCQEEGIQERLAEMLPSVSSILT

>d1koha1 c.10.2.3 (A:201-362) mRNA export factor tap {Human (Homo sapiens)}

LNELKPEQVEQLKLI
MSKRYDGSQQALDKLGRSDPDLVAQNIDVV
LNRRSSMAATLRI
IEENIPEL
LSNLSNNR
LYRLDDM
SIVQKAPNL
KILNLSG
NELKSEREL
DKIKGL
KLEELWLD
GNSLSDT
FRDQSTY
ISAIRER
FPKLLR
DGHEL
PPIAF

>d1a9na_c.10.2.4 (A:) Splicesomal U2A' protein {Human (Homo sapiens)}

VKLTAELIEQAAQY
TNAVRDRE
DLRGYKIP
VIENLGAT
LDQFDAID
FSDNEIR
KLDGFPL
RRLKTL
VNNN
RICRIGE
GLDQAL
PDLTE
ILTNN
SLVEL
GDLDPLASL
KSLS
TYLC
ILRN
PV
TNKK
HYR
LYVI
KVPQ
VR
LDFQ
VK
KL
KER
QEA
KMFK

>d1igra1 c.10.2.5 (A:1-149) L1 and L2 domains of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

EICPG
GIDIR
NDYQQL
KRLEN
CTVIE
GYLH
ILLIS
KAEDY
RSYRF
PKLT
VITEY
LLL
RV
AGLES
LGD
LFP
NLTV
IRGW
KLF
YNY
ALV
FEM
TNL
DIGLY
NLR
NITR
GAIR
IEKN
ADLC
YLST
WDWS
LILDA
SVNN
YIVGN
KPP
KECG

>d1igra2 c.10.2.5 (A:300-478) L1 and L2 domains of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

KVCEEE
KKTKT
IDS
VTS
SAQM
LQG
CTIF
KG
NLL
NIR
RG
NNI
ASE
LEN
FMGL
IEV
VTG
YV
KIR
HS
HAL
V
SLS
FLK
NLRL
L
GEE
QLEG
NYSF
YV
LDN
QNL
QL
WDW
DH
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IKAG
KMY
FA
NP
KLC
VSE
IYR
MEE
VTG
TKG
RQS
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NGER
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>d1ds9a_c.11.1.1 (A:) Outer arm dynein light chain 1 {Green algae (Chlamydomonas reinhardtii)}

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>d1jj2k_c.12.1.1 (K:) Ribosomal protein L15 (L15p) {Archaeon Haloarcula marismortui}
TSKKRQRGSRTHGGGSHKNRRGAGHRRGRDAGRDKHEFHNEPLKGSKFQKVQEEAATIDVREIDENVTLAADDVAEVEDGGFRDV
DVVEEADDADYVKVLGAGQVRHELTIAADDFSEGAREKVEGAGGSVELDLGEERQ

>d1jj2n_c.12.1.1 (N:) Ribosomal protein L18e {Archaeon Haloarcula marismortui}
SKTNPRLSSLIADLKAARSSGAVWGDVAERLEKPRRTAECNLGRIERYAQEDETVVPGKVLGSGVLQKDVTAAVDFSGTAETKIDQVGEAVSL
EQAIENNPEGSHVRVIR

>d1aua_2.c.13.1.1 (97-299) C-terminal domain of phosphatidylinositol transfer protein sec14p {Baker's yeast (Saccharomyces cerevisiae)}
YDEKPLIAKFYPQYYHKTDKDRPVYFEELGAVNLHEMINKVTSEERMLKNLVWEYESVVQYRLPACSRAAGHLVETSTIMDLKGISISSAYSVMSYV
REASYISQNYYPERMGKFYIINAPFGSTAFLFKPFDPVTISKIFLGSSYQKELLQKIPAENLPVKFGGKSEVDESKGLYLSDIGPWRDPKYIGPEGE
APE

>d1h4xa_c.13.2.1 (A:) Anti-sigma factor antagonist Spollaa {Bacillus sphaericus}
AFQLEMVTRETVVIRLFGEVDHHAVEQIRAKISTAIQGAVTTIWNFERLSFMDSSGVGLVGRMRELEAVAGRTILLNPSPTMRKVQFSGLGPW
MMDATEEEAIDRVR

>d1auz_c.13.2.1 (-) Anti-sigma factor antagonist Spollaa {Bacillus subtilis}
SLGIDMNVKESVLCIRLTGELDHHTAETLKQKVTSQLEKDDIRHIVLNLEDLSFMDSSGLGVILGRYKQIKQIGGEMVVCAISPAVKRLFDMSGFLKIIRF
EQSEQQQALLTGVAS

>d1tyfa_c.14.1.1 (A:) Clp protease, ClpP subunit {Escherichia coli}
SRGRERSFDIYSRLLKERVIFLTGQVEDHMANLIVAQMLFLEAENPEKDIYLYINSPGGVITAGMSIYDTMQFIKPVDSTICMGQAASMGAFLLTAGAKG
KRFCLPNSRVMIHQPLGGYQQATDIEIAREILKVKGKRMNELMALHTGQSLEQIERDTERDRFLSAPEAVEYGLVDSILTHRNN

>d1fc6a4_c.14.1.2 (A:78-156,A:249-463) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}
VTSEQLLFLEAWRAVDRAYVDKSFNGQSWFKLRETYLKKEPMDRRAQTYDAIRKMLAVLDDPFTRLEPSRLAALRRGTXKVTINPVFTTCNVAA
AALPPGAAKQQLGYVRLATFNSNTAAQQAFTELSKQGVAGLVDIIRNNGGGLFPAGVNVARMLVDRGDLVLIADSQGIRDYISADGNSIDSATPL
VVLVNRGTASASEVLAGALKDSKRGGLIAGERTFGKGLIQTVDLSDGSGVAVTVARYQTPAGVDINKIGVSPDVQLPVEVLPTDLEGCRVLGSDAAP
RLF

>d1k32a4_c.14.1.2 (A:680-762,A:854-1061) Tricorn protease {Archaeon Thermoplasma acidophilum}
SSIHEEFLQMYDEAWKLARDNYWNEAVAKEISERIYEKYRNVLPLCKTRYDLSNVIVEMQGEYRTSHSYEMGGTFTDKDPFRSXDDRFIRYRSWVEA
NRRYVHERSKGTIGYIHIPDMGMMGLNEFYRLFINESSYQGLIVDVRNGGGFVSQLIIEKLMNKRIGYDNPRRGTLSPYPTNSVRGKIIAITNEYAGS
DGDIFSFSFKLGLGLKLIGTRTWGGVGITPKRRLIDGTVLTQPEFAFWFRDAGFGVENYGVDPDVEIEYAPHDYLSGKDPQIDYAIDALIEELRN

>d1j7xa_c.14.1.2 (A:) Interphotoreceptor retinoid-binding protein IRBP {African clawed frog (Xenopus laevis)}
DPSVTHVLHQLCDILANNYAFSERIPTLLQHLPNLDYSTVISEEDIAAKLNYELQSLTEDPRLVLSKTDLVMPGDSIQAEINIPEDEAQMLQALVNTVFK
VSILPGNIGYLRFDQFADSVIAKLAPEVNTVWEPIITENLIIIDLRYN VGGSSTAVPLLSYFLDPETKIHFLTLHNRRQNSTDEVYSHPKVLGKPYGSK
KGVYVLTHQTATAAEEFAYLMQSLSRATIIGEITSGNLMHSKVFPFGDTQLSVTVPIINFIDSNGDYWLGGGVVPDAIVLADEALDKAKEIIAFHPPLA

>d1nzya_c.14.1.3 (A:) 4-Chlorobenzoyl-CoA dehalogenase {Pseudomonas sp., strain CBS-3}
MYEAIGHRVEDGVAEITIKLPRHRNALSVKAMQEVTDALNRAEEDDSVGAVMITGAEDAFCAGFYLREIPLDKGVAGVRDHFRIAALWWHQMIHK
IIRVKRPVLAINGVAAGGGLGISLASDMAICADSAAFKVCAWHITIGIGNDTATSYSLARIVGMRRAMEMLTNRTLYPEEAKDWGLVSRVYPKDEFRE
VAWKVARELAAAPTHLQVMAKERFHAGWMQPVEECTFEIQNVIASVTHPHFMPCLTRFLDGHRA DRPQVELPAGV

>d1ey3a_c.14.1.3 (A:) Enoyl-CoA hydratase (crotonase) {Rat (Rattus norvegicus)}
FQYIITEKKGNSSVGLIQLNRPKALNALCNGLIEELNQALETFEEDPAVGAI LTGGEKAFAAGADIKEMQNRTFQDCYSGKFLSHWDHITRKPVIA
AVNGYALGGGCELAMCIDIYAGEKAQFGQPEILLGTIPGAGGTQRLTRAVGKSLAMEMVLTGDRISAQDAKQAGLVS KIFPVETLVEEAIQCAEKIA
NN SKIIVAMAKESVNAAFEMTLTEGNKLEKKLFYSTFATDDRRREGMSAFVEKRKANFKDH

>d1dcia_c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Rat (Rattus norvegicus)}
AYESIQVTSAQKHVLHVQLNRPEKR NAMNRAFWRELVECFQKISKDSCRAV VSGAGKMFSGIDLDMMASDILQPPGDDVARI AWYLRDLISR
YQKFTVIEKCPKPVIAAIHGGCIGGGVDLISACDIRYCTQDAFFQVKE DVGLAADVGLQRLPKVIGNRS LVNELTFTARKMMADEALDGLVSRVF

PDKDVMLNAAFALAADISSKSPAVQGSKINLIYSRDHSVDESLDMATWNMSMLQTQDIKSQAAMEKKDSKSITFSKL
>d1hnua_c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Baker's yeast (*Saccharomyces cerevisiae*)}
NEKISYRIEGPFFIILINPDNLNALEGEDYIYLGELLELADRNRDVYFTIIQSSGRFFSGADFKGIAKAQGDDTNKPSETSKWVSNFVARNVYVTDAF
IKHSKVLCICLNGPAIGLSAALVALCDIVSINDKVYLLYPFANGLITEGGTTVLPLKFGTNNTYECLMFNPKFYDIMCENGFISKNFNMPSSNAEFA
NAVKLEELREKVKGLYLPSCLMKLLKSNHIDAFNKANSVEVNESLKYWVDGEPLKRFRQ
>d1hzda_c.14.1.3 (A:) AUH protein {Human (*Homo sapiens*)}
EDELVRVRHLEENRGRIVVGLINRAYGKNLSKLNKMLSKAVDALKSDKKVRTIIRSEVPGIFCAGADLKERAKMSSSEVGPVSKIRAVINDIANLPVPT
IAAIDGLALGGGLELACDIRVAASSAKMGLVETKLAIIPGGGTQRPLPRAIGMSLAKELIFSARVLDGKEAKAVGLISHVLEQNQEGDAAYRKALDL
AREFLPQGPVAMRVAKLAINQGMEVSDLVTGLAIEEACYAQTIPTKDRLEGLLAFKEKRPPRYKGE
>d1ef8a_c.14.1.3 (A:) Methylmalonyl CoA decarboxylase {Escherichia coli}
MSYQYVNVVTINKAVIEFNYGRKLNALSKVFIDDLMQALSDLNRPEIRCILRAPSNSKVSAGHDHELPSSGRDPLSYDDPLRQITRMIQKFPKPIIS
MVEGSVWGGAFEMIMSSDILIAASTSTFSMTPVNLGVYPYNLVGIHNLTRDGFHIVKELIFTASPITAQRALAVGILNHVVEEELEDFTLQMAHHISE
KAPLAIAVIKEELRVLGEAHTMNSDEFERIQGMRRAYVDSQEDYQEGMNAFLKRKPNFVGH
>d1jnxx1_c.15.1.3 (X:1649-1757) Breast cancer associated protein, BRCA1 {Human (*Homo sapiens*)}
RMSMVSVGLTPEEFMLVYKFARKHHITLTNLITEETTHVVMKTDAEFVCERTLKYFLGIAGGKWVSYFWVTQSICKMLNEHDFEVRGDVVNGR
NHQGPKRARESQD
>d1jnxx2_c.15.1.3 (X:1758-1859) Breast cancer associated protein, BRCA1 {Human (*Homo sapiens*)}
RKIFRGLEICCYGPFTNMPTDQLEWMVQLCGASVVKELSSFTLGTGVHPIVVVQPDAWTEDNGFHAIQMCEAPVVREWVLDVALIDQCQELDT
YLIPQIP
>d1cdza_c.15.1.1 (A:) DNA-repair protein XRCC1 {Human (*Homo sapiens*)}
ELPDFFQGKHFFLYGEFPGDERRKLIRYVTAFNGELEDYMSDRVQFVITAQEWDPSEEEALMDNPSLAFVRPRWIYSCNEKQKLLPHQLYGVVPQA
>d1in1a_c.15.1.2 (A:) DNA ligase III alpha {Human (*Homo sapiens*)}
GSADETLCQTKVLLDIFTGVRVLYLPPSTPDFSRLRRYFVAFDGDVLQEFDMTSATVLSRDKNPAAQQVSPEWIWACIRKRLVAPC
>d1dtb3_c.15.1.2 (B:2582-2660) NAD+-dependent DNA ligase, domain 4 {Thermus filiformis}
EEVSDLLSGLTFLTGECSRPREEVKALLGRLGAKVTDSVSRKTSYLVVGENPGSKLEKARALGVAVLTEEFWRFLKE
>d1rvv1_c.16.1.1 (1:) Lumazine synthase {Bacillus subtilis}
MNIIQGNLVGTGLKIGIVVGRFNDITSKLLSGAEDALLRHGVDTNDIDVAWVPGAFEPAAKKMAETKKYDAITLGTIVRGATTHYDYVCNEAAKG
IAQAANTTGVPIFGIVTTENIEQAIERAGTKAGNKGVDCAVSAIEMANLNRSF
>d1di0a_c.16.1.1 (A:) Lumazine synthase {Brucella abortus}
TSFKIAFIQARWHADIVDEARKSFVAELAAKTGGSVEVEIFDVPGAYEIPHLAKTLARTGRYAAIVGAVIDGGYDHDFVATAVINGMMQVQLETE
VPVLSVVLTPHHFESKEHHDFFAHFVKVKGVEAAHALQIVSERSRIAA
>d1hqka_c.16.1.1 (A:) Lumazine synthase {Aequifex aeolicus}
MQIYEGKLTAEGLRGIVASRFNHALVDRIVEGAIDCIVRHGGREEDITLVRVPGSWEIPVAAGELARKEDIDAVIAIGVLIRGATPHFDYIASEVSKGLA
NLSLELRKPTFGVITADTLEQAIERAGTKHGNKGWEAALSAIEMANLFKSLR
>d1c41a_c.16.1.1 (A:) Lumazine synthase {Rice blast fungus (*Magnaporthe grisea*)}
GPTPQQHDGSALRIGIVHARWNETIIEPLLLAGTKAKLLACGVKESNIVVQSPGSWELPIAVQRQLYASQLQTSSGPGSAGDLLGSSTDLTALPTTT
ASSTGPFDALIAIGVLIKGETMHFEYIADSVSHGLMRVQLDTGPVIFGVLTLDQAKARAGVIEGSHNHGEDWGLAAVEMGVRRDWAAGKT
>d1c2ya_c.16.1.1 (A:) Lumazine synthase {Spinach (*Spinacia oleracea*)}
MNELEGYVTKAQSFRFAIVVARFNEFVTRRLMEGALDFKKYSVNEDIDVVWVPGAYELGVTAQALGKSGKYHAIVCLGAVVKGDTSHYDAVNSA
SSGVLSAGLNSGVPCVFGVLTCNDMDQAINRAGGKAGNKGAEASALTAIEMASLFEEHHLK
>d1ejba_c.16.1.1 (A:) Lumazine synthase {Baker's yeast (*Saccharomyces cerevisiae*)}
AVKGLGKPDQVYDGSKIRVGIIHARWNRIIDALVKGAIERMASLGVEENNIIETVPGSYELPWGKRFVDRQAKLGKPLDVVIPIGVLIKGSTMHFEY
ISDSTTHALMNLQEKVDMMPVIFGLLCTMEEQALARAGIDEAHSMHNHGEDWGAAVEMAVKFGKNAF
>d1cp3a_c.17.1.1 (A:) Apopain (caspase-3, cpp32) {Human (*Homo sapiens*)}

NSYKMDYPEMGLCIIINNKNFHKGSTGMSRSQTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKEHDKRSSFVCVLLSHGEEGIIFGTNG
PVDLKKITNFFRGDRCRSLTGPKLFIIQACRGTEDCGIETDSGVDDDMACHKIPVDAFLYAYSTAPGYYSWRNSKGWSFIQLCAMLKQYADKL
EFMHILTRVNRKVATEFESFSFDATFHAKKQPCIVSMLTKELYFYH
>g1bc.1 c.17.1.1 (A;B) Interleukin-1beta converting enzyme (a cysteine protease) {Human (Homo sapiens)}
GNVKLCLEEAQRIWKQKSAEIYPIMDKSSRTRLALIICNEEFDSPRTGAEVDTGMTMLLQNLGYSVDVKKNLTASDMTTELEAFahrpehktSDS
TFLVFMSSHGIREGICGKKHSEQVPDILQLNAIFNMLNTKNCP SLKDPKVIIQACRGDSPGVVFKDXAIKKAHIEKDFIAFCSSPDNVWRHPTM
GSVFIGRLIEHMQEYACSCDVVEIFRKVRFSFEQPAGRAQMPTTERVTLTRCFYLFPGH
>d1f1ja_c.17.1.1 (A;) Caspase-7 {Human (Homo sapiens)}
YQYNMNFKEKGKCIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGF D VIVYNDCSAKMQDLKKASEEDHTNAACFACILLSHGEENVIYGKD
GVTPIKDLTAHFRGDRSKTLEPKLFFIQACRGTELDDGIQADSGPIN D TDANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHG
KDLEIMQILTRVNDRVARHFESQSDDPHFHEKKQPCIVSMLTKELYFS
>g1qtn.1 c.17.1.1 (A;B) Caspase-8 {Human (Homo sapiens)}
DKVYQMKSKPRGYCLIINNNHNFAKAREKVPKLHSIRDRNGTHLDAGALTTFEELHFEIKPHDDCTVEQIYEILKIYQLMDHSNMDCFICCILSHGDKG
IYGTDGQEAPIYELTSQFTGLKCP SLAGKPKVFFIQACQGDNYQKGIPVETDXTRYIPDEADFLGMATVNNCVSYRNAEGTWYIQSLCQLRERCPR
GDDITLTVENYEVSNKDDKKNMKGKQMPQPTFLRKKLVFP SD
>d1jxqa_c.17.1.1 (A;) Caspase-9 {Human (Homo sapiens)}
MGALESLRGNADLAYILSMEP CGHCLII NNVNFCRESGLRTGGSNIDCEKLRRFSSLHFMVEVKGDLTAKMV LALLELARQDHGALDCVVVILS
HGCQASHLQFPGAVYGTGCPVSVEKIVNIFNGTSCPSLGGKP KLF FIQACQGDNYQKGIPVETDXTRYIPDEADFLGMATVNNCVSYRNAEGTWYIQSLCQLRERCPR
LPTPSDIFVSYSTFPGFVSRDPKSGSWYVETLDDIFECWAHSEDLQSLLRVANAVSVKG IYKQMPGCFNLRKKLFFKTS
>d1cvra2 c.17.1.2 (A:1-350) Gingipain R (RgpB), N-terminal domain {Porphyromonas gingivalis}
YTPVEEKENRMIVIVAKK YEGDIKDFWDWKNQRGLRTEVKVAEDIASPV TANA IQQFVKQ EYEGNDLTYVLLVGHDHKDIPAKITPGIKSDQVYQ
IVGNDHYNEVFIGRFSCESKEDLKTQIDRTIH YERNITTEDKWL GQALCIAAE GGPSADNGESDIQHEN VIANLLTQYGYTKIICKYD PGVTPKNIIDAF
NGGISLVNYTGHGSETAWGTSHFGTTVKQLTN SNQLP FIFDVACVNGDFLSMPCFAE ALMRAQKDGKPTGTVAIIASTIDQYWAPP MRGQDEM
NEILCEKHPPNNIKRTFGGVTMNGMFAMVEKYKKDGENMLDTWTVFGDPSLLVRTLV
>d1akz_c.18.1.1 (-) Uracil-DNA glycosylase {Human (Homo sapiens)}
MEFFGESWKKHLSGEFGKPYFIKLMGFVAEERKHYTVPPPQHVFTWTQMC DIKDV KV VILGQDPYHGPNAHGLCFSVQRPVPPPSLENIYKEL
STDIEDFVHPGHGDLSGWAKQGVLLLNAVLT VRAHQANSHKERGWEQFTDAV SVLNQNSNGLVFLWGSYAQKKGSAIDRKRHV/LQTAHPSP
LSVYRGFFGCRHFSKTNELLQKSGKKPIDWKE L
>d1laue_c.18.1.1 (E;) Uracil-DNA glycosylase {Herpes simplex virus type 1}
LDWTTFRRVFLIDDAWRPLMEPE LANPLTAHLLAEYNRRCQTEEVLP PREDVFSWTRYCTPDEV RVVIIQ QDPYHHPGQA HGLAF SVRANVPPPS
LRNVLA AVKNCYPEARMSGHG CLEKWARDGVLLNTLTVKRGAAASHS RIGWDRFVGGVIRRLAARRPGLVFM WGTHAQN AIRPDPRVHC VL
KFSHPSPLSKV PFGTCQHFLVANRYLETR SISPIDW S V
>d3euga_c.18.1.1 (A;) Uracil-DNA glycosylase {Escherichia coli}
LTWHDV LAE KKQPHFLNLTQTVASERQSGVTIYPPQKDVNAFRFT ELDGV KV VILGQDPYHGPQAHGLAF SVRPGIAIPPSLLNMYKELENTIP
GFTRPNHGYLESWARQGVLLNTLTVRAGQAHSHASLGWETFTDKVISLINQHREGV VFLWGSHAQKKGAIIDKQRHHVLKAPHPSPLSAHRGF
FGCNHFV LANQW LEQHGETPIDWMPVLP AE
>d1muga_c.18.1.2 (A;) G:T/U mismatch-specific DNA glycosylase {Escherichia coli}
MVEDILAPGLRVFCGINPGLSSAGTGFPAH PANR FWKVIYQAGFTDRQLKPQEAQHLLDYRCGVTKL VDRPTVQANEVSKQELHAGGRKIEKIE
DYQPQALAILGKQAYEQGFSQRGAQWGKQTLTIGSTQIWVLPNPSGLSRV SLEKLVEAYRELDQALVV
>d1mla_1 c.19.1.1 (3-127,198-307) Catalytic domain of malonyl-CoA ACP transacylase {Escherichia coli}
QFAFVFPGQGSQTVGMLADMAASYPIVEETFAEASAALGYDLWALTQQGPAEELNKWTQTPALLTASVALYRVWQQQGGKAPAMMAGHSLGE
YSALVCAGV IDFADAVRLVEMRGKFMQEA VPEXVPSHAC LMKA ADKLA VELAKITFNAP TVPV VNN DVK C ETNGDAIR DALV RQL NPV QWTK
SVEYMAAQGV EHLYEV GPGK VLT GLT KRIV D TLTA SALNEPSAMAAL
>d1g7sa3 c.20.1.1 (A:329-459) Initiation factor IF2/eIF5b, domain 3 {Archaeon Methanobacterium thermoautotrophicum}

DPEKVREEILSEIEDIKIDTDEAGVVVKADTLGSLEAVVKILRDMYVPIKVADIGDVSRDVVNAGIALQEDRVYGAIIAFNVKVIPSAAQELKNSDIKF
QGNVIYRLMEEYE EWVRGIEEEEKKKKWMEA

>d1jj2i_c.21.1.1 (I:) Ribosomal protein L13 {Archaeon Haloarcula marismortui}

AEFDADIVDARDCIMGRVASQVAEQALDGETVAVVNAERAVITGREEQIVEKYEKRVDIGNDNGYFYPKRPDGIFKRTIRGMLPHKKORGREA FES
VRVYLGPNPYDEDGEVLDGTSLDRLSNIKFVTLGEISETLGANKTW

>d1dmga_c.22.1.1 (A:) Ribosomal protein L4 {Thermotoga maritima}

AQVDLLNVKGEVKGTLEISDFVFNIDPNYDMQLSNRRAGTASTKTRGEVSGGGRKPWPQKHTGRARHGSIRSPIWRHGGVVHGPKP
RDWSKKLNKKMKKLALRSALSVKYRENKLLVDDLKLERPKTKSLKEILQNLQLSDKTLIVLPWKEEGYMNVKLSGRNLPDVKVIADNPNNSKNGE
KA VR RIDGLNVFDMLKYDYLVLTRDMVSKIEEV LG

>d1jj2c_c.22.1.1 (C:) Ribosomal protein L4 {Archaeon Haloarcula marismortui}

MQATIYDLGNTDGEVDPDVFTEPVRSIDLIGKAVRAAQANRKQDYGSDEYAGLRTPAESFGSGRGQAHV PKL DGRARRVPQAVKGRSAHPPKTE
KDRSLDNLNDKERQLAVRSALAATADADLVADRGHEFDRDEVPVVSDDFEDLVKTQE VVSLEALDVHADIDRAETKIKAGQGSARGRKYRRPASIL
FVT SDE PSTA RNL AGADV ATASEVN TEDLA PG GAP GRL TVF TES ALAEVAER

>d1hey_c.23.1.1 (-) CheY protein {Escherichia coli}

DKELKFLVVGNGGTGKSTVRNLLKELGFNNVEDGV DALNKLQAGGYGFVSDWNMPNMDGLELLKTIRADGAMSALPVLMVTA EAKKENIIA
AAQAGASGYVVKPFTAATLEE KLN KIFE KLG M

>d1jbea_c.23.1.1 (A:) CheY protein {Escherichia coli}

ADKELKFLVDDFSTMRRIVRNLLKELGFNNVEEAEDGV DALNKLQAGGYGFVSDWNMPNMDGLELLKTIRADGAMSALPVLMVTA EAKKENIIA
AAQAGASGYVVKPFTAATLEE KLN KIFE KLG M

>d1tmy_c.23.1.1 (-) CheY protein {Thermotoga maritima}

GKRVLIVDDAAFMRMMI KDIITKAGYEVAGEATNGREAVEKYKELKPDIVTMDITMPEMNGIDAIEKIMKIDPNAKII VCSAMGQQAMVIEAIKAG
AKDFIVKPFQPSRV VEALNK V

>d1a04a2_c.23.1.1 (A:5-142) Nitrate/nitrite response regulator (NARL), receiver domain {Escherichia coli}

EPATILLIDDHPMLRTGVKQLISMAPDITVGEASNGEOQGIELAESLDPDLILDLNMPGMNGLETLDKLREKSLSGRIVVFSVS NHEEDVVTALKRGA
DGYLLKDM EPEDLLKALHQAAAGEMVLSEALTPVLAASL

>d1ntr_c.23.1.1 (-) NTRC receiver domain {Salmonella typhimurium}

MQRGIVVVVDDDSSIRWVLERALAGAGLTCTTFENGNEVLAALASKTPDVLLSDIRMPGMDGLALLKQIKQRHPMLPVII MTAHS LDAA VSAYQ
QGAFDYL PKPFDIDEAVALVERAISHYQE

>d1dbwa_c.23.1.1 (A:) Transcriptional regulatory protein FixJ, receiver domain {Rhizobium meliloti}

MQDYTVHIVDDEE PVKSLAFMLTMNGFAVKMHQS AEAFLA FAPDVRNGVLVTDLRMPDMMSGVELRNLGDLKINIPSIVITGHGDVPM AVEAM
KAGAVDFIEKPFEDTVII EIERASEHLV

>d1qkka_c.23.1.1 (A:) Transcriptional regulatory protein DctD, receiver domain {Sinorhizobium meliloti}

PSVFLIDDDRDLRKAMQQTLELAGFTVSSFASATEALAGLSADFAGIVISDIRMPGMDGLALFRKILALPDPLMILVTGHGDIPMAVQAIQDGAYDFI
AKPFAADRLVQSARRAEEKRRLV MENRSLRRAAE AASEGL

>d1dz3a_c.23.1.1 (A:) Sporulation response regulator Spo0A {Bacillus stearothermophilus}

SIKVCIA DDNR ELV SLL DEYISSQPDMEVIGTAYNGQDCLQM LEEKRPDILLLDIIMPHLDGLAVLERIRAGFEHQPNVIMLTA FGQEDVTKA VELGA
SYFILKPFDMENLAHHIRQVY GKT

>d1nat_c.23.1.1 (-) Sporulation response regulator Spo0F {Bacillus subtilis}

NEKILIVDDQY GIRILLNEV FNKEGYQTFOA ANGLQAL DIVTKERPDVL LLD MKIPGMDGIEILKRMKVIDENIRVIIMTAYGEL DM IQESKELGAL THFA
KPF DIDEIRDAV KYLPL

>d1a2oa1_c.23.1.1 (A:1-140) Methylesterase CheB, N-terminal domain {Salmonella typhimurium}

MSKIRVLSVDDSALMRQIMTEIINSHSDMEMVATAPDPLVARDLIKFNPDVLTLDVEMPRMDGLDFLEKLMRLRPMPVVMVSSLTGKGSEVTLRA
LELGAIDFVTKPQLGI REGMLAY SEMIAEKV RTAARARIAAHKP

>d1kgsa2_c.23.1.1 (A:2-123) PhoB receiver domain {Thermotoga maritima}

NVRVLVVEDERDLADLITEALKKEMFTVDVCYDGEEGMYMALNEPFDVVILDIMLPVHDGWEILKSMRESGVNTPVLMLTALSDVEYRVKGKLNMG
ADDYLPKPFDLRELIARVRALIRRKE

>d1b00a_c.23.1.1 (A:) PhoB receiver domain {Escherichia coli}

ARRILVVEDEAPIREMVCVLEQNGFQPVEAEDYDSAVNQLNEPWPDILLLDWMLPGGGSIQFIKHLKRESMTRDIPVVMLTARGEEDRVRGLET
GADDYITKPFSPKELVARIKAVMRRI

>d1dcfa_c.23.1.2 (A:) Receiver domain of the ethylene receptor {Thale cress (Arabidopsis thaliana)}

HMSNFTGLKVLVMDENGVRMVTKGLLVHGCEVTTSSNEECLRVVSHEHKVVFMDCMPGVENYQIALRIHEKFTKQRHQRPLLVALSGNTDK
STKEKCMSFGLDGVLLPKVSLDNIRDVLSLDLEPRVLYE

>d1qo0d_c.23.1.3 (D:) Negative regulator of the amidase operon AmiR {Pseudomonas aeruginosa}

SANSLLGSRELQVLVLPNPPGEVSDALVLQLIRIGCSVRCWPPPEAFDPVDPVVFTSIFQNRHHDEIAALLAAGTPRTTLVALVEYESPAVLSQIIELEC
HGVTQPLDAHRLVLPVLVSARRISEEMAKLKQKTEQLQDRQARINQAKVLLMQRHGWDEREAHQHLSREAMKRREPILKIAQELL

>d1fyva_c.23.2.1 (A:) Toll-like receptor 1, TLR1 {Human (Homo sapiens)}

NIPLEELQRNLQFHAFISYSGHDSFWVKNELLNPNEKEGMQICLHERNFVPGKSIVENIITCIEKSYKSIFVLSPNFVQSEWCHYELYFAHHNLFHEGSN
SLILILLEPIPQYSIPSSYHKLKSLMARRTYLEWPKEKSKRGLFWANLRAAINIKLTEQAK

>d1fywa_c.23.2.1 (A:) Toll-like receptor 2, TLR2 {Human (Homo sapiens)}

SRNICYDAFSYSERDAYVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNIIDSIEKSHKTVFVLSENFKSEWCKYELDFSHFRLFDENNDAAIIL
LLEPIEKKAIPQRFCKLKIMNTKTYLEWPMDAQREGFWVNLAIAIKS

>d1eiwa_c.23.3.1 (A:) Hypothetical protein MTH538 {Archaeon Methanobacterium thermoautotrophicum}

VTAEIRLYITEGEVEDYRVFLERLEQSGLEWRPATPEDADAVIVLAGLGTRDEILGAVDLARKSSKPIITVRPYGLENVPPELEAVSSEVGWNPHCI
RDALEDALDVI

>d1jkja2_c.23.4.1 (A:122-287) Succinyl-CoA synthetase, alpha-chain, C-terminal domain {Escherichia coli}

NCPGVITPGECKIGIQPGHIHKPGKVGIVSRSGTLTYEAVKQTTDYFGQSTCVGIGGDPIPGSNFIDILEMFKEKDPQTAEIVMIGEIGGSAEEAAAYIK
EHVTKPVVGYIAGVTAPKGKRMGHAGAIAGGKGTADKEFAALEAAGVKTVRSLASDICEALKTVL

>d1euca2_c.23.4.1 (A:131-306) Succinyl-CoA synthetase, alpha-chain, C-terminal domain {Pig (Sus scrofa)}

NCPGVINPGECKIGIMPGBIHKKGRIGIVSRSGTLTYEAVHQTQVGLQSLCVGIGGDPFNGTDFTDCLEIFLNDPATEGIILGEIGGNAEENAAEFL
KQHNSGPKSKPVVFSIAGLTAPPGRRMHGAGAIAGGKGGAKEITALQSAGVVVMSSPAQLGTTIYKEFEKRKML

>d1jkjb1_c.23.4.1 (B:239-388) Succinyl-CoA synthetase, beta-chain, C-terminal domain {Escherichia coli}

DPREAQAAQWELNYVALDGNIGCMVNAGLAGMTMDIVKLHGGE PANFLVGGGATKERVTEAFKIIISDDKVAKLVNIFGGIVRCCLIADGIIG
AVAEVGVNVPVVRLLEGNNAELGAKKLADSGLNIIAKGLTAAQQVVAAVEGK

>d1eucb1_c.23.4.1 (B:246-393) Succinyl-CoA synthetase, beta-chain, C-terminal domain {Pig (Sus scrofa)}

EPIENEAAKYDLKYIGLDGNIACFVNAGLAGMATCDIIFLNGGK PANFLDLGGGVKESQVYQAFKLTADPKVEAILVNIFGGIVNCIAIANGITKACREL
ELKPLVVRLEGTVNVHEAQNIINTNSGLPITS AVDLEAAKKAVASVT

>d2fcr_c.23.5.1 (-) Flavodoxin {Chondrus crispus}

KIGIFFSTGNTTEVADFIGKLGAKADAPIDVDDVTPDQALKDYDLLFGAPT WNTGADTERGTSWDEFLYDKLPEVDMKDLPAIFGLGDAEGY
PDNFCDIAIEEIHDCAFKQGAKPVGF SNPPDYEEESKSVRDGKFLGPLDMVNDQIPMEKRVAGWVEAVVSETGV

>d1f4pa_c.23.5.1 (A:) Flavodoxin {Desulfovibrio vulgaris}

PKALIVYGSTTGNT EYTAETIARELADAGYEVD SRDAASVEAGGLFEGFDLVLGCSTWGDDSIELQDDFIPLDSLEETGAQGRKVACFGCGDSSWE
YFCGA VDAIEEKLKNL GAEIVQDG LRIDGDPRA ARD DIVGWAHDVRGA

>d1rcf_c.23.5.1 (-) Flavodoxin {Anabaena, pcc 7119 and 7120}

SKKIGLFYGTQTKTESVAEIRDEFGNVVTLHDVSQAEVTDLNDYQYIIGCPTWNIGELQSDWEGLYSELDDVDFNGKLVAYFGTGDQIGYADNF
QDAIGILEEKISQRGGKTVGYWSTDGYDFNDSKALRNGKFVGLALDEDNQSDLTDDRIKS WVAQLKSEFGL

>d1ag9a_c.23.5.1 (A:) Flavodoxin {Escherichia coli}

AITGIFFGSDTGNTE NIAKMIQKQLGKDADVHDIAKSSKEDLEAYDILLG IPTWYYGEAQCDWDDFFPTLEEIDFNGKLVALFGCGDQEDYAEYFCD
ALGTIRDIIERPGATIVGHWPTAGYHF EASKGLADDDHHVGLAIDEDRQPELTAERVEKWKQISEELHLDEILNA

>d1czna_c.23.5.1 (A:) Flavodoxin {Anacystis nidulans and Synechococcus, pcc 7942}
AKIGLFYGTQTVTQIAESIQQEFGGESIVDLNDIANADASDLNAYDYLIGCPTWNVGEIQLSDWEGIYDDLSVNFGKKVAYFGAGDQVGYSND
FQDAMGILEEKISSLGSQTGVYWPPIEGYDFNESKAVRNQFVGLAIDEDNQPDLTKNRIKTWSQLKEFGL
>d5nul_c.23.5.1 (-) Flavodoxin {Clostridium beijerinckii}
MKIVYWSGTGNTEKMAELIAKGIESGKDVTINTVSDVNIDELLNEDILILGCSAMTDEVLESEFEPFIEEISTKISGKKVALFGSYGWGDGKWMRDF
EERMNGYGCVVETPLIVQNEPDEAEQDCIEFGKKIANI
>d1fuea_c.23.5.1 (A:) Flavodoxin {Helicobacter pylori}
GKIGIFFGTDSGNAEAIAEKISKAIGNAEVVVDVAKASKEQFNGFTKVILVAPTAGAGDLQTDWEDFLGLEASDFANKTIGLVLGLDQDTYSETFAEGIF
HIYEKAKAGKVVGQTSTDGYHFAASKAVEGGKFVGLVIDEDNQDDLTDERIAKWWVEQVRGSFA
>d1bvyf_c.23.5.1 (F:) FMN-binding domain of the cytochrome P450bm-3 {Bacillus megaterium}
NTPLLVLYGSNMGTAEGTARDLADIAMSKGFPQVATLDASHAGNLREGAVLITASYNGHPPDNAKQFVDWLQASADEVKGVRYSVFGCGDKN
WATTYQKVPAFIDETLAAGAENIADRGEADASDDFEGTYEEWREHMWSDVAAYFNL
>d1e5da1_c.23.5.1 (A:251-402) Rubredoxin oxygen:oxidoreductase (ROO), C-terminal domain {Desulfovibrio gigas}
PTNKVVIFYDSMWHSTEKMARVLAESFRDEGCTVKLMWCKACHHSQIMSEISDAGAVIVGSPTHNNNGILPYVAGTLQYIKLRPQNKIGGAFGSFG
WSGESTVKVLAEWLTGMGFDMPATPKVKNVPTHDAYEQLKTMQTIARALKAKLAA
>d1ja1a2_c.23.5.2 (A:63-239) NADPH-cytochrome p450 reductase, N-terminal domain {Rat (Rattus norvegicus)}
PVKESSFVEKMKKTGRNIVFYGSQTGTAAEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDKSLVVFCCMATYGEGDPTDNAQDFYDWLQED
TDVDLTGVKFAVFGGLGNKTYEHFNAMGKYVDKRLEQLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEFFGVETGEE
>d1b1ca_c.23.5.2 (A:) NADPH-cytochrome p450 reductase, N-terminal domain {Human (Homo sapiens)}
SSFVEKMKKTGRNIVFYGSQTGTAAEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDNALVVFCCMATYGEGDPTDNAQDFYDWLQED
DLGVKFAVFGGLGNKTYEHFNAMGKYVDKRLEQLGAQRIFELGLGDDGNLEEDFITWREQFWPAVCEHFGV
>d1dxqa_c.23.5.3 (A:) NAD(P)H:quinone reductase {Mouse (Mus musculus)}
AARRALIVLAHSEKTSFNYAMKEAAVEALKRGWEVLESIDLAMNFNPISRNDITGEKLDSKNFQYPSESSLAYKEGRSLSPDIVAEHKKLEAADLVIFQ
FPLQWFGVPAILKGWFERVLVAGFAYTYAACMYDNGPFQNKKTLLSITTGGSGSMYSLQGVHGDMNVILWPIQSGILRFCGFQVLEPQLVYSIGHTPP
DARMQILEGWKKRLETVWEETPLYFAPSSLFDLNQAGFLLMKEVQEEQKKNKFGLSVGHHLGKSIPADNQIKARK
>d1qrda_c.23.5.3 (A:) NAD(P)H:quinone reductase {Rat (Rattus rattus)}
AVRRALIVLAHAERTSFNYAMKEAAVEALKKGWEVVESIDLAMNFNPISRNDITGEPKDSENQYPVESSLAYKEGRSLSPDIVAEQKKLEAADLVIF
QFPLYWFGVPAILKGWFERVLVAGFAYTYATMYDKGPFQNKKTLLSITTGGSGSMYSLQGVHGDMNVILWPIQSGILRFCGFQVLEPQLVYSIGHTPP
DARVQVLEGWKKRLETVWEETPLYFAPSSLFDLNQAGFLLMKEVQEEQKKNKFGLSVGHHLGKSIPADNQIKARK
>d1d4aa_c.23.5.3 (A:) NAD(P)H:quinone reductase {Human (Homo sapiens)}
VGRRALIVLAHSEKTSFNYAMKEAAAALKKGWEVVESIDLAMNFNPISRNDITGEPKDSENQYPVESSLAYKEGRSLSPDIVAEQKKLEAADLVIF
QFPLQWFGVPAILKGWFERVFIGEFAYTYAACMYDKGPFRSKKAVLSITTGGSGSMYSLQGVHGDMNVILWPIQSGILHFCGFQVLEPQLTYSIGHTPP
DARIQILEGWKKRLENIWDETPLYFAPSSLFDLNQAGFLMKEVQDEEKNKKFGLSVGHHLGKSIPADNQIKARK
>d1qr2a_c.23.5.3 (A:) Quinone reductase type 2 (menadione reductase) {Human (Homo sapiens)}
AGKKVLIVYAHQEPKSFNGSLKNVADELRSQGCTVTSIDLAMNFEPRTDKDITGTLNSPEVNYGVETHEAYKQRSLASDITDEQKKVREADLVIF
QFPLYWFSVPAILKGWMDRVLCQGFADFIPGFYDSGLLQGKLALLSVTTGGTAEMYTKTGVNGDSRYFLWPLQHGTLLHFCGFKVLPQISFAPEIASE
EERKGMVAAWSQRLQTIWKEEPICHTAHWHFGQ
>d1bmta2_c.23.6.1 (A:741-896) Methionine synthase, C-terminal domain {Escherichia coli}
EQGKTNGKMWATVKGDVHDIGKNIVGVVLCQNNYEIVDLGVMVPAEKILRTAKEVNADLIGLGLITPSLDEMNVNAKEMERQGFTIPLLIGGATT
KAHTAVKIEQNYSGPTVYVQNASRTVGVVAALLSDTQRDDFVARTRKEYETVRIQHGR
>d1fmfa_c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium tetanomorphum}
MEKKTIVLGVIGSDCHAVGNKILDHSFTNAGFNVNIGVLSSQEDFINAAIETKADLICVSSLYGQGEIDCKGLREKCDEAGLKGIKLFVGGNIVVGKQ
NWPDVEQRFKAMGFDRVYPPGTSPETTIADMKEVLGVE
>d1ccwa_c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium cochlearium}

MEKKTIVLGIVGSDCHAVGNKILDHAFTNAGFNVNIGVLSPQELFIKAAIETKADAILVSSLYGQQEIDCKGLRQKCDEAGLEGILLYVGGNIVVGKQH
WPDVEKRKDMGYDRVYAPGTPPEVGIADLKKDLNIE

>d7reqa2 c.23.6.1 (A:561-728) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

AQIRTISGVYSKEVKNTPEVEARELVEEFEQAEGRRPRILLAKMGQDGHDHGQKVIAATAYADLGFVDVGPLFQTPEETARQAVEADVHVGVSSL
AGGHLTLPALRKELDKLGRPDILITVGGVPIEQDFDELRKDGAVEIYTPGTVIPESAISLVKKLRASLDA

>d7reqb2 c.23.6.1 (B:476-638) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta subunits {Propionibacterium freudenreichii, subsp. shermanii}

TKPFPAAAPARKGLAWHRDSEVFQLMDRSTSVERPKVFLACLGTRRDFFGREGFSSPVWHIAGIDTPQVEGGTTAEIVEAFKKSGAQVADLCSSAK
VYAQQGLEVAKALKAAAGAKALYLSGAFKEFGDDAAEAEKLIDGRLFMGMDDVVDTLSSTDILGVAK

>d1c4ka1 c.23.7.1 (A:1-107) Ornithine decarboxylase N-terminal "wing" domain {Lactobacillus sp., strain 30a}

SSSLKIASTQEARNQYFDTRVVVDAVGSDFTDVGAVIAMDYETDVIDAADATKFGIPFAVTKDAQAIASADEKKIFHIIDLENKFATVNAREIETAVN
NYEDSIL

>d1qcza_c.23.8.1 (A:) N5-carboxyaminoimidazole ribonucleotide (N5-CAIR) mutase PurE {Escherichia coli}

PARVAIVMGSKSDWATMQFAAEIFEILNVPHHVEVSAHRTPDKLFSAESAEENGYQVIAGAGGAHLPGMIAAKTLVPVLGVPVQSAALSGVDS
LYSIVQMMPRGIPVGTIAIGKAGAANAALLAAQILATHDKELHQRLNDWRKAQTDEVLENPDPRGAA

>d1cex_c.23.9.1 (-) Cutinase {Fungus (Fusarium solani), subsp. pisi}

RTTRDDLINGNSASCADVIFIYARGSTETGNLGLPSIASNLAFGKDGVIQGVGGAYRATLDNALPRGTSAAIREMLGLFQQANTKCPDATL
IAGGYSQGAALAAASIEDLDSAIRDKIAGTVLFGYTKNLQNRRIPNYPADRTKVFCTGDLVCTGSLIVAAPHLAYGPDARGPAPEFLIEKVRAVRGS

>d1g66a_c.23.9.1 (A:) Acetylxyran esterase {Penicillium purpurogenum}

SCPAIHVFGARETTASPGYGSSTVVNGVLSAYPGSTAEEAINYPACGGQSSCGGASYSSVAQGIAAVASAVNSFNSQCPSTKIVLVGYSQGGEIMDVA
LCGGGDPNQGYTNATAVQLSSAVNMVKAIFMGDPMFRAGLSYEVGTCAAGGFQDRPAGFSCPSAAKIKSYCDASDPYCCNGSNAATHQGYGSE
YGSQALAFVSKLG

>d1qoza_c.23.9.1 (A:) Acetylxyran esterase {Trichoderma reesei}

ECPAIHVFGARETTVSQGYGSATVVNLVIQAHPGTTSEAIVYPACGGQASC GGISYANSVNGTAAAAAANFHNSCPDTQLVLVGYSQGAQIFD
NALCGGGDPGEGITNTAVPLTAGAVSAVKAIFMGDPNRNIHGLPYNVGTCTQGFDARPAGFVCPASKIKSYCDAADPYCCTGNDPNVHQGYGQE
YGQQALAFINSQLS

>d1esc_c.23.10.1 (-) Esterase {Streptomyces scabies}

DPPVTFFGDSYTANFGIAPVTNQDSERGWCFQAKENYPAVATRSLADKGITLDVQADVSCGGALIHHFWEKQELPFGAGELPPQQDALKQDTQLT
VGSLGGNTLGFNRILKQCSDELRKPSLLPGDPVDGDEPAAKCGEFFGTGDKQWLDDQFERVGAELEELDRIGYFAPDAKRVLVGYPRVLVPEDTTKC
LTAAPGQTQLPFADIPQDALPVLQIQKRLNDAMKKAADGGADFVDLYAGTGANTACDGADRGIGGLLEDSQLELLGTKIPWYAHPNDKGRDIQ
AKQVADKIEEILN

>d1flca2 c.23.10.2 (A:1-150,A:307-427) Esterase domain of haemagglutinin-esterase-fusion glycoprotein HEF1 {Influenza C virus}

EKIKICLQKVQNSFSLHNFGGNLYATEEKRMFELVKPKAGASVNLNQSTWIGFGDSRTDKNSAFPRSADVSAKTADKFRFLSGGSLMLSFGPPG
KVDYLYQGCGKHVKFYEGVNWSPHAAINCYRNWTDIKLNFKQNIYELASQSHXEKGPTAVQSIWGKGRESDYAVDQACLSTPGCMLIQKQKPYI
GEADDHHGDQEMRELLSGLDYEARCISQSGWVNETSPFTEKYLLPPKFGRCPLAAKEEISPKIPDGLLIPTSGTDTTVT

>d1es9a_c.23.10.3 (A:) Platelet-activating factor acetylhydrolase {Cow (Bos taurus)}

ENPASKPTPVQDVGQDGKWMSPQHNRFLDCKDKEPEVVFQDSLVQLMHQCEIWRELFSPLHALNFGIGGDSTQHVLWRLENGELHIRPKIVVV
WVVTNNNHGHTAEQVTGGIKAIQLVNERQPQARVVVLGLLPRGQHPNPLREKNRRVNEVRAALAGHPRAHFLADPGFVHSDDTISHDMYD
YLHLSRLGYTPVCRALHSLLRL

>d1fxwf_c.23.10.3 (F:) Platelet-activating factor acetylhydrolase {Cow (Bos taurus)}

SNPAAIPHAEDIQGDDRWSMSQHNRFVLDCDKDEPDVLFVGDSMVQLMQQYEIWRELFSPLHALNFGIGGDSTQHVLWRLNGELENIPKIVIV
VVWGTNNNHNTAEEVAGGIEAIVQLINTRQPQAKIIVLGLLPRGKEPNPLRQKNAKVNQLKVSPLKLANVQLLTDGGFVHSDDGAISCHDMFDFL
HLTGGGYAKICKPLHELIMQLL

>d1k7ca_c.23.10.4 (A:) Rhamnogalacturonan acetylesterase {Fungus (*Aspergillus aculeatus*)}

TTVYLAGDSTMKGNGGSGTNGWGEYLASYLSATVVNDAVGRSARSYTREGRFENIADVVTAGDVIVEFGHNDGGSSTDNGRTDCSGTGAEV
CYSVYDGVNELTLPAYLENAAKLFTAKGAKVILSSQTPNNPWEITGTFVNSPTRFVEYALAAEVAGVEYVDHWSYVDSIYETLGNATVNSYFPIDHT
HTSPAGAEVVAEAFLKAVCTGTSLKSVLTTTSFEGTCL

>d1iexa2 c.23.11.1 (A:389-603) Beta-D-glucan exohydrolase, C-terminal domain {Barley (*Hordeum vulgare*)}

LVLLKNGKTSTDAPLLPLPKKAPKILVAGSHADNLGYQCGGWIEWQGDTGRTTVGTTILEAVKAADVDPSTVVFAENPDAEFVKSGGFSYAIVAVGE
HPYETKGDNLNLTIPEPGLSTVQAVCGGVRCATVLISGRPVVQPLLAASDALVAAWLPGSEGQGVTDALFGDFGFTGRPLRTWFKSVDQLPMNV
GDAHYDPLFRLGYGLTTNATK

>d2naca2 c.23.12.1 (A:1-147,A:336-374) Formate dehydrogenase {Pseudomonas sp., strain 101}

AKVLCVLYDDPVGDYPKTYARDLKPIDHYPGQTLPTKAIDFTPQGQLGSVSGELGLRKYLESNGHTLVTSDKDPDSVFERELVDADVVISQPF
WPAYLTPERIAKAKNLKLALTAGIGSDHVDLQSAIDRNVTVAEVTCNSXTLTAQARYAAGTREILECFEGRPIRDEYLIVQGGALA

>d1qp8a2 c.23.12.1 (A:1-82,A:264-302) Putative formate dehydrogenase {Archaeon *Pyrobaculum aerophilum*}

MELYVNFEPEAEELRKYFKIVRGGDLGNVEAALVSITAEELAKMPRLKFIQVVTAGLDHLPWESIPPHVTVAGNAGSNXGYGNERVWRQMVM
EAVRNILITYATGGPRNIAKREDYIG

>d1dxy_2 c.23.12.1 (1-100,300-330) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}

MKIIAYGARVEDIQYFKQWAKDTNTLEYHTEFLDENTVEWAKGFDGINSLQTPYAAVGFEKMHAYGIKFLTIRNVGTDNIDMTAMKQYGIRLSNV
PAYXTETAVHNMVYFSLQHLVDFLTKGESTEVTG

>d1gdha2 c.23.12.1 (A:2-100,A:292-321) D-glycerate dehydrogenase {Hyphomicrobium methylovorum}

KKKILITWPLPEAACMARARESYDVIAGDDPKITIDEMIETAKSVDALLTNEKCRKEVIDRIPIENIKCISTYSIGFDHIDLACKARGIKVGNAPHGXAT
QAREDMAHQANDLIDALFGGADMSYAL

>d1psda2 c.23.12.1 (A:7-107,A:296-326) Phosphoglycerate dehydrogenase {Escherichia coli}

EKD KIKFLLVEGVHQKALESLRAAGYTNIEFKHGALDDEQLKESIRDAHFIGLRSRTHLTEDVINAEEKLVAGCFCIGTNQVLDAAKRGIPVFNAPFS
XSTQEAQENIGLEVAGKLIKYSNDNGSTLSAVN

>d2ldla2 c.23.12.1 (A:1-103,A:301-337) D-lactate dehydrogenase {Lactobacillus helveticus}

MTKVFAAIRKDEEPFLNEWKEAHKDIDVYTDKLLTPETAKLAKGADGVVVYQQLDYTADTLQALADAGVTKMSLRNVGVDNIDMDKAKELGFQI
TNVPVSYXTTHAVRNMVVKAFNNNLKLINGEKPDSPVALNKNKF

>d1pjca2 c.23.12.2 (A:1-135,A:304-361) L-alanine dehydrogenase {Phormidium lapideum}

MEIGVPKEIKNQEFRVGLSPSSVRTLVEAGHTVFIETQAGIGAGFADQDYVQAGAQVVPASKADAWSREMVVVKVEPLPAEYDLMQKDQLLFTYLHL
AAARELTEQLMRVGLTIAIAYETVELPNRSLPLTPMSIIXVPWTATQALNNSTLPYVVKLANQGLKALETDDALAKGLNVQAHRVLHPAVQQVFPDLA

>d1f8ga2 c.23.12.2 (A:1-143,A:327-384) Nicotinamide nucleotide transhydrogenase dl component {Rhodospirillum rubrum}

MKIAIPKERRPGEDRVAISPEVVKLVLGLFEVIVEQGAGVGASITDDALTAAGATIASTAAQALSQADVWWKVRPMTAEGTDEVALIKEGAVLM
CHLGALTNRPVVEALTKRKITAYAMELMPRISRAQSMDILSSQSNLXVAADASPLFAKNNFLTPHVDKDTKTLVMKLEDETSGTCVTRDGAIHV
ALTGQGA

>d1a7aa2 c.23.12.3 (A:2-189,A:353-432) S-adenosylhomocysteine hydrolase {Human (*Homo sapiens*)}

SDKLPYKVADIGLAAWGRKALDIAENEMPGLMRMREMYASKPLKGARIAGCLHMTVETAVLIETLTLGAEVQWSSCNIFSTQNHAAAIAKAGIP
VYAWKGETDEEYLWCIEQTLYFKDGPLNMIIDDGGDLTNIHTKHPQLLPGIRGISEETTTGVHNLYKMMANGILKVPAINVNDSVTSKFXHPSFVFM
SNSFTNQVMAQIELWTHPDKYPVGVHFLPKLDEAVAEEAHGKLNVKLTKEKQAAQYLGMSCDGPFKPDHYRY

>d1b3ra2 c.23.12.3 (A:4-189,A:353-431) S-adenosylhomocysteine hydrolase {Rat (*Rattus norvegicus*)}

LPYKVADIGLAAWGRKALDIAENEMPGLMRMREMYASKPLKGARIAGCLHMTVETAVLIETLVALGAEVRWSSCNIFSTQDHAAAIAKAGIPVFA
WKGETDEEYLWCIEQTLHFKDGPLNMIIDDGGDLTNIHTKHPQLLPGIRGISEETTTGVHNLYKMMANGILKVPAINVNDSVTSKFDXPSFVMSN
SFTNQVMAQIELWTHPDKYPVGVHFLPKLDEAVAEEAHGKLNVKLTKEKQAAQYLGMPINGPFKPDHYRY

>d2dhqa_c.23.13.1 (A:) Type II 3-dehydroquinate dehydratase {Mycobacterium tuberculosis}

LIVNVINGPNLGLRLRREPavyggTTDELVALIERAAEGLKAVVRQSDSEAQLLDWIHOAADAAEPVILNAGGLHTSVALRDACAELSAPLIEVH
ISNVHAREFRRHSYLSPIATGVIVGLGIQGYLLALRYLAEH

>d1d0ia_c.23.13.1 (A:) Type II 3-dehydroquinate dehydratase {Streptomyces coelicolor}
PRSLANAPIMLNGPNLNLLGQRQPEIYGSIDLADVEALCVAAAAHGGTVDFRQSNHEGELVDWIHEARLNHCIVINPAAYSHTSVAILDALNTC
DGLPVVEVHISNIHQREPFRHSYVSQRADGVVAGCGVQGYVFGVERIAALAG

>d1f8ya_c.23.14.1 (A:) Nucleoside 2-deoxyribosyltransferase {Lactobacillus leichmannii}
PKKTIYFGAGWFTDRQNKAKEAMEALKENPTIDLENSYVPLDNQYK GIRDEHPEYLHDKVWATATYNNDLNGIKTNDIMLGVYIPDEEDVGLGM
ELGYALSQGKYVLLVIPDEDYGKPINLMSWGVSDNVIKMSQLDFNFKPRFDYEGAVY

>d1fjgb_c.23.15.1 (B:) Ribosomal protein S2 {Thermus thermophilus}
VKELLEAGVHFGHERKRWNPKFARYIYAERNGIHIIDLQKTMEELERTFRFIEDLAMRGGTILFGTKKQAQDIVRMEAERAGMPYVNQRWLGGML
TNFKTISQRVHRLEELEALFASPEIEERPKKEQVRLKHELRLQKLYSGFRLKRLPDAIFVVDPTEKAIAVREARKLFIPVIALADTDSPDLVYIIPGND
DAIRSIQLILSRAVDLIIQARGGVVEPSPSYALVQEAE

>d1f2va_c.23.17.1 (A:) Precorrin-8x methylmutase {Pseudomonas denitrificans}
PEYDYIRDGNAYERSFAIRAEADLSRFSEEADLAVRMVHACGSVEATRQFVSPDFVSSARAALKAGAPILCDAEMVAHGVTRARLPAGNEVICTI
RDPRTPALAAEIGNTRSAAALKLWSERLAGSVVAIGNAPTAFLLEMLRDGAPKPAAILGMPVGFVGAAESKDALAENSYGVFAIVRGRGLGGSAM
TAAALNSLARPGL

>d1gpm2_c.23.16.1 (A:3-207) GMP synthetase {Escherichia coli}
ENIHKHRILIDFGSQYTQLVARRVRELGVYCELWAADVTEAQIRDFNPSGIILSGGPESTTEENSPRAPQYVFEAGVPVFGVCYGMQTMAMQLGG
HVEASNEREFGYAQVEVVNDSALVRGIEDALTADGKPLDVWMSHGDKVTAIPSDFITVASTESCPFAIMANEKRFYGVQFHPEVTHTRQGMRML
ERFVRDICQCEAL

>d1a9xb2_c.23.16.1 (B:1653-1880) Carbamoyl phosphate synthetase, small subunit C-terminal domain {Escherichia coli}
LNGMDLAKEVTTAEAYSWTQGSWLTGGLPQAKKEDELPHVYADFGAKRNILRMLVDRGCRLTIVPAQTSADVLKMNPDGIFLSNGPGDPAPC
DYAITAIQKFLTDIPVFGICLGHQLLALASGAKTVKMKFGHHGGNHPVKDVEKNVVITAQNHFVADEATLPANLRVTHKSLFDGTLQGIHRTDK
PAFSFQGNPNEASPAGPHDAAPLFDFHIELEQYRKT

>d1qdlb_c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Archaeon Sulfolobus solfataricus}
MDLTLIINDYDSFVYNIAQIVGELGSYPIVIRNDEISIKGIERIDPDRLIISPAGPTPEKREDIGVSLDVKYLKRTPILGCLGHQAIGYAFGAKIRRKVF
HKGKISNIIVLVNNSPSLYYGIAKEFKATRYHSLVVDEVHRPLIVDAISAEDNEIMAIHHEEYPIYGVQFHPEVGTSGLYKILYNFLNRV

>d1i1qb_c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Salmonella typhimurium}
ADILLLDNIDSFTWNLADQLRTNGHNVVIYRNHIPAQTLDRLATMKNPVLMLSPGPVPSEAGCMPELLTRLRGKLIIGICLGHQAIVEAYGGYVG
QAGEILHGKATSIEHDGQAMFAGLANPLPVARYHSLVGSNVPAGLTINAHFNGMVMAVRHDADRVCFGQFHPESILTTQGARLLEQTLAWAQKK

>d1i7qb_c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Serratia marcescens}
ADILLLDNVDSFTYNLVQDQLRASGHQVVIYRNQIGAEVIIERLQHMEQPVLMSPGPVPSEAGCMPELLQLRGQLPIIGICLGHQAIVEAYGGQVG
QAGEILHGKASAIAHDGEGLFAGMANPLPVARYHSLVGSNIPADLTNARFGEMVMARDDRRVCGFQFHPESILTTQGARLLEQTLAWALAK

>d1k9vf_c.23.16.1 (F:) GAT subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}
MRIGIISVPGNIMNLYRGVKRASENFEDVSIELVESPRNDLYDLLFIPGVGHFEGMRRRENDLIDFVRKHVEDERYVVGCLGMQLFEESEEAP
GVKGLSLIEGNVVKLRSRRLPHMGWNEVIFKDTFPNGYYYFVHTYRAVCEEHVLTTEYDGEIFPSAVRKGRILGFQFHPEKSSKIGRKLEKVICSL
SR

>d1jvna2_c.23.16.1 (A:-3-229) GAT subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}
GSHMPVVHVIDVESGNLQLSLTNAIEHLGYEVQLVKSPKDFNISGTSRLILPGVGNYGHFVDNLFNRGFEKPIREYESGKPIIMGICVGLQALFAGSVESP
KSTGLNYIDFKLSRFDDSEKPVPEIGWNSCIPSENLFGLDPYKRYYFVHSFAILNSEKKNLENDGWKIAKAKYGEFFIAAVNKNNIFATQFHPEKS
GKAGLNVENFLKQQSPPIPNSAEEKELLMN

>d1g2ia_c.23.16.2 (A:) Intracellular protease {Archaeon Pyrococcus horikoshii}
MKVLFLTANEFDVELIYPYHRLKEEGHEVYIASFERGTTGKHGSVKVDLTFDKVNPEEFDALVLPGRAPERVRLNEKAVSIARKMFSEGKPVASIC
HGPQILISAGVLRGRKGTSPGKDDMINAGVEWWDAEVVVDGNWSSRVPADLYAWMREFVKLLK

>d1cf9a1_c.23.16.3 (A:598-753) Catalase, C-terminal domain {Escherichia coli, HPII}

VKGRRVVAILLNDEVRSADELLAILKALKAKGVHAKLLYSRMGEVTADDGTVLPIAATFAGAPSLTVDAIVPCGNIADIADNGDANYYLMEAYKHLKPIA
LAGDARKFKATIKIADQGEEGIVEADSADGSFMDELLTMAAHRVWSRIPKIDKIPA

>d1fyea_c.23.16.4 (A:) Aspartyl dipeptidase PepE {Salmonella typhimurium}

MELLLLSNSTLPGKAWLEHALPLIANQLNGRRSAVFIPFAGVTQTWDEYTDKTAEVLAFLGVNVTVIHRVADPLAAIEKAIIIVGGGNTFQLLKESE
RGLLAPMADRVKRGALYIGWSAGANLACPTIRTTNDMPIVDPNGFDALDLFPLQINPHFTNALPEGHKGETREQRIELLVVAPELTIVGLPEGNW
QVSNGQAVLGGPNTTWFKAGEEAVALEAGHRF

>d1a9xa2 c.24.1.1 (A:936-1073) Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain {Escherichia coli}

NSTMKKHGRALLSVREGDKERVVVDLAALKLKGFEKDATHGTAIVLGEAGINPRLVNKVHEGRPHIQDRIKNGEYTYIINTTSGRRAIEDSRVIRRSAL
QYKVHYDTTLNGGFATAMALNADATEKVISVQEMHAQIK

>d1b93a_c.24.1.2 (A:) Methylglyoxal synthase, MgsA {Escherichia coli}

MELTTRTPARKHIALVADHDCKQMLMSWVERHQPLQEHQVLYATGTTGNLISRTGMNVNAMLSGPMGGDQQVGALISEGKIDVLIFFWDPLN
AVPHDPDVKALLRLATVVNIPVATNVATDFIIQSPHFNDAVDILIPDYQRYLA

>d1g8ma1 c.24.1.3 (A:4-200) IMP cyclohydrolase domain of bifunctional purine biosynthesis enzyme ATIC {Chicken (Gallus gallus)}

RQQLALLSVSEKAGLVEFARSLNALGLGLIASGGTATALRDAGLPVRDVSQDTGFPEMLGGRVKTLHPAVHAGILARNIPEDNADMNKQDFSLRVVV
CNLPFVKTSSPGTVPEAVEKIDIGGVALLRAAKNHARTVVCDPADYSSVAKEMAASKDKTSVETRRHLAKFTHTAQYDAISDYFRKEYS
K

>d1fnc_2 c.25.1.1 (155-314) Ferredoxin reductase (flavodoxin reductase) {Spinach (Spinacia oleracea)}

MLMPKDPNATIIMLGTTGIAPFRSFLWKMFKEHDDYKFNGLAWLFLGVPTSSLLYKEEFKMKEAPDNFRLDFAVSREQTNEKGEKMYIQTR
MAQYAVELWEMLKKDNTVYVMCGLKGMEKGIDDIMVSLAAAEGIDWIEYKRQLKKAEQWNVEVY

>d1qfza2 c.25.1.1 (A:154-308) Ferredoxin reductase (flavodoxin reductase) {Garden pea (Pisum sativum)}

DPNATVIMLGTTGIAPFRSFLWKMFKEHDDYQFNGLAWLFLGVPTSSLLYKEEFKMKEAPENFRLDFAVSREQVNDKGEKMYIQTRMAQYA
EELWELLKKDNTFVYMCGLKGMEKGIDDIMVSLAAKDGIDWIEYKRTLKKAEQWNVEVS

>d1fb3a2 c.25.1.1 (A:208-362) Ferredoxin reductase (flavodoxin reductase) {Paprika (Capsicum annuum)}

DPNATVIMLGTTGIAPFRSFLWKMFKEHDDYKFNGLAWLFLGVPTSSLLYKEEFKMKEAPENFRLDFAVSREQTNEKGEKMYIQTRMAQYA
ELWTLLKKDNTFVYMCGLKGMEQGIDDIMSSLAAKEGIDWADYKKQLKKAEQWNVEVY

>d1gawa2 c.25.1.1 (A:157-314) Ferredoxin reductase (flavodoxin reductase) {Maize (Zea mays), leaf isoform}

MPKDPNATIIMLATGTGIAPFRSFLWKMFKEHDDYKFNGLAWLFLGVPTSSLLYKEEFKMKERAPENFRVDYAVSREQTNAAGERMYIQTRMA
EYKEELWELLKKDNTVYVMCGLKGMEKGIDDIMVSLAEKDGIDWFDYKKQLKRGDQWNVEVY

>d1jb9a2 c.25.1.1 (A:163-316) Ferredoxin reductase (flavodoxin reductase) {Maize (Zea mays), root isoform}

DPNATHIMIATGTGVAPFRGYLRRMFMDVPNRYRFGGLAWLFLGVANSDSLDEEFTSYLKQYPDNFRYDKALSREQKNRSGGKMYVQDKIEEYS
DEIFKLDDGAHIYFCGLKGMMPIQDTLKKVAERRGESWDQKLAQLKKNKQWHVEVY

>d1que_2 c.25.1.1 (142-303) Ferredoxin reductase (flavodoxin reductase) {Cyanobacterium (Anabaena sp.), pcc 7119}

LPDDPEANVIMLATGTGIAPMRTYLWRMFKAERAANPEYQFKGFSWLFGVPTTPNILYKEELEIQQKYPDNFRITYAISREQKNPQGGRMYIQD
RVAEHADQLWQLIKNQKTHYICGLRGMEEGIDAALSAAAEGVTWSDYQKDLKKAGRWHVETY

>d1fdr_2 c.25.1.1 (101-248) Ferredoxin reductase (flavodoxin reductase) {Escherichia coli}

DEVPHCETLWMLATGTAIGPYLSILRLGKLDLRFKNLVLVHAARYAADLSYLPQMCELEKRYEGKLRIQTVSRETAAGSLTGRIPALIESGELESTIGLP
MNKETSHVMLCGNPQMVRDTQQLKETRQMTKHLRRPGHMTAEHYW

>d1a8p_2 c.25.1.1 (101-258) Ferredoxin reductase (flavodoxin reductase) {Azotobacter vinelandii}

TSDLPPGKHLYMLSTGTGLAPFMSLIQDPEVYERFEKVVLIHGVRQVNELAYQQFITEHLPQSEYFGEAVKEKLIYYPTVTRSFHNQGRLTLMRSGK
LFEDIGLPPINPQDDRAMICGSPSMLDESCEVLDGFLKISPRMGEPGDYLIERAFVEK

>d1qfja2 c.25.1.1 (A:98-232) NAD(P)H:flavin oxidoreductase {Escherichia coli}

RDDEERMILIAAGGTGFSYARSILLTALARPNRDIITIYWGGREEQHLYDLCELEALSLKHPGLQVVPVVEQPEAGWRGRGTVLTAVLQDHGTIAEH
DIYIAGRFE MAKIARDLFCSERNAREDRFGDAFAFI

>d2cnd_2 c.25.1.1 (125-270) Nitrate reductase {Corn (Zea mays)}

GSFVINGKQRNARRLAMICGGSGITPMYQIIQAVLRDQPEDHTEMHLVYANRTEDDILLRDELDRAAEEYPDRLKVVYVIDQVKRPEEGWKYSVG
FVTEAVLREHVPEGGDDTLALACGPPPMIQFAISPNEKMKYDMANSFVF

>d1ndh_2 c.25.1.1 (126-272) cytochrome b5 reductase {Pig (Sus scrofa), liver}

GKFAIRPDKKSSPVIKTVKSVGMIAGGTGITPMIQLQVIRAIMKDPPDHVCCHLLFANQTEKDILLRPELEELRNEHSARFKLWYTVDRAPEAWDYSQGF
VNEEMIRDHLPPPSEEPLVMCGPPPMIQYACLPNLERVGHPKERCFAF

>d1i7pa2 c.25.1.1 (A:154-300) cytochrome b5 reductase {Rat (Rattus norvegicus)}

GKFAIRADKKSNPVRTVKSVGMIAGGTGITPMIQLQVIRAVLKDPNDHTVCYLFFANQSEKDILLRPELEELRNEHSARFKLWYTVDKAPDAWDYSQG
FVNEEMIRDHLPPPGEETLILMCGPPPMIQFACLPNLERVGHPKERCFTF

>d2pia_2 c.25.1.2 (104-223) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}

EFPLDKRAKSFILVAGGIGITPMIQLRQEGLRSFRLLYLTDPGTAFFDELTSDERSDVKIHHDHGDKAFDFWSVFEKSKPAQHVYCCGP
QALMDTWRDMTGHWPSGTVHF

>d1ep3b2 c.25.1.3 (B:103-262) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}

PVAEVSTDKILIIGGGIVPPLYELAKQLEKTGCQMTILLGFAENVKILENEFSNLKNVTLKIATDDGSYGTKGHVGMLMNEIDFEVDALYTCGAPAM
LKAVAKKYDQLERLYISMESRMACGIGACYACVEHDKEDESHALKVCEDGPVFLGKQLSL

>d1ja1a3 c.25.1.4 (A:519-678) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}

RLPKSTTPVIMVPGTGIAPFMGIQERAWLREQGKEVGETLYYGCRSSDEDLYREELARFHKGALTQLNVAFSREQAHKVYVQHLLKRDREHL
WKLIHEGGAHIYVAGDARNMAKDVTQNTFYDIVAEFGPMEHTQAVDYVKKLMTKGRYSLNVWS

>d1ddga2 c.25.1.4 (A:447-599) Sulfite reductase flavoprotein {Escherichia coli}

LPANPETPVIMIGPGTGIAPFRAFMQQRAADEAPGNWLFFGNPHFTEDFLYQVEWQRYVKEGVLTRIDLAWSRDQKEKVVQDKLREQGAELW
RWINDGAHIYVCGDANRMAKDVEQALLEVIAEFGGMDEAADEFSELRVERRYQRDVY

>d1f20a2 c.25.1.4 (A:1233-1397) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat (Rattus norvegicus)}

SFHLPNRNPQVPCILVPGTGIAPFRSFWQQRQFDIQHKGMNPCKMVLFVFCRQSNDIHYREELTQAKNKGVFRELYTASREPDRPKYVQDVLQE
QLAESVYRALKEQGGHIYVCGDVTMAADVLIKAIQRIIMTQQGKLSEEDAGVFIISRLRDNRYHEDIFGV

>d1cqxa3 c.25.1.5 (A:262-403) Flavohemoglobin, C-terminal domain {Alcaligenes eutrophus}

DVDAKTPIVLISGGVGLTPMVSMLKVALQAPPRQVFVHGARNSAVHAMRDRRLREAATYENLDLFVYDQPLPEDVQGRDYDYPGLVDVKQIEKS
ILLPDADYYICGPIPFMRMMQHDALKNLGIHEARIHYEVFGPDLFAE

>d4ts1a_c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Bacillus stearothermophilus, nca 1503}

MDLLAELQWRGLVNQTTDEDGLRKLLNEERTVLYCGFDPTADSLHIGHLATLTMRFFQQAGHRPIALVGGATGLIDPSGKKSERTLNAKETVEAW
SARIKEQLGRFLDFEADGNPAKIKNNYDWIGPLDVITFLRDVGKHFVNYMMAKESVQSRIETGISFTFSYMMQLQAYDFLRLYETEGCRLQIGGSDQ
WGNITAGLELIRLTKGEARAFGLTIPVTKADGTFKGKTESGTIWLDEKTSFYQFWINTDDRDVIRYLKYFTFLSKEEIALEQELREAPEKRAAQK
TIAEEVTKLVHGEEARLQAIRYA

>d1jila_c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Staphylococcus aureus}

TNVLIEDLKWRLIYQQTDEQGIEDLLNEQVTLYCGADPTADSLHIGHLLPFLTERRFQEHGHRPIVLIGGGTMIGDPSGKSEERVLQTEEQVDKNI
EGISKQMHNIFEGTDHGAVLVNNRDWLQGQISLISFLRDYGKHFVNYMLGKDSIQSRLEHGISYTEFTYTIQLQAFGHLNRELNCIQQVGGSDQW
GNITSGIELMRRMYGQTDAYGLTIPVTKSDGKKFGKSESGAVWLDAEKTSFYQFWINQSDDEVIKFLKYFTFLGKEEIDRLEQSKNEAPHLREAQ
KTLAEEVTKFIHGEGDALNDAIRISQALF

>d1i6la_c.26.1.1 (A:) Tryptophanyl-tRNA synthetase (TrpRS) {Bacillus stearothermophilus}

MKTIFSGIQPSGVITIGNYIGALRQFVELQHEYNCYFCIVDQHAITVWQDPHELQRQNIIRRLAALYLVAGVIDPTQATLFIQSEVPAHAQAAWMLQCIVYI
GELEMRTQFKEKSAGKEAVSAGLLTYPPLMAADILLYNTDIVPGVEDQKQHIELTRDAERFNKRYGELEFTIPEARIPKVGARIMSLVDPKKMSKSDP
NPKAYITLDDAKTIEKKIASVTDSEGTTIRYDKEAKPGISNLLNIYSTLSGQSIEELERQYEGKGYGVFKADLAQVVIETLRPIQERYHHWMESEELDRVL
DEGAEKANRVASEMVRKMEQAMGLR

>d1gtra2 c.26.1.1 (A:8-338) Glutaminyl-tRNA synthetase (GlnRS) {Escherichia coli}

TNFIRQIIDELASGKHTTVHTRFPPEPNGLYIGHAKSICLNFGIAQDYKGQCNLRDDTNPKEDIEYVESIKNDVEWLFHWSGNVRYSSDYFDQ
LHAYAIELINKLAYVDELTPEQIREYRGTLTQPGKNSPYRDRSVEENLALFEKMRAGGFEEGKACLRAKIDMASPFIVMRDPVLYRIKFAEHHTQGNK

WCIYPMYDFTHCISDALEGITHSLCTLEFQDNRRLYDWVLDNITIPVHPRQEFSRLNLEYTVMSKRKLNLVTDKHVEGWDDPRMPTISGLRRGYT
AASIREFKRIGVTKQDNTIEMASLESCIREDLNE

>d1gln_2 c.26.1.1 (1-305) Glutamyl-tRNA synthetase (GluRS) {Thermus thermophilus}

MVVTRIAPSPTGDPHVGAYIAFLNYAWARRNGGRIVRIEDTDRARYVPGAEERILAALKWLGLSYDEGPDVAAPTGPYRQSERLPLYQKYAEELLKR
GWAYRAFETPSEELEQIRKEKGGYDGRARNIPPEEAERARRGEVIRLKVRPGTTEVKDELRGVVYDNQEIPDVLLKSDGYPTYHLANVVDDH
LMGVTDVIRAEEWLVSTPIHVLLYRAFGWEAPRFYHMPLRNPDKTISKRSHTSLDWKAEGFLPEALRNYLCLMGFSMPDGREIFLEIFIQAFT
WERVSLGGPVF

>d1a8h_2 c.26.1.1 (1-348) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}

MEKVVFYVTTPIYYVNAEPLHGHAYTTVADFLARWHRLDGYRTFLGTDEHGETVYRAAQAGEDPKAFVDRVSGRFKRAWDLLGIAYDDFIRTTE
ERHKKVVQLVKKVYEAGDIYGEYEGLYCVSCRFYTEKEVLEGLCPIHGRPVERRKEGNYFRMMEYRPWLQEYIQENPDLIRPEGYRNEVLAMILAE
PIGDLISRPKSRVPWGIPLPWDENHTVVFWDALLNVSALDYPEGEAYRTFWPHAWHLIGKDILKPHAVFWPTMLKAAGIPMYRHLNVGGFL
GPDGRKMSKTLGVNVVDPFALLEYGDRALYYREIYGQDTPVSEEARTRYEAD

>d1f4la2 c.26.1.1 (A:4-140,A:176-388) Methionyl-tRNA synthetase (MetRS) {Escherichia coli}

AKKILVTCALPYANGSIHLGHMLEHIQADVWVRYQRMRGHEVNFIACDDAHGTPIMLKAQQLGITPEQMIGEMSQEHQTDAGFNISYDNYHSTH
SEENRQLSELIYSRLKENGFIKNRTISQLYDPEKGMFLPDRFXVSGATPVMRDSEHFFDLSFSEMLQAWTRSGALQEQQVANKMQEWFESGLQQ
WDISRDAPYFGFEIPNAPGKYFYVWLDAPIGYMGSKNLCDKRGDSVSFDEYWKKDSTAELYHFIGKDIVFHSLFWPAMLEGSNFRKPSNLVHG
VTVNGAKMSKSRGTFIKASTWLNFADSLRYYTAKLSSRIDDIDLNLNLEDVFQRVNADIVNK

>d1ile_3 c.26.1.1 (1-197,387-641) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}

MFKEVGEPNFPKLEEVLAFWKREKIFQKSVENRKGGPRYTVEGPPANTGLPHVGAQARSYKDLFPRYKTMRGYYAPRRAGWDTHGLPVELEV
EKKGLLKSREIEAYGIERFNQACRESVFTYEKEWEAFTERIAYWDLEDAYATLEPTYIESIWWSLKNLFDRGGLYRDHKVVYPYCPCGTPLSSHEVALG
YXPHCWRCSTPLMYYATESWFIKNTLFKDELIRNNQEIHWVPPHIKEGRYGEWLKNLVDWALSRNRYWGPLPIWCQACGKEEAIGSFQELKARA
TKPLPEPFDPHPYVQVELACACGGTMRRVPPVYDQVWDSGAMPFASLHYPFEHEEVFRESFPADIFIAEGIDQTRGFNSLHQLGVMLFGSIAFK
NVICHGLILDEKGQKMSKSGNVVDPWDIIRKFGADALRWIYVSAPPEADRRFGPNLVRETVRD

>d1ffya3 c.26.1.1 (A:1-200,A:395-644) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

MDYEKTLLMPKTDFPMRGGLPNKEPQIQEKWDAEDQYHKALEKNKGNETFILHDGPPYANGNLHMGHALNKILKFIVRYKTMQGFYAPYVPG
WDTHGLPIEQALTKKGVDRKKMSTADEFREKCKEFALEQIELQKKDFRRLGVRGDFNDPYITLKPEYEAQIRIFGEMADKGLIYKGKKPVYWSPSSESS
LAEAEIEYXPHDWRTKKPVIFRATPQWFASISKVRQDILDAIENTNFKVNWGKTRIYNMVRDRGEWVISRQRVVGVLPLVFAENGEIIMTKETVN
HVADLFAEHGSNIWFEREAKDLLPEGFTPHGSPNGTFTKETDIMDVWFDSGSSHGVLETRPELSFPADMYLEGSDQYRGWFNSSITTSVATRGVS
PYKFLLSHGFVMDGEGKKMSKSLGNVIVPDQVVKQKGADIARLWVSSTDYLADVRISDEILKQTSD

>d1gaxa3 c.26.1.1 (A:1-189,A:343-578) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}

MDLPKAYDPKSVEPKWAEKWAKNPVANPKSGKPPFVIFMPPPNTGSLHMGHALDNSLQDALIRYKRMRGFEAVWLPGDHAGIATQVVERL
LLKEGKTRHDLGREKFLERVWQWKEESGGTILKQLKRLGASADWSREAFTMDEKRSRAVRYAFSRYYHEGLAYRAPRLVNWCPCRTTLSLEVEXT
CSRCGTPIEYAIFPQWWLRLRPLAEEVLKGLRRGDIAVPERWKKVNMDWLENVKDWNSRQLWWGHQIPAWCEDCQAVNPRPERYLEDPT
SCEACGSPRLKRDEDVFDTWFSSALWPLSTLGWPEETEDLKFYPGDVLVGYDILFLWVSRMEVSGYHFMGERFVLLHGLVLDEKGQKMSKS
KGNVIDPLEMVERYGADALRFALIYLATGGQDIRDLRWLEMARNF

>d1f7ua2 c.26.1.1 (A:136-483) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast (Saccharomyces cerevisiae)}

SCKLVENKKVIEFSSPNIAKPFHAGHLRSTIIGGLANLYEKLGVIRMNYLGDWKGKQFGLAVGFERYGNEEALVKDPIHHLFDVYRINKDIEEG
DSIPLEQSTNGKAREYFKRMEDGDEEALKIWKRFRFESIEKYIDTYARLNKIKYDVYSGESQVSKESMILKAIDLKFKEGLTHEDKGAVLIDLTKFNKLGKA
IVQKSDGTTLYLTDVGAAMDREYEKYHFDKMIYVIASQQLHAAQFFEILKQMGFEWAKDLQHVNFQGMVQGMSTRKGTVVFLDNILEETKEKMH
EVMKKKENKYAQIEHPEEVALVGISAVMIQDMQGKRINNNYEFKWERMLSSEG

>d1iq0a2 c.26.1.1 (A:97-466) Arginyl-tRNA synthetase (ArgRS) {Thermus thermophilus}

PFPRRPGVVLVEHTSVNPNKELHVGHLRNIALGDAIARILAYAGREVLVNYIDDTGRQAAETLFALRHGTLWDGKEKYDHFAGRAYVRLHQDPEYE
RLQPAIEEVHLALERGELREEVNRLLAQMATMHALNARYDLVVWESDIVRAGLQLKAALLEQSPHVFRPREGKYAGALVMDASPVIPGLEDPFFVL
LRSNGTATYYAKDIAFQFWKMGILEGLRFRPYENPYYPGLRTSAPEGEAYTPKAETINVVDVRQSHPQALVRAALALAGYPALAEEAHAYETVLL

GRQMSGRKGLAVSVDEVLEEATRRARAIVEEKNPDPKKEAARMVALGAIRFSMVKTEPKKQIDFRYQEALSFE

>d1coza_c.26.1.2 (A:) CTP:glycerol-3-phosphate cytidylyltransferase {Bacillus subtilis}

MKKVITYGTFDLLHWGHKLLERAKQLGDLVVAISTDEFNLQKQKKAYHSYEHRKLILETIRYVDEVIPEKNWEQKKQDIIDHNIDVFVMGDDWEGK

DFFLKDQCEVVYLPRTEGISTTKIKEI

>d1qjca_c.26.1.3 (A:) Phosphopantetheine adenylyltransferase {Escherichia coli}

KRAIYPGTDPITNGHIDIVTRATQMFDHVILIAASPSKKPMFTLEERVALAAQQATAHLGNVEVGFSDLMANFARNQHATVLIRGLRAVADFEYE

MQLAHMNRLMPELESVFLMPSKEWSFISSSLVKEVARHQGDVTHTLPENHVQALMAKLA

>d1f9aa_c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase {Archaeon Methanococcus jannaschii}

LRGFIIGRFQPFHKGHLEVKKIAEEVDEIIIGSAQKSHTLENPFTAGERILMITQSLKDYLTYPIPICKIEFNSIWVSYVESLTPFDIVSGNPLVRVL

FEERGYEVKRPEMFNRKEYSGTEIRRMLNGEKWEHLPKAVVDIKEIKGVERLRKLA

>d1ej2a_c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase {Archaeon Methanobacterium thermoautotrophicum}

MRGLLVGRMMPFHGRGHLQVIKSILEEVDELICIGSAQLSHSIRDPTAGERVMMMLTKALSENGIPASRYIIPVQDIECNALWVGHIKMLTPFDdrvys

GNPLVQRLFSEDGYEVTTAPPLFYRDRYSGTEVRRMLDDGDWRSLLPESVVEVIDEINGVERIKHLA

>d1hoa_c.26.1.4 (A:) Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC) {Escherichia coli}

MLIIETLPLLQQIRRLRMEGKRVVALVPTMGNLHDGHMKLVDEAKARADVVVSIFVNPMQFDRPEDLARYPRTLQEDCEKLNRKVDLVFAPSVK

EIYPNGTETHTYDVPGLSTMLEGASRPGHFRGVSTIVSKLFNLVQPDIAFCGEKDFQQQLALIRKMVADMGF DIEIVGPIMRAKDGALSSRNGLT

AEQRKIAPIGLYKVLSIADLKQAGERDLDEIIITIAGQELNEKGFRADDIQIRDADTLLEVSETS KRAVILVAAWLG DARLIDNKMVEL

>d1g8fa2 c.26.1.5 (A:169-389) ATP sulfurylase central domain {Baker's yeast (Saccharomyces cerevisiae)}

YPGLRKTPAQLRLEFQSQRQWDRVVAFQTRNPMHRAHRELTVAAREANAKVLIHPVVGTLKPGDIDHHTRVRVYQEIKRYPNGIAFLSLLPLAMRM

SGDREAVWHAIIRKNYGASHFIVGRDHAGPGKNSKGVDYGPYDAQELVESYKHELDIEVVPFRMVTYLPDEDRYAPIDQIDTTKRTLNISGTELRR

RLRVGGEIPEWFSYPEVVKILRESNP

>d1i2da2 c.26.1.5 (A:171-390) ATP sulfurylase central domain {Fungus (Penicillium chrysogenum)}

YVALRYTPAELRVHFDKLGWSRVVAFQTRNPMHRAHRELTVAARSRQANVLIHPVVGTLKPGDIDHHTRVRVYQALLPRYPNGMAVLGLLGLAM

RMGGPREAIWHAIIRKNHGATHFIVGRDHAGPGNSNSKGEDFYGPYDAQHAVEKYKDELGIEVVEFQMVTL PDTDEYRPVDQVPAGVKTLNISGTE

LRRLRLRSGAHIPEWFSYPEVVKILRESNP

>d1jhda2 c.26.1.5 (A:174-396) ATP sulfurylase central domain {unnamed symbiont of Riftia pachyptila}

PDTFRTAVEIRNEIKEHGW SKVVAFQTRNPMHRAHEELCRMAMESLDADGVVVHMLGKLKGDPAPVRDAIRTMAEVYFPPTVMVTGYGF

DMLYAGPREAVLHAYFRQNMGATHFIIGRDHAGVGDDYYGAFDAQTI FDEVP EGAMEIEIFRADHTAYS KLNKIVMMRDVPDHTKEDFVLLSGTK

VREMLGQGIAPPPEFSRPEVAKILMDYYQSIN

>d1gpm a1 c.26.2.1 (A:208-404) GMP synthetase, central domain {Escherichia coli}

WTPAKIIDDVAARIREQVGDDKVLGLSGGV DSSVTAMILHRAIGKNLTCVFDNGLRLNEAQV LDMFGDHFGLNIVHVAEDRFLSALAGENDP

EAKRKIIGRV FVEVFDEEALKLEDVKWL A QGTIY PDVIESAASATGKAHVIKSHHNVGLPKEMKMG LVEPLKELFDEVRKIGLELGLPYDMLYRHPP

P

>d1ih8a_c.26.2.1 (A:) NH3-dependent NAD+-synthetase {Bacillus subtilis}

SMQE KIMRELHV KPSIDPKQ EIDRVNFLKQYVKKTGA KGFV LGISGGQD STLAGRLA QLAVESI REEGGDAQFIA VRLPHGTQQD EDDA QLALKFIK

PDKSWKF DIKSTV AFSDQYQQETGDQLTDFNKG NVKARTRMIAQYAI GGQEG LLV LGTDHAAEAVTGFT KYGDGGADLLPLTGLK RQGRTLLKE

LGAPERLYLKEPTADLLDEKPQQSDET LGLIS YDEIDDYLEG KEVSAK VSEALEK RYSMTEH KRQ VPAS MFDDWWK

>d1ct9a1 c.26.2.1 (A:193-516) Asparagine synthetase B, C-terminal domain {Escherichia coli}

RDWFDYDAVKDNVTDKNELRQALED SVKSHLMSDVPYGVLLSGGLD SIIASITKKYARRVEDQER SEAWWPQLHSFAVGLPGSPDLKAAQEVAN

H LGTVHHEIHTVQEGLDAIRDVIYHIETYDVT TIRASTPMYLM SRKIKAMGIK MVLSGEGSDEVFGGYLYFHKAPNAKELHEETVRKLLALHMYDCA

RANKAMS A伟GVEARVPFLDKKFLDVAMRINPQDKMCNGKMEKHILREC FEA YLPASVAWRQKEQFS DVG VG SWIDLKEVAAQQVSDQQLET

ARFRFPYNTPTSKEAYLYREI FEELPLPSAAECVPG

>d1jgta1 c.26.2.1 (A:210-508) beta-Lactam synthetase {Streptomyces clavuligerus}

PGLSRRILPEGEAVAAVRAALEKAVAQRVTGDTPLVLSGGIDSSGVAACAHRAAGELDTVSMGTDTSNEFREARAVVDHLRTRHREITPTTELLA
QLPYAVWASESVDPDIIEYLLPLTALYRALGPERRILTGYGADIPLGGMHREDRLPALDTVLAHDMATFDGLNEMSPVLSTLAGHWTTHPYWDR
LDLVSLEAGLKRGRDKWVLAAMADALPAETVNRPKLGHEGSHTSSFSRLLDHGVAEDRVHEAKRQVVRELFDTVGGRHPSEVDTDDV
VRSVADRT

>d1k92a1 c.26.2.1 (A:1-188) Argininosuccinate synthetase, N-terminal domain {Escherichia coli}

TTIKHLPVGQRIGIAFSGGLDTSAALLWMRQKGAVPYAYTANLGQPDEEDYDAIPRRAMEYGAENARLIDCRKQLVAEGIAAIQCGAFHNTTGGLT
FNTTPLGRAVTGTMVLAAMKEDGVNIWGDGSTYKGNIDIERFYRYGLTNAELQIYKPWLTDTFIDEGLGRHEMSEFMIACGFDYKMSVEK

>d1sur__ c.26.2.2 (-) Phosphoadenylyl sulphate (PAPS) reductase {Escherichia coli}

SKLDLNALNELPKVDRILALAETNAELEKLDAGEGRVAWALDNLPGEVLSSSGIQAAVSLHVNQIRPDIPVILTDGYLPETYRFIDE
YRATESAAWQEARYGKLWEQGVEGIEKYNDINKVEPMNRALKELNAQTWFAGLRREQSGSRANLPVLAIRQGVFKVLPIDWDNRTIYQYLQKHGL
KYHPLWDEGYLSVGDTK

>d1dlja3 c.26.3.1 (A:295-402) UDP-glucose dehydrogenase (UDPGDH), C-terminal (UDP-binding) domain {Streptococcus pyogenes}

AKQIINVLKEQESPVKVVGVYRLIMKSNSDNFRSAIKDVIDILSKDIKIIYEPMLNKLESEDQSVLVNDLENFKKQANIIVTNRYDNELQDVKNKVYS
RDIFGRD

>d2tpt_2 c.27.1.1 (71-335) Thymidine phosphorylase {Escherichia coli}

DWKSLHLNGPIVDKHSTGGVGDTVSLMLGPMVAACGGYIPMISGRGLGHTGGTLDKLESIPGFDIFPDDNRFREIICKDVGVAIIQQTSSLAPADKRFY
ATRDITATVDSIPLITASILAKKLAEGLDALVMVDVKVSGAFMPYELSEALAEAIVGANGAVGVRTTALLDMNQVLASSAGNAVEVREAQFLTGEY
RNPRLFVDVTMALCVERMLISGKLAQDAEARAKLQAVLDNGKAAEVFGRMVAAQKGPTDFVENYAKLP

>d1brwa2 c.27.1.1 (A:71-330) Pyrimidine nucleoside phosphorylase {Bacillus stearothermophilus}

LSSIRGVVKDKHSTGGVGDTTLVLGPLVASVGVPVAKMSGRGLGHTGGTIDKLESVPGFHV
EISKDEFIRLVNENGIAIIQQTGDLTPADKKLYALRDV
TATVNSIPLIASSIMSKKIAAGADAIVLDVKTGAGAFMKLDEARRLARVMV
DIGKRVGRRTMAVSDMSQLGYAVGNALEVKEAIETLKNGNGPHD
LTELCCTLGSHMVYLAEKPSLDEARRLLEEIRSGAAIAAFKTFLAQQGGDASV
VDDLDKLP

>d1dnpa2 c.28.1.1 (A:1-200) N-terminal domain of DNA photolyase {Escherichia coli}

TTHLVWFRQDRLHDNLALAAACRNSSARVLALYIATPRQWATHNMSPRQAELINAQLNGLQIALAEKGIPLLFREVDDFVASVEIVKQVCAENS
THTLFNYQYEVNERARDVEVERALRNVCEGFDDSVILPPGAVMTGNHEMYKV
FTPFKNawlKRLREGMPECVAAPKVRSSGIEPPSITLNYPHQ
SFDTAHF

>d1iqlra2 c.28.1.1 (A:2-171) N-terminal domain of DNA photolyase {Thermus thermophilus}

GPLLWHRGDLRLHDHPALLEALARGPVGLVLDPNNLKTPRRRAWFLEN
VRALREAYRARGGALWVLEGLPWEKVEAARRLAKAVYALTSH
TPYGRYRDGRVREALPVPLHLLPAPHLPPDLPRAVYTPFSRLYRG
AAPPLPPPEALPKGPEEGIPREDPG

>d1qnf_2 c.28.1.1 (1-204) N-terminal domain of DNA photolyase {Anacystis nidulans}

MAAPILFWHRDRLRSLDNLGAAARAQSAQLIGLFCLDPQJLQSADMAP
PARVAYLQGCLQELQQRYQQAGSRLLLLQGDPQHLIPQLAQQLQAEAV
YWNQDIEPYGRDRDGQVAAALKTAGIRAVQLWDQLLHSPDQILSGSG
NPYSVYGPFWKNWQAQPKPTVATPTELVDSLPEQLTAIPLLSELPT
KQLGFDWDGGF

>d1efva1 c.29.1.1 (A:20-207) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}

QSTLVIAEHANDSLAPITLNTITAATRLGGEVSCVL
AGTKCDKVAQDLCVKVAFQV
AQNHDVYKGLPEELPLILATQKQFN
YTHICAGASAFGK
PRVAAKLEVAPI
SDIIAIKSPDT
FVRTIYAGNALCT
VKCDEKV
KFVFSVR
GTSFDA
ATSGGS
ASSEK
ASTSP
VEISEW
LDQKLTKS

>d1efvb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}

LRVLVAVKRV
VIDYAVKIRV
KPDRTGV
VTDGVKH
SMNP
FCEIA
VEEAVR
LKEKKLV
KEVIA
VSCGP
AQCO
ETIRT
ALAM
GAD
RG
IH
EV
VPP
AE
ERL
GPL
QVAR
VLA
KLA
KEK
V
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>d1efpa1 c.29.1.1 (A:2-184) Electron transfer flavoprotein, ETFP {Paracoccus denitrificans}

AVLLLGEVTNGALNR
DATAKAVA
AVKALGD
TVLCAG
ASAK
AAA
EEA
AKIAG
VAK
VLA
EPTA
ALI
V
LAG
DY
SHIA
AP
TT
DA
K
NV
MP
RVA
ALL
DVM
V
LSD
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>d1efpb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETPP {Paracoccus denitrificans}
MKVLPVKRLIDYNVKARVKSDGSGVDLANVKMSMNPDEIAVEEAIRLKEKGQAEEIAVGVKQAAETLRTALAMGADRAILVVAADDVQQDIE
PLAVAKILAAVARAEGTEIIAGKQAIIDNDMNATGQMLAAILGWAQATFASKVEIEGAKAKVTREVDGLQTIASLPAVVTADLRLNEPRYASLPNI
MKAKKKPLDEKTAADYGVDVAPRLEVVSREPEGRKAGIKVGSVDELVGKL

>d1mjha_c.29.1.2 (A:) "Hypothetical" protein MJ0577 {Archaeon Methanococcus jannaschii}
VMYKKILYPTDFSETAEIALKHVKAFKTLKAEEVILLHVIDEREIKKRDIIFSLLGAGLNKSVEEFENELKNKLTEEAKNMENIKKELEDVGFKVKDIIVV
GIPHEEIVKIAEDEGVDIIMGSHGKTNLKEILLGSVTENVIKKSNSKPVLVVKRKNS

>d1jmva_c.29.1.2 (A:) Universal stress protein A, UspA {Haemophilus influenzae}
MYKHILVAVDLSEESPILLKAVGIAKRHDALKSIIHVDFVNFSDLYTGLIDVNMMSSMQDRISTETQKALLDAAESVDYPISEKLSGSGDLGQLSDAIEQY
DVDLLVTGHHQDFWSKLMSTRQVMINTIKIDMLVPLRD

>d1dv1a2 c.30.1.1 (A:1-114) Biotin carboxylase (BC) subunit of acetyl-CoA carboxylase {Escherichia coli}
MLDKIVIANRGEIALRILRACKELGIKTVAVHSSADRDLKHVLLADETCIGPAPSVKSYLNIPAIISAAEITGAVALHPGYGFLSENANFAEQVERSGFIFI
GPKAETIRLMG

>d1gsoa2 c.30.1.1 (A:-2-103) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}
EFMKVLVINGNGGREHALAWKAAQSPLVETVFVAPGNAGTALEPALQNVAVGVTIDPALLDFAQNEKIDLTVPEALVKGVVDTFRAAGLKIFGPTA
GAAQLEG

>d1b6ra2 c.30.1.1 (A:1-78) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}
MKQVCVLNGNQLGRMLRQAGEPLGIAVWPVGLDAEPAAVPFQQSVITAEIERWPETALTRQLARHPAFVNDRVPIIA

>d1eyza2 c.30.1.1 (A:2-112) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}
TLLGTALRPAAATRVMLLGSGELGKEVAIECQRLGVEVIAVDRYADAPAMHVahrshvinMLGDALRRVVELEKPHYIVPEIEAIATDMLIQLEEGLN
VVPCARATKLTM

>d1a9xa3 c.30.1.1 (A:1-127) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}
MPKRTDIKSILILGAGPIVGQACEFDYSGAQACKALREEGYRVINVNSNPATIMTDPEMADATYIEPIHWEVVRKIIEKERPDAVLPTMGQTALNCA
LELERQGVLEFGVMTIGATAIDAIDKAE

>d1a9xa4 c.30.1.1 (A:556-676) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}
STDREKIMVLGGPNRIGQQIEFDYCCVHASLALREDGYETIMVNCNPETVSTDYDTSDRLYFEPVTLEDVLEIVRIEKPKGIVQYGGQTPLKLARALE
AAGVPVIGTSPDAIDRAEDRE

>d1iow_1 c.30.1.2 (1-96) D-Ala-D-Ala ligase {Escherichia coli, gene ddIB}
MTDKIAVLLGTSAAREVSLNSGAAVLAGLREGGIDAYPVDPKEVDTQLKSMGFQKVFIALHGRGGEDGTLQGMLELMGLPYTGSGVMASALSM
D

>d1ehia1 c.30.1.2 (A:3-134) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}
KKRVALIFGGNSEHDVSKRSAQNFYNAIEATGKYEIIVFAIAQNGFFLDTESSKKILALEDEQPIVDAFMKTVDASDPLARIHALKSAGDFDIFFPVVHG
NLGEDGTLQGLFKLLDKPYVGAPLRGHAVSF

>d1e4ea1 c.30.1.2 (A:2-131) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}
NRIKVAILFGGCSEEHDVSVKSAIEIAANINKEKYEPLYIGITKSGVWKMCEKPCAEWENENCYSAVLSPDKMHGLLVKKNHEYEVNHVDVAFSALH
GKSGEDGSIQGLFELSGIPFGCDIQSSAICM

>d1gsa_1 c.30.1.3 (1-122) Prokaryotic glutathione synthetase, N-terminal domain {Escherichia coli}
MIKLGIVMDPIANINIKKDSSFAMILLEAQRRGYELHYMEMGDLYLINGEARAHTRLNVKQNYEEWFSFVGEQDPLPLADLDVILMRKDPPFDTEFYI
ATYILERAEEKGLTLVNKPQLRDC

>d2hgsa1 c.30.1.4 (A:202-303) Eukaryotic glutathione synthetase {Human (Homo sapiens)}
PNALVLLIAQEKEERNIFDQRAlENELLARNIHIVRRTFEDISEKGSDLQDRLFVDGQEIAVYYFRDGYMPRQYSLQNWEARLLERSHAAKCPDIATQ
LAG

>d1auva1 c.30.1.5 (A:112-213) Synapsin Ia domain {Cow (Bos taurus)}

AARVLLVIDEPHTDWAKYFKGKKIHGEIDIKVEQAEFSNLVAHANGGFSVDMEVLRNGVKVVRSLPDFVLIRQHAFSMARNGDYRSVLVIGLQYA

GIPSI

>d1dhs__ c.31.1.1 (-) Deoxyhypusine synthase, DHS {Human (Homo sapiens)}

APAGALAAVLKHSSTLPPESTQVRGYDFNRGVNRYRALLEAFGTTGFQATNFGRAVQQVNAMIEKKLEPLTSCTIFLGYTSNLISSGIRETIRYLVQHNM
VDVLVTAGVEEDLIKCLAPTYLGEFSLRGKELRENGINRIGNLLVPNEYCKFEDWLMPILDQMVMEQNTEGVWTPSKMIARLGKEINNPESVY
YWAQKNHIPVFSALTDGLDGMIFFSYKNPGLVLIVEDLRLINTQAIFAKCTGMIIILGGGVVKHHIANANLMRNGADYAVYINTAQEFGDSDG
ARPDEAVSWGKIRVDAQPVKVYADASLVFPLLVAETFAQKMDAFMHEKNED

>d1efva2 c.31.1.2 (A:208-331) C-terminal domain of the electron transfer flavoprotein alpha subunit {Human (Homo sapiens)}

DRPELTGAKVVVSGGRGLKSGENFKLLYDLADQLHAAVGASRAAVDAGFVNPDMQVGQTGKIVAPELYIAGISGAIQHLAGMKDSKTIVAINKDPE
APIFQVADYGIVADLFKVPPMTEILK

>d1efpa2 c.31.1.2 (A:185-308) C-terminal domain of the electron transfer flavoprotein alpha subunit {Paracoccus denitrificans}

SDRPELTSAARRVVSRRGGLGSKESFAIIELADKLGAAGVGASRAAVDGSYAPNDWQVGQTGKVAPELYVAVGISGAIQHLAGMKDSKVIAINKDEE
APIFQIADYGIVADLFKVPPMTEILK

>d1poxa1 c.31.1.3 (A:183-365) Pyruvate oxidase {Lactobacillus plantarum}

YASANNYQTPLLPEPDVQAVTRLTQTLAAERPLIYYIGARKAGKELEQLSCTLKIPLMSTYPAKGIVADRPAYLGSANRVAQKPANEALAQADVVL
VGNNYPFAEVSKAFKNTRYFLQIDIDPAKLGRHKTDIAVLADAQKTLAIALAQVSERESTPWWQANLANVNKNWRAYLASLED

>d1pvda1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

QTPIDMSLKPNDAESEKEVIDTILALVKDAKNPVILADACCSRHDVKAETKKLIDLTQFPATPMGKGSIDEQHPRYGGVVGTLSKPEVKEAVESADL
ILSVGALLSDKTKNIIVEFHSDHMKIRNATFPGVQMKFLQKLLTNAADAAGYKPVAVPARTPANAAVP

>d1qpba1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

QTPIDMSLKPNDAESEKEVIDTILALVKDAKNPVILADACCSRHDVKAETKKLIDLTQFPATPMGKGSIDEQHPRYGGVVGTLSKPEVKEAVESADL
ILSVGALLSDFNTGSFSYSYKTKNIIVEFHSDHMKIRNATFPGVQMKFLQKLLTNAADAAGYKPVAVPARTPANAAVP

>d1zpda1 c.31.1.3 (A:188-362) Pyruvate decarboxylase {Zymomonas mobilis}

EASDEASLNAAVDETAKFIANRDKVAVLVGSKLRAAGAEAAVKFTDALGGAVATMAAKSFFPEENALYIGTSWGEVSYPGVEKTMKEADAVIALA
PVFDNDYTTGWTIDPDPKKLVAEPRSVVVNGIRFPSVHLKDYLTRLAQKVSKKTGSDDPKSLNAGEKKAAPADPS

>d1bfd_1 c.31.1.3 (182-341) Benzoylformate decarboxylase {Pseudomonas putida}

SVRLNDQDLDILVKALNSASNPAIVLGPDVDAANANADCVMLAERLKAPVWVAPSAPRCFPTRHPCFRGLMPAGIAISQLLEGHDVVLVIGAPVF
RYHQYDPGQYLKPGTRLISVTCPLEAARAPMGDAIVADIGAMASALANLVEESSRQLPTAAP

>d1jsca1 c.31.1.3 (A:280-460) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

AQDEFVMQSINKAADLINLAKKPVLVGAGILNHADGPRLLKELSDRAQIPVTTLQGLGSFDQEDPKSLDMILGMHGCATANLAVQNADLIIAVGA
RFDDRTGNISKFAPEARAAAEGRRGGIHFEVSPKNINKVQQTQIAVEGDAATTNLGKMMMSKIFPVKERSEWFQINKWKKEYPY

>d1d4oa_ c.31.1.4 (A:) Transhydrogenase domain III (dIII) {Cow (Bos taurus)}

GTHTEINLDNAIDMIREANSIIITPGYGLCAAKAQYPIADLVKMLSEQGKKVRFGIHPVAGRMPGQLNVLLAEAGVPYDIVLEMDEINHDFPDTDLV
VIGANDTVNSAAQEDPNIIAGMPVLEVWKSQKVIVMKRSLGVGYAAVDNPIFYKPNTAMLLGDAKKTCDALQAKVRES

>d1hzzc_ c.31.1.4 (C:) Transhydrogenase domain III (dIII) {Rhodospirillum rubrum}

SVKAGSAEDAFAIMKNASKVIIVPGYGMAVAQAAQHALREMADVLKEGVESYAIHPVAGRMPGHMNVLAAEANVPYDEVFELEEINSSFQTADV
AFVIGANDVTNPAAKTDPSSPIYGMPILDVKEAGTVLFIKRSMASGTYAGVENELFRNNNTMMLFGDAKKMTEQIVQAMN

>d1icia_ c.31.1.5 (A:) AF1676 sir2 homolog {Archaeon Archaeoglobus fulgidus}

GSHHHHHHGSHMDEKLLKTIAESKYLVALTGAGVSAESGIPTFRGKDGFLWNRYRPEELANPQAFAKDPEKVVWVWYAWRMEKFVNAQPNKAHQA
FAELERLGVLKCLITQNVDDLHERAGSRNVIHLHSLRVVRCTSCNNSEVESAPKIPPLPKCDKGSLRPGVVWFGEMLPPDVDRAMREVERAD
VIIVAGTSAVQPAASLPLIVKQRGGAIIEINPDETPLTPIASLRKGAGEVMDELVRHVRKALS

>d1j8fa_ c.31.1.5 (A:) Sirt2 histone deacetylase {Human (Homo sapiens)}

GEADMDFLRLNLSQTLGSQKERLLDELLEGVARYMQSERCRRVICLVGAGISTSAGIPDFRSPSTGLYDNLEKYHLPYPEAIFEISYFKKHPEPFFALA
KELYPGQFKPTICHYFMRLLKDKGLLRCYTQNIOTLERIAGLEQEDLVEAHGTFYTSCHVSASCRAHEYPLSWMKEKIFSEVTPKCEDCQLSVKPDIVFF
GESLPARFFSCMQSDLKVVDLVMGTSQVQPFASLISKAPLSTPRLLINKEKAGQSDPFLGMIMGLGGGMDFDSKKAYRDVAWLGECDQGCLAL

AELLGWKKELEDLVRREHASIDAQS

>d1fsz_1 c.32.1.1 (23-231) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}

SPEDKELLEYLQQKTAKITVVGCGGAGNNITRLKMEIGAKTVAINTDAQQLIRTKADKKILIGKKLTRLGAGGNPKIGEEAAKESAEIKAQDS
DMVFITCGGGGTGTGSAPVVAEISKKIGALTAVVTPFVMEGVRMNAMEGLERLKQHTDTLVIPNEKLFEIVPNMPLKLAFKVADEVLINAVK
GLVELITKDGL

>d1tuba1 c.32.1.1 (A:1-245) Tubulin alpha-subunit {Pig (Sus scrofa)}

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRAVFVDLEPTVIDEVRTGTYRQLFHPEQLITGKE
DAANNYARGHYTIGKEIIDLVLDRIRKLADQCTGLQGFSVHSFGGGTSGFTSLLMERLSVDYGKKSKLEFSIYPAPQVSTAVVEPYNSILTHTTLEHS
DCAFMDVNEAIYDICRRNLDIERPTYTNLNRLIGQIVSSITASLRFD

>d1tubb1 c.32.1.1 (B:1-245) Tubulin beta-subunit {Pig (Sus scrofa)}

MREIVHIQAGQCGQNQIGAKFWEVISDEHGDIDPTGSYHGDSDLQLERINVYYNEAAGNKYVPRAILVDLEPGTMDSVRSGPFGQIFRPDNFVGQSG
AGNNWAKGHYTEGAELVDSVLDVVRKESES CDCLQGFQLTHSGGGTGSGMTLLISKIREEYPRIMNTFSVVPSPKVSDTVVEPYNATLSVHQLV
ENTDETYCIDNEALYDICFR TLKLTTPTYGDNLNHLVSATMSGVTTCLRFP

>d1nbaa_c.33.1.1 (A:) N-carbamoylsarcosine amidohydrolase {Arthrobacter sp.}

TFNDIEARLA VEEAFAEGTSIYNERGFKRRIGYGNRPAVIHD LANAWTQPGHPFSCPMETIIPNVQRINEAARAKGPVVFYTTNVYRN RDASSG
TN DMLWYSKIPTETLPADSYWAQIDDRIAPADGEVIEKNRASA FPGTNLEFLTSNRIDLTVTGATAAGCVRHTVEDAIKGFRPIIPRETIGDRVP
GVVQWNLYDIDNKFGDVESTDSVVQYLDALPQFEDTVPKTLSDPQP EVA PADPV

>d1im5a_c.33.1.2 (A:) Pyrazinamidase/nicotinamidase {Archaeon Pyrococcus horikoshii}

PEEALIVVDMQRDFMPGGA LPVPEGDKIIPKVNEYIRKFKEKGALI VATRDWH PENHISFRERGGPWRHC VQNT P GAEFVV DLPEDA VIISKATEP
DKEA YSGFEGTDLAKI RLNGNGVKRVYICGVATEYCV RATALDALKHGFEVYLLRDAVKGIKPEDEERA LEEMKS RG IKIVQF

>d1yaca_c.33.1.2 (A:) YcaC {Escherichia coli}

TKPV VRLDKNDAA VLLV DHQAGL LSLVRDIEPD KFKNNV ALGDLAKYFNLPTIL TTS AETGPNGPLV PELKAQF P DAPIAR PGNIN AWDN EDV KA
VKATGKKQ LIIAGV VTECV AFPALSAIEEGFDV FVT DAS GTF NEITR HSAWDRMSQAGAQLMTWFGVACELHRDWRNDIAGLATLFSN HIPD YR
NLMTSYDTLT

>d1hi9a_c.99.1.1 (A:) Zn-dependent D-aminopeptidase DppA {Bacillus subtilis}

MKLYMSV DMEG ISGLP DDTF VDSG KRN YERGR LIMTEE ANYCIAE AFNS GCTE VLVN DS HS KM NN LM VE KLH PEADL ISGDV KPF SMV EG LDD TF
RGALFLGYHARASTPGVMSHSMIFGVRFYINDRPV GEL GLNAYVAG YYDVPVLMVAGDDRAAKEAEELIPN VTAAV KQT ISRS AV/KCL SPAKR GR
LLTEKTAFA LQNKDKV KPLT PDP RVLSIE FANYG QAEWANL MPGTE IKT GTTTVQF QAK DMLE AYQAM LV MTEL AMRTS FC

>d1e20a_c.34.1.1 (A:) Halotolerance protein Hal3 {Mouse-ear cress (Arabidopsis thaliana)}

RKPRVLLA SGSVAAIKFGNLCHCFTEWA EVRAV VTKS LHFLDKL SLPQEV TLTD EWE SS WNKIG DPV LHI EL RRW ADVL VIAL P SANT LGK IA
GLCDNLL CIR RAWD YT KPLF VAPAM NTLMWNNP FTERHLLS LDEL GITLIPPIKKRLAC GDY NGAMAEP SLIYSTVRLF WESQAH

>d1g5qa_c.34.1.1 (A:) Epidermin modifying enzyme (peptidyl-cysteine decarboxylase) EpiD {Staphylococcus epidermidis}

MYGKL LICATAS INVININ HYI VELKQHF DEV NILF SPSS KNF INT DV LKFC DNLY DEIKD PLNN NIV ENHEYI LVPASANTINKIANGICDNLL TVCL
TGYQKLF IFPP NMN IRM WGNPFLQKNIDLLK NNDV KVYSP DMN KS F EISS GRY KNN IT MP NIEN VLFVN

>d1k1ea_c.108.1.5 (A:) Probable phosphatase YrbI {Haemophilus influenzae, HI1679}

KLENIKFV ITDVGVL TDGQLHYDANGEAIKSF VRD GLG KML MDADI QVAVLS GRD SPIR RRIADLG I KLF LGK LEK TA CF DLM KQAG VTA EQT
AYIGDD SV DLP AFAAC GT SFAV AD APIY VKNAV DHLV LST HGGKA FREM SDM ILQA QGK SS VF DT AQGFLK SV KSM GQ

>d1zrn_c.108.1.1 (-) L-2-Haloacid dehalogenase, HAD {Pseudomonas sp., strain YL}

YIKGIAFD LYGT LFDV HSVV GRC DEAF PGR G REIS ALW RQK QLEY TWL RSL MN RYV NF QQ ATE DAL RFT CRH LG LD DAR TRS T LCD AY RL AP FSE V
PDSL REL KRR GLK LAI LS NGSP QSI DAVV SHAG LR DGF DH LL S VPQ VY KPD NR VY EL AE QAL GLD RS AIL FV AS NAW DAT GARY FG FPT C W IN RTG
NVF EEM GQ TP DWEV TSL RAV VEL F

>d1qq5a_c.108.1.1 (A:) L-2-Haloacid dehalogenase, HAD {Xanthobacter autotrophicus}

MIKAVV FDAY GTL FDV QS VAD AT ERAP GR GEY ITQV WRQ KQ LEY SW LRAL MG RY ADF WS VTR EAL Y LTG L GLE PDES FLAD MAQ AY NR LTP YP
DAAQ CLA EAP LK RAI LS NGAP DML QAL V ANA GL LTD SF DAVI S VD A KRV FK PH PDS Y AL VEE V LGV TPA E VLF VSS NG FD VGG A KNF GFS VAR VAR LS

QEALARELVSGTIAPLTMFKALRMREETYAEAPDFVVPALGDLPLRVRGMA

>d1ek1a1 c.108.1.2 (A:4-225) Epoxide hydrolase, N-terminal domain {Mouse (Mus musculus)}

RVAAFDLGVLALPSIAGAFRSEEALPRDFLLGAYQTEFPEGPTEQLMKGKITFSQWVPLMDESYRKSSKACGANLPENFSISQIFSQAMAARSIN
RPMILQAAIALKKKGFTTCIVTNNWLDDGDKRDSLAQMMCELSQHFDFLIESCQVGMIKPEPQIYNFLDTLKAKPNEVVFLDDFGSNLKPARDMG
MVTILVHNTASALRELEKVGTGTOFPAP

>d1feza_c.108.1.3 (A:) Phosphonoacetaldehyde hydrolase {Bacillus cereus}

KIEAVIFDWAGTTVDYGFCAFLEVFMEIFHKRGVAITAEEARKPMLLKIDHVRALTEMPIASEWRVFRQLPTEADIQEMYEFFEEILFAILPRYASP
INAVKEVIASLRERGKIGSTTGYTREMMDIVAKEAALQGYKPDLVTDPDVPGRPYPWMCYKNAMELGVYPMNHHMIKVGDTVSDMKEGRNAG
MWTVGVILGSSELGLTEEVENMDSVELREKIEVVRNRFVENGAHTIETMOELESVMHEIE

>d1j97a c.108.1.4 (A:) Phosphoserine phosphatase {Archaeon Methanococcus jannaschii}

EKKKLILFDSTLVNNETIDEIAREAGVEEVKKITKEAMEGKLNFQSLRKRVSSLKDPIEKVEKAIRTPTEGAETIKELKNRGYVVAVVSGGFID
AVNKIKEKGLDYAFANRLIVKDGKLTGDVEGEVLKENAKGEILEKIAKIEGINLEDTVAVGDANDISMFKAGLKIAFCAPKILKEKADICIEKRDLREI
KYIK

>d1fs5a c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Escherichia coli}

MRLIPLTTAEQVGKWAARHIVNRINAFKPTADRPVFLGLPTGGTPMTTYKALVEMHKAGQVSFKHVTFNMDEYVGLPKEHPESYYFSMHRNFFD
HVDIPAENINLLNGNAPDIDAECRQYEKIRSYKGKIHLMGGVGNDGHIAFNEPASSLASRTRIKTLTHDTRVANSRRFFNDVNQVPKYALTGVGVTLL
DAEFFVMIIVLGSOKAI ALOAAVEGCVNHMWTISCIQI HPKAIMVCDFPSTMELKVTKT IRYFNEFI FAFNIKGJ

>d1d9ta c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Human (Homo sapiens)}

MKLIILEHYSQASEWAAKYIRNRIIQFNPGEKYFTLGLPTGSTPLGCYKKLIEYYKNGDLFSKYVKTBNMDEYVGLPRDHPESYHSFMWNFFKHIDI
HPENTHILDGNAVDLQAECDAFEKIKAAAGGIELFVGIGPDGHIAFNEPGSSLVRTRVKTLAMDTILANARFFDGELEVPTMALTGVGVGTVMDA
REVMUJITGAHKAFALYKAJEEGVNHMWTVSAFOOHRTVEVCDERATEIJKV/KTV/KYEKGJMLVHNKLVDPLVISKEKETEKSQ

>d1ig3a2_c100.1.1 (A:10-178) Thiamin pyrophosphokinase, catalytic domain {Mouse (Mus musculus)}

HSSGLVPRGSHMEHTPLEPLLPTGNLKYCLVVLNQPLDARFRHLWKALLRACADGGANHLYDLTEGERESFLPEFVGDFDSIRPEVKKEYTKKG
CDLSTPDDOHDTEFKLOVJORKIEEKFELQDVIVTJGGGGGREDOIMASVNTLEOATHITPVJUUIOK

>d1jg0a2 c_100.1.1 (A:3-223) Thiamin pyrophosphokinase, catalytic domain {Baker's yeast (*Saccharomyces cerevisiae*)}

EECINPERIKIGTDLINIRNKMNLKELIHPNEDENSTLLINQKIDIPRPLFYKIWKLHDLKVCADGAANRLYDYLDDETLRIKYLPNYIIGDLDLSKEV
YKYYRKNKVTIKQTTQYSTDFTKCVNLISLHFNSPEFRSLISNKDNLQSNHGIELEKGITHLYNTMTESLVFSKVTPISLLALGGIGGRFDQTVHSITQLYT
ISENASYEKLCYMTP

>d1f75a_c 101.1.1 (A:) Undecaprenyl diphosphate synthase {Micrococcus luteus}

NINAAQIPKHIAIMDGNGRWAQKKMPRIKGHYEGMQTVRKITRYASDLGVKYLTLYAFSTENWSRPKDEVNYLMKLPGDFLNTFLPELIEKNVKV
ETIGFIDDLPDHTKKAVLEAKETKHNTGLTLVFALNYGGRKEIISAVQLIAERYKSGEISLDEISETHFNEYLFTANMPDPPELLRTSGEERLSNFLIWQCS
YSEEVEFIDEWPDENEEFSIACOCISIVNBR

>d1ip3a_c101.1.1 (A:) | Undecaprenyl diphosphate synthase {Escherichia coli}

LPAHGCRHVAIIMDGNGRWAKKQGKIRAFGHKAGAKSVRAVSFAANNGIEALTYAFSSENWRPAQEVSALMELFWALDSEVKSLHRHNVR
RIIIGDTSRFNSRLQERIRKSEALTAGNTGLTNAANYGGRWDIVQGVRQLAEKVQQGNLQPDQIDEEMLNQHVCMHELAPVDLVIRTGGEHRSNF
LIWQIAYAFYETDVLWPDEDFQDEFGALNAAFANRE

>d1pyda2_c 36.1.1 (A2-181) Pyruvate decarboxylase {Baker's yeast (*Saccharomyces cerevisiae*)}

SEITLGKYLFERLKQVNNTVFGPLGDFNLSSLDKIYEVGMRWAGNANELNAAYAADGYARIKGMSIITTFGVGELSALNGIAGSYAEHVGVLHVVGVSISHHTLGNIGDFTVFEHRSANISSETTAMITDUTAPAFIDRCIRTTVYTORPVYGLPANLVDLNVPAKL

>d1pyda3 c 36.1.1 (A:361-556) Pyruvate decarboxylase {Baker's yeast (*Saccharomyces cerevisiae*)}

ASTPLKQEWWMWNQLGNFLQEGDVIAETGTSAGFINQTTFPNNTYGISQVLWGSIGFTTGATLGAAFAAEIDPKKRVLFIGDGLQLTVQEISTMI
RW/GI KPYI EVI NNDGVTIEKLIHGPKAQYNEIOGW/DHLISLPTEGAKDVTHRVATTGEWDKUTODKSENDNSKIRMIEIMI PVEDAPONLVKOAKL

T

>d1zpda2 c.36.1.1 (A:2-187) Pyruvate decarboxylase {Zymomonas mobilis}

SYTVGTYLAERLVQIGLKHFAVAGDYNLVLDNLLNKMEQVYCCNELNCGSAEGYARAKGAAAVVTYSVGALSAFDAIGGAYAENLPVILSGA
PNNNDHAAGHVLHALGKTDHYQLEMAKNITAAAEEAIYTPPEAPAKIDHVIKTALREKKPVYLEIACNIASMPCAAPGPASALFND
>d1zpda3 c.36.1.1 (A:363-566) Pyruvate decarboxylase {Zymomonas mobilis}
APLVAEIAIRQVEALLPTNTVIAETGDSWFNAQRMKLPGNGARVEYEMQWGHIGWSVPAAFGYAVGAPERRNILMVGDSFQLTAQEVAQMVR
LKLPIIFLINNYGYTIEVMIHDPYNNIKNWDYAGLMEVFNGNGGYDSGAAKGLAKTGELAEAIKVALANTDGPTLIECFIGREDCTEELVKWKGK
RVAAANSRKPVNK
>d1poxa2 c.36.1.1 (A:9-182) Pyruvate oxidase {Lactobacillus plantarum}
TNILAGAAVIKVLEAWGVDHLYGIPGGSINSIMDALSAERDRHYIQVRHEEVGAMAAAADAKLTGKIGVCFGSGAGPGGTHLMNGLYDAREDHPV
LALIGQFGTTGMNMDTFQEMNENPIYADVADYNTAVNAATLPHVIDEARRAYAHQGVAVVQIPVDPWPQQISAEDW
>d1poxa3 c.36.1.1 (A:366-593) Pyruvate oxidase {Lactobacillus plantarum}
KQEGPLQAYQVLRAVNKIAEPDAIYSDVGDINLNANRHLKLTPSNRHITSNLFATMVGVIPGAIAAKLNYPERQVFNLAGDGGASMTMQDLVTQV
QYHLPVINVVFTNCQYGFIDEQEDTNQNDFIGVEFNIDFSKIADGVHMQAFRVNKIEQLPDVFFEQAKAIAQHEPVLIADAVITGDRPLPAEKLRLDS
AMSSAADIEAFKQRYEAQDLQPLSTYLQFGLDD
>d1bfd_2 c.36.1.1 (2-181) Benzoylformate decarboxylase {Pseudomonas putida}
ASVHGTTYELLRRQGIDTVFGNPGSNEPLFLKDFPEDFRYILALQEACVVGIAQASRKPAFINLHSAAAGTGNAMGALSNAWNNSHSPLIVTAGQ
QTRAMIGVEALLTNVDAANLPRPLVKWSYEPASAAEVPHAMSRAIHMASMAPQGPVYLSVPYDDWDKDADPQSHHLFDRHVSS
>d1bfd_3 c.36.1.1 (342-524) Benzoylformate decarboxylase {Pseudomonas putida}
EPAKVDQDAGRLLHPETVFDTLNDMAPENAIYLNESTTTAQMWQRQNMNRNGSYFCAAAGGLGFALPAAIGVQLAEPERQVIAIGDGSANYISA
LWTAAQYNIPTIFVIMNNNTYGALRWFAGVLEAENVPGLDVPGIDFRALAKGYGVQALKADNLQELKGLSLQEALSAKGPVIEVSTV
>d1jsca2 c.36.1.1 (A:83-270) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}
PDMDTSFVGLTGGQIFNEMMSRQNVDTGFYPPGAILPVYDAIHNSDKFNFVLPKHEQGAGHMAEGYARASGKPGVVLVTSGPGATNVTPMA
DAFADGIPMVVFTGQVPTSAIGTDAFQEADEVVGISRSCKWNVMVKVEELPLRINEAFEIATSGRGPVPLVDPKDVTAAIRNPIPTKTLPS
>d1jsca3 c.36.1.1 (A:461-648) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}
AYMEETPGSKIKPQTVIKKLSKVANDTGRHIVTTGVGHQHMWAQHWTWRNPHTFITSGLGTMGYGLPAAIGAQVAKPESLVIDIDGDASFN
MTLTELSSAVQAGTPVKILINNEEQGMVTQWQSLFYEHRYSHTHQLNPDFIKLAEAMGLKGLRVKKQEELDAKLKEFVSTKGPVLLEVEVDKK
>d1gpus1 c.36.1.2 (A:3-337) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}
QFTDIDKLAVSTIRILAVDTVKANSGHPGAPLGMAPAAHVLWSQMRMNPTNPDWINRDRFVLSNGHAVAQLYSMLHTGYDLSIEDLKQFRQLGS
RTPGHPEFELPGVEVTGPGQGQISAVGMAMAQANLAATYNKPGFTLSDNYTYVFLGDCLQEGLSEASSLAGHLKGLNLIAIYDDNKITIDGATSI
SFDEDVAKRYEAYGWEVLYVENGNEGLAGIAKIAQAKLSKDPTLIKMTTIGY GSLHAGSHSVHGAPLKAADVQQLSKFGFPDKSFVVPQEYV
DHYQKTIKPGVEANNWKNLFSEYQKKFPELGAELARRLSGQ
>d1gpus2 c.36.1.2 (A:338-534) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}
LPANWESKLPTYTAKDSAVATRKLSETVLEDVYNQLPELIGGSADLTPSNLTRWKEALDFQPPSGSGNYSGRYIRYIREHAMGAIMNGISAFGANY
KPYGGTFLNFVSYAGAVRLSALSGHPVIWATHDSIGVGEDGPTHQPIETLAHFRSLPNIQVWRPADGNEVSAAYKNSLESKHTPSIIALSRQNLQL
>d1dtwa1 c.36.1.3 (A:) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}
PQFPGASAEIFDKLEFIQPNVISGIPYRVMDRQGQIINPSEDPLPKEVLKLYKSMTLLNTMDRILYESQRQGRISFYMTNYGEEGTHVGSAAALDN
TDLVFGQYREAGVLMYRDYPLELFMAQCYGNISDLGKGRQMPVHYGCKERHFVTISSPLATQIPQAVGAAYAKRANANRVVICYFGEAASEGDA
HAGFNFAATLECPUIFFCRNNGYAISTPTSEQYRGDGIAARGPGYGYIMSIRVDGNDVFAYVNTKEARRRAVAENQPFIEAMTYRIGHHSTSDDSSAY
RSVDEVNYWDKQDHPISLRHYLLSQGWDEEQEKAWRKQSRRKVMFAFEQAERKPKPNPNNLLFSDVYQEMPAQLRKQQESLARHLQTYGEHY
PLDHFDFK
>d1dtwb1 c.36.1.3 (B:17-204) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}
QTQKMNLFQSVTSALDNSLAKDPTAVIFGEDVAFGGVFRCTVGLRDKYGRKDRVFNTPLCQGIVGFGIGIAVTGATAIAEIQFADYIFPAFDQIVNEAA
KYRYRSGDLFNCGSLTIRSPWGCVGHGALYHSQSPEAFFAHCPIKVVIPRSPFQAKGLLSCIEDKNPCIFFEPKILYRAAAEVP
>d1qs0a1 c.36.1.3 (A:) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}
NEYAPLRLHVPEPTGRPGCQTDFSYLRNDAGQARKPPDVDAADTADLSYSLVRVLDEQGDAQGPWAEDIDPQILRQGMRAVLKTRIFDSRMVV

AQRQKKMSFYMQSLGEEAIGSGQALALNRTDMCFPTYRQQSILMARDVSLVEMICQLLSNERDPLKGRQLPIMYSVREAGFFTISGNLATQFVQAV
GWAMASAIAKGDTKIASAWIGDGATAESDFHTALTFAHVYRAPVILNVVNNQWAISTFQAIAGGESTTFAGRGVCGIASLRVDGNDFVAVYASRW
AAERARRGLGPSLIEWVTYRAGPHSTSDPSKYRPADDWSHFLGDPIALKQHLIKIGHWSEEHQATTAEFEAAVIAAQKEAEQYGTLANGHIPS
AASMFDVYKEMPDHLRRQRQEL

>d1qs0b1 c.36.1.3 (B:2-205) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

ATTMTMIQALRSAMDVMLERDDNVVYGDVGYFGGVFRCTEGLQTGYKSRVFDAPISESGIVGTAVMGAYGLRPVVEIQFADYFYPASDQI
VSEMARLRYRSAGEFIAPLRLMPCCGGIYGGQTHSQSPEAMFTQVCLRTVMPNSPYDAKGLLIAECDDPVIFLEPKRLYNGPDFGHHDRPVTP
WSKHPHSAVPDG

>d1ik6a1 c.36.1.3 (A:1-191) E1-beta subunit of pyruvate dehydrogenase {Archaeon Pyrobaculum aerophilum}

VAGVVMMANMAKAINMALHEEMERDERVVVLGEDVGKKGGVFLTEGLYERFGPERVIDTPLNEGGILGFAMGMAMAGLKPVAEIQFVDFIWL
GADELLNHIAKLRSGGNKAPLVVRTPGSGTRGGLYHSNSPEAIVHTPGLVVMPSTPYNAKGLKAAIRGDDPVVFLEPKILYRAPREEVPEG
>d1keka1 c.36.1.4 (A:2-258) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

GKKMMTTDGNTATAHVAYAMSEVAIIYIPSTSMTGEEADDWAAQGRKNIFGQTLTIREMQSEAGAAGAVHGALAAGALTTFTASQGLLMIPN
MYKISGELLPGVFHVTARAIAAHALSIFGDHQDIYAARQTFAMLAQSSVQEADMALVAHLAAIESNVPFMHFFDGFRTSHEIQKIEVLDYADMAS
LVNQKALAEFRAKSMNPEPHVRGTAQNPDIFYFQGREAANPYYLKVPGIVAEYMVKVASLTGRSY

>d1keka2 c.36.1.4 (A:786-1232) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

VKSEVLPRDSLKGSQFQEPLMEFSGACSGCGETPYVRVITQLFGERMFIANATGCSSIW GASAPSMPYKTNR LGQGP AWGN SLFEDA EYFG MN
MSMFARRTHLADLAKALES DASGDVKEALQGWLAGKNDPIKSKEYGDKLKLLAGQKDG LLGQIAAMSDLYTKSVWIFGGDGW AYDIGYGLD
HV LASGEDVN VFM DTEV YNTGGQSS KATPTG AVAK FAAAGK RTG KKD LARM VMTY GY VV ATVSMG YSK QQFL KV LKEA E SFP GP S LVI AYAT CI
NQGLRKGMGK SQDV MINT AVK SG YW P LFRY DP RL AAQG KNP FQL DS KAP DG SVEE FL MA QN RFA V LDRS FP EDA KRL RAQ V AH ELD VRF KE LEH
MAATNIFSFAPAGGKADGSVDFGEGAEFCTR DTP MMAR PD SG EACD QN RAG TSE QQG DLS KRT KK

>d1gky__ c.37.1.1 (-) Guanylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SRPIVISPGSGTGKSTLLKLF AEPDSFGFSVSSTTRPRA GEVNGKDYNF VS VDEFKSMIKNN EFIEWAQFSGNYYGSTVASVKQVSKGKTCILDID
MQGVKSVKAPEL NARFL FI APPS VEDL KKRLEG RGTETEESINKR LSAQA QELAYA ETGA HDK VIVN DLDKAY KELK DFIA EK

>d1kgda_ c.37.1.1 (A:) Guanylate kinase-like domain of Cask {Human (Homo sapiens)}

HMRKTLVLLGAHGVGRRIKNTLITKHPDRFAYPIPHTRPPKKDEENGKNYYFVSHDQMMQD ISNNEYLEYGS HEDAMY GTKLETIRKIHEQGLIAI
LDVEPQALKVLR TAEFAPFV FIA P T PGLNEDES LQRLQ KESD ILQ RTYAHYFD LTIN NEIDE TIRH LEEA VELVC

>d1kjwa2 c.37.1.1 (A:526-724) Guanylate kinase-like domain of Psd-95 {Rat (Rattus norvegicus)}

VTQMEVHYARPII LGPTKDRAND DLLSEFPDKFGSCVPHTRPKREYEIDGRDYHFVSSREKMEKDIQAHKFIEAGQYNSHLYGTSVQS VREVAEQG
KHCILDVSANAVRRLQAAHLPIAIFPRSL ENV L EINKRITEEQARKAFDRATKLEQEFTECFS AIVEGDSFEEIYHKV KRVIEDLSGP YIW PARERL

>d1ukz__ c.37.1.1 (-) Uridylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

PAFSPDQVS VIFVLGGPGAGKGTQCEKLV KDYSFVHLSAGD L RAEQGRAGS QYGE L KNCI KEQG QIVPQE ITL ALL RNAISDNV KANKHKFL IDG PR
KMDQ AISFER DIVES KFIL FDCP EDIM L LER GKTSGRS DDDNIESIKR FNTFK ETS MPVIEYFET KSKV VRCD RS VEDV YK DV QDA IRDSL

>d1deka_ c.37.1.1 (A:) Deoxyribonucleoside monophosphate kinase {Bacteriophage T4}

MKLIFLSGVKRS GKDTTADFIMS NYS AVKY QLAG PIK DALAYA WGV FAANTD YPC LTR K FEG IDYD RETNL NLTK LEVITIME QAF CYL NGK SPIK GV
VFD DEG KES VN FV AFN KITD V INNIED DQW SVR RL M Q ALG TD LIV NN FDR MYW V KLF ALD YL DKF NS GYD YYI VP DTR QDHE M DA ARAM GATV IH
VVR PGQ K S ND THI TEAGLPI RD GDL VIT ND GS LEEL FS KI KNTL KV L

>d1j90a_ c.37.1.1 (A:) Deoxyribonucleoside kinase {Fruit fly (Drosophila melanogaster)}

TQPFTV LIEGNIGSGKTTYLNHFEKYKNDICL L TEP VEK VWR NVNGVN L L ELMYKDPKKWAMPFQS YV TLMLQS HTAP TNKL KIMER SIFS ARY CFV
ENMR RRG NSL E QGM YN TLE WYK FIE ESI HV QADL II YLRT S P E V AY E R I QRAR SE E C VPL K YLQ E L H E L H E DW L I H Q R R P Q SCK VL DAD LN L E

>d1jaga_ c.37.1.1 (A:) Deoxyguanosine kinase {Human (Homo sapiens)}

GPRRLSIEG NIAVGK STFVKLLT KTY PEWH VATE PVATW QNIQA AGNQ KACTA QSLGNL LDMMY REPAR WS YTF QTFS LSR LKV QLEPFPEKLLQA
RKP VQIFERSV YSDR YIFAKN L FENG SLS DIE WHI YQD WHS FLLWE FASR ITL HGFI YLQASPQV CLK RLY QRAREEEK GIEL AY LEQL HGQ HEAW LIHK
TTKLHFEALMNIPV LVLDV NDDF SEE VT KQED LM REV NT FV KNL

>d1cke_a_c.37.1.1 (A:) CMP kinase {Escherichia coli}

AIAPVITIDGPSGAGKGTLCAMAELQWHLLSGAIYRVLALAALHHHVDASEDALVPLASHLDVRFVSTNGNLEVILEGEDVSGEIRTQEVA
SQVAAFPRVREALLRRQRARFRELPGIADGRDMGTVVFPDAPVKIFLDASSEERAHRRMLQLQVKGFSVNFERLLAEIKERDDRNRAVAPLPAA
DALVLDSTTLSIEQVIEKALQYARQKLALA

>d1qf9a_c.37.1.1 (A:) UMP/CMP kinase {Dictyostelium discoideum}

MEKS KPNVVFLGGPGSGKGTQCANIVRDFGVWHL SAGD LRLR QEQ QSGSKD GEMIA TMKNG EIVPSIVTVKLLNAIDANQGKNFLVDGFPRNE
ENNN SWEENMKDFVDTKFVLFDCPEEVMTQRLKRGESSGRSDDNIESIKKRFTNVQTKL VIDHYNKFDKVII PANRDVNEVYNDVENLFK
MGF

>d1e2ka_c.37.1.1 (A:) Thymidine kinase {Herpes simplex virus type 1, different strains}

MPTLLRVYIDGPHGMGKTTTQLVALGSRDDIVVPEPMTYWRVLGASETIANIYTQHRLDQGEISAGDAAVMTSAQITMGMPYAVTDAVLA
PHIGGEAGSSHAPPALTLIFDRHPIAACLLCYAPAARYLMGSMTPQAVLAFLVIPPTLPGTNIVLGALPEDRHIDRLAKRQRPGERLDLAMLAIRR
GLLANTVRYLQCGGSWREDWGQLSGTAVPPQGAEPQSAGPRPHIGDTLFTLRAPELLAPNGDLYNVFAWALDVLAKRLRSMHVFILDYDQSPA
GCRDALLQLTSGMVQTHVTPGSIPTICDLARTFAREMGE

>d3adk_c.37.1.1 (-) Adenylate kinase {Pig (Sus scrofa)}

MEEKLKSKII FVVGGPGSGKGTQCEKIVQKYGYTHLSTGDLRAEVSSGSARGKMLSEIMEKGQLVPLETVLDMLRDAMVAKVDTSKGFLIDGYPRE
VKQGEEFERKIGQPTLLYV DAGPETMTKRLKRGETSGRVDDNEETIKRLEYYKATEPVIAFYEKRGIVRKVNAEGSVDDVFSQVCTHLDTLK

>d1nksa_c.37.1.1 (A:) Adenylate kinase {Archaeon Sulfolobus acidocaldarius}

MKIGIVTGIPVGKSTVLA KVKEILDNQGINNKIINYGDFMLATALKLG YAKDRDEM RKL SVEKQKKLQIDA AKGIAEEARAGGEGYL FIDTHA VIRTPS
GYLPGPLPSVITEINPSVIFLEADPKIILSRQKRDTTRNRNDYDES VILETINFARYAATASAVLAGSTV KIVNV EGDP SIAANEIIRSMK

>d2ak3a1_c.37.1.1 (A:0-124,A:162-225) Adenylate kinase {Cow (Bos taurus), mitochondrial izozyme-3}

GASARLLRAAIMGAPGSGKGTVSSRITKH FELKHLSSGDL RDNMLRGTEIGV LA KTFIDQGKLIPDDVMTRLV LHEK NL TQYNWL LDGF PRTL PQA
EA LDRAYQIDTVINLNVPFEVKQRLTXDRP ETVV KRL KAYEAQTEPV LEY YRK KV LET FSGT ETNK IWP H VY AFL QT KLP QR SQET SVTP

>d1ak2_1_c.37.1.1 (14-146,177-233) Adenylate kinase {Cow (Bos taurus), mitochondrial izozyme-2}

PKGVR A VLLGPGAGKGTQAPKLA KNF CVCH LATG DML RAM VAS GSEL GKKL KATMDAG KLV DEM VLE LIE KNL ET PPK NGFL LDGF PRT VRQA
EM LDD LME KRKE KLD S VIE FSIP DS LIRR ITG RL IHXS DDN K KALK IR LEAY HT QT TP LVE YY SKR GIHS AID AS QTP DV V FA SI LA FSK AT S

>d1aky_1_c.37.1.1 (3-130,169-220) Adenylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

ESIRMV LIGPPGAGKGTQAPNLQERFHAAH LATG DML RSQIA KGT QLG LEAK KIMDQ GGL VSD D M VNM IK DELT NN P ACK NGFL DG FP RT VR QA
EKLDQMLKEQGT PLE KAI ELKV DELL VARIT X NAD ALK KRL AYHA QTEP IVDFY KKT G I WAG VD AS QPP AT V WAD ILN KLG KN

>d1e4ya1_c.37.1.1 (A:1-121,A:157-214) Adenylate kinase {Escherichia coli}

MRII LL GAL VAG KGTQA QF IME KYG IP QI STG DML RAAV KGS E LG KQ A K D M D AG K L V D E L V I A L V KERIA QED CRNG FLL DG FP RT IP QAD AM KE
AG IN VD YV LE FD VP D E L I V D RIV X KDD Q E E T V R K RL VEY HQM TAP LIG Y S K E A E AG NT K YAK VDG TK P VAE VR AD LE K IL G

>d1zaka1_c.37.1.1 (A:3-127,A:159-222) Adenylate kinase {Maize (Zea mays)}

ADPLK VMI SGAP ASG KGTQ C E LI KT K YQ LA HIS A G D L R AE IA AG S E N G K R AKE F M E K G Q L V P D E I V V N M V K E R L R Q P D A Q E N G W L L D G Y P R S Y S Q
A MALE T L E I R P D T F I L L D V P D E L L V E R V V X F D D T E E V K V K L R L E T Y Y Q N I E S L L S T Y E N I I V K V Q G D A T V D A V F A K I D E L L G S I L E K K N E M V S S T

>d1zin_1_c.37.1.1 (1-125,161-217) Adenylate kinase {Bacillus stearothermophilus}

MNL VLM GLPGAGKGTQA EK IVA AY GIP HISTG DMF RAAM KEG TPL GLQ AK QY M DRG D L V P D E V T I G I V R E R L S K D D C Q N G F L L D G F P R T V A Q A E A
LET M L A D I GRK LDY V I H D V R Q D V L M E R L T X ADD NEAT V A N R L E V N M K Q M K P L V DF Y EQ K G Y L R N I N G E Q D M E K V F A D I R E L L G G L A R

>d1tmka_c.37.1.1 (A:) Thymidylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

GR GK L I L I E G L D R T G K T T Q C N I L Y K K L Q P N C K L L K F P E R S T R I G G L I N E Y L T D D S F Q L S D Q A I H L L F S A N R W E I V D K I K K D L L E G K N I V M D R Y V S G V A Y S A
A K G T N G M D L D W C L Q P D V G L L K P D L T L F L S T Q D V D N N A E K R G A F G H E R Y E N G A F Q E R A L R C F H Q L M K D T T L N W K M V D A S K S I E A V H E D I R V L S E D
P V L S T H I D H D K F S F F

>d1e9ea_c.37.1.1 (A:) Thymidylate kinase {Human (Homo sapiens)}

ARR G A L I V L E G V D R A G K S T Q S R K L V E A L C A A G H R A E L L R F P E R S T E I G K L L S S Y L Q K K S D V E D H S V H L L F S A N R W E Q V P L I K E K L S Q G V T L V V D R Y A F S G
V A Y T G A K E N F S L D W C K Q P D V G L P K P D L V L F L Q L Q L A D A K R G A F G H E R Y E N G A F Q E R A L R C F H Q L M K D T T L N W K M V D A S K S I E A V H E D I R V L S E D

AIATATEKPLKELWK

>d4tmka_c.37.1.1 (A:) Thymidylate kinase {Escherichia coli}

RSKYIVIEGLEGAGKTTARNVVVETLEQLGIRDMVFTRPGBTQLAEKLRSLLLDSVGDEVITDKAEVLMFYAARVQLVETVIKPALANGTWIGDR
HDLSQTAYQGGGRGIDQHMLATLRDAVLGDFRPDLTLYLDVTPEVGLKRARARGELDRIEQESFDFFNRTRARYLELAQDKSIHTIDATQPLEAVMD
AIRTTVTHWVKEL

>d1g3ua_c.37.1.1 (A:) Thymidylate kinase {Mycobacterium tuberculosis}

MILIAIEGVGDAGKRTLVEKLSGAFRAAGRSVATLAFPRYQGSVAADIAAEALHGEHGDLASSVYAMATLFALDRAGAVHTIQGLCRGYDVVILDYVA
SNAAYSAARLHENAAAGKAAAWVQRIEFARLGLPKPDWQVLLAVSAELAGERSRGRAQRDPGRARDNYERDAELQQRTGAVYAEAAQGWGGR
WLWVGADVDPGRLAATLA

>d1e6ca_c.37.1.2 (A:) Shikimate kinase {Erwinia chrysanthemi}

MTEPIFMVGARGCGMTTGVRELARALGYEFVDTDIFMQHTSGMTVADVVAEGWPGFRRRESEALQAVATPNRVVATGGMVLLQEQRQFMR
AHGTVVYLFAAPEELALRLOASLQAHQRPTLTGRPIAEEMEAVLREREALYQDVAHYVVDATQPPAAIVCELMQTMRL

>d1qhxa_c.37.1.3 (A:) Chloramphenicol phosphotransferase {Streptomyces venezuelae}

MTTRMIILNGSSAGKSGIVRCQLQSVLPPEPWLAFGVDSLIEAMPLKMQSAGGIEFDADGGVSIGPEFRALEGAWAEGVVAMARAGARIIDDVFL
GGAAAQERWRSFVGDLVLWVGVRCDGAVAEGRETARGDRVAGMAAKQAYVVHEGVEYDVEVDTTHKESIECAWAIAAHVV

>d1d6ja_c.37.1.4 (A:) Adenosine-5'-phosphosulfate kinase (APS kinase) {Penicillium chrysogenum}

HASALTRSERTELRNQRGLTIWTGLSAGKSTLAVEREHLQLVRDRRVHAYRLDGDNIRFLNKLGFSEADRNEENIRRIAEVAKLFADSNSIAITSFISP
YRKDRDTARQLHEVATPGEETGLPVEVYVDVPVEAEQRDPKGLYKKAREGVIKEFTGISAPYEPANPEVHVKNYELPVQDAVKQIIDYLDKGYLP
AKK

>d1g8fa3_c.37.1.15 (A:390-511) ATP sulfurylase C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

PRPKQGFSIVLGNSLTVSREQLSIALSTFLQFGGGRRYYKIFEHNNKTELLS LIQDFIGSGSGLIIPDQWEDDKDSVVGKQNVYLLDTSSADIQLESAD
PISHIVQKVVLFEDNGFFF

>d1i2da3_c.37.1.15 (A:391-573) ATP sulfurylase C-terminal domain {Fungus (Penicillium chrysogenum)}

PRATQGFTIFLTGYMNNSGKDAIARALQVTLNQQGGRSVSLLGDTVRHESSELGFTREDRHTNIQRIAFVATELTRAGAAVIAAPIAPYEESRKFARDA
VSQAGSFFLVHVATPLEHCEQSDKRGIYAAARRGEIKGFTGVDDPYETPEKADLVDFSKQSVRSIVHEIIIVLESQGFLERQ

>d1aqua_c.37.1.5 (A:) Estrogen sulfotransferase {Mouse (Mus musculus)}

EYYEVFGFRGVLMDKRFTKYWEDVEMFLARPDDLVIATPKSGTTWISEVVYMIYKEGDVEKCKEDAIFNRIPYLECRNEDLINGIKQLKEKESPRIVK
THLPKLLPASFWEKNCKMIYLCRNAKDVAVSYYFLIMITSYPNPKSFSEFVEKFMQGQVPGWSYDHVKAWWEKSNSRVLFMFYEDMKEDIR
REVVKLIEFLERKPSAELVDRIIQHTSFQEMKNNPSTNYTMMPEEMMNQKVSPFMRKGIIGDWKNHFPICALRERFDEHYKQQMKDCTVKFRME

>d1efha_c.37.1.5 (A:) Hydroxysteroid sulfotransferase {Human (Homo sapiens)}

DFLWFEGIAFPTMGFRSETLRKVRDEFVIRDEDVIIYTPKSGTNWLAEILCLMHSGDAKWIQSVPWVSEIGYTALSETESPRLFSSHLPIQ
LFPKSSFKAKVIYLMRNPDRDVLVSGYFWKNMKFIKKPKSWEEYFEWFCQGTLYGWSFDIHGWMPMREEKNFLLSYEELQDTGRTIEKICQ
FLGKTLPEEELNLKNSFSQSMKENKMSNYSLLSDYVVDKAQLLRKGVSGDWKNHFTVAQAEDFDKLQEKMAADLPRKLAAALE

>d1cjma_c.37.1.5 (A:) Aryl sulfotransferase sult1a3 {Human (Homo sapiens)}

SRPPLYVKGVPLIKYFAEALGPLQSFQARPDDLIINTPKSGTTWVSQLDMIYQGGDLEKCNRAPIYVVPFLEVNDPGEPSGLETLKDTPPPRLIKS
HLPLALLPQTLDDQKVVVVARNPDKAVSYHFHRMEKAHEPEPGTWDSSFLEKFMAGEVSYGSWYQHVQEWWEELSRTHPVLYFYEDMKENPK
REIQKILEFVGRLSPEETMDFMVQHTSFKEMKKNPMTNYTTVPQELMDHSISPFMRKG MAGDWKTTFTVAQNERFDADYAEKMAGCSLSFRS

>d1insta_c.37.1.5 (A:) Heparan sulfate N-deacetylase/N-sulfotransferase domain {Human (Homo sapiens)}

DPLWQDPCEDKRHKDIWSKEKTCRFPKLIIGPQKTGTTALYLFGLMHPDLSNYPSETFEEIQFFNIGHNYHKGIDWYMEFFPIPNTTSDFYFEKS
ANYFDSEVAPRRAAALLPKAKVLTILINPADRAYSWYQHQRADDPVALKYTFHEVITAGSDASSKLRALQNRCCLVPGWYATHIERWLSAYHANQILV
LDGKLLRTEPAKVMMDMVQKFLGVNTIDYHKTAFDPKKGFWCQLLEGGTKCLGKSKGRKYPEMDLDSRAFLKDYYRDHNIELSKLLYKMGQLPT
WLREDLQ

>d1fmja_c.37.1.5 (A:) Retinol dehydratase {Fall armyworm (Spodoptera frugiperda)}

PFPYEFRELNPPEEDKLVKANLGAFPTTYVKLGPKGYMVYRPLKDAANIYNMPLRPTDVFVASYQRSGTTMTQELVWLIENDLNFEAKTYMSLRYIY

LDGFMIDPEKQEEYNDILPNPENLDMERYLGLLEYSSRGSSLLAAPPTEKRFVKTHLPLSLMPPNMLDTVKMVYLARDPRDVAVSSFHHARLLYL
LNKQSNFKDFWEMFHRLGYLTLPYFEHVKEAWAKRHDNPMLFLFYEDYLKDPLPGCIARIADFLGKKLSEEQIQLCEHNFKEFKNNNGAVNMEDYRE
IGILADGEHFIRKGKAGCWRDYFDEEMTKQAEKWKDNLKDTDLRYPNM

>d1a7j_c.37.1.6 (-) Phosphoribulokinase {Rhodobacter sphaeroides}

SKKPIISVTGSSGAGTSTVKHTFDQIFRREGVKAVSIEGDAFHFRNRAADMKAELDRRYAAGDATFSHFSYEANELKELERVFREYGETGQGRTRTYV
HDDAEAARTGVAPGNFTDWRDFDSHLLFYEGLHGAVVNSEVNIAGLADLKIGVVVINLEWIQKIHDRATRGYTTEAVTDVILRRMHAYVHCIV
PQFSQTDINFQRVPVVDTSPNFIARWIPTADESVVIRFRNPRGIDFPYLTSMIHGSWMSRANSIVPGNKLDLAMQLITPLIDRVVRESKV

>d1esma_c.37.1.6 (A:) Pantothenate kinase PanK {Escherichia coli}

QTLMTPYLQFDRNQWAALRDSVPMTLSDEIARLGKINEDLSLEEVAEIYLPLSRLNFYISSNLRQAVLEQFLGTNGQRIPYIISIAGSVAVGKTTAR
VLQALLSRWPEHRRVELITDGFLHPNQLKERGLMKKGFPESYDMHRLVKFSDLKSGVPNTAPVYSHLIYDVIDPGDKTVVQPDILILEGLNVL
QSGMDYPDPHHVFVSDVDFSIYVDAPEDLLQTWYINRFLKFREGAFTDPDSYFHNYAKLTKEEAKTAMTLWKEINWLNLQNILPTRERASLILTK
SANHAVEEVRLRK

>d1bif_1 c.37.1.7 (37-249) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain {Rat (Rattus norvegicus)}

CPTLIVMVGLPARGKTYISKKLTRYLNFIGVPTRFNVGQYRRDMVKTYKSFEFFLPDNEEGLKIRKQCALAALNDVRKFLSEEGGHVAVFDATNTRE
RRAMIFNFGEQNGYKTFVESICVDPEVIAANIVQVKLGSPDYVNRSDEATEDFMRRIECYENSYESLDEEQRDLSYIKIMDVGQSYVVNRVADHI
QSRIVYYLMNIHVTPR

>d1ctqa_c.37.1.8 (A:) ch-p21 Ras protein {Human (Homo sapiens)}

MTEYKLVVGAGGVGKSALTQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHQYRE
QIKRVKDSDDVPMVLVGNKCDLAARTVESRQAQDLARSYGIPYIETSAKTRQGVEDAFTLVREIRQH

>d1ds6a_c.37.1.8 (A:) Rac {Human (Homo sapiens)}

MQAICKVVGDGAVGKTCCLIYTTNAFPGEIPTVFDNYSANVMVDSKPVNGLWDTAGQEDYDRLRPLSYPQTDVFLICFLVSPASYENVRAKW
FPEVRHHCPSTPIILVGTKLDLRDDKDTIEKLKEKKLAPITYPQGLALAKEIDSVKYLECSALTQRGLKTVFDEAIRAVLCQP

>d1mh1_c.37.1.8 (-) Rac {Human (Homo sapiens)}

GSPQAICKVVGDGAVGKTCCLIYTTNAFPGEIPTVFDNYSANVMVDGKPVNLGLWDTAGQEDYDRLRPLSYPQTDVFLICFLVSPASFENVRAK
WYPEVRHHCPNTPIIILVGTKLDLRDDKDTIEKLKEKKLAPITYPQGLAMAKEIGAVKYLECSALTQRGLKTVFDEAIRAVLCPP

>d1c1ya_c.37.1.8 (A:) Rap1A {Human (Homo sapiens)}

MREYKLVVLGGGVGKSALTQFVQGIFVEKYDPTIEDSYRKQVEVDCQQCMLEILDTAGTEQFTAMRDLYMKNGQGFALVYSITAQSTFNDLQDLR
EQILRVKDTEDVPMILVGNKCDLEDERVERGKEQQNQLARQWCNCAFLESSAKSKINVNEIFYDLVRQINR

>d1kao_c.37.1.8 (-) Rap2a {Human (Homo sapiens)}

MREYKVVVLGGGVGKSALTQFVQGIFVEKYDPTIEDSYRKQVEVDCQQCMLEILDTAGTEQFTAMRDLYMKNGQGFALVYSITAQSTFNDLQDLR
IRVKRYEKVPIVLGNKVDESEREVSSSEGRALAAEWGCPFMETSAKSKTMVDELFAEIVRQMNYA

>d3raba_c.37.1.8 (A:) Rab3a {Rat (Rattus norvegicus)}

NFDYMFKILIIGNSSVGKTSFLFRYADDSFTPAPVSTVGIDFKVKTIRNDKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITNEESFNAVQDW
TQIKTYSWDNAQVLLVGNKCDMEDERVSSSERGRQLADHLGFEFFEASAKDNINVKQTFERLVDVICEK

>d1huqa_c.37.1.8 (A:) Rab5c {Mouse (Mus musculus)}

ICQFKLVLGESAVGKSSLVLFVKGQFHEYQESTIGAACFLTQVCLDDTTVKFEIWDTAGQERYHSLAPMYRGAQAAIVYDITNTDFARAKNW
KELQRQASPNIVIALAGNKADLASKRAVEFQEAQAYADDNSLLFMETSAKTAMNVNEIFMAIAKKL

>d1d5ca_c.37.1.8 (A:) Rab6 {Malaria parasite (Plasmodium falciparum)}

KYKLVFLGEQAVGKTSIITRFMYDFTDNNYQSTIGIDFLSKTLYLDEGPVRLQLWDTAGQERFRSLIPSYIRDSAAAIVYDITNRQSFENTTKWIQDILN
ERGKDVIIALVGNKTDGLRKVTYEEGMQKAQEYNTMFHETSAKAGHNIKVLFKKTASKL

>d1g16a_c.37.1.8 (A:) Rab-related protein Sec4 {Baker's yeast (Saccharomyces cerevisiae)}

SIMKILLIGDGVGKSCLLVRFVEDKFNPSETTIGIDFKIKTVINGKKVKLQIWDTAGQERFRSLIPSYIRDSAAAIVYDITNRQSFENTTKWIQDILN
HANDEAQLLGVGNKSDMETRVTADQGEALAKELGIPFISSAKNDDNVNEIFFTLAKLIQEKI

>d1byua_c.37.1.8 (A:) Ran {Dog (Canis familiaris)}

EPQVQFKLVLVGDDGTGKTFVKRHLTGEFEKKYVPTLGVEVHPLVFHTNRGPIKFNVWDTAGQEKGGLRDGYIQAQCAIIMFDVTSRVTYKNVP
NWHRLVRVCENIPIVLCGNVKDIKDRVKAKSIVFHRKKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFVAMPALAPPEV/MDPALAAQYEH
DLEVAQTT

>d1i2ma_c.37.1.8 (A:) Ran {Human (Homo sapiens)}

QVQFKLVLVGDDGTGKTFVKRHLTGEFEKKYVATLGVEVHPLVFHTNRGPIKFNVWDTAGQEKGGLRDGYIQAQCAIIMFDVTSRVTYKNVPN
WHRDLVRVCENIPIVLCGNVKDIKDRVKAKSIVFHRKKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFV

>d1tx4b_c.37.1.8 (B:) RhoA {Human (Homo sapiens)}

AIRKKLVIVGDGACGKTCLIVNSKQDFPEVYVPTVFENYVADIEVDGAQVELALWDTAGQEDYDRLRPLSYPTDVILMCFSIDSPDSLENPEKWTP
EVKHFCNPVPIILVGNKKDLRNDEHTRRELAKMKQEPVKPEEGRDMANRIGAFGYMECSAKTKDGREVFMATRAAL

>d1hura_c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF1}

GNIFANLFKGLFGKEMRILMVGDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYKNISFTVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSNDRERV
NEAREELMRMLAEDELRAVLLFANKQDLPNAMNAEITDKLGHSLRHRNWWYIQATCATSGDGLYEGLDWLSNQLRNQK

>d1e0sa_c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF6}

GKVLSKIFGNKEMRILMLGLDAAGKTTILYKLKGQSVTIPTVGFNVETVTYKNVKFNVWVWDVGGQDKIRPLWRHYTGTQGLIFVVDCADRDRIDE
ARQELHRIINDREMRDAIIIFANKQDLPDAMPKHEIQEKGTRIRDRNWYVQPCATSGDGLYEGLTWLTSNYK

>d1fzqa_c.37.1.8 (A:) ADP-ribosylation factor {Mouse (Mus musculus), ARL3}

GLLSILRKLSAPDQEVRILLGLDNAGKTTLLKQLASEDISHITPTQGFNIKSQSQGFKLNVWDIGGQRKIRPYWRSYFENTDILYVIDSADRKRFE
TGQELTELLEEEKLSCVPVLIFANKQDLLTAAPASEIAEGLNLHTIRDRVWQIQSCSALTGEVQDGMNWVCKNV

>d1f6ba_c.37.1.8 (A:) SAR1 {Chinese hamster (Cricetulus griseus)}

SSVLQFLGLYKKTGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPTLHPTSEELTIAGMTFTFDLGGHQARRVWKNYLPAINGIVFLVDCADHERLLES
KEELDSLMTDETIANVPILGNKIDRPEAISEERLREMFGLYGQTTKGGSVSLKELNARPLEVFMCVSLKRQGYGEGFRWMAQYID

>d2ngr_a_c.37.1.8 (A:) CDC42 {Human (Homo sapiens)}

MQTIKCVVVGDAVGKTCCLIYTTNKFSEYVPTVFDNYAVTVMIGGEPTYLGLFDTAGQEDYDRLRPLSYPTDVFVLCFSVSPSSENVKEKWW
PEITHHCPKTPFLVGQTQIDLRDDPSTIEKLAKNKQKIPTEAEKLARDLKAVKYVECSALTQKGLKNVFDEAILAALEPPKKSRRCVLL

>d1ek0a_c.37.1.8 (A:) Ypt51 {Baker's yeast (Saccharomyces cerevisiae)}

VTSIKLVLLGEAVGKSSIVLRFVSNDFAENKEPTIGAFLTQRVTINEHTVKFEIWTAGQERFASLAPMYYRNAQAALVYDVTKPCSFIKARHWVK
ELHEQASKDIIIALVGNKIDMLQEGGERKVARREEGEKLAEEKGLLFFETSAKTGENVNDVFLGIGEKIPLK

>d1h65a_c.37.1.8 (A:) Chloroplast protein translocon GTPase Toc34 {Garden pea (Pisum sativum)}

VREWSGINTFAPATQTKLLELLGNLKQEDVNSLTLVMGKGVGKSSTVNSIIGERVVSISPFQSEGPRPMVSRSRAGFTLNIIDTPGLIEGGYINDMA
LNIIKSFLLDKTIDVLLYVDRLDAYRVDNLDKLVAKAITDSFGKGIWNKAVALTHAQFSPPDGLPYDEFFSKRSEALLQVVRSGASLKKDAQASDIPVVL
ENSGRCNKNDSDKEVLPNGIAWIPHVLVQTITEVALNKSESIFVDKNLIDKLAAD

>d1azsc2_c.37.1.8 (C:36-66,C:202-393) Transducin (alpha subunit) {Cow (Bos taurus)}

YVRATHRLLLGGAGESGKSTIVKQMRILHVNXVLTSGIFETKFQVDKVNFMFDVGGQRDERRKWIQCFNDVTAIFVASSSYNMVIREDNQTNRL
QEALNLFKSIWNNRWLRTISVILFLNKQDLLAEVKLAGKSKIETYFPEFARYTTPEDATPEPGEDPRVTRAKYFIRDEFRLISTASGDGRHYCYPHTCAV
DTENIRRNFNDCRDIIQRMHLRQYEL

>d1tada2_c.37.1.8 (A:27-56,A:178-342) Transducin (alpha subunit) {Cow (Bos taurus)}

ARTVKLLLLGAGESGKSTIVKQMKIIHQDGXTGIIETQFSFKDLNFRMFVGGQRSERKKWIHCSEGVTIIFIAALSAYDMVLVEDDEVNRMHESLHL
FNSICNHRYFATTSIVLFLNKKDVFSEKIKKAKHLSICFPDYNGPNTYEDAGNYIKVQFLELMRMRDVKEIYSHMTCATDTQNVKFVFDATDIIKE

>d1bof_2_c.37.1.8 (10-60,182-354) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

KAAVERSKMIDRNLREDGEKAAREVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHFTFKDLHFKMFVGGQRSERKKWIHCSEGVTIIFCVALS
DYDLVLAEDEEMNRMHESMKLFDSCNNKWFDTDSIILFLNKKDLFEKIKKSPLTICYPEYAGSNTYEEAAAYIQCQFEDLNKRKDKEIYTHFTCATD
TKNVQFVFDATVDVIKNNLKDCCGLF

>d1cipa2_c.37.1.8 (A:32-60,A:182-347) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

REVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHFTFKDLHFKMFVGGQRSERKKWIHCSEGVTIIFCVALSVDLVAEDEEMNRMHESMKL

FDSICNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAAAYIQCQFEDLNKRKDTKEIYTHFTCATDTKNVQFVFDAVTDVIKNN
>d1fqa2 c.37.1.8 (A:28-60,A:182-344) Transducin (alpha subunit) {Rat (Rattus norvegicus)}
RTVKLLLGAESGKSTIVKQMIIHQDGLEXETQFSFKDLNFRMFDVGGQRSERKKWIHCFCGTIAIFCVALSDYDLVLAEDEEMNRMHESMKL
FDSICNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAGNYIKVQFLELNMRDVKEIYSHMTCATDTQNVKFVFDAVTDIIKENL
>d1gota2 c.37.1.8 (A:6-60,A:182-343) Transducin (alpha subunit) {Rat (Rattus norvegicus)}
SAEEKHSRELEKKLGEDAKDARTVKLLLGAESGKSTIVKQMIIHQDGLEXETQFSFKDLNFRMFDVGGQRSERKKWIHCFCGTIAIFCVALSD
YDLVLAEDEEMNRMHESMKLFDSCNNKWFTDTSIILFLNKKDLFEEKIKKSPLTICYPEYAGSNTYEEAGNYIKVQFLELNMRDVKEIYSHMTCATD
TQNVKFVFDAVTDIIKENL
>d1efca3 c.37.1.8 (A:8-204) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}
TKPHVNVTIGHVDHGKTTAAITVLAKTYGGAARAFDQIDNAPEEKARGITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAIL
VVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVDDDEELLEVEMEVRELLSQYDFPGDDTPIVRGSAKALEGDAEWEAKILELAGFLDSYIPEP
ER
>d1efm_1 c.37.1.8 (12-190) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}
VNVGTIGHVDHGKTTAAITVLAKTYGGAARXXXXXXXXXXXXGITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAAT
DGPMQPTREHILLGRQVGVPYIIVFLNKCDMVDDDEELLEVEMEVRELLSQYDFPGDDTPIVRGSAKALEGDAEWEAKILEAGFLDSYIPEP
>d1etu_1 c.37.1.8 (5-200) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}
FERTKPHVNVTIGHVDHGKTTAAITVLAKTYGGAAXXXXXXXXXXXXXGITINTSHVEYDTPTRHYAHVDCPGHADYVKNMITGAAQMDG
AILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVDDDEELLEVEMEVRELLSQYDFPGDDTPIVRGSAKALEGDAEWEAKILEAGFLDSYI
P
>d1exma3 c.37.1.8 (A:3-212) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Thermus thermophilus}
GEFIRTKPHVNVTIGHVDHGKTTAAITVLAEGGGAKFKKYEEIDNAPEERARGITINAAHVEYSTAARHYAHTDCPGHADYVKNMITGTAPLDGCILVVA
DGAIIVVSAADGPMPQTREHILLARQVGVPYIIVFMNKVDMVDDPELLLVEMEVRELLSQYDFPGDDTPIVRGSAKALEGDAEWEAKILEAGFLDSYIPEP
WVDKIWELDAIDEYIPT
>d1d2ea3 c.37.1.8 (A:55-250) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Cow (Bos taurus), mitochondrial}
KPHVNVTIGHVDHGKTTAAITKLAEGGGAKFKKYEEIDNAPEERARGITINAAHVEYSTAARHYAHTDCPGHADYVKNMITGTAPLDGCILVVA
ANDGPMPQTREHLLARQIGVEHVVVVVNKADAVQDSEMVLELEIRELLTEFGYKGEETPIIVGSALCALEQRDPGLKSVQKLLDAVDTYIPV
>d1f60a3 c.37.1.8 (A:2-240) Elongation factor eEF-1alpha, N-terminal (G) domain {Baker's yeast (Saccharomyces cerevisiae)}
GKEKSHINVVVIGHVDGKSTTGHLYKCGGIDKRTIEKFEEAAELGKGSFYAWVLDKLKAERERGIFTIDIALWKFETPKYQVTVIDAPGHRDFIKN
MITGTSQADCALIIAGGVGEFEAGISKDGQTREHALLAFTLGVRLIVAVNKMDSVKWDESRFQEIVKETSNIKKVGYNPKTVFVPISGWNGDN
MIEATTNAPWYKGWEKETKAGVVKGKTLLEAIDAEQPSRPT
>d1jnya3 c.37.1.8 (A:4-227) Elongation factor eEF-1alpha, N-terminal (G) domain {Archaeon Sulfolobus solfataricus}
KPHLNLIVGHVDHGKSTLVRLLMDRGFIDEKTVKEAAEEAKKLGKESEKFAFLDRLEERERGVTINLTFRMFETKKYFTIIDAPGHRDFVKNMIT
GASQADAAILVVSACKGEYEAGMSVEGQTREHILAKTMGLDQLIVAVNKMDLTEPPYDEKRYKEIVDQVSKFMRSYGFNTNKVRFPVVAPSGDNI
THKSENMKWYNGPTLEEYLDQLELPK
>d1dar_2 c.37.1.8 (1-282) Elongation factor G (EF-G), N-terminal (G) domain {Thermus thermophilus}
MAVKVEYDLKRLRNIGIAAHIDAGKTTTERILYYTGRHIKIGEVHEGAATMDFMEQERERGIFTAAVTTCFWKDHRNIIDTPGHVDFTIEVERSMR
VLDGAIIVFDSSQGVEPQSETVWRQAKEYKVPRIAFANKMDKTGADLWLVRTMQERLGPVVMQLPIGREDTFSIIDVLRMKAYTYGNDLGT
DIREIPIPEEYLDQAREYHEKLVEAADFDENIMLKYLEGEETPEEEVAAIRKGTIDLKITPVFLGSALKNGVQLLDAVVDYLP
>d1g7sa4 c.37.1.8 (A:1-227) Initiation factor IF2/eIF5b, N-terminal (G) domain {Archaeon Methanobacterium thermoautotrophicum}
MKIRSPIVSVLGHVDHGKTLHDHIRGSAVASREAGGITQHIGATEIPMDVIEGICGDFLKKFSIRETPGLFFIDTPGHEAFTTLRKRGALADLAILIVD
INEGFKPQTQEALNIRMYRTPFVVAANKIDRIHGWVHEGRPFMETFSKQDIQVQQKLDTKVYELVGLKHEEGFESERFDRVTFASQVSIIPISAIT
GEGIPELLTMLMGLAQQYLREQLKIE
>d1egaa1 c.37.1.8 (A:4-182) GTPase Era, N-terminal domain {Escherichia coli}

DKSYCGFIAIVGRPNVGKSTLLNKLLGQKISITSRKAQTRHRIVGIHTEGAYQAIYVDTPLGHMEEKRAINRLMNKAASSSIGDVELVIFVVEGTRWTP
DDEMVNLKREGKAPVILAVNKVDNVQEKAQADLLPHLQLASQMNFLDIVPISAETGLNDTIAIVRKHLPEATHHFPE

>d1f5na2 c.37.1.8 (A:7-283) Interferon-induced guanylate-binding protein 1 (GBP1), N-terminal domain {Human (Homo sapiens)}
MTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLAKKKGFSLGSTVQSHTKGIWWMWCVPHPKKPGHILVLLDTEGLG
DVEKGDNQNDSWIFALAVLLSSTFVYNSIGTINQQMDQLYYVTELTHRIRSKSSPDENENEVEDSADFVSFFPDFVWTLRDFSLDEADGQPLTPDE
YLTYSLKLKGTSQKDETFLNPLRCIRKFPKKCFVDRPVHRRKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTKLS

>d1jwyb_c.37.1.8 (B:) Dynamin G domain {Slime mold (Dictyostelium discoideum)}

DQLIPVINKLQDVFTNLGSDPLDPQIVVGSQSSGKSSVLENIVGRDFLPRGSGIVTRRPLILQLTHLPIADDGSQTQEWFELHKPNDMFYDFSEIR
EEIIRDTRMTGKNGISAQPINLKIYSPHVNLTVLDPGITKVPVGQDQPTDIEQQIRRMVMAYIKKQNAIIAVTPANTDLANSALQLAKEVDPEG
KRTIGVITKLDLMDKGTDAMEVLTGRVIPLTGFIVINRSQEDIIAKKSIRESLKSEILYFKNHPYKSIANRSGTAYLSKTLNKL MFHIRDTLPDLKVKS
KMLS

>d1br2a2 c.37.1.9 (A:80-789) Myosin S1, motor domain {Chicken (Gallus gallus), pectoral muscle}

PPKFSKVEDMAELTCNEASVLHNLRERYFSGLIYTSGLFCVVNPYKQLPIYSEKIIDMYKGKKRHEMPPHIYIAIDTAYRSMLQDREDQSILCTGESG
AGKTENTKKVIQYLVAVVASSHKGKKDTSITQGPFSYGELEKQLQANPILEAFGNAKTVKNDNSSRGKFIRINFDTGYIVGANIETYLEKSRAIRQA
KDERTFHIFYIAGASEQMRNDLLEGFNNYTFSLNSNGHVPIPAQQDDEMFFQTELAMTIMGTEEEQTSILRVVSSVQLGNIVFKKERNTDQASM
PDNTAAQKVCHLMGIVNTDTRSILTPTKVRDVVKQAKTKEQADFAIEALAKFERLFRWLTRVNKALDKTRQGASFGLGILDAGFEIFEINSFE
QLCINYTNEKLQQLFNHTMFQEEYQREGIEWNFIDFGDLQPCIELIERPTNPPGVALLDEECWFPKATDTSFVEKLIQEQQNHAKFQKSQLKD
KTEFCILHYAGKVTYNASAWLTKNMDPNDNNTSLLNQSSDKFVADLWVDVDRIVGLDQMAKMTTESSLPSASKTKGFMRTVGQLYKEQLTKLMT
TLRNTNPVRCIIPNHEKRAGKLDALVLEQLRCNGVLEGIRICRQGPNRIVFQEFRQRYEILAANAIPKGFMDGKQACILMIKALELDPNLYRIGQS
KIFFRTGVLAHLEEIRD

>d2mysa2 c.37.1.9 (A:4-33,A:80-843) Myosin S1, motor domain {Chicken (Gallus gallus), pectoral muscle}

DAEAMAAFGEAAPYLRKSEKERIEAQNKPFDXMNPPKYDKIEDMAMMTHLHEPAVLYNLKERYAAWMIYTSGLFCVTNPYKWLVPVNPKVVLAY
RGKKRQEAPPHFSISDNAYQFMLTDRENQSILITGESGAGKTVNTKRVIQYFATIAASGEKKKEEQSGKMQGTLEDQIISANPLLEAFGNAKTVRNDN
SSRGFKFIRHFATGKLASADIETYLLEKSRTFQLPAERSYHIFYQIMSNKKPELIDMLLITTNPYDHYVSEGEITVPSIDDQEELMATDSAIDILGFA
DEKTAIYKLTGAVMHYGNLKFQKQREEQAEPDGTEVADKAAYLMGLNSAELLKALCYPRVGVGNEAVTKGETVSEHNSVGALAKAVYEKMF LW
MVIRINQQLDTKQPRQYFIGVLDIAGFEIFDFNSFEQLCINFTNEKLQQFFNNHHMFVLEQEEYKKEGIEWEFIDFGMDLAACIELIEKPMGIFSILEECC
MFPKATDTSFKNKLYDEHLGKSNNFQPKPAKGKAEAHFSLVHYAGTVDYNISGWLEKNKDPLNETVIGLYQKSSVTLALLFATYGGEAEGGGGKKG
GKKKGSSFQTVALFRENLNKLMLANLRSTHPHFVRCIIPNETKTPGAMEHEHLVHQLRCNGVLEGIRICRKGFPSRVLYADFKQRYRVLNASAIPEGQF
MDSKKASEKLLGGGDVDHTQYAFGHTKVFVKAGLLLEEMRDDKLAEIITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNVKHWPW
MKLFFKIKPLLK

>d1b7ta4 c.37.1.9 (A:5-28,A:77-835) Myosin S1, motor domain {Bay scallop (Aequipecten irradians)}

FSDPDFQYLVDRKKLMKEQTAAXMNPPKFEKLEDMANMTYLNEASVLYNLSRTSGLIYTYSGLCIAVNPYRRLPIYTDSSIAKYRGKRKTEIPP
HLFSVADNAYQNMVTDRENQSCLITGESGAGKTENTKKVIMYLAKVACAVKKDDEASDKKEGSLEDQIQQANPVLEAYGNAKTRNNNSRGKF
RIHFGPTGKIA GADIETYLLEKSRTVYQQSAERNYHIFYQICNSNAIPELNDVMLVTPDGSGLYSFINQGCLTVNDIDDVEEFLKDCDEAFDILGFTKEEKQSM
FKCTASILHMGE MKFQRPREEQAESDGAEAEKVAFLCGINAGDLLKALLKPKVKVGTEMVTKGQNMNQVVNSVGALAKSLYDRMFNWLVRRV
NKTLDTAKRNYYIVGLDIAGFEIFDFNSFEQLCINYTNERLQQFFNNHHFILEQEEYKKEGIAWEFIDFGMDLQMCIDLIEKPMGILSILEECCMFPKA
DDKSFQDKLYQNHMGKNRMFTKPGKPTRPNQGPAHFELHHYAGNVPSITGWLEKNKDPINENVVALLGASKEPLVAELFKAPEEPAGGGKKKG
KSSAFQTISAVHRESLNKLMKNLYSTPHFVRCIIPNELKQPGGLVDAELV LHQLQCNGVLEGIRICRKGFPSRLIYSEFKQRYSLAPNAIPQGFVDGKTV
SEKILAGLQMDPAEYRLGTTKVFVKAGVLGNLEEMRDERLSKISMFQAHRGYLIRKAYKKLQDQRIGLSVIQRNIRKWLVRNWQWWKLYSKV
P>d1lvk_2 c.37.1.9 (2-33,80-759) Myosin S1, motor domain {Slime mold (Dictyostelium discoideum)}

NPIHDRTSDYHKYLKVQGDSLFLKLTVDKXRNPPIKFDGVEDMSELSYLNEPAVFHNLRVRYNQDLIYTYSGLFLVAVNPFKRIPYQEMVDIFKGR
RRNEVAPHIFAISDVAYRSMLDDRQNQSLLTGESGAGKTENTKKVQYLASVAGRNCANGSGVLEQQILQANPILEAFGNAKTRNNNSRGKF
IQFNNAGFISGASIQSYLEKSRRVVFQSTSERNYHIFYQLLAGATAEEKKALHLAGPESFNYLNQSGCVDIKGVSDDEFKITRQAMDIVGFSQEEQMSI
FKIIAGILHLGNIKFEKGAGEGAVLKDKTALNAASTVFGVNPBVLEKALMEPRILAGRDLVAQHLLNEKSSSRDALVKA LYGRLFLWLKKINNNVLCSE

RKAYFIGVLDISGFEIFKVNSFEQLCINYTNEKLQQFFNHMFKEQEKYLKEKINWTFIDFGLDSQATIDLIDGRQPPGILALLDEQSVPNATDNTLIT
KLHSHFSKKNAKYEEPRFSKTEFGVTHYAGQVMYEIQDWLEKNKDPLQQDLELCFKDSSDNVTKLFDNPNIASRAKKGANFLTVAAQYKEQLASL
MATLETTNPHFVRCIIPNNKQLPACKEDKVLDQLRCNGVLEGIRITRKGFNPRIIYADFVKRYYDAPNVRDAEDSQKATDAVLKHLNIDPEQFRGI
TKIFFRAGQLARIEEARE

>d1mnd_2 c.37.1.9 (2-33,80-690) Myosin S1, motor domain {Slime mold (*Dictyostelium discoideum*)}

NPIHDRSDYHKYLKVQGDSDLFKLTVDKRXRNPICKFDGVEDMSELSYLNEPAVFHNLRVRYNQDLITYSGFLFLAVNPFKRIPYQTQEMVDIFKGR
RRNEVAPHIFAISDVAYRSMLDDRQNQSLITGESGAGKTENKKVIQYLASVAGRQANGSGVLEQQILQANPILEAFGNAKTRNNNNSSRGKFIE
IQFNNAGFISGASIQSYLEKSRRVVFQSETERNYHIFYQLLAGATAEEKKALHLAGPESFNYLNQSGCVDIKGVSDEDEFKITRQAMDIVGFSQEEQMSI
FKIIAGILHGNIKFEKGAGEGAVLKDKTALNAASTVFGVNPSSVLEKALMEPRILAGRDLVAQHNLNEKSSSRDALVKALYGRFLWLVKKINNVLCE
RAAYFIGVLDISGFEIFKVNSFEQLCINYTNEKLQQFFNHMFKEQEYLKEKINWTFIDFGLDSQATIDLIDGRQPPGILALLDEQSVPNATDNTLIT
KLHSHFSKKNAKYEEPRFSKTEFGVTHYAGQVMYEIQDWLEKNKDPLQQDLELCFKDSSDNVTKLFDNPNIASRAKKGANFITVAAQYKEQLASL
MATLETTNPHFVRCIIPNNKQLPACKEDKVLDQLRCNGVLEGIRITRK

>d1bg2__ c.37.1.9 (-) Kinesin {Human (*Homo sapiens*)}

DLAECNIKVMCRFRPLNESEVNPGDKYIAKFQGEDTVVIASKPYAFDRVFSQSTSQEQQVYNDCAKKIVKDVLEGYNGTIFAYGQTSSGKHTMEGKL
HDPEGMGIIPRIVQDFNYYISMDENLEFHFIKVSFYEIYLDKIRDLLDVSKTNLSVHEDKNRVPYVKGCTERFVCSDEVMDTIDEKGSNRHVAVTNM
NEHSSRSHSIFLINVKQENTQTEQKLSGKLYLVDLAGSEKVKSGTGAEGAVLDEAKNINKSLSALGNVISALAEGSTVPYRDSKMTRILQDSLGGNCRTT
IVICCPSSYNESETKSTLLFGQRAKTI

>g2kin.1 c.37.1.9 (A;B;) Kinesin {Rat (*Rattus norvegicus*)}

ADPAECSIKVMCRFRPLNEAEILRGDKFIPFKGEETVVIGQGKPYVDRVLPPNTTQEQQVYNACAKQIVKDVLEGYNGTIFAYGQTSSGKHTMEGK
LHDPQLMGIIPRIAHDFDHIYSMDENLEFHFIKVSFYEIYLDKIRDLLDVSKTNLAVHEDKNRVPYVKGCTERFVSSPEEVMDVIDEGKANRHVAVTNM
MNEHSSRSHSIFLINIKQENVETEKLSGKLYLVDLAGSEKVKXAKNINKSLSALGNVISALAEGTKTHVPYRDSKMTRILQDSLGGNCRTTIVICCPSPVF
NEAETKSTLMFGQRAKTIKNTVSNLETAEEWKKYEKEKE

>d1i6ia_c.37.1.9 (A;) Kinesin {Mouse (*Mus musculus*), kif1a}

GASVKAVVRVPFNSREMSRDSKCIQMSGTTIVNPQPKETPKSFSDYWSHTSPEDINYASQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTG
AGKSYTMMGKQEKDQQGIIPQLCEDLSRINDTTNDNMSYSVEVSYMEIYCERVRDLPNPKNKGRLVREHPLLGPYVEDLSKLAVTSYNDIQDLM
DSGNKARTVAATNMNETSSRSSHAVFNIIFTQKRHDAETNITTEKVKISLVDLAGSERADSTGAKGTRLKEGANINKSLTLGKVISALAEMDSGPKN
KKKKKTDIFPYRDSVLTWLLRENLLGGNSRTAMVAALSPADINYDETLSTLRYADRAKQIRNTVSVNHHHHH

>d1i6a_c.37.1.9 (A;) Kinesin {Human (*Homo sapiens*), mitotic kinesin eg5}

GKNIQVVVRCPFNLAERKASAHSIVECDPVRKEVSRTGLADKSSRKTYTFDMVFGASTKQIDVYRSVCPILDEVIMGYNCTIFAYGQTGTGKTF
TMEGERSPNEEYTWEEDPLAGIIPRTLHQIFEKLTNGTEFSVKSLLEIYNEELFDLLNPSSDVSERLQMFDDPRNKRKGVIKGLEEITVHNKDEVYQIL
EKGAAKRTTAATLMNAYSSRSSHSVFSVTHMKETTIDGEELVKIGKLNLVDLAGSENIGRSGAVDKRAREAGNIQSLTLGRVITALVERTPHVPYRES
KLTRILQDSLGGRTTSIIATISPASLNLEETLSTLEYAHRAKNILNKPEV

>d1goja_c.37.1.9 (A;) Kinesin {Neurospora crassa}

SSANSIKVVARFRPQNRVEIESGGQPIVTFQGPDTCTVDSKEAQGSFTFDRVFDMSCQSDIFDFSIKPTVDDILNGYNGTVFAYGQTGAGSYTM
MGTSIDDPDGRGVIPRIVEQIFTSILSSAANIEYTVRSYMEIYMERIRDLLAPQNDNLPVHEEKNRGVYVKGLLEIYVSSVQEYEVMRGGNARAV
AATNMNQESSRSHSIFVITITQKNVETGSAKSGQLFLVLAGSEKVGKTAGSGQTLEEAKKINKSLSALGMVINALTGKSSHVPYRDSKLTRILQESLG
GNSRTTLIINCSPSSYNTAETLSTLRFGMRAKSINKAKVNAELSPAELKQMLAKAKTQ

>d2ncda_c.37.1.9 (A;) Kinesin motor Ncd (non-claret disjunctional) {Fruit fly (*Drosophila melanogaster*)}

LRQRTEELLRCNEQQAAELETCKEQLFQSNMERKELHNTVMDLRGNIRVFCRIRPLEEENRMCCWTYHDESTVELQSIDAQAKSKMGQQIFS
DQVFHPLSSQSDIFEMVSPLIQSALDGYNICIFAYGQTGSGKTYTMDGVPESVGVIPRTVLLFDSIRGYRNGLWEYEIKATFLEIYNEVLYDLSNEQK
DMEIRMAKNNKNDIYVSITEETVLPNHLRHLMTAKMNRTASTAGNERSSRSHAVTKLELIGRHAEKQEISVGSINLVLAGSESPTSTRMTET
KNINRSLSELTNVILALLQKDHIPYRNSKLTLLMPSLGGNSKLMFINVSPFQDCFQESVKSLRFAASVNSC

>d1f9va_c.37.1.9 (A;) Kinesin motor Ncd (non-claret disjunctional) {Baker's yeast (*Saccharomyces cerevisiae*), Kar}

GNIRVYCRIRPALNKLENSDTSLINVNEFDDNSGVQSMEVTKIQNTAQVHEFKFDKIFDQQDTNVDFKEVGQLVQSSLGYNVCIFAYGQTGSGKT

FTMLNPGDGIIPSTISHIFNWINKLTKGWDYKVNCIEFIEIYNENIVDLRSDDNNNKEDTSIGLKHEIRHDQETKTTITNTSCKLESEEMVEIILKKAN
KLRSTASTASNEHSSASHSIFIILSGSNAKTGAHSYGTNLVLAGSERINVSQVGDRLRETQNINKSLCLGDIHALGQPDSTKRHIFRNSKLTYLL
QYSLTGDSKTLMFVNISPSSHHINETLNSRFASKVNSTRV
>d1byi_c.37.1.10 (-) Dethiobiotin synthetase {Escherichia coli}
SKRYFVTGTDTEVGKTVASCALLQAAKAAGYRTAGYKPVASGESEKTPEGLRNSDALALQRNSSLQLDYATVNPYTFAEPTSPHIISAQEGRPIESLMSA
GLRALEQQADWVLVEGAGGWFTPLSDTFTADWVTQEQLPVILVVGVLGCINHAMLTAQVIQHAGLTLAGWVANDVTPPGKRHAEYMTTLR
MIPAPLLGEIPWLAENPENAATGKYINLL
>d1qf5a_c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Escherichia coli}
GNNVVVLGTQWGDEGKGKIVDLTERAKYVVRYQGGHNAGHTLVINGEKTVLHLIPSGILRENTSIIGNGVVLSPALMKEMKELEDRGIPVRERLL
LSEACPLILDYHVALDNAREKARGAKAIGTTGRGIGPAYEDKVARGLRVGDLFDKETAELKEVMEYHNFQLVNYYKAЕAVDYQVKLDDTMAVAD
ILTSMVVDVSDLLDQARQRGDFVMFEAQGTLIDHGTYPVTSSNTAGGATGSGLGPYVDDYVLGILKAYSTRVGAGPFPTELFDETGEFLCKQ
GNEFGATTGRRRTGWLDTVAVRRAVQLNSGFCLTKLDVLGLKEVKLCVAYRMPDGREVTTPLAADDWKGVEPIYETMPGWSESTFGVKDR
SGLPQAALNYIKRIEELTGVPIDIISTGPDRTETMILRDPFA
>d1dj2a_c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Mouse-ear cress (Arabidopsis thaliana)}
IGSLSQVSGVLCQWGDEGKGKLVILAQHFDIVARCQGGANAGHTIYNSEGKKFALHLVPSGILNEDTCVINGVHVLPGLFKEIDGLESNGVSC
KGRILVSDRAHLLFDHQEVDFLRESELAKSFIGTTKRGIGPAYSSKIRNGIRVGDLRHMDSLQKLDLLSDAAARFQGFKYTPEMLREEVEAKRYA
DRLEPYITDTVHFINDISQKKVLVEGGQATMLIDFGTYPVTSSPSAGGICTGLGIAPSVVGDLIGVVKAYTRVSGGPFTENLGTGGDRLLAG
QEFGTTTGRPRRCGWLIDIVALFSCQINGFASLNLTKLDVSDLNEIQLGVAYKRSRGDTPVKSFPGLRLEELHVEYEVLPGWKSDISSVRNYSLDPKA
AQQYVERIEELVGVPHYIGIGPGGRDALIYK
>d1dj3a_c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Bread wheat (Triticum aestivum)}
ADRVSSLSNVSGVLSQWGDEGKGKLVDLAPRFDIVARCQGGANAGHTIYNSEGKKFALHLVPSGILHEGTLCVVGNGAVIHVGPGFFEIDGLQSN
GVSCDGRILVSDRAHLLFDLHQTVDFLREELANSFIGTTKRGIGPCYSSKVRNGLRCVCDLRHMDSLQKLDVLFEDAARFEGFKYSKGMILKEEVE
RYKKFAERLEPFIADTVHVLNESIRQKKKILVEGGQATMLIDFGTYPVTSSPSAGGICTGLGIAPRVIGDLIGVVKAYTRVSGGPFTELLGEEGDIV
LRKAGMЕFGTTTGRPRRCGWLIDIVALKYCCDINGFSSLNLTKLDVSLGLPEIKLGVSYNQMDGEKLQSFPGDLDTLEQVQVNYEVLPGWSDISSVR
SYSELPQAARRYVERIEELAGVPVHYIGVGPGGRDALIYK
>d1j4ba_c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Mouse (Mus musculus)}
AAATGSRTVVLGAQWGDEGKGKVV DLLADIVSRCQGGNNAGHTVVVDGKEYDFHLLPSGIINTKAVSFIGNGVVIHPLGLFEEAKNEKKGL
KDWEKRLIISDRAHLLFDHQAVDGLQEVQRQAQEGKNIGTTKGIGPTYSSKAARTGLRICDLSDFEFSARFKNLAHQHQSMFPTLEIDVEGQLK
RLKGFAERIRPMVRDGVFMYEALHGPPKKVLEGANAAALLDIDFGTYPVTSSNCTVGGVCTGLGIPPQNIQDVYGVVKAYTRVIGAFPTEQINE
IGDLLQNRGHEWGVTTGRKRCGWLDMILRYAHMVNGFTALALTLDILVSEIKVGISYKLNKGRIPYFPANQEILQKVEVEYETLPGWKADTTG
ARKWEDLPPQAQSYYRFVENHMGAVKVGVKSGRESMIQLF
>d1eg7a_c.37.1.10 (A:) Formyltetrahydrofolate synthetase {Moorella thermoacetica}
DIEIAQAAMKPKVMEARGLGIQEDEVELYGKYKAKISLDVYRRLKDPDKLILVTAITPTPAGEGKTTSVGLTDALARLGKRVMVCLREPSLGPFG
IKGGAAGGGYAQVVPMEDINLHFTGDIHAVTYAHNLLAAMVDNHLLQQGNVLNIDPRTITWRRVIDLNERALRNIVIGLGGKANGVPRETGFDISVA
SEVMACLCLASDLMDLKERFSRKVVGTYDGKPVTAGDLEAQGSMALLMKDAIKPNLVQTLENTPAFIHGGPFANIAHGCNSIIATKALKLADYVVT
EAGFGADLGAEKFYDVKCRYAGFKPDATVIVATVRALKMHGGSVPKSDLATENLEALREGFANLEKHNIKGFGVPAVVAINAFPTDEAELNLLYELC
AKAGAEVALSWAKGGEGGLELARKVLQTLERSPSNFHVLYNLDLSIKDKIAKIATEIYGADGVNYTAEADKAIQRYESLGYGNLPVVMAKTQYSFSD
MTKLGRPRNFTITVREVRSLAGGRILVPIGAIMTMPGLPKRPAACNIDIDADGVIT
>d1fp6a_c.37.1.10 (A:) Nitrogenase iron protein {Azotobacter vinelandii}
AMRQCAIYGKGGIGKSTTQNVLAALEMGGKVMIVGCDPKADSTRLLHSAQNTIMEMAAEAGTVEDLELEDVLKAGYGGVKCVESGGPEPGV
GCAGRGVITAINFEEGAYEDDFVYDVLGVCGGFAMPIRENKAQEIYIVCSGEMMAMYAANNISKGIVKYANSGSVRLGGLICNSRNTDRE
DELIALANKLGTQMIHFVPRDNVVQRAEIRRMTVIEYDPKAKQADEYRALARKVVDNKLVIPNPITMDELELLMEFGIMEVEDESIVGKTAEEV
>d1cp2a_c.37.1.10 (A:) Nitrogenase iron protein {Clostridium pasteurianum}
MRQVAIYGKGGIGKSTTQNLTSGLHAMGKTIMVVGCDPKADSTRLLGGLAQKSVLDTLREEGEDVELDSILKEGYGGIRCVESGGPEPGVGAGR

GIITSINMLEQLGAYTDDLDYFVYDVLGVCGGFAMPIREGKAQEYIIVASGEMMALYAANNISKIQKYAKSGGVRLGGIICNSRKVANEYELDAF
AKELGSQLIHVFPRSPMVTKAEINKQTIVIEYDPTCEQAEEYRELARKVDANELFVIPKPMTQERLEEILMQYG
>d1hyqa_c.37.1.10 (A:) Cell division regulator MinD {Archaeon Archaeoglobus fulgidus}
VRTITVASGKGGTGKTTITANLVALAQLGHDTIVDADITMANLELILGMEGLPVTLQNVLAGEARIDEAIYVGPGGVKVPAGVSLEGLRANKPEK
LEDVLTLQIMESTDILLDAPAGLERSAVIAIAAAQELLVVNPEISSITDGLKTIVAEERLGTKVLGVVNRITTLGIEMAKNEIEAILEAKVIGLIPEDPEVR
RAAAYGKPVVLRSPPNSPAARAIVELANYIA
>d1g3qa_c.37.1.10 (A:) Cell division regulator MinD {Archaeon Pyrococcus furiosus}
MGRIISIVSGKGGTGKTTVTANLSVALGDRGRKVLAVDGDLTMANLSLVGVDDPDVTLHDVLAGEANVEDAIYMTQFDNVYVLPGAVDWEHVLK
ADPRKLPEVKSLKDKFDFILDCPAGLQLDAMSAMLSGEAEALLVTNPEISCLDTMKVGIVLKKGALILGFVLNRYGRSDRDIPPEAAEDVMEVPLA
VIPEDPAIREGTLEGIPAVKYKPESKGAKAFVLAEEIEKLA
>d1iona_c.37.1.10 (A:) Cell division regulator MinD {Archaeon Pyrococcus horikoshii}
MTRIISIVSGKGGTGKTTVTANLSVALGEMGRKVLAVDGDLTMANLSLVGVDDVNITLHDVLAGDAKLEDAIYMTQFENVYILPGAVDWEHVIKAD
PRKLPEVKSLKGKYDFILDCPAGLQLRAMSAMLSGEAEALLVTNPEISCLDTMKVGIVLKKGALILGFVLNRYGRSERDIPPEAAQDVMDVPLAVI
PEDPVIREGTLEGIPAVKYKPESKGAKAFVLAEEIEKLA
>d1jpn2 c.37.1.10 (A:89-296) GTPase domain of the signal sequence recognition protein Ffh {Thermus aquaticus}
EARLPVLKDRNLWFLVGLQGSGKTTAAKLALYYKGKGRPPLLVAADTQRPAAREQLRLGEKVGVPLEVMDGESPESIRRRVEEKARLEARDLILVD
TAGRLQIDEPLMGELARKEVLPDDEVLLVLDAMTQEQALSVARAFDEKVGVTGLVTKLDGDARGGAALSARHVTGKPIYFAGVSEKPEGLEPFYPE
RLAGRILGMGD
>d1j8mf2 c.37.1.10 (F:87-297) GTPase domain of the signal sequence recognition protein Ffh {Archaeon Acidianus ambivalens}
DKEPKVIPDKIPYVIMLVGVQGTGKTTAGKLAYFYKKKGFKVGLVGADVYRPAALEQLQLQQQIGVPVYGEPEKDVVGIAKRGVEKFLSEKMEII
VDTAGRHYGEEAALLEEMKNIYEAIKPDEVTLVIDASIGQKAYDLASKFNQASKIGTIITKMDGTAKGGAALSAVAATGATIKFIGTGEKIDELEVFN
RRFVARLHHHH
>d1fts_2 c.37.1.10 (285-495) GTPase domain of the signal recognition particle receptor FtsY {Escherichia coli}
PLNVEGKAPFVILMVGNGVGKTTIGKLARQFEQQGKSVMLAAGDTFRAAAVEQLQVWGQRNNIPVIAQHTGADSASVIFDAIQAAKARNIDVL
IADTAGRLQNKSMLMEELKKIVRVMKKLDVEAPHEVMLTIDASTGQNAVSQAKLFHEAVGLGITLKDGTAKGGVIFSADQFGIPIRYIGVGERIED
LRPFKADDFFIEALFAR
>d1ihu1 c.37.1.10 (A:1-296) Arsenite-translocating ATPase ArsA {Escherichia coli}
MQFLQNIPPYLFFTGKGGVGKTSISCATAIRLAEQGKRVLVSTDPASNQVFSQTIGNTIQAIASVPGLSEIDPQAAAQQYRARIVDPIKGVLPDD
VVSSINEQLSACTTEIAAFDEFTGLTDASLLTRFDHIIFDAPTGHTIRLLQLPGAWSSFIDSNSPEGASCLGPMAGLEKQREQYAYAVEALSDPDKRTL
VLVARLQKSTLQEVARTHLELAAIGLNQYLVINGVLPKTEAANDTLAAIWEREQEAALANLPADLAGLPTDTLFLQPVNVMGVGSALSRLLSTQP
>d1ihu2 c.37.1.10 (A:308-586) Arsenite-translocating ATPase ArsA {Escherichia coli}
QRPDIPSLSALVDDIARNEHGLIMLMGKGGVGKTTMAAAIAVRLADMGFVHLTTSDPAHLSMTLNGSLNQLQSRIDPHEETERYRQHVLETKG
KELDEAGKRLLEDLRSPCTEEIAVQAFSRVIREAGKRFVVMMDTAPTGHTLILLDATGAYHREIAKKMGEKGHFTTPMMLLQDPERTKVLLVTLPETT
PVLAAANLQADLERAGIHPWGWIINNSLISADTRSPLLRMRAQQELPQIESVKRQHASRVALPVLAEPGTIDKLKQLAGHHH
>d2reb_1 c.37.1.11 (3-268) RecA protein, ATPase-domain {Escherichia coli}
DENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSDLIALGAGGLPMGRIVEIYGPESSGKTTLQVIAAAQREGKTCFIDAHEHALD
IYARKLGVDIDNLLCSQPDTEQALEICDALARSGAVDVIVVDSVAALTPKAEIEGEIGDSHMLAARMMSQAMRKLAGNLKQSNTLLFINQIRMKI
GVMFGNPETTGGNALKFYASVRDIRRIGAVKEGENVVGSETRVKVVKNKIAAPFKQAEFQJLYGEGI
>d1g19a1 c.37.1.11 (A:1-269) RecA protein, ATPase-domain {Mycobacterium tuberculosis}
MTQTPDREKALELAVAQIEKSYGKGSVMRLGDEARPISVIPTGSIALDVALGIGGLPRGRVIEIYGPESSGKTTVALHAVANAQAAGGVAAFIDA
LDPDYAKKLGVTDSSLVSPDTGEQALEIADMLIRSGALDIVVDSVAALPRAELEGEMGDSHVGLQARLMSQLRKMTGALNNSGTTAIFINQL
RDKIGVMFGSPETTGGKALKFYASVRMDVRRVETLKGTVGNRTRVKVVKNKCLAPFKQAEFDILYGKGI
>d1cr1a_c.37.1.11 (A:) Gene 4 protein (g4p, DNA primase), helicase domain {Bacteriophage T7}
MRERIREHLSSESVGLLFGCCTGINDKTLGARGEVIMVTSQSGMKGKSTFVRQQALQWGTAMGKKVGLAMLEESVEETAEDLIGLHNRRVRLRQS

DSLKREIIENGKFDQWFELFGNDTFHLYDSFAEAETDRLLAKLAYMRSGLGCDVIILDHISIVVSAGESDERKMDNLMTKLGFAKSTGVVLVVICH
LKNPDKGKAHEEGRPVSITDLRGSGALRQLSDTIIALERNNQQGDMPNVLVRILKCRFTGDTGIAGYMEYNKETGWLEPSSY

>d1g8ya_c.37.1.11 (A:) Hexameric replicative helicase repA {Escherichia coli, plasmid rsf1010}

ATHKPINILEAFAAAAPPPLDYVLPNMVAGTVGALVSPGGAGKSMLALQLAAQIAGGPDLLEVGELEPTGPVIYLPAAEDPPTAIHHLHALGAHLSAER
QAVADGLLIQPLIGSLPNIMAPEWFGLKRAAEGRRLMVLDLTLRRFHIEENASGPMAQVIGRMEAIAADTGCISVFLHHASKGAAMMGAGDQQ
QASRGSSVLDNIRWQSylssMTSAEAEEWGVDDQRRFFVRFGVSKANYGAPFADRWFRRHDGGVLKPA

>d1e9ra_c.37.1.11 (A:) Bacterial conjugative coupling protein TrwB {Escherichia coli}

VGQGEFGGAPFKRFLRGTRIVSGGKLKRM TREKAKQVTAGVPMRDAEPRHLLNGATGTGKSLLRELAYTGLLRGDRMVIVDPNGDMLSKFG
RDKDIIINPYDQRTKGWSFFNEIRNDYDWQRYALS VVPRGKTDEAEWASYGRLLRETAKKLALIGTPSMRELFHWTTIATFDDL RG FLEGTLAESL
AGSNEASKALT SARFVLSKLPEHV TMPDGFSIRSWLED P N GGN L F IT WRED M GP AL RPL IS AWV D V CTS ILS L PEEPK RRLWLF IDE LAS LEK L AS
LAD AL TKGRKAGL RVVAGL QSTS QL DDV YGV K EA QT L RAS FRSL VV LGGS RT DP K TN ED M S L S L G E HEVERDRYS K NTG K HH STG RA L ER VR ER VV
MPAEIANLPDLTAYVG FAGRPIAKV PLEIKQFANRQPAFVEGT

>d1e79a3 c.37.1.11 (A:95-379) Central domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

VDVPVGEELLGRVVDALGNAIDKGKPIGSKARRVGLKAPGIIPRISVREPMQTGIKAVDSLVPIGRGQRELIIGDRQTGKTSIAIDTIINQKRNDGTD
EKKKLYCIYVAIGQKRSTVAQLVKRLTDADAMKYTIVS ATASDAAPLQY LAPYSGCSMGEYFRDNGKH ALIYDDLSKQAVAYRQMSLLRRPPGREA
Y PGDV FYLHSRLERA AKM ND AFGG S LTALPV ETQAGD VSAY IPTN VISIT DGQI FLE TELFYKGIRPA INV GLS VSR VGSAQ

>d1e79d3 c.37.1.11 (D:82-357) Central domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

IRIPVG PETLGRIMNVIGEPIDERGPIKTKQFAAIHAEAPEF VEMS VEQE ILVTGIKVVDLLAPYAKGGKIGLFGGAGVGKTVLIMELINNVA KAHGGY S
VFAGVGERTREGNDLYHEMIESGVINLK DATSKVALVYQMNEPPGARARVALTGLTV AEYFRDQEGQDVLLFIDNI FRFTQAGSEV S ALL GRIPSAV
GYQPTLATDMGT M QER ITT KKGSITSVQAIYV PADDL TD PAPATT FAH LD ATT VLS RAI AELG IYPAV DPL DSTS RI

>d1skyb3 c.37.1.11 (B:96-371) Central domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

EV PVGETLIGRVNPLGQPV DGLGPVETT ETRPIESRAPGVMDRRSVHEPLQTG KAI DALVPIGRGQRE LIIGDRQTGKTSVA IDTI INQKDQ NMIC Y
VAIGQKESTVATV VETLA KH GAPD YTI VVTASASQPAPLLF LAPYAGVAMGEYFMIMGKH VLV IDDL SKQAA YRQMSLLRRPPGREA YPGDIFYL H
SRLLERA AKLSDAKGG S LTALPFV ETQAGD ISAY IPTN VISIT DGQI FLC SDL FFSG V RPAINAGL SVR VGAAQ

>d1sky e3 c.37.1.11 (E:83-356) Central domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

ISPVGQV TLGRV FNVLGE PIDE GLDIPADAR RDPI HR PAPK FEELATE VEI LETGIKVVDLLAPYIKGGKIGLFGGAGVGKTVL IQELIH NI AQEHGGIS V
FAGVGERTREGNDLYHEM KDSGVIS KTAMVFGQMNEPPGARM RVALTGLT MAEYFRDQEGQDGLL FIDNIFRFTQAGSEV S ALL GRM PSAIGYQP
T LATE MGQLQER ITSTAKGSITSIQAIYV PADDY TD PAPATT FSHLD ATT NLERK LAEM GIYPAV DPLV STS RALAP

>d1fx0a3 c.37.1.11 (A:97-372) Central domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

QIPVSEAYLGRVINALAKPIDGRGEITASESRLIESPAPGIMSRRS VYEPLQTGLIAIDAMIPVGRGQRELIIGDRQTGKTA VATDTILNQQQN VCVY V
AIGQKASSVAQV VTNFQER GAMEY TIVVA ETADSPATLQY LAPYTGAA LAEYFMYRERHTL IIYDDLSKQAAQYRQMSLLRRPPGREA YPGDVFY LH
SRLLERA AKLSSLLGE GSMT ALPIV ETQAGD VSAY IPTN VISIT DGQI FLSADLFNAGIRPA INV G ISV SRV GSAAQ

>d1fx0b3 c.37.1.11 (B:98-377) Central domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

LSVPVGGPTLGRIFNV LGE PV DNLRPV DTRT SPIH RSA PAFT QLDTKLSIFETGIKV VNLLAPYRGGKIGLFGGAGVGKTVLIMELINNIAK AHGGV S
VFGVGERTREGNDLYMEMKESGVINEQ NIAESKVALVYQMNEPPGARM RVGLT ALTMAEYFRDVNEQDVLLFIDNIFRFTQAGSEV S ALL GRM
PSAVGYQPTL STEM G S L QER ITST KEGSITSIQAVYV PADDL TD PAPATT FAH LD ATT VLS RGLA AKGIYPAV DPL DSTS MLQ P

>d1cbua_c.37.1.11 (A:) Adenosylcabinamide kinase/adenosylcabinamide phosphate guanyltransferase CobU {Salmonella typhimurium}

MILVTGGARSGKSRHAEALIGDAPQVLYIATSQLDEMAARIQHHKDGRPAHWRTAECWRHLDLTITADLAPDDA ILLCITTMVTNLLF ALGGEND
PEQWDYAA MER AID DEI QLIAACQRC PAKV VL VTNE VMGIVPEN RLARHFRDIAGRVNQRLAAADEVWLVSGIGV KIK

>d1g5ta_c.37.1.11 (A:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}

ERGIIIVFTGNGKGKTTA AF GTAARAVGHGKNVGVVQFI KGTWPNGERNLLEPHGVEFQVMATGFTWETQNREADTAACMAVWQHGKRMLAD

PLLDLWVVLDELTYMVAYDYLPLEEVISALNARPGHQTVIITGRGCHRDILDLADTVSELRPVKHA

>d1g64b_c.37.1.11 (B:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}

QQRQQKVKDVRDARVAQAQEERGIIVFTGNGKGKTTAAFGTAARAVGHGKNVVQFIKGTWPNGERNLLEPHGVEFQVMATGFTWETQNRE

ADTAACMAVWQHGKRMЛАDPLDMWVVLDELTYMVAYDYLPLEEVISALNARPGHQTVIITGRGCHRDILDLADTVSELRPVKHAFDAGVKAQMGI
DY

>d1b0ua_c.37.1.12 (A:) ATP-binding subunit of the histidine permease {Salmonella typhimurium}

NKLHVIDLHKRYGGHEVLKGVSQARAGDVSIIGSSSGKSTFLRCINFLEKPSEGAIIVNGQNIINLRDKDGQLKVADKNQLRLRTRLTMVFQHFН
LWSHMTVLENVMEAPIQVGLSKHDARERALKYLAKVGIDERAQGKYPVHLSGGQQQRVSIARALAMEPDVLLFDEPTSALDPELVGEVLRIMQQL
AEEGKTMVVVTHEMGFARHVSSHVIFLHQGKIEEGDPEQVFGNPQSPRLQQFLKGSSLKLEH

>d1g6ha_c.37.1.12 (A:) MJ1267 {Archaeon Methanococcus jannaschii}

TMEILRTENIVKYFGEFKALDGVSISVNKGDTVLIIGPNGSGKSTLINVTGFLKADEGRVYFENKDITNKEPAELYHYGIVRTFQTPQPLKEMTVLENLLI
GEICPGESPLNSLFYKKWIPKEEEMVEKAFAKILEFLKLSHLDRKAGELSGGQMKLVEIGRALMTNPKMIVMDEPIAGVAPGLAHDIFNHVLELKAGI
TFLIIERLIDLVNYIDHLYMFNGQIIAEGREEEIKNVLSDPKVVEIYIGE

>d1f3oa_c.37.1.12 (A:) MJ0796 {Archaeon Methanococcus jannaschii}

MIKLKNVTKYKMEEIIYALKNVNLNIKEGEFVSIMPGSGKSTMLNIIGCLDKPTEGEVYIDNIKTNDLDDDELTKIRRDKGIVFQFNLIPLTALE
NVELPLIFKYRGAMSGEERRKRAECLKMAELEERFANHKNPQLSGGQQQRVAIARALANNPPIIADEPGTGALDSKTGEKIMQLKKLNEEDGKTV
VVVTHDINVARFGERIIYKLGEVEREELKRGF

>d1jj7a_c.37.1.12 (A:) Peptide transporter Tap1, C-terminal ABC domain {Human (Homo sapiens)}

GLLTPLHLEGVLVQFQDVFSAYPNRPDVVLQGLTFLRPGEVTALVGPNGSGKSTVAALLQNLQPTGGQLLDGKPLQYEHRYLHRQVAAVGQEPQ
VFGRSLQENIAYGLTQKPTMEEITAAAVKSGAHSFISGLPQGYDTEVDEAGSQLSGGQRQAVALARALIRKPCVLILDDATSALDANSQLQVEQLLYES
PERYSRSVLLITQHLSLVEQADHILFLEGGAIREGGTHQQQLMEEKKGCYWAMVQA

>d1g2912_c.37.1.12 (1:1-240) Maltose transport protein MalK, N-terminal domain {Archaeon Thermococcus litoralis}

MAGVRLVDWVKVFGEVTVARMSLEVKGDFMILLGPSGCGKTTLRMIAGLEEPSRGQIYIGDKLVADPEKGIFVPPKDRDIAMVFQSYALYPHMT
VYDNIAFPLKLRKVPRQEIDQRVREVAELLGLTELLNRKPRELSSGGQRQVALGRAIVRKPVFLMDEPLSNLDAKLRVRMRAELKKLQRQLGVTTIY
VTHDQVEAMTMDRIAVMNRGVLQQVGSPDEVYDKPANTFVAGFI

>g1f2t.1_c.37.1.12 (A.;B:) Rad50 {Archaeon Pyrococcus furiosus}

MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFTKVGARDTYIDLIFEKDGTYRITRRFLKGYSSGEIHAK
RLVGNEWKHVTEPSSKAISAFMEKLIPYNIFLNAYIRQGQIDALESXAREAALSKIGELASEIFAETEGKYSEVVRAEENKVRFLVWEGKERPLTFL
SGGERIALGLAFRLAMSPLYLAGEISLLIDEPPTYLDEERRRKLTIMERYLKKIPQVILVSHDEELKDAADHVIRISLENGSSKVEVVS

>g1ii8.1_c.37.1.12 (A.;B:) Rad50 {Archaeon Pyrococcus furiosus}

MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFTKVGARDTYIDLIFEKDGTYRITRRFLKGYSSGEIHAK
RLVGNEWKHVTEPSSKAISAFMEKLIPYNIFLNAYIRQGQIDALESDEAREKVVRREVNLNDKFETAYKKLSELKTTINRNRIKEYRDILARTEXRERVKKEI
KDLERAKDFTEELIEKVKKYKALAREAALSKIGELASEIFAETEGKYSEVVRAEENKVRFLVWEGKERPLTFLSGGERIALGLAFRLAMSPLYLAGEISL
LILDEPTPYLDEERRRKLTIMERYLKKIPQVILVSHDEELKDAADHVIRISLENGSSKVEVVS

>d1e69a_c.37.1.12 (A:) Smc head domain {Thermotoga maritima}

MRLKKLYLGKFSGRPSLIGFSDRVTAIVGPNGSGKSNIIDA WKVFGEQSKKELRASEKFDMIFAGSENLPAGSAYVELVFEENGEEITVARELKRTG
ENTYYLNGSPVRLKDIRDRFAGTGLGVDFYSIVGQGQIDRIVNASPEELRLESSKHPTSLVPRGSYQRVNESFNRFISLLFFGGEGRLNIVSEAKSILDAG
FEISIRKPGRRDQKLSLLSGGEKALVGLALLFALMEIKPSPFYVLDEVDSLDDYNAERFKRLLKENSHTQFIVITHNKIVMEAADLLHGVTMVNGSA
IVPVEV

>d1qhl_a_c.37.1.12 (A:) Cell division protein MukB {Escherichia coli}

RGKFRSLTLINWNGFFARTFDLDELVTLSSGGNGAGKSTTMAAFVTALIPDLTLLHFRNTTEAGATSGSRDKGLHGKLKAGVCYSMLDTINSRHQRVV
VGVRLLQQVAGRDRKVDIKPFAIQGLPMSVQPTQLVTETLNERQARVPLNELKDKLEAMEGVQFKQFNSITDYHSLMFDLGIIARRRSASDRSKFYR
LIEASLYGGISSAITRSRSLRDYLLPEN

>d1ewqa2_c.37.1.12 (A:542-765) DNA repair protein MutS, the C-terminal domain {Thermus aquaticus}

YVRPRFGDRLQIRAGRHPVVERRTEFPNDLEMAHELVLITGPNMAGKSTFLRQTALIALLAQVGFSVPAEEAHPLFDGIYTRIGASDDLGGKSTF
MVE MEEVALILKEATENSLVLLDEVGRGTSSLDGVAIATAEALHERRAYTLFATHYFELTALGLPRLKNLHVAAREEAGGLVFYHQVLPGPASKSYGV
EVAAMAGLPEVKVARARALLQAMAAR

>d1e3ma2 c.37.1.12 (A:567-800) DNA repair protein MutS, the C-terminal domain {Escherichia coli}
YTCPTFIDKPGIRITEGRHPVVEQVLNEPIANPLNLSQRRMLIITGPNMGGKSTYMRQTA LIALMAYIGSYVPAQKVEIGPIDRIFTRGAADDLASG
RSTFMVEMTETANILHNATEYSLVMDEIGRTSTYDGLSLAWACAENLANKIKALTIFATHYFELTQLPEKMEGVANVHDALEHGDTIAFMHSVQ
DGAASKSYGLAVAALAGVPKEVIKRARQKLRELESIS

>d1pj_1 c.37.1.13 (1-318) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}
MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFTNAKAAREMRERVQSLLGAAEDVVISTFHSMC
VRILRRDIDRIGINRNFSILDPTDQLSVMKTI LKEKNIDPKKFEPRTILGTISA AKNELLPEQFAKRASTYYEVSDVYQEYQQRLLRNHSDFDDLIMT
TIQLFDRVPDVLYHQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNICAVGDADQSIYRWRGADIQNLSFERDYPNAKVILLEQNYRSTKRILQAAN
EVIEHNVNRKPKRWTENPEG

>d1pj_2 c.37.1.13 (319-651) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}
KPILYYEAMNEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANI PYQIVGGLKFYDRKEIKDILAYLRVIANPDDDSLRLIINVP
KRGIGASTIDKLVRYAADHESLFEALGELEMIGLAKAAGALAAFRS QLEQWTQLQEYVS VTELVEEVLDKSGYREMLKAERTIAQSRLENLDEFLS
VTKH FENVSDDKS LIAFLTD LALISDLDELDGTEQAAEGDAVMLMTLHAAKGLEFPVVFLIGMEEGIFPHNR SLEDDDEMEEERRLAYVGITRAEEELV
LTSAQMRTLFGNIQMDPPSRFLNEIPAHLLETASR

>g1qhh.1 c.37.1.13 (A;B;C;D:) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}
MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFTNAKAAREMRERVQSLLGAAEDVVISTFHSMC
VRILRRDIDRIGINRNFSILDPTDQLSVMKTI LKEKNIDPKKFEPRTILGTISA AKNELLPEQFAKRXYYEVSDVYQEYQQRLLRNHSDFDDLIMTTI
QLFDRVPDVLYHQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNICAVGDADQSIYRWRGADIQNLSFERDYPNAKVILLEQNYRSTKRILQAANEV
IEHNVNRKPKRWTENPEGK PILYYEAMNEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANI PYQIVGGLKFYDRKEIKDILAY
LRVIANPDDDSLRLIINVPKRGIGASTIDXLFEALGELEMIGLAKAAGALAAFRS QLEQWTQLQEYVS VTELVEEVLDKSGYREMLKAERTIAQSR
ENLDEFLSVTKH FENVSDDKS LIAFLTD LALISXGDAVMLMTLHAAKGLEFPVVFLIGMEEGIFPHNR SLEDDDEMEEERRLAYVGITRAEEELVLTSAQ
MRTLFGNIQMDPPSRFLNEIPAHLLETASR

>d1uaaa1 c.37.1.13 (A:2-307) DEXX box DNA helicase {Escherichia coli, RepD}
RLNPGQQQAVEFVTGPCLLAGAGSGKTRVITNKIAHLIRGCGYQARHIAAVFTNKAAREMKERVGQTLGRKEARGLMISTFHTLGLDIKREYAAL
GMKANFSLFDDTDQALLKELTEGLIEDDKVLLQQLISTISNWKNDLKTPSQAASAIGERDRIFAHCYGLYDAHLKACNVLDFFDDILLPTLLQANEE
VRKRWQN KIRYLLVDEYQDTNTSQYELVKLLVGSRARFTVVGDDDSIYSWRGARPQNLVLSQDFPALKVIKLEQNYRSSGRILKAANILIANNPHV
FEKRLFSELG

>d1uaaa2 c.37.1.13 (A:308-640) DEXX box DNA helicase {Escherichia coli, RepD}
YGAELKVL SANNEEHEAERV T GELIAHHFVNKTQYKDYL RGNHQS RVEKFLMQN R I PYKISGGTSFFS RPEIKDLLAYLRVLTNPDDSAFLRIVN
TPKREIGPATLKKLGEWAMTRNKS MFTASFDMGLSQLTSRGYEA LTRFTHWLAEIQRLAEREPIAAVRDLIHGM DYEWLYETSPSPKAAEMRMK
NVNQLFSWMTEMLEGSELDEPM T LQV VTRFTL RDMMERGESEEE LDQVQLMTLHASKGLEFPYVYMG MEEGFLPHQSSIDE NIDEERRLAY
VGITRAQKELTFLCKERRQYGE VRPEPSRFLLELPQDDLIW

>d1hv8a1 c.37.1.13 (A:3-210) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}
VEYMFNFELNLSDNILN A IRNKGFEKPTDIQMVKV I PLFLNDE YNIVA QARTGSGKTASFAIPLIELVNENNGIEAI ILPTRELAIQVADEIESLKGKNLKI
AKIYGGKAIY P QIKALK NANIVV GTPGRILDH INRGTNLKNV KYFILDEADEMLNMGFIDV EKILNACNKDKRILLFSATMPREI LN LAKKYM GDY SF
IKAKI

>d1hv8a2 c.37.1.13 (A:211-365) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}
NANIEQS YVEVNENERFEALCRL KNKEFYGLVFC KTKRDTKELASMLR D IGF KAGAI HGDL SQREKVIRLFKQKKIRI IATD VMSRG IDVNDLNCV
INYHLPQNPESYMH RIGRTGRAGKKG KAI SIINR REYKKL RYIERAMKL KIKKLK

>d1gm5a3 c.37.1.13 (A:286-549) RecG helicase domain {Thermotoga maritima}
ETLPERILEKRKLLGVKDAYYGMHFPKTFYHLEKARERLAYELFVLQLA FQKIRKEREK HGGIPKKIEGKLAEEFI KSLPFKLTNAQKRAHQEIRNDMISE

KPMNRLLQGDVGSGKTVVAQLAILDNYEAGFQTAFMVPTSLAIQHYRRTVESFSKFNHVALIGATTPEKEKIKSGLRNGQIDVVIGTHALIQEDV
HFKNLGLVIIDEQHRFGVKQREALMNKGKMDTLVMSATPIPRSMALAFYGDLDVTVIDEMPP

>d1gm5a4 c.37.1.13 (A:550-755) RecG helicase domain {Thermotoga maritima}

GRKEVQTMVLVPMDRVNEVYEFVRQEVMRGGQAFIVYPLIEESDKLNKSAVEMYEYLSEVFPEFKLGLMHGRLSQEEDRVMLEFAEGRYDILVS
TTVIEVGIDVPRANVMVIENPERFGLAQLHQLRGRVGRGGQEAYCFLVVGDVGEAMERLRFITLTDGFKIAEYDLKTRGPGEFFGVQHQHLSGFK
VADLYRDLKLLEW

>d1fuka_c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IKQFYVNVEEEYKYECLTDYDSISVTQAVIFCNTRRKVEELTTKLRNDKFTVSAYSDLPQQERDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYD
LPANKENYIHRIGRRGRFKGVAINFVTNEDVGAMRELEKFYSTQIEELPSDIATLLN

>d1qdea_c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IQTNYDKVVKFDDMELDENLLRGVFGYGFEEPSAIQQRRAIMPIIEGHHDVLAQAQSGTGTGKTSIAALQRIDTSVKAPQALMLAPRELALQIQKV
MALAFHMDIKVHACIGGTSFVEDAEGLRDAQIVVGTPGRVFDNIQRRFRTDKIKMFILDEADEMLSSGFKEQIYQIFTLLPPTQVLLSATMPNDV
LEVTTKFMNRNPVRILV

>d1c4oa1 c.37.1.13 (A:2-409) Nucleotide excision repair enzyme UvrB {Thermus thermophilus}

TFRYRGSPKGQPKIAIGLVEALRDGERFVTLGATGTGKTVTMAKVEALGRPALVAPNKILAAQLAEEFRELFPENAVEYFISYYDYYQPEAYVPG
KDLYIEKDASINPEIERLRHSTTRSLLTRRDVIVVASVSAIYGLGDPREYRARNLVVERGKPYPREVLLERLLELGYQRNDIDLSPGRFRAKEVLEIFPAYE
TEPIRVELFGDEVERISQVHPVTGERLRELPGFVLFPAATHYLSPEGLEEILKEIEKELWERVRYFEERGEVLYAQRKLERTLYDLEMLRVMGTCGVENYA
RYFTGKAPGEPPYTLLDYFPEDFLVFLDESHVTVPQLQGMYRGDYARKKTLVDYGRFLPSALDNRPLRFEELERSQVVFSATPGPFELAHSGRVVE
QIIRP

>d1c4oa2 c.37.1.13 (A:410-583) Nucleotide excision repair enzyme UvrB {Thermus thermophilus}

TGLLDPLVRVKPTENQILDLMEGIRERAARGERTLTVLTVRMAEELTSFLVEHGIRARYLHHELDAKRQALIRDLRLGHYDCLVGINLLREGLDIPEVS
LVAILDADKEGLRSERSLIQTIGRAARNARGEVWLYADRVSSEMQRAIEETNRRRALQEAYNLEHGTIPETV

>d1d9xa1 c.37.1.13 (A:2-414) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}

EGRFQLVAPYPEPQGDQPQIAKLVGDRGGVKHQTLGATGTGKFTISNVIAQVNKPTLIAHNKTLAGQLYSELKEFFPHNAVEYFVSYDYYQPEA
YVPQTDTYIEKDAKINDEIDKLRHSATSALFERRDVIIASVSCIYGLGSPEEYRELVSLRVGMEIERNALLRRLVDIQYDRNDIDFRGTFRVRGDVVEIF
PASRDEHCIRVEFFGDEIERIRAEVDALTGKVLGEREHVAIFPASHFVTREEKMRLAIQNIEQEELERLAEQKGLLEAQRLEQRTRYDLEMMREM
FCGSIENYSRHHLARPPGSTPYTLLDYFPDDFLIIVDESHVTLPLQLRGMYNGDRARKQVLVDHGFRFLPSALDNRPLTFFEEQKINQIYVSATPGPYELE
HSPGVVEQIIRP

>d1d9xa2 c.37.1.13 (A:415-595) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}

TGLLDPTIDVRPTKGQIDDLIGEIRERVERNERLTVTTLKKMAEDLTDYLKEAGIKVAYLHSEIKTLERIEIIRDRLGKYDVLGINLLREGLDIPEVSLVAIL
DADKEGLRSERSLIQTIGRAARNANGHVIMYADTTKSMEIAIQETKRRRAIQEEYNRKHGIVPRTVKKEIRDV

>d1jr3a2 c.37.1.13 (A:3-242) gamma subunit of DNA polymerase III, N-domain {Escherichia coli}

YQLVARKWRPQTADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAKGLNCETGITATPCGVCDNCREIEQGRFVDSLIEIDAASRTKV
EDTRDLDNVQYAPARGRFKVKYLIDEVHMLSRSFNALLKTLLEPPEHVKFLLATTDPQKLPVTILSRCLQFLKALDVEQIRHQLEHILNEEHIAHEPR
ALQLLARAEGSLRDALS LTDQIA SGDQVSTQAVSAMLG

>d1a5t_2 c.37.1.13 (1-207) delta prime subunit of DNA polymerase III, N-domain {Escherichia coli}

MRWYPWLRPDXEKLVASYQAGRHHALLIQALPGMGDDALIYALSRYLLCQQPQGHKSCGHRCGQLMQAGTHPDYTLAPEKGKNTLGVD
REVTEKLNEHARLGGAKVWWVTDAAALLTDAANALLKTLLEPPEATWFFLATREPERLLATLSRCLHYLAPPPEQYAVTWSREVTMSQDALLAAL
RLSAGSPGAALALFQG

>d1jqlb_c.37.1.13 (B:) delta subunit of DNA polymerase III, N-domain {Escherichia coli}

MIRLYPEQLRQLNEGLRAAYLLLNDPLLQESQDAVRQAAAQGFEHHTFSIDPNTDWNAIFSLCQAMSFLASRQTLLLLPGPNAAINEQLL
TLTGLLHDDLLIVRGNKLSKAQENAAWFTALANRSVQVTCQ

>d1jr3d2 c.37.1.13 (D:1-211) delta subunit of DNA polymerase III, N-domain {Escherichia coli}

MIRLYPEQLRQLNEGLRAAYLLLNDPLLQESQDAVRQAAAQGFEHHTFSIDPNTDWNAIFSLCQAMSFLASRQTLLLLPGPNAAINEQLL

TLTGLLHDDLLLIVRGNKLASKAQENAAWFTALANRSVQVTCQTPEQAQLPRWVAARAKQLNLEDDAANQVLCYEGNLLALAQALERLSLLWPD
GKLTPRVEQAVNDAAH

>d1iqa2 c.37.1.13 (A:2-232) Replication factor C {Archaeon Pyrococcus furiosus}

SEEIREVKVLEKPWVEKYPQRQLDDIVGQEHIVKRLKHVKTGSMPHLLFAGPPVGKTTAALALARELFGENWRHNFLNASDERGINVIREKVKE
FARTKPIGGASFIIFLDEADALTQDAQQALRRTMEMFSSNVRILSCNYSSIIPIQSRCIAFRRPLRDEDIAKRLRYIAENEGLTEEGLQAILYIAEG
DMRRAINILQAAAALDKITDENVMVAS

>d1hqca2 c.37.1.13 (A:5-242) Holliday junction helicase RuvB {Thermus thermophilus}

ALRPKTLDEYIGQERLKQKLRVYLEAAKARKEPLEHLLLFGPPGLKTTLAHVIAHELGVNLRVTSGPAIEKPGDLAAILANSLEEGDILFIDEIHRLSRQA
EEHLYPAMEDFVMDIVIGQGPAARTIRLELPRFTLIGATTRPGLTAPLLSRFGIVEHLEYYTPEELAQGVMRDARLLGVRITEEAALEIGRRSRGTMRVA
KRLFRRVRDFAQVAGEEVTRERALEALAALGLDE

>d1in4a2 c.37.1.13 (A:17-254) Holliday junction helicase RuvB {Thermotoga maritima}

QFLRPKSLDEFIQENVKKKSLALEAAKMRGEVLDHVLLAGPPGLKTTLAHIASELQTNIHVTSGPVLVKQGDMAILTSLERGDVLFIDEIHRLNK
AVEEELYSAIEDFQIDIMIGKGPSAKSIRIDIQPFTLVGATRSGLSSPLRSRFGIILEDFYTVKELKEIKRAASLMDVDIEDAAAEMIAKRSRGTPRIAIRL
TKRVRDMLTVVKADRINTDIVLKTMEVNLNIDD

>d1fnna2 c.37.1.13 (A:1-276) CDC6, N-domain {Archaeon Pyrobaculum aerophilum}

AIVVDDSVSPSYVPKRLPHREQQLQQLDILLGNWLNRNGHHYPRATLLGRPGTGKTVTLRKLWEYKDCTTARFYINGFIYRNFTAIIGEIARSLNIPF
PRRGLSRDEFALLVEHLRERDLYMFVLDDAFNLAPDILSTFIRLGQEADKLGAFRIALIVGHNDALNNLDPSTRGIMGKYVIRFSPYTKDQIFDILL
DRAKAGLAEGSYSDELQMIADITGAQTPLDTNREGDARLAIDILYRSAYAAQQNGRKHIAPEDVRKSSKEVLFG

>d1d2na_c.37.1.13 (A:) Hexamerization domain of N-ethylmaleimide-sensitive fusion (NSF) protein {Chinese hamster (Cricetulus griseus)}

EDYASYIMNGIICKWGDPTVRLDDGELLVQQTKNSDRTPLVSVLLEGPPHSGTKALAAKIAEESNPFKICSPDKMIGFSETAKCQAMKKIFDDAYKS
QLSCVVVVDIERLLDYVIPGPRFSNLVQLQALLVLLKAPPQGRKLIIGTSRKDVQEMEMLNAFSTTHVPNIATGEQLLEALELLGNFKDKERTTIAQ
QVKGKKWIGIKKLLMIELMSLQMDPEYVRKFALLREEGASPLD

>d1e32a2 c.37.1.13 (A:201-458) Membrane fusion atpase p97, D1 domain {Mouse (Mus musculus)}

VGYDDVGGCRKQLAQIKEMVELPLRHPAIRKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFLINGPEIMSKLAGESESNLRAFEEAKNAPAI
FIDELDAIAPKREKTHGEVERRIVSQLTLMGLKQRAHIVVMAATNRPNSIDPALRRFGRFDREVDIGIPDATGRLEILQIHTKNMKLADDVDLEQVA
NETHGHSVADLAALCSEAALQAIRKKMDLIDLEDETIDAEMVNSLAVTMDDFRWALSQ

>d1g6oa_c.37.1.13 (A:) Hexameric traffic ATPase, HP0525 {Helicobacter pylori}

LSAEDKKFLEVERALKEALNPLRHATEELFGDFLKWMENITEICYNGNKVVVVLKNNGEWQPDFVRDRKAFSLRMLHFARCCASFKKKTIDNYENP
ILSSNLANGERVQIVLSPVTNDETISISIRIPSCKTYPHSFEEQGFYNNLDNKEQAIKDGIAIGKNVIVCGGTGSGKTTIYKSIMEFIPKEERIISIEDTE
EIVFKHHKNTQLFFGNITSADCLSKLCSRMRPDRILGELRSSEAYDFYNVLCSGHKGTLTTLHAGSSEAFIRLANMSSNSAARNIKFESLIEGFKD
DMIVHINHHKQCDEFYIK

>d1ht1e_c.37.1.13 (E:) Hs1U {Escherichia coli}

HSEMPREIVSELDKHIIGQDNAKRSVAIALRNRWRRMQLNEELRHEVTPKNILMIGPTVGKTEIARRLAKLANAPFIKVEATKFTEVGVGVKEVDSI
IRDLTDAAVKMVRVQAIKNRYRAEELAEERILDVLIPPAKNNWGQTEQQQEPASAQRQAFRKKLREGQLDDKEIEIDAAAPMGVEIMAPPGMEE
MTSQLQSMFQNLGGQKQKARLKIKDAMKLIEEEAKLNPNEELQDAIDAVEQHGIVFIDEIDKICKRGESSGPDSREGVQRDLLPVEGCTVST
KHGMVKTDHILFIASGAFQIAKPSDLIPELQGRLPIRVELQALTTSDFERILTEPNASITVQYKALMATEGVNIEFTDSGIKRIAEEAWQVNESTENIGAR
RLHTVLERLMLMEEISYDASLGSQGNITADYVSKHLDVALVADEDLSRFIL

>d1g41a_c.37.1.13 (A:) Hs1U {Haemophilus influenzae}

SEMTPREIVSELDQHIIQGQADAKRAVIALRNRWRRMQLQEPLRHEVTPKNILMIGPTVGKTEIARRLAKLANAPFIKVEATKFTEVGVGVKEVDSII
RDLTDSAMKLVRQQEIAKNRARAEDVAEERILDALLPPAKNQWGEVENHDSHSSTRQAFRKKLREGQLDDKEIEIDVSAGVSMGVEIMAPPGMEE
MTNQLQSLFQNLGSDKTKKRKMKIKDALKALIDDEAAKLINPEELQKAIDAVEQNGIVFIDEIDKICKGEYSGADVSRREGVQRDLLPVEGSTVSTK
HGMVKTDHILFIASGAFQVARPSDLIPELQGRLPIRVELTALSAADFERILTEPHASLTEQYKALMATEGVNIAFTDAVKKIAEEAFRVNEKTEENIGARR
LHTVMERLMDKISFSASDMNGQTVNIDAAYVADALGEVVENEDLSRFIL

>d1g8pa_c.37.1.13 (A:) ATPase subunit of magnesium chelatase, BchI {Rhodobacter capsulatus}
RPVFPFSAIVGQEDMKLALLTAVDPGIGGVLFVGDRTGKSTAVRALAALLPEIEAVEGCPVSSPNEMIPDWATVLSTNVIRKPTPVVDLPLGVSED
RVVGALDIERAISKGEAFEPGLLARANRGYLYIDECNLLEDHVLDLLDVAQSGENVERDGLSIRHPARFVLVGSNPEEGDLRPQLLDRFGLSVEVL
SPRDVETRVEVIRRRTDYADPKAFEEWRPKDMDIRNQLEARERLPKVEAPNTALYCAALCIALGSDGLRGEELLRSARALAALEGATAVGRDHL
KRVATMALSHRLRRDPLEAGSTARVARTVEETLP

>d1a1va1 c.37.1.14 (A:190-325) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}
PPAVPQSFQVAHLHAPTGGSKSTKVPAAYAAQGYKVLVLPNSVAATLGFAYMSKAHGVDPNIRTGVRTTGSPITYGKFLADGGCSGGAYDIII
CDECHSTDATSLIGITVLDQAETAGARLVVLTATP

>d1a1va2 c.37.1.14 (A:326-624) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}
PGSVTVPHNIEEVALSTTGEIPFYGKAIPIEVKGGRHLIFCHSKKKCDELAALKVALGINAVAYYRGLDVSPIVTSGDVVVVATDALMTGFTGFDIVI
DCNTCVTQTVDFSLDPTFTIETTLPQDAVSRTQRRGRTGRGKPGIYRFVAPGERPSGMFDSSVLCCECYDAGCAWYELTPAETTVRLRAYMNTPGLP
VCQDHLEFWEGVFTGLTHIDAHFLSQTKQSGENFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEVTLHPITKYIM
TCMS

>d1cu1a3 c.37.1.14 (A:326-631) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}
PGSVTVPHNIEEVALSTTGEIPFYGKAIPIEVKGGRHLIFCHSKKKCDELAALKSGLGINAVAYYRGLDVSPIVTIGDVVVVATDALMTGFTGFDIVI
DCNTCVTQTVDFSLDPTFTIETTLPQDAVSRSQRGGTGRGRRGIYRFVTPGERPSGMFDSSVLCCECYDAGCAWYELTPAETSVRLRAYMNTPGLP
CQDHLEFWESVFTGLTHIDAHFLSQTKQAGDNFPYLVAYQATVCARAQAPPPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEVTLHPITKYIMA
CMSADLEVVT

>d1gkub1 c.37.1.16 (B:1-250) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}
AAAAAAAAAAAAAAAAAAAAASLCLFPEDFLLKEFVEFFRKCVGEPRAIQKMWAKRILRKESFAATAPTVGKTSFGLAMSLFLA
KGKRCYVIFPTSLVIQAAETIRKYAEKAGVGTENLIGYYHGRIPKREKENFMQNLRFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVDKLL
HLLGFHYDLKTKSWVGEARGCLMVSTATAKKKAELFRQLLNFDIGSSRIT

>d1gkub2 c.37.1.16 (B:251-498) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}
VRNVEDVAVNDESISTLSSILEKLGTGGIIYARTGEEAEIYESLKNFKRIGIVTAKKGDYKEFVGEIDHLIGTAHYYGTIVRGLDLPERIRFAVFVGCPSF
RVTIEDIDSPLSPQMVKLLAYLRNVDEIERLLPAVERHIDEVREILKKVMGKERPQAQDKVVREGEVIFPDRLTYIQGSGRTSRLFAGGLTKGASFLL
SELLSAFIERAKLYDIEFKSIDEVDFEKLSELDESDRDRYRRR

>d1gl9b1 c.37.1.16 (B:2-250) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}
IPVVYSNLCPVCGGDLESKEIEKHVCFRKRSRSLCLFPEDFLLKEFVEFFRKCVGEPRAIQKMWAKRILRKESFAATAPTVGKTSFGLAMSLFLA
KGKRCYVIFPTSLVIQAAETIRKYAEKAGVGTENLIGYYHGRIPKREKENFMQNLRFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVDKLLHLLGFH
YDLTKTSWVGEARGCLMVSTATAKKKAELFRQLLNFDIGSSRIT

>d1ble_c.38.1.1 (-) Fructose permease, subunit IIb {Bacillus subtilis}
MNIVLARIIDDRFIHGQILTRWIKVHAADRIIVVSDDIAQDEM RKTLSVAPS NVKASAVSVKMAKFHS PRYEGVTAMLLFENPSDIVSLIEAGVPIK
TVNVGGMRFENHRRQITKS VSTEQDIKAFETLSDKGVKLELRQLPSASEDFVQILRNVT

>d1d0va_c.39.1.1 (A:) Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) {Salmonella typhimurium}
LHALLRDIPAPDAEAMARTQQHIDGLKPPGSLRLETAVQLAGMPGLNGTPQVGEKAVLVMCADHGVWDEGVAVSPKIVTAIQAANMTRGTT
GVCVLAQAGAKVHVIDVGIDAEPIPGVVNMRVARGCGNIAVGPM SRLQAEALLVEVSRYACDLAQRGVTLFGVGE LGMAN TPAAMVS VFT
GSDAKEVVGIGANLPPSRIDNKV D VV RRAIAIN QPNPRDGIDVLSKVGFFDLVGM GTVMLGAARCGLPVLLDGFLSYA ALAACQIAPAVRPY LIPS
HFSAEKGARIALAHLSMEPYLHMAMRLGEGSGAALAMP IVEAACAMFHNM GELAASNIVLP

>d1chd_c.40.1.1 (-) Methyleneesterase CheB, C-terminal domain {Salmonella typhimurium}
LLSSEK LIAIGASTGGTEAIRHVLQPLPLSSPAVIITQHMPPGFTRSFAERLN KLCQISVKEAEDGERVLP GHAYIAPGDKHMELARSGANYQIKIH DGPP
VNRHRPSDVLFHSVAKHAGR NAVGVL TGMGNDGAAGMLAMYQAGAW TIAQNEASC VVFGMPREAINMGGVSEV DLSQV SQQMLAKISA
GQAIRI

>d1csee_c.41.1.1 (E:) Subtilisin {Bacillus subtilis, carlsberg}

AQTPYGIPLIKADKVQAQGFKGANVKAVLDTGQASHPDNVGGASFVAGEAYNTDGNHGTHVAGTVAAALDNTTGVGVAPS VSLYAVKVL
NSSSGSGS YSGIVSGIEWATTNGMDVINMSLGGASGSTAMQAVDNAYARGVVVAAAGNSGNSGNTIGYPAKYDSVIAVGAVDSNSNRASFSS
VGAELVMAPGAGVYSTPTNTYATLNGTSMASPHVAGAAALILSKHPNLSASQVRNRLSSTATLGSSFYKGKLINVEAAAQ
>d1bh6a_c.41.1.1 (A:) Subtilisin {Bacillus licheniformis}
AQTPYGIPLIKADKVQAQGKGANVKVIIIDTGIASSHTDLKVGASFVSGESYNTDGNHGTHVAGTVAAALDNTTGVGVAPNVS LYAIVLNS
SGSGSYSAIVSGIEWATQNGLDVINMSLGGPSGSTALKQAVDKAYASGIVVVAAGNSGNSGSQNTIGYPAKYDSVIAVGAVDSNKNRASFSSVGSE
LEVMAPGVSVYSTPSNTYTSNGTSMASPHVAGAAALILSKYPTLSASQVRNRLSSTATNLGDSFYKGKLINVEAAAQ
>d1gci_c.41.1.1 (-) Subtilisin {Bacillus lentus}
AQSPWGIRVQAPAAHNRGLTSGVKAVLDGISTHDPLNIRGGASFVPGEPSTQDGNGHGTHVAGTIAALNNSIGVLGVAPS AELYAVKVL GAS
GSGSVSSIAQGLEWAGNNGMHVANLSGSPSPSATLEQAVNSATSRGVLVAAASGNSGAGSISYPARYANAMA AVGTDQNNNRASFSSQYGAGLDI
VAPGVNVQSTYPGSTYASLN GTSMATPHVAGAAALVKQKNPWSNVQIRNHLKNTATLGS TNLGYGSGLVNAEAATR
>d1s01_c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}
AQSPYGVSQIKAPALHSQGYTGSNVKAVIDSGIDSSHPLKVAGGASFVPS ETNP FQDDNSHGTHVAGTVAA LDNSIGVLGVAPSSALYAVKVL
DAGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVASGVVVVAAAGNEG STGSSTVGYPGKYP SVIAVGAVDASNQRASFSS
GPELDV MAPGVSI C STLPGNKYGA KSGTSMASPHVAGAAALILSKHPNWTNTQVRSSQLNTT KLGD SFYYKGKLINVQAAAQ
>d1sue_c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}
AKCVSYGV SQIKAPALHSQGYTGSNVKAVIDSGIDSSHPLNVAGGASFVPS ETNP FQDDNSHGTHVAGTVLA VAPS ALYAVKVL GADGSGQYS
WIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVASGVVVVAAAGNEG STGSSTVGYPGKYP SVIAVGAVDSSNQRASFSSVGPELDVMA
PGVSI C STLPGNKYGA KSGTSMASPHVAGAAALILSKHPNWTNTQVRSSLEN TT KLGD SFYYKGKLINVQAAAQ
>d1sup_c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}
AQSPYGVSQIKAPALHSQGYTGSNVKAVIDSGIDSSHPLNVAGGASFVPS ETNP FQDDNSHGTHVAGTVAA LDNSIGVLGVAPS ALYAVKVL
GADGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVASGVVVVAAAGNEG STGSSTVGYPGKYP SVIAVGAVDSSNQRASFSS
VGPELDV MAPGVSI QSTLPGNKYGA NGTSMASPHVAGAAALILSKHPNWTNTQVRSSLEN TT KLGD SFYYKGKLINVQAAAQ
>d1meea_c.41.1.1 (A:) Messentericopeptidase {Bacillus mesentericus}
AQSPYGISQIKAPALHSQGYTGSNVKAVIDSGIDSSHPLNVAGGASFVPS ETNPYQDGSSHGTHVAGTIAALNNSIGVLGVAPS ALYAVKVL D
GSGQYSWIINGIEWAIANNMDVINMSLGGPTGSTALKVVDKAVSSGIVVAAAGNEG STGSSTVGYPGKYP SVIAVGAVDSSNQRASFSSAGSEL
DVMAPGVSI QSTLPGGTYGA NGTSMASPHVAGAAALILSKHPTWTNAQVRDRLESTATYLGS FYYKGKLINVQAAAQ
>d1dbia_c.41.1.1 (A:) Thermostable serine protease {Bacillus sp., AK.1}
WTPNDTYQGYQGPQNTYTDYAWDVTKGSSQEI AVDTGVDYTHPDLGKVIGYDFVDNDYDPMDLNNHGTHVAGIAAAETNNATGIAGM
APNTRILAVRALDRNGSGTLSIADAIYAADSGAEVINLSLCDCHTTLENAVNYAWNKGSVVVAAGNNGSSTFEPASYENVIAGVADQYDRL
ASF SNYGTWVDVVA PGVDIVSTITGNRYAYMSGTSMASPHVAGLA ALLASQGRNNIEIRQAIEQTADKISGTGYFKYGRINSYNAV
>d1thm_c.41.1.1 (-) Thermitase {Thermoactinomyces vulgaris}
YTPNDPYFSSRQYGPQKIQAPQAWDIAEGSGAKIAIVDTGVQSNHPDLAGKV VGGWDFVDNDSTPQNGNGHGTHCAGIAAAVNNSTGIAGTAP
KASILAVRVLDSNGSGTWTAVANGITYAADQGAKVISLSLGGTGVNGLQQAVNYAWNKGSVVVAAGNAGNTAPNPYAYNSNIAVSTDQNDN
KSSFSTYGSWV DVAAPGSSIYSTYASLSGTSMATPHVAGVAGLLASQGRSASNIRAAIENTADKISGTGYWAKGRVNAYKAVQY
>d1ic6a_c.41.1.1 (A:) Proteinase K {Fungus (Tritirachium album), strain limber}
AAQTNAPWGLARISSTSPGTSTYYDESAGQGSCVYV IDT GIEASHPEFEGRAQMVKYYSSRDGNHGTHCAGTVGSRTYGVAKKTQLFGV
DDNGSGQY STIAGMDFVASDKNNRNCPKGVVASLSSGGYSSVNSAARLQSSGVMVAVAAGNNNADARNYSPASEPSVCTVGASDRYDRRS
SFSNYGSVLDIFGPGTDILSTWIGGSTRISGTSMATPHVAGLAAYLMTLGKTTAASACRYIADTANKGDSLIPFGTVNLLAYNNYQA
>d1ga6a_c.41.1.2 (A:) Serine-carboxyl proteinase PSCP {Pseudomonas sp.}
AGTAKGHNPTEFPTIYDASSAPTAANTVGIITIGGSQTLQDLQQFTSANGLASVNTQTIQGSSNGDYSDDQQGQGEWDLDSQSIVGSAGGA
VQ QLLFYMADQSASGNTGLTQAFNQAVSDNVAKVINVSLGWC EADANADGTLQAEDRIFATAAAQGQTFSVSSGDEGVYECNNRGYPDGSTY
SVSW PASSPNVIAVGGTTLYTTSAGAYSNETVNEGLDSNGKLWATGGGVSYESKPSWQSVSGTPGRRLPDISFDAAQGTGALI NYGQLQQIGG
TSL ASPIFVGLWARLQSANSNSLGFPAAFSYASSTPSLVDVKSGNNGYGGYGYNAGTGWDYPTGVGSLSIAKLSAYIRSNGF

>d1d3va_c.42.1.1 (A:) Arginase {Rattus norvegicus}

KPIEIGAPFSKGQPRGGVEKGPAAALKAGLVEKLKETEYNVRDHGDLAFDVPNDSPFQIVKNPRSVGKANEQLAAVVAETQKNGTISVLGGDHS
MAIGSISGHARVHPDLCIVWVDAHTDINTPLTTSSGNLHGQPVAFLKELKGKFPDVPGFSWTPCISAKDIVYIGLRDVDPEHEYIITLGKIKYFSMTE
VDKLIGKVMEETFSYLLGRKKRPIHLSFDVGDLPVFTPATGTPVVGGLSYREGLYITEEYKTGLSGLDIMEVNPTLGKTPPEVTRTVNTAVATLSCF
GTKREGNHK

>d2ceva_c.42.1.1 (A:) Arginase {Bacillus caldovelox}

KPISIIGVPMDLGQTRRGVDMGSPAMRYAGVIERLERLHYDIEDLGDIPIGKAERLHEQGDSRLRNKAVAEEANEKLAADVQVVQRGRFPLVGGD
HSIAIGTLAGVAKHYERLGVIWYDAHGDVNTAETSPSGNIHGMPLAASLGFGHPALTQIGGYSPKIKPEHVVLIGVRSLSDEGEKKFIREKGKIKYTMHEV
DRLGMTRVMEETIAYLKERTDGVHLSLDGLDPSDAPGVGTPVIGGLTYRESHLAMEMLAEAQIITSAECVNPILDERNKTAVALMGSLFGE
KLM

>d1c3pa_c.42.1.2 (A:) HDAC homologue {Aequifex aeolicus}

KKVKLIGTLDYGKYRYPKNHPLKIPRVSLLRFKDAMNLIDEKELIKSRPATKEELLFHTEYINTLMEAERCQCVPKGAREKYNIGGYENPVSYAMFTG
SSLATGSTVQAIEFLKGNVAFNPAGGMHHAFKS RANGFCYINNP AVGIEYLRKKGFKRILYIDLDAH HCDGVQE AFYTDQVFVLSLHQ SPEYAFPFE
KG FLEEIGEGKGKGKGNLNIPLPKGLNDNEFLFALEKSLEIVKEVFEPEVYLLQLGTDPLLEDYLSKFNLNSNVAFKAFNIVREVFGEGVYLG GGYHPYAL
ARA WTLIWC ELSG REVPE KLN NKAKELLK SDFE FDEV DR SYM LETLK DPW RGGE VR KEV KDT LEKAKA

>d1hf2a2 c.102.1.1 (A:1-99) Cell-division inhibitor MinC, N-terminal domain {Thermotoga maritima}

MVDFKMTKEGLVLLIKDYQNLEEVLNAISARITQMGGFFAKGDRISLMIENHNKHSQDIPRIVSHLRNLGLEVSQILVGSTVEGKENDLKVSRTTVE

>d1jke_a_c.110.1.1 (A:) D-Tyr tRNA_{tr} deacylase {Escherichia coli}

MIALIQRVTRASVTVEGEVTFGEIGAGLLVLLGVEKDDDEQKANRLCERV LGYRIFSDAE GKMN LN VQQAGGSVLV VSQFTLAADTERGMRPSFSKG
ASPDRAE ALYD YFVER CQQEM NTQT GRFAADM QVSLV NDGPV FWLQV

>d1nocb_c.43.1.1 (B:) Chloramphenicol acetyltransferase {Escherichia coli}

ITGYTTVDISQWHRKEFQSVAQCTYNQTVQLDITAFLKTVKKNNKHFYPAFIHLARLMNAHPEFRMAMKDGEVWDSVHPCYTVFHEQTET
FSSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWV/SFTSF DLNVANMDNFFAPVFTMGKYYTQGDVKLMP LAIQVHHAVC
DG FHVG RMLN ELQQYC DEWQG

>d3cla_c.43.1.1 (-) Chloramphenicol acetyltransferase {Escherichia coli}

MNYTKFDVKNWVRRHFEFYRHLPCGFSLTSKIDITLKKSL DD SAYKFPVMIY LIAQAVNQF DELRMAIKDDELIVWDSVDPQFTV FHQETETFS
ALSCP YSSD IDQFMVN YLSVM ERYKSDT KLF PQGV TPEN HLN ISAL PWV NFDSFN LN V ANFT DYF API ITMA KYQQEGDR LLPLS VQV HAVCDGF
HVARFINRLQELCNSKLK

>d1eaf_c.43.1.1 (-) Dihydrolipoamide acetyltransferase {Azotobacter vinelandii}

IPPIPPVDFAKYGEIEE VPMT RLQMIGATNLHRSWLNVPHV TQFESADITEA FRVAQK A VAKKAGV KLT VLP LLLKACAY LLKEL PDFN S LAPS GQA
LIRKKYVHIGFAV DTPD GLL VPV IRN VDQ KSL LQ AEA EAE AELA EKAR SKKL GADAM MQG ACFT ISSL GHIG GT AFT PIV NAPE VAI LGV SK AS M QPV WD
GKA FQ PRL M LPL SLSYD H RVING AAA ARFT KRL GDLL ADIR AILL

>d1b5sa_c.43.1.1 (A:) Dihydrolipoamide acetyltransferase {Bacillus stearothermophilus}

AAA KPATTEGE F PETRE KMSGIR RAI AKAMVHSKHTAPV TLMD EAD VTKL V AHRKKF KAIA AEKG IKL FLPY VV KALV SAL REY PV LNT SIDDE TEII
QKH YYNIGIAAD TD RG L LPV I KHAD RKPI FALA QE INELA EKAR DGK LTPG EMKG ASCT ITN IG SAGG QWFTP V NHPE VAI LGI RIA EK PIV RD GEI
VAAPMLA LSLS FD HRM IDG DATA QK ALN HIKR LL SDPE LLM

>d1e2o_c.43.1.1 (-) Dihydrolipoamide succinyltransferase {Escherichia coli}

ARSEKRVPMTRLRK RVA ER LLEAKN STAM LTT FNEV NMK PIMDLR KQYGEA FEK RH G IRL GFMS FYV KAV VEAL KRY PEVN ASID GDD VV HNY FD
VS MAVS T PRGLV TPV LRD VT LGM ADIE KKI KELA VKG RDG KLT VED LT GG NFT IT NGG VFG SLM STI IN PP QSA IL GMH AI KDR PM A VNG QV EIL P
MMYL ALSYD HRL IDG RES VGFL VTI KEL LED PT RLL DV

>d1phr_c.44.1.1 (-) Tyrosine phosphatase {Cow (Bos taurus)}

VTKS VL FV CLGN CRSP IA EAV FRKL VTD QN ISDN WVIDSGA VSDW NVGR SPD PRA V SCLRN HG INTA H KAR QV T KED FV T FDY ILC MDE SNL RD LN
RKS NQV KNCR A KIELL GS YDPQ KQ LI ED PYY GN DAD FET VY QQ CVRC RA FLE KV R

>d5pnt_c.44.1.1 (-) Tyrosine phosphatase {Human (Homo sapiens)}

AEQATKSVLFVCLGNICRSPIAEAVFRKLVDQNISENWRVDSAATSGYEIGNPPDYRGQSCMKRHGIPMSHVARQITKEDFATFDYILCMDESNLRD
LNRKSNNQVKTCAKIELLGSDPQKQLIIEDPYYGNDSDFETVYQQCVCCRAFLEKAH
>d1d1qa_c.44.1.1 (A:) Tyrosine phosphatase {Baker's yeast (Saccharomyces cerevisiae)}
IEKPKISVAFIALGNFCRSPMAEAIFKHEVEKANLENRFNKIDSFGTSNYHGESPDHRTVSICKQHGVKINHKGKQIKTKHFDEYDYIIGMDESNNLN
KKIQPEGSKAKVCLFGDWNTNDGTVQTIIEDPWYQDIQDFEYNFKQITYFSQFLKKEL
>d1jf8a_c.44.1.1 (A:) Arsenate reductase ArsC {Staphylococcus aureus}
DKKTIYFISTGNSARSQMAEGWGKEILGEGWNVYSAGIETHGVNPKAIEAMKEVDIDISNHTSDLIDNDILKQSDLVTLCSADNNCPILPPNVKE
HWGFDDPAGKEWSEFQRVRDEIKLAIKFKLR
>d1jl3a_c.44.1.1 (A:) Arsenate reductase ArsC {Bacillus subtilis}
NKIIYFLCTGNSCRSQMAEGWAKQYLGEWKVYSAGIEAHGLNPNAVKAMKEVGIDISNQTSIDIISDILNNADLVTLGDAADKCPMTPPHVKR
EHWGFDPPARAQGTEEEKW AFFQRVRDEIGNRLKEFAETGK
>d1iiba_c.44.2.1 (A:) Enzyme IIB-cellulose {Escherichia coli}
KKHIYLSSAGMSTSLLSKMRAQAEKYEVPIIAFPETLAGEKGQNA DVVLLGPQIAYMLPEIQRLLPKPVEVIDSLLYGVGDGLGVLA VAAIKK
AAA
>d1vhra_c.45.1.1 (A:) VH1-related dual-specificity phosphatase, VHR {Human (Homo sapiens)}
SVQDLNDLSSDGCGYSLPSQPCNEVTPRIYVGASVAQDIPKLQKLGITHVLNAAEGRSFMHVNNTANFYKDGSITYLGKANDTQEFLNLSAYFERA
ADFDQALAQKNGRVLVHCREGYRSRPTLVIA YLMMRQKMDVKSALSIVRQNREIGPNDGFLAQLCQLNDRLAKEGKLKP
>d1mkp_c.45.1.1 (-) Mapk phosphatase Pyst1 (mkp3) {Human (Homo sapiens)}
ASFVVEILPFLYLGCAKDSTNLDVLEFGIKYILNVTNPNLNFENAGEFKYKQIPISDHWSQNL SQFFPEAISFIDEARGKNCGVLVHSLAGISRSVT
VTV
AYLMQKLNLSMN DAYDIV/KMKKS NISPNFNMFGQ LLD FERTL
>d1d5ra2_c.45.1.1 (A:14-187) Phosphoinositide phosphatase Pten (Pten tumor suppressor), N-terminal domain {Human (Homo sapiens)}
RRYQEDGF DLDLT YIPNIIAMGPAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNLC AERHYDTAKFNCRVAQYPFEDHNPPQLELIKPF CEDLDQW
LSEDDNHVAIHCAGKGR TGMICAYLLH RGKFLQA QEA LDFYGEV RTRD KKGVTIPSQ RRYVYY SYLLKNHLD
>d1i9sa_c.45.1.1 (A:) mRNA capping enzyme, triphosphatase domain {Mouse (Mus musculus)}
KIPPRWLNCPRRGQPVAGRFLPLKTM LGRYD SQAEE NFHPSMLS NYLKSLKV KMSL LVDT NT SRFYDR NDIE KEGIKYIKLQCKGH GECPTTEN
TETFIRLCERFNERSPPELIGVHCTHGFNRTGFLICAFLVEKMDWSIEAAVATFAQARPGIYKG DYLKE LFRRYGDIEEAPPVLPDWC FEDED
>d1fpza_c.45.1.1 (A:) Kinase associated phosphatase (kap) {Human (Homo sapiens)}
TPIHISWLSLSRVNCSQFLGLCALPGCKFDVRRNVQKDTEELKSCGIQDIFVFCTR GELSKYRVPNLLDLYQQCGIITHHHPIADGGTPDIASCCEIME
ELTTCLKNYRKTLIHSYGGLGRSCLVAACLLYLSDTISPEQAI DSRLRGSGAI QT KQYNYLHEFRDKLA AHL
>d1eeoa_c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), 1B}
EMEKEFEQIDKSGSWAAIYQDIRHEASDFPCRVAKLPKKNRNRYRDVSPFDHSRIK LHQEDNDYINASLIK MEEAQRSYILTQGPLNTCGFWEM
VWEQKSRGVVMLNRVMEKGLKCAQYWPQKEEKEMIFEDTNLKLTLISEDIKSYYTVRQLELENLTQETREILHFHYTTWPDFGV PESPASFLNLF
KVRESGSLSPHEGPVVHSSAGIGRSGTFCLADTC LLLMDKRDPSSDIKKV LLEM RKF RMGLI QTADQLRFSYLA VIEGAKFIMGDSSVQDQWKE
LSHED
>d1rpma_c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), mu}
AIRVADLLQHITQMKAEGYGFKEEYESFFEGQSAPWDSAKKDENRMKRNRYGNIIAYDHSRVR LQTI EGDTNSD YINGNYIDGYHRPNHYIATQGP
MQETIYDFWRMVWHENTASIIMVTNLVEGRVKCKYW PDDTEIYKDIKVTLIETELLA EYVIRTFAVEKRGVHEIREIRQFHFTGWP DHGV PYHAT
GLLG FVRQVKSKSPPSAGPLVHCSAGAGRTGCFIVIDIMLDMAEREGVV DIYNCV RELRSRRV NMVQTEEQYVFIHDAILEACL
>d1yfoa_c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus)}
KYPPLPVDKLEEINRRMADDNKL FREEFNALPACPIQATCEAASKEENKEKNRYVNILPYDHSRVHLTPVEGVPDS DYINASFINGYQEKNKFIAAQG
PKEETVNDFWRMIWEQNTATIVMVTNLKERKECKCAQYWPDQGCWTYGNVRV SEDVTVLVDYTVRKFCIQQVGDVTNRKPQRLITQFHTSW
PDFGV PFTPIGMLKFLKKVACNPQYAGAI VVHCSAGVGR GTFV VIDAM LDMMH SERKV DVG FV SRIRA QRCQ MVQ TD MQYVFIYQ ALLEHY
LY

>d2shpa1 c.45.1.2 (A:219-525) Tyrosine phosphatase {Human (Homo sapiens), shp-2}

TRINAAEIESRVRELSKLAETTDVKQGFWEETLQQQECKLLYSRKEGQRQENKNKNRYKNILPDFDHTRVLHDGDPNEPVSDYINANIIMPEFET
KCNNSKPCKSYIATQGCLQNTVNDFWRMVFQENSERVMTTKEVERGKSKCVCYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKGQQN
TERTVWQYHFRTWPDHGVPSPGGVLFLEEVHHKQESIMDAGPVVHCSAGIRGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRQRSGMVQ
TEAQYRSIYMAVQHYIETL

>d1fpra_c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), shp-1}

GFWEETFESLQKQEVKNLHQRLEGQRPENKGKNRYKNILPDFHSRVLQGRDSNIPGSYDINANYIKNQLGPDENAKTYIASQGCLEATVNDFWQM
AWQENSERVMTTREVEKGRNKCVPYWPEVMQRAYGPYSVTNCGEHTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGPSEPGGVLSF
LDQINQRQESLPHAGPIVHSSAGIRGTFIIVIDMLMENISTKGLDCDIQKTIQMVRQSRGMVQTEAQYKFIYVAIAQFIEETKKKLEV

>d1jlna_c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus), ptp-sl/br7}

GSPREKVAMEYLQSASRVLTRSQLRDVVASSHLLQSEFMEIPMFVDPKEIDIPRHTKNRYKTIPLNPLSRVCLRPNITDSLSTYINANYIRGYSKE
KAFIATQGPMINTVNDFWQMWWQEDSPVIVMITKLKEKNEKCVCVLYWPEKRGIFYGKVEVLVTGVTECDNYTIRNLVLKQGSHIQHVHYWTSWP
DHKTPDSAQPQLQLMLDVEEDRLASEGRGPVVHCSAGIRGCFIATSIGCQLKEEGVVDAISVCQLRVDRGGMVQTSEQYEFVHALCLFESR
LSPETV

>d1ypta_c.45.1.2 (A:) Tyrosine phosphatase {Yersinia enterocolitica}

PEARAEELSSRLTTLRNTPATNDPRYLQACGGKEKLNFRDIQCRRQTAVRADLNANYIQVGNTRTIACQYPLQSQLESHFRMLAENRTPVLA
SEIANQRFGMPDYFRQSGTYGSITVESKMTQQVGLGDGIMADMYTLTIREAGQKTISPVVHGNWPDTAVSSEVTKALASLVQDQTAETKRNM
ESKGSSAVADDSSKLRPVIHCRAVGRATAQLIGAMCMNDSRNSQLSVEDMVQSQMRVQRNGIMVQKDEQLDVLIKLAEGQGRPLLNS

>d1g4us2 c.45.1.2 (S:297-539) SptP tyrosine phosphatase, catalytic domain {Salmonella typhimurium}

PQTMMSGPTLGLARFAVSSIPINQQTQVKLSDGMPVPVNTLFDGKPVLAGSYPKNTPDALEAHMKMILEKECSCLVLTSEDQM
SYTFGEVHTNSQKVSSASQGEIDQYNMQLSCGEKRYTIPVHLVKNWPDHQPLSTDQLEYLADRVKNSNQNGAPGRSSDKHLP
RTGTMAAALVLKDNPNSNLEQVRADFRDSRNNRMLEDASQFVQLKAMQAQLLM

>d1lara1 c.45.1.2 (A:1307-1623) RPTP Lar {Human (Homo sapiens)}

MITDLADNIERLKANDGLKFSQEYESIDPGQQFTWENSLEVNPKNRYANVIAYDHSRVIITSIDGVPGSDYINANYIDGYRKQNAYIATQGPLPET
MGDFWRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVTLDTVELATYVRTFALKSGSSEKRELRFQFM
TPILAFLRRVKACNPLDAGPMVVHCSAGVGRGCFIVIDAMLERMKHEKTVDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEATCGHTEVPAR
NLYAHIQKLGQVPPGESVTAMELEFKLASS

>d1lara2 c.45.1.2 (A:1628-1876) RPTP Lar {Human (Homo sapiens)}

SRFISANLPCNFKNRLVNIMPYELTRVCLQPIRGVEGSDYINASFLDGYRQQKAYIATQGPLAESTEDFWRMLWEHNSTIIVMLTKLREMGREKCHQ
YWPAERSARYQYFVDPMAEYNMPQYILREFKVDARDGQSRTIRQFQFTDWPEQGVPKTGEGFIDFIGQVHKTKEQFGQDG
GVFITLSIVLERMRYEGVVDMFQTVKTLTQRPMVQTEDQYQLCYRAALEYLSF

>d1larb1 c.45.1.2 (B:1340-1623) RPTP Lar {Human (Homo sapiens)}

TWENSNLEVNPKNRYANVIAYDHSRVIITSIDGVPGSDYINANYIDGYRKQNAYIATQGPLPETMGDFWRMVWEQRTATVMMTRLEEKSRVK
DQYWPARGTETCGLIQVTLDTVELATYVRTFALKSGSSEKRELRFQFM
CFIVIDAMLERMKHEKTVDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLASS

>d1c25_c.46.1.1 (-) CDC25a {Human (Homo sapiens)}

MLIGDFSKGYLFHTVAGKHQDLKYISPEIMASVLNGKFANLIKEFVIIDCRYPYEYEGGHIKGAVNLH
MEEVEDFLLKKPIVPTDGKRVIVVFHCEFSSE
RGPRMCRYVRERDRLGNEYPKLHYPELYVLKGGYKEFFMKCQSCEPPSYRPMHHEDFKE

>d1qb0a_c.46.1.1 (A:) CDC25b {Human (Homo sapiens)}

DHRELIBGDSKAFLQTVGDGHQDLKYISPETMVALLTGKFSNIVDKFIVDCRYPYEYEGGHIKTAVNLPLERDAESFLKSPIAPCSLDKRV
SERGPRMCRFIRERDRAVNDYPSLYPEMYILKGGYKEFPQHPNFCEPQDYRPMNHEAFKDELKTRLKTRS
WA

>d1hzma_c.46.1.1 (A:) Erk2 binding domain of Mapk phosphatase mkp-3 {Human (Homo sapiens)}

MIDTLRVPFASEMAISKTVawlNEQLEGNERLLMDCRPQELYESSHIESAINVAIPGIMLRLQKG
NLPVRALFTRGEDRDRFTRRCGTDVVLYD
ESSSDWNENTGGESLLGLLKKLDEGCRAFYLEGGFSKFQAEFSLH
CETNLDGs

>d1gmx_ c.46.1.3 (A:) Sulfurtransferase GlpE {Escherichia coli}

MDQFECINVADAHQKLQEKEAVLDIRDPQSFAMGHAVQAFHTNDLGAFMRDNDFTPVMVMCYHGNSSKGAAQYLLQQGYDVVSIDGG
FEAWQRQFPAEVAYGA

>d1rhs_1 c.46.1.2 (1-149) Rhodanese {Cow (Bos taurus)}

VHQVLYRALSTKWLAESVRAVGKVGPGRLVLDASWYSPGTREARKEYLERHVPGASFFDIECRDKASPYEVMLPSEAGFADYVGSLGISNDTHVV
YDGDDLGSFYAPRVVWMFRVFGHRTSVLNGGFRNWLKEGHPVTSEPSRPEP

>d1rhs_2 c.46.1.2 (150-293) Rhodanese {Cow (Bos taurus)}

AIFKATLNRSLLTYEQVLENLESKRFQLVDSRAQGRYLGTQPEPDAVGLDSGHIRGSVNMPFMNLTEDGFEKSPEELRAMFEAKVKDLTKPLIATCR
KGVTACHIALAAYLCGKPDVAIYDGSWF EW FHRAPPETWVQSQKG

>d1e0ca1 c.46.1.2 (A:1-135) Sulfurtransferase {Azotobacter vinelandii}

MDDFAISLPLVIEPADLQARLSAPELILVDTSAARYAEHIPGARFVDPKRTQLGQPPAPGLQPPREQLESLFGE LGH RPEAVVVYDDEGGGWAGR
IWLLDVGQQRYHYLNNGGLTAWLAEDRPLSREL PAPA

>d1e0ca2 c.46.1.2 (A:136-271) Sulfurtransferase {Azotobacter vinelandii}

GGPV A SLHDEPTASRDYLLGRLGAADLAIWDARSPQEYRGEKVLAAKGGHIPGAVNFEWTAAMDPSRALRIRTDIAGRLEELGITPDKEIVTHCQT
HHRSGLTYLI AKALGYPRVKG YAG SWGE WGNHPDTPVEL

>d2trxa_ c.47.1.1 (A:) Thioredoxin {Escherichia coli}

SDKIIHLTDDSFD TDV LKADGAI LVDF WAEWCGPCKMIAPI LDEIADEYQGKLT VAKLNIDQNP GTAP KYGIRG IPT LLLFKNGEVAAT KV GAL SKG QLK
EFL DANLA

>d1thx_ c.47.1.1 (-) Thioredoxin {Anabaena sp., pcc 7120}

SKGVITITDAEFESEVLKAEQPVLVYFWASWCGPCQLMSPLINLAANTYSDRLKVV KLEIDPNPTTVKKYKVEGVPALRLVKGEQILDSTEGVISKDLL
SFLD THLN

>d1dbya_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}

MEAGAVNDDTFKNVLESSVPVLFDFWAPWCGPCRIIAPVVDEIAGEYKDKLKCVKLNTDESPNVASEYGIRSIPTIMVFKGKGCETIIGAVPKATIV
QTVEKYL N

>d1ep7a_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}

GGSVIVIDS KA AWDQ ALQAGK EEH KPI VDFT ATW CGPCKMIAPLFETLSNDYAGKVIFLKVDV DAVA A AEAAGITAMPTFHVYKDGVKA DDLVG
ASQDKL KALVAKHAAA

>d1quwa_ c.47.1.1 (A:) Thioredoxin {Bacillus acidocaldarius}

ATMTLTDANFQQAIQGDKPVLDFWAAWC GPCRMMAPVLEFAEAHADKVTVA KLNVDENPETTSQFGIMSI TLIFKG GRPVKQLIGYQPKEQ
LEAQLADVLQ

>d1f9ma_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin F}

MEAIVGKVTEVN KDT FWPIVKAAGDKPVV LDMFTQWCGPCKAMAPKYE KLAEEYLDVIFLKDCNQENKTLAKELGIRV VPTFKILKENS VVGEV
T GAKYDKL KLEAIQAARS

>d1fb6a_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin M}

VQDVNDSSWKEFVLESEVPVMVDFWAPWC GPKLIA PVIDE LAKEYSGKIAVYKLNTDEAPGIATQY NIRSIPTVLFFKNGERKESIIGAVPKSTLDS
EKYL

>d1erv_ c.47.1.1 (-) Thioredoxin {Human (Homo sapiens)}

MVKQIESKTA FQE ALDA AGDKLVV DFSATW CGPCKM IKPFFHSLSEKYSNVIFLEV DVDDCQDVASECEVKS MPTFQFFKGQKVGE FSGANKEKL
EATIN ELV

>d1aba_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Bacteriophage T4}

MFKVYGYDSNIHKCGPCDNAKRLTVKKQPFEFINIMPEKGVF DDEKIAELLTKLGRDTQIGLTMPQVFAPDGSHIGGF DQLREYFK

>d1qfna_ c.47.1.1 (A:) Glutaredoxin (Thioltransferase) {Escherichia coli}

MQTVIFGRSGCPYSVRAKDLAEKLSNERDDFQYQYVDIRAEGITKEDLQQKAGKP VETVPQIFDQQHIGGYTDFAAWVKENLDA

>d3grx_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Escherichia coli, GRX3}

ANVEIYTKECPYSHRAKALLSSKGVSFQELPIDGNAAKREEMIKRSGRRTVQPQFIDAQHIGGYDDLYALDARGGLDPLK
>d1kte__ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Pig (Sus scrofa)}
AQAFVNLSKIQPGKVVVFICPTCPFRKTQELLSQLPKEGLLEFDITATSDTNEIQDYLQQLTGARTVPRVFIGKECIGGCTDLESMHKRGEELLRLQQ
VGAVK
>d1jhb__ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Human (Homo sapiens)}
AQEFVNCKIQPGKVVVFICPTCPYCRRAQEILSQLPIKQGLLEFDITATNHTNEIQDYLQQLTGARTVPRVFIGKDCIGGCSDLVSLQQSGELLRLKQI
GALQ
>d1h75a__ c.47.1.1 (A:) Glutaredoxin-like NRDH-redoxin {Escherichia coli}
MRITIYTRNDCVQCHATKRAMENRGDFEMINVDRVPEAAEALRAQGFRQLPVVIAGDLSWSGFRPDMINRLHPAP
>d1fo5a__ c.47.1.1 (A:) MJ0307, thioredoxin/glutaredoxin-like protein {Archaeon Methanococcus jannaschii}
MSKVVKIELTSPMCPHCPAAKRVVEEVANEMPADEVYEINVMENPQKAMEYGIMAVPTIVINGDVEFIGAPTKEALVEAIKKRL
>d1iloa__ c.47.1.1 (A:) MTH985, a thioredoxin {Archaeon Methanobacterium thermoautotrophicum}
MMKIQIYGTGCANCQMILEKNAREAVKELGIDAEFEKIEMDQILEAGLTALPGLAVDGEKIMGRVASKEEIKKILS
>d1gh2a__ c.47.1.1 (A:) Thioredoxin-like protein, N-terminal domain {Human (Homo sapiens)}
GVGVKPVGSDPDFQPELSGAGSRLAVVKFTMRCGPCLRIAPAFSSMSNKYPQAVFLEVVDVHQCGTAATNNISATPTFFRNKVRIDQYQGADAV
GLEEKIKQHLE
>d1bjx__ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}
AATTLPDGAAAESLVESSEAVIGFFKDVEDSAKQFLQAAEADDIPFGITSNSDVFSKYQLDKDGVVLKKFDEGRNNFEGEVTKENLLDFIKHNQLP
LVIEFTEQTA
>d1mek__ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}
DAPEEEEDHVLVLRKSNAEAALAAHKYLLVEFYAPWCGHCKALAPEYAKAAGKLKAEGSEIRLAKVDATEESDLAQYGVRYGPTIKFFRNGDTASPKEY
TAGREADDIVNWLKRTGPAA
>d1a8l_1 c.47.1.2 (1-119) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}
MGLISDADKKVIKEEFFSKMVNPVKLIVFVRKDHCQYCDQLKQLVQELSELTDKLSYEIVDFDTPEGKELAKRYRIDRAPATTITQDGKDFGVRYFGLPA
GHEFAAFLEDIVDVSREET
>d1a8l_2 c.47.1.2 (120-226) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}
NLMDETKQAIRNIDQDVRILVFVTPTCYCPLAVRMAHKFAIENTKAGKGKILGDMVEAIEYPEWADQYNVMAVPKIVIQVNGEDRVEFEGAYPEK
MFLEKLLSALS
>d1hyua3 c.47.1.2 (A:1-102) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}
MLDTNMKTQLRAYLEKLTKPVELIALDDSAKSAEIKELAEIAELSDKVTFKEDNTLPRKPSFLTNPGSQGPRFAGSPLGHEFTSLVALLWTGGH
PS
>d1hyua4 c.47.1.2 (A:103-198) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}
KEAQSLLEQIRDIDGDFEFETYSLSCNCVDVQALNLMALVNPRIKHTAIDGGTFQNEITERNVGMGVPAVFVNGKEFGQGRMTLTEIVAKVDTG
>d1a8y_1 c.47.1.3 (3-126) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
GLDFPEYDGVDRLINVNAKNYKNVFKYEVALLYHEPPEDDKASQRQFEMEELILEAAQVLEDKGVGFLVDSEKDAAVAKKLGTEEDSIYVFKE
DEVIEYDGEFSADTLVEFLLDVLED
>d1a8y_2 c.47.1.3 (127-228) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
VELIGERELQAFENIEDEIKLIGYFKNKDSEHYKAFKEAAEEFHPIPFATFDSKVAKKLTKLNEIDFYEAFMEEPVTIPDKPNSEEEIVNFVEEHRRS
>d1a8y_3 c.47.1.3 (229-347) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
TLRKLKPESMYETWEDDMGDIHIVAFEEADPDGYFLEILKSVAQDNTDNPDLIIWIDPDDFPLLVPYWEKTFIDLSAPQIGVNVNTDADSVWM
EMDDEEDLPSAEELEDWLEDVL
>d1fvka2 c.47.1.4 (A:1-64,A:129-188) Disulphide-bond formation facilitator (DSBA) {Escherichia coli}
AQYEDGKQYTTLEKPVAGAPQVLEFFSFCPHCYQFEEVLHISDNVKKLPEGVKMTKYHVNFMXFVVKSLVAQQEKAADVQLRGVPAMFVNGK
YQLNPQGMDTSNMDVFVQQYADTVKYLSEK

>d1bed_2 c.47.1.4 (1-62,127-181) Disulphide-bond formation facilitator (DSBA) {Vibrio cholerae}
AQFKEGEHYQLKTPASSSPVVSEFFSFYCPHCNTFEPIIAQLQQQLPEGAKFQKNHVSFMGXFAVDSMVRRFDKQFQDSGLTGVPAAVNNRVLQGQSVKSLDEYFDLVNYLLTK
>d1aqwa2 c.47.1.5 (A:1-76) Glutathione S-transferase {Human (Homo sapiens), class pi}
PPYTVVYFPVRGRCAALRMILLADQQSWKEEVVTETWQEGSLKASCLYQGLPKFQDGDLTLQSNITLRLHGRRTL
>d2gsra2 c.47.1.5 (A:1-76) Glutathione S-transferase {Pig (Sus scrofa), class pi}
PPYTITYFPVRGRCEAMRMILLADQQSWKEEVVTMETWPPLPKSCLFRQLPKFQDGDLTLQSNAILRHLGRSFGL
>d1glqa2 c.47.1.5 (A:1-78) Glutathione S-transferase {Mouse (Mus musculus), class pi}
PPYTIVYFPVRGRCEAMRMILLADQQSWKEEVVTIDTWMQGLLKPTCLYQGLPKFEDGDLTLQSNAILRHLGRSLGL
>d1gtua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
PMILGYWDIRGLAHAIRLLETDSSYEKKYTMGDAPPYDRSQWLNEFKLGLDFPNLPYLIDGAHKITQSNAILCYIARKHN
>d1hna_2 c.47.1.5 (1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
PMTLGYWNIRGLAHSIRLLETDSSYEKKYTMGDAPPYDRSQWLNEFKLGLDFPNLPYLIDGTHKITQSNAILRYIARKHN
>d3gtub2 c.47.1.5 (B:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
SCESSMVLGYWDIRGLAHAIRLLEFTDTSYEKKYTCGEAPDYDRSQWLNEFKLGLDFPNLPYLIDGKRNKITQSNAILRYIA
>d2gsta2 c.47.1.5 (A:1-84) Glutathione S-transferase {Rat (Rattus norvegicus), class mu}
PMILGYWNVRGLTHPIRLLETDSSYEKKYAMGDAPPYDRSQWLNEFKLGLDFPNLPYLIDGSRKITQSNAIMRYLARKHH
>d1gsua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Chicken (Gallus gallus), class mu}
VVTLGWDIRGLAHAIRLLETYTETPYQERRYKAGPAPDFDPSDWTEKEKLGLDFPNLPYLIDGDKLTQSNAILRYIARKHN
>d1gsea2 c.47.1.5 (A:2-80) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}
AEKPKLHYFNARGKMESTRWLAAAGVEFEKKFIKSAEQLDKLRNDGYLMFQQVPMVEIDGMKLVQTRAILNYIASKYN
>d1gula2 c.47.1.5 (A:4-80) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}
RPLKHYPNGRGRMESVRVVLAAGVEFEEFKLEQLYKLQDGHNHLLFQQVPMVEIDGMKLVQTRAILNYIASKYN
>d1f3aa2 c.47.1.5 (A:1-79) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-1)}
AGKPVLYFNARGRMECTIRWLAAAGVEFEKKFIQSPEDEKLKKDGNLMDQVPMVEIDGMKLAQTRAILNYIATKYD
>d1b48a2 c.47.1.5 (A:2-79) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-4)}
AAKPKLYYFNNGRGRMESIRWLAAAGVEFEEEFLETREQYEKMQKDGHLLFGQVPLVEIDGMMLTQTRAILSYLAKEY
>d1ljra2 c.47.1.5 (A:1-79) Glutathione S-transferase {Human (Homo sapiens), class theta}
MGLELFSDLVSPQRSAVYIFAKKNGIPLERTLVDLKGQHKSKEFLQINSLGKLPDKDFILTTESSAIIYLSCKYQ
>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}
PKYTLHYFPLMGRAELCRFVLAHGEETDRVEMADWPNLKATMYSNAMPVLDIDGTKMSQSMCIARHLAREFG
>d1eema2 c.47.1.5 (A:5-102) Glutathione S-transferase {Human (Homo sapiens), class omega}
SARSLGKGSAPPGPVPEGSIRIYSMRFCPFAERTRLVLKAKGIRHEVININLNKPKEWFFKKNPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKLL
>d1fw1a2 c.47.1.5 (A:5-87) Glutathione S-transferase {Human (Homo sapiens), class zeta}
KPILYSYFRSSCSWRVRIALALKIDYKTPINLIKDGQQFSKDFQALNPMKQVPTLKIDGITIHQSLAIIEYLEETRPTPR
>d1duga2 c.47.1.5 (A:1-80) Glutathione S-transferase {Schistosoma japonicum}
SPILGYWKIGLVQPTRLLEEKYEEHLYERDEGDKWRNKKFELGLEFPNLPLYIDGDVKLTQSMAIIRYIADKHNM
>d1fhe_2 c.47.1.5 (1-80) Glutathione S-transferase {Fasciola hepatica}
PAKLGWKLRLAQPVRFLFELYLGEEYEEHLYGRDDREKWMSEKFNMGLDLPNLPLYIDDKCKLTQSVAIMRYIADKHGM
>d2fhea2 c.47.1.5 (A:1-80) Glutathione S-transferase {Fasciola hepatica}
PAKLGWKRGLQQPVRLLLEYLGEKYEEQIYERDDGEKWFSSKKFELGLDLPNLPLYIDDKCKLTQSLAIRDYIADKHGM
>d1gnwa2 c.47.1.5 (A:2-85) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}

GIKVFHGPASIATRRVIALHEKNLDFELVHVELKDGEHKKEPFLSRNPGQVPAFEDGDLKFESRAITQYIAHRYENQGTNL
>d1axda2 c.47.1.5 (A:1-80) Glutathione S-transferase {Maize (Zea mays), type I}
APMKLYGAVMSWNLTCACTAAEAGSDYEIVPINFATAEHKSPEHLVRNPFGQVPALQDGDLYLFESRAICKYAARKNKP
>d1aw9_2 c.47.1.5 (2-82) Glutathione S-transferase {Maize (Zea mays), type III}
APLKLYGMPLSPNVVRATVLNEKGDFEIVPVDLTTGAHKQPDFALNPFGQIPALVDGDEVLFESRAINRYIASKYASE
>d1e6ba2 c.47.1.5 (A:8-87) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana), class zeta}
KLKLYSYWRSSCAHRVIALALKGLDYEYIPVNLLKGDDQFDSDKINPMGTVPALVGDVWINDSFAIMYLDEKYPEP
>d1a0fa2 c.47.1.5 (A:1-80) Glutathione S-transferase {Escherichia coli}
MKLFYKPGACSLASHITLRESGKDFTLVSVDLMKKRLENGDDYFAVNPKGQVPALLDDGTLTEGVAIMQYLADSVPR
>d1pmt_2 c.47.1.5 (1-80) Glutathione S-transferase {Proteus mirabilis}
MKLYYTPGSCSLSPHIVLRETGLDFSIERIDLRTKKTESGKDFLAIPKGQVPVLQDNGDILTEGVAIVQYLADLPDR
>d1f2ea2 c.47.1.5 (A:1-80) Glutathione S-transferase {Sphingomonas paucimobilis}
MKLFISPGACSLAPHIALRETGADFEAVKVDLAVRKTEAGEDFLTVNPMSGKVPALTDSGETLTENPAILLYADQNPAS
>d1g7oa2 c.47.1.5 (A:1-75) Glutaredoxin 2 {Escherichia coli}
MKLYIYDHCPYCLKARMIFGLKNIPVLEHVLLNDAETPRMVQGKQVPLQKDDSRYPMPESMDIVHYVDKLDGK
>d1k0da2 c.47.1.5 (A:109-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}
QPLEGYTLFSHRASPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSNPNARVPALIDHGMDNLSIWESGAILLHVNKYYKETGNPL
>d1k0dd2 c.47.1.5 (D:99-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}
YSRITKFFQEQQLEGYTLFSHRASPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSNPNARVPALIDHGMDNLSIWESGAILLHVNKYYKETGN
PL
>d1k0ma2 c.47.1.5 (A:6-91) Chloride intracellular channel 1 (clic1) {Human (Homo sapiens)}
PQVELFKAGSDGAKIGNCPFSQRLFMVLWLKGVTNFVTTVDTKRRTEVQKLCPGELPFLLYGTEVHTDTNKIEEFLEAVLCPP
>d2trcp_c.47.1.6 (P:) Phosducin {Rat (Rattus norvegicus)}
EGQATHGPKGVIDWRKFKESEDGDSIPPSKKEILRQMSSPQRDDKDSKERMSRKMSIQEYELIHQDKEDEGCLRKYRRQCMQDMHQKLSFG
PRYGFVYELETGEQFLETIEKEQKVTTIVNIYEDGVRGCDALNSSLECLAAEYPMVKFCIKASNTGAGDRSSVLPTLLVYKGELISNFISVAEQFA
EDFFAADVESFLNEYGLLPER
>d1a0rp_c.47.1.6 (P:) Phosducin {Cow (Bos taurus)}
FEGQASHTGPKGVIDWRKFKESEDSDSVAHSKKEILRQMSSPQRDDKDSKERMSRKMSVQEYELIHDKDEDENCLRKYRRQCMQDMHQKLSF
GPRYGFVYELESQEQLTIEKEQKITTIVHIYEDGIKGCDALNSSLICLAAEYPMVKFCIKASNTGAGDRSSVLPTLLVYKGELISNFISVTEQLAE
EFFTDGVESFLNEYGLLPER
>d1g7ea_c.47.1.7 (A:) Endoplasmic reticulum protein ERP29, N-domain {Rat (Rattus norvegicus)}
LHTKGALPLDTVTFYKVIPKSFKVLKFDTQYPYGEKQDEFKRLAENSASSDDLLAEVGISDYGDKLNMESEKYKLDKESYPVYFRDGFENPVPY
SGAVKVGAIQRWLKGQGVYLG
>d1qgva_c.47.1.8 (A:) spliceosomal protein U5-15Kd {Human (Homo sapiens)}
SYMLPHLHNGWQVDQAILSEEDRVVIRFGHDPTCMKMDVLYSIAEKVKNFAVIYLVDITEVPDFNKMELYDPCTVMFFFNRKHIMIDLGTG
NNNKINWAMEDKQEMVDIETVYRGARKGRGLVVSPKDY
>d1eeja1 c.47.1.9 (A:61-216) Disulfide bond isomerase, DsbC, C-terminal domain {Escherichia coli}
NVTNKMLKQLNALEKEMIVYKAPQEKGKHTVFTDITCGYCHKLHEQMADYNALGITVRYLAFPRQGLDSDAEKEMKAIWCAKDNKAFDDVMA
GKSVAPASCDVDIADHYALGVQLGVSGTPAVVLSNGTLVPGYQPPKEMKEFLDEHQKMTSGK
>d1gp1a_c.47.1.10 (A:) Glutathione peroxidase {Cow (Bos taurus)}
RTVYAFSARPLAGGEPEFNSSLRGKVLLIENVASLXGTTVRDYTMNDLQRRRLGPRGLVVLGFPCNQFGHQENAKNEEILNCLKYVRPGGGFEPNFM
LFEKCEVNGEKAHPLFAFLREVLPPTSDDATALMTDPKFITWSPVCRNDVSWNFEKFLVGPDPGVPRRYSRFLTIDIEPDIELLSQ
>d1qk8a_c.47.1.10 (A:) Tryparedoxin I {Crithidia fasciculata}
GLDKYLPGIEKLRRGDGEVEVKSLAGKLVFFYFSASWCPPCRGFTPQLIEFYDKFHESKNFEEVVFCTWDEEDGFAGYFAKMPWLA
VPAQSEAVQK

LSKHFNVESIPTLIGVDADSGDVVTTRARATLVKDPEGEQFPWKDA
>d1i5ga_c.47.1.10 (A:) Tryparedoxin II {Crithidia fasciculata}
SGLKKFFPYSTNVLGAAADIALPSLAGKTVFYFSASWCPPSRAFTPQLIDFYKAHAEKKNFEVMLISWDESAEDFKDYYAKMPWLALPFEDRKGMEFLTTGFDVKSIPTLGVVEADSGNIITTOARTMVVKDPEAKDFPWPN
>d1e2ya_c.47.1.10 (A:) Tryparedoxin peroxidase (thioredoxin peroxidase homologue) {Crithidia fasciculata}
GAAKLNHPAPEFDDMALMPNGTFKKVSLSSYKGKYVLFYPMDFTFVCPTEIIFQSDDAKRFAEINTEVISCDSEYSHLQWTSVDRKKGLGPM
AIPMLADKTKAIARAYGVLDDESGVAYRGVFIIDPNGKLQRQIIINDMPIGRNVEEVIRLVEALQFVEEHG
>d1qq2a_c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys peroxiredoxin) {Norway rat (Rattus norvegicus)}
SGNAKIGHPAPSFKATAVMPDGQFKDISLDYKGKYVVFYPLDFTFVCPTEIIFSDRAEEFKLNCQVIGASVDSHFLAWINTPKQGGLGPM
NIPLVSDPKRTIAQDYGVLKADEGISFRGLFIIDDKGILRQITINDLPVGRSVDEILRLVQAFQFTDKHGEVCPA
>d1qmva_c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys peroxiredoxin) {Human (Homo sapiens)}
SGNARIGKPAPDFKATAVVVGAFKEVKLSDYKGKYVVFYPLDFTFVCPTEIIFSNRAEDFRKLGCEVLGVSVDSQFTHLAWINTPRKEGLGPLNIP
LLADVTRRLSEDYGVLKTDGKGLRQITNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKGSDTIKPNVDDSKEYFSKHN
>d1hd2a_c.47.1.10 (A:) Peroxiredoxin 5 {Human (Homo sapiens)}
APIKVGDAIPAVEVFEPEGPNKVNLAEFLKGKGVFGVPGAFTPGCSKTHLPGFVEQAEALKAKGVQVVACLSVNDAFVTGEWGRAHKAEKGKVRLLADPTGAFGKETDLDLDSLVSIFGNRRLKRFMSMVQDGIVKALNVEPDGTGLTCSLAPNIISQL
>d1prxa_c.47.1.10 (A:) HorF6 peroxidase {Human (Homo sapiens)}
LLGDVAPNFNEANTTVGRIRFHDFLGSWGLFSHPRDFTPVCTTELGRAAKLAPEFAKRNVKLIALSIDSVEDHLAWSKDNAYNSEEPTEKLPFPIIDRNRELAILGMLPAEKDEKGMPVTARVFVFGPDKKLKSILYPATTGRNFDEILRVVSLQLTAEKRVATPVWDKGDSVMVLPTIPEEEAKKLFPKGFTKELPSGKKYLRYTPQ
>d1kyga_c.47.1.10 (A:) Alkyl hydroperoxide reductase AhpC {Salmonella typhimurium}
SLINTKIKPFKNQAFKNGEFIEVTEKDETRGSVFFFYPADFTFVCPTELGDVADHYEELQKLGVDVYSSTDTHFTHKAWHSSSETIAKIKYAMIGDPTGALTRNFDNMREDEGLADRATFVDPQGIIQAEVTAEGIGRDASDLRKIKAAQYVAAHPGEVCP
>d1jfua_c.47.1.10 (A:) Membrane-anchored thioredoxin-like protein TlpA, soluble domain {Bradyrhizobium japonicum}
TGDPACRAAVATAQKIAPLAHGEVAALTMASAPLKLPLDADGKPKKLSDFRGKTLVNLWATWCPCRKEPALDELQGKLSGPNEVVAINIDTRDPEKPKTFLKEANLTRGLGFNDQKAKVQFDLKAIGRALGMPTSVLVDPQGCEIATIAGPAEWASEDALKLIRAATG
>d1foha3 c.47.1.10 (A:462-662) Phenol hydroxylase, C-terminal domain {Soil-living yeast (Trichosporon cutaneum)}
NLVTDKKSSQKELAKNCVVGTRFKSQPVVRHSEGLWMHFGDRLVTDGRFRIIVFAGKATDATQMSRKKFSAYLDSENSVISLYTPKVSDRNSRIDVTHSCHRDDIEMHDFPAPALHPKWQYDFIYACDSWHHPHPKSYQAWGVDETKGAVVVVPDGYTSVTDLEGTAEIDRYFSGILVEPKEKSGAQTEADWTKS
>d1f37a_c.47.1.11 (A:) Thioredoxin-like 2Fe-2S ferredoxin {Aquifex aeolicus}
AEFKHVFCVQDRPPGHPQGSCAQRSREVQAFMEKIQTDPQLFMTTIVPTGCMNACMMGPVVYPDGVVYQGV/KPEDVDEIVEKHLKG
GEPVERLVIKGKPPGM
>d1j9ba_c.47.1.12 (A:) Arsenate reductase ArsC {Escherichia coli}
NITIYHNPACGTSRNTLEMIRNSGTEPTIILYLENPPSRDELVKLIADMGISVRALLRNVEPYEQLGLAEDKFTDDQLIDFMLQHPILINRPIVVTPLGTRLCRPSEVVLDILQDAQKGAKTKEDEGEKVVDEAGKRL
>d1qmha1 c.47.2.1 (A:185-279) RNA 3'-terminal phosphate cyclase, RPTC, insert domain {Escherichia coli}
ERGNIVQMRGEVLAGVPRHVAEREIATLAGSFSLHEQNIHNLPRDQGPGNTVSLEVESENITERFFVVGKEKRSVSAEVVAAQLVKEVKRYLASTA
>d1gpua3 c.48.1.1 (A:535-680) Transketolase {Baker's yeast (Saccharomyces cerevisiae)}
EGSSIESASKGGYVLQDVANPDIILVATGSEVLSVEAKTLAAKNIKARVVSLPDFFTFDQPLEYRLSVPDNVPIMSVEVLATTCWGKYAHQSFGID
RFGASGKAPEVFKFFGTPPEGVAERAQKTIAYKGDKLISPLKKAF
>d1dtwb2 c.48.1.2 (B:205-342) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}
PYNIPLSQAEVIQEGSDVTLVAWGTQVHVIREVASMAKEKLGVSCVIDLRTIIPWDVDTICKSVIKTGRLLISHEAPLGGFAEISSTVQEECFLNLEAP
ISRCVCGYDTPFPHIFEPFYIPDKWKCYDALRKMINY

>d1qs0b2 c.48.1.2 (B:206-339) 2-oxoisovalerate dehydrogenase E1b {Pseudomonas putida}
YYTVPLDKAAITRPGNDSVLTYGTTVVAQVAAEESGVDAEVIDLRLWPLDLDTIVESVKTGRCVVHEATRTCGFAELVSLVQEHCFFHLEAPI
ERVTGWDTPYPHAQEWYFPGPSRVGAALKKVM

>d1ik6a2 c.48.1.2 (A:192-326) E1-beta subunit of pyruvate dehydrogenase {Archaeon Pyrobaculum aerophilum}
DYVVEIGKARVAREGDDVTLVGAVVHAKLEAAERVKASVEVVDLQLTNPLDFDTVLKSRSKTGRLIAHDSPKTGGGLGAEVRALVAEKALDRLTAPV
IRLAGPDVPQSPIAADAAAYAPTVERIIKAIYEYVMRY

>d1keka3 c.48.1.3 (A:259-415) Pyruvate-ferredoxin oxidoreductase, PFOR, domain II {Desulfovibrio africanus}
KLFDYVGAPDAERVIVSMGSSCETIEEVINHLAAKGEKIGLIKVRLYRPFVSEAFFAALPASAKVITVLDRTKEPGAPGDPLYLDVCSAFVERGEAMPKIL
AGRYGLGSKEFSPAMVKSVDNMSGAKKNHFTVGIEDDVTGTSPLPVNAFADTPK

>d1a49a3 c.49.1.1 (A:396-530) Pyruvate kinase, C-terminal domain {Rabbit (Oryctolagus cuniculus)}
ELARSSSHSTDLMEAMAMGSVEASYKCLAAALIVTESGRSAHQVARYRPRAPIIAVTRNHQTARQAHLYRGIFPVVCKDPVQEAWAEDVDLRVNLA
MNVGKARGFFKKGDVVVLTGWRPGSGFTNTMRVPPV

>d1pkla3 c.49.1.1 (A:358-498) Pyruvate kinase, C-terminal domain {Leishmania mexicana}
NEYVFFNSIKKLQHIPMSADEAVCSSAVNSVYETKAKAMVVLNTGRSARLVAKYRPNCPICVTTRLQTCRQLNITQGVESVFFDADKLGHDEGKEH
RVAAGVEFAKSKGYVQTDYCVVIHADHKVKGYANQTRILLVE

>d1a3wa3 c.49.1.1 (A:367-500) Pyruvate kinase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
DMRNCTPKPTSTTETVAASAVAATFEQKAKAIIVLSTSQTTPRLVSKYRPNCPICLVTCPRAARFSHYRGVFPVFEKEPVSDWTDDVEARINFOIEK
AKEFGILKKGDTYVSIQGFKAGAGHSNTLQVSTV

>d1e0ta3 c.49.1.1 (A:354-470) Pyruvate kinase, C-terminal domain {Escherichia coli}
ITEAVCRGAVETAEKLDAPLIVVATQGGKSARAVRKYFPDATILATTNEKTAHQVLVLSKGVVPPQLVKEITSTDDFYRLGKELALQSGLAHKGDVVVMVS
GALVPSGTTNTASVHVL

>d1e79g_c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Cow (Bos taurus)}
ATLKDIRRLSIKNIQKITSMKMVAAAKYARAERELKPARVYGVGLALYEKADIKPEDKKHLLIGVSSDRGLCGAIHSSVAKQMSEAANLAAAG
KEVVIIGVGDKIERSILHRTHSDQFLVTKEVGRPPFTGDAVIALELLNSGYEFDEGSIIFNFRRSVISYKTEEKPIFSLDTISSAESMSIYDDIDADVLRNY
QEYSLANIIYSLKESTTSEQSARMATMDNASKNASEMIDKLTTFNRTRQAVITKELIEIISGAAALD

>d1mabg_c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Rat (Rattus norvegicus)}
RDITRRLSIKNIQKITSMKMVAAAKYARAERELKPARVYGTGLALYEKAEIKGPEDKKHLLIGVSSDRGLCGAIHSSVAKQMNDMAALTAAGKE
VMIVGIGEIKSILYRTHSDQFLVSFKDVGKRPPFTGDAVIALELLNSGYEFDEGSIIFNQFKSVISYKTEEKPIFSTVVAENMSIYDDIDADVLQNY
QEYNLANIIYSLKESTTSEQSARMATMDNASKNASDMIDKLTTFNRTRQAVITKELIEIISGAAALD

>d1fs0g_c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Escherichia coli}
KITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGNLEYKHPYLEDRDVKRVGYLVVSTDRLCGGLNINLFKKLLAEMKTWTDKGVQ
CDLAMIGSKGVSSFNSVGGNVVAQVTGMGDNPSLSELIGPVKVMLQAYDEGRLDKLYIVSNKFINTMSQVPTISQLLPLPASDDDLKHKSWDYLYE
PDPKALLDTLLRRYVESQVYQGVVENLASEQAARMVAMK

>d1lam_1 c.50.1.1 (1-159) Leucine aminopeptidase, N-terminal domain {Cow (Bos taurus)}
TKGLVLGIYSKEKEDEPQFTSAGENFNKLVSGKLREILNISGPPLKAGKTRTFYGLHEDFPSVVVGLGKKTAGIDEQENWHEGENIRAABAAGCRQ
IQDLEIPSVEVDPCGDAQAAAEGAVLGLYEYDDLQKQRKVVVSAKLHGSEDQEAWQRGV

>d1kmma1 c.51.1.1 (A:326-424) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Escherichia coli}
DPVVDIYLVASGADTQSAAMALAERLRDELPGVKLMTNHGGGNFKQQFARADKWGARAVVGESEVANGTAVVKDLRSGEQTAQAQDSVAAHL
RTLLG

>d1qe0a1 c.51.1.1 (A:326-420) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Staphylococcus aureus}
IEENLDLFIVTMGDQADRYAVKLLNHLRHNGIKADKDYLQRKIKGQMKQADRLGAKFTIVIGDQELENNKIDVKNMOTTGESETIELDALVEYFKK

>d1h4vb1 c.51.1.1 (B:326-421) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Thermus thermophilus}
EKGPDLYLIPTEEAVAEAFYLAELRPLRRAEYALAPRKPAGGLEALKRGAAFAGFLGEDELRAVEVTLKRLATGEQVRLSREEVPGYLLQALG

>d1atia1 c.51.1.1 (A:395-505) Glycyl-tRNA synthetase (GlyRS), C-terminal domain {Thermus thermophilus}

QLAPIKVAIPLVKNRPEITEYAKRLKARLLALGLGRVLYEDTGNIGKAYRRHDEVGTPFAVTVDYDTIGQSKDGTTRLKDTVTVRDRDTMEQIRLHVDELEGFLRERLRW
>d1qf6a1 c.51.1.1 (A:533-642) Threonyl-tRNA synthetase (ThrRS), C-terminal domain {Escherichia coli}
FPTWLAPVQVIMNITDSQSEYVNELTQKLSNAGIRVKADLRNEKIGFKIREHTLRRVPYMLVCGDKEVESGKVAVRTRRGKDLGSMDVNEVIEKLOQEIRSRSLKQLEE
>d1hc7a1 c.51.1.1 (A:277-403) C-terminal domain of ProRS {Thermus thermophilus}
RGLVLPPRRLAPIQVIVPIYKDESREVLEAAQGLRQALLAQGLRVHLDLDRDQHTPGYKFHEWELKGVPFRVELGPKDLEGGQAVLASRLGGKETPLAALPEALPGKLDAFHEELYRRALAFREDH
>d1g5ha1 c.51.1.1 (A:343-469) The aaRS-like accessory subunit of mitochondrial polymerase gamma, C-terminal domain {Mouse (Mus musculus)}
RKVLKLHPCLAPIKVALDVGKGPTVELRQVCQGLLNELLNGISVWPGYSETVHSSEQLHSKYDEMMSVLFSVLVTETTLENGLIQLRSRDTTMKEMMHISKLRLDFLVKYLASASNVAALDHHHHH
>d1crza2 c.51.2.1 (A:7-140) TolB, N-terminal domain {Escherichia coli}
DSGVDSGRPIGVVPFQWAGPGAAPEDIGGIVADLRNSGKFNPPLDRARLPQQPGSAQEVQPAAWSALGIDAVVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNKQWLRYAGHTASDEVFEKLGTGKG
>d1eexb_c.51.3.1 (B:) Diol dehydratase, beta subunit {Klebsiella oxytoca}
GFLTEVGEARQGTQQDEVIIAVGPAFLQAQTNVNIVGIPHKSILREVIAGIEEEGIKARVIRCFKSSDVAFAVEGNRLSGSGISIGIQSKGTTVIHQQGLPPLSNLELFQAPLLTETYRQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHIKETKYVVTGKNPQELRVA
>d1b78a_c.51.4.1 (A:) XTP pyrophosphatase {Archaeon Methanococcus jannaschii}
KIYFATGPNPKIKEANIIKLKDLKDVIEQJKISYPEIQQTLEEVAEFGAKWWVNILKKPVIVEDSGFFVEALNGFPGTYSKFVQETIGNEGIILKLEGKDNRNAYFKTVIGYCDENGVRFLKGIVKGRVSEEIRSKGYGFAYDSIFIPEEEERTFAEMTTEKSQISHRKKAFFEFKKFLDRI
>d1ex2a_c.51.4.2 (A:) Maf protein {Bacillus subtilis}
MTKPLILASQSPRRKELLDLQLPYSIIVSEVEEKLNRNFSPPEENVQWLAKQKAKAVADLHPHAIVIGADTMVCLDGECLGPQDQEAAASMLRRLSGRSHSVITAVSIQAENHSETFYDKTEVAFWSLSEEEIWTYIETKEPMKDAGAYGIQGRGALFVKKIDGDYYSMGLPISKTMRALRH
>d1ihna_c.103.1.1 (A:) Hypothetical protein MT938 (MTH938) {Archaeon Methanobacterium thermoautotrophicum}
SHMFSDCRFGSVTYRGREYRSDIVVHVDGSVTPRRKEISRRKGTYGTSHVMAEEEELLEEKPESIIGSGVHGALETGFRSDATVLPTCEAIKRYNEERSA
GRRVAAIIHVTC
>d1ckqa_c.52.1.1 (A:) Restriction endonuclease EcoRI {Escherichia coli}
SQGVIGIFGDYAKAHDLAVGEVSKLVKKALSNEYPQLSFRYRDSIKKTEINEALKKIDPDLGTLFVSNSSIKPDGGIVEVKDDYGEWRVVLVAEAKHQ
GKDIINIRNGLVGKRGDQDLMAAGNAIERSHKNISEIANFMLSHEHFPYVLFLEGSNFLTENISITRPDGRVNLEYNSGILNRLDLTAANYGMPINS
NLCINKFVNHKDKSIMLQAASIYTQGDGREWDSKIMFEIMFDISTTSRLVLRDLFQLTSK
>d1az3a_c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia coli}
SLRSDLINALYDENQKYDVGCIISAEGKIYPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEPKQQNHYPDFTLYKPSEPNKKIAIDIKTYYTNKENEKIKFT
LGGYTSFIRNNNTKNIVYPFDQYIAHWIIGYVYTRVATRKSSLKTYNINELNEIPKPYKGVKVFLQDKWVIAGDLAGSGNTTNIGSIHAHYKDFVEKGIF
DSEDEFLDYWR
>d1eona_c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia coli}
SLRSDLINALYDENQKYDVGCIISAEGKIYPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEPKQQNHYPDFTLYKPSEPNKKIAIDIKTYYTNKENEKIKFT
LGGYTSFIRNNNTKNIVYPFDQYIAHWIIGYVYTRVATRKSSLKTYNINELNEIPKPYKGVKVFLQDKWVIAGDLAGSGNTTNIGSIHAHYKDFVEKGIF
DSEDEFLDYWRNYERTSQLRNDKYNNSIEYRNWIYRGRK
>d1bam_c.52.1.3 (-) Restriction endonuclease BamHI {Bacillus amyloliquefaciens}
MEVEKEFITDEAKELLSKDKLIQQAYNEVKTSCSPLICWPATSKTFTINNTEKNCNGVVPIKELCYTLLEDTYNWYREKPLDILKLEKKGGPIDVYKEFIEN
SELKRVGMFETGNISSAHRSMNKLLGLKHGEIDLAIILMPIKQLAYYLTDRVTFEELEPYFELTEGQPFIFIGFNAEAYNSNVPLPKGSDGMSKRSIK
KWKDKVENK
>d1dmua_c.52.1.4 (A:) Restriction endonuclease BglII {Bacillus subtilis}

MYNLHREKIFMSYNQNQKYLEDNPEIQEKIELYGLNLLNEVISDNEEIRADYNEANFLHPFWMNYPPLDRGKMPKGQDQIPWIEVGEKAVGSKLTRL
VSQRREDITVREIGLPTGPDERYLTSPTISLTNGFTDSIMMFVDIKSVGPRDSYDLVSPNQVSGNGDWAQLEGGIQQNQQTIQGPRSSQIFLPTIP
PYILSDGTIAPVVHLFIKIYAMRSLTKGDTGQSLYKIKLASVPNGLGLFCNPYAFDSAYKFLFRPGKDRTKSLLQKRVRLVLDKIGPRVMTIDM
DK

>d1dfma_c.52.1.5 (A:) Restriction endonuclease BgIII {Bacillus subtilis}

MKIDITDYNHADEILNPQLWKEIEETLLKMPHLVKASDQASKVGSLIFDPVGTNQYIKDELVPKHWKNNIPIPKRFDLGTIDFGKRDTLVEVQFSNY
PFLLNNNTVRSELFHSNMDIDEEGMKVAAITKGHMFPASNSSLYYEAQANQLNSLAEVNVFDVPIRLVGLIEDFETDIDIVSTTYADKYSRTITKRTDV
KGKVIDTNTPNTRRRKRGTVTY

>d3pvia_c.52.1.6 (A:) Restriction endonuclease Pvull {Proteus vulgaris}

SHPDLNKLLELWPHIQEYQDLALKHGINDIFQGNGGKLLQVLLTGLTVLPREGNDAVDNAGQEYELKSINIDLTKGFSTHHHMNPVIIAKYRQWPW
IFAIYRGAIAEAIYRLEPKDLEFYDKWERKWYSDGHKDINNPKIPVVKVMEHGTKIY

>d1cfr_c.52.1.7 (-) Restriction endonuclease Cfr10I {Citrobacter freundii}

MDIISKSGEGNKYTINSIAFAVAYASHIDINTTEFSKVLSGLRDFINDEAIRLGGKISDGFSFKCNGDWYEWLIGIRAEFFLESETNFIVVKMPNATSFDV
MSIYKSCLSEFIYDLRSKLSNNVNLTSPDFSIIDIRGRREELKSMLKDISFSNISLSTISEIDNLYKNFIDYAELEHIKSFLSVKTTFRPDRLQLAHEGSLM
KALYTHLQRTWTINPTGIRYYAATSIGNADVIGLKTVAHTSITDVKSPLQSAVDEIFKINSVLDVDSCLSHIL

>d1knva_c.52.1.7 (A:) Restriction endonuclease Bse634I {Bacillus stearothermophilus}

NLTNSNCVEEYKENGKTKIRIKPFLNALIELYHHQPTGSIKENLDKLENYVKDVKAKGLAITSGAFSNTRGTWFEVMIAIQSWNYRVKRELNDYLIICK
MPNVKTFDFRKIFDNETREKLHQLEKSLTHKQQVRLITSNPDLIIRQKDLIKESEYNLPINKLTHEIDVALTLFKDIEGKCKWDSDLVAGVGLKTSLRPDR
RLQLVHEGNILKSLFAHLKMRWNPKAEFKYYGASSEPVSKADDALQTAATHTIVNVNSTPERAVDDIFSLTSFEDIDKMLDQIICK

>d1d02a_c.52.1.8 (A:) Restriction endonuclease MunI {Eubacteria (Mycoplasma unidentified)}

LSGRLNWQALAGLKASGAEQNLYNVFNAVFEGTKYVLYEKPKHLKNLYAQVVLPPDVKEIFNPLIDLSTTQWGVSPAFAIENTETHKILFGEIKRQDG
WVEGKDPSAGRGAHERSCKLFTPGLLKAYRTIGGINDEEILPFWVVFEGDITRDPKRVREITFWYDHQDNYFMWRPNESGEKLVQHFNEKLKKY
LD

>d1ev7a_c.52.1.9 (A:) Restriction endonuclease Nael {Nocardia aerocolonigenes}

EPDDDLERVATLVSQDPGDRTAGVLRDTLDQLYDGQRTGRWNFDQLHKTEKTHMGTIVEINLHREFQFGDGFETDYEIAGVQVDCFKFSMSQGA
WMLPPESIGHICLVIWASDQQCAWTAGLVKVIPQFLGTANRDLKRRLTPEGRAQVVKLWPDHGKLQENLLLHIPGDVRDQIFSAKSSRGNQHGQA
RVNELFRRVHGRLIGRAVIATVAQQDDFMKRVRGSGGARSILRPEGIILGHQDNDPKVANDLGLPVRKGQVVAARVVADEGDQRQTAEIQGRR
WAWAVPGDPIVEAPVV

>d1fua_c.52.1.10 (A:) Restriction endonuclease NgolV {Neisseria gonorrhoeae}

MQPLFTQERRIFHKKLLDGNILATNNRGVVSNAQDSNTRSFNIAKGIADLLHSETVSERLPGQTSGNAFEACSEFVQSAFEKLQHIRPGDWNVKQV
GSRNRLEIARYQQYAHITALAKAAEENPELAAALGSDYITTPDIIVTRNLIAADEINRNEFLVDENIATYASLRAGNGNMPLLHASISCKWTIRSRAQN
ARSEGGLNLVRNRKGRPHIVVVTAEPTPSRISSIALGTGEIDCVYHFALYELEQILQLQSLNEYDALDLFYIMVNGKRLKDISDPLPLDIAV

>d1dc1a_c.52.1.11 (A:) Restriction endonuclease Bsobl {Bacillus stearothermophilus}

KPFENHLKSVDDLKTTYEEYRAGFIAFALEKKNRSTPYIERARALKVAASVAKTPKDLLYLEDQDALLYASGISDKAKKFLEDDKESINNLIENFLEPAG
EEFIDEIIFYLLFQGDSLGGTMRNIAAGALAQQKLTRAISALDIANIPYKWLDSDRKYTNWMDKPEDDYELETFAKGISWTINGKHRTLMYNITVSL
VKKNVDICLNFNCEPIYTPQKVHQPKYLLGELKGGIDPAGADEHWKTANTLIRRNFKSEKGLSPKTFIGAAIEHMSMAEEIWDLQLQSGSLTNSA
NLTKTEQVGSLCRWIINI

>d1kc6a_c.52.1.19 (A:) Restriction endonuclease HinclI {Haemophilus influenzae}

SFIKPIYQDINSILIGQKVKRPKGTLGHAAGEPFEKLVYKFLKENLSDITFKQYELNDLFMKNPAIIGHEARYKLFNSPTLLFLSRGKAATENWSIENL
FEEKQNDTADILLVKDQFYELLDVKTRNISKAQAPNIISAYKLAQTCAMIDNKEFDLFDINYLEVDWELNGEDLVCVSTSFAELKSEPESELINYINWAAA
MQIQFHVRDLDDQGFNGTREEWAKSYLKHFVTQAEQRAISMIDKFVKPFKKYIL

>d2foka4_c.52.1.12 (A:387-579) Restriction endonuclease FokI, C-terminal (catalytic) domain {Flavobacterium okeanokoites}

KSELEEKKSELHKLKYVPHHEYIELIEIARNSTQDRILEMKVMEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDYGVIVDTKAYSGGYNLPIQADEM
QRYVEENQTRNKHINPNEWWKVYPSSVTEFKFLFVSGHFKNYKAQLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLTEEVRRKFNNNGEINF

>d1avqa_c.52.1.13 (A:) lambda exonuclease {Bacteriophage lambda}
SHMTPDILQRTGIDVRAVEQGDDAWHKLRLGVITASEVHNVIAPRSGKKWPDMKMSYFHTLLAEVCTGVAPEVNAKALAWGKQYENDARTLFE
FTSGVNVTESPIYRDESMRTACSPDGLCSDGNGLELKCPFTSRDFMKFRLLGGFEAIKSAYMAQVQYSMWVTRKNAWYFANYDPRMKREGLHYVVI
ERDEKYMASFDEIVPEFIEKMDEALAEIGFVGEOQWR

>d1azo_c.52.1.14 (-) DNA mismatch repair protein MutH from {Escherichia coli}
PRPLSSPPETEEQLLAQAAQQLSGYTLGELAALVGLVTPENLKRDKGWIGVLLEIWL GASAGSKPEQDFAA LGVELKTI PVDLGRPLETTFCVAPLTGN
SGVTWETSHVRHKLKRVLWIPVEGEASIPLAQRRVGSP LLWSPNEEDRQLREDWEELMDMIVLGQVERITARHGEYLQIRPKAANAKALTEAIGAR
GERILTLPRGFYLKKNFTSALLARHFLIQ

>d1cw0a_c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {Escherichia coli}
ADVHDKATRSKNMRAIATRDTAIEKRLASLLTGQGLAFRVQDASLPGRPDFVVDEYRCVIFTHGCFWHHHHCYLFKVPATRTEFWLEKIGKNVERDR
RDISRLQELGWRVLLWECALRGREKLTDEALTERLEEWICGEGASAQIDTQGIHLLA

>d1vsra_c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {Escherichia coli}
AIEKRLASLLTGQGLAFRVQDASLPGRPDFVVDEYRCVIFTHGCFWHHHHCYLFKVPATRTEFWLEKIGKNVERDRDISRLQELGWRVLLWECAL
RGREKLTDEALTERLEEWICGEGASAQIDTQGIHLLA

>d1f1za2 c.52.1.16 (A:8-168) TnsA endonuclease, N-terminal domain {Escherichia coli}
FSEVQIARRIKEGRGQGHGKDYIPWLTQEVPPSSGRSHRIYSHKTGRVHHLLSDLEAVFLSLEWESSVLDIREQFPLPSDTRQIAIDSGIKHPVIRGVD
QVMSTDFLVDCDKDGPFEQFAIQVKPAAALQDERTLEKLELERRYWQQKQIPWFIFTDKE

>d1fzra_c.52.1.17 (A:) Endonuclease I (Holliday junction resolvase) {Bacteriophage T7}
SGLEDKVSQLESKGKFEYEEWKVPVIPASNHTYTPDFLLPNGIFVTKGLWESDDRKKHLLIREQHPELDIRIVFSSRTKLYKGSPTSYGEFCEKHG
KFADKLIPAEWIKEPKKEVFPFDRLLRK

>d1gefa_c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Pyrococcus furiosus}
MYRKGAQAERELIKLLEKHGFAVRSAGSKVDLVAGNGKKYLCIEVKTKKDHLVKGKDMGRLLIESRRFGGIPVLAVKFLNVGWRFIEVSPKIEKF
VFTPSSGVSLVLLGIQKTEL

>d1hh1a_c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Sulfolobus solfataricus}
SAVERNIVSRLRDKGFAVVRAPASGSKRKDPIPDIALKNGVIILEMKSRKDIEGKIYVRREQAEGIIEFARKSGGSLFLGVKKPGVLKFIPFEKLRRTETG
NYVADSEIEGLDLEDLVRLEAKISRTL

>d1a79a1 c.52.2.1 (A:83-179) tRNA splicing endonuclease, C-terminal domain {Archaeon Methanococcus jannaschii}
ERLCLKYLVKDLRTRGYIVKTLKYGADFRLYERGANIDKEHSVYL/KVFPEDSSFLLELTGFVRAHSVRKLLIAIVDADGDIVYYNMTYVKP

>d1dzfa1 c.52.3.1 (A:5-143) Eukaryotic RPB5 N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
NERNISRLWRAFRTVKEMVKDRGYFITQEEVELPLEDFKAKYCDSMGRPQRKMMMSFQANPTEESISKFPDM GSLWVFCDEPSVGKTMKTFVIHI
QEKNFQTGIFVYQNNITPSAMKLVPSIPPATIETFNEAAVNVN

>d1gdta2 c.53.1.1 (A:1-140) gamma,delta resolvase, catalytic domain {Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDVILVKKLDLRLGRDTADMQLIKEFDAQGVSI RFIDDGIST
DGEMGKVMVVTILSAVAAQERQRILERTNEGRQEAMAKGVVF

>d1hx7a_c.53.1.1 (A:) gamma,delta resolvase, catalytic domain {Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDVILVKKLDLRLGRDTADMQLIKEFDAQGVSI RFIDDGIST
DGEMGK

>d2rsla_c.53.1.1 (A:) gamma,delta resolvase, catalytic domain {Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALKDAGVKANRIFTDKASGSSSDRKGLDLLRMKVEEGDVILVKKLDLRLGRDTADMQLIKEFDAQGVSI RFIDDGIST
DGEMGKVMVVTILSAVAAQERQR

>d1tfr_2 c.53.1.2 (12-180) T4 RNase H {Bacteriophage T4}
KEGICLIDFSQIALSTALVNFPDKEKINLSMRHLIILNSIKFNVKKAKTLGYTKIVLCIDNAKSGYWRRDFAYYYKKNRGKAREESTWDWEGYFESSHKVI
DELKAYMPYIVMDIDKYEADDHIAVLKKFSLEGHKILIISSDGDFTQLHKYPNVKQWSPMHKKWVKI

>d1bgxt2 c.53.1.2 (T:1-173) 5' to 3' exonuclease domain of DNA polymerase <i>Taq</i> {Thermus aquaticus}

MRGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTSRGEPVQAVYGFAKSLKALKEDGDAIVVFDAKAPSFRHEAYGGYKAGRPTPEDFPRQLA
LIKELVDLGLARLEVPGYEADDVLASLAKKAKEKEYEVRLTADKDLYQLLSDRIHVLHPEGYLITPAWLWEKYG

>d1xo1a2 c.53.1.2 (A:19-185) T5 5'-exonuclease {Bacteriophage T5}

RRNLMIVDGTNLGFRFKHNNSSKKPFASSYVSTIQLAKSYSARTTIVLGDKGSVFRLEHLPEYAGRNRDEKYAQRTEEEKALDEQFFEYLKDAFELCKTT
FPTFTIRGVVEADDMAAYIVKLIGHLYDHVWLSTDGDWDTLTDKVSRSFTTRREYHLRDHYEHHN

>d1a77_2 c.53.1.2 (2-208) Flap endonuclease-1 {Archaeon Methanococcus jannaschii}

GVQFGDFIPKNIISFEDLKGKKVAIDGMNALYQFLTSIRLRDGSPLRNKGITSAYNGVFYKTIHLLENDITPIWVFDGEPPKLKEKTRKVRREMKEKAE
LKMKEAIKKEDFEEAAKYAKRVSYLPKMVENCKYLLSMGIPYVEAPSEGEAQASYMAKKGDVWAVSQDYDALLYGAPRVVRNLTTKEMPELIE
LNEVLEDLR

>d1b43a2 c.53.1.2 (A:1-219) Fen-1 nuclease {Archaeon Pyrococcus furiosus}

GVPIGEIIPRKIELENLYGKKAIDALNAYQFLSTIRQKDGTPLMDSKGRITSHLSGLFYRTINLMEAGIKPVYVFDGEPPFKKELEKRREAREEAEKK
WREALEKGIEEARKYAQRATRVNEMLIEDAKLLEMIGIPIVQAPSEGEAQAAAYMAAKGSVYASASQDYDSLLFGAPRLVRNLTITGKRKLPGNVV
VEIKPELIILEEVLKELK

>d1ekja_c.53.2.1 (A:) beta-carbonic anhydrase {Pea (*Pisum sativum*)}

EASERIKTGFLHKKEYDKNPALYGELAKGQSPPFMVFACSDSRVCPSHVLDQGPGEAFVVRNVANLVPPYDQAKYAGTGAAIEYAVLHLKVSNIVVI
GHSACGGIKGLLSFPFDGTYSTDFIEEWVKIGLPAKAKVKAQHGDAPFAELCTHCEKEAVNASLGNLLTPFVREGLVNKTLALKGGYYDFVKGSFELW
GLEFGSSTFSV

>d1g5ca_c.53.2.1 (A:) beta-carbonic anhydrase {Archaeon Methanobacterium thermoautotrophicum}

IIKDLIRENQDFRFRDLSLKHSPKLCIITCMDSRLIDLLERALGIGRGDAKVIKNAGNIVDDGVIRSAAVAIYALGDNEIIIVGHTDCGMARLDEDLIVSR
MRELGVVEEEVNIENFSIDVLNPVGDEEENVIEGVKRLKSSPLIPESIGVHGLIIDINTGRLKPLYLDE

>d1i6pa_c.53.2.1 (A:) beta-carbonic anhydrase {Escherichia coli}

KDIDTLISNNALWSKMLVEDPGFFEKLAQAKPRLWIGCSDSRVPAERLTGLEPGEFLVHRNVANLVHTDLNCLSVVQYAVDVLVEHIIICGHYG
CGGVQAAVENPELGLINNWLLHIRDIWFKHSSLGEMPKERRLDLCELNVMEQVYNLGHSTIMQSAWKRGQKVTHGWAYGIHDGLLRDLDVTA
TNRETLEQRYRHGISNLKLK

>d1ddza1 c.53.2.1 (A:84-325) beta-carbonic anhydrase {Red alga (*Porphyridium purpureum*)}

VMSDLEKKFIELEAKLVAQPGQAMPGKSNIFANNEAWRQEMLKQDPFFNRLANGQSPEYLWIGCADSRVPANQLLDPAGEVFVHRNIANQCI
HSDISFLSVLQYAVQYLKVKHILVCGHYGCGGAKAALGDSRLGLIDNWLHIRDVRRMNAKYLDKCKDGDEELNRLIELNVLEQVHNVCATSIVQDA
WDAGQELTVQGVVYGVGDGKLRDLGVLVVNSDDISKFYRTKSDSGALKAG

>d1ddza2 c.53.2.1 (A:326-564) beta-carbonic anhydrase {Red alga (*Porphyridium purpureum*)}

NPNAPLVQVTKGGESELSTMEKLTAEVQQTPGKLKEGANRWFVNNEWRQKMLKQDPQFFSNLAHTQTPEILWIGCADSRVPANQIINLPAGEV
FVHRNIANQCIHSDMSFLSVLQYAVQYLKVKRVVVCGHYACGGCAAALGDSRLGLIDNWLHIRDVRRHNQAELSRTDPKDSLNRLIEINVLEQMI
NVCATSIVQDAWDAGQELEVQGVVYGVGDGKLRDMGVVAKANDDI

>d1pdo_c.54.1.1 (-) IIA domain of mannose transporter, IIA-Man {Escherichia coli}

TIAIVIGTHGWAEEQQLKTAEMILLGEQENVGVWIDFVPGENAETLIEKYNQALAKLDTTKGVLFVDTWGSPFNAASRIVVDKEHYEVAGVNIPML
VETLMARDDPSFDELVALAVETGREGVKALK

>d1bupa1 c.55.1.1 (A:4-188) Heat shock protein 70kDa, ATPase fragment {Cow (*Bos taurus*)}

GPAVGIDLGSTYSCGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVAMNPTNTVDAKRLIGRRFDDAVQSDMKHWPFMVVND
AGRPKVQVEYKGETKSFPYEEVSSMVLTKMKEIAEAYLGKTVNAVTPAYFNDSQRQATKDAGTIAGLNVLRINNEPTAAAIAYGLDKK

>d1bupa2 c.55.1.1 (A:189-381) Heat shock protein 70kDa, ATPase fragment {Cow (*Bos taurus*)}

VGAERNVLIFDLGGGTDFVSLTIEDGIFEVKSTAGDTHLGGEDFDNRMVNHFIAEFKRKHKKDISENKRAVRLRTACERAKRTLSSSTQASIEIDSLEY
GIDFYTTSITRARFEELNADLFRGTLDPVEKALRDAKLDKSQLHDIVLGGSTRIPKIQKLLQDFNGKELNKSINPDEAVAYGAAVQAAILS

>d1hjoa1 c.55.1.1 (A:3-188) Heat shock protein 70kDa, ATPase fragment {Human (*Homo sapiens*)}

KAAAIGIDLGTTSCGVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVDAKRLIGRKFGDPVVQSDMKHWPFQVIND
GDKPKVQSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYFNDSQRQATDAGVIAGLNVLRINNEPTAAAIAYGLDR

>d1hjoa2 c.55.1.1 (A:189-382) Heat shock protein 70kDa, ATPase fragment {Human (Homo sapiens)}

GKGERNVLIFLGGGTFDVSILTIDGIFEVKATAGDTHLGGEFDNRLVHFVEEFKRKHKDISQNRAVRRLTACERAKRTLSSTQASLEIDSLFE
GIDFYTSITRARFEELCSDLFRSTLEPVKEALKDQAQIHDLVGGSTRIPVKVQKLLQDFNGRDLNKSINPDEAVAYGAAVQAALMG

>d1dkgd1 c.55.1.1 (D:3-185) Heat shock protein 70kDa, ATPase fragment {Escherichia coli, gene dnaK}

KIIGIDLGTTNSCVAIMDGTTPRVLENAEGDRTPSIIAYTQDGETLVGQPAKRQAVTNPQNTLFAIKRIGRRFQDEEVQRDVSIIMPFKIIADNGDA
WVEVKGQKMAPPQISAEVLKKMKTAEDYLGEPVTEAVITVPAYFNDAQRQATKDAGRIAGLEVKRINNEPTAAALAYGLDKGT

>d1dkgd2 c.55.1.1 (D:186-383) Heat shock protein 70kDa, ATPase fragment {Escherichia coli, gene dnaK}

GNRTIAVYDLGGGTFDISIIEIDEVDGEKTFEVLATNGDTHLGGEFDSSLINYLVEEFKKDQGIDLRLNDPLAMQRLKEAAEKAKIELSSAQQTDVNLPY
ITADATGPKHMKVTRAKLESVDELVRNSIELLKVALQDAGLSVSDIDDVILVGGQTRMPMVQKKVAEFFGKEPRKDVNPDDEAVAIGAAVQGGVLT

>d1j6za1 c.55.1.1 (A:4-146) Actin {Rabbit (Oryctolagus cuniculus)}

ETTALVCDNGSGLVKAGFAGDDAPRAVFPSSIVGRPRHQGVGMGQKDSYVGDEAQSKRGILTLYPIEHGIITNWDDMEKIWHHTFYNELRVAP
EEHPTLLEAPLNPKANREKMTQIMFETFNVPAMYVAIQAVLSLYASG

>d1j6za2 c.55.1.1 (A:147-372) Actin {Rabbit (Oryctolagus cuniculus)}

RTTGIVLDSDGVTHNPIYEGYALPHAIMRLDLAGRDLTDYLMKILTERGYSFTTAEREIVRDIKEKLCYVALDFENEMATAASSSLEKSYLEPDGQ
VITIGNERFRCPETLFQPSFLGMESAGIHETTYNSIMKCDIDIRKDLYANNVMSGGTTMYPGIADRMQKEITALAPSTMKIKIAPPBKYSVWIGGSIL
ASLTFQQMWITKQEYDEAGPSIVHR

>d1d4xa1 c.55.1.1 (A:4-146) Actin {Nematode (Caenorhabditis elegans)}

EVAALVVDNGSGMCKAGFAGDDAPRAVFPSSIVGRPRHQGVGMGQKDSYVGDEAQSKRGILTLYPIEHGIITNWDDMEKIWHHTFYNELRV
APEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASG

>d1d4xa2 c.55.1.1 (A:147-375) Actin {Nematode (Caenorhabditis elegans)}

RTTGIVLDSDGVTHNPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTAEREIVRDIKEKLCYVALDFEQEMATAASSSLEKSYLEPDGQVI
TVGNERFRCPEAMFQPSFLGMESAGIHETTYNSIMKCDIDIRKDLYANTVLSGGTTMYPGIADRMQKEITALAPSTMKIKIAPPBKYSVWIGGSILA
SLSTFQQMWISKQEYDESGPSIVHRKCF

>d1c0fa1 c.55.1.1 (A:1-146) Actin {Slime mold (Dictyostelium discoideum)}

DGEDVQALVIDNGSGMCKAGFAGDDAPRAVFPSSIVGRPRHTGKDSYVGDEAQSKRGILTLYPIEHGIITNWDDMEKIWHHTFYNELRV
VLLTEAPLNPKANREKMTQIMFETFNTPAMYVAIQAVLSLYASG

>d1dgaa2 c.55.1.1 (A:147-375) Actin {Slime mold (Dictyostelium discoideum)}

RTTGIVMDSDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYMMKILTERGYSFTTAEREIVRDIKEKLCYVALDFEQEMATAASSSALEKSYLEPDGQ
VITIGNERFRCPEALFQPSFLGMESAGIHETTYNSIMKCDVDIRKDLYGNVVLGGTTMYPGIADRMNKEITALAPSTMKIKIAPPBKYSVWIGGSIL
ASLTFQQMWISKQEYDESGPSIVHRKCF

>d1yaga1 c.55.1.1 (A:4-146) Actin {Baker's yeast (Saccharomyces cerevisiae)}

EVAALVIDNGSGMCKAGFAGDDAPRAVFPSSIVGRPRHQGVGMGQKDSYVGDEAQSKRGILTLYPIEHGIITNWDDMEKIWHHTFYNELRV
PEEHPVLLTEAPMNPKNREKMTQIMFETFNVPAFYVSIQAVLSLYSSG

>d1yaga2 c.55.1.1 (A:147-375) Actin {Baker's yeast (Saccharomyces cerevisiae)}

RTTGIVLDSDGVTHVPIYAGFSLPHAILRIDLAGRDLTDYLMKILSERGYSFTTAEREIVRDIKEKLCYVALDFEQEMTAQSSIEKSYLEPDGQVI
TIGNERFRAPEALFHPVSGLGLESAGIDQTNTNSIMKCDVDIRKELYGNVIMSGGTTMYPGIADRMNKEITALAPSSMKVKIIAPPBKYSVWIGGSIL
SLTTFQQMWISKQEYDESGPSIVHHKCF

>d1jcfa1 c.55.1.1 (A:1-140) Prokaryotic actin homolog MreB {Thermotoga maritima}

MLRKDIGIDLTANTLVFLRGKGIVVNEPSVIAIDSTTGEILKVGLEAKNMIGKTPATIKAIRPMRDGVIADYTVLVMRYFINKAKGGMNLFKPRVVI
GVPIGITDVERRAILDAGLEAGASKVFLIEEPMAAIGSN

>d1jcfa2 c.55.1.1 (A:141-336) Prokaryotic actin homolog MreB {Thermotoga maritima}

LNVEEPGNMVDIGGGTTEAVISLGSIVTWSIRIAGDEMDEAIVQYVRETYRAIGERTAERVKIEIGNVFPSENDELETTVSGIDLSTGLPRKTL
KGGEVREALRSVVAIVESVRTTLEKTPPELVDIIRGIFTGGGSLLRGDLTLLQKETGISVIRSEEPLTAVAKGAGMVLKVNILKKLQGAG

>d1k8ka1 c.55.1.1 (A:3-160) Actin-related protein 3, Arp3 {Cow (Bos taurus)}

GRLPACVVDGCGTGYTKLGAGNTEPQFIIPIASCIAIKESAKVGDQAQRVMKGVDLDFIGDEAIEKPTYATKWPIRHGIVEDWDLMERFMEQVIFKY
LRAEPEDHYFLTEPPLNTPENREYTAEIMFESFNVPGLYIAVQAVLALAASWTSRQVGE
>d1k8ka2 c.55.1.1 (A:161-418) Actin-related protein 3, Arp3 {Cow (Bos taurus)}
RTLTGTVIDSGDGVTIVIPVAEGYVIGSCIKHIPIAGRDTYFIQQLLRDREVGPPEQSLETAKAVKERYSYVCPDLVKEFNKYDTDGSWKWIKQYTGINAI
SKKEFSIDVGYERFLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVRRPLYKNIVLSGGSTMFRDFGRRLQRDLKRTVDARLKSEELSGGRLPKPPI
DVQVITHHMQRYAVWFGGSMLASTPEFYQVCHTKKDYEIGPSICRHNPVFGVMS
>d1k8kb1 c.55.1.1 (B:154-343) Actin-related protein 2, Arp2 {Cow (Bos taurus)}
GVVVDSGDGVTHICPVYEGFSLPHLTRLDIAGRDTYLIKLLLRYAFNHSADFETVRMIKEKLCYVGYNIEQEQQKLAETTVLVESYLPDGRIIKVG
GERFEAPEALFQPHLINVEGVGVAELLFTIQAADIDTRSEFYKHIVLSSGSTMYPGLPSRLERELKQLYLERVLKGDVEKLSKFIR
>d1e4ft1 c.55.1.1 (T:7-199) Cell division protein FtsA {Thermotoga maritima}
TVFVTSIDIGSRYIKGLVLGKRDQEWEALAFSSVKSRLGEDEIKDAIAFKESVNTLKEEEQLQKSLRSDFVISFSSVSFEREDTVIERDFGEEKRSITLDI
LSEMQUEALEKLKENGKTPHLHIFSKRYLDDERIVFNPLDMKASKIAIEYTSIVVPLKVYEMFYNFLQDVKSPFQLKSSLVSTAEGVL
>d1e4ft2 c.55.1.1 (T:200-390) Cell division protein FtsA {Thermotoga maritima}
TTPEKDRGVVVNLGYNFTGLIAYKNGVPIKISYVPVGMKHKVIKDVSAVLDTSFEESERLIITHGNAVNDLKEEEIQYRGLDGNTIKTTAKKLSVIIHA
RLREIMSKKKFREVAKIVEEGEIGIPGGVVLTGGAKIPRINELATEVFKSPVRTGCYANSDRPSIINADEVANDPSFAAFGNVFA
>d1huxa_c.55.1.5 (A:) Hydroxyglutaryl-CoA dehydratase component A {Acidaminococcus fermentans}
SIYTLGIDVGSTASKCILKDGKEIVAKSLVAVGTGTSGPARSIEVLEAHMKKEDMAFTLATGYGRNSLEGIADKQMSELSCHAMGASFIWPNVHTVI
DIGGQDVKVIHVNGTMTNFQMNDKAAGTGRFLDVMANILEVKVSDLAELGAKSTKRAISSTCTVFAESEVISQLSKGTDKIDIAGIHRSVASRV
GLANRVGIVKDVVMTGGAQNYGVRGALEEGLVIEKTSPLAQYNGALGAALYAYKKA
>d1g99a1 c.55.1.2 (A:1-156) Acetate kinase {Archaeon Methanoscincus thermophila}
MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIIQKKFDGKKEKLTDLPTHKDALEEVVKALTDEFVVKDMGEINAVGHRVVGGEKF
TTSALYDEGVEKAIKDCFELAPLHNPPNMMSGISACAEIMPGTPMVIVFDTAFHQTMP
>d1g99a2 c.55.1.2 (A:157-398) Acetate kinase {Archaeon Methanoscincus thermophila}
PYAYMYALPYDLYEKHGVRYKGFGHTSHKYVAERAALMLGKPAEETKIITCHLNGNSSITAVEGGKSVETSMGFTPTEGLAMGTRCGSIDPAIVPFLME
KEGLTTREIDTLMNKSGVGLVSGLSNDFRDLDEAASKGNRKAELALEIFAYVKKFIGEYSAVLNGADAVVFTAGIGENSASIRKRILTGLDGIGIKIDDE
KNKIRGQEIDISTPDAKVRVFVPIVNEELAIARETKEIVET
>d1ig8a1 c.55.1.3 (A:18-224) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}
DVPKELMQQIENFEKIFTVPTETLQAVTKHFISELEKGLSKGGNIPMIPGWVMDFTGKESGDFLAIDLGGTNLRVVLVKGDDRTFDTTQSKYRLP
DAMRTTQNPDDELWEFIADSLKAFIDEQFPQGISEPIPLGFTFSFPASQNKINEGILQRWTGFDIPNIENHDVVPMLQKQITKRNIPIEVVALINDTTG
LVASYYTDP
>d1ig8a2 c.55.1.3 (A:225-486) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}
ETKMGVIFGTGVNGAYYDVCSDIEKLQGKLSDDIPPSAPMAINECEYGSFDNEHVVLPRTKYDITIDEESPRPGQQTFEKMSSGGYLGEILRLALMDMY
KQGFIFKNQDLSKFDKPFVMDTSYPARIEEDPFENLEDTDDLFQNEFGINTTVQERKLIRRSELIGARAARLSVCGIAACQKRGYKTGHIAADGSVYN
RYPGFKEKAANALKDIYWTQTSLDDYPIKIVPAEDGSGAGAAVIAALAQKRIAEGKSGVIGA
>d1bdg_1 c.55.1.3 (13-222) Hexokinase {Blood fluke (Schistosoma mansoni)}
FSDQQLFEKVVIEKPFDLSVVDYEEICDRMGESMRLGLQKSTNEKSSIKMFPSYVTKPTNGTETGNFLADLGGSYRVLVTLLEGKGKSPRIQERTY
CIPAEKMSGSGTELFKYIAETLADFLENNMGKDKKFDLGFTSFPCVQKGLTHATLVRWTGFSADGVEGHNVAILLQTELKRELNVKCVAVVNDT
VGTLASCALEDP
>d1bdg_2 c.55.1.3 (223-460) Hexokinase {Blood fluke (Schistosoma mansoni)}
KCAVGLIVGTGTNVAYIEDSSKVELMDGVKEPEVVINTEWGAEGEKGELDCWRTQFDKSMIDSLHPGKQLYEKMIVSGMYLGEVRHIIIVLVEQKI
LFRGDLPERLKVRNSLLTRYLTDVERDPAHLLYNTHYMLDDLHVPVVEPIDNRIVRYACEMVVKRAAYLAGAGIACILRRINRSEVTGVGDGSYKFHP
KFCERMTDMVDKLKPKNTRFCLRLSEDGSGKGAAIAASC
>d1czan1 c.55.1.3 (N:16-222) Mammalian type I hexokinase {Human (Homo sapiens)}
DDQVKKIDKLYAMRLSDETLIDIMTRFRKEMKNGLSRDNPTATVKMLPTFVRSIPDGSEKGDFIALDGGSSFRILRVQVNHEKNQNVHMESEVY

DTPENIVHGSGSQLFDHVAECLGDFMEKRKIKDKKLPVGFTSFPCQSKIDEAILITWTKRFKASGVEGADVVKLLNKAIIKKRGDYDANIVAVVNDT
VGTMMTCGYDDQ

>d1czan2 c.55.1.3 (N:223-465) Mammalian type I hexokinase {Human (Homo sapiens)}

HCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDAIDAYSNPGKQLFEKMVSGMYLGEVLRLILVKMAKEGLLF
EGRITPELLTRGFNTSDVSAIEKNKEGLHNAKEILTRLGVEPSDDDCSVQHVCTIVSFRSANLVAATLGAILNRLRDNGTPRLRTTVGDGSLYKTH
PQYSRRFHKTLLRRLVPDSVRFLLSESGSGKGAAMVTAVAYRLAE

>d1czan3 c.55.1.3 (N:466-670) Mammalian type I hexokinase {Human (Homo sapiens)}

QHRQIEETLAHFHLTKDMILLEVKKRMRAEMELGLRKQTHNNAVVKMLPSFVRRTPDGTENGDFALDLGGTNFRVLLVKIRSGKKRTVEMHNKIYA
IPIEIMQGTGEELFDHIVSCISDFLDYMGIGKPRMPLGFTSFPCQQTSLDAGILITWTKGFKATDCVGHVDVVTLLRDAIKRREEFDLDVVAVVNDTVG
TMMTCAYEEP

>d1czan4 c.55.1.3 (N:671-913) Mammalian type I hexokinase {Human (Homo sapiens)}

TCEVGLIIVGTGSNACYMEEMKNVEMVEGDQGQMCINMEWGAFFGDNGLDDIRTHYDRLVDEYSLNAGKQRYEKMIISGMYLGEIVRNILIDFTKK
GFLFRGQISETLKTRGIFETKFLSQIESDRALLQVRAILQQQLGNSTCDDSLVKTVCGVVSRRAAQLCGAGMAAVVDKIRENRGLDRLNVTVGDGT
LYKLHPHFSRIMHQTVKELSPKCNVSFLLEDGSKGKAALITAVGVRLRT

>d1bg3a1 c.55.1.3 (A:1-222) Mammalian type I hexokinase {Rat (Rattus norvegicus)}

MIAAQLLAYYFTELKDDQVKKIDKYLAMRLSDEIILIDILTRFKEMKNGLSRDNPTASVMLPTFVRSIPDGSEKGDFAIDLGGSSFRILRVQVNHEK
NQNVSMEIYDTPENIVHGSGTQLFDHVADCLGDFMEKKKIKDKKLPVGFTSFPCRQSKIDEAVLITWTKRFKASGVEGADVVKLLNKAIIKKRGDY
DANIVAVVNDTGTMMTCGYDDQ

>d1bg3a2 c.55.1.3 (A:223-465) Mammalian type I hexokinase {Rat (Rattus norvegicus)}

QCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDAIDRGSNPGKQLFEKMVSGMYMGEVLRLILVKMAKEGL
LFEGRITPELLTRGFNTSDVSAIEKDKEGIQNAKEILTRLGVEPSDVDCSVQHICITIVSFRSANLVAATLGAILNRLRDNGTPRLRTTVGDGSLYKM
HPQYSRRFHKTLLRRLVPDSVRFLLSESGTGKGAAAMVTAVAYRLAE

>d1bg3a3 c.55.1.3 (A:466-670) Mammalian type I hexokinase {Rat (Rattus norvegicus)}

QHIRQIEETLAHFRLSKQTLMEVKKRLTEMEMGLRKETNSKATVKMLPSFVRSIPDGTEHDFLALDLGGTNFRVLLVKIRSGKKRTVEMHNKIYSIP
LEIMQGTGDELFDHIVSCISDFLDYMGIGKPRMPLGFTSFPCQHQTNLDCGILISWTKGFKATDCEGHVASLLRAVKRREEFDLDVVAVVNDTVG
MMTCAYEEP

>d1bg3a4 c.55.1.3 (A:671-911) Mammalian type I hexokinase {Rat (Rattus norvegicus)}

TCEIGLIVGTGTNACYMEEMKNVEMVEGNQGQMCINMEWGAFFGDNGLDDIRTDFDKVVDEYSLNSGKQRFEKMIISGMYLGEIVRNILIDFTKK
GFLFRGQISETLKTRGIFETKFLSQIESDRALLQVRAILQQQLGNSTCDDSLVKTVCGVVSKRAAQLCGAGMAAVVEKIRENRGLDHLNVTVGDGT
LYKLHPHFSRIMHQTVKELSPKCTVSFLLEDGSKGKAALITAVGVRL

>d1bu6o1 c.55.1.4 (O:3-253) Glycerol kinase {Escherichia coli}

KKYIVALDQGTTSSRAVVMDHDANIISVSQREFEQIYPKPGWVEHDPMIEIWATQSSTLVEVLTAKADISSDQIAAIGTNQRETTIVWEKETGKPIYN
VWQCRRTAEICEHLKRDGLEDYIRSNTGLVIDPYFSGTKVKWILDHVEGSRERARRGEFFGTVDTWLIWKMTQGRVHVTDYTNASRTMLFNIHTL
DWDDKMILEVDIPREMLPEVRRSSEVYQQTNIGGGTRIPISGIAGDQQAALFGQ

>d1bu6o2 c.55.1.4 (O:254-499) Glycerol kinase {Escherichia coli}

LCVKEGMANKTYGTGCFMLMNTGEKAVKSENLTTIACGPTGEVNYALEGAVFMAGASIQLRDEMKLINDAYDSEYFATKVQNTNGVYVPAF
TGLGAPYWDYARGAIFGLTRGVNANHIIRATLESIAYQTRDVLEAMQADSGIRLHALRVDDGAVANNFLMQFQSDILGTRVERPEVREVTALGAAY
LAGLAVGFWQNLDELQEKAVIDERFRPGIETTERNYRYAGWKKAVKRAMAWEEH

>d1chma1 c.55.2.1 (A:2-156) Creatinase {Pseudomonas putida}

QMPKTLRIRNGDKVRSTFSQAQYEANRQARLRAHAAENIDAAIFTSYHNINYYSDFLYCSFGRPYALVVTEDDVISANIDGGQPWRRTVGTDNIVYT
DWQRDNYFAAIQQALPKARRIGIEHDHNLQNQNDKLAARYPDAELVDAVAAACMRMR

>d1az9_1 c.55.2.1 (1-176) Aminopeptidase P {Escherichia coli}

SEISRQEQQRRQALVEQMOPGSAALIFAAPEVTRSADSEYPYRQNSDFWYFTGFNEPEAVLVLIKSDDTNHHSVLFNVRDLTAEIWFGRRLGQDA
APEKLGVDRALAFSEINQQLYQLLNGLDVYHAQGEYAYADVIVNSALEKLKRGSRQNLTAPATMIDWRPVVHEMRLF

>d1jl1a_c.55.3.1 (A:) RNase H (RNase HI) {Escherichia coli}
KQVEIFTAGSALGNPGPGGYGAILRYGREKTFSAKYRTTNNRMELMAAIVALEALKEHAEVILSTDQSQVRQGITQWIHNWKRGWKTADKKPV
KNVDLWQRQLDAALGQHQIKWEWVKGHAGHPENERADELARAAAMNPNTLEDTGYQVE

>d1rii_c.55.3.1 (-) RNase H (RNase HI) {Thermus thermophilus}
RKRALFTDGACLGNGPVGWAALLRFHAHEKLLSGGEACTTNNRMELKAAIEGLKALKEPAEVLDYTDSHYLKAFTEGWLEGWRKRGWRTAEG
KPVKNRDLWEALLAMAPHRVRFHFVKGHTGHPENERVDREARRQAQSQAKT

>d1jl2a_c.55.3.1 (A:) RNase H (RNase HI) {Chimeric (Escherichia coli/Thermus thermophilus)}
KQVEIFTDGSALGNPGPGGYGAILRYGREKTFSAKYRTTNNRMELKAAIEGLKALKEPAEVLDYTDSHYLKAFTEGWLEGWRKRGWRTAEGKPV
KNRDLWEALLAMAPHRVRFHFVKGHTGHPENERADELARAAAMNPNTLEDTGY

>d1ekea_c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Methanococcus jannaschii}
MIIIGIDEAGRGPVLGPMMVCAFAIEKEREELKKLGVKDSKELTKNKRAYLKKLENLGYVEKRILEAEEINQLMNSINLNDIEINAFSKVAKNLIEKLNIR
DDEIEIYIDACSTNTKKFEDSFKDIEDIICKERNLNKIIAEHKADAKYPVVAASIIAKAERDEIIDYYKKIYGDIGSGYPSDPKTIKFLEDYFKKKLPLDIAR
THWKTCRILDKSKQT

>d1i39a_c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Archaeoglobus fulgidus}
MKAGIDEAGKGCVIGPLVAVGACSDEDRLRKLVKDSKKLSQGRREELAEEIRKICRTEVLKVSPENLDERMAAKTINEILKECYAEILRKPEIAYVDS
PDVIPERLSRELEEITGLRVVAEHKADEKYPVLAASIIAKVEREREIERLKEFGDFGSGYASDPRTRVLKEWIASGRIPSCVRMRWKTVSNLRQK

>d1io2a_c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Thermococcus kodakaraensis}
MKIAGIDEAGRGPVIGPMVIAAVVVDENSLPKLEELKVRDSKKLTPKRREKLNEILGVLDYVILELPPDVIGSREGTLNEFEVENFAKALNSLKVKPD
VIYADAADVDEERFARELGERLNFEAEVVAKHKADDIFPVVAASILAKVTRDRIVEKLKEEYGEIGSGYPSDPRTAFLENYYREHGEFPPIVRKGWKT
TLKKIAEKVESEKK

>d1c9ra1_c.55.3.1 (A:430-558) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}
EKEPIVGAETFYVDGAANAATKLGKAGYVTNKGQRQKVPLNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAPDKSESELVNQIEQLIKKE
AVYLAWVPAHAGIGGNAAVDALVSAGIAA

>d1hrha1_c.55.3.1 (A:432-556) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}
EPIVGAETFYVDGAANRET KLGKAGYVTNKGQRQKVPLNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAPDKSESELVNQIEQLIKKE
YLAWVPAHKIGGGNEQVDKLV SAGI

>d1jlaa1_c.55.3.1 (A:430-553) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}
EKEPIVGAETFYVDGAANRET KLGKAGYVTNKGQRQKVPLNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAPDKSESELVNQIEQLIKKE
KVYLAWVPAHKIGGGNEQVDKLV SAGI

>d1vrta1_c.55.3.1 (A:430-539) HIV RNase H (Domain of reverse transcriptase) {Human immunodeficiency virus type 1}
EKEPIVGAETFYVDGAANRET KLGKAGYVTNKGQRQKVPLNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGIIQAPDKSESELVNQIEQLIKKE
KVYLAWVPAH

>d1asu_c.55.3.2 (-) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}
PLREPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAQHHWATAIAVLRPKAIKTDNGSCFTSKSTREWLGIAHT
TGIPGNSQQAMVERANRLLKDKIRVLAEGDGFMKRIPTSKQGELLAKAMYALNHFERGENTKTNL

>d1c0ma2_c.55.3.2 (A:49-216) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}
GVNPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAQHHWATAIAVLRPKAIKTDNGSCFTSKSTREWLGIAHT
TGIPGNSQQAMVERANRLLKDKIRVLAEGDGFMKRIPTSKQGELLAKAMYALNHFERGENTKTPQKHWRPT

>d1cxqa_c.55.3.2 (A:) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}
GRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAQHHWATAIAVLRPKAIKTDNGSCFTSKSTREWLGIAHTTGIP
GNSQQAMVERANRLLKDKIRVLAEGDGFMKRIPTSKQGELLAKAMYALNH

>d1exqa_c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}
SSPGIWQLDCTHLEGKVLVAVHVASYIEAEPVIAETGQETAYFLKLAGRPVKTIHTDNGSNFTGATVRAACDWAGIKQEDGIPYNPQSQGVVES
MNKELKKIIGQVRDQAHLKTAQMAVFIHNKKRKGIGGIGYSAGERIVDIIATDIQ

>d1hyva_c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}
SPGIWQLDCTHLEGKVLVAVHVASGYIAEVIPAETGQETAYFLLLAGRWPVKTVHTDNGSNFTSTVKAACWWAGIKQEFGIPYNPQSQGVIES
MNKELKKIIGQVRDQAHLKTAQMAVFIFHNKKRGGIGGYSAGERIVDIIATDIQ
>d1c6va_c.55.3.2 (A:) Retroviral integrase, catalytic domain {Simian immunodeficiency virus}
NSDLGTWQMDCTHLEGKIVIVAHVASGFIAEVIPQETGRQTALFLLLAGRWPVTHLHTDNGANFASQEVMVAWWAGIEHTFGVPYNPQSQ
GVVEAMNHHLKNQIDRIREQANSVETIVLMAVHCMNHKRRGGIGDMTPAERLINMITTEQEIQFQ
>d1bco_2 c.55.3.3 (258-480) mu transposase, core domain {Bacteriophage mu}
EHLDAMQWINGDGYLHNVFVRWFNGDVIRPKTFWQDVKTRKILGWRCDVSENIDSIRLSFMDVVTRYGIPEDFHITIDNTRGAANKWLTGGAP
NRYRFVKVEDDPKGFLLMGAKMHWTSSVAGKGWQAKPVERAFGVGGLEYVDKHPALAGYTGPNPQAKPDNYGDRAVDAEFLKTLAEGV
AMFNARTGRETEMCGGKLSFDDVFEREYARTIVRKP
>d1b7ea_c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}
SAEAIRKAGAMQTVKLAQEFPELLAIEDTTSLSYRHQVAEELGKLSIQDKSRGWWVHSVLLLEATTFRVTGLHQEWWMRPDDPADADEKESGK
WLAAAATSLRMGSMSMSNVIAVCDREADIHAYLQDKLAHNERFVVRSKHPRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPAR
KASLSLRSRITLKQGNITLNAVLAEEINPPKGETPLKWLLTSEPVESLAQALRVIDIYTHRWRIEEFHKAWKTGAGAERQRMEEPDNLERMVSILSFV
AVRLQLRESFTLPQALRAQGLLKEAHVESQSAETVLPDECQLLGYLDKGKRKRKEGSLQWAYMAIARLGGFMDSKRTGIASWGLWEGWEAL
QSKLDGFLAAKDLMAQ
>d1f3ia_c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}
ALHRAADWAKSVFSSAALGDPRRTARLVNVAQLAKYSGKSITISSEGSKAAQEGAYRFIRNPVSAEAIRKAGAMQTVKLAQEFPELLAIEDTTSLY
RHQVAEELGKLSIQDKSRGWWVHSVLLLEATTFRVTGLHQEWWMRPDDPADADEKESGKWLAAAATSLRMGSMSMSNVIAVCDREADIHAY
LQDKLAHNERFVVRSKHPRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKRPARCASLSLRSRITLKQGNITLNAVLAEEINPPKGETP
LKWLTTSEPVESLAQALRVIDIYTHRWRIEEFHKAWKTGAGAERQRMEEPDNLERMVSILSFVAVRLQLRESFTLPQALRAQGLLKEAHVESQSA
ETVLPDECQLLGYLDKGKRKRKEAGSLQWAYMAIARLGGFMDSKRTGIASWGLWEGWEALQSKLDGFLAAKDLMAQGKIG
>d1kfsa1 c.55.3.5 (A:324-518) Exonuclease domain of prokaryotic DNA polymerase {Escherichia coli}
MISYDNYVTILDEETLKAWIAKLEKAPVFADFDTEDSLDNISANLVGLSFAIEPGVAAVYIPVAHDYLDAPDQISRERALELLPILLEDEKALKVGQNLKYD
RGILANYGIELRGIAFDTMLESYILNSVAGRHDMDSLAERWLKHKTITFEEIAGKGKQNLTFNQIALEEAGRYAAEDADVTQLHLKMWPDLQK
>d1qtma1 c.55.3.5 (A:293-422) Exonuclease domain of prokaryotic DNA polymerase {Thermus aquaticus}
ALEEAPWPPPPEGAFVGFLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDSLVLALREGLGLPPGDDPMLLAYLLPSNTTPE
GVARRYGEWTEEAGERAALSERLFANLWGRLEG
>d1xwl_1 c.55.3.5 (297-468) Exonuclease domain of prokaryotic DNA polymerase {Bacillus stearothermophilus, newly identified strain as yet unnamed}
AKMAFTLADRTEEMIADKAALVVEVVEENYHDAPIVGIAVVNEHGRFFLRPETALADPQFVAWLDETKKSMFDKRAAVALKWKGIELCGVSF
DLLAAAYLLDPAQGVDDVAAAAMKQYEAVRPDEAVYKGAKRAVPDEPVLAELHLRKAAAIWELERPFLDELRRN
>d1t7pa1 c.55.3.5 (A:1-210) Exonuclease domain of T7 DNA polymerase {Bacteriophage T7}
MIVSDIEANALLESVTFKHCGVIYDYSTAELYVSYRPSDFGAYLDAEAEVARGGLIVFHNGHKYDVPALTAKLQLNREFHLPRENCIDTLVLSRLIHSN
LKDTDMGLLRSKGKLPAGEAWGYRLGEMKGEYKDDFKRMLEEQQEYVDGMMEWWNFNEEMMDYNVQDVVTKALLEKLLSDKHYFPPEIDFT
DVGYTTFWSES
>d1noya_c.55.3.5 (A:) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Bacteriophage T4}
DEFYISIETVGNVINYIDENGKERTREVEYLPTMFRHCKEESKYKDIYGKNCAPQKFPMSMKDARDWMKRMEDIGLEALGMNDFKLAYISDTYGEI
VYDRKFVRVANCDIEVTGDKFPDMKAELYIDAITHYDSIDDRFYVF DLLNSMYGSVSKWDALKAAKLCEGGDEVQEILDRIYMPFDNERDML
MEYINLWEQKRPAlFTGWNIEGFDVPIYIMNRVKMILGERSMKRSPIGRVKSLLQNMYGSKEIYSIDGVSILDLYKKFAFTNLPSFSLESVAQHET
KKGKLPYDGPINKLRETNHQRYISYNIIDVESVQAIDKIRGFIDLVLMSMSYYAKMPFSGVMSPIKTWDAlIIFNSLKGE
>d1ih7a1 c.55.3.5 (A:1-375) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Bacteriophage RB69}
MKEFYLTVSEQIGDSIFERYIDSNGRERTREVEYKPSLFAHCPCESQATKYFDIYGKPCPTRKLFanMRDASQWIKRMEDIGLEALGMDDFKLAYLSDTYNY
EIKYDHTKIRVANFDIEVTSPDGFPEPSQAKHPIDAITHYDSIDDRFYVF DLLNSPYGNVEEWSIEAKLQEQQGDEVPEIIDKIIYMPFDNEKELLME

YLNFWQQKTPVLTGWNVESFDIPYVYNRIKNIFGESTAKRLSPHRKTRVKVIENMYGSREIITFGISVLDYIDLYKKFSFTNQPSYSLDYISEFELNVGKL
KYDGPISKLRESNHQRYISYNIIDVYRVLQIDAKRQFINLSLMGYYAKIQSVPPIKTDAAIFNSLKE

>d1tgoa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Thermococcus gorganarius}

MILDTDYITEDGKPVIRFKKENGEFKIDYDRNFEPYIALLKDDSAIEDVKKITAERHGTTVRVRAEKVKKFLGRPIEVWKLKFTHPQDVPAIRDKIKE
HPAVVDIYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNIDLPYDVVSTEKEMIKRFLKVKEKDP
DVLITYNGDNDFAYLKRSEKLGVKFILGREGSEPQIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLAIVEAIFGQPKEKVYAEELAQAWETGEG
LERVARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSR

>d1qhta1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Thermococcus sp., 9on-7}

MILDTDYITEDGKPVIRFKKENGEFKIEYDRTFEPYFYALLKDDSAIEDVKKVTAKRHGTVVKVRAEKVQKKFLGRPIEVWKLKFTHPQDVPAIRDRI
RAHPAVVDIYDIPFAKRYLIDKGLIPMEGDEELMLAFAITALYHEGEEFGTGPILMISYADGSEARVITWKKIDLPYDVVSTEKEMIKRFLRVVREK
DPDVILITYNGDNDFAYLKRCEELGIKFTLGRDGSEPQIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLAIVEAIVFGKPKEKVYAEELAQAWES
EGGLERVARYSMEDAKVTYELGREFFPMEAQLSRLIGQSLWDVSR

>d1d5aa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Desulfurococcus tok{}}

MILDADYITEDGKPVIRFKKEKGKIDYDRDFEPYIALLKDDSAIEDIKKITAERHGTTVRVTRAERVKKFLGRPVEVWKLKFTHPQDVPAIRDKIRE
HPAVVDIYDIPFAKRYLIDRGLIPMEGDEELRMLAFDIETLAHAGAAAGAGPILMISYADEEGARVITWKNIDLPYDVVSTEKEMIKRFLKVQEKD
PDVLITYNGDNDFAYLKRSEMLGVKFILEGRDGSEPQIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLAIVEAIVFGQPKEKVYAEELAQAWSG
EGGLERVARYSMEDAKATYELGKEFFPMEAQLSRLVGQSLWDVSR

>d1gcxa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Pyrococcus kodakaraensis}

MILDTDYITEDGKPVIRFKKENGEFKIEYDRTFEPYFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLGRPVEVWKLKFTHPQDVPAIRDKE
EHPAVIDIYDIPFAKRYLIDKGLIPMEGDEELKMLAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNIDLPYDVVSTEREMIKRFLRVVKEKD
PDVLITYNGDNDFAYLKRCEKLGINFALGRDGSEPQIQRMGDRFAVEVKGRIHFDLYPVIRRTINLPTYTLAIVEAIVFGQPKEKVYAEELITTAWETG
ENLERVARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSR

>d1fxxa_c.55.3.5 (A:) Exonuclease I {Escherichia coli}

QSTFLFHDYETFGTHPALDRPAQFAAIRTDSEFNVIGEPEVYCKPADDYLQPQGAVALGITPQEARAQGENEAAFAARIHSLFTVPKTCILGYNNVRF
DDEVTRNIFYRNFYDPYAWSQHDNSRWDLDDVMRACYALRPEGINWPENDDGLPSFRLEHTKANGIEHSNAHDAMADVATIAMAKLVKTR
QPRLFDFYLTHRHKHLMALIDVPQMKPLHVSGMFGAWRGNTSWAPLAWHPENRNAVIMVLAGDISPLESDTLRERLYTAKTDLDNA
AVPVKLVHNKCPVLAQANTLRPEDADRLGINRQHCLDNLKILRENPNQVREKVAIAEAEPFTPSDNVDAQLYNGFFSDADRAAMKIVLETEPRNLP
ALDITFVDKRIEKLNYRARNPGTLDYAEQQRWLEHRRQVFTPEFLQGYADELQMLVQQYADDKEKVALLKALWQYADEIVEH

>d1hjra_c.55.3.6 (A:) RuvC resolvase {Escherichia coli}

AIILGIDPGSRTVGYVIRQVGRQLSYLGSGCIRTKVDDLPSRLKIYAGVTEIITQFQPDYFAIEQVFMAKNADSALKLGQARGVAIAAVNQELPVFEY
AARQVKQTVGIGSAEKSQVQHMVRTLLKLPANPQADAADALAIATHCHVSQNAMQ

>d1kcfa2 c.55.3.7 (A:39-256) Mitochondrial resolvase ydc2 catalytic domain {Fission yeast (Schizosaccharomyces pombe)}

TSRVLGIDLGIKNFSYCFASQNEDSKVIIHNSVENLTEKNGLDIQUWTEDFQPSMADLSIQLFNTLHEKFNPVILMERQYRSGIATIPEWTLRVN
MLESMLYALHYAEKRNSIEQKIQYFPFLSLSPKSTSYWASVNLTKASFSSKKSRVQMVKELEDGQKILFENEALYKWNNNGSRVEFKKDDMADSALIA
SGWMRWQAQLKHYRNFCQFL

>d1jj2m_c.55.4.1 (M:) Ribosomal protein L18 (L18p) {Archaeon Haloarcula marismortui}

ATGPRYKVPMRRREARTDYHQRLRLKSGKPRLVARKSNKHVRAQLVTLGPNGDDTLASAHSSDLAEYGWEAPTGNMPSAYLTGLLAGLRAQEAG
VEEAVLDIGLNSPTPGSKVFAIQEGAIDAGLDIPHNDVLAQWQRTRGAHIAEYDEQLEPLYSGDFDAADLPEHFDELRETLLDGDIEL

>d1fjgk_c.55.4.1 (K:) Ribosomal protein S11 {Thermus thermophilus}

KRQVASGRAYIHASYNNNTITDPDGNPITWSSGGVIGYKGSRKTPYAAQLAALDAAKKAMAYGMQSVDIVRGTGAGREQAIRALQASGLQVK

SIVDDTPVPHNGCRPKKKFRKAS

>d1dt9a1 c.55.4.2 (A:143-276) Middle domain of eukaryotic peptide chain release factor subunit 1, ERF1 {Human (Homo sapiens)}

DSKFGFIVIDGSGALFGTLQGNTREVLHKFTVDPKKHGRGGQSALRFLRMEKRHNYVRKVAETAVQLFISGDKVNAGLVLAGSADFKEELSQS
DMFDQRLQSKVLLVDISYGGENGFNQAIELSTEVLs

>d1eo1a_ c.55.5.1 (A:) Hypothetical protein MTH1175 {Archaeon Methanobacterium thermoautotrophicum}

MKIAIASSTGDLGSEVSRRFFGRAPYFMIVEMKKGNIESSEVIENPSASASGGAGIRTAQIIANNGVKAVIASSPGPNAFEVLNELGIYRATGTSVEENL
KLFTEGNLEEIRSPGSRGRRRR

>d1ewqa3 c.55.6.1 (A:121-266) DNA repair protein MutS, domain II {Thermus aquaticus}

LLQESLLPREANYLAIAITGDGWGLAFLDVSTGEFKGTVLKSKSALYDELFHRPAEVLLAPELLENGAFLDEFRKRFPVMLSEAPFEPEEGGPLRRA
RGALLAYAQRTQGGALSLQPFRFYDPGAFMRLPEATLRALEVFEPL

>d1e3ma3 c.55.6.1 (A:117-269) DNA repair protein MutS, domain II {Escherichia coli}

GTISDEALLQERQDNLLAAIWQDSKGFGYATLDISSLGRFLSEPADRETMMAELQRTNPAELLYAEDFAEMSIEGRRLRRPLWEFEIDTARQQLNQ
QFGTRDVLVGFVENAPRGLCAAGCLLQQYAKDTQRRTLPHRSITMEREQDSIIM

>d1sfe_2 c.55.7.1 (12-92) Ada DNA repair protein {Escherichia coli}

LAVRYALADCELGRCLVAESERGICAIIIGLDDDATLISELQQMFPAADNAPADMFFQQHVREVIASLNQRDTPLTPLDIR

>d1qnta2 c.55.7.1 (A:6-91) O6-alkylguanine-DNA alkyltransferase {Human (Homo sapiens)}

EMKRTTLDSPPLGKLELSGCSEQLHEIKLLKGTSAAADAEVPAPAAVLGGPEPLMQCTAWLNAYFHQPEAIEFPVPAHHPVFQQ

>d1mgta2 c.55.7.1 (A:1-88) O6-alkylguanine-DNA alkyltransferase {Archaeon Pyrococcus kodakaraensis}

MLSVEKFRVGERVVWIGVIFSGRVQGIAFAFDRGTLMKRIHDLAELHGKRGVSISLDVQPSDYPEKFVFKVLIGELDNASFLRELSFEG

>d1cfza_ c.56.1.1 (A:) Hydrogenase maturing endopeptidase HybD {Escherichia coli}

MRILVLGVGNILLTDEAIGVRIECALEQRYILPDYVEILDGGTAGMELLGDMANRDHLIIADAIVSKKNAPGTMMILRDEEVPALFTNKISPHQLGLAD
VLSALRFTGEFPKKLTLVGVIPESLEPHIGLTPTVEAMIEPALEQVLAALRESGVPAIRSDS

>d1c8ba_ c.56.1.2 (A:) Germination protease {Bacillus megaterium}

MEKELDLSQSYVRTDLAVEAKDIALENQPKPNQSEIKGVIVKEKEEQGVKISMVEITEGAEIAKKGRYVTLESVGIREQDTEKQEEAMEEVFAKE
LNFFIKSLNIPDDASCLVVGGLNLSVTPDALGPKAVIDNLLTRHLFELQPSVQDGFRPVAIVPGVMGMTGIETSDIIFGVVKVNPDFIIADALAARS
IERVNATIQSDSGIHPGSGVGNKRKEISYETLGIPVIAIGIPTVDAVSITSDTIDFILKHFGREMKEQGKPSKSLPSGMFTGEKKLTEDDLPNEEQRQ
TYLGMIGTLPEEKRRRIHEVLAPLGHNLMTPKEVDMFIEDMANVVAGGLNAALHHEVDQENFGAYTH

>d1ulb__ c.56.2.1 (-) Purine nucleoside phosphorylase, PNP {Human (Homo sapiens)}

MENGYTYEDYKNTAEWLLSHTKHRPQVAICGSGLGGTDKLTQAQIFDYSEIPNFPRESTVPGHAGRLVFGFLNGRACVMMQGRFHMYEGYPLWK
VTFPVVFHLLGVETLVTNAAGGLNPKEVGDIMLIRDHINLPGFSGQNPLRGPNDERFGDRFPAMS DAYDRTMRQRALSTWKQMGEQRELQE
GTYVMVAGPSFETVAECRVLQKLGADAVGMSTVPEVIVARHCGLRVFGFSITNKVIMDYESLEKANHEEVLAAGKQAAQKLEQFVSLMASIPLPD
KAS

>d1b8oa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cow (Bos taurus)}

NGYTYEDYQDTAKWLLSHTEQRPVAVICGSGLGGTDKLTQAQIFDYSEIPNFPRESTVPGHAGRLVFGFLNGRACVMMQGRFHMYEGYFWKVTF
FPVRVFRLLGVETLVTNAAGGLNPFEVGDIIMLIRDHINLPGFSGENPLRGPNERFGVRFPMASDAYDRTMRQKAHSTWKQMGEQRELQEGT
YVMLGGPNFETVAECRLLRNGLGADAVGMSTVPEVIVARHCGLRVFGFSITNKVIMDYESQGKANHEEVLEAGKQAAQKLEQFVSLMASI

>d1k9sa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Escherichia coli}

ATPHINAEMGDFADVVLMPGDPLRAKYIAETFLEDAREVNNVRGMLGFTGTYKGRKISVMGHGMIPSCSIYTKELITDFGVKKIIRVGSCGAVLPH
VKLRDVVIGMAGCTDSKVNIRFKDHDFAAIAFDMVRNAVDAAKALGIDARVGNLFSADLFYSPDGEMFDVMEKYGILGVEMEAAGIYGVAEEF
GAKALTICTVSDHIRTHEQTTAACERQTTFNDMIKIALESVLLGDK

>d1qe5a_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cellulomonas sp.}

PPLDDPATDPFLVARAAADHIAQATGVEGHDMALVLGSGWGGAAELLGEVVAEVPTHEIPGFSSVTRSIRVERADGSVRHALVLGSRTHLYEGKGVR
AVVHGVRATAATGAETLITNGCGGLNQEWGAGTPVLLSDHINLTARSPLEGPTFVDLTDVYSPRLRELAHRVDPTLPEGVYAQFPGPHYETPAEV
MAGILGADLVGMSTTLEAIAARHCGLEVGLVSLVTNLAAGISPTPLSHAEVIEAGQAAQPRISALLADIAKR

>d1g2oa_c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Mycobacterium tuberculosis}

DPDELARRAAQVIADRTGIGEHDVAVVLGSGLPAVAALGSPPTVLPQAELPGFVPPAAGHAGELLSPIGAHRVLVLAGRIHAYEGHDLRYVVHP
VRAARAAGAQIMVLNTAAGGLRADLQVGQPVISDHNLNTARSPLVGGEFVLDTASPRRLRELARQSDPQLAEGVYAGLPGPHYETPAEIRMLQTL
GADLVGMSTVHETIAARAAGAEVLGVSLVTNLAAGITGEPLSHAEVLAAGAASATRMGALLADVIARF

>d1k3fa_c.56.2.1 (A:) Uridine phosphorylase {Escherichia coli}

MSKSDVFHLGLTKNDLQGATLAVPGDPDRVEKIAALMDKPVKLASHREFTTWRAELDGKPVICSTGIGGPSTSIAVEELAQLGIRTFLRIGTTGAIQ
PHINVGDVLTASVRDGAISLHFAPLEPAVADFECKTALVEAAKSIGATTGVTASSDTYPGQERYDTYSGRVVRHKGSMEEWQAMGVMNY
EMESATLLTMCAASQGLRAGMVAGVIVNRQQEIPNAETMKQTESHAVKIVVEAARRLL

>d1cb0a_c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Human (Homo sapiens)}

AVKIGIIGGTGLDDPEILEGRTEKVDTPGKPSDALILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKKEEGCTHVITTAGSLREEIQPGDIVI
IDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVIETAKKGLRCHSKGTMVTFEGRPFSSRAESFMFRWGADVINMTTVPEVVLAK
EAGICYASIAMATDYDCWKEHEEAWSVDRVLTKELENANKAKSLLTTIPQIGSTEWSETLHNLNKMAQFSVLL

>d1je0a_c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Archaeon Sulfolobus solfataricus}

PVHILAKKGEVAERVLVVGDPGRARLLSTLQNPKLTNENRGFLVYTGKYNGETVSIATHGIGGPSIAVLEELAMLGANVFIRYGGTGTALVPIYLGEYII
VTGASYNQGGLFYQYLRDNACVASTPDFELTNKLVTSFSKRNLKYYGVNFSSDAFYAEDEEFVKKWSSRGNIAVEMECATLFTLSVKKGWKSATVLV
VSDNLAKGGIWITKEELEKSVMGDGAKAVLDTLTS

>d2pth_c.56.3.1 (-) Peptidyl-tRNA hydrolase {Escherichia coli}

TIKLVGLANPGAEYAATRHNAGAWFV DLLAERL RAPLREEAKFFGYTSRVTLGGEDV RLLVPTT FMNL SGKAVAAMASFR INPDEILV AHD ELD LPP
GVAKFKLGGGHGGHNGLKDII SKLGNNPNFHRLRIGIGHPGDKNKVVGFLGKPPVSEQ KLI DEAIDE ARCT EMWF TDGLT KATN RLH AFKA Q

>d1a2za_c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Archaeon Thermococcus litoralis}

MKKVLITGFEPFGGDSKNPTEQIAKYFDRKQIGNAMVYGRVLPVSVKRATIELKRYLEEIKPEIVINGLAPTYSNITVERIAVNII DARIPDNDGYQPIDE
KIEEDAPLAYMATLPVRAITKTLRDNGIPATISYSAGTYLCNYVMFKTLHFSKIEGYPLKAGFIHV PYTPDQV VNKFFLGKNTPSMCLEAEIKAIELAVKV
SLDYLEKDRDDIKIPL

>d1auga_c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Bacillus amyloliquefaciens}

MEKKVLLTGDFPFGGETVNP SWEAVKRLNGAAEGPASIVSEQVPTV FYKSLAVLREAIKKHQDIIICVGQAGGRMQITPERVAINLNEARIPDNEG N
QPVGEDISQGGPAAYWTGLPIKRIVEIKKEGIPAAVS YTAGTFVCNHLFYGLMDEISRHHPHIRGGFIHPIYIPEQLTQKSAPSLSLDHITKALKIAAVTA
AVHEDDIETG

>d1iofa_c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Archaeon Pyrococcus furiosus}

MKVLVTGFEPFGGEKINPTERIAKDLGIKIGDAQVFG RVL PVV FG KAKEV LEK TLE EIKPDIAIH VGLAPGRSAISIERIAVNAIDARIPDNEG KKI EDE PI
VPGAP TAYFSTLPIKKM KK LHERG I PAYI NSAG LYLC NYV M YL S LHSATKG YPK MSG F IH V PYI PEQ I IDKIGKGQVPPSMC YEME LEAV KV AIEVAL
EELL

>d2ctc_c.56.5.1 (-) Carboxypeptidase A {Cow (Bos taurus)}

ARSTNTFNYATYHTLDEIYDFMDLLVAEHPQLVSKLQIGRSYEGRPIYVLKFSTGGSNRPAIWIDLG IHSREWITQATGVWF AKKFTEDY GQDPSFTAIL
DSMDIFLEIVTNP DGFAT HSQNRLWRKTRSVTSSLCVGVDANRNWDAGFGKAGASSPCSETYHGKYANSEVEVKSIVDFVKDHGNFKAFLSIHS
YSQLLLPYGYTTQSIPDKTELNVAKSAVEALKSLYGT SYKGSIITIYQASGGSIDWSYNQGKYSFTELRTG RYGFLLPASQI IPTAQETWLGVLT
MEHTLNN

>d1pca_1 c.56.5.1 (1-308) Carboxypeptidase A {Pig (Sus scrofa)}

ARTTSTFNYATYHTLEE IYDFMDILV AEHPALVSKLQIGRSYEGRPIYVLKFSTGGSNRPAIWIDSGIHSREWITQASGVWF AKKITE NYGQNSFTA ILD
SMDIFLEIVTNPNGFA FTHSDNRLWRKTRSKASGSLCVGSDSNRNWDAGFGGAGASSPCAETYHGKP NSEVEVKSITDFVKNNNGNIKA FISIHSY
SQLLLPYGYKTQSPADKSELNQIAKSAVAALKSLYGT SYKGSIITIYQASGGSIDWSYNQGKYSFTELRTG RYGFLLPASQI IPTAQETWLALLTIM
EHTLNNS

>d1dtda_c.56.5.1 (A:) Carboxypeptidase A {Human (Homo sapiens)}

FNFGAYHTLEE ISQEMDNLVAEHPGLVSKVNIGSSFENRPMNVLFSTGGDKPAIWL DAGIHAREWV TQAT ALWTANKIVSDYGDPSITSILD A IF
LLPV TNPDGYVFSQTKNRMWRKTRSKV SAGSLCVGVDPNRNW DAGFGGP GASSN P CSDSYH GPSAN SEVEVKSIVDFIKSHGKV KAFIILH S YSQL

LMFPYGYKCKLDDFDELSEVAQKAAQSLSLHGTKYVGPICSVIYQASGGSIDWSYDYGKYSFAELRTGTYGFLLPARQILPTAEETWLGLKAIM
EHVRDHYPY
>d1nsa_1 c.56.5.1 (4-308) Carboxypeptidase B {Pig (Sus scrofa)}
TTGHSYEKYNWETIEAWTEQVTSKNPDLISRSAIGTTFDGDNIYLLKGKPGSNKPAIFMDCGFHAREWISQAFCQWFVRDAVRTGYEAHMTEF
LDNLDFYVLPVLNIDGYIYTWTKNRMWRKTRSTNAGSSCTGTDPNRNFAGWCTGAVSNPCNETYCGSAAESEKETKALADFIRNNLSSIKAYLTI
HSYSQMILYPYSYDYKLPPENDAELNSLAKGAVKELASLYGTSYSGPGSTTIYPAAGGSDDWAYNQGKYSFTFELRDKGRRGFLVLPESQIQATCQETM
LAVKYVTNTYTHEHL
>d1cpb__ c.56.5.1 (-) Carboxypeptidase B {Cow (Bos taurus)}
TTGHSYEKYNWETIEAWTEQVASENPDLISRSAIGTFLGNTIYLLKGKPGSNKPAVFMDCFGHAREWISPAFCQWFVRREXXXXXIEHMTEFL
DKLDFYVLPVVNIDGYIYTWTNRMWRKTRSTRAGSSCTGTDLNRFAGWCSIGASNNSPCSETYCGSAAESEKESKAVADFIRNHLSIKAYLTIHS
YSQMMILYPYSYDYKLPPNDLNTLAKGAVKKLASLHGTTSYGPGATTIYPASGGSDDWAYDQGKYSFTFELRDKGRRGFLVLPESQIQPTCEETM
AIKYVTSVLEHL
>d1h8la2 c.56.5.1 (A:4-304) Carboxypeptidase D, catalytic domain {Crested duck (Lophonetta specularioides)}
QAVQPVDFRHHHFSDEMEIFLRRYANEYPSITRLYVGKSVLRELYVMEISDNPGIHEAGEPEFKYIGNMHGNEVVGRLELLNLIEYLCKNFGTDPEVT
DLVQSTRIHIMPSMNPDGYEKSQEGDRGGTVGRNNNSNYDLNRNFPDQFFQVTDPQQPETLAVMSWLKTPFVLSANLHGSSLVNVYPFDDDE
QGIAIYSKSPDDAVFQLALSYSKENKKMYQGSPCKDLYPTEYFPHGITNGAQWVNVPGGMQDWNYLNTNCFEVTIELGCVKYPKAELPKYWEQ
NRRSLLQFIKVQVR
>d1obr__ c.56.5.2 (-) Carboxypeptidase T {Thermoactinomyces vulgaris}
DFPSYDGSYHNYNEMVNKINTVASNYPNIVKKFSIGKSYEGRELWAVKISDNVGTDENEPREVYTALHHAREHTLVEMALYTLDFLTQNYNLDRTN
LVNNREIYIVFNINPDGGEYDISSGSYKSWRKRNQPNSSYYGTDLNRYGYKWGCCGSSGSPSSETYGRSAFSAPETAAMRDFINSRVVGGK
QQIKLTIFHTYSELILYPGYTYTDVPSDMTQDDFNFKTMANTMAQTNGYTPQQASDLYITDGMNTDWAYGQHKIAFTFEMYPTSYNPGFYPP
DEVIGRETSRNKEAVLYVAEKADCPYSVIGKSC
>d1lam_2 c.56.5.3 (160-484) Leucine aminopeptidase, C-terminal domain {Cow (Bos taurus)}
FASGQNLLARRLMEPTPKFAEIVEENLKSASIKTDVFIRPKSWIEEQEMGSFLSVAKGSEEPVFLEIHYKGSPNASEPPLVFVGKGTDFSGGI
SIKAAANMDLMRADMGGATICAISAAKLDLPIINVGLAPLCENMPGSKANKPGDVVRARNGKTIQVDNTDAEGRLLADALCYAHTFNPKVII
AATLGAMDIALGSGATGVFTNSSLWNKLFEASIEITGDRVWRMPLFEHYTRQVIDCQLADVNNIGKRSAGACTAAFLKEFVTHPKWAHLDIAG
VMTNKDEVPLYLRKGGMAGRPTRTLIEFLFRFSQ
>d1amp__ c.56.5.4 (-) Aminopeptidase {Aeromonas proteolytica}
MPPITQQATVTAWLPQVDASQITGTISSLESFTNRFTTSGAQASDWIASEWQALSASLPNASVKQVSHSGYNQKSVMITGSEAPDEWIVIGG
HLDSTIGSHTNEQSVPAGADDASGIAAVTEVIRVLSENNFQPKRSIAFMAYAAEVGLRGSQDLANQYKSEGKNNVSALQDMTNYKGSAQDVF
ITDYTDNFTQYLTQLMDEYLPSTYGFDTGYACSDHASWHNAGYPAAMPFESKFNDYNPRIHTTQDTLANSPTGSHAKKFTQLGLAYAIEMGSA
TG
>d1qc9a_ c.56.5.4 (A:) Aminopeptidase {Streptomyces griseus}
APDIPLANVKAHLQLSTIAANNGNRAHGRPGYKASVDYVKAALKDAAGYTTLQQFTSGGATGYNLIANWPGDPNKVLMAGAHLDVSSGAGI
NDNGSGSAAVLETALAVSRAGYQPDKHLRFWWGAELGLIGSKFYVNNLPSADRSKLAGYLNFDLIGSPNPGYFVYDDDPVIEKTFKNYFAGLNV
PTEIETEGDGRSDHAPFKNVGVPVGGIFTGAGYTKSAAQAKWGGTAGQAFDRCYHSSCDLSNINTALDRNSAAAHHAIWTLSS
>d1cg2a1 c.56.5.4 (A:26-213,A:327-414) Carboxypeptidase G2, catalytic domain {Pseudomonas sp., strain rs-16}
QKRDNVLFQAATDEQPAVITLEKLVNIETGTGDAEGIAAAGNFLEALKNLGFTVTRSKSAGLVGDNIVGKIKGRGGKNNLLMSHMDTVLKGILA
KAPFRVEGDKAYGPGIADDKGNAVLHTLKLKEYGVRDYGTITVLFNTDEEKGSFGSRDLIQEEAKLADYVLSFEPTSAGDEKLSLGTXFNAGEGGK
KLVDKAVAYYKEAGGTLGVVEERTGGGTDAAAYAALSGKPVIIESLGLPGFGYHSDKAEYVDISAIPRRLYMAARLIMDLGAG
>d1de4c3 c.56.5.5 (C:122-189,C:383-608) Transferrin receptor ectodomain, protease-like domain {Human (Homo sapiens)}
LYWDDLKRKLSEKLDSTDFSTIKLNNENSYVPREAGSQKDENLALYVENQFREFKLSKVWRDQHFVXEIKILNIFGVIKGFVEPDHYVVVGAQRDA
WGPGAAKSGVGVTALLKLAQMFSDMVLKDGFQPSRSIIFASWSAGDFGSVGATEWLEGYLSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYTIEKT
MQNVKHPVTGQFLYQDSNWASKVEKLTLDNAAPFLAYSGIPAVSFCCEDTDYPGLGTTMDTYKELIERIPELNKVVARAAAEVAGQFVILTHDVEL

N

>d1boub_c.56.6.1 (B:) LigB subunit of an aromatic-ring-opening dioxygenase LigAB {Pseudomonas paucimobilis}
ARVTGITSCHIPALGAAIQTGTSNDYWGPVFKGYQPIRDWIKQPGNMMPDVILVYNDHASAFDMNIIPTFAIGCAETFKPAEGWGPRPVPDVKG
GHPDLAWHIAQSLILDEFDMTIMNQMDVHDGCTVPLSMIFGEPEEWPCVKIPFPVNVTYPPPSGKRCFALGDSIRAAVESFPEDLNVHVWGTGG
MSHQLQGPRAGLINKEFDLNFIDKLISDPEELSKMPHIQYLRESGSEGVELMWLIMRGALPEKVRDLYTFYHIPASNTALGAMILQPEETAGTPLEPR
KVMSGHSL

>d1di6a_c.57.1.1 (A:) MogA {Escherichia coli}
ATLRIGLVSISDRASSGVYQDKGIPALEEWLTSALTPFELETRLIPDEQAIIEQTLCELDEMSCHLVTGGTGPARRDVTPDATLAVADREMPGFGEQ
MRQISLHFVPTAILSQRQVGVRKQALILNLPGQPKSIKETLEGVKDAEGNVVVGIFASPVYCQLLEGPYVETAPEVVAFRPKSARR

>d1jlja_c.57.1.1 (A:) Gephyrin N-terminal domain {Human (Homo sapiens)}
HQIRVGVLTVSDSCFRNLAEDRSGINLKDLVQDPSSLGGTISAYKIVPDEIEEKETLIDWCDEKELNLLTTGGTFAPRDVTPPEATKEVIEREAPGMALA
MLMGSLNVTPLGMLSRRPVCIGRKTLIINLPGSKGSQECFQFILPALPHAIDLLRAIVKVKEVHD

>d1eava_c.57.1.1 (A:) Plant CNX1 G domain {Mouse-ear cress (Arabidopsis thaliana)}
GPEYKVAILTVSDTVSAGAGPDRSGPRAVSVDSSSEKLGAKVVATAVVDEVERIKDILQKWSDVDEMDLILTLGGTGFTPRDVTPEATKKVIERET
PGLLFVMMQESLKITPFAMLSRSAAIGRGSTLIINMPGNPNAVAECMEALLPAALKHQI

>d1g8la3_c.57.1.2 (A:178-326) MoeA, central domain {Escherichia coli}
VRVALFSTGDELQLPGQPLGDGQIYDTNRLAVHLMLEQLGCEVINLGIIRDDPHALRAAFIEADSQADVVISSGGVSVEADYTKTILEELGEIAFWKL
AIKPGKPFAFGKLSNSWFCGLPGNPVSATLTYQLVQPLLAQLSGNTASG

>d1bgva2_c.58.1.1 (A:1-194) Glutamate dehydrogenase {Clostridium symbiosum}
SKYVDRVIAEVEKKYADEPEFVQTVEEVSSLGLPVDAHPEYEVEALLERMVIPERVIEFRVPWEDDNGKVVHNTGYRVQFNAGAIGPYKGGLRFAPS
VNLSIMKFLGFEQAFKDSLTLPMGGAKGGSDFDPNGKSDREVMRFCQAFMTELYRHIGPDIDVPAGDLGVGAREIGYMYGQYRKIVGGFYNGVLT
G

>d1gtma2_c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}
ADPYEIVIKQLERAQYMEISEEAEFLKRQPRIVEVTIPVEMDDGSVKVFTGFRVQHNWARGPTKGIRWHPEETLSTVKALAAWMTWKAVMD
LPYGGGKGGIIVDPKKLSDREKERLARGYIRAIYDVISPYEDIPAPDVYTNPQIMAWMMDYEYETISRRKTPAFGIITGKPLSI

>d1euza2_c.58.1.1 (A:4-180) Glutamate dehydrogenase {Archaeon Thermococcus profundus}
IDPFEMAVKQLERAQYMDISEEAEWLKKPMRIVEVSPVEMDDGSVKVFTGFRVQHNWARGPTKGIRWHPEETLSTVKALATWMTWKAV
VDLPHYGGGKGGIIVNPKELESEREQERLARAYIRAVYDVIGPWTIDIPAPDVYTNPKIMGWMMDEYEYETIMRRKGPAGVITGKPLS

>d1bvua2_c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Thermococcus litoralis}
QDPFEIAVKQLERAQYMDISEEAEFLKRQPRIVEVSPVEMDDGSVKVFTGFRVQHNWARGPTKGIRWHPEETLSTVKALAAWMTWKAVM
DLPHYGGGKGGIICNPKELESEREQERLARAYIRAIYDVISPYTDIPAPDVYTNPQIMAWMMDYEYETISRRKDPFGVITGKPPSV

>d1b26a2_c.58.1.1 (A:4-178) Glutamate dehydrogenase {Thermotoga maritima}
SLYEMAVEQFNRAASLMLESDEAHLRRPKRVLIVEFPVRMDDGHVEVFTGYRVQHNVARPAKGGIRYHPDVTLDEVKALAFWMTWKAVMN
LPFGGGKGGVRDPKKLRSNELERLSRRFFSEIQLVIIQPYNDIPAPDVNTNADVIAWYMDTYSMNVGHTVLGIVTGPVEL

>d1hwxa2_c.58.1.1 (A:1-208) Glutamate dehydrogenase {Cow (Bos taurus)}
ADREDDPNFFKMVEGFFDRGASIVEDKLVEDLKRQEQKRNRVRLRIIKPCNHLVLSFPIRRDDGSWEVIEGYRAQHSHQRTCPKGIRYSTD
VSVDEVKALASLMTYKCAVVDPFGGAKAGVKINPKNYTDEDLEKIRRFTMELAKKGFIGPGVDVPAPNMSTGEREMSWIADTYASTIGHDINA
HACVTGKPISQGGI

>d1leha2_c.58.1.1 (A:1-134) Leucine dehydrogenase {Bacillus sphaericus}
MEIFKYMELYDYEQLVFCQDEASGLKAVIAIHDTLGPALGGARMWTYNAEEAIEDALRLARGMTYKNAAGLNLGGGKTVIIGDPFADKNEDMF
RALGRFIQGLNGRYITAEDVGTVDMDLIHQETDYVT

>d1c1da2_c.58.1.1 (A:1-148) Phenylalanine dehydrogenase {Rhodococcus sp., M4}
SIDSALNWDGEMTVTRFDAMTGAHFVIRLDSTQLGPAAAGGTRAAQYSNLADALTDAKLAGAMTLKMAVSNLPMGGKSVIALPAPRHSIDPST
WARILRIHAENIDKLSGNWTGPDVNTNSADMINTLNDTEFVGRSLERGGAGS

>d1a4ia2 c.58.1.2 (A:2-126) Tetrahydrofolate dehydrogenase/cyclohydrolase {Human (Homo sapiens)}

APAEILNGKEISAQIRARLKNQVTQLKEQVPGFTPRLAILQVGNRDDSNLINVKLKAAEIGIKATHIKLPRTTSEVMKYITSLNEDSTVHGFLVQLP
LDSENSINTEEVINAIAPERKDVDG

>d1b0aa2 c.58.1.2 (A:2-122) Tetrahydrofolate dehydrogenase/cyclohydrolase {Escherichia coli}

AAKIIDGKTIQQVRSEVAQKVQARIAAGLRAPGLAVLVGSNPASQIVASKRKACEEVGFVSRSYDLPETTSEAELLEIDLNTADNTIDGILVQLPLP
AGIDNVKVLERIHPDKDVDG

>d1edza2 c.58.1.2 (A:3-148) Tetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}

KPGRTILASKVAETFNTEIINNVEEYKKTHNGQGPLLGVFLANNPAAKMYATWTQKTSESMGFRYDLRVIEDKDFLEEAIIQANGDDSVNGIMVYF
PVFGNAQDQYLQQVVCERKDVGLNHVYYQNLYHNVRYLDKENRLKSIL

>d1do8a2 c.58.1.3 (A:21-279) Mitochondrial NAD(P)-dependent malic enzyme {Human (Homo sapiens)}

IKEKGKPLMLNPRTNKGMATLQERQMLGLQGLPPKETQDIQALRFHRNLKKMTSPLKEYIYIMGIQERNEKLFYRILQDDIESLMPIVTPTVGLA
CSQYGHIFRRPKGLFISIDRGHVRSIVDNWPENHVKA VVTDGERILGLDLGVYGMGIPVGKCLTYACAGIRPDRCLPVCIDVGTNDIALLKDPFY
MGLYQKRDRQQYDDLIDEFMKAITDRYGRNTLIQFEDFGNHNAFRFLRKYREKYCTFNDD

>d2uaga2 c.59.1.1 (A:298-437) UDP-N-acetyl muramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}

GLPHRFEVVLEHNGVRWINDSKATNVGSTEALNLHVGDGLHLLGGDGKSADFSPLARYLNGDNVRLYCFGRDGAQLAALRPEVAEQTETMEQ
AMRLLAAPRVQPGDMVLSPACASLDQFKNFQERGNEFARLAKELG

>d1e8ca2 c.59.1.1 (A:338-497) UDP-N-acetyl muramyl tripeptide synthetase MurE {Escherichia coli}

VCGRMVEVFTAPGKPTVVVDYAHPTDALEKALQAARLHCAGKLWCVFCGGDRDKGRPLMGIAEEFADVAVVTDDNPRTEEPRAIINDILAGML
DAGHAKVMEGRAEAVTCAVMQAKENDVVLVAGKGHDYQIVGNQRDYSRVTVARLLGVIAHSH

>d1gg4a1 c.59.1.1 (A:313-447) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

VPGRLFPIQLAENQLLDDSYNANVGSMTAAVQVLAEMPGYRVLVVGDMAELGAESACAHVQVGEAAKAAGIDRVLSGVKQSHAISTASGVGEHF
ADKTALITRLKLLIAEQQVITILVKGSRSAAMEEVVRALQ

>d1jbwa1 c.59.1.2 (A:297-425) Folylpolyglutamate synthetase, C-terminal domain {Lactobacillus casei}

WPARLEKISDTPLVIDGAHNPDGINGLITALKQLFSQPITVIAGILADKDYAAMADRITAFTVYLVPVPGTPRALPEAGYEALHEGRLKDSWQEALA
ASLNDVDPDQPIVITGSLYLASAVRQTLLG

>d1qhfa_c.60.1.1 (A:) Phosphoglycerate mutase {Baker's yeast (Saccharomyces cerevisiae)}

PKLVLVRHGQSEWNEKNLFTGWVDVLSAKGQQEARAGELLKEKKVYPDVLYTSKLSRAIQTANIALEKADRLWIPVNRSWRLNERHYGDLQKD
KAETLKKFGEKFNTYRRSFDPPPPDAASSPSQKGDERKYVDPNVLPETESLALVIDRLLPYWQDVIAKDLSGKTVMIAHGNSLRGLVKHLEGIS
DADIAKLNIPGTILVFELDENLKPSPSYLDPEAAAAGAAAV

>d3pgm_c.60.1.1 (-) Phosphoglycerate mutase {Baker's yeast (Saccharomyces cerevisiae)}

PKLVLVRHGQSEWNEKNLFTGWVDVLSAKGQQEARAGELLKEKGVNVLVDYTSKLSRAIQTANIALEKADRLWIPVNRSWRLNERHYGDLQKD
DKAQTLLKFGEEKFNTYRRSFDPPPPDAASSPSQKGDERKYVDPNVLPETESLALVIDRLLPYWQDVIAKLVGKTSMIAHGNSLRGLVKHLEGIS
DADIAKLNIPPGTILVFELDENLKPSPSYLDPEA

>d1fzta_c.60.1.1 (A:) Phosphoglycerate mutase {Yeast (Schizosaccharomyces pombe)}

MTTEAAPNLLVTRHGESEWNKLNLTGKDPALSETGIKEAKLGGERLKSRGYKFDIAFTSALQRAQKTCQIILEEVGEPNLETIKSEKLNERYYGDQ
GLNKDDARKKGAEQVQIWRRSYDIAPPNGESLKDTAERVLPIYYKSTIVPHILKGEVKLIAHGNSLRALIMDLEGTDQIVKRELATGVPIVYHLDK
DGKYVSKELIDN

>d1e58a_c.60.1.1 (A:) Phosphoglycerate mutase {Escherichia coli}

AVTKLVLVRHGESQWNKENRFTGWWYDVLSEKGVSEAKAAGKLLKEEGYSDFAYTSVLKRAIHTLWNVLDLDQAWLPVEKSWKLNERHYGALQ
GLNKAETAEKYGDEQVKQWRRGFAVTPPELTKDDERYPGHDPRYAKLSEKEPLTESLALTIDRVIPYWNTELPRMKSGERVIAAHGNSLRALVKYLD
NMSEEEILENIPTGVPLVYEFDENFKPLKRYYLGNADEIAAKAAAVANQK

>d1ebba_c.60.1.1 (A:) Broad specificity phosphatase YhfR {Bacillus stearothermophilus}

ATTLYLTRHGETKWNVERRMQGWQDSPLTEKGRQDAMRLGKRLEAVELAAIYTSTSgraletaeivrggripiyqderlreihlgdwegkthdeir
QM DPIAFDHFWQAPHYAPQRGERFCDVQQRALEAVQSIVDRHEGETVLIVTHGVVLLKTLMAAFKDTPLDHLWSPPYMYGTSVIIEDGGTFHV

AVEGDVSHIE

>d1rpa__ c.60.1.2 (-) Acid phosphatase {Rat (Rattus norvegicus)}

KELKFVTLVFRHGDRGPIETFPNDPIKESSWPQGFGQLTKWGMGQHYELGSYIRRGRFLNNSYKHDQVYIRSTDVRTLMSAMTNLAALFPPEG
NSIWNPRLLWQPPIPHTVLSEDRLLYLPFRDCPRFQEKLSEEFKRLQPYKSFIIDLPSLSGFEDQDLFEIWSRLYDPLYCESVHNTLPTWATE
DAMTKLKELSELSSLSYGIHKQKEKSRLQGGVLVNEILNMKLATQPQKARKLIMYSAHDTTVSGLQMAVDVYNGLLPPYASCHIMELYQDNGGHF
VEMYYRNETQNEPYPLTPGCTHSCPLEKFAELLDVIPQDWATECMG

>d2hpaa_ c.60.1.2 (A:) Acid phosphatase {Human (Homo sapiens)}

KELKFVTLVFRHGDRSPIDTFPTDPIKESSWPQGFGQLTQLGMEQHYELGEYIRKRYRKFLNESYKHEQVYIRSTDVRTLMSAMTNLAALFPPEGVSI
WNPILLWQPPIPHTVPLSEDQQLYLPFRNCPRFQELESETLKSEEFQKRLHPYKDFIATLGKLSLHGQDLFGIWSKVVYDPLYCESVHNFTLPSWATEDT
MTKLRELSELSSLSYGIHKQKEKSRLQGGVLVNEILNMKRAZQIPSYKKLIMYSAHDTTVSGLQMAVDVYNGLLPPYASCHLTELFEKGEYFVEMYY
RNETQHEPYPLMLPGCSCPCLERFAELVGPVIPQDWSTECMT

>d1ihp__ c.60.1.3 (-) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus ficuum}

SCDTVDQGYQCFCSETSHLGWQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHARYPTDSKGKKYSALIEIQQNATTFDGKYAFLKTNYSLGADDL
TPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKDPRAQPGQSSPKIDVVISEASSNNTLDPGTCTVFEDSELADTVAN
FTATFVPSIRQLENDLSGVTLTDTEVTYLMDMCSFTISTSTVDTKLSFCDLFTHDEWINYDYLQSLKYYGHGAGNPLGPTQGVYANEIARLTH
SPVHDDTSNNHTLDSSPATFPNLSTYADFSDHNGIISIFALGLYNGTKPLSTTVENITQTDGFSSAWTPFASRLYVEMMQCQAQEPLVRVLVND
RVVPLHGCPVDALGRCTRDSFVRGLSFARSGGDWAECFA

>d1qfxa_ c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus niger}

KQFSQEFRDGYSILKHGGNGPYSERVSIGIARDPPTCEVDQVIMVKRHGERYPSPSAGKDIEEALAKVSYINTTEYKGDIAFLNDWTYYVPNECY
NAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETVPPFSSGYGRVIETARKFGEGFFGYNYSTNAALNIISESEVMGADSLPTCDNDQTTCDN
LTYQLPQFKVAAARLNSQNPGMNLTASDVYNLMVMASFELNARPSNWINAFTQDEWVSFGYVEDNYYYYCAGPGDKNMAAVGAVYANASLTL
NQGPKEAGSLFFNFAHDTNITPIALAQLVLPNEDLPLDRVAFGNPYSIGNIVPMGGHHTIERLSCQATALSDEGTYVRLVNEAVLPFNDCTSGPGYSC
PLANYTSILNKNLPDYTTTCNVSASYPQYLSFWNNYNTTELNYRSSPIACQEGDAMD

>d1dkla_ c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Escherichia coli}

SEPELKLESVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGWLPRGGELIAYLGHYQRQLVADGLLAKKGCPQSGQVIIADVDERTRKTG
EAFAAGLAPDCAITVHTQADTSSPDLFNPLKTGVCQLDNANVTDAILSRAGGSIAFTGHRQTAFRELERVLNFPQSNLCLKREKQDESCSLTQALPS
ELKVSADNVLGAVSLASMLTEIFLQQAQGMPEPGWGRITDSHQWNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIKTALTPHPPQKQAYGVTL
TSVLFIAGHDTNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRSLSDNSQWIQSVLVTQLQMRDKTPLSNTPPGEVKLTAGCEERNAQG
MC5LAGFTQIVNEARIPACSL

>d1bif_2 c.60.1.4 (250-468) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain {Rat (Rattus norvegicus)}

SIYLCRHESENLKGRIGGDGPLSPRGREFSKHLAQFISDQNIKDLKVFTSQMKRTIQTAEALSPVYEQFKVLNEIDAGVCEEMTYEEIQDHYPF
RDQDKYRYRYPKGESYEDLVQRLEPVIMELERQENVLVICHQAVMRCLLAYFLDKAAEELPYLKCPHTVVKLTPVAYGCKVESIFNVAVNTHRDRP
QNVDIRPSEEALTVPAH

>d1fbta_ c.60.1.4 (A:) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain {Rat (Rattus norvegicus)}

RSIYLCRHESENLRGRIGGDGLSARGKQYAYALANFIRSQGIISSLKVWTSHMKRTIQTAEALGPVYEQWKALNEIDAGVCEEMTYEEIQEHYPEEF
ALRDQDKYRYRYPKGESYEDLVQRLEPVIMELERQENVLVICHQAVMRCLLAYFLDKSSDELPYLKCPHTVVKLTPVAYGCRVESIYLN

>d1nula_ c.61.1.1 (A:) Xantine-guanine PRTase (XPRTase) {Escherichia coli}

EKYIVTWDMQLQIHARKLASRLMPSEQWKGIIAVSRGGLVPGALLAREL GIRHVDTVCISSYDHNDNQRELKVLKRAEGDGE GFIVIDDVDTGGTAVAI
REMYPKAHFVTIFAKPAGRPLVDDYVVDIPQDTWIEQPWDMGVVFVPPISGR

>d1hgxa_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Tritrichomonas foetus}

MDDLERVLYNQDDIQKRIELAELTEFYEDKNPVMICVLTGAVFFYTDLLKHLDFQLEPDYIICSSYSGTKSTGNLTISKDLKTNIEGRHVLVVEDI
LTMYQLNNLQMRKPASLKVCTLCDKDICKKAYDVIDYCGFVVENRYIIGYGFDFHNKYRNLPVIGILKE

>d1fsga_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Toxoplasma gondii}

GSHMASKPIEDYGKGKGRIEPMYIPDNTFYNADDFLVPPHCKPYIDKILLPGGLVKDRVEKLAYDIHRTYFGEELHIICLKGSRGFFNLLIDYLATIQKS
GRESSVPPFEHYVRLKSQYQNDNSTGQLTVLSDDLSIFRDKHVLIVEDIVDTGFTLTEFGERLKAvgPKSMRIATLVEKRTDRSNSLKGDFVGFSIEDVWI
VGCCYDFNEMFRDFDHAVLSDAARKKFEK

>d1gph11 c.61.1.1 (1:235-465) Glutamine PRPP amidotransferase, C-terminal domain {Bacillus subtilis}

ICSMYEIYFSRPDSNIDGINVHSARKNLGKMLAQESAVEADVVTPDSSISAIGYAETGIPYELGLIKNRVGRTEIQPSQALREQGVRMJKLSAVR
GVVEGKRVVMVDDSIVRGTTSRIVTMLREAGATEVHKISSPPIAHPCFYGIDTSTHEELIASSHSVDEIRQEIGADTLSFLSVEGLKGIGRKYDDSN
CGQCLACFTGKYPTIEYQDTVLPHVKEAVLTK

>d1ecfa1 c.61.1.1 (A:250-492) Glutamine PRPP amidotransferase, C-terminal domain {Escherichia coli}

NPCLFYVVFARPDFSFDIKISVYSARVNMGTKLGEKIAREWEDLDIDVVVPIPETSCDIALEIARILGKPYQGFVKNRVGRTEIMPQQQLRRKSVRRKL
NANRAEFRDKNVLLVDDSVRGTTSSEQIEMAREAGAKKVYLASAAPEIRFPNVYGDMPSATELIAHGREVDEIRQIIGADGLIFQDLNDLIDAVRAE
NPDIQQFECFSVNGVYVTVDQGYLDFLTLRNDDAKAVQRQ

>d1dqna_c.61.1.1 (A:) Guanine PRTase {Giardia lamblia}

MICSVTGPVKDVLSFFFDRNDVLESEVKFKHLLATFECKALAADTARRMNEYKDVAEPVTLVALLGAYLYASLLTVHLTFPYTLHFVVKSSYKGTR
QESVVFDEEDLQLKEKREVVLIDEYVDSGHTIFSQEQIKHAKICSCFVKDVDAIKKHSALADTKMFYGYTPMPKGWSLIGFGLDDNGLRRGWAHLF
DINLSESEVTEFRRRLTEHIKGLNINGVNRY

>d1bzya_c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGPTase) {Human (Homo sapiens)}

SPGVVISDDEPGYDLDLFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKEMGGHHIVALCVLKGYYKFFADLLDYIKALNRNSDRSIPMTVDFIRLK
SYCNDQSTGDIKVIGGDDSLTGKNVLIVEDIIDTGTKTMQTLSSLRQYNPKMVVKASLLVKRTPRSVGYKPDFVGFEIPDKFVVGYALDYNEYFRDL
NHVCVISETGKAKYKA

>d1cjba_c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGPTase) {Plasmodium falciparum}

PIPNNPGAGENAFDPVFVNNDDGYDLSFMIPAHYKKYLTKVLVPNGVIKNRIEKLAYDIKKVYNNEEHILCLLKGSRGFTTALKHLSRIHNYSAVET
SKPLFGEHYVVRVSKSYCNDQSTGTLEIVSEDLSCLKGKHVLIVEDIIDTGTKTLVFCCEYLKKFEIKTVIAACLIKRTPLWNGFKADFVGFSIPDHVVGVYSLD
YNEIFRDLHDHCLVNDEGKKKYKAT

>d1tc1a_c.61.1.1 (A:) Hypoxanthine PRTase {Trypanosoma cruzi}

YEFAEKILFTEEEIRTRIKEVAKRIADDYKGKGRLPYVNPLVLISVLKGSFMFTAACLCAFDFNVPVRMEFICVSSYGEGLTSSGQVRMLLDTRHSIEGH
HVIVEDIVDTATLNYLYHMYFTRRPASLKTVVLLDKREGRRVPSADYVANIPNAFVIGYGLYDDTYRELRDIVVLRPE

>d1qb7a_c.61.1.1 (A:) Adenine PRTase {Leishmania donovani}

PFKEVSPNSFLDDSHALSQKKSYRWYSPVFSPRNVPRFADVSSITESPETLKAIRDFLVQRYRAMSPAPTHILGFDARGFLFGPMIAVELEIPFVLM
RKADKNAGLLIRSEPYEKEYKEAAPEVMTIRYGSIGKGSRVVLIDDVLATGGTALSGLQLVEASDAVVEMVSILSIPFLKAAEKIHSTANSRYKDIKFISLL
SDDALTEENCNGDSKNYTPRVLSCGVDVLAEPH

>d1g2qa_c.61.1.1 (A:) Adenine PRTase {Baker's yeast (Saccharomyces cerevisiae)}

MPIASYAQELKLALHQYPNFPSEGILFEDFLPIFRNPGFLFQKLIDAFKLHLEEAFPEVKIDYIVGLESRGFLFGPTLALALGVGFVPRKAGKLPGECKAT
YEKEYGSDLFEIQKNAIPAGSNVIIVDDIIATGGSAAAAGELVEQLEANLLEYNFVMEFLDFLKGRSKLNAPVFTLL

>d1oroa_c.61.1.1 (A:) Orotate PRTase {Escherichia coli}

MKPYQRQFIEFALKQVLKGEFTLKGSRKSPYFFNAGLFNTGRDLALLGRFYAEALVDSGIEFDLLFGPAYKGPIATTAVA LAEHHHDLDPYCFNRKE
AKDHGEGGNLNGVGSALQGRVMLVDDVITAGTAIRESMIEIIQANGATLAGVLISLDRQERGRGEISAIQEVERTDYNCKVISIITLKDIAVLEEKPEMAEH
AAVKAYREEFGV

>d1a3c_c.61.1.1 (-) Uracil PRTase {Bacillus subtilis}

QKAVILDEQAIRRALTRIAHEMIERNKGMMNCILVGKTRGIYLAKRLAERIEQJEGNPVTVGEIDITLYRDDLSSKTSNDEPLVKGADIPVDTDQKVILV
DDVLYTGRTRVAGMDALVDVGRPSSIQLAVLVDRGHRELPYRADIYIGKNIPTSKSEKVMVQLDEVDQNDLVAIYEN

>d1bd3a_c.61.1.1 (A:) Uracil PRTase {Toxoplasma gondii}

QEESILQDIITRFPNVVLMKQTAQLRAMMTIIRDKETPKEEFVFYADRIRLIEEALNELPFQKKEVTTPLDVSYHGVSFYSKICGVSVRAGESMESGL
RAVCRGVRIGKILIQRDETTAEPKLIYEKL PADIRERWVMLLDPMCATAGSVCKAIEVLLRLGVKEERIIFVNILAAPQGIERVFKEYPKVRMVTAAVDIC
LNSRYYIVPGIGDFGDRYFGTM

>d1dkra1 c.61.1.2 (A:8-166) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}
NLKIFSLNSNPELAKEIADIVGVQLGKCSVTRFSDEQVQINIEESIRGDCYIIQSTSVDNEHIMELLIMDALKRASAKTINIVIPYYGYARQDRKARSREPITAKLFANLLETAGATRVIADLHAPQIQGFFDIPDHLMGVPLGEYFEGKNLE

>d1dkra2 c.61.1.2 (A:167-316) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}
DIVIVSPDHGGVTRARKLADRKAQIAIIDKRRPRPNVAEVNMIVGNIEGKTAILIDDIITAGTITLAANALVENGAKEVYACCTHPVLGPAVERINNSTIKELVVTNSIKLPPEKKIERFKQLSVGPLLAEAIIRVHEQQSVSYLFS

>d1lfaa_c.62.1.1 (A:) Integrin CD11a/CD18 (Leukocyte function associated antigen-1, LFA-1) {Human (Homo sapiens)}
GNVDLVLFQDGMSMLQPDEFQKILDFMKDMKKLSNTSYQFAAVQFSTSYKTEFDSDYVKRKDPAALLKHVKHMLLNTFGAINYVATEVFREELGARPDAKVLIIITGEATDSGNIDAQKDIIRYIIGIGKHFQTKESQETLHKFASKPASEFVKILDFTKLDFTELQKKIYVIE

>d1atza_c.62.1.1 (A:) von Willebrand factor A3 domain {Human (Homo sapiens)}
QPLDVILLDGSSFPASYFDEMKSFAKAFISKANIGPRLTQVSVLQYGSITTIDVPWNVVPEKAHLLSLVDMQREGGPSQIGDALGFAVRYLTSEMHHARPGASKAVVILVTDVSDVSDAAADAARSNRVTVFPIGIGDRYDAAQLRILAGPAGDSNVVKLQRIEDLPTMVTGNSFLHKL

>d1fnsa_c.62.1.1 (A:) von Willebrand factor A1 domain {Human (Homo sapiens)}
MYCSRLLDLVFLDGSSRLSEAEFEVLKAFVVDMMERLRSQKWRVRAVVEYHDGSHAYIGLKDKRKPSELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKEIDRPEASRIALLMASQEPQRMSRNFRVYVQGLKKKIVIPVGIGPHANLKQIRLIEKQAPENKAFLSSVDELEQQRDEIVSYLCDLAPEAP

>d1ido_c.62.1.1 (-) Integrin CR3 (CD11b/CD18, Mac-1), alpha subunit {Human (Homo sapiens)}
DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSKTLFSLMQYSEEFRIHFTKEFQNNPNPRSLVKPITQLLGRHTATGIRKVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVPEADREGVIRYVIGVDAFRSEKSQRLNTIASKPPRDHVQVNNEALKTIQNQLREK

>d1qc5a_c.62.1.1 (A:) Integrin alpha1-beta1 {Human (Homo sapiens)}
STQLDIVIVLDGSNSIYPWDSVTAFLNDLLERMDIGPKQTQVGIVQYGENVTHEFNLNKYSSTEELVAAKIVQRGGRQTMALGDTARKEAFTEARRGARRGVKKVMVITDGESHDNHRLKKVIQDCEDENIQRFISIAILGSYNRGNLSTEKFVEEIKSIASEPTEKHFFNVSDELALVTIVKTLGERI

>d1ck4a_c.62.1.1 (A:) Integrin alpha1-beta1 {Rat (Rattus norvegicus)}
TQLDIVIVLDGSNSIYPWESVIAFLNDLLKRMIDIGPKQTQVGIVQYGENVTHEFNLNKYSSTEELVAANKIGRQGGLQTMALGDTARKEAFTEARGARRGVKKVMVITDGESHDNHRLKKVIQDCEDENIQRFISIAILGHYNRGNLSTEKFVEEIKSIASEPTEKHFFNVSDELALVTIVKALGERIFAGT

>d1aoxa_c.62.1.1 (A:) Integrin alpha2-beta1 {Human (Homo sapiens)}
SCPSLIDVVVCDESNSIYPWDAVKNFLEKFVQGLDIGPTKTQVGLIQYANNPRVVFNLNNTYKTEEMIVATSQTSQYGGDLNTFGAIQYARKYASAASGGRRSATKVMVVVTDGESHDGSMILKAVIDQCNHDNILRFGIAVLGYLNRNALDTKNLIKEIKAIASIPTERYFFNVSDEAALLEKAGTLGEQIFSIEGT

>d1jv2b2 c.62.1.1 (B:107-354) Integrin beta A domain {Human (Homo sapiens)}
VEDYPVDIYIYLMDSLQYQNLGKLTQMRKLTNSLRIGFGAFVDKPVSPYMYISPPPEALENPYCYDMKTTCLPMFGYKHLVLTQDVTRFNEEVKKQSRSNRDAPEGGFDAIMQATVCDEKIGWRNDASHLLFTDAKTHIALDGRLAGIVQPNQDGQCHVGSNDNHYSASTMDYPSLGLMTEKLSQKNIINLIFAVTENVNVNLYQNYSELIPGTTVGVLVLSMDSSNVQLIVDAYGKIRSK

>d1poia_c.63.1.1 (A:) Glutaconate-CoA transferase alpha {Acidaminococcus fermentans}
SKVMTLKDAIAKYVHSGDHIALGGFTDRKPYAAVFEILRQGITDLTGLGGAAGGDWMLIGNGRVKAYINCYTANSVTVNSRRFRKWFEAGKLTMEDYSQDVYIYMMWHAAALGLPFLPVTLMQGSGLTDEWGKSVRKTLKVPDDKFKYIDNPFKPGEKVVAVPVPQVDVAIHAQQASPDGTVRIWGGKFQDVIAEAAKYTIVTCEEISDEEIRRPTKNDIPGMCMVDAVVLAPYGAHPSQCYGLYDYDNPLKVDKVKSTQEDFDAFCKEWVFDLKDHDDEYLNKLGATRLINLKVVPGLYHIDMTKE

>d1poib_c.63.1.1 (B:) Glutaconate-CoA transferase beta {Acidaminococcus fermentans}
DYTNTNKEMQAVTIAKQIKNGQVVTGTLPLIGASVAKRVYAPDCHIIVESGLMDSCPVEVPRSGDLMFMAHCGCIWPNVRFVGFINEYLHANRLIAFIGGAQIDPYGNVNSTSIGDYHHPKTRFTGSGGANGIATYSNTIIMMQHEKRRFMNKIDYVTSPGWIDGPGRERLGLPGDVGPQLVTDKGILKFDEKTKRMYLAAYYPTSSPEDVLENTGFQDLDVSKAVELEAPDPAVIKLIREEIDPGQAFIQVP

>d1keka4 c.64.1.1 (A:416-668) Pyruvate-ferredoxin oxidoreductase, PFOR, domain III {Desulfovibrio africanus}
GTIQCQFWGLGADGTVGANKQAQKIIQDNTDLFAQGQFSYDSKKSGGTTSHLRFGEKPIQSTYLVNRADYVACHNPAYVGIYDILEGIKDGGTFVLNSPWSSLQEDMDKHLPSGIKRTIANKLLKFYNIQAVKIATDVLGGRINMIMQTAFFKLAGVLPFEKAVDLLKKSIIHKAYGKKGEKIVKMNTDAVDQAVTS

LQEFKYPDSWKDAPAETKAEPMTNEFFKNVVKPILTQQGDKLPVSAFEADGRFPLG
>d1jkxa_c.65.1.1 (A:) Glycinamide ribonucleotide transformylase, GART {Escherichia coli}
MNIVVLISNGNSNLQAIIDACKTNKIKGTVRAFSNKADAFGLERARQAGIATHLIASAFDSREAYDRELIEHDIMYAPDVVLAGFMRIILSPAFVSHY
AGRLLNIHPSLLPKYPGLHTHRQALENGDEEHGTSVHFVTDELGGPVILQAKVPVFAGDSEDDITARVQTQEHAIYPLVISWFADGRLKMHENAA
WLDGQRLLPPQGYA
>d1fmta2 c.65.1.1 (A:1-206) Methionyl-tRNAfmet formyltransferase {Escherichia coli}
SESLRIIFAGTPDFAARHLDALLSSGHNVVGFTQPDRPAGRKKLMPSPVKVLAEEKGLPVFQPVSLRPQENQQLVAELQADVMMVVAYGLILPKAV
LEMPRLGCINVHGSSLPRWRGAAPIQRSLWAGDAETGVTIMQMDVGLDTGDMILYKLSCPITAEDSGTLYDKLAEGLPQGLITTLKQLADGTAKPEV
QDETGVTYAEK
>d1vid_c.66.1.1 (-) Catechol O-methyltransferase, COMT {Rat (Rattus norvegicus)}
TKEQRILRYVQQNAKPGDPQSVEAIDTYCTQKEWAMINVGDAKGQIMDAVIREYSPSLVLELGAYCGYSAVRMARLLQPGARLLTMEMNPDYAAIT
QQMLNFAGLQDKVTILNGASQDLIPQLKKYDVTLDMVFLDHWDKDRYLPDTLLKCGLRKGTLLADNVIVPGTPDFLAYVRGSSSFECTHYSSY
LEYMKVVDGLEKAIYQGPS
>d1fp1d2 c.66.1.12 (D:129-372) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}
RGYLASFPTFLCYPALLQVMNFKEAVVDEDIDLKVNHGVTKYEFMGKDKKMNQIFNKSMDVCATEMKRMLEITYGFEGISTLVGGGSGRN
LELIISKYPLIKGINFDLPQVIENAPPLSIEHVGDMFASPVQGDAMILKAVCHNWSDEKCIIFLSNCHKALSPNGKVIIVEFILPEEPNTSEESKLVSTL
DNLMFITVGGRRERTEKQYEKLSKLSGFSKFQVACRAFNLSLGVMIFYK
>d1fp2a2 c.66.1.12 (A:109-352) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}
LCLAPMVECVLDPTLSGSYHELKKWIYEEDLTLFGVTLGSGFWDFLDKNPEYNTSFNDAMASDSLKLINLALRDCDFVFDGESIVDGGGTGTTAKIIC
ETFPKLKCVIFDRPQVVENLGSNNLTYVGDMFTSIPNADAVLLKYLHNWTDKDCLRLKKCEAVTNDGKRGKVIIIDMVIDKKKDENCQVTQIKLL
MDVNMACLNGKERNEEEWKKLFIEAGFQHYKISPLTGFLSIEIYP
>d1ej0a_c.66.1.2 (A:) RNA methyltransferase FtsJ {Escherichia coli}
GLRSRAWFKLDEIQQSDKLFPGMTVVDLGAAPGGWSQYVTQIGGKGRIIACDLLPMDIVGVDFLQGDFRDELVMKALLERVGDSKVQVVMS
DMAPNMSGTPAVDIPRAMYLVELALEMCRDVLAPGGSFVVKVFQGEFGDEYLREREIRSLFTKVKVRKPDRSSRARSREVIVATGRKP
>d1fbna_c.66.1.3 (A:) Fibrillarin homologue {Archaeon Methanococcus jannaschii}
MEDIKIKEIFENIYEVDLGDGLKRIATKSIVKGKKVYDEKIIKGDEEYRIWNPNSKLAAIIKGLKVMPIKRDSDKIYLGASAGTPSHVADIADKGIVYAI
EYAPRIMRELLDACAERENIIPILGDANKPQEYANIVEKVDVIYEDVAQPNQAEILIKNAKWFLKGGYGMIAIKARSIDVTKDPKEIFKEQKEILEAGGF
KIVDEV DIEPFKEDHVMFVGIWEKG
>d1dusa_c.66.1.4 (A:) Hypothetical protein MJ0882 {Archaeon Methanococcus jannaschii}
FSEKPTTKSDVKIVEDILRGKKLKFTDGSVFSYGKVDKGTKILVENVVV/DKDDIILGCGYVGIGALADEVKSTTMADINRRAIKLAKENIKLNNLD
NYDIRVVHSDLYENVKDRKYNKIITNPIRAGKEVLHRIIEGKELLKDNGEWVVIQTKQGAKSLAKYMKDVFGNVETVTIKGGYRVLKSKKL
>d1im8a_c.66.1.14 (A:) Hypothetical protein HI0319 (YecO) {Haemophilus influenzae}
FIFDENVAEVFPDMIQRSPVGYSNIITAIGMLAERFVTADSNNVYDLGCSRGAATLSARRNINQPNVKIIGIDNSQPMVERCRQHIAAYHSEIPVEILND
IRHVEIKNASMVLNFTLQFLPEDRIALLTKEYEGLNPNGVLSEKFREDTCKINHLLIDHHQFKRANGYSELEVSQKRTALENVMRDTSIETHKVR
KNVGFSQVELWFQCFNFGSMIAVK
>d1d2ha_c.66.1.5 (A:) Glycine <i>N</i>-methyltransferase {Rat (Rattus norvegicus)}
TAEYKAWLLGLLRQHGCHRVLVDACGTGVDSIMLVEEGFSVTSVDASKMLKYALKERWNRRKEPAFDKWVIEEANWLTDKDVPGDGFDAVICL
GNSFAHPDSKGDQSEHRLALKNIASMVRPGGLLVIDHKNYDYILSTGCAPPGKNIYYKSDLTKDITTSVLTNNKAHMVTLDYTVQPGAGRDGAP
GFSKFRLSYYPHCLASFTELVQEAFGGRCQHSVLGDFKPYRPGQAYVPCYFIHVLKKTG
>d1xvaa_c.66.1.5 (A:) Glycine <i>N</i>-methyltransferase {Rat (Rattus norvegicus)}
VDSVYRTRSLGVAAEGIPDQYADGEAARVWQLYIGDTRSRTAEYKAWLLGLLRQHGCHRVLVDACGTGVDSIMLVEEGFSVTSVDASKMLKYALKE
RWNRRKEPAFDKWVIEEANWLTDKDVPGDGFDAVICLGNFAHPDSKGDQSEHRLALKNIASMVRPGGLLVIDHRNYDYILSTGCAPPGKNIYY
KSDLTKDITTSVLTNNKAHMVTLDYTVQPGAGRDGAPGFSKFRLSYYPHCLASFTELVQEAFGGRCQHSVLGDFKPYRPGQAYVPCYFIHVLKKTG
>d1hnna_c.66.1.15 (A:) Phenylethanolamine N-methyltransferase, PNMTase {Human (Homo sapiens)}

AVASAYQRFEPRAYLRNNYAPPRGDLCPNGVGPWKLRLAQTATGEVSGRTLIDIGSGPTVYQLLSACSHFEDITMTDFLEVNRQELGRWLQEEP
GAFNWSMYSQHACLIEKGKGEWCQDKERQLRARVKRVLPIDVHQPLGAGSPAPLPADALVSACLEAVSPDLASFQRALDHITLLRPGGHLLIG
ALEESWYLAGEARLTVPVSEEEVREALVRSGYKVRDLTYIMPAHLQTGVDDVKGVFFAWAQKVG
>d1khha_c.66.1.16 (A:) Guanidinoacetate methyltransferase {Rat (*Rattus norvegicus*)}
RWETPYMHSLAAAASRGGRVLEVGFGMAIAASRVQQAPIKEHWIIECNDGVFQRLQNWLKQPHKVVPLKGLWEVAPELTDHGFDGILYDTY
PLSEETWHTHQFNFIKTHAFRLLKPGGILTYCNLTSWGEMLMSKYTDITAMFEETQVPALEAGFQRENICTEVMALVPPADCYYAFPQMTPVTK
H
>d1g6q1_c.66.1.6 (1:) Arginine methyltransferase, HMT1 {Baker's yeast (*Saccharomyces cerevisiae*)}
DYYFDSYDHYGIHEEMLQDTVRTLSRNAAIQNKDLFKDKIVLDVCGTGILSMFAAKHGAKHVIGVDMSSIEMAKELVNGFSDKITLLRGKLEDV
HLPFPKVDIISEWMGYFLYESMMDTVLYARDHYLVEGLIFPDKCSIHLAGLEDSQYKDEKLNWQDVYGFDSFVPLVHEPIVTVERNNVNT
TSDKLIEFDLNTVKISDLAFKSNFNLAKRQDMINGIVTWFDIVFPAPKGKRPVEFSTGPHAPYTHWKQTIFYFPDDLDAETGDTIEGELVCSPNEKNN
RDNIKISYKFESNGIDGNRSRKNEGSYLMH
>d1f3la_c.66.1.6 (A:) Arginine methyltransferase, HMT1 {Rat (*Rattus norvegicus*)}
DLQEDEDGVYFSSYGHYGIHEEMLKDKVRTESYRDFIYQNPHEFKDKVVLVDVCGTGILSMFAAKAGAKKVIADQSEILYQAMDIIRLNKLEDTIVLIK
GKIEEVSLPVEKVDVIISWMGYFLFESMLDSVLYAKSKYLAKGGSVYPDICTISLVAVSDVSKHADRIAFWDDVYGFNMSCMKKAVIPEAVVEVVD
HKTLISDPDCDIKHIDCHTTISDLEFSSDFTLRTKTAMCTAVAGYFDIYFEKNCHNRVFSTGPQSTKTHWKQTIFLLEKPFPVKAGEALKGKITVHKNK
KDPRSLIVTTLNSSTQTYSLQ
>d1d15a1_c.66.1.7 (A:1-213) Protein-L-isoaspartyl O-methyltransferase {Thermotoga maritima}
MREKLFWILKKYGVSDHIKAFLIPREEFLTSYPLSYVVEDIVLVSYDDGEEYSTSSQPSLMAFMIEWVGLDKGMRVLEIGGGTGYNAAVMSRVVG
EKGLVSVESRKICEIAKRNRVERLGIVENIFVCGDGYYGVPEFSPYDVIFVTGVDEVPETWFTQLKEGGRIVVPINLKLRRQPAFLFKKKDPYLVGNY
KLETRFITAGGNLG
>d1jg1a_c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Archaeon *Pyrococcus furiosus*}
EKELEYKWMRTVEMLKAEGIIRSKEVERAFLKYPRYLSVEDKYKKYAHIDEPLPIPAGQTVSAPHMVAIMLEIANLPGMNNILEVGTGSGWNAALISEI
VKTDVYTIERIPELVEFAKRNLERAGVKNVHVLGDGSKGFPKAPYDVIIVTAGAPKIPEPLIEQLKIGGKLIIPVGSYHLWQELLEVRKTKDGKIKNHG
GVAFVPLIGEYGWK
>d1kr5a_c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Human (*Homo sapiens*)}
ASHSELIHNLRKNGIITDKVFEVMLATDRSHYAKCNPYMDSPQSIFQATISAPHMHAYALELLFDQLHEGAKALDVGSGLTACFARMVGCTKG
VIGIDHIKELVDDSVNNVRKDDPTLSSGRVQLVGDGRMGYAEAPYDAIHVGAAAPVVPQALIDQLKPGGRLILPVGPGAGGNQMLEQYDKLQDG
SIKMPLMGVIYVPLTDKEKQWSR
>d1i9ga_c.66.1.13 (A:) Probable methyltransferase Rv2118c {Mycobacterium tuberculosis}
TGPFSIGERVQLDAKGRRTMSLTPGAEEFHTRGSIAHDAVIGLEQGSVVKSSNGALFLVLRPLLVDYVMSMPRGQVYPKDAAQIVHEGDFIPGA
RVLEAGAGSGALTSLRAVGPAGQVISYEQRADHAEHARRNVSGCYGQPPDNWRLVSDLADSELPDGSVDRAVLDMAPWEVILDAVSRLLVAG
GVLMVYVATVQLSRIVEALRAKQCWTPEPRAWETLQRGWNVVGAVRPQHSMRGHTAFLVATRRLAPGAVA
>d1af7_2_c.66.1.8 (92-284) Chemotaxis receptor methyltransferase CheR, C-terminal domain {Salmonella typhimurium}
NLTAFFREAHHFPIAEHARRRHGEYRVWSAAASTGEEPYSAITLADALGMAPGRWKVFASDIDTEVLEKARSGIYRSELKTLSPQQLQRYFMRGT
GPHEGLVVRQELANYVEFSSVNLLKQYQNVPGFDAIFCRNVMIYFDKTTQEDILRFPVLLKPDGLLFAGHSENFSNLVREFSLRGQTVYALS
>d3mag_c.66.1.9 (-) Polymerase regulatory subunit VP39 {Vaccinia virus}
MDVVSLSKPKFMYFEEIDNEYEPESANEVAKLPYQGQLKLLGELFFLSKLQRHGILDGATVYIGSAPGTHIRYLRDHFYNLGVIIKWMLIDGRHH
DPILNGLRDVTLVTFRVDEEYLRSIKKQLHPSKIIILSDVRSPKRGGNESTADLLSNYALQNVMSILNPVASSLKWRCPFDQWIKDFYIPHGNKMLQP
FAPSYAEMRLLSIYTGENMRLTRVTKSDAVNYEKMMYLNKIVRNKVVNFDPNQEYDFHMYFMLRTVYCNKTFPTTAKVFLQQSIFRFLNIP
>d1yub_c.66.1.9 (-) rRNA methyltransferase {Streptococcus pneumoniae, Ermam}
MNKNIKYSQNFLTSEKVLNQIQLNLKETDTVYEIGTGHGHTTAKISKQVTSIELDHLFNLSSSEKLNTRVTLIHQDILQFQFPNKQRYKIVGNIP
YHLSTQIICKVVFESRASDIYLIVEEGFYKRTLDIERTLGLLHTQVSIQQLKLPAECFHPKPKVNSVLIKTRHTTDVPDFYWKLYTYFVSKWWNREYRQ
LFTKNQFHQAMKHAKVNNLSTITYEQVLSIFNSYLLFNGRK

>d1qama_c.66.1.9 (A:) rRNA methyltransferase {Bacillus subtilis, Ermc'}

QNFITSKHNIDKIMTNIRLNEHDNIFEIGSGKGHFTLELVQRCNFVTAIEIDHKLCCTTENKLVDHDNFQVLNKDILQFKFPKNQSYKIFGNIPYNISTDII
RKIVFDSIADEIYLIVEYGFAKRLLNTRSLALFLMAEVDISILSMVPREYFHPKPKVNSSLIRLNRKKSRISSHDKQKYNVFVMKWVNKEYKKIFTKNQF
NNSLKHAGIDDLNNISFEQFLSLFNSYKLFNK

>d1i4wa_c.66.1.9 (A:) Transcription factor sc-mtTFB {Baker's yeast (Saccharomyces cerevisiae)}

PIPGIKDISKLKFFYGFYLWNPTVYNKIFDKLDLTKYKHPEELKVLDPYQGVIQSAIFYNKCPHQYSLLEKRSSLYKFLNAKFEGSPLQLKRDPYDWS
TYSNLIDEERIFVPEVQSSDHINDKFLTVANVTGESEGLIMQWLSCIGNKNWLYRGKVKMILLWMPSTTARKLLARPGMHSRSRKCSVVREAFTDTK
LIAISDANELKGFDSDQCIEEWDPILSAAEIWPTKGKPIALVEMDPIDFDFDVNWYTRHLMILKRTPLNTVMDSLGHGGQQYFNSRITDKDLLKK
CPIDLTNDEFIYLTKLMEWPFPK

>d6mhta_c.66.1.10 (A:) DNA methylase Hhal, coenzyme-binding domain {Haemophilus haemolyticus}

MIEIKDKQLTGLRFIDLFLAGGGFRRAESCGAECVYSNEWDKYAQEYVEMNFGEKPEGDITQVNEKTIKDHDILCAGFPCQAFSISGKQKGfedSRGT
LFFDIARIYREKKPKVVFMENVKNFASHDNGNTLEVVKNTMNELDYSFHAKVLNALDYGIPQKRERIYMICFRNDLNIQNFOFPKPFEINTFKDLLL
PDSEVEHLVIDRKDLVMTNQIEQTTPKTVRLGIVGKGGQGERIYSTRGIAITLSAYGGGIFAKTGGYLVNGKTRKLHPRECARVMGYPDSYKVHPSTS
QAYKQFGNSVSVINVLQYIAYNIGSSLNFKPY

>d1g38a_c.66.1.10 (A:) DNA methylase Taql, coenzyme-binding domain {Thermus aquaticus}

VETPPEVVDVMVSLAEAPRRGRVLEPACAHGPFLRAFREAHGTGYRFGVVEIDPKALDLPPWAEGILADFLWEPGEAFDLILGNPPYGIVGEASKYP
IHVFKAVKDLYKKAFSTWKYKLYGAFLKEAVRLLKPGGVLFVVPATWLWLEDFAFLREFLAREGKTSVYYLGEVFPQKKVSAVVIRFQKSGKGLSLW
DTQESESGFTPILWAEPHYWEGEIIRFETEETRKLEISGMPMLGDLFHIRFAARSPEFKKHPAVRKEPGPGLPVLTGRNLKPGWVDYEKNHSGLWMPK
ERAKELRDFYATPHLVAHTKGTRVVAAWDERAYPWREEFHLLPKEGVRLDPSSLVQWLSEAMQKHVRTRYRDFVPHLRLMLERLPVREYGFH
T

>d1dcta_c.66.1.10 (A:) DNA methylase HaeIII, coenzyme-binding domain {Haemophilus aegyptius}

MNLISLFSAGGLDGFQKAGFRIICANEYDKSIWKTYESNHSAKLIKGDISKISSDEFPKCDGIIGGPPCQSWEAGSSLRGIDDPRGKLFYERYIRLKQK
KPIFFLAENVKGMMMAQRHNKAVQEFIQEFDNAGYDVHILLNANDYVAQDRKRVFYIGFRKELNINYLPPIPHLIKPTFKDVIWDLKDNPIPALKDN
KTNGNKCIYPNHEYFIGSYSTIFMSRNVRQWNEPAFTVQASGRQCQLHPQAPVMLVSKNLNKFVEGKEHYRRLTVRECARVQGFPDDFIFHYE
SLNDGYKMIGNAVPVNLAYEIAKTIKSAL

>d2dpma_c.66.1.10 (A:) DpnM DNA adenine methyltransferase {Streptococcus pneumoniae}

TLQPFTKWTGGKRQLLPVIRELIPKTYNRYFEPFVGGGALFFDLAPKDAVINDFNAELINCYQQIKDNPQELIEILKVKHQEYNSKEYYDLRSADRDERI
DMMSEVQRAARILYMLRVNFNGLYRVNSKNQFNVPYGRYKNPKIVDEELISAISVYINNNQLEIKVGDFEKAIVDVRTDFVYFDPPYIPLSETSAFTS
YTHEGFSFADQVRLDAFKRLSDTGAYVMLSNSSSALVEELYKDFNIHYVEATRTNGAKSSRGKISEIIVTNYEK

>d1g55a_c.66.1.10 (A:) DNMT2 {Human (Homo sapiens)}

EPLRVLELYSGVGGMHHALRESCIPAQVVAIDVNTVANEVYKYNFHTQLLAKTIEGITLEEFDRLSFDMILMSPPCPFTRIGRQGDMTDRTNSF
LHILDILPRLQKLPKYILLEVNKGFEVSSTRDLLIQTENCGFQYQEFLSPSLGIPNSRLRYFLIAKLQSEPLPFQAPGQVLMEFPKIEIHRKNQQDSDL
VKMLKDFLEDDTDVNQYLLPPKSLLRYALLDIVQPTCRSSCFTKGYGSYIEGTGSVLQTAEDVQVENIYKSLTLSQEEQITKLLILKLYFTPKEIANLL
GFPPEFGFPEKITVKQRYRLLGNSLNVHVVAKLKILY

>d1booa_c.66.1.11 (A:) m.Pvull N4 cytosine-specific DNA methyltransferase {Proteus vulgaris}

NFGKKPAYTTSNGSMYIGDSLELESFPEESISLVMTSPPFALQRKKEYGNLEQHEYVDWFLSFAKVNNKKLKDGSFVVDGGAYMKGPARSIFYNF
RVLIRMIDEVGFFLAEDFYWFNPSKLPSPIEWVNKRKIRVKDAVNTVWWFSKTEWPKSITKVLAPYSDRMKKLIEDPDFYTPKTRPSGHDIGKSFS
KDNGGSIPPNLQISNSENGQYLANCKLMGIKAHPARFPALKPEFFIRMLETPEDDLVDIFGGSNTTGLVAERESRKWISFEMKPEYVAASAFRFLDN
NISEEKITDIYNRILNGESLDLNSI

>d1eg2a_c.66.1.11 (A:) m.Rsrl N6 adenosine-specific DNA methyltransferase {Rhodobacter sphaeroides}

GTTRHVDVCDCLDTLAKLPDDSVQLIICDPPYNIMLADWDDHMDYIGWAKRWLAEAERVLSPSGSIAIFGGLQYQGEAGSGDLISIISHMRQNSK
MLLANLIIWNPNGMSAQRFANRHEEIAWFAKTKYFFDLDAVREPYDEETKAAYMKDKRLNPESVEKGRNPTVWWRMSRLNGNSLERVGHPT
QKPAAVIERLVRALSHPGSTVLDFAGSGVTARVAIQEGRNSICTDAAPVFKEYYQKQLTFLQDDGLIDKARSYEIVEGAANFGAALQR

>d1inla_c.66.1.17 (A:) Spermidine synthase {Thermotoga maritima}

RTLKELELRELQPRQHLWYFEEYTGNVGLFMKMNRYIYSGQSDIQRIDIFENPDLGVVFALDGITMTTEKDEFMYHEMLAHVPMFLHPNPKKVLII
GGGDGGTLREVLKHDSEKAILCEVDGLVIAARKYLQTCGFDPPRAEVIANGAEYVRKFNEFDVIIIDSTDPTAGQGGHLFTEEFYQACYDALK
EDGVFAETEDPFYDIGWFKLAYRRISKVFPITRVYLGFMTPSGMWSYTFASKGIDPKDFDPEKVRKFNKELKYNEEVHVASFALPNFKKELGL
M

>d1kpga_c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1 {Mycobacterium tuberculosis}

DELKPHFANVQAHYDLSDDFFRLFLDPTQTYSCAYFERDDMTLQEAQIAKIDLALGKGLQPGMTLLDVGCGWGATMMRAVEKYDVNVGLTLSK
NQANHVQQLVANSENLRSKRVLLAGWEQFDEPVDRIVSIGAFEHGHERYDAFFSLAHRLLPADGVMLLHTITGLHPKEIHERGLPMSFTARFLKFI
VTEIFPGGRPLSIPMVQECASANGFTVTRVQLQPHYAKTLDLWSAALQANKQAIALQSEEVYERYMKYLTGCAEMFRIGYIDVNQFTCQK

>d1kpia_c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1 {Mycobacterium tuberculosis}

QLKPPVEAVRSHYDKSNEFFKLWLDPSMTYSCAYFERPDMLTEEAQYAKRKLALDKLNLEPGMTLLDIGCWGSTMRHAVAEDVNvigLTLSENQ
YAHDKAMFDEVDSPRKREVRIQGWEEFDEPVDRIVSLGAFEHFADGAGDAGFERYDTFFKKFYNLTPDDGRMILLHTIPDKEEAQELGLTPMSLL
RFIKFILTEIFPGGRPLRISQVYYSSNAGWKVERYHRIGANYVPTLNAWADALQAHKDEAIALKGQETCDIYMHYLRCSDLFRDKYTDVCQFTLVK

>d7aata_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken (Gallus gallus), mitochondria}

SSWWSHVEMGPPDPILGVTEAFKRDTNSKKMNLGVGAYRDDNGKPVVLNCVRKAEAMIAAKMMDKEYLPIAGLADFTRASEALALGENSEAFKS
GRYVTVGQISGTGSLRVMANFLQRFFKSRDVYLPKPSGNHPTIFRDAGLQLQAYRYYDPKTCSDLFTGAMEDISKIPEKSIILLHACAHNPTGVDR
QEIQWKELASVVKRNLLAYFDMAYQGFASGDINRDAWALRHIEQGIDVLSQSYAKNMGLYGERAGAFTVICRDAEAKRVESQLKILIRPMYSNP
PMNGARIASLILNTPELRKEWLVEVKGMADIISMRQLVSNLKKEGSSHWNQHITDQIGMFCTGLKPEQVERLTKEFSIYMTKDRISVAGVASS
NVGYLAHAIHQVTK

>d2csta_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken (Gallus gallus), cytosolic form}

AASIFAAVPAPPVAVFKLADFREDGDSRKVNLLGVGAYRTDEGQPWVLPVVRKVEQLIAGDGSLNHEYLPILGLPEFRANASRIALGDDSPAIAQKR
VGSVQGLGGTGALRIGAEFLRWYNGNNNTATPVYVSSPTWENHNSVFMDAGFKDIRTYRYWDAAKRGLDLQGLDDMEKAPEFSIFILHACAH
NPTGTDPTPDEWKQIAAVMKRRCFLPFFDSAYQGFASGSLDKDAWAVRYFVSEGFEFLCAQSFSKNFGLYNERVGNLSVVGKDENDNVQRVLSQME
KIVRTTWSNPPSQGARIVATTLSPOQLFAEWKDNVKTMDRVLLMRSELRSRLESGLTPGTWNHITDQIGMFSTGLNPQVEYMIKEKHIYLMAS
GRINMCGLTTKNLDYVAKSIHEAVTKIQ

>d1ajsa_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Pig (Sus scrofa), cytosolic form}

APPSVFAEPQAPQPVLFVFKLADFREDPDKVNLGVGAYRTDDCQPWVLPVVRKVEQRIANSSLNHEYLPILGLAEFRTCASRLALGDDSPALQE
RVGGVQSLGGTGALRIGAEFLRWYNGNTNNKDPVYVSSPTWENHNGVFTAGFKDIRSYRYWDTEKRGQLDQFLSDLENAPEFSIFVLHACAH
PTGTDPTPEQWKQIASVMKRRCLPFFDSAYQGFASGNLEKDAWAIRYFVSEGFEFLCAQSFSKNFGLYNERVGNLTVAKEPDSLRLVLSQMOKIVR
VTWSNPPAQGARIVARTLSDPELFHEWTGNVKTMDRILSMRSELRARLEALKTPGTWNHITDQIGMFSTGLNPQVEYLINQKHIYLLPSGRIN
MCGLTTKNLDYVATSIHEAVTKIQ

>d1yaaa_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Baker's yeast (Saccharomyces cerevisiae), cytosolic form}

SATLFNNIELLPPDALFGIKQRYGQDQRATKVDLGIGAYRDDNGKPWVLPVKAAEKLHNDSSYNHEYLGITGLPSLTSNAAKIIFGTQSDALQEDRVI
SVQSLSGTGALHISAKFFSKFPDKLVLSKPTWANHMAIFENQGLKTATPYWANETKSSDLNGFLNAIQKAPEGSIFVLHSCAHNPTGLDPTSEQW
VQIVDAIASKNHIALFDTAYQGFATGDLKDDAYAVRLGVEKLSTVSPVFVCSFAKNAGMYGERVGCFLHALTKQAQNKTICKPAVTSQQLAKIIRSEVN
PPAYGAKIVAKLLETPELTEQWHKDMVTMSSRITKMRHALRDHLVKGTPGNWDHIVNQCGMFSFTGLTPQMVKRLEETHAVYLVASGRASIAGL
NQGNVEYVAKAIDEVVRFYA

>d1qisa_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Escherichia coli}

MFENITAAPADPILGLADLFRADERPGKINLGIGVKDETGKTPVLTSVKKAEQYLLNETTKNYLGINIDGIPEFGRCTQELLFGKGSALINDKRARTAQTP
GGTGALRVAADFLAKNTSVKRVVVSNSPWNHKSVFNSAGLEVREYAYDAENHTLDFDALINSLNEAQAGDVVLFHGFCHNPTGIDPTLEQWQT
LAQLSVEKGWLPDFAYQGFARGLEEDAEGLRAFAAMHKELIVASSYSKNFGLYNERVGACTIONSETVDRAFSQMKAAIRANYSNPPAHGASV
VATILSNDALRAIWEQELTDMRQRIQRMRQLFVNLTQEKGANRDFSIIKQNGMFSFGLTKEQVRLREEFGVYAVASGRVNAGMTPDNMAPLC
EAIAVAVL

>d1bjwa_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Thermus thermophilus}

MRGLSRRVQAMKPSATVAVNAKALELRRQGVDLVALTAGEPDFDTPEHVKEARRALAQGKTKYAPPAGIPELREALAEKFRRENGLSVTPEETIVTV

GGKQALFNLFQAILDPGDEVILSPYWVSYPEMVRFAGGVVVEVTLPEEGFVPDPERVRRAITPRTKALVVNSPNPTGAVYPKEVLEALARLAVE
HDFYLVSDIEYHLLYEGERHSPGRVAPEHTLTNGAAKAFAMTGWIGYACGPKEVIKAMASVSSQSTTSPDTIAQWATLEALTNQEASRAFVEMA

REAYRRRRDLLLEGITALGLKAVRPGAFYVLMDSPIADEVRAAERLLEAGAVAVPGTDFAFGHVRLSYATSEENLRKALERFARVL

>d2ay1a_c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Paracoccus denitrificans}

MLGNLKQPAPDKILALMGFEPFRPRQKGIDLGVGVYKDATGHTPIMRAVHAAEQRMLETTTKYAGLSGEPEFQKAMGEILGDGLKSETTATLA
TVGGTGALRQALELARMANPDLRVFSDPTWPNHVSIMNFMLPVQTYRFDAETRGVDSEGKADLAAAKGDMVLLHGCHNPTGANLTL
DQWAEIASILEKTGALPLIDLAYQGFGDGLEEDAAGTRLIASRIPEVLLIAASCNSKNGIYERTGCLLACADAATRELAQGAMAFLNRQTSFPPFHGA
KIVSTVLTTPELRADWMAELEAVRSGMLRLREQLAGELRDLGSDRFGVAEHRGMFSRLGATPEQVKRIKEFGIYMGDSRINIAGLNDNTIPILA
RAIIEVGV

>d3tata_c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Escherichia coli}

MFQKVDAYAGDPILTLMERFKEDPRSDKVNLSIGLYNNEDGIIPQLQAVAEEARLNAQPHGASLYLPMEGLNCYRHAIAPLLGADHPVLKQQRVAT
IQLGGSGALKVGADFLKRYFPESGVVSDPTWENHVAIFAGAGFEVSTPYWDEATNGVRFNDLTLKTPARSIVLLHPCCHNPTGADLTNDQ
WDIAVIEILKARELIPFLDIAYQGFGAGMEEDAYAIRAISAGLPAVLVSNSFSKIFSLYGERVGGLSVMCEDAEAAGRVLGQLKATVRRNYSPPNFGAQV
VAAVLNDEALKASWLAEEVEMRTRILAMRQELVKVSTEMPERNFYLLNQRMFSYTGLSAAQVDRLREEFGVYLIASGRMCVAGLNTANVQRV
AKAFAAVM

>d1gdea_c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Archaeon Pyrococcus horikoshii}

ALSDRLELVSASEIRKLFIAAGMKDVISLGIGEPDFDTPQHIKEYAKEALDKGLTHYGPNIQLLELREAIAEKLKKQNGIEADPKTEIMVLLGANQAFLM
GLSAFLKDGEELIPTPAFVSYAPAVILAGGKPVEVPTYEDEFRLNVDELKKYVTDKTRALIINSPCNPTEGAVLTKDLEEADFVVEHDLVISDEVYEH
FIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGWRLGFVAAPSWIERNMVKFQMYNATCPVTIQQAAKALKDERSWKAVEEMRKEYDRRK
VWKRLNEMGLPTVKPKGAFYIFPRIRDGLTSKKFSELMLKEARAVAVPGSAFGKAGEGYVRISYATAYEKLEEAMDRMERVLKERKL

>d1bw0a_c.67.1.1 (A:) Tyrosine aminotransferase (TAT) {Trypanosoma cruzi}

WDVMSMNAGLNFNPIRTVSDNAKPSPKPIIKLSDGPTLDKNLLTSAQIKKLKEAIDSQECNGYFPTVGSPEAREAVATWWRNSFVKEELKSTI
VKDNVVLCSGGSHGILMAITAICDAGDYALVPQPGFPHYETVCKAYIGMHFYNCRPENDWEADLDEIRRLKDDKTLIIVTNPNSPCGSNSRKH
EDIVRLAEELRPLFSDEIYAGMVFKGKDPNATFTSVADFETTVPRVILGGTAKNLVPGWRLGWLWVDPHNGNPSFLEGLKRVGMLVCGPCTVQ
AALGEALLNTPQEHDQIVAKIEESAMYLYNHIGECIGLAPTMRGAMYLMSRIDLEYRDIKTDVEFFEKLLEEENVQVLPGTIFHAPGFTRLTTRPV
EVYREAVERIKAFQRHAA

>d1fg7a_c.67.1.1 (A:) Histidinol-phosphate aminotransferase {Escherichia coli}

TTITDLARENVRNLTPYQSARRLGGNGDVWLNANEYPTAVEFQLTQQTLNRYPECCQPKAVIENYAQYAGVKPEQVLVSRGADEGIELLRAFCEPGK
DAILYCPPTYGMYSVSAETIGVECRTVPTLDNWQLDLQGISDKLDGVKVVYVCPNNPTGQLINPQDFRTLLETRGKAIVVADEAYIEFCPQASLAG
WLAEPYHLLRTLSKAFALAGLRCGFTLANEEVINLLMKVIAPYPLSTPVADIAAQALSPQGIVAMRERVAQIIAEREYLIAALKEIPCVEQVFDSETNYI
LARFKASSAVFKSLWDQGIILRDQNQKQPSLSGCLRITVGTRERSQRVIDALRAEQV

>d1kusa_c.67.1.1 (A:) L-threonine-O-3-phosphate decarboxylase CobD {Salmonella enterica}

HGGNIREPATVLGISPQDQLLDFSANINPLGMPVSVKRALIDNLDCIERYPDADYFHLHQALARHHQVPASWILAGNGETESIFTVASGLKPRRAMIVT
PGFAEYGRALAQSGCEIRRWSLREADGWQLTDAILEALTPDLDCFCTPNPNTGGLPERPLQAIADRCKSLNINLILDEAFIDFIPHETGFIPALKDNP
HIWVLRSLTKFYAIPLGLRGYLVNSDDAAMARMRRQQMPWSVNALAALAGEVALQDSAWQQATWHWLREEGARFYQALCQLPLTVYPGRANY
LLRCEREDIDLQRRLLTQRILRSCANYPGLDSRYRVAIRSAQNERLAAALRNVLGIAP

>d1jg8a_c.67.1.1 (A:) Low-specificity threonine aldolase {Thermatoga maritima}

MIDLRSDTVKPTEEMRKAMAQAEVGDDVYGEDPTINELERLAAETFGKEAALFVPSGTMGNNQVSIMAHTQRGDEVILEADSHIFWYEVGAMAV
LSGVMMPVPGKNGAMDPDDVRKAIRPRNIHFPRTLSIAENTHNRSGGRVVPLENIKEICTIAKEHGINVHIDGARIFNASIASGVPKEYAGYADSV
MFCLSKGLCAPVGSSVVGDRDFIERARKARKMLGGGMRQAGVLAAGIIALTJMVDRLKEDHENARFLALKKEIGYSVNPEDVKTNMVILRTDNL
KVNAHGFIEALRNSGVLANAVSDTEIRLVTWKDVSRSNDIEEALNIFEKLFRKFS

>d1tpla_c.67.1.2 (A:) Tyrosine phenol-lyase {Citrobacter intermedium}

MNYPAEPRIKSVETVSMIPRDERLKKMQEAGYNTFLNSKDIYIDLLTDSGTNAMSDKQWAGMMMGDEAYAGSENFYHLERTVQELFGFKHIVP
THQGRGAENLLSQLAIPGQYVAGNMYKNGAVFVDIRDEAHAGLNAFKGDIDLKKLQKLIDEKGAENIAYICLAVTVNLAGGQPVS MANMRA

VRELTAAHGIKVFYDATRCVENAYFIKEQEQQGFENKSIAEIVHEMFSYADGCTMSGKKDCLVNIGGFLCMNDDEMSSAKELVVYEGMPSYGGLAG
RDMEAMAIGLREAMQYEYIEHRVKQVRYLGDKLKAAGVPIVEPVGGHAVFLDARRFCEHLTQDEFPAQSLAASIYVETGVRSMERGIKLETVRLTIPR
RVYTYAHMDVVADGIKLYQHKEDIRGLKFIYFFTARFDYI

>d1ax4a_c.67.1.2 (A:) Tryptophan indol-lyase (tryptophanase) {Proteus vulgaris}

AKRIVEPFRIKVMVEKIRVPSREEREALKEAGYNPFLPPSAVYIDLLTDGTNAMSDHQWAAMITGDEAYAGSRNYDLKDKAKELFNYDYIIPAHQG
RGAENILFPVLLKYKQKEGKAKNPVFISNFHFTAAHVVELNGCKAINIVTEKAFDSETYDDWKGDFDIKKLENIAQHGADNIVAIYSTVTCNSAGG
QPVSMSNLKEVYEIAKQHGFVVMDSARFCENAYFIKARDPKYKNATIKEVIFDMYKADALTMSSAKKDPLLNIGGLVAIRDNEEIFTLARQRCVPME
GFVTYGGLAGRDMAMAVQGLEEGTEEEYLHYRIGQVKYLGDRLREAGIPIQYPTGGHAVFVDCKKLVPQIPGDQFPAQAVINALYLESGVRAVEIGS
FLLGRDPATGEQKHADMEFMRLTIARRVTNDHMDYIADALIGKLEKFATLKGLFELYEPVLRHTARLKPI

>d1js3a_c.67.1.6 (A:) DOPA decarboxylase {Pig (Sus scrofa)}

MNASFRRRGKEMVDYMADELEGIRQRQVYDPDVQPGYLRPLIPATAPQEPDTFEDILQDVEKIIMPGVTHWHSPYFFAYFPTASSYPAMLADMCG
AIGCIGFSWAASPACELETVMMDWLGKMLQLPEAFLAGEAGEEGGGVIQGSASEATLVALLAARTKVVRRLQAASPLTQGALEKLVAYASDQAH
SSVERAGLIGGVKLKAIPSDGKFAMRASALQEALERDKAAGLIPFFVATLGTSCSFNLLEVGPICHEEDIWLHVDAAYAGSAFICPEFRHLLNGVE
FADSFNPNPHKWLLNFDCSAMWVKRRTDLTGAFKLDPVYLKHSQGSLITDYLHWQLPLGRRFRSLKMWVFVFRMYGVKGLQAYIRKHVQLSH
EFEAFVLQDPRFEVCAEVTLGLVCFRLKGSDGLNEALLERINSARKIHLVPCRLRGQFVRLFACSRKVESGHVRLAWEHIRGLAAELLA

>d1cl1a_c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Escherichia coli}

KLDTQLVNAGRSKYTLGAVNSVIRASSLVFDSVEAKKHATRNRANGELYGRRGLTHFSLQQAMCELEGGAGCVLPCGAAAVANSILAFIEQG
DHVLMNTAYEPSQDFCSKILSKLGVTTSWFPLIGADIVKHLQPNTKIVFLESFGSITMEVHDVPAIAAVRSVVPDAIMIDNTWAAGVLFKALDFG
IDVSIIQATKYLVGHSDAMIGTAVCNARCWEQLRENAYLMGQMVDADTAYITSGLRTLGVRRLQHHESSLKVAEWLAEPQVARVNHPALPGSK
GHEFWKRDFTGSSGLFSVLLKKLNNEELANYLDNFSLFSMAYSWGGYESLILANQPEHIAAIRPQGEIDEFGSTLIRLHIGLEDVDDLIADLDAGFARI

>d1ibja_c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Thale cress (Arabidopsis thaliana)}

ASVSTLLNVLDNKFDPMSTPLYQTATFKQPSAIENGPYDTRSGNPRDAESLLAKLKDRAFTSGMAALSAVTHLIKNGEEIVAGDDVYG
GSDRLLSQVPRSGVVVKRVNTKLDEAAAIGPQTKLVWESPTNPRQQISDIRKISEMAHAQGALVLDNSIMSPVLSRPLELGADIVMHSATKFI
AGHSDVMAGVLAVKGEKLAKEVYFLQNSEGSGLAPFDWLCLRGIKTMALRIEKQQENARKIAMYLSSHPRVKVYAGLPDHPGHHLFHSQAKG
AGSVFSFITGSVALSKHLVETTKYFSIASFGSVKSLISMPCFMASHASIPAEVREARGLTEDLVRISAGIEDVDDLISLDLIAFKTFPL

>d1cs1a_c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Escherichia coli}

RKQATIAVRSGLNDDEQYGCVPPIHLSSTYNFTGFNEPRAHDYSRRGNPTRDVVQRALAELEGGAGAVLNTGMSAHLVTTVFLPGDLLVAPH
CYGGSYRLFDLAKRGCYRVLFDQGDEQALRAALAEKPVLVESPNSPPLRVDIAKICHLAREVGAVSVVDTFLSPALQNPLALGADLVLHSCTK
YLNHGSDVVAGVVIAKDPDVTELAWWANNIGVTGGAFDSYLLRGLRTLVRMELAQRNAQAIVKYLQTQPLVKKLYHPSLPENQGHEIAARQQK
GFGAMLSFELDGDEQTLRRLGGSLFTLAESLGGVESLISHAATMTHAGMAPEARAAAGISETLLRISTGIEDGEDLIADLENGFRAANKG

>d1qgna_c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Common tobacco (Nicotiana tabacum)}

MKYASFLNSDGSVAIHAGERLGRGIVTDAITPPVNTSAYFFNKTSELIDFKEKRRASFEYGRYGNPTTVVLEEKISALEGAESTLLMASGMCASTVML
LALVPAGGHIVTTDCYRKTRIFIETILPKMGITATVIDPADVGALEALANQKKVNLFFTESPTNPFLRCVDIELVSKLCHEKGALVCIDGTATPLNQKAL
ALGADLVLSATKFLGGHNDVLAGCISGPLKLVSEIRNLHHILGGALNPNAAYLIIRGMKTLHLRVQQNSTALRMAEILEAHPKVRHVYPGLQSH
EHIIAKKQMTGFGGAVSFEVDGLLTTAKFDALKIPIYAPSFGCESIVDQPAIMSVDLSQSDRAKYGIMDNLVRFSFGVEDFDDLKADILQALDS

I

>d1e5ea_c.67.1.3 (A:) Methionine gamma-lyase, MGL {Trichomonas vaginalis}

ERMPATACIHANPQKQDFGAAIPPIYQTSTFVFDNCQCQGGNRFAGQESGYIYTRLGNPTVSNLEGKIAFLEKTEACVATSSGMGIAATVLTILKAGD
HLISDECLYGCALTHALFEHALTKFGIQVDFINTAIPGEVKHHMKPNTKIVYFETPANPTLKIIDMERVCKDAHSQEGVLVIADNTFCSPMITNPVDFGVDV
VVHSATKYINGHTDVVAGLICGKADLQQIRMVGKIDITGSVISPHDAWLTRLSTLNIRMKAESENAMKVAEYLKSHPAVEKVVYPGFEDHEGHDI
AKKQMRMIGSMITFILKSGFEGAKLDDNLKLTLAVSLGGCESLIQHPASMTHAVVPEKEERAAGITDGMIRLSVGIEDADELIADFKQGLDALLR

>d1d2fa_c.67.1.3 (A:) Modulator in mal gene expression, MalY {Escherichia coli}

LLPFTISDMDFATAPCIIEALNQRLMHGVFGYSRWKNDEFIAIAHWFSTQHYTAIDSQTVVYGPSVIYMSVSELIRQWSETGEGVVIHTPAYDAFYKAI
EGNQRTVMPVALEKQADGWFCMDGKLEAVLAKPECKIMLLCSPQNPTGKVWTCDDELEIMADLCERHGVRVISDEIHMDMVWGEQPHIPWSNV

ARGDWALLSGSKSFNIPALTGAYGIIENSSSRDAYLSALKGRDGSSLSPVLAHTAHIAAYQQGAPWLDALRIYLKDNLTYIADKMNAAFPELNWQIPQS
TYLAWLRLRPLNIDDNALQKALIEQEKAIMPETYGEERGFVRLNAGCPRSKEKGVAGLINAIRAVR

>d1c7na_c.67.1.3 (A:) Cystalysin {Treponema denticola}

MIYDFTTKISRKNLGSLKWDLMSQNPEVGNEVVPLSADMEEFKNPPEIELGLKKYLDENVLGYTGPTEEYKKTVKKWMKDRHQWDIQTDWINTA
GVVPAVFNAVREFTKPGDGVIIITPVYYPFFMAIKNQERKIIECELLEKDGYYTIDFQKLEKLSKDKNNKALLFCSPHNPVGRVWKDELQKIKDIVLSD
LMLWSDEIHFDLIMPGYEHTVFQSIDEQLADKTITFTAPSFTNIAGMGMSNIIKNPDIRERTKSRDATSGMPFTLGYKACEICYKECGKWLDCI
KVIDKNQRIVKDFEVNHPEIKAPLIEGTLYQWIDFRALKMDHKAMEEFMIHKQAQIFFDEGYIFGDGGIGFERINLAAPSSVIQESLERLNKALKDLK

>d1eg5a_c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Thermotoga maritima}

MRVYFDNNATTRVDDRVLEEMIVFYREKYGNPNSAHGMGIEANLHMEKAREKVAKVLGVSPSEIFFSCATESINWILKTVAAETFEKRKRTIITPIEH
KAVLETMKYSMKGFVKVYVPVDSRGVVKLEELEKLVDEDFTFLVSIMAANNEVGTIQPVEDVTRIVKKNKETLVHDAVQTIGKIPFSLEKLEV
FSAHKFHGPKGVGITYIRKGPVIRPLIHGQQGERLRSQTQNVPVGIAARAMEIAVEELSEAKHMEKLRSKLVSGLMNLGAHIITPLEISLPNTLSV
FPNIRGSTLQNLLSGYGIYVSTSSACTSKDERLRHVLDAMGVDRRIAQGAIRSLCKYNTEEEVDYFLKIEEILSFL

>d1jf9a_c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Escherichia coli}

IFSVDKVRADFPVLSREVNGLPLAYLDSAASAQKPSQVIDAEAEFYRHGYAAVHRGIHTLSAQATEKMFENVRKRALFINARSAELVFRGTTEGINL
VANSWGNNSNRAGDNIIISQMEHHANIPWQMLCARVGAELRVIPNPDGTLQLETLPRLFDEKTRLLAITHVSNLGTTENPLAEMITLAHQHGAK
VLVDGAQAVMHHPPDVQALCDFYVFSGHKLYGPTGIGLYVKEALLQEMPPWEGGSMAITVSLSEGTTWTKAPWRFEAGTPNTGGIIGLGAAL
EYVSALGLNNIAEYEQNLMHYALSQLESVPDLTLYGPQNRLGIAFNLGKHAYDVGSLDNYGIAVRTGHHCAMPLMAYYNVPAMCRASLAMYN
THEEVDRLVTLGLQRIHRLLG

>d1elua_c.67.1.3 (A:) Cystine C-S lyase {Synechocystis sp.}

QFPGLANKTYFNFGGQQLPTEVALEITAMYGYLQENGPFISAANQHQQLIAQLRQALAETFNVDPNTITTDNVTTGCDIVLWGLDWHQGDEILLT
DCEHPGIIAIVQAIARFGITYRFFPVAATLNQGDAAVLANHLGPKTRLVILSHLLWNTQVPLAEIMAVCRRHQGNYPVRLVLDGAQSAGSLPLD
FSRLEVDDYAYFTGHKWFAFPAGVGGLYIHGDCLGEINPTYVGWSITYGAKGEPTGWAEGGKRFEVATSYPQYAGLLAQLHQQRQTAEERYQAI
CQRSEFLWRGLNQLPHVHCLATSAPQAGLVSFTVDSPLGHRAIVQKLEEQRILRTIADPDCIRACCHYTDEEEINHLLARLADFGP

>d2dkb_c.67.1.4 (-) Dialkylglycine decarboxylase {Pseudomonas cepacia}

LNDATFWRNARHHLVRYGGTFEPMIIERAKGSFVYDADGRAILDFTSGQMSA/LGHCHPEIVSIGEYAGKLDHLFSEMLSRPVVDLATRLANITPP
GLDRALLSTGAESNEAIRMAKLVTGKYEIVGFAQSWHGMTGAAASATYSAGRKGVGPAAVGSFAIPAPFTYRPRFERNGAYDYLAEELDYAFDLIDR
QSSGNLAAFIAEPILSSGGIILPDGYMAALKRCEARGMILLDEAQTVGVRTGTMFACQRDGVTDPILTSKTLGAGLPLAAIVTSAAIERAH
LFYTTVSDPLPAVGLRVLVVQRDGLVARANVMGDRRLRGLLDLMERFDCIGDVRGRGLLLGVIEV/KDRRTKEPADGLGAKITRECMNLGSMN
IVQLPGMGGVFRIAPPLTSEDEIDLGLSLLGQAIERAL

>d2gsaa_c.67.1.4 (A:) Glutamate-1-semialdehyde aminomutase (aminotransferase) {Synechococcus sp., strain GR6}

FKTIKSDEIFAAAQKLMPGGVSSPVRAFKSVGGQPIVFDRVKD DAYAWDV DGNRYIDYVGTW GPAICGH AHEPEVIEALKVAMEKGTSFGAPCALEN
LAEMVNDAVPSIEMVRVFNSGTEACMAVLRLMRAYTGRDKIIFEGCYHGHADMFLVKAGSGVATLGPSSPGVPKTTANTLTPYNDLEAVKALF
AENPGEIAGVILEPIVGNSGFIVPDAGFLEGRLREITLEHDALLFDEVMTGFRIAYGGVQEKGVT PDLTLGKIIGGGLPVGAYGGKREIMQLVAPAGP
MYQAGT LSGNPLAMTAGIKTLELLRQPGTYEYLDQITKRLSDGLLIAQETGHAACGGQVSGMFGFFFTEGPVHNYEADKSDLQKFSRFHGM
QGIYLAPSQFEAGFTSLAHTEDIDATLAAARTVMSAL

>d2oata_c.67.1.4 (A:) Ornithine aminotransferase {Human (Homo sapiens)}

GPPTSDDIFEREYKGHNHYHPLPVALERGKG IYLWDVEGRKYFDLSSYSAVNQGHCHPKIVNALKSQVDKLTLSRAFYNNVLGEYEYITKLFNYH
KVLPMNTGVEAGETACKLARKWGYTVKGQKAKIVFAAGNFWGRTLSAISSTDPTSYDGF GPFMPGFDIIPYNDLPA LERALQDPNVA AFMVEP
IQGEAGVVVPDPG YLMGVRELCTRHQVLFIADEI QTGLARTGRWLADYENV RPDIVLLGKALSGG LYPVSAVLCDDIMLTI KPG EHGSTYGGNPL
GCRVAIAALEVLEENLAENADKLGII RLNEMLKLP SDVVTAVRGKG LNAIVIKETKDWD AWKVCLRLRDNGLLAKPTHGDIIRFAPPV LKEDELRESI
EIINKTILSF

>d1gtxa_c.67.1.4 (A:) 4-aminobutyrate aminotransferase, GABA-aminotransferase {Pig (Sus scrofa)}

F DYDGPLMKTEVPGP RSRELMKQLNIIQNAEAVHFFCN YEE SRG NYL DV DGNR MLDL YSQISSIPIGYSHPALV KL VQQPQNV STF INR PA L GIL PPE
NFVEKLRESLLS VAPKGMSQLITMACGSCSNENA FKTIFM WYRSK ERG QSAFS KEE LCTC MINQAPGCPD YSILS FMGAF HGR TMG CLAT THSKAIH

KIDIPSFDWPIAPFPRLKYPLEEFVKENQQEEARCLEEVEDLIVKYRKKKKTAVGIIVEPIQSEGGDNHASDDFRKLRDISRKHGCALVDEVQTGGGS
TGKFWAHEHWGLDDAADVMTFSKKMMTGGFFHKEEPRNAPYRIFNTWLGDPSKNLLAEVINIIKREDLLSNAAHAGKVLLTGLLDLQARYPQFI
SRVRGRGTFCSFDTPDESIRNKLSIARNKGVMGGCGDKSIRFRPTLVFRDHHAHLFLNIFSDILADFK

>d1bt4a_c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Bacillus circulans, subsp. alkalophilus}
SERAYNFNAGPAALPLEVLERAQAEFVDYQHTGMSIMEMSHRGAVYEAVHNEAQARLLALLGNPTGYKVLFIQGGASTQFAMIPMNFLKEGQTAN
YVMTGSWASKALKEAKLIGDTHVAASSEASNYMTPLKLQEIQLQDNAAYLHLTSNETIEGAQFKAFPDTGSVPLIGDMSSDILSRPFDLNQFGLVYAG
AQKNLGPSPGVTVVIVREDLVAESPCKLPTMLRYDTYVKNNSLYNTPPSFGIYMVNEVWKWIEERGGLEGVQQANRKASLIYDAIDQSGGFYRCVD
VDSRSMDMNITFRLASEELEKEFVKASEQEGFVGLKGHRSGVGLRASIYNAVYESCEALVQFMEHFKRSRG

>d1bjna_c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Escherichia coli}
QIFNFSSGPAMILPAEVLKQAQQELRDWNGLTSVMEVSHRGKEFIQVAEEAEKDFRDLNVPSNYKVLFCGGGRGQFAAVPLNILGDKTTADYVD
AGYWAASAIAKEAKKYCTPNVFDAKVTVDGLRAVKPMREWQLSDNAAYMHCPNETIDGIADETPDFGADVVAADFSSTILSRPIDVSRYGVYAG
AQKNIGPAGLTIIVVREDLLGKANIACPSILDYSILNDNGSMFNTPPTFAWYLSGLVFKWLKANGVAEMDKINQQKAELLYGVIDNSDFYRNDVAKR
NRSRMNVFQLADSALDKLFLEESFAAGLHALKGHRVVGGMRASIYNAMPLEGVKALTDFMVEFERRHG

>d1cj0a_c.67.1.4 (A:) Serine hydroxymethyltransferase {Rabbit (Oryctolagus cuniculus)}
WSSHEQMLAQPLKDSDAEVYDIKKESNRQRVGLELIASENFASRAVLEALGSCNNKYSEGPGQRYYGGTEHIDELETLCQKRALQAYGLDPQCW
GVNVQPYSGSPANFAVYTALVEPHGRIMGLDLPDGHLTHGFMTDKKKISATSIFFESMAYKVNPDGTGIDYDRLEENARLFHPKLIAGTSCSRNL
YGRRLKIADENGAYLMADMAHISGLVAGVVPSPFEHCHVTTTHKTLRGCRAGMIFYRGGVRSVDPKTGKEILYNLESLINSAVFPGLQGGPHNH
AIAGVAVALQAMTPEFKEYQRQVVANCRLSAALVELGYKIVTGGSDNHLILVDLRSKGTDGGRAEKVLEACSIACNNTCPGDKSALRPSGLRLGT
PALTSRGLLEKDFQKVAHFIRGIELTVQIQDDTGPRTLKEFKEKLAGDEKHQRAVRALRQEVEFAFLPLPGLPGF

>d1ejia_c.67.1.4 (A:) Serine hydroxymethyltransferase {Mouse (Mus musculus)}
MADRATLWASHEKMLSQPLKDSDAEVYIIKKESNRQRVGLELIASENFASRAVLEALGSSLNNKYSEGPGQRYYGGTEFIDELEMICQKRALQAY
HLDPQCWGTVNQPYSGSPANFAVYTALVEPHGRIMGLDLPDGHLTHGFMTDKKKISATSIFFESMPYKVPETGYINYDQLEENASLFHPKLIAGT
SCYSRNLDYARLRKIADDNGAYLMADMAHISGLVAAGVVPSFEHCHVTTTHKTLRGCRAGMIFYRGGVRSVDPKTGKETYELESLINSAVFPGL
QGGPHNHAIAGVAVALQAMTTEFKIYQLQVLANCRALSDALTELGYKIVTGGSDNHLILMDLRSKGTDGGRAEKVLEACSIACNNTCPGDKSALR
PSGLRLGTPALTSRGLLEDFQKVAHFIRGIELTLQIQSHMATKATLKEFKEKLAGDEKIQSAVATLREEVENFASNFSLPGPDF

>d1bj4a_c.67.1.4 (A:) Serine hydroxymethyltransferase {Human (Homo sapiens)}
DADLWSSHADMLAQPLKDSDVEVYIIKKESNRQRVGLELIASENFASRAVLEALGSCNNKYSEGPGQRYYGGTEFIDELETLCQKRALQAYKLD
QCWGVNVQPYSGSPANFAVYTALVEPHGRIMGLDLPDGHLTHGFMTDKKKISATSIFFESMPYKVNPDGTGIDYDQLEENARLFHPKLIAGTSC
RNLEYARLRKIADENGAYLMADMAHISGLVAAGVVPSFEHCHVTTTHKTLRGCRAGMIFYRGGVRSVDPATGKEILYNLESLINSAVFPGLQGGP
HNHAIAGVAVALQAMTLEFKVYQHQQVANCRLSEALTELGYKIVTGGSDNHLILVDLRSKGTDGGRAEKVLEACSIACNNTCPGDRSALRPSGLR
LGTPALTSRGLLEKDFQKVAHFIRGIELTLQIQSDTGVAATLKEFKERLAGDKYQAAVQALREEVESFASLFLPLPGF

>d1dfoa_c.67.1.4 (A:) Serine hydroxymethyltransferase {Escherichia coli}
LKREMNIADYDAELWQAMEQEKRQEEHIELIASENYTSPRMQAQSQLTNKYAEYPGKRYGGCEYVDIVEQLAIDRAKELGADYANVQPHS
GSQANFAVYTALLEPGTVLGMNLAHGHHLTHGSPVNFSGKLYNIPYGDATGHIDYADLEKQAKEHKPKMIIIGGSAYSQVVDWAKMREIADSIG
AYLFVDMAHVAGLVAAGVVPNPVPHAHVTTTHKTLAGPRGGLILAKGGSEELYKKLNSAVFPGGQGGPLMHVIAGKAVALEAMEPEFKTYQQ
QVAKNAKAMVEFLERGYKVVSGGTDNHLFLVDVKNLTGKEADAALGRANITVNKNVPNDPKSPFVTSGIRGTPAIRRGFKEAEAKELAGW
MCDVLDISINDEAVIERIKGVLDICARYPVYA

>d1b9ha_c.67.1.4 (A:) 3-amino-5-hydroxybenzoic acid synthase (AHBA synthase) {Amycolatopsis mediterranei}
KAPEFPWPQYDDAERNGLVRALEQQQWWRMGGDEVNSFEREFAAHGAAHALAVTNGTHALELALQVMGVPGTEVIVPAFTFISSQAAQR
LGAVTVPDVDAATYNLDPEAAAVTPRTKVIMPVHMAGLMADM DALAKISADTGVPLLQDAAHGARWQGKRVGELEDSIATFSFQNGKLM
TAGEGGAVVFDPGETEKYETAFLRHSGCGRPDDRRYFHKIAGSNMRLNEFSASVLAQLARLDEQI AVRDERWLLSRLGAIDGVVPPQGGDVRAD
RNSHYMAMFRIPGLTEERRNALVDRLEAGLPAAFAFRAIYRTDAFWELGAPDESVDIAIARRCPNTDAISSDCVWLHHRVLLAGEPELHATAEIADA
VARA

>d1fc4a_c.67.1.4 (A:) 2-amino-3-ketobutyrate CoA ligase {Escherichia coli}

GSHMRGEFYQQLTNDLETARAEGLFKEERIITSAQQADITVADGSHVINFCANNYGLANHPDLIAAAKAGMDSHGFGMASVRIFICGTQDSHKELE
QKLAFLGMEDAILYSSCFDANGGLFETLLGAEDAIISDALNHASIIDGVRLCKAKRYRYANNMDQELEARLKEAREAGARHVLATDGVSMDGVIA
NLKGVCVDLADKYDALMVDDSHAVGFVGENGRGSHEYCDVMGRVDIITGTLKALGGASGGYTAARKEVVWLRQRSPYLSNLSLAPAIAVASIK
VLEMVEAGSELRDRWLWANARQFREQMSAAGFTLAGADHAIIPVMLGDAVVAQKFARRELQKEGYVTGFYPVVPKGQARIQMSAAHTPEQITR
AVEAFTRIGKQLGVIA

>d1bs0a_c.67.1.4 (A:) PLP-dependent acyl-CoA synthase (8-amino-7-oxonanoate synthase, AONS) {Escherichia coli}

SWQEKINAALDARRAADLRRYRPAQGAGRVLWADDRQYLNFSNSNDYLGLSHHPQIIRAWQQGAEQFGIGSGGSGHVGYSVHQALEEELAE
WLGYSRALLFISGFAANQAVIAAMMAKEDRIAADRSLHASLLEAASLSPSQLRRFAHNDVTHLARLLASPCPGQQMVTEGVFSMDGDSAPLAEIQ
QVTQQHNGWLMVDDAHTGVIGEQGRGSCWLQVKPELLVVTFGKGFGVSGAAVLCSSTVADYLLQFARHLIYSTMPPAQALRASLAVIRSD
EGDARREKLAALITRFRAGVQDLPFTLADSCSAIQPLIVGDNRSALQLAEKLQRQGCWVTAIRPPTVPGTARLRLTAAHEMQDIDRLLEVHGNG
>d1qj5a_c.67.1.4 (A:) Adenosylmethionine-8-amino-7-oxononanoate aminotransferase, BioA {Escherichia coli}

MTTDDLAFDQRHILHPYTSMTSPLPVVSAEGCELIISDGRRLVDMSSWWAAIHGYNHQPQNAAMKSQIDAMSHVMFGGITAPAIELCRKL
VAMTPQPLECVFLADSGSVAVEAMKMAQYWQAKGEARQFLTRNGYHGDTFGAMSVCDPDSMHSLSKGYLPENLFAPAPQSRMDGEW
DERDMVGFARLMAAHRHEIAVIIEPIVQGAGGMRMYHPEWLKRIRKICDREGILLIADEIATGFRTGKLFACEHAEIAPDILCLGKALTGGTMTLSA
TLLTREVAETISNGEAGCFMHGPTFMGNPLACAAANASLAILESGDWQQQVADIEVQLREQLAPARDAEMVADVRVLGAIGVVETTHPVNMAAL
QKFFVVEQGVWIRPFGKLIYLMPPYIILPQQLQRLTAVNRAVQDETFFCQ

>d1b8ga_c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {Apple (Malus domestica)}

MLSRNATFNSHGQDSSYFLGQYEKNPYHEVHNTNGIIQMGLAENQLCFDLLESWAKNPEAAFKNGESIFAEALFQDYHGLPAFKKAMVD
FMAEIRGNKVTFDPNHLVTAGATSANETFIFCLADPGEAFLIPTYYPGFDRDLKWRGVEIVPIHCTSSNGFQITETAEEAYQEAERNLRVKGVLV
TNPSNPLGTTMTRNELYLLSFVEDKGIGHLISDEIYSGTAFSSPSFISVMEVLDKRNCDENSEWVQRVHVYSLSKDGLPGFRVGAIYSNDDMVVA
ATKMSSFGLVSSQTQHLLSAMLSDKKLTKNYIAENHKRLQRQKKLVSLQKSGISCLNGNAGLFCWVDMRHLLRSNTFEAEMELWKKIVYEVHLNI
SPGSSCHCTEPGWFRVCANLPERTLAMQRLKAFVG

>d1iaya_c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {Tomato (Lycopersicon esculentum)}

ILSKLATNEEHGENSPYFDGWKAYDSDPFPHPLKNPNGVIQMGLAENQLCLDIEDWIKRNPKGSCSEGIKSFKAIANFQDYHGLPEFRKAIAKFMEK
TRGGRVRFDPERVVMAGGATGANETIIFCLADPGDAFLVPSYPAFNRDLRWRTGVQLPIHCESNNFKITSKAVKEAYENAQKSNIKVKGLILTNP
SNPLGTTLDKDTLKSLSFTNQHNIHLVCDEIYAATVFDTQFVSSIAEILDEQEMTYCNKDLVHIVYSLSKDMGLPGFRVGIIYSFNDDVNCARKMSS
FGLVSTQTQYFLAAMLSDEKFDVDFLRESAMRLGKRHKHTNGLEVVGKCLKNNAGLFCWMDLRPLLRESTFDSEMSLWRVIINDVKNVSPGSSF
ECQEPGWFRVCANMDDGTVDIALARRFVGVEK

>d1c4ka2_c.67.1.5 (A:108-569) Ornithine decarboxylase major domain {Lactobacillus sp., strain 30a}

PPFFKSLKEYVSRYLIQFDPCGHQGGQYYRKHPAGREFYDFFFGETVFRADLCNADVALGDLLIHEGPAVAEKHAARVNADKTYVILGGSSNANN
VTSALVNGDLVLFDRNNHKSVYNSALAMAGGRPVLQTNRNPYGFIGGIYDSDFDEKKIRELAALKVPERAKWKRPFRLAVIQLGTYDGTIYNAHE
VVKRIGHLCDYIEFDSA伟VGYEQFIPMMRNSSPLIDLGPEDPGIIVVQSVHKQQAGFSQTSQLHKKDSHIKGQLRYCDHKHFNNSFNLFMSTSPF
YPMYAALDVNAAMQEAGEAGRKLWHDLLITIEARKLIKAGSMFRPVPPVNGKKWEDGDTEDMANNIDYWRFEKGAKWHAYEGYGDNQYY
VDPNKFMILTPGINPETG DYEDFGVPATIVYLRDHGIIPEKSDLNSILFLMTPAETPAKMNLLTQLLQLQRLIED

>d1qg8a_c.68.1.1 (A:) Spore coat polysaccharide biosynthesis protein SpsA {Bacillus subtilis}

PKVSIMTSYNSKSDYVAKSISSILSQTFSDFELFIMDDNSNEETLNIRPFLNDNRVRFYQSDISGVKERTEKTRYAALINQAIEMAEGEYITYATDDNIY
MPDRLLKMVRELDTHPEKAVIYSASKTYHLNENRDIVKETVRPAQVTWNAPCAIDHCSVMRYSVLEVKKEKFGSYWDESPAFYRIGDARFFWRV
NHFPYFPLDEELDNYITDQSIFHQLFELEKNEFVRNLPPQRNCRELRESLKKLGMG

>d1j8wb_c.68.1.2 (B:) beta 1,4 galactosyltransferase (b4GalT1) {Cow (Bos taurus)}

TACPEESPLVGPMLIEFNIPVDLKLVEQQNPKVKGGRYTPMDCISPHVAAIIIPFRNRQEHLYWLYLHPILQRQQLDYGIYVINQAGESMFNRALK
LNVGFKEALKDYYDYNCFVFSVDLIPMNDHNTYRCFSQPRHISVAMDKGFSLPVQYFGGSALSQQFLSINGFPNNYWGWGGEDDIYNRLA
FRGMSVSRPNAVIGKCRMIRHSRDKNEPNPQRFDRIAHTKETMLSDGLNSLTYMVLLEVQRYPLYTKITVDIGTPS

>d1ezia_c.68.1.3 (A:) CMP acylneuraminate synthetase {Neisseria meningitidis}

MEKQNIAVILARQNSKGLPLKLNRLKMNGISLLGHTINAAISSKCFDRIIVSTDGLIAEAKNFGVEVVLRPAELASDTASSISGVIALETIGNSGTVL

LQPTSPLRTGAHIREAFSLFDEKIKGSVVACPMEEHPLKTLQINNGEYAPMRHLSDEQPRQQLPQAFRPNGAIYINTASLIANNCFIAPTKLYIM
SHQDSIDIDTELDLQQAENILN

>d1ga8a_c.68.1.4 (A:) Galactosyltransferase LgtC {Neisseria meningitidis}

MDIVFAADDNYAAAYLCVAAKSVEAAHPDTEIRFHVLADAGISEANRAAVAANLRGGGNIRFIDVNPEDFAGFPLNIRHISITTYARLKGEYIADCDKV
LYLDIDVLVRDSLTPWDTDLGDNWLGASIDLVERQEGYKQKIGMADGEYYFNAVGVLINLKKWRRHDIFKMSSEWVEQYKDVMQYQDQDILNG
LFKGGVCYANSRFNMPTNYAFMANWFASRHTDPLYRDRNTVMPAVSHYCGPAKPWHRDCTAWGAERFTELAGSLTTVPEEWRGKL

>d1g93a_c.68.1.9 (A:) alpha-1,3-galactosyltransferase catalytic domain {Cow (Bos taurus)}

KLKLSDFWFNPFKRPEVVMTKWAPVVEGTYNRAVLNDNYYAKQKITVGLTVFAVGRYIEHYLEELTSANKHFMVGHPVIFYIMVDDVSRMPLIEL
GPLRSFKVFKIKPKEKRWQDISMMRMKTIGEHIVAHIQHEVDFLCMDVDQVFQDKFGVETLGESVAQLQAWWYKADPNFTYERRKESAAYIPFG
EGDFYYHAAIFGGPTQVLNITQECFKGILKDKKNDIEAQWHDESHLNKYFLLNKPTKILSPEYCWDYHIGLPADIKLVKMSWQT

>d1hv9a2_c.68.1.5 (A:4-251) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, N-terminal domain {Escherichia coli}

NAMSVVILAAGKGTRMYSQDPKVLHTLAGKAMVQHVDAANELGAAHVHLVYGHGGDLLKQALKDDNLNWVVLQAEQLGTGHAMQQAAPFFAD
DEDILMLYGDVPLISVETLQRRLDAKPQGGIGLLTVKLDDPTGYGRITRENGKVTGIVEHKDATDEQRQIQEINTGILIANGADMKRWLAKLTNNNAQ
GEYYITDIIALAYQEGREIVAVHPQLSEVEGVNNRLQLSRLERVYQSEQAEKLLAG

>d1hm9a2_c.68.1.5 (A:2-251) N-acetylglucosamine 1-phosphate uridyltransferase GlmU, N-terminal domain {Streptococcus pneumoniae}

SNFAIIILAAGKGTRMKSDLPKVLHKVAGISMLEHVFRSGAIQPEKTVVGHKAELVEEVLAGQTEFVTQSEQLGTGHAVMMTEPILEGLSGHTLV
AGDTPLITGESLKNLIDFHINHKNVATILTAETDNPFYGRIVRNNDNAEVLRIVEQKDATDFEKQIKEINTGTYVFDNERLFEALKNINTNNAQGEYYITD
VIGIFRETGEKVGAYTLKDFDESLGVNDRVALATAESVMRRINHKHMNG

>d1fxoa_c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Pseudomonas aeruginosa}

KRKGIILAGGSGTRLHPATLAISKQLLPVYDKPMIYPLSTLMLAGIREILIISTPQDTPRFQQLLGDSNWGLDLYAVQPSPDGLAQAFIIGESFIGND
LSALVLGDNLYGHDFHELLGSASRQRTGASVFAYHVLDLPERGYVVEFDQGGKAISLEEKPLEPKNSNYAVTGLYFYDQQVVDIARDLKPSRGELEITD
VNRAYLERGQLSVEIMGRGYAWLDTGTHDSLLEAGQFIATLENRQGLKVCPEEIAYRQKWIADAQLEKLAAPLAKNGYQYQYKRLLTETVY

>d1iina_c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Salmonella enterica}

MKTRKGIILAGGSGTRLYPVTMAVSQQLPIYDKPMIYPLSTLMLAGIRDILIIISTPQDTPRFQQLLGDSQWGLNLQYKVQPSPDGLAQAFIIGEEFI
GHDDCALVLDNFIFYGHDLPLKLMEEAVNKESGATVFAYHVNDPERGYVVEFDQKGTAWSLEEKPLEPKNSNYAVTGLYFYDNSVVEMAKNLKPSSARG
ELEITDINRIYMEQGRSLVAMMGRGYAWLDTGTHQSIEASNFIATIERQGLKVCPEEIAFRKNFINAQVIELAGPLSKNDYGYLLKMV

>d1h5ra_c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Escherichia coli}

KMRKGIILAGGSGTRLYPVTMAVKQLLPIYDKPMIYPLSTLMLAGIRDILIIISTPQDTPRFQQLLGDSQWGLNLQYKVQPSPDGLAQAFIIGEEFIG
GDDCALVLDNFIFYGHDLPLKLMEEAVNKESGATVFAYHVNDPERGYVVEFDQKGTAWSLEEKPLEPKNSNYAVTGLYFYDNDVVQMAKNLKPSSARG
EITDINRIYLEQGRSLVAMMGRGYAWLDTGTHQSIEASNFIATIERQGLKVCPEEIAFRKGFIIDVEQVRKLAQPLKNNYGGQYLYKMTKD

>d1fgga_c.68.1.7 (A:) 1,3-Glucuronyltransferase I (glcAT-I) {Human (Homo sapiens)}

MTIYVVTPTYARLVQKAELVRLSQLTSLVPRLHWLLVEDAEGPTPLVSGLLAASGLLFTHLVLTPKAQRRLREGEPGWVHPRGVEQRNKALDWLRGR
GGAVGGEKDPGGTQGVVYFADDNTSRELFEEMRWTRGVSVWPVGLVGGLRFEGPQVQDGRVVFHTAWEPSRFPVDMAGFAVALPLL
DKPNAQFDSTAPRGHLESSLLSHLDPKDLEPRAANTRVLVWHTRTEKPKMKQEEQLQRQGRGSDPAIEV

>d1fo8a_c.68.1.10 (A:) N-acetylglucosaminyltransferase I {Rabbit (Oryctolagus cuniculus)}

LAVIPILVIACDRSTVRRLCDKLLHYRPSAELFPIIVSQDCGHEETAQVIASYGSAVTHRQPDLSNIAVQPDHRKFQGYYKIAHYRWALGQIFHNFNYP
AAVVVEDDLEVAPDFFEYFQATYPLLKADPSLWCVSAWNDNGKEQMVDSSKPELLYRTDFFPGLWLLAELWAELEPKWPKAFWDDWMRRPE
QRKGRACVRPEISRTMTFGRKGVSHGQFFDQHLKFIKLNQQFVPTQLDLSYLQQEAYDRDFLARVYGAQPLQVEKVRTNDRKELGEVRVQYTGRD
SFKAFAKALGVMDLKSGVPRAGYRGIVTFLFRGRRVHLAPPQTWDGYDPSWT

>d1e5ka_c.68.1.8 (A:) Molybdenum cofactor biosynthesis protein MobA {Escherichia coli}

MTTITGVVLAGGKARRMGGVDKGLELNGKPLWQHVADALMTQLSHVVVANRHQEIQASGLKVIDSLADYPGAGMLSVMQQEAGEWF
LFCPCDTPYIPPDLAARLNHQRKDAPVVVHDGERDHPTIALVNRAIEPLLLEYLQAGERRVMVFMRLAGGHAVDFSDHKDAFNVNNTPEELARW
Q

>d1i52a_c.68.1.13 (A:) 4-diphosphocytidyl-2-c-methylerythritol (CDP-me) synthase (YgbP) {Escherichia coli}
HLDVCAVVAAGFGRRMQTECPKQYLSIGNQTILEHSVALLAHPRVKRVVIAISPGDSRFAQLPLANHPQITVVDGGERADSVLAGLKAAGDAQ
WVLVHDAARPCLHQDDLARLLALSETRTGGILAAPVRDTMKRAEPGKNAIAHTVDRNGLWHALTPQFFPRELLHDCLTRALNEGATITDEASALEY
CGFHPQLVEGRADNIKVTRPEDLALAEFLTR

>d1h7ea_c.68.1.13 (A:) CMP:2-keto-3-deoxy-manno-octonic acid (CMP-KDO)synthetase, KdsB {Escherichia coli}
SKAVIVIPARYGSSRLPGKPLLDIVGKPMIQHVYERALQVAGVAEVWVATDDPRVEQAVQAFGGKAIMTRNDHESGTDRLVEMHKVEADIYINLQ
GDEPMIRPRDVETLLQGMRDPALPVATLCHAISAAEAEpstVKVVVNTRQDALYFSRSRPIPYPRNAEKARYLKHVGIYAYRRDVLQNYSQLPESMP
EQAESLEQLRLMNAGINIRTFEVAATGPGVDTPACEKVRALMAQELAENA

>d1jyka_c.68.1.13 (A:) CTP:phosphocholine cytidylytransferase LicC {Streptococcus pneumoniae}
EIRVKAIILAAAGLGLTRPLTENTPKALVQVNQKPLIEYQIEFLKEKGINDIIIVGYLKEQFDYLKEKYGVRLVNDKYADYNNFYSLYLVKEELANSYVIDA
DNYLFKNMFRNDLRTSTYFSVYREDCTNEWFLVYGDYKVQDIIVDSKAGRILSGVSFWDAPTAEKIVSFIDKAVSGEFVDLYWDNMVKDNIKELD
VYVEELEGNSIYEIDSQVQDYRKLEEILK

>d1jw9b_c.111.1.1 (B:) Molybdenum cofactor biosynthesis protein MoeB {Escherichia coli}
AELSDQEMLRYNRQIILRGFDGQEAALKDSRVLIVGLGGCAASQYLASAGVGNLTLLDFDTVSLSNLQRQLHSDATVGQPKVESARDALTRINP
HIAITPVNALLDAELAALIAEHDVLDCDNTNAVRNQLNAGCFAAKVPLVSGAACRMEGQITVFTYQDGEPYCRLSRLFGENALTCEAGVMAPLI
GVIGSLQAMEAIKMLAGYKGKPASGKIVMYDAMTCQFREMKLMRNPGEVCG

>d1ea5a_c.69.1.1 (A:) Acetylcholinesterase {Electric ray (Torpedo californica)}
SELLVNTSGKVMGTRVPVSSHISAFLGIPFAEPPVGNMRFRREPKKPWGVWNASTYPNNCCQQYVDEQFPFGSGSEMWPNPREMSEDCLYL
NIWVPSPRPKSTTVMVWIYGGGFYGSSTLDVYNGKYLAYTEEVVLSYRVGAFLALHGSQEAPGNVGLDQRMALQWVHDNIQFFGGDPK
TVTIFGESAGGASVMHILSPGSRDLFRRAILQSGSPNCWPASVVAEGRRRRAVELGRNLNCNLNSDEELIHLREKKPQEIDVENVLPFDSIFRFS
FVPVIDGEFFPTSLESMLNSGNFKKTQILLGVNKDEGSFFLYGAPGFSKDSESKISREDFMSGVKLSVPHANDLGLDAVTLQYTDWMDDNNGIKR
DGLDDIVGDHNVICPLMHFNKYTKFGNGTYLYFFNHRASNLVWPEWMGVIGHYEIEFVFLGPLV/KELNYTAEEALSRRIMHYWATFAKTGNPNE
PHSQESKWPLFTTKEQKFIDLNEPMKVHQQLRVQMCVFWNQFLPKLLNAT

>d1maaa_c.69.1.1 (A:) Acetylcholinesterase {Mouse (Mus musculus)}
EDPQLLVRVGGQLRGIRLKAPGGPVSALGIPFAEPPVGSRRFMPEPKRPWGVLDATTQNVCYQYVDTLYPGFEGTEMWNPNPRELSEDCLYL
NVWTPYPRPASPPTVLIWYGGGFYSGAASLDVYDGRFLAQVEGAVLVSMNYRVGTFGLALPGSREAPGNVGLDQRLALQWVQENIAAFGGDP
MSVTLFGEASAGAASVMHILSLPSRSLFHRAVLQSGTPNGPWATVSAGEARRATLLARLVCPPGGAGGNDELIACLRTRPAQDLDHEWHVLP
QESIFRFSSFPVVDGDFLSDTPEALINTGDFQDLQVLVGVVKDEGSYFLVYGVPGFSKDNEISLRAQFLAGVRGVRGPQASDAAEAVVLYHTDWLHP
EDPTHLRDAMSAVVGDHNVCPVAQLAGRLAAQGARVYAYIFEHRASTLTWPLWMGVPHGYEIEFIFGLPLDPSLNYYTEERIFAQRLMKYWTNFA
RTGDPNDPRDRKSPQWPPYTAAQQYVSLNLKPLEVRRGLRAQTCAFWNRFPLPKLLSAT

>d1f8ua_c.69.1.1 (A:) Acetylcholinesterase {Human (Homo sapiens)}
DAELLVTVRGGRLRGIRLKPGGPVSALGIPFAEPPMGPRLPPEPKQPWGVVDATTQNVCYQYVDTLYPGFEGTEMWNPNPRELSEDCLYLNV
WTPYPRPTSPPTVLIWYGGGFYSGASSLDVYDGRFLVQAERTVLVSMNYRVGAFLALPGSREAPGNVGLDQRLALQWVQENIAAFGGDPTS
VTLFGQSAGAASVMHLLSPSRLFHRAVLQSGAPNGPWATVGMGEARRATQLAHLVGCPPGGTTGNDTELVACLTRPAQV/LVNHEWHV
PQESVFRFSFVPPVVDGDFLSDTPEALINAGDFHGLQVLVGVVKDEGSYFLVYGVPGFSKDNEISLRAEFLAGVRGVRGPQVSDAAEAVVLYHTDWL
HPEDPARLREALSDVVGDHNVCPVAQLAGRLAAQGARVYAYIFEHRASTLSWPLWMGVPHGYEIEFIFGIPLDPSRNYYTAEEKIFQRLMRYWAN
FARTGDPNEPRDPKAPQWPPYTAGAQYVSLDLRPLEVRRGLRAQACAFWNRFPLPKLLSAT

>d1dx4a_c.69.1.1 (A:) Acetylcholinesterase {Fruit fly (Drosophila melanogaster)}
DRLVQTSSGPVRGRSVTVQGREVHVTGIPYAKPPVEDLFRKPVPAEPWHGVLDATGLSATCVQERYEYFPFGSGEEIWPNTNVSEDCLYINVW
APAKARLRHGRGANGGEHPNGKQADTDHLLHNGNPQNTTNGLPLIWIYGGGFMTGSATLDIYNADIMAAGVNIVASFQYRVGAFLHLAPE
MPSEFAEEAPGNVGLWDQALAIRWLKDNAHAFGGNPEWMTLFGESAGSSVNAQLMSPVTRGLVKRGMMQSGTMNAPWSHMTSEKAVEIG
KALINDCNCSNMLKTNPAHVMSCMRSDAKTISVQQWNSYSGILSFPSAPTDGAFLPADPMTLMKTADLKDYDILMGNVRDEGYFLLYDFIDY
FDKDDATALPRDKYLEIMNNIFGKATQAEREAIIFQYTSWEGNPGYQNQQQIGRAVGDHFTCPTNEYAQLAERGASVHYYFTHRTSTSLLGEW
MGVLHGDEIEYFFGQPLNNSLQYRPVERELGKRMILSAVIEFAKTNPAQDGEWPNSKEDPVYYIFSTDDEKIELKARGLPLAARCSFWNDYLPKVR

W

>d2bce__ c.69.1.1 (-) Bile-salt activated lipase (cholesterol esterase) {Cow (Bos taurus)}

AKLGGSVYTEGGFVEGVNKKLSQLGDSVDIFKGIPFAAAPKALEKPERHPGWQGTLKAKSFKKRCLQATLTQDSTYGNEDCLYLNIWPVPGRKEVSHDL
PVMIWIYGGAFMLMGASQGANFLSNLYDGEIATRGNVIVVTNFNYRVGPLGLSTGDSNLPGNYGLWDQHMAIAWVKRNIEAFGGDPDNITLFGE
SAGGASVSLQTLSPYNKGLIKRAISQSGVGLCPWAIQQDPLFWAKRIAEKVGCPVDDTSKMAGCLKITDPRALTLAYKLPLGSTEYPKLHYLSFPVID
GDFIPDDPVNLYANAADVYIAGTNMDGHLFVGMDVPAINSNKQDVTEEDFYKLVSLTVTKGLRGANATYEVYEPWAQDSSQETRKKTMDL
ETDILFLIPTKIAVAQHKSHAKSANTYTFLSQPSRMPYIPKWMGADHADDLQYVFGKPFATPLGYRAQDRTVSKAMIAYWTNFARTGDPNTGHST
VPANWDPYLEDNYLEINKQMDNSMSMKLHLRTNYLQFWTQTQYQALPTVTSAGASLLPPEDNSQASPVPPADNSGAPTEPSAGDSEVAQMPVVI
GF

>d1f6wa_ c.69.1.1 (A:) Bile-salt activated lipase (cholesterol esterase) {Human (Homo sapiens)}

AKLGAVYTEGGFVEGVNKKLQLGDSVDIFKGIPFAAPTAKALENPQPQPHGWQGTLKAKNFKKRCLQATITQDSTYGDDEDCLYLNIWPVPGRKQVSRD
LPVMIWIYGGAFMLMGSGHGANFLNNYLDGEIATRGNVIVVTNFNYRVGPLGLSTGDSNLPGNYGLRDQHMAIAWVKRNIAAFGGDPDNITLFGE
ESAGGASVSLQTLSPYNKGLIRRAISQSGVALSPWVIQKNPLFWAKKVAEKVGCPVGAARMAQCLKVTDPRALTLAYKVPLAGLEYPMILHYVGFP
VIDGDFIPDDPINLYANAADIDYIAGTNMDGHIFASIDMPAINGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYTESWAQDPSQENKKTVVDF
ETDVFLFLVPTEIALAQHRANAKSAKTYAYLFSHPSRMPVYVKWVGADHADDIQYVFGKPFATPLGYRPQDRTVSKAMIAYWTNFAKTGDPNMGDS
AVPHTWEPYTTENSGYLEITKKMGSSSMKRSLRTNFLRYWLTLYLALPTV

>d1qe3a_ c.69.1.1 (A:) Thermophytic para-nitrobenzyl esterase (PNB esterase) {Bacillus subtilis}

THQIVTTQYGKVKGTTENGVHKWKGIPYAKPPVGQWRFKAPEPEPVEWEDVLDATAYGPICPQPSDLSLSYTELPRQSEDCLYVNFPDTPSQNLP
VMVWIHGGAFYLGAGSEPLYDGSKLAAQGEVIVVTNLNRLGPFGFLHLSFDEAYSNDLGLDQAAALKWVRENISAFGGDPDNVTVFGESAGGM
SIAALLAMPAAKGLFQKAIMESGASRTMTKEQAACAAFLQVLGINESQLDRLHTVAAEDLLKAADQLRIAKENIFQLFFQPALDPKTLPEEPEKSI
AEGAASGIPLIGTTDEGYLFFTPSDVHSQETLDALEYLLGKPLAEKAADLYPRSLESQIHMMTDLLFWRPAYASAQSHYAPVWMYRFDWHP
EKPPYNKAFAHLELPFVFGNLDGLERMAKEITDEVKQLSHTIQSAWITFAKTNPSTEAVNWPAYHEETRETVILDSEITENDPESEKRQKLF

>d1jkma_ c.69.1.2 (A:) Carboxylesterase {Bacillus subtilis, brefeldin A esterase}

PGRLGDESSGPRTDPRFSPAMVEALATFGLDAVAAAAPPVSASDDLPTVLAAGVASHDGFQAVYDSIALDLPTRDDVETSTETILGVDGNEITLVFR
PAGVEGLPLVYTHGGMTLTTDNRVHRRWCTDLAAAGSVVVMDFRNAWTAEGHHPFPSGVEDCLAFLWVDEHRESLGLSGVVQGESG
GGNLAIATLLAKRRGRRLDAIDGVYASIPYISGGYAWDHERRLTELPSLVEDNGYFIENGGMALLVRAYDPTGEHAEDPIAWPYFASEDELRLGLPPFVV
AVNELDPLRDEGIAFARRLARAGVDVAARVNIGLVHGADVIFRHWLPAALESTVRDVAGFAADRARLR

>d1evqa_ c.69.1.2 (A:) Carboxylesterase {Alicyclobacillus acidocaldarius}

LDPVIQQVLDQLNRMPAPDYKHLAQQQFRSQSQLFPPVKKEPVAEVREFDMDPGRTLKVRMRYRPEGVEPPYPALVYHGGWVVGDLTHEDPV
CRVLAKDGRAVVFSVDYRLAPEHKFPAAVEDAYDALQWIAERAADFHDLPARIAVGGDSAGGNLAATSLAKERGGPALAFQQLIYPSTGYDPAHPP
ASIEENAEGYLLTGGMMILWFRDQYLNSELTHPWFSVPVLYPDLSGLPPAYIATAQYDPLRDEVGKLYAEALNKAGVKVEIENFEDIHGFAQFYSLSPG
ATKALVRIAEKLRDALA

>d1jjia_ c.69.1.2 (A:) Carboxylesterase {Archaeon Archaeoglobus fulgidus}

MLDMPIDPVYYQLAEYFDLSPKFDFQSSAREYREAINRIYEERNRQLSQHERVERVEDRTIKGRNGDIRVRVYQQKPDSPVLVYHGGGFICSIESH
DALCRRRIARLSNSTVSVSDYRLAPEHKFPAAVYDCYDATKVAENAELRIDPSKIFVGGDSAGGNLAAAVSIMARDSGEDFIKHQILIYPVNVFAP
PSLLEFGEGLWILDQKIMSWFSEQYFSREEDKFNPLASVIFADLENLPPALIITAEDPLRDEGEVFGQMLRAGVEASIVRYRGVLHGFINYYPLKAA
RDAINQIAALLVFD

>d1jjfa_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase z {Clostridium thermocellum}

SLPTMPPSGYDQVRNGVPRGQVVNISYFSTATNSTRPARVYLPYGSKKYSLVLLHGIGGSENDWFEGGGRANVIADNLIAEGKIKPLIIVTPNTN
AAGPGIADGYENFTKDLLNSLIPYIESNYSVYTDREHRAIAGLSMGGGQSFNIGLTDKFAYIGPISAAPNTYPNERLFPDGGKAAREKLKLLFIACGT
NDLIGFGQRVHEYCVANNINHVWLIQGGGHDNVWKPGLWNFLQMADEAGLTD

>d1gkla_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase y {Clostridium thermocellum}

SFKYESAVQYRPAPDSYLNPCPQAGRIVKETYTGINGTKSLNVLPYGYDPNKKYNIYLMHGGGENENTISNDVQLQNILDHAIMNGELEPLIVTP
TFNNGNCTAQNFYQEFRQNVPFVESKYSTAESTTPQGIAASRMHRGFGFAMGGLTWYVMVNCLDYVAYFMPLSGDYWGNSPQDKANSIA

EAINRSGLSKREYFVFAATGSEDIAYANMNPQIEAMKALPHFDYTSDFSKGNFYFLVAPGATHWWGYVRHYIYDALPYFFHELEHHHHHH

>d1f0na_c.69.1.3 (A:) Antigen 85b {Mycobacterium tuberculosis}

SRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYYQSGLSIVMPVGGQSSFYSDWSPACGKAGCQTY
KWETFLTSELQPWLSANRAVKPTGSAAIGLMSAGSAMILAAYHPQQFIYAGLSALLPSQGMGPMPLIGLAMGDAGGYKAADMVGPPSDPAWE
RNDPTQQPKLVANNTRLWVYCGNGTPNELGGANIPAEFLENFVRSSNLKFQDAYNAAGGHNAVFNFPNGTHSWEYWGQLNAMEKGDLQSSL
GAG

>d1dqza_c.69.1.3 (A:) Antigen 85c {Mycobacterium tuberculosis}

RPGLPVEYLQVPSPASMGRDIKVQFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEWYYQSGLSIVMPVGGQSSFYTDWYQPSQSNGQNYTYKW
ETFLTREMPAWLQANKGVSPGTGNAAVGLSMGGSLALIAAYPQQFPYAASLSGFLNPSESWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKR
NDPMVQIPRLVANNTRIWVYCGNGTPSDLGGDNIPAKFLEGTLRTNQTFRDTYADGGRNGVFNFPPNGTHSWPYWNEQLVAMKADIQHVLN
G

>d1ju3a2 c.69.1.21 (A:5-351) Bacterial cocaine esterase N-terminal domain {Rhodococcus sp. mb1}

NYSVASNVMPMRDGVRLAVDLYRPDADGPVPVLLVRNPYDKFDVFAWSTQSTNWLEFVRDGYAVVIQDTRGLFASEGEFVPHVDEADAEDTL
SWILEQAWCDGNVGMFGVSYLGVQTQWQAAVSGVGGLKAIAPSMASADLYRAPWYGGPGALSVEALLGWSALIGTGLITSRSARPEDAADFVQL
AAILNDVAGAASVTPLAQPLLGRLIPWVIDQVVDHPDNDESWQSISLFERLGLATPALITAGWYDGFVGESLRTFVAVKDNADARLVVGPWSHS
NLTRGRNADRKGIAATYPIQUEATTMHKAFFDRHLRGETDALAGVPKVRLFVMGIDEWRDETGW

>d1qfma2 c.69.1.4 (A:431-710) Prolyl oligopeptidase, C-terminal domain {Pig (Sus scrofa)}

DASDYQTVQIFYPSKDGTKIPMFIVHKKGIKLDGSHPAFLYGGGFNISITPNYSVSRLIFVRHMGGLAVANIRGGGEYGETWHKGGLANKQNCDF
DFQCAAELYIKEGTSPKRLLTINGGSNGGLLVATCANQRPDLFGCVIAQVGVMMDMLKFHKYTIGHAWTTDYGCSDSKQHFEWLKYPLHNVKLPEA
DDIQYPSMILLTADHDDRVVPLHSLKFIATLQYIVGRSRKQNNPLLIHVDTKAGHGAGKPTAKVIEEVSDMFAFIARCLNIDWIP

>g1wht.1 c.69.1.5 (A;B:) Serine carboxypeptidase II {Wheat (Triticum vulgaris)}

GHAADRIARLPGQPAVDFDMYSGYITVDEGAGRSLFYLQEAPEDAQPAPLVLWLNGGPGCSSVAYGASEELGAFRKPRGAGLVLNEYRWNKVAN
VLFLDSPAAGVGFSYNTSSDIYTSVDNRTAHDSAFLAKWFERPHYKYRDFYIAGESYAGHYVPELSQLVHRSKNPVINLGFMVGNGLIDDYHDYV
GTFEFWWNHGIVSDDTYRRLKEACLHDSFIHPSPACDAATDVATAEQGNIDMYSLYTPVCNIIXSYDPCTERYSTAYNRRDVQMALHANVTGAMNY
TWATCSDTINTHWHDAPRSMPIYRELIAAGLRIWVFSGDTDADVPLATRYSIGALGLPTTSWYPWYDDQEVGGWSQVYKGLTLSVRGAGHEV
PLHRPRQALVLFQYFLQGKPMPGQ

>d1cpy__ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (Saccharomyces cerevisiae)}

KIKDPKILGIDPNTQYTGYLDVEDEKHFFFWTFESRNPDPAKDPVILWLNGGPGCSSLTGLFFALGPSSIGPDLKPIGNPYSWNSNATVIFLDQPVNV
GFSYSGSSGVNTVAAGKDVNLFELFFDQFPEVNKGQDFHIAGASYAGHYIPVFASEILSHKDRNFNLTSVLIGNGLTDPLTQNYYPEMACGEgg
EPSVLPSEECSAMEDSLERCLGLIESCYDSQSVCVPATIYCNAQLAPYQRTGRNVYDIRKDCEGGNLCYPTLQDIDDLNQDYVKEAVGAEVDH
YESCNFDINRNFLFAGDWMKPYHTAVTDLNQDLPILVYAGDKDFICNWLGNKAWTDVLPWKYDEFASQKVNRWTASITDEVAGEVKSYKHFTY
RVFNGGHMVPFDVPENALSMVNEWIHHGGSF

>d1ac5__ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (Saccharomyces cerevisiae), kex1(delta)p}

LPSSEEEYKVAYELLPGLEVPDPNSNIPQMAGHIPLRSEADEQDSSDLEYFFWFKFTNNDSNGNVDRPLIWLNGGPGCSSMDGALVEGPFRVNS
DGKLYLNEGWSISKGDLLFIDQPTGTGFSVEQNKKDEGKIDKNKFDEDLEDVTKHFMDFLENYFKIFPEDLTRKIIISGESYAGQYIPFFANAILHNHNFsk
IDGDTYDLKALLINGWIDPNTQSLSYLPFAMEKKLIDESNPNFKHLTNNAHENCQNLINSASTDEAAHFSYQECEPINLNLSSYTRESSQKGTADCLNM
YNFNLKDSYPSCGMNWPKDISFVSKFFSTPGVIDSLHLDSDKIDHWKECTNSVGTKLSPNPKSIHLLPGLLESGIEIVLFNGDKDLICNNKGVLDTID
NLKWWGGIKGFSDDAVSFDWIKHSKSTDSEEFSGYVKYDRNLTVFVSYNASHMVPFDKSLVSRGIVDIYNSNDVMIIDNNNGKNVMITT

>d1ivya_c.69.1.5 (A:) Human 'protective protein', HPP {Human (Homo sapiens)}

APDQDEIQLPGLAKQPSFRQYSGYLKSSGSKHLHYWFVESQKDPENSPVVLWLNGGPGCSSLDGLLTEHGPFLVQPDGVTEYNPYSWNLIANVLY
LESPAGVGFSYDDKFYATNDTEVAQSNFEALQDFRLPEYKNNKFLTGESYAGIYIPTLAVLVMQDPSMNQGLAVGNGLSSYEQNDNSLVFAYY
HGLLGNRLWSSLQTHCCSNKCNFYDNKDLCEVTNLQEVARIVGNSGLNIYNLYAPCAGGVPSSHFRYEKDTVVQDLMNIFTRLPLKRMWHQALLR
SGDKVRMDDPCTNTTASTYLNPNYVRKALNIPEQLPQWDMCNFLVNLQYRRLYRSMNSQYKLSSSQKYQILLYNGDVMACNFMGDEWFVDS
LNQKMEVQRRPWLVKGDSGEQIAGFVKEFShIAFLTIKGAGHMVPTDKPLAFTMFSRFLNKQPY

>d1hlga_c.69.1.6 (A:) Gastric lipase {Human (*Homo sapiens*)}

SPEVTMNSIQMITYWGPNEEYEVTEDGYILEVNIRPYGKNSGNTQRPVFLQHGLLASATNWISNLPNNSLAFILADAGYDVWLGNRGNT
WARRNLYYSPDSVEWFASFDEMAKYDLPATIDFIVKKTGQKLYHGVSQGTTIGFIAFSTNPSLAKRIFTYALAPVATVKYTSLINKLRFVPQSLFK
FIGDKIFYPHNFFDQFLATEVCSCREMLNLLCSNALFIICGFDKSNFTSRLDVYLSHNPGTSVQNMFHWTQAVKGKFQAYDWGSPVQNRMHYD
QSQQPPYYNTAMNVPIAVWNGKDLLADPQDVGLLPKLPNLIYHKEIPFYNHLDIFIAMDAPQEYNDIVSMISEDKK

>d1azwa_c.69.1.7 (A:) Proline iminopeptidase {Xanthomonas campestris, pv. citri}

MRTLYPEITPYQQGSLKVDDRHTLYFEQCGNPHGKPVMLHGGPGGCNDKMRFRHDPAKYRIVLFDQRGSGRSTPHADLVNTTWDLVADIER
LRTHLGVDRWQVFQGSWGSTLALAYAQTHPQQVTELVRGIFLRRFELEWFYQEGASRLFPDAWEHYLNAIPPVERADLMSAFHRRLTSDDEATRL
AAAKAWSVWEGETSFHLVDEDFTGHEDAFAFARIENHYFVNGGFEVEDQLLRDAHRIADIPGVIVHGRYDVVCPLQSAWDLHKAWPKAQL
QISPASGHSAFEPEVNDAVLVRATDGFA

>d1qtra_c.69.1.7 (A:) Proline iminopeptidase {Serratia marcescens}

LRGLYPPLAAYDSGWLDTGDGHRIWELSGNPNGKPAVFIHGGPGGGISPHRQLFDPERYKVLFDQRGCGRSRPHASLDNNNTWHLVADIERL
EMAGVEQWLVFQGSWGSTLALAYAQTHPERVSEMLRGIFTLRQRLHWYYQDGASRFFPEKWERVLSILSDDERKDVIAYRQRILTSADPQVLE
AAKLWSVWEGETVTLLPSRESASFGEDDFALAFARIENHYFTHLGFLESDDQLLRNVPLRHIPAVIVHGRYDMACQVQNAWDLAKAWPEALHIVE
GAGHSYDEPGILHQMLIATDRFAGK

>d1b6g_c.69.1.8 (-) Haloalkane dehalogenase {Xanthobacter autotrophicus}

MVNAIRTPDQRFSNLQYPFSPNYLDDLPGYPGPLRAHYLDEGNSDAEDVFLCLHGEPTWSYLYRKMIPIVFAESGARVIAPDFFGFKSDKPVDEEDY
TFEFHRNFLLALIERDLRNITLVQDWGGLGLTPMADPSRFKRLLIMNACLMTDPVTQPAFSAVTQPADGFTAWKYDLVTPSDLRLDQFMKRW
APLTTEAEASAYAAPFPDTSYQAGVRKFPKMVAQRDQACIDISTEISFWQNDWNGQTMAIGMKDKLLGPDVMYPMKALINGCPELEIADAGH
FVQEFGEQVAREALKHFAETE

>d1bn7a_c.69.1.8 (A:) Haloalkane dehalogenase {Rhodococcus sp.}

IGTGFPFDPHYVEVLGERMHYDVGPRDGTVFLHGNPNTSSYLWRNIIIPHVAPSHRCIAPDLIGMGKSDKPDLYFFDDHVRYLDAFIEALGLEEVV
LVIHDWGSALGFHWAKRNPERVKGIACMEFIRPIPTWDEWPEFARETQAFRTADVGRELIIDQNAFIEGVLPKCVVRPLTEVMDHYREPFLKPD
REPLWRFPNEPIAGEPANIVALVEAYMNWLHQSPVPKLLFWGTPGVLIPIAAEALRASELPNCKTVDIGPLHYLQEDNPDLIGSEIARWLPGLA

>d1cv2a_c.69.1.8 (A:) Haloalkane dehalogenase {Sphingomonas paucimobilis, UT26, LinB}

GAKPFGEKKFIEIKGRRMAYIDEGTGDPILQHGHPNTSSYLWRNIMPHCAGLGRLIACDLIGMGDSDKLDPGSPERYAYAEHRDYLDALWEALDLGD
RVVLLVHDWGSALGFDWARRHRERVQGIAYMEAIAMPIEWADFPEDQFQAFRSQAGEELVLDQNVFVEQLPGLILRPLSEAEMAAYREPFL
AAGEARRPTLSWPRQJPIAGTPADVVAIARDYAGWLSESPIPKLFINAEPGALTTGRMRDFCRTWPQNQTEITVAGAHFIQEDSPDEIGAAIAAFVRR
RPA

>d1din_c.69.1.9 (-) Dienelactone hydrolase {Pseudomonas sp., B13}

MLTEGISIQSYDGHFTGALVGSPA KAPAPVIVIAQEIFGVNAFMRETVSWLVDQGYAAVCPDLYARQAPGTALDPQDERQREQAYKLWQAFDMEAG
VGDLLEAIRYARHQPSNGKVGVLGYALGGALAFLVAAGYDRAVGGYVGLEKQLNKVPEVKHPALFHMGGQDHFVAPSRQLITEGFGANPLL
QVHWYEEAGHSFARTSSGYVASAAA LANERTLDFLAPLQS

>d1c4xa_c.69.1.10 (A:) 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (BPHD) {Rhodococcus sp., strain rha1}

TVEIIKRFPSGTASHALVAGDPQSPAVLLHGAGPGHAASNWRPIIPDLAENFFVAPDLIGFGQSEYPETYPGHIMS WVGMRVEQILGLMNHF
GIEKSHIVGNSMGGAVTLQLVVEAPERFDKVALMGSGVAPMNARPPELARLLAFYADPRLTPYRELIHSFVYDPENFFGMEEIVKSREFEVANDPEVR
RIQEVMFESMKAGMESLVPPATLGLP HDVLVHGRQDRIVPLDTSLYLT KHLKHAELVLDRCGHWAQLERWDAMGPMLMEHFRA

>d1ek1a2_c.69.1.11 (A:226-544) Mammalian epoxide hydrolase, C-terminal domain {Mouse (*Mus musculus*)}

LPVPCNPNDVSHGYTVKPGIRLFVEMGSGPALCLCHGFPESWFSWRYQIPALAQAGFRVLAIDMKGYGDSSPPEIEYAMELLCKEMVTFLDKL
GIPQAVFIGHDWAGVMVWNMALFYPERVRAVASLNTPFMPPDPDVS PMKVI RSI PVFN YQLYFQEPGVAEAELEKNMSRTFKSFRASDETGFIAV
HKATEIGGILVNTPEDPNLSKITTEEEIEFYIQQFKKTGFRGPLNWYRNTERNWKWSCKGLRKILVPA LMVTAEKDIVLRPEMSKNMEKWIPFLKG
HIEDCGHWTQIEKPTEVNQILIKWLQTE

>d1ehya_c.69.1.11 (A:) Bacterial epoxide hydrolase {Agrobacterium radiobacter}

AIRRPEDFKHYEVQLPDVKIH VREGAGPTLLLHGWP GFWWEWSK VIGPLAEHYDVIVPDLRGFGDSEKPD LNDLSKYSLKAADDQA ALD ALG

IEKAYVVGHDFAAIVLHKFIRKYSDRVIAAAIFDPIQPDFGPVYFGLGHVHESWYSQFHQLDMAVEVGSSREVCKYFKHFFDHWSYRDELLTEEELE
VHVNDNCMKPDNIHGGFYRANIRPDAALWTLDHTMSDLPVTMIWGLGDTCPYAPLIEFVPKYNSYTMETIEDCGHFLMVEKPEIAIDRIKTA
FR

>d1qo7a_c.69.1.11 (A:) Bacterial epoxide hydrolase {Aspergillus niger}

KAFAKFPSSASISPNTVSIPDEQLDDKLTLVRLSKIAPPYTESLQADGRFGITSEWLTTMREKWLSFEDWRPFEARLNFPQTTEIEGLTIHFAALFSE
REDAVPIALLHGWPGBVEFYPILQLFREYEYTPETLPFHVVPSLPGYTFSGGPPPLDKDFGLMDNARVVDQLMKDLGFGSGYIIQGGDIGSFVGRLLGV
GFDACKAVHLNLCAKRAPPGEPSIESLAAKEGIARMKFTDGLAYAMEHSTRPSTIGHVLSSPIALLAWIGEKYLQWVDKPLPSETILEMVSLY
WLTESTFPRAIHTYRETTPTASAPNGATMLQKELYIHKGFSFFPKDLCVPVRSWIATTGNLVFFRDHAEGGHFAALERPRELKTDLTAFVEQVW

>d1brt_c.69.1.12 (-) Bromoperoxidase A2 {Streptomyces aureofaciens}

PFITVGQENSTSIDLYYEDHGTGQPVLIHGFPPLSGHSWERQSAALLDAGYRVITYDRRGFGQSSQPTGYDYDTFAADLTVLETLDLQDAVLVGS
TGTGEVARYVSSYGTARIKVAFLASLEPFLKTDNDNPDGAAPQEFDGIVAAVKADRYAFYTFNDFYNLDENLGRTRISEEAVRNSWNTAASGGFF
AAAAAPTTWYTDFRADIPRIDVPALILHGTGDRTLPIENTARVFHKALPSAEYVEVEGAPHGLWTHAEEVNNTALLAFLAK

>d1a8q_c.69.1.12 (-) Bromoperoxidase A1 {Streptomyces aureofaciens}

PICTTRDGVEIFYKDWGQGRPVVFIHGWPNGDAWQDQLKAVV DAGYRGIAHDRRGHGHSTPVWDGYDFDTFADDLNDLTLDRDVTLVAH
SMGGELARYVGRHGTGRLRSAVLLSAIPPVMIKSDKNDPDPVDEVFDALKNGVLTTERSQFWKDTEGFFSANRPGNKVTQGNKDAFWYMAMA
QTIEGGVRCVDAFGYTDFTEDLKFDIPTLVHGDDQQVPIATGRKSAQIIPNAELKVYEGSSHGIAMVPGDKEKFNRDLLEFLNK

>d1a88a_c.69.1.12 (A:) Chloroperoxidase L {Streptomyces lividans}

GTVTSDDGTNIFYKDWGPRDGLPVFFHGWPALSADDWDNQMLFLSHGYRVIADRRGHGRSDQPSGNDMDTYADDLAQIEHLDLRDAVLF
GHSTGGGEVARYVARAEPGRVAKAVLVAVPPVMVKSDTNPDGLPLEVDEFRAALAANRAQFYIDVPSGPYGFNREGATVSQGLIDHWLWQG
MMGAANAHYCIAAFSETDFTDDLKRIDVPVLVAHGDDQVVPYADAAPKSAELLANATLKSYEGLPHGMLSTHPEVLPNDLLAFVKS

>d1a8s_c.69.1.12 (-) Chloroperoxidase F {Pseudomonas fluorescens}

TTFTTRDGQTQIYKDWGSGQPIVFSHGWPNALDWESQMFIAAQGYRVIADRRGHGRSSQPSGNDMDTYADDLAQIEHLDLRDAVLF
TGGGEVARYGRHGTARVAKAGLISA VPLMLKTEANPGGLPMEVFDGIRQASLADRSQLYKDLASGPFFFNQPGAKSSAGMVDFWFWLQGMA
AGHKNAYDCIKAFSETDFTEDLKIDVPTLVHGDDQVVPYADAAPKSAELLANATLKSYEGLPHGMLSTHPEVLPNDLLAFVKS

>d1thta_c.69.1.13 (A:) Myristoyl-ACP-specific thioesterase {Vibrio harveyi}

QCKTIAHVLRVNNQELHVWETPPKENVPFKNNTLIASGFFARRMDHFAGLAEYLSTNGFHVFRYDSLHHVGLSSGSI
DEFTMTGKNSLCTVYHW
LQTKGQTQNIGLIAASLSARVAYEVISDLESLFLITAVGVVNLRTDLEKALGFYLSLPIDELPNLDLFEHGKLGSEVFVRDCFEHHWDTLDSTLDKVANTS
VPLIAFTANNDDWWVKQEEVYDMLAHIRTGHCKLSSLLGSHDLDGENLVLRNFYQSVTKAIAAMDGGSLEIDVDFIEPDEQLTIATVNERRLKAEIEN
RTPEMA

>d1ei9a_c.69.1.13 (A:) Palmitoyl protein thioesterase 1 {Cow (Bos taurus)}

DPPAPLPLVWHGMGDSCCNPLSMGAIKKMVEKKIPGIHVSLEIGTLREDVENSFLNVNSQVTVCQILAKDPKLQQGYNAMGFSQGGQFLRA
VAQRCPSPPMVNLISVGGHQHGQVFGLPRCPGESSHICDFIRKTLNAGYNAKIQERLVQAELYWDPIREDIYRNHSIFLADINQERGVNESYKKNL
ALKKFVFMVKFLNDTIVDPDSEWFGFYRSGQAKETIPLQESTLYTQDRLGLKAMDKAGQLVFLALEGDLQLSEEWFYAHIIPLF

>d1auoa_c.69.1.14 (A:) Carboxylesterase {Pseudomonas fluorescens}

MTEPLILQPAKPADACVIWLHGLGADRYDFMPVAEALQESLLTRFVLPQAPTRPVTINGGYEMPSWYDIKAMSPARSISLEELEVSAKMVTDLIEAQ
KRTGIDASRIFLAGFSQGGAVVFHTAFINWQGPLGGVIALSTYAPTFGDELELSASQQRIPALCLHGQYDDVVQNAMEGRSAFEHLKSRGVTVTW
YPMGHEVLPQEIHDIGAWLAARLG

>d1fj2a_c.69.1.14 (A:) Acyl protein thioesterase 1 {Human (Homo sapiens)}

MDPEFMSTPLPAIVPAARKATAAVIFLHGLGDTGHWAEEAFAGIRSSHIFYCIPHPVPRVTLNMNVAMPSWF DIIGLSPDSQEDESGIKQAAENIK
ALIDQEVKNGIPSNRIILGGFSQGGALSLYTALTTQQKLAGVTALSCWLPLRASFPQGPPIGGANRDISILQCHGDCDPLVPLMFGSLTVEKLKTLVNPAN
VTFKTYEGMMHSSCQQEMMDVKQFIDKLLPI

>d1qlwa_c.69.1.15 (A:) A novel bacterial esterase {Alcaligenes sp.}

VPKTPAGPLTSGQGSFFVGGRDVTSSETLSLSPKYDAHGTVDQMYVRYQIPQRACKRYPITLIHGCCLTGMTWETPDGRMGWDEYFLRKYSTY
VIDQSGRGRSATDISAINAVKLKAPASSPLDFAAGHEAAWAIFRFGPRYPDAFKDTQFPVQAQAEWLQQMVPDWLGSMPNPTVANLSKLAIK

LDGTVLLSHSQSGIYPFQTAAMNPKGITAIVSVEPGECPKPEDVKPLTSIPVLVFGDHIEEPRWAPRLKACHAFIDALNAAGGKGQLMSLPALGVH
GNSHMMMQDRNNLQVADLILDWIGRNTA

>d1jfra__ c.69.1.16 (A:) Lipase {*Streptomyces exfoliatus*}

NPYERGPAPTNASIEASRGPYATSQTSVSSLVASGFGGTIYYPSTADGTFGAVVISPGFTAYQSSIAWLGPLASQGFVVFTIDNTTLQDQPDSRGRQ
LLSALDYLTQRSSVRTRVDATRLGVMGHSMGGGSLEAAKSRTSLKAIPLGWNTDKTWPRLRTPTLVVGADGDTAVPATHSKPFYESLPGSLDK
AYLELRGASHFTPNTSDTTIAKYSISWLKRFDSDTRYEQFLCPIPRPSLTIAEYRGTCPHTS

>d1tca__ c.69.1.17 (-) Triacylglycerol lipase {*Candida antarctica*, form b}

LPSGSDPAFSQPKSVLDAGLTCQGASPSSVSKPILLVPGTGTGPQSFDSNWPLSTQLGYTPCWISPPFMNDTQVNTEYMVNAITALYAGSGNNK
LPVLTWSQGGLVAQWGLTFFPSIRSKVDRMAFAPDYKGTVLAGPLDALAVSAPSWSQQTGSALTTALRNAGGLTQIVPTTNLYSATDEIVQPQVS
NSPLDSSYLNGKNVQAQAVCGPLFVIDHAGSLTSQFSYVGRSALRSTTGQARSADYGITDCNPLPANDLTPEQKVAAAALLAPAAAAIVAGPKQN
CEPDLMMPYARPAVGKRTCSGIVTP

>d3tgl__ c.69.1.17 (-) Triacylglycerol lipase {*Rhizomucor miehei*}

GIRAATSQEINELTYTTLSANSYCRTVPGATWDCIHCDATEDLKIITWSTLIYDTNAMVARGDSEKTIYIVFRGSSSIRNWIADLTFPVSYPPVSGTK
VHKGFLDSYGEVQNELVATVLDQFKQYPSYKVAVTGHSLGGATVLLCALDLYQREEGLSSNLFLYTQGQPRVGDPAFANYVSTGIPYRRTVNERDIV
PHLPPAAGFLHAGEEYWIDNSPETVQVCTSLETSDCSNSIVPFTSVLDHLSYFGINTGLCT

>d1tia__ c.69.1.17 (-) Triacylglycerol lipase {*Penicillium camembertii*}

DVSTSELDQFEFWVQYAAASYEADYTAQVGDKLSCSKNCPEVEATGATVSYDFSDSTITDTAGYIAVDHTNSAVVLAFRGSYSVRNWADATFVH
TNPGLCDGCLAELGFWSSWKLVRDDIIKELKEVVAQNPNEYELVVGHSGLGAAVATLAATDLRGKGYPASKLYASPRVGNAALAKYITAQGNFRFT
HTNDPVPKLPLLSMGYVHVSPEYWITSPNNATVTS DIKVIDGDSFDGNTGTGLPLTDFEAHIWYFVQVDAGKG

>d1tib__ c.69.1.17 (-) Triacylglycerol lipase {*Thermomyces (Humicola) lanuginosus*}

EVSQDLFNQFNLAQYSAAYCGKNNDAAGTNTCTGNACPEVEKADATFLYSFEDSGVGDVGTGFLALDNTNKLIVLSFRGSRSIENWIGNLNFDLK
EINDICSGCRGHDGFTSSWRSVADTLRQVEDAVERHPDYRVFTGHSLGGALATVAGADLRGNGYDIDVFSYGA PRVGNAFAEFLTVQTGGTLYR
ITHTNDIVPRLPPREFGYSHSSPEYWIKGTLVPVTRNDIVKIEGIDATGGNNQPNIPDIPAHLYWYFGLIGTCL

>d1lgya__ c.69.1.17 (A:) Triacylglycerol lipase {*Rhizopus niveus*}

KVVAATTAAQIQEFTKYAGIAATAYCRSVVPGNKWDCVQCQKWVPGKIIITFTSLLSDTNGYVLRSDKQKTIYLFRGTSFRSAITDIVFNFSDYKPVK
GAKVHAGFLSSYEQVNVDFPVVQEQLTAHPTYKVIVTGHSLGQAALLAGMDLYQREPLSPKNLISFTVGGPRVGNPTFAYYVESTGIPFQRTVHK
RDIVPHVPPQSFGFLHPGVESWIKSGTSNVQICTSEITKDCNSIVPFTSILDHLSYFDINEGSCL

>d1thg__ c.69.1.17 (-) Type-B carboxylesterase/lipase {*Fungus (Geotrichum candidum)*, ATCC 34614}

EAPTAVLNGNEVISGVLEGKVDTFKGIPFADPPLNDRFKHPQFTGSYQGLKANDFSPACMQLDPGNSLTLLDKALGLAKVPEEFRGPLYDMAKGT
VSMNEDCLYLNVRPAGTKPDAKLPVMWVYIGGAFVYGSAAYPGNSYVKE SINMGQPVFVSINYRTGPFGFLGDDAITAEGNTNAGLHDQRKG
LEWVSDNIANFGGDPDKVMIFGESAGAMSVAHQLIAYGKDNTYNGKKLFHSAILQSGGFLPYHDSSVGPDISYNRFAQYAGCDSASANDTLECL
RSKSSVSLHDAQNSYDLKDLFGLLPQFLGPRPDGNIIPDAAYELFRSGRYAKV PYISGNQDEGTAFAPVALNATTPHVKKWLQYIFYDASEASIDR
VLSLYPQTLSVGSPFRTGILNALTPQFKRVAAILSDMLFQSPRRVMLSATKDVNRWTYLSTLHNLPFLGTFHGNELIFQFNVNIGPANSYLRFISFA
NHHDPNVGTNLLQWDQYTDEGKEMLEIHMTDNVMRTDDYRIEGISNFETDVNLYG

>d1lpp__ c.69.1.17 (-) Type-B carboxylesterase/lipase {*Fungus (Candida rugosa)*, formerly Cylindracea}

APTA LANGDTITGLN AII NEAFLGIPFAEPPVGNLRFKDPV PVYSGSLDGQKFTSYGPSCMQQNPEGTYEENLPKAALDLVMQSKVFEAVSPSEDCLT
IN VVRPPGT KAGANLPVMLWIFGGGFEVGGTSTFPPAQMITKSIAMGKPIIHSVNVYRVS SWGFLAGDEIKAEGSANAGLKDQRLGMQWVADNIA
AFGGDPTKVTIFGESAGSMSVMCHI LWNDGDNTYKGKPLFRAGIMQSGAMVPSDAV DGIY GNEIFDLLASNAGCGSASDKLACLRGVSSDTLEDA
TNNTPGFLAYSSLRLSYLPPDGVNITDDMYALVREGKYANIPVIIGDQNDEGTFFGTSSLNVTDAQAREYFKQSFVHASDAEIDLMTAYPGDITQG
SPFDTGILNALTPQFKRISA VGLDLGFTLARRYFLNHYGGTKYSFLSKQLSGLPVLT FHNSNDIVFQDYL LGSGSLIYNNAFIAFATDLPNTAGLLVKW
PEYTSSSQSGNNLMMIN ALGLYTGKDNFR TAGYDALFSNPPSFFF

>d1clea__ c.69.1.17 (A:) Type-B carboxylesterase/lipase {*Candida cylindracea*, cholesterol esterase}

APTA LANGDTITGLN AII NEAFLGIPFAEPPVGNLRFKDPV PVYSGSLDGQKFTSYGPSCMQQNPEGTYEENLPKAALDLVMQSKVFEAVLPQSEDCL
TIN VVRPPGT KAGANLPVMLWIFGGGFEVGGTSTFPPAQMITKSIAMGKPIIHSVNVYRVS WGFLAGDDIKAEGSGNAGLKDQRLGMQWVADN

IAGFGGDPSKVTIFGESAGSMSVLCHLIWNGDNTYKGKPLFRAGIMQSGAMVPSDPVDGTYGNEIYDLFVSSAGCGSASDKLACLRSASSDTLLDA
TNNTPGFLAYSSLRLSYLPRPDGKNITDDMYKLVRDGKYASVPVIIGDQNDEGTVGFLSSLNVTNAQARAYFKQSFHISDAEIDLMAAYPQDITQ
GSPFDTGIFNAITPQFKRISAVLGLDAFIHARRYFLNHFQGGTKYSFLSKQLSGLPIMGTFHANDIVWQDYLLGSMSVIYNNAFIAFATDLDPTAGLLV
NWPKYTSSSQSGNNLMMINALGLYTGKDNRFTAGYDALMTNPSSFFV

>d1i6wa_c.69.1.18 (A:) Lipase A {Bacillus subtilis}

HNPPVMVHGIGGASFNFAGIKSYLSQGWSRDKLYAVDFWDKTGTNYNNGPVLSRFVQVKLDETGAKVDIVAHSMGGANTLYYIKNLDDGNKV
ANVVTLGGANRLTGKALPGTDPNQKILYTSIYSSADMIVMNYLSRLDGARNVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN

>d4lipd_c.69.1.18 (D:) Lipase {Burkholderia cepacia (formerly Pseudomonas cepacia)}

DNYAATRYPIILVHGLTGTQYAGVLEYWYGIQEDLQQRGATVYVANLSGFQSDDGPNGRGEQLLAYVKTVAATGATKVNVLVGHSGQGLTSRYVAA
VAPDLVASVTITGTPHRGSEFADFVQGVLAYDPTGLSSTVIAAFVNFGILTSSNNNTNQDALAALKLTQAATYNQNYPASGLGAPGSCQTGAPT
ETVGGNTHLLYSWAGTAIQPTISVFGVTGATDTSTIPLVDPANALDPSTLAFLGTGTVMVNRSGSGQNDGVSKCSALYGQVLSTSJKWNHLDEINQL
LGVRGANAEDPVAVIRTHANRLKLAGV

>d1ex9a_c.69.1.18 (A:) Lipase {Pseudomonas aeruginosa}

STYTQTKPIVLAHGMLGFDNILGVYWFIPSALARLDRGAQVYVTEVSQLDTSEVRGEQLLQQVEEIVALSGQPKVNIGHSHGGPTIRYAAVRPDL
IASATSGVAPHKGSDTADFLRQIPPGSAGEAVLSGLVNSLGALISFLSSGSTMQNSLGSLESNSEGARFNAKYPQGIPTSACGEGAYKVNGVSY
WSGSSPLTNFLDPSDAFLGASSLTFKNGTANDGLVGTCSHLGMVIRDNYRMNHLDENQVFGLTSFETSPVSYRQHANRLKNASL

>d1cvt_c.69.1.18 (-) Lipase {Chromobacterium viscosum}

ADTYAATRYPVILVHGLAGTDKFANVVDYWYGIQSDLQSHGAKVYVANLSGFQSDDGPNGRGEQLLAYVQVLAATGATKVNIGHHSQGGLTSRYV
AAVAPQLVASVTITGTPHRGSEFADFVQDVLTDPGLSSTVIAAFVNFGTLVSSHNTDQDALAALRTTAAQATYNRNFPASGLGAPGSCQTGA
ATETVGGSQHLLYSWGGTAIQPTSTVGLVTGATDTSTGTLDVANVTDPSTLALLATGAVMINRASGQNDGLVSRCSLFGQVISTSYHWNHLDEINQ
LLGVRGANAEDPVAVIRTHVNRLKLQGV

>d1hpla2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Horse (Equus caballus)}

NEVCYERLGCFSDDSPWAGIVERPLKILPWSPKDVTRFLYTNENPDNFQEIVADPSTIQSSNFNTGRKTRIIHGFIDKGEESWLSTMCMQNMFKVE
SVNCICVDWKGSRTAYQSASNQVRIVGAEVAYLVGVLQSSFDYSPSNVHIGHSLGSHAAGEAGRRTNGAVGRITGLDPAEPCFQGTPELVRLDPSD
AQFVDVIHTDIAPFIPNLGFGMSQTAGHLDFFPNGGKEMPGCQKNVLSQIVDIDGIWQGTRDFAACNHLRSYKYYTDSILNPDGFAGFPCASYSDF
ANKCFPCSEGPQMQGHYADRFPGRKTGVGQLFYLNTGDASNFA

>d1etha2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Pig (Sus scrofa)}

SEVCFPRLGCFSDDAPWAGIVQRPLKILPWSPKDVTRFLYTNQNQNQNYQELVADPSTITNSNFRMDRKTRIIHGFIDKGEEDWLSNICKNLFKVE
SVNCICVDWKGGSRGTQASQNIHVGAEVAYFVEVLKSSLGSPSNVHIGHSLGSHAAGEAGRRTNGTIERITGLDPAEPCFQGTPELVRLDPSD
KFVDVIHTDAAPIPNLGFQMSQTVGHLDFPNNGKQMPGCKNQILSQIVDIDGIWEGTRDFAACNHLRSYKYYTDSILNPDGFAGFPCDSYNVFTA
NKCFPCPSEGPQMQGHYADRFPGKTNQVSVQFYLNTGDASNFA

>d1lpbb2 c.69.1.19 (B:1-336) Pancreatic lipase, N-terminal domain {Human (Homo sapiens)}

KEVCYERLGCFSDDSPWSGITRPLHILPWSPKDVTRFLYTNENPNNFQEVADSSISGSNFNKRTRIIHGFIDKGEENWLANVCKNLFKVES
VNCICVDWKGGSRGTQASQNIHVGAEVAYFVEFLQSAFGYSPSNVHIGHSLGSHAAGEAGRRTNGTIGRITGLDPAEPCFQGTPELVRLDPSD
KFVDVIHTDGAPIPNLGFQMSQTVGHLDFPNNGKQMPGCKNQILSQIVDIDGIWEGTRDFAACNHLRSYKYYTDSIVNPDGFAGFPCASYNVFTA
ANKCFPCPSEGPQMQGHYADRFPGKTNQVSVQFYLNTGDASNFA

>d1gpl_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain {Guinea pig (Cavia porcellus)}

AEVCYSHLGCFSDEKPWAGTSQRPIKSLPSDPKKINTRFLYTNENQNSYQLITADIKASNFNLRKTRIIHGFIDKGEENWLLDMCKNMFQVE
KVNCICVDWKGGSKAQYSQASQNIHVGAEVAYLVQVLSTSINYAPENVHIGHSLGAHTAGEAGKRLNGLVGRITGLDPAEPCFQDTPPEEVRLDPSD
AKFVDVIHTDISPILPSLGFQMSQKVGHMDFFPNNGKDMMPGCKTGISCNHHRSIEYYHSSILNPEGFLGYPACASYDEFQESGCPACKGCPKMGHF
ADQYPGKTNNAVEQTFFLNTGASDNFT

>d1rp1_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain {Dog (Canis familiaris)}

KEVCYEQIGCFSDAEPWAGTAIRPLKLPWSPERIGTRFLYTNKNPNNQFTLLPSDPSTIGASNFQTDKTRIIHGFIDKGEENWLLDMCKNMFKV
EEVNCICVDWKKGQSQTSYTQAANNVRVVGQAQMMSMLSANYSYSPSQVQLIGHSLGAHVAEGASRTPLGRITGLDPVEASFQGTPPEEVRLD

PTDADFDVVIHTDAAPLIPFLFGFTSQQMGGHLDFFNGGEEMPGCKKNALSQIVDLDGIWEGTRDFACNHLRSYKYYSESILNPDGFAFASYPCASYR
AFESNKCFPCPDQGCPQMGHYADKFAQKYFLNTGDSSNFA

>d1bu8a2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Rat (*Rattus norvegicus*)}

KEVCYGHLCFSNDKPWAGMLQRPLKIFPWSPEDIDTRFLLYTNENPNNYQKISATEPDTIKFSNFQLDRKTRFIVHGFIDKGEDGWLLDMCKMFQ
VEVKNCICWDWRRSGSRTETYQASYNTRVVGAELFLVQLSTEMGYSPEVNHLIGHSLGAHVGEAGRRLEGHVGRTGLDPAEPCFQGLPEEVRLD
PSDAMFVDVIHTDSAPIIPLGFGMSQKVGHLDFFNGGKEMPGCQKNILSTIVDINGIWEGTQNFACNHLRSYKYYASSILNPDGLGYPCCSYEK
FQQNDCFCPEEGCPKMGHYADQFEGKTATVEQTVYLNTGDSGNFT

>d1qj4a_c.69.1.20 (A:) Hydroxynitrile lyase {Rubber tree (*Hevea brasiliensis*)}

AFAHFVLIHTICHGAWIWHKLPLLEALGHKVTALDLAASGVDPQRQIEEIGSFDEYSEPLLTFLALPPGEKVILVGESCGGLNIAIAADKYCEKIAAAVFH
NSVLPDTEHCPSYVVDKLMEVFPDWKDFTYTKDGKEITGLKGFTLLRENLYTCGPEEYELAKMLTRKGSLFQNILAKRPFFTKEGYGSIKKIYVW
TDQDEIFLPEFQLWQIENYKPDVKYVKVEGGDHKLQLTKTKEIAEILQEVADEADTYN

>d1e89a_c.69.1.20 (A:) Hydroxynitrile lyase {Cassava (*Manihot esculenta*)}

PISKMVTAHFLIHTICHGAWIWHKLPALEGRAGHKVTALDMAASGIDPRQIEQINSFDEYSEPLLTFLKLPQGEKVIVGEACAGLNIAIAADRYVDK
IAAGVFHNSLLPDTVHSPTYVEKLLESFPDWDRTEYFTFTNITGETITMKLGFLVLLRENLFTKCTDGEYELAKMVMRKGSFQNVLARPKFTEKGY
GSIKKVVYIWTDQDKIFLPDFQRWQIANYKPDVKYQVQGGDHKLQLTKTEVAHILQEVADEADAYA

>d1keza_c.69.1.22 (A:) Erythromycin polyketide synthase {Saccharopolyspora erythraea}

SSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLVDMADGPGEVTVICAGTAISGPHEFTRLAGALRGIAPIVRAVPQPGYEEGEP
LPSSMAAVAAVQADAIVRTQGDKPFVAGHSAGALMAYALATELLDRGHPPRGVVLIDVYPPGHQDAMNAWLEELTATLFDRETVRMDDTRLAL
GAYDRLTGQWRPRETGLPTLLVSAGEPMGPWPDDSWKPTWPFEHDVTAVPGDHFTMVQEHAIAIRHIDAWLGGG

>d2masa_c.70.1.1 (A:) Inosine-uridine nucleoside N-ribohydrolase, IU-NH {Crithidia fasciculata}

AKKIILDCDPGLDDAVAILAHGNPEIELLAITTVVGNQTLAKVTRNAQLVADIAGITGVPIAGCDKPLVRKIMTAGHIHGESGMGTVAYPAEFKNKV
DERHAVNLIIIDLVMSHEPKTITLVTGGLTNIAMAARLEPRIVDRVKEVVLGGGYHEGNATSVAEFNIIIDPEAAHIVFNESWQVTMVGDLTHQAL
ATPPILQRVKEVDTNPARFMLEIMDYTKIYQSNRYMAAAAVHDPCAVAYVIDPSVMTTERVPVDIELTGKLTGMMTVADEFRNPRPEHCHTQAVKL
DFEKFWGLVLDALERIGDP

>d1ezra_c.70.1.1 (A:) Nucleoside hydrolase {Leishmania major}

PRKIILDCDPGIDDAVAIFIAGHNPEIELLAITTVVGNQSLKVTQNARLIVADAGIVGVPIVAAGCTKPLVRGVRNASHIHGETGMGNVSYPPEFKTKL
DGRHAVQLIIDLIMSHEPKTITLVTGGLTNIAMAARLEPRIVDRVKEVVLGGGYHTGNASPVAEFNVFIDPEAAHIVFNESWNVTMVGDLTHLA
LATPAVQKRVREVGTKPAAFMLQILDFTKVEYEKEHDTYGKVHDPCAVAYVIDPTVMTTERVPVDIELNGALTGMTVADFRYPRPKNCRTQAVKL
DFDKFWCLVIDALERIGDP

>d1hoza_c.70.1.1 (A:) Inosine-adenosine-guanosine preferring nucleoside hydrolase {Trypanosoma vivax}

GSAKNVLDHDGNLDDFVAMVLLASNTEKVRLIGALCTDADCFVENGFNVTGKIMCLMHNNMNPLFPIGKSAATAVNPFPKEWRCRAKNMDD
MPILNIPENVELWDKIAKENEKYEGQQLLADLVMNSEEKVTICVTGPLSVNAWCIDKYGEKFTSKVEECVIMGGAVDVRGNVFLPSTDGTAEWNIY
WDPASAKTVFGCPGLRRIMFSLDNTPVRSVPYQRFGEQTNFLLSILVGTMWAMCTHCELLRDGDGYAWDALTAAYVVDQKVANVDPVPIDV
VVDKQPNEGATVRTDAENYPLTFVARNPEAEFFLDMILLRSARAC

>d1ra9_c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Escherichia coli}

MISLIAALAVDRVIGMENAMPWNLPADLAWFKRNTLDKPVIMGRHTWEISGRPLPGRKNIILSSQPGTDDRTWVKSVDIAAACGDVPEIMVIG
GGRVYEQFLPKAQKLYLTHIDADEVEGDTHFPDYEPDDWESVFSEFHADAQNSHSYCFEILERR

>d3dfr_c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Lactobacillus casei}

TAFLWAQNRNGLIGKDGHLWHLDDLHYFRAQTVGKIMVVGRRTYESFPKRPLPERTNVVLTHQEDYQAQGAVVVHDVAAVFAYAKQHLDQEL
VIAGGAQIFTAFKDDVDTLLVTRLAGSFEGDTKMIPLNWDDFTKVSSRTVEDTNPALHTTYEVWQKKA

>d1df7a_c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Mycobacterium tuberculosis}

MVGLIWAQATSGVIGRGGDIPWRLPEDQAHFREITMGHTIVMGRRTWDSLPAVRLPGRNNVLSRQADFMASGAEVVGSLEEALTPETWVI
GGGQVYALALPYATRCEVTEVTDIGLPRREAGDALAPVLDLDETWRGETGEWRSRSGLRYRLYSYHRS

>d1d1ga_c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Thermotoga maritima}

AKVIFVLAMDVSGKIASSVESWSSFEDRKNFRKITTEIGNVVMGRITFEEIGRPLPERLNVLTRRPKTSNNPSLVFFNGSPADVVKLEGKGYERAVI
GGKTVFTEFLREKLVDLFVTVEPYVFGKGIPFFDEFEGYFPLKLEMRRRLNERGTLFLKYSVE
>d1vdra_c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Haloferax volcanii}
ELVSVAALAENRVIGRDGELPWPSSIPADKKQYRSRIADPVVLGRTTFSMRDDLPGSAQIVMSRSERSFSVDTAHRASVEEAVDIAASLDAETAYVI
GGAAIYALFQPHLDRMVLSPVGPEYEGDTYYPEWDAAEWELDAETDHEGFTLQEWR
>d8dfr_c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Chicken (Gallus gallus)}
VRSLSNSIVAVCQNMIGKGDGNLPWPPLRNESRYFQRMTTSSVEGKQNLVIMGKKTWFPSIPEKNRPLKDRINIVSRELKEAPGAHYLSKSLDDAL
ALLDSPELKSKVDMVVWVGGTAVYKAAMEKPINHRLFVTRILHEFESDTFFPEIDYKDFKLLEYPGVPADEIQEEDGIQYKFEVYQKSV
>d1hfq_c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Human (Homo sapiens)}
VGSLNCIVAVSQNMIGKNGDLPWPPLRNESRYFQRMTTSSVEGKQNLVIMGKKTWFPSIPEKNRPLKGRINLVLSRELKEPPQGAHFLSRSLDDAL
KLTEQPELANKVDMVVWVGGSSVYKEAMNHPGHLKLFVTRIMQDFESDTFFPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKFEVYEKND
>d1dyr_c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Fungus (Pneumocystis carinii)}
NQQKSLSLIVALTTSYGIRSNSLPWKLKEISYFKRVTSFVPTFESMNVVLGMRKTWEISIPLQFRPLKGRINVVITRNESLDLNGNIHSAKSLDHA
LELLYRTYGSESSVQINRIVIGGAQLYKAAMDHPKLDIMATIYKDIHCDVFFPLKFRDKEWSSVWKEKHSLESWVGTVPHGKINEDGFDYEFE
MWTRDL
>d1aoea_c.71.1.1 (A:) Dihydrofolate reductases, eukaryotic type {Yeast (Candida albicans)}
MLKPNVIAIVAAALKPALGIGYKGKMPWRLRKEIRYFKDVTRTTKPNTRNAVIMGRKTWEISIPQKFRPLPDRLNIIILRSYNEIIDNIIHASSIESLNL
VSDVERVFIIAGAEIYNELINNSLVSHLLITEIEHPSPESIEMDTFLKFPLESWTKQPKSELQKFVGDTVLEDDIKEGDFTYNYTLWTRK
>d1ekqa_c.72.1.2 (A:) Hydroxyethylthiazole kinase (THZ kinase, ThiK) {Bacillus subtilis}
MDAQSAAKCLTAIRRHSPLVHSITNNVVNTNFTANGLLALGASPVMAYAKEEVADMAKIAGALVNLIGTLSKESVEAMIIAGKSANEHGPVILDPVG
AGATPFRTESARDIIREVRЛАAIRGNAEIAHTVGVTDWLIKGVDAEAGEGGGDIIRLAQQAAQKLNTVIAITGEVDVIADTSHVTLHNGHKLLTKVTGA
GCLLTSVVGAFCAVEENPLFAAIAAISSYGVAAQLAQQTADKGPGSFQIELLNKLSTVTEQDVQE沃ATIERV
>d1jxha_c.72.1.2 (A:) 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate kinase (HMP-phosphate kinase, ThiD)
{Salmonella typhimurium}
MQRINALTIAGTDPGGAGIQADLKTFSALGAGCSCVITALVAENTCGVQSVYIEPDFVAAQLDSVFSVDIRDTKIGMLAETDIVEAVAERLQRHHV
RNVVLDTVMLAKSGDPLSPSAIETLRVRLPQVSLTPNLPEAAALLDAPHARTEQEMLAQGRALLAMGCEAVLMKGHHLEDAQSPDWLFTREGE
QRFSAPRVNTKNTHTGCTLSAALAALRPRHRSWGETVNEAKAWLSAALAQADTLEVKGIGPVHFHAWW
>d1rkd_c.72.1.1 (-) Ribokinase {Escherichia coli}
AGSLVVLGSINADHILNLQSFPTPGETVTGNHYQVAFGGGANQAVAAGRSGANIAFIACTGDDSIGESVRQQLATDNIDITPVSIVKGESTGVALIFV
NGEGENVIGHAGANAALSPALVEAQRERIANASALLMQLESPLESVMAAKIAHQNKITVALNPAPARELPDELLALVDIITPNETAEAKLTGIRVEND
EDAAKAAQVLHEKGIRTVLITLGSRGVVASVNGEGQRPGFRVQAVDTIAAGDTFNGALITALLEEKPLPEAIRFAAAAAIAVTRKGQAQPSVPWRE
EIDAFLDRQR
>d1bx4a_c.72.1.1 (A:) Adenosine kinase {Human (Homo sapiens)}
VRENILFGMGNPLLDISAVVDKDFLDKYSLKPNQDQI LAEDKHKELFDELVKKFKVEYHAGGSTQNSIKVAQWMIQQQPKAATFFGCIGIDKFGIEILRK
KAAEAHVDAHYYEQNEQPTGTCACITGDNRSLIANLAAANCYKKEHLDLEKNWMLVEKARVCYIAGFFLTVSPESVLKVAHHASENNRIFTLNLS
APFISQFYKESLMKVMPYDILFGNETEATFAREQGFETKDIKEIAKKTQALPKMNSKRQIVIFTQGRDDTIMATESEVTAFAVLDQDQKEIIDTNG
AGDAFVGGLSQLVSDKPLTECIRAGHYAASIIIRRTGCTFPKPDFH
>d1dgya_c.72.1.1 (A:) Adenosine kinase {Toxoplasma gondii}
GPMRVFAIGNPILDVVAEVPSFLDEFFLKGDATLATPEQMRIYSTLDQFNPTS LPGGSALNSVRVVKLLRKPGSAGYMGAI GDDPRGQVLKELCD
KEGLATRFMVAPGQSTGTCAVLINEKERTLC THLGACGSFRIPENWTFASGALIFYATAYTLATPKNALEVAGYAHGIPNAIFTLNSAPFCVELYKDA
MQSLLLHTNILFGNEEEFAHLAKVHNLAEEKVALSVANKEHAVEVCTGALRLTAGQNTGATKLVVMTRGHNPVIAAEQTADGTVVVHEGVGPVV
AAEKIVDTNGAGDAFVGGLYGLSQGKTVKQCIMCGNACAQDVIQHVGFSLSF
>d1gc5a_c.72.1.3 (A:) ADP-dependent glucokinase {Archaeon Thermococcus litoralis}
MKESLKDRIRLWKRLYVN AFENALNAIPNVKGVLAYNTNIDA IKYLDADDLEKRVTEK GKEKV FEEIENPPEKISSIEELGGILRSIKLGKAMEWFVSE

EVRRYLREWGWDDELIGGQAGIMANLGGVYRIPTIVHPQNPQLQAEFLVDGPIYVPVFEGNKLKVHPKDAIAEEELIHYIYFPRGFQVFVQA
PRENRFIANADDYNARVMRREFREGFEITRNVELAIISGLQLKEYYPDGTYYKDVLDRVESHLNLNRYNVKSHFEFAYTANRRVREALVELLPKFT
SVGLNEVELASIMEIIGDEELAKEVLEGHFSIDAMNVLMDETGIERIHFTYGYALALTQYRGEEVRDALLFASLAAAAMKGNLERIEQIRDALSV
PTNERAIVLEEELEKEFTEFENGLIDMVDRLQAFVPTKIVASPSTVIGDTISSAFSEFGMRKR

>d2uaga3 c.72.2.1 (A:94-297) UDP-N-acetyl muramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}

DIELFCREAQAPIAVITGSNGKSTVTLVGEMAKAAGVN VGVGGNIGLPA MLLDEC ELYVLE LSSF QLE TSSLQAVAATILNVTEDHMDRYPFGLQ
QYRAAKLRIYENAKVCVNADDALTMPIRGADERCVSFGVNMGDYHLNHQQGETWLRVKGEKVLNKEMKLSGQHNYTNALAALALADAAGLP
RASSLKALTTFT

>d1e8ca3 c.72.2.1 (A:88-337) UDP-N-acetyl muramyl tripeptide synthetase MurE {Escherichia coli}

QLNERLSALAGR FYHEPSDNRLVGTGNGKTTTQLLAQWSQLGEISAVMGTVGNGLGKVIPTENTTGSADVQHELAGLV DQGATFCAME
VSSHGLVQHRVAALKFAASVFTNLSRDHDYHGDMEH YEA AKWL LYSEHHCGQAI INAD DEVGR RWLA KLPDAV AVSMEDHINPNCHGRWLKAT
EVNYHDSGATIRFSSSWGDGEIESHL MGAF NVSN LLLA LATLL ALGYP LADLL KTAARLQP

>d1gg4a4 c.72.2.1 (A:82-312) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

DTRLA FGELAA WVRQQV PARVVALTGSSGKTSV KEMTA AILSQCGNTLYTAGNL NNDIGV PMTLL RTPEYDYAVIELGANHQGEIAWTVSLTRPEA
ALVNNLAAAHLEGFGSLAGVAKAKGEIFSGLPENGIAIMNADNN DWLNWQS VIGSRKVWR FSPNAANS DFTATNIHVTSHGTEFTLQTPTGSV DVL
LPLPGRHN HNIANALAAAALMSVGATLDAIKAGLANLKA

>d1jbwa2 c.72.2.2 (A:1-296) Folylo polyglutamate synthetase {Lactobacillus casei}

MNYTETVAYIHSF PRLAKTGD HRRIL TLHAL GNPQQQ GRYI HVTG NGK GS AANAI AHV LEAS GLTV GLY TSPF IMRF NERIM IDHE PIP DA ALV NAV
AFV RAALERLQQQQAD FNVTE FITALAYWYFRQRQDV AVIEVGIGG DTD STNV ITPV SVL TEVALD HQK LLGHT ITIAK HKAG I KRG IPVV TG
NL VPDA AAAVVA AKVATT GSQW LRF DRDF SVP KAKL HGW GQRFTY EDQ DGR ISD LEV PLV GDY QQ RNMAIA IQTA KV YAK QT EWPL TPQ NIRQ GLA
ASH

>d1jzta_c.104.1.1 (A:) Hypothetical protein YNL200c (YN00_YEAST) {Baker's yeast (Saccharomyces cerevisiae)}

LKVSSK LAEID KELM GPQIGFTLQQLM ELAG FSVAQAV CRQFPL RGKT ET EKG KH VFIAGPGNNGGDGLV CARHLKLF GYN PV FYPK R SERTE
FYKQLVHQLNFFKVPVLSQ DEGNWLEYLKPEK TLCIVDA IFGFSFKPPMREP FK GIVE ELCKVQ NIPI VSDV PTG WDVKGP ISQPSINPA VL S LT
PKPCSSHIREN QTTHYV GGRFIP RDF FANKFG FEPFG YESTD QILKL

>d1b7ba_c.73.1.1 (A:) Carbamate kinase {Enterococcus faecium}

GKKMVVALGGNAILSNDASAHAQQQALVQTSAYLVHLIKQGHRLIVSHGN GPQVGN LLLQQQA DSEKNPAMPL DTCVAM TQGSIG YWLSN ALN
QELNKAGIKKQV ATVLTQ VVDPADE AFKNPTKPIGPFLTE AEAK EAM QAGA IFKED AGR GWRK VVPS PKP DIHEA TINT LIKNDI ITIS CGGGGIPV
VGQELKGVEAVIDKDFASEKLAELVDADALVILTGV DYVCINYGPDEKQLTNVTVAELE EYKQAGHFAPGSM LPKIEAAIQF VESQPNKQAIITSLENL
GMSGD EIV GTVV

>d1e19a_c.73.1.1 (A:) Carbamate kinase {Archaeon Pyrococcus furiosus}

GKRVVIALGGNALQQRGQKGSYEEMMDNVRK TARQIA EIARGYEV /I THGNGPQVGSLLLHMDAGQATY GIPA QPM DVAGAM SQGWIG YM IQ
QALKNE LRKRGMEKKV VTII QTIVDKNDPAFQNPTKPVGPFYDEETAKRLAREKGWIVKEDSGRGWRRV VPSPD PKH VEAETIKLVERGVIVIAS
GGGGVPVILEDGEIKGVEAVIDKDLAGEKLAEEVNADIFMILTDVNGA ALYYGTEKEQW/L REV KVEELRK YYEEGHFKAGSMGPKVLA AIRFIEWGG
ERAIIAHLEKAVEALEGKTGTQVLP

>d1eqja1_c.105.1.1 (A:77-310) 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain {Bacillus stearothermophilus}

QSLTRINIA REG E FDR NETFLA AMNHV KQHGT SLH LGFL L SDGGV HSHI HHLY ALL RLAA KEV KRV YIH GFL DGR DV GP QT APQ YI KE KI KE YG
VGEIATLSGRYYSM DRD KR WDR VE KAY RAM VV GEG PTY RDPLE CIED SYKH GIYDEFV LPS VIV RED GRP V ATIQDN DAI IFY NFRP DRA IQS NTFTN
EDFREF DRGP KHPKHL FFV CLTH FSET VAGY VAFKP

>d1eqja2_c.76.1.3 (A:3-76,A:311-510) 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain {Bacillus stearothermophilus}

KKPVALIILDGFALRDETYGNAVAQANKPNFDRYWNEYPTTLKACGEAVGLPEGQMGNS EVGHLNIGAGRIVYXTLDNTIGEVL SQHGLRQLRIA
ETEKYPHVTFMSGGREEEFPGEDRILINSPK VPTYDLKPEMSAYEVTD ALLKEIAD KYD AIIL NYAN PDMV GHSGK LEPTI KAVEAV D ECLG KVVD A I

LAKGGIAITADHGNADEVLTPDGKPQTAHTTNPVPVIVTKKGKILRDGGILGDLAPTMDDLLGPQPKEMTGKSLIV

>d1ed8a_c.76.1.1 (A:) Alkaline phosphatase {Escherichia coli}

TPEMPVLENRAAQGDITAPGGARRLTGDDQTAALRDSLSDKPAKNILLIGDMGDSEITAARNYAEGAGGFFKGIDALPLTGQYTHYALNKKTGKPDY
VTDSAASATAWSTGVKYNGALGVDIHEKDHPITLEMAKAAGLATGNVSTAELQDATPAALVAHVSRKCYGPSATSEKCPGNALEGGKGSITEQLL
NARADVTLGGGAKTFAETATAGEWQGKTLREQAQARGYQLVSDAASLSNTEANQQPKLLGFADGNMPVRWLGPKATYHGNIDKPAVTCTPNP
QRNDSVPTLAQMKTDAKIELLSNEKGFFLQVEGASIDKQDHAANPCGGQIGETVLDDEAVQRALEFAKKEGNTLVITADHAHASQIVAPDTKAPGLT
QALNTKDGAVMVMSYGNSEEDSQEHTGSQRLIAAYGPHAANVVGLTDQTLFYTMAALKL

>d1ew2a_c.76.1.1 (A:) Alkaline phosphatase {Human (Homo sapiens)}

IIPVEENPDFWNREAAEALGAAKKLQPAQTAAKNLIIFLGDMGVSTVTAARILKGQKKDKLGPEIPLAMDRFPYVALSKTYNVDKHVPDSGATATA
YLCGVGNFQTIGLSAARFNQCNTTRGNEVISVMNRACKAGKSVGVVTTTRVQHASPGTYAHTVNRNWYSDADVPASARQEGCQDIATQLISN
MDIDVILGGGRKYMFRMGTDPPEYPPDDYSQGGTRLDGKNLVQEWAQRLRGARYVWRNTELMAQASLDPSTHLMGLFEPGDMKYEIHRDSTLD
PSLMEMTEAALRLSRRNPRGFFLVEGGRIDHGHHESRAYRALTETIMFDDAIERAGQLTSEEDTLSVTADHSHVFSFGGYPLRGSSIFGLAPGKARD
RKAYTVLLYNGNGPGYVLKDGPDTESGSPEYRQQSAVPLDEETHAGEDVAVFARGPQAHLVHGVQEQTIAHVMFAACLEPYTACDLAPP

>d1auk_c.76.1.2 (-) Arylsulfatase A {Human (Homo sapiens)}

PPPNIVLIFADDLGCGYGHPSSTPNLDQLAGGLRTDFYVPVSLCTSRAALLTGRLPVRMGMYPGVLVPSSRGGLPLEEVTVAEVLAARGY
LTGMAGKWHLGVGPEGAFLPPHQGFHFRFLGIPYSHDQGQPCQNLTCFPATPCDGGCDQGLVPIPLANLSVEAQPPWLPGLEARYMAFAHDLMA
DAQRQDRPFFLYASHHTHYPQFSGQSAERSGRGPFGDSLMEELDAAVGTLMTAIGDGLLEETLVIFTADNGPETMRMSRGCGSLLRCGKGTTY
EGGVREPALAFWPGBHIAPGVTHEASSLDLPTLAALAGAPLNVTLDFDLSPLLLGTGKSPRQLFFYPSYPDEVRGFAVRTGKYKAHFTQGSA
HSDTTADPACHASSLTAHEPPLYDLSKDPGENYNLLGGVAGATPEVLOAKLQLLKAQLDAAVTFGPSQVARGEDPALQICCHPGCTPRPACCHC
P

>d1fsu_c.76.1.2 (-) Arylsulfatase B (4-sulfatase) {Human (Homo sapiens)}

SRPPHLVFLLADDLGWNDVGFHGSIRTPHLDALAAGGVLLNDYYTQLXTPRSRQLLTGRYQIRTGLQHQIIWPCQPSVPLDEKLPLQLKEAGYT
THMVGKWHLGMYRKECLPTRRGFDTYFGYLLGSEDYYSHERCTLIDALNVTRCALDFRDGEVATGYKNMYSTNIFTKRAIALITNHPPKPLFLYAL
QSVEPLQVPEEYLKPYDFIQDKNRHYAGMVSLMDEAVGNVTAALKSSGLWNNTVIFSTDNGGQLLAGGNWPLRGRKWSLWEGGVRGVG
FVASPLLKQKGVKNRELIHISDWLPTLVKLRGHTNGTKPLDGFDVWKTISEGSPSPRIELLHNIDPNFDSSPCPRNSMAPAKDDSSLPEYAFNTSV
HAAIRHGNWKLTGPGCGWFPPPSQYNVEIPSSDPTKTLWLFIDRDPEERHDLREYPHIVTKLLSRQFYHKHSVYFPAQDPRCDPKATG
VWGPWM

>d1hdha_c.76.1.2 (A:) Arylsulfatase B (4-sulfatase) {Pseudomonas aeruginosa}

KRPNFLVIVADDLGFSIDAGFGEIATPNLDALAIAGLRLTDFTASTCSPTRSMLLTGTDHHIAGIGTMAEALTPELEGKPGYEGHLNERVVALPELLRE
AGYQTLMAGKWHGLKPEQTPHARGFERSFLPAGAANHYGFEPPYDESTPRILKGTPALYVEDERYLDTLPEGFYSSDAFGDKLQLYKERDQSRPF
AYLPFSAPHWPLQAPREIVEKYRGRYDAGPEALRQERLARLKEGLVADVEAHPVLAITREWEALEDEERAKSARAMEVYAMVERMDWNIGRV
VDYLRQQGELDNTFVLFMSDNGAEGALLEAFPKFGPDLLGFLDRHYDNSLENIGRANSVWYGRWAQAAATAPSRLYKAFTTQGGIRVPALVRYPRL
SRQGAISHAFATVMDVTPTLTLAGVRHPGKRWRGREIAEPRGRSWLGWLGETEAAHDENTVTGWELFGMRAIRQGDWKAVYLPAPVGPATW
QLYDLARDPGEIHDLADSQPGKLAELIEHWKRYVSETGVV

>d1k30a_c.112.1.1 (A:) Glycerol-3-phosphate (1)-acyltransferase {Cushaw squash (Cucurbita moschata)}

SHSRKFVLVRSEEEELSCIKKETEAGKLPPNVAAGMEELYQNYRNAVIIESGNPKADEIVLSNMTVALDRILLDVEDPFVSSHHKAIREPDFYYIFGQNY
IRPLIDFGNSFVGNLSQLFDIEEKLQQGHNVLISNHQTEADPAIISLLLEKTNPYIAENTIFAGDRVLAIDLCKPFSIGRNLLCIVYSKKHMFDELTETK
RKANTRSLKEMALLRGGSQLIWIAPSGGRDRPDPSTGEWYPAPFDASSVDMRRLIQHSDVPGHFLPALLCHDIMPSSQVEIEIGEKRVIAFNG
AGLSVAPEISFEEIAATHNPEEVREAYSKALFDVAMQYNVLKTAISGKQGLGASTADVSLSQPW

>d1e4bp_c.74.1.1 (P:) L-fuculose-1-phosphate aldolase {Escherichia coli}

MERNKLARQIIDTCLEMTRLGLNQGTAGQVSVRYQDGMLITPTGIPYEKLTSHIVFIDGNGKHEEGKLPSEWRFHMAAYQSRPDANAVVHNHAV
HCTAVSILNRSPAIHYMIAAGGNSIPCAYATFGTRELSEHVALALKNRKATLLQHHGLIACEVNLEKALWLAHEVEVLAQYLTTLAITDPVPLSDE
EIAVVLEKF

>d1jdia_c.74.1.1 (A:) L-ribulose-5-phosphate 4-epimerase {Escherichia coli}

MLEDLKRQVLEANLALPKHNLVTWTGNVSAVDRERGVFVKPSGVDSIMTADDMVVSIETGEVVEGAKKPSSDTPTHRLLYQAFPSIGGIVHTH
SRHATIWAQAGQSIPATGTTADYFYGTIPCTRKM岱EINGEYEWETGNVIVETFEKQGIDAAQMPGVLVSHGPF AWGKNAEDAVHNAIVLEE
VAYMGIFCRQLAPQLPDMQQTLLNKHYLRKH

>d1j9la_c.106.1.1 (A:) SurE homolog TM1662 (TM107 ?) {Thermotoga maritima}

MIRILVTNDGIQSKGIIVLAELLSEEHEFVVAAPDKERSATGHISITIHVPLWMKKVFISERVAYSTTGPADCVKLAYNVVMDKRVDLIVSGVNRGPN
MGMDILHSGTVSGAMEAMMNIPSIASSANYESPDFEGAARFLIDFLKEFDLSLLDPFTMLNINVPAGEIKGWRFRQSRRWNDYFEERVSPFG
EKYYWMGEVIEDDDRDVDYKAVREGYVSITPIHPFLTNEQCLKLREVDY

>d1cjya2 c.75.1.1 (A:142-721) Cytosolic phospholipase A2 catalytic domain {Human (Homo sapiens)}

PDLRFSMALCDQEKTFRQRKEIRESMKKLLGPKNSEGLHSARDVPVAILGSGGGFRAMVGFSVMKALYESGILDATYVAGLSGSTWYMSTL
YSHPDFPEKGPEEINEELMKNVSHNPLLTPQKVKRYVESLWKKSSGQPVTFTDIFGMLIGETLIHNRMNTTSSLKEKVNTAQCPPLFTCLHVKP
DVSELMFADWVEFSPYEIGMAKYGTMAPDLFGSKFFMGTVKKYEEENPLHFLMGVWGSASFILNVRVLGVSGSQSRGSTMEEELENITKHIVSN
DSSSDSDESHEPKGTESEDAGSDYQSDNQASWIHRMIMALVSDSALNFTRERAGKVHNFMGLNLNTSYPLSPLSDFATQDSFDDDELAAVAD
PDEFERIYEPLDVKSKKIHVVDSGLTFNLPYPLILRPQRGVDLIISFDSARPSDSSPPFKELLAEKWAKMNKLFPKIDPYVFDREGLKECYVFKPNPD
MEKDCPTIIHFVLANINFRKYKAPGVPRETEEKEIADFIDFDDPESPFSTFNQYPNQAFKRLHDLMHFTLNNIDVIKEAMVESIEYRRQ

>d1xaa_c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Thermus thermophilus}

MKVAVLPGDGIGPEVTEAALKVLRALDEAEGLGLAYEVFPFGGAAIDAFGEPEPTRKGVEEAEAVLLGSVGGPKWDGLPRKIRPETGLLSRKSQD
LFANLRPAKVFPGLERLSPKKEEARGVDVLIVRELTGGYIYFGEPRGMSEAEAWNTERYSKPEVERVARVAFAARKRKHVVSDKANLEVGEFWR
KTVEEVGRGYPDVALEHQYVDAMAMHVRSPARFDVVTGNIFGDIISLDLASVPGSLGLPSASLGRGTPVFEPVHGSAPDIAGKGIANPTAAILSA
AMMLEHAFLVELARKVEDAVAKALLETPPPDLGGSAGTEAFTATVLRHLA

>d1xad_c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Chimera (Thermus thermophilus) and (Bacillus subtilis)}

MKVAVLPGDGIGPEVTEAALKVLRALDEAEGLGLAYEVFPFGGAAIDAFGEPEPTRKGVEEAEAVLLGSVGGPKWDQNPRLPEKGLLSRKQLD
LFANLRPVKFESLSDASPLKEYIDNVDVIVRELTGGYIYFGEPRGMSEAEAWNTERYSKPEVERVARVAFAARKRKHVVSDKANLEVGEFWR
KTVEEVGRGYPDVALEHQYVDAMAMHVRSPARFDVVTGNIFGDIISLDLASVPGSLGLPSASLGRGTPVFEPVHGSAPDIAGKGIANPTAAILSA
AMMLEHAFLVELARKVEDAVAKALLETPPPDLGGSAGTEAFTATVLRHLA

>d2ayqa_c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Bacillus coagulans}

MKMKLAFLPGDGIGPEVMDAAIRVLKTVLDNDGHEAVFENALIGGAAIDEAGTPLPEETLDICRRSDAILLGAVGGPKWDHNPASLRPEKGLLRLK
EMGLFANLRPVKAYATLLNASPLKRERVENVDLVIVRELTGGYIYFGRPSERRGPGENEVVDTLAYTREEIERIIKAFQLAQRKKLASVDKANVLESSR
MWREIAEETAKKPDVELSHMLVDSTSMLIANPGQFDVITENMFGLDLSDEASVITGSLGMILPSASLRSDRFGMYEPVHGSAPDIAGQGKANPL
GTVLSAALMLRYSFGLEKEAAIEKAVDDVLQDGYCTGDLQVANGKVVSTIELDRLIEKLN

>d1a05a_c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Thiobacillus ferrooxidans}

MKKIAIFAGDGIGPEIVAAARQVLDQDAHQAHGLRCTEGLVGGAALDASDDPLPAASLQLAMAADAVILGAVGGPRWDAYPPAKRPEQGLLRLK
GLDLYANLRPAQIFPQLLDASPLRPELVRDVLDVRELTGGYIYFQPKGREGSGQYEKAFTDEVYHRFEIERIARAFRAAQGRRKQLCSVDKANVLE
TTRLWREVTEVARVDYDVRVLSHMYVDNAAMQLIRAPAQFDVLLTGNMFGDILSDEASQLTGSIGMLPSASLGEGRAMYEPVHGSAPDIAGQDKA
NPLATILSVAMMLRHSLSNAEPWAQRVEAAVQRVLDQGLRTADIAAPGTPVIGTKAMGAVVNALNK

>d1cnza_c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Salmonella typhimurium}

MSKNYHIAVLPDGIGPEVMAQALKVMDAVRSRFDMRITTSHYDVGGAIDNHGHPLPKATVEGCEQADILFGSVGGPKWEHLPDQQPERGAL
LPLRKHFKLFNSNLRPAKLYQGLEACPRLRADIAANGFDILCVRELTGGYIYFQPKGREGSGQYEKAFTDEVYHRFEIERIARAFESARKRRKVTSIDKA
NVLQSSILWREIVNDVAKTYPDVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMITGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGK
NIANPIAQILSALLRYSLDANDAATAIEQAINRALEEGIRTGDLARGAAA VSTDEMGIARYVAEGV

>d1cm7a_c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Escherichia coli}

MSKNYHIAVLPDGIGPEVMTQALKVLDAVRNRFAMRITTSHYDVGGAIDNHQPLPPATVEGCEQADAVLFGSVGGPKWEHLPDQQPERGA
LLPLRKHFKLFNSNLRPAKLYQGLEACPRLRADIAANGFDILCVRELTGGYIYFQPKGREGSGQYEKAFTDEVYHRFEIERIARAFESARKRRKVTSIDKA
NVLQSSILWREIVNEIATEYPDVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMITGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGK
NIANPIAQILSALLRYSLDADDAACAIERAINRALEEGIRTGDLARGAAA VSTDEMGIARYVAEGV

>d1iso__ c.77.1.1 (-) Isocitrate dehydrogenase, ICDH {Escherichia coli}

SKVVVPAQGKKTQLNGKLNPENPIPYIEGDGIGVDVTAPMLKVDAAVEKAYGERKISWMEYTGEKSTQVGQDVWLPATLDLIREYRAIK
GPLTPVGGIIRSLNVALRQELDLYICLRPVRYQQGTSPVKHPLETDMVIFRENSEDIYAGIEWKADSADAEVKFLREEMGVKKIRFPEHCGIGIKP
MSEEGTKRLVRAAIEYAIANDRSVTLVHKGNIMKFTEGAFKDWTGYQLAREEFGELIDGGPWLKVNPNNTGKEIVIKDVIADAFLQQILLRPAEYDV
IACMNLNGDYISDALAAQVGIGIAPGANIGDEYALFEATHGTAPDIAGQDKANPGSIILSAEMMLRHMGWTEAADLIVKGMEGAINAKTVKDFF
SLMDGAKLLKCSEFGDAIIENM

>d1hqsa_c.77.1.1 (A:) Isocitrate dehydrogenase, ICDH {Bacillus subtilis}

MAQGEKITVSNGVLNPNNPIIPFIEGDTGPDWNAASKVLEAAVEKAYGEKKITWKEVYAGEKAYNKTGEWLPATLDVIREYFIAKGPLTPVG
GGIRSLNVALRQELDLFVCLRPVRYFTGPSPVKRPEDTMVIFRENTEDIYAGIEYAKGSEEVQKLFLQNELNVNKIRFPETSGIGIKPVSEEGTSRLV
RAAIDYIAEHGRKSVTLVHKGNIMKFTEGAFKNWGYELAEKEYGDKVFTWAQYDRIAEEQGKDAANKAQSEAEAAGKIIKDSIADIFLQQILTRPNEF
DVVATMNLNGDYISDALAAQVGIGIAPGANINETYGHAFEAHTGTAQPKYAGLDKVNPSVILSGVLLHELGWNEAADLVIKSMETIASVVTYD
FARLMDGATEVKCSEFGEELIKNMD

>d1ekxa1 c.78.1.1 (A:1-150) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}

ANPLYQKHISINDSRDDNLVLATAAKLKANPQPPELLKKVIASCFFEASTRTRLSFETSMHRLGASVVGFSDSANTSLGKKGTLADTISVISTYDAI
VMRHPQEGAARLATEFSGNVLPVLNAGDGSNQHPTQLLDLFTIQETQG

>d1ekxa2 c.78.1.1 (A:151-310) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}

RLDNLHVAMVGDLKYGRTVHSLTQALAKFDGNRFYFIAPDALAMPQYILDMLDEKGIAWSLHSSIEEVMAEVDIRLYMTRVQKERLDPSEYANVKAQ
FVLRASDLHNNAKANMKVLHPLPRVDEIATVDKTPHAWYFQQAGNGIFARQALLALVNRDLVL

>d2atca2 c.78.1.1 (A:151-305) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}

RLNNLHVAMVGDLKYGRTVHSLTQALAKFDGNRFYFIAPDALAMPEYILDMLDEKGIAWSLHSSIEEVMTRVQKERLDPSEYABVKAQFLVRANSLG
GLHNAKMNAKVLHPLPRVDEIATVDKTPHAWYFQQAGNGIFARQALLALVNRDLVL

>d2at2a1 c.78.1.1 (A:1-144) Aspartate carbamoyltransferase catalytic subunit {Bacillus subtilis}

MKHLTTMSELSTEEIKDLLQTAQELKSGKTDNQLTGKFAANLFFEPSTRTRFSFEVAEKLGGMNVNLNDGTSTSVQKGTELTYDTIRTLESIGVDVCVIRH
SEDEYYEELSVQNVIPILNAGDGCQHPTQSLLDLMTIYEEFNT

>d2at2a2 c.78.1.1 (A:145-295) Aspartate carbamoyltransferase catalytic subunit {Bacillus subtilis}

FKGLTVSIHGDIKHSRVARNSAEVLTGARVLFSGPSEWQDEENTFGTYVSMDEAVESSDVMILLRIQNERHQSAVSEQYLNKYGLTVERAERMK
RHAIIMHPAPVNRGEIDDLSVESEKSRIFKQMKGNGVFIRMAVIQCALQTNVKR

>d1dxha1 c.78.1.1 (A:1-150) Ornithine transcarbamoylase {Pseudomonas aeruginosa}

AFNMHRNLLSLMHSTRELRYLLDLRDLKRAKYTGTEQQHLKRKNIALIFEKTSTRTRCAFEVAAYDQGANVTYIDPNSSQIGHKESMKDTARVLG
RMYDAIEYRGFKQEIVEELAKFAGVPVFNGLTDYHPTQMLADVLTMRHSD

>d1dxha2 c.78.1.1 (A:151-335) Ornithine transcarbamoylase {Pseudomonas aeruginosa}

KPLHDISAYLGDARNNMGSNLLIGAKLGMDVRIAAPKALWPHEDEFVAQCKKFAEESGAKLTTEDPKEAVKGDFVHTDVWVSMGEPEAWGE
RIKELLPYQVNMEIMKATGNPRAKFMHCLPAFHNSETKVGKQIAEQYPNLANGIEVTEDVFESPYNIAFEQAENRMHTIKAILVSTLADI

>d1duvg1 c.78.1.1 (G:1-150) Ornithine transcarbamoylase {Escherichia coli}

SGFYHKHFLKLLDFTPAELNSLLQLAALKADKSGKEEAKLTGKNIALIFEKDSTRTRCSFEVAAYDQGARVTLGPSGSQIGHKESIKDTARVLGRMY
DGIQYRGYQGEIVETLAEYASPVWNGLTFNEHPTQLADLLTMQEHLPG

>d1duvg2 c.78.1.1 (G:151-333) Ornithine transcarbamoylase {Escherichia coli}

KAFNEMTLYAGDARNNMGSNMLEAAALTGLDLRVAPQACWPEALVTECRALAAQQNGGNLTDEDVAKGVEGADFIYTDVVWVSMGEAKEKW
AERIALLREYQVNSKMMQLTGNPEVKFLHCLPAFHDDQTTLGKMAEEFGLHGGMEVTDEVFESAASIVFDQAENRMHTIKAVMVATLSK

>d1a1s_1 c.78.1.1 (1-150) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}

VVSLAGRDLCLQDYTAEEIWITLEAKMFKIWQKIGKPHRLLEGKTLAMIFQKPSTRTRVSFEVAMAHLGGHALYLNAQDLQLRRGETIADTARVL
RYVDAIMARVYDHKDVEDLAKYATVPVINGLSDFSHPCQALADYMTIWEKKG

>d1a1s_2 c.78.1.1 (151-313) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}

TIKGVKVVVGDGNNAHSLMIAGTKLGADVVVATPEGYEPDEKVIKWAEQNAAESGGSFELLHDPVKAVKDADVIYTDVWASMGQEAEERRK

IFRPFQVNKDLVKHAKPDYMFHMCLPAHRGEEVTDDVIDSPNSVWDQAENRLHAQKAVLALVMGGIK
>d1otha1 c.78.1.1 (A:34-184) Ornithine transcarbamoylase {Human (Homo sapiens)}
KVQLKGDRDLTLKNFTGEEIKYMLWLSADLKFRKQKGELPLQGKSLGMIFEKRSTRTRLSTETGFALLGGHPCFLTTQDIHLGVNESLTDATARVLSSM
ADAVALARVYKQSDLDTLAKEASIPPIINGLSDLYHPIQLADYLTLQEHY
>d1otha2 c.78.1.1 (A:185-354) Ornithine transcarbamoylase {Human (Homo sapiens)}
SLKGTLTSWIGDGNNILHSIMMSAAKFGMHLQAATPKGYEPDASVTKLAEQYAKENGTKLLTNDPLEAHGGNVITDTWISMGREEEKKRLOA
FQGYQVMTAKVAASDWTFLHCLPRKPEEVDEVFYSPRSLVFPEAENRKWTIMAVMVSLLTDSPQLQKPKF
>d1b74a1 c.78.2.1 (A:1-105) Glutamate racemase {Aequifex pyrophilus}
MKIGIFDSVGGLTVLKAIRNRYRKVDIVYLGDTARPYGIRSKDTIYRSLCAGFLDKGVDIIVVACNTASAYALERLKKEINVPVFGVIEPGVKEALKK
SR
>d1b74a2 c.78.2.1 (A:106-252) Glutamate racemase {Aequifex pyrophilus}
NKKIGVIGTPATVKSGAYQRKLEEGGADVFAKACPLFAPLAEEGLLEGEITRKVVEHYLKEFKGKIDTLILGCTHYPLLKEIKKFLGDAEVVDSSEALSL
HNFIKDDGSSLELFFDLSPNLQFLIKLILGRDYPVKLAEGVF
>d1qopb_ c.79.1.1 (B:) Tryptophan synthase, beta-subunit {Salmonella typhimurium}
TTLLNPYGFEGGMVYVPQILMPALNQLEEA FVSAQKDPEFQAFQADLLNYAGRPTALKCQNITAGTRTTLYLKREDELLHGGAHKTNQVLGQALLA
KRMGKSEIIAETGAGQHGVASALASALLGLKRIYMGAKDVERQSPNVRMRLMGAEVIPVHGSATLKDACNEALRDWSGSYETAHYMLGTAAG
PHPYPTIVREFQRMIGEETKAQILDKEGRLPDAVIACVGGGSNAIGMFADFIN DTSVGLIGVEPGGHGIETGEHGAPLKGRVGIYFGMKAPMMQT
ADGQIEESYSISAGLDFPSVGPQHAYLNSIGRADYVSITDDEALEAKTLCRHEGIIPALESSHALAHALKMMREQPEKEQLVVNLSGRGDKDIFTVH
DIL
>d1fcja_ c.79.1.1 (A:) O-acetylserine sulfhydrylase (Cysteine synthase) {Salmonella typhimurium}
SKIYEDNSLTIGHTPLVRLNRIGNGRILAKVESRNPSFSVKCRIGANMIWDAEKRGVLKPGVELVEPTNGNTGIALAYVAAARGYKLTLMPETMSIERR
KLLKALGANLVLTEGAKGMKGAIQKAEEIVASDPQKYLLLQQFSNPANPEIHEKTTGPEIWEDTDGQVDFVFIGVGTGTLGVTRYIKGKTDLIT
VAVEPTDSPVIAQALAGEEI KPGPHKIQGIGAGFIPGNLDLKLIDKVVGITNEEAISTARRLMEEEGILAGISSGAAVAAALKLQEDESFTNKNIVVILPSS
G
>d1tdj_1 c.79.1.1 (5-335) Allosteric threonine deaminase N-terminal domain {Escherichia coli}
QPLSGAPEGAELYRLAVLRAVAPVYEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGLTEEQKAHGVTASAGNHAQGVAFSSAR
LGVKALIVMPTATADIKVDAVRGFGEVLLHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGT LAELLQQDAHDRVFPVGGGLAAG
VAVLQLMPQKIVIAVEAEDSACLKAALDA GHPV DLPVRGLFAEGVAVKRIGDETFRLCQEYLDIITVDSAICAAMKDLFEDVRAVEPS GALALA
GMKKYIALHNIRGERLAHILSGANVNHFGLRYV SERCELGE
>d1e5xa_ c.79.1.1 (A:) Threonine synthase {Mouse-ear cress (Arabidopsis thaliana)}
IETAVKPPHRTEDNIRDEARRNRNAVNPFSAKYVPFNAAPGSTESYSLDEIVYRSRSGGLLDVEHDMEALKRFDGAYWRDLFDSRVGKSTWPYGSG
VWSKKEWLVP EIDDDDIVSAFEGNSNLFWAERFGKQFLGMNDLWVKHCGISHTGSFKD LGMTVLVSVNRLRKMKRPVVGCASTGDTSAALS
AYCASAGIPSIVFLPANKISMAQLVQPIANGAFVLSIDTDFGCMKLIREITAELPIYLANSLNSLRLEGQKTAIEILQQFDWQVPDWVIVPGGNLGNI
YAFYKGFKMCQELGLVDRIPRMVCAQAAANPPLYLHYKSGWKDFKPMTASTTFASAIQIGDPVSIDRAVYALKCNGIVEEATEEELMDAMAQADS
TGMFICPHTGVALTALFKLRNQGVIAPTDRTVVSTAHLKFTQSKIDYHSNAIPDMACRFSNPPDVKA DFGAVMDVLKS YLGSNTLTS
>d1f2da_ c.79.1.1 (A:) 1-aminocyclopropane-1-carboxylate deaminase {Yeast (Hansenula saturnus)}
AGVAKFAKYPLTFGPSPISLNRLSQHLGSKVN VYAKRED CNSGLAFGGNKL RKEYIPDIVEG DYTHLVSIGGRQSNQTRMVA ALA AKLGKKCVLIQ
EDWVPIPEAEKD VYNRVGNIELS RIMGADVRVIEDGFDIGMRKS FANALQELEDAGHKPYPPIPAGCSEHKYGLGFVGFAD EVINQEVELGIKFDKIV
VCCVTGSTTAGLAGMAQYGRQDDVIAIDASFTSEK TKEQTLRIANNTAKLIGVEHEFKDFTLDTRFAYPCYGV PNEG TIEAIRTCAEQGVLTDPVYEG
KSMQGLLAI LIKDYFKPGANVLYVHLGGAPAL SAYSSFFPTKTA
>d1jbqa_ c.79.1.1 (A:) Cystathionine beta-synthase {Human (Homo sapiens)}
WIRPDAPS RCTWQLGRPASESPHHHTAPAKSPKILPDILKIGDTPMVRINKIGKKFGLCELLAKCEFFNAGGSVKDRISLRM IEDAERDGT LKPGDTI
IEPTSGNTIGLALAAA VRGYRCIIVMPEKMSSEKVDVLRALGAEIVRPTPTNARFDSPESHVGVAWRLKNEIPNSHILDQYRNASNPLAHYDTTADEIL
QQCDGKLDMLVASVGTGGITGIARKLKEKCPGCR II GVDPEGSILAEPEELNQTEQTTYEVEGIGYDFIPTVLDRTVVDKWFKS NDEEAFTFARMLIA

QEGLLCGGSGAGSTVAVAKAAQELQEGQRCVVILPDSVRNYMTKFLSDRWMQLKGFL

>d1jeoa_c.80.1.3 (A:) Probable 3-hexulose-6-phosphate isomerase MJ1247 {Archaeon Methanococcus jannaschii}

LEELDIVSNNILKKFYTNDEWKNLDSLIDRIIKAKKIFIGVGRSGYIGRCFAMRLMHLGFKSYFVGETTPSYEKDDLILISGSRTESVLTAKKAK
NINNNIIIAIVCECGNVVEFADLTIPLEVKKS KYLPMGTTFEETALIFLDLVIAEIMKRLNLDESEIIKRHCNLL

>d1moq_c.80.1.1 (-) "Isomerase domain" of glucosamine 6-phosphate synthase (GLMS) {Escherichia coli}

GDKGIYRH YM QKEIYEQPNAIKNTLGRISHGQVDLSELGPNADELLSKVEHIQILACGTSNSGMVSRYWFESLAGIPCDVEIASEFRYRKSAVRNS
LMITLSQSGETADTLA GLRLS KELGYLGS LAICNVPGSSLVRESDLALMNTAGTEIGVASTKAFTTQLTVLLMLVAKLSRLKG LDASIEHDIVHGLQALPS
RIEQMLSQDKR I EALAEDFS DKHH ALFLGRGDQ YPIA LEGALKLKE ISYIHA EAAYAAGE LHGPLA LIDADMPVIVVAPNNEL EKLKS NIEEV RARGQQ
LYVFADQDAGFVSSDNM HIIEMPH VEEVIAPIFYTVPLQLL AYHVALIKGTDV DQPRNLAKSVT VE

>d1g98a_c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Rabbit (*Oryctolagus cuniculus*)}

AALTRNPQFQKLQQWHRHGESELNRHLFDTDKERFNHFSLTNTNHGHILLDYSKNLVTEVMHMILLDLAKSRGV EAARESMFN GKEINSTEDRA
VLHVALRNRSNTPIVVDGKDV MPEVN KVL DMKAFCQR VRSGDWKGYTGKTITDV INIGGSDLGPLMVTEALKPYSSGGPRVWFVSNIDGTHIA
KTLACLNPESSLFIIASKTFTTQETITNAK TAKDWFLSAKDPSTVAKHFVALSTNTAKVKEFGIDPQNM FEFWDWVGGRYSLWSAIGLSIALHVGFDN
FEQLLSGAHWMDQHFRTPLEKNAPVLLA MLGIWYINCFG C ETQAVLPYDQYLHRFAAYFQQGDMESNGKYITKSGARV DHTQGPIVWGE PG TN
GQHAFYQLIHQGTMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMKGKSTE EARKE LQAGKSPEDLMKLLPHKV FEGNRPTNSIVFTKLT
ILGALIAMYEHKIFVQGVVWDINSFDQWGVELGKQLAKKIEPELDGSSPVTS HSSTNGLINFIKQQREAK

>d1iata_c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Human (*Homo sapiens*)}

AALTRDPQFQKLQQWREHRSELNRLRFDANKDRFNFHFSLTNTNHGHILV DYSKNLVTEDVMRMLV DLA KSRGV EAARERMFN GKEINYTEGR
AVLHVALRNRSNTPIVLDGKDV MPEVN KVL DMKSF CQR VRSGDWKGYTGKTITDV INIGGSDLGPLMVTEALKPYSSGGPRVWYVSNIDGTHI
AKTLAQLNPESSLFIIASKTFTTQETITNAETAKEWFLOQAKDPSAVAKHFVALSTNTTKVKEFGIDPQNM FEFWDWVGGRYSLWSAIGLSIALHVG
DNFEQLLSGAHWMDQHFRTPLEKNAPVLLALLGIWYINCFG CETHA MLPYDQYLHRFAAYFQQGDMESNGKYITKSGTRV DHTQGPIVWGE PG
TNGQHAFYQLIHQGTMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMKGKSTE EARKE LQAGKSPEDLERLLPHKV FEGNRPTNSIVFTKLT
PFMLGALVAMYEHKIFVQGIIWDINSFDQWGVELGKQLAKKIEPELDGSAQVTSHDASTNGLINFIKQQREAK

>d1c7qa_c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Bacillus stearothermophilus}

AISFDYSNALPFMQENELDYLSEFVKAHHMLHERKGPGDFLGWVDWPIRYDKNEFSRIKQAAERIRNHSDALV VIGGSGYLGARA AIEALSHTFH
NQMNDTTQIYFAGQNISSTYISHLLDVL EGK DLSINVISKSGTTPEAIAFRFRDYMEKKYKGEE ARK RYI VTTDRKGALKLADQEGYETFVIPDNIG
GRYSVLTAVGLPIAVAGLNIDRMMEGAASAYHKYNPDLLTNE SYQYAVRNILYRKGKAIELLV NYEPSLHYSEWWKQLFGESEGKDQKGLFPAS
VDFTTDLHSMGQYQVEGRRNLIETVLHVKKPQIELTIQED PENIDGLN FLAGKTLDEVNKKA FGQTLAHVDGGVPNLIVE LDEMNEYTFGE MVYFF
EKACGISGHLLGVNPFDQPGVEAYKKNMALLGKPGF EDEKA ALMKRL

>d1eu1a2_c.81.1.1 (A:4-625) Dimethylsulfoxide reductase, PGI {Rhodobacter sphaeroides}

ANGEVMSGCHWGVFKARVENGRAFAEPWDKDPAPSHQLPGVLDIYSPTRIKYPMVRREFLEKGVNADRSTRNGDFVRV TWDEALDLVAREL
KRVQESYGTGTFGGSYGWKSPGRLHN CQVLMRRA LNL AGGFVNSSGDYSTAAQIIMPHVMGTL EYEQQTAWPVV VENTDLMVFWAADPM
KTNEIGWVIPDHGAYAGM KALKEKGTRVIAINPVRTETADYFGADV VSPRPQTDVALMLGMAHTLYSED LHD KDFLENCTTGFDLFAA YLTGESDGT
PKTAEWAAEICGLPAE QIRELARS FVAGRTMLAAGWSIQRMMHGEQAHWMLVTLASMLGQIGLPGGGFGLSYHYSNGGPTSDG PALGGISDGG
KAVEGA AWLSESGAT SIPC ARV VDMILLNPGGEFQNGATA TYP DVKLAYWAGGNPFAH HQDRNRM LKAWEKLET FIVQDFQWTATARHADIVLP
ATT SYERNDIESVG DYSNRAILAMKKVVDPL YEARSDYDIFA ALAERLGKGA EFT EGR DEMGWISSFYEA VQAE FKNVAM PSFED FWSEGIVEFPI
TEGANFVRYAD FREDPLFNPLGTPSGLIEIYSK NIEK MGYDDCPA HPTWMEPA

>d1dmr_2_c.81.1.1 (3-625) Dimethylsulfoxide reductase, PGI {Rhodobacter capsulatus}

LANGTVMSGSHWGVFTATVENGRATAFTPWEKDPHPSPMLAGVLDIYSPTRIKYPMVRREFLEKGVNADRSTRNGDFVRV SWDQALDLVAAE
VKRVEETYGPEGVFGGSYGWKSPGRLHN CQVLMRRA LNL AGGFVNSSGDYSTAAQIIMPHVMGTL EYEQQTAWPVLAENTEV MVFWAADPM
KTSQIGWVPIEHGAYP GLEALKAKGTVIVIDPVRTKTVEFFGA EHITPKPQTDVA IMLGMAHTLVAEDLYDKDFIANYTSGFDKFLPYLDGETDSTPK
TAEWAEGISGVPAETIKELARLFESK RTMLAAGWSMQRMMHGEQAHWMLVTLASMLGQIGLPGGGFGLSYHYSNGGPTSDG PALAGITDGGAA
TKGPEWLAAS GASVIPV ARV VDMILENPGAE FDFNGTRSKFP DVK MAYW VGGNP FVHHQDRNRM VKAWEKLET FVHDFQWTPTARHADIVLP
ATT SYERNDIETIGDYSNTGILAMKKI VEP LYEARSDYDIFA AVAERLGKGA EFT EGR DEMGWISSFYEA VQAE FKNVAM PSFED FWSEGIVEFPI

VTDGADFVRYASFREDPLLNPLGPTGLIEYSKNEKMGYDDCPAHPTWMEPL

>d1aa6_2 c.81.1.1 (1-564) Formate dehydrogenase H {Escherichia coli}

MKKVVTVCPCASGCKINLVVDNGKIVRAEAAQGKTNQGTLCKGYYGDFINDTQLTPRLKTPMIRRQRGGKLEPVSWDEALNYVAERLSAIKEK
YGPDAIQTGSSRTGNETNYVMQKFARAVIGTNNDCCARVCHGPSAGLHQSVNGAMSNAINEIDNTDLVFVFGYNPADSHPIVANHVINA
RNGAKIIVCDPRKTIETARIADMHIALKNNSNIALLNAMGHVIEENLYDKAFVASRTEGFEYRKIVEGYTPESEDITGVSASEIRQAARMYAQAKSAA
ILWGMGVTQFYQGVETVRSLSLAMILGNLGKPHAGVNVRGQNNVGACDMGALPDTPGYQYVKDPANREKFAKAWGVESLPAHTGYRISEL
PHRAAHGEVRAAYIMGEDPLQTDALSAVRKAFADEDLELVQDIFMTKASAADVLPSWEHEGVFTAADRGFQRFFKAVEPKWDLKTDWQIIS
EIATRMGYPMHYNNTQEIWDELRLHLCPDFYGATYEKMGEGLFIQWPGRDTSADQGTSYLFKEKFDTPNGLAQFFTCDWVA

>d1tmo_2 c.81.1.1 (5-631) Trimethylamine N-oxide reductase {Shewanella massilia}

NEDEWLTTGSHFGAFKMKRKNGVIAEVKPDFLDKYPTDMINGIRGMVYNPSRVYPMVRLDFLLKGHKSNTHQRGDFRFVRTWDKALTFLKHSL
DEVQTQYGPSLHAGQTGWRATGQLHSSTSHMQRAVGMHGNYVKKIGDYSTGAGQTILPYVLGSTEVEAQGTSWPLILEHSDTIVLWSNDPYKNL
QVGWNAETHESFAYLAQLKEKVQKGKIRVISIDPVVTKTQAYLGCEQLYVNPQTDVTMLAIAHEMISKLYDDKFIQGYSLGFEFVPPVYMGTKDGV
AKTPEWAAPICGVEAHVIRDLAKTLVKGRTQFMMGWCIQRQQHGEQPYWMAAVLATMIGQIGLPGGGISYGHYSSIGVPSSGAAAPGAFRNL
DENQKPLFDSSDFKGASSTIPVARWIDAILEPGKTIDANGSKVVYPDIKMMIFSGNNPWNHHQDRNRMQAFHKLECVVTVDVNWTATCRFSDIV
LPACTTYERNDIDVYGYAYANRGILAMQKMEVPLFDLSDFEIFTRFAAVLGKEKEYTRNMGEMEWLETLYNECKAANAGKFEMPDFATFWKQGYV
HFGDGEVWTRHADFRNDPEINPLGTPSGLIEIFSRKIDQFGYDDCKGHTWMEKT

>d1g8ka2 c.81.1.1 (A:4-682) Arsenite oxidase large subunit {Alcaligenes faecalis}

NDRITLPPANAQRTNTCHFCIVCGYHVYKWPTELEGGRAPEQNALGLDFRKQLPPLAVTLPAMTNVTEHDGARYDIMVVPDKACVVNSGLS
STRGGKMASMYPTGDKERLSAPRLYAADEWVDTTDWDHAMALYAGLIKTLKDGPQGVFFSCFDHGGAGGGFENTWGTGKLMFSAIQTP
MVRIHNRPAYNSECHATREMIGIELNNAYEDAQLADVWSIGNNPYEQSTNYFLNHWLPNLQGATTSKKERFPNENFPQARIIFVDPRETPSVAIA
RHVAGNDRLHLIAEPGTDALFNGLFTYVEQGWIDKPFIEAHTKGFDAAVKTNRLSDECSNITGVPVDMIKRAAEWSYKPKASGQAPRTMHAY
EKGIWGNNDNYVIQSALLDLIATHNVGRRGTGCVRMGGHQEGYTRPPYPGDKKIYDQELIKGKGRIMTWWGCNNFQTSNNAQALREAILQRSAI
VKQAMQKARGATTEEMVDVIEATQNGGLFVTSINLYPTKLAEEAHMLPAAHPGEMNLTSMNGERRIRLSEKFMDPPGTAMADCLIAARIANAL
RDMYQKDGKAEMAAQFEGFDWKTEEDAFNDGFRRAGQPGAPAIDSQGGSTGHLVTYDRLRKSGNNGVQLPVVSWDESKGLVGTEMLYTEGKF
DTDDGKAHFKPAPWNG

>d2napa2 c.81.1.1 (A:4-600) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}

RPEKWVKVCRYCGTCGVLGVKDGKAVAIQGNPNHHNAGLLCLKGSLIPVLSKERVTQPLVRRHKGKLEPVSWDEALDLMASRFRSSIDMY
GPNSVAWYGSQCLTEESVANKIFKGGFTNNVDGNPRLCMASAVGGYVTSFGKDEPMGYADIDQATCFFIIGSNTSEAHPVLFRRIARRKQVEP
GVKIIVADPRTNTSRIADMHVAFRPGTDLAFMHMSMAWVIIENEELNPRFWQRYVNFMADAEGKPSDFEGYKAFLENYRPEKVAEICRPVVEQIYGA
ARAFESAATMSLWCMGINQRVQGVFANNLIHLITGQICRPGATFSLTGQPNACGGVRDGGALSHLLPAGRAPINAKHRAEMEKLWGLPEG
RIAPEPGYHTVALFEALGRGDVKCMIICETNPAHTLPNLNKVHKAMSHPESFIVCIEAPDAVTLEYADLVPFAFWCERDGVYGGCERRYSLTEKAVD
PPGQCRPTVNTLVEFARRAGVDPQLVNRNAEDVWNEWRMVSKGTTDFWGMTRERLRKESGLIWPCPSEDHPGTSRLYVRGQDPCVPADHP
DRFFFYGKPDGRAVIWMRPAKG

>d1ad3a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus norvegicus)}

SISDTVKRAREAFNSGKTRSLQFRIQQLEALQRMINENLKSISGALASDLGKNEWTSYYEVAHVLEELDTTIKELPDWAEDEPVAKTRQTQQDDLYIH
SEPLGVVLVIGAWNYPFNLTIQPMVGAVALGNAVILKPKSEVSGHMADLLATLIPQYMDQNLYLVKGGVPETTELLKERFDHIMYTGSTAVGKIVMA
AAAKHLPTVTELGKSPCYVDKDCDLDVACRRIAWGKFMNSGQTCVAPDYILCDPSIQNQIVEKLKSLKDFYGEDAKQSRDYGRIINDRHFQRVK
GLIDNQKVAHGGTWDQSSRYIAPТИLDVDPQSPVMQEEIFGPVMPICVRSLEEAIQFINQREKPLALYVFSNNEKVIKKMIAETSSGGVTANDVIV
HITVPTLPFGGVGNNSGMAYHGKKSFTFSHRRSCLVKSLLNEAHKARYPPSPA

>d1bi9a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus norvegicus), retinal type II}

MASLQLLPSTPNLEIKYTKIFINNEWQNSESGRVFPVCNPATGEQVCEVQEAQKVDIKAVQAARLAFLGSVWRRMDASERGRLLDKLADLVERD
RATLATMESLNGGKPFLQAFYIDLQGVIKTLRYAGWADKIHGMITPVDGDYFTFRHEPIGVCQIIPWNFPLLMFTWKIAPALCCGNTVVIKPAEQ
TPLSALYMGALIKEAGFPPGVVNILPGYGYPTAGAAIASIGIDKIAFTGSTEVGKLIQEAGRSNLKRVTLELGGKSPNIIFADADLDYAVEQAHQGVFF
NQGQCCTAGSRIFVEESIYEFVKRSVERAKRIVGSPFDPTTEQGPQIDKKQYNKILEIQSGVAEGAKLECGGKGLGRKGFFIEPTVFSNVTDDMRIA

KEEIFGPVQEILRFKTMDEVIERANNSDFGLVAAVFTNDINKALMVSSAMQAGTVW/INCYNALNAQSPFGGFKMSGNGREMGEFGLREYSEVKTV
TVKIPQKNS

>d1ag8a_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Cow (Bos taurus), mitochondrial}
VPTPNQQPEVLYNQIFINNEWHDAVS KKT FPTVN P STGDV ICHVAEGDKADVDRAVKAARAAFQLGSPWRRMDASERGRLLNRLADLIERDRTYL
AALETLDNGKPYIISYLV DLMVLKCLRYYAGWADKYHGKTIPIDG DYFSYTRHEPVG VCGQIIPWNFP LLMQAWKLGPALATGNVV VMKVAEQTPL
TALYVANLIKEAGFPPGVNVNIPFGPTAGAAIASHEDVDKVAFTGSTEVGHLIQVAAGKSNLKRVTL EIGGKSPNIIMSDADMDWAVEQAHFALFF
NQGQCCCAGSRTFVQEDIYAEFVERSVARAKSRVGNPFD SRTEQGPQVDETQFKKVLGYIKSGKEEGLKLCGGGAA DRGYFIQPTVFGDLQDG
MTIAKEEIFGPVMQILKF KSMEEV GRANNSKYGLAAAVFTKDLKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKLSGSRELGEYGLQAYTE
VKTVTVRVPQKNS

>d1cw3a_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Human (Homo sapiens), mitochondrial}
AVPAPNQQPEVFCNQIFINNEWHDAVRKTFPTVN P STGEVICQVAEGDKEDVDKAVKAARAAFQLGSPWRRMDASHRGRLLNRLADLIERDRTY
LAALETLDNGKPYVISYLV DLMVLKCLRYYAGWADKYHGKTIPIDG DYFSYTRHEPVG VCGQIIPWNFP LLMQAWKLGPALATGNVV VMKVAEQTPL
PLTALYVANLIKEAGFPPGVNVNIPFGPTAGAAIASHEDVDKVAFTGSTEIGRV IQVAAGSSNLKRVTL EIGGKSPNIIMSDADMDWAVEQAHFALFF
FNQGQCCCAGSRTFVQEDIYDEFVERSVARAKSRVGNPFD SKTEQGPQVDETQFKKVLGYINTGKQEGAKLLC GGGIAADRGYFIQPTVFGDVQD
GMTIAKEEIFGPVMQILKF KTIIEVV GRANNSTYGLAAAVFTKDLKANYLSQALQAGTVWVNCYDVFGAQSPFGGYKMSGSGRELGEYGLQAYTE
VKTVTVKVPQKNS

>d1bxsa_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Sheep (Ovis aries)}
DVPAPLTNLQFKYT KIFINNEWHSSVSGKKFPV FN PATEEKLC EVEEGDKEDVDKAVKAARQAFQIGSPWRTMDASERGRLLNKLADLIERDRLLAT
MEAMNGGKLFNSAYLMDLGGCIKTLRYCAGWADKIQGRTIPMDGNFTYTRSEPVG VCGQIIPWNFP LLMFLWKGPA LSCGNTVVVKPAEQTPL
TALHMGS LIKEAGFPPGVNVNIPGYGPTAGAAISHMDVDKVAFTGSTEVGK LIKEAAGKSNLKRVSL EGGKSPCIVFADADLDNAVEFAHQGVFYH
QGQCCIAASRLFVEESIYDEFVRSVERAKKV LGNPLPGVSQGPQIDKEQYEKILDIESGKKEGA KLECGGGPWGNKG YFIQPTVFSVTDDMRI
AKEEIFGPVQQIMKFKSLDDVIRANNTFYGLSAGIFTNDIKAITVSSALQSGTVWVNCYDVSAQCPFGGFKMSGNGRELGEYGFHEYTEVKVTI
KISQKNS

>d1a4sa_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Baltic cod (Gadus callarias)}
AQLVDSMPSASTGSVVVTDLNYWGGRRIKS KDGATTEPVFEPATGRVLCQM VPCGAEV DQAVQSAQAYLKW SKMAGIERSRVMLEAARIIRE
RRDNIAKLEVINNGKTITEAEYDIDAAWQCIEYYAGLAPL TSQH IQLPGGAFA YTRREPLGV CAGIL AWNP FMIAW KCAPALACGN AVFKPSP
MTPVTGVILAEIFHEAGVPVGLNVVQGGAETGSLLCHHPNVAKSFTGSVPTGKVMEMSAKTVKHVTLEGGKSPLLIFKDCELEN A VR GALMA
NFLTQGQVCTNGTRV FVQREIMPQFLEEVVKRTKAIVVGDPLLTETRMGGLISKPQLDKVLGFVAQAKKEGARVLC GGEPLTPSDPKLKNGYFMSPC
VLDNCRDDMTCVKEE IFGPVMSVLPFDTEEVLQRANNTFGLASGVTRDISRAHRVAANLEAGTCYINTYSISPVEV PFGGYKMSGFGRENGQAT
VDYYSQQLKTVIVE MG DVDSL F

>d1euha_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Streptococcus mutans}
TKQYK NYVNGEW KLSENEIKIYEPAS GAE LGSVPAMSTEEV D YVYASAKKAQPAW RALSYIERAAYLHKVADILMRDKEKIGA ILSKEVAKGYKSAVSE
VVR TAEIINYAAE EGLR MEGEVLEGG SFEAASKKIAV VRREP VGLV LAISPFNYPVNLAGSKIA PALIAGN VIAFKPPTQGSISG LLAEAFAEAGL PAG
VFNTITGRGSEIGDYI VEHQAVNF INFTGSTGIGERIGK MAGMRPIM L EGGKDSAIV LEDADLE TAKN IIAGAFG YSGQRCTAVK RVLMESVADEL
VEKIREKVLA LTIGNP EDDADITPLIDTKSAD YVEGLINDANDKGATALTEIKREGN LICPILFDKVTTDMRLAWE EPFGPVLP IIRVTS VEEAIEISNKSEY
GLQASIFTNDPRAFGIAE QLVE GTVHIN NK TQRGTDNFPFLGAKKSGAGI QGVKYSIEAMTTVKS VVFDI K

>d1ez0a_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Vibrio harveyi}
TDNVFYATNAFTGEALPLA FPV HTEEV NQAA TAAK VARD FRR NN SKRAS LLRTIAS ELEAR SDDIIARAH LETALPEV RL TGEIARTANQLRFADV
VNSGSYHQAILDTPNTRAPLKPDIRQQIALGPVAVFGASNPLAFSAAGGDTASALAAGCPVIVKGHTAHPGTSQIVAE CIEQALKQEQLPQAI FT
LLQGNQRALGQALVSHPEIKA VGFTG VGGGRALFNL AHERPEPIPFY GELGAINPTFIFPSAMRAKADLADQFVASMTMGCQFCTKPGVVFALN
TPETQAFIETAQSLIRQQSPSTLTPGIRD SYQS QVSRGSDD IDVTF SQAES PCV ASALFVTSENWRKHPAWE EEEIFGPQSLIVVCEN VADM LSL
EMLAGSLTATIHATEEDYD PQVSQLP RLEEAGRLV FNGWPTGV EGYAMV HGGPYPASTHS ASTVGA EAIHRWLRPVAYQALPESLLPDSLKAENP
LEIARAVDGKA

>d1k75a_c.82.1.2 (A:) L-histidinol dehydrogenase HisD {Escherichia coli}

NTIIDWNSCTAEQQRQLLMRPAISASESITRTVNDLNVKARGDEALREYSAFKDCKTALKVSAEIAASERLSDELKQAMAVAV/KNIETFHTAQ
KLPPVDVETQPGVRCQQVTRPVASVGLYIPGSAPLSTVLMLATPASIAGCKVVLCSPPPIDEILYAAQLCGVQDVNVGGAQIAALAFGTESVP
KVDKIFPGNAVFTEAKRQVSQRLDGAIDMPAGPSEVLVIADSGATPDFVASDLSQAEGPDSQVILLTPAADMARRVAEAVERQLAELPRAETA
RQALNASRLIVTKDLAQCVIEISNQYGPEHIIQTRNARELVDSITSAGSVFLGDWSPEASGDYASGTNHVLPTYGYTACSSLGLADFQKRMTVQELSK
EGFSALASTIETLAAAERLTAHKNAVTLRVNALKEQA

>d1aco_2 c.83.1.1 (2-528) Aconitase, first 3 domains {Cow (Bos taurus)}

RAKVAMSHFEPHEYIRYDLLEKNIDIVRKRLRNPLTLSEKIVYGHLDPPANQEIERGKTYLRLPDRVAMQDATAQMAMLQFISSGLPKVAVPSTIHCD
HLIEAQLGGEKDLRRAKDINQEVENFLATAGAKYGVGFWRPGSGIIHQIILENYAYPGVLLIGTDHSHTPNGGGICIGVGGADAVDMAGIPWEL
KCPKIVGVLGSLSGWTSPKDVILKVGAGLTVKGGAIVEYHGPGVDSISCTGMATICNMGAEGATTSTFPYNHRMKYLSKTGRADIANLADEFK
DHLVPDSGCHYDQLIEINLSELKPHINGPFTPDALHPVAEVGSVAEKEGWPLDIRVGLIGSCTNSSYEDMGRSAAVAKQALAHGLKCKSQFTITPGSE
QIRATIERDGYAQVLRDVGIVLANACGPGCIGQWDRKDIKKGEKNTIVTSYRNFTGRNDANPETHAFVTSPEITALAIAGTLKFNPETDFTGKDG
KKFKLEAPDADELPRAEFDPGQDQTYQHPPKDSSGQR

>d3pmga1 c.84.1.1 (A:1-190) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

VKIVTVKTKAYPDQKPGTSLRKRVKFQSSTNYAENFIQSIISTVEPAQRQEATLVVGGDGRFYMKEAQIQLIVRIAANGIGRLVIGQNGILSTPAVSCII
RKIKAIIGGIILTASHNPGGPNDFGIKFNISNGGPAPEAITDKIFQISKTIEEYACPDLKVDLGVLGKQQFDLENKFKPFTVEIVDS

>d3pmga2 c.84.1.1 (A:191-303) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

VEAYATMLRNIFDFNALKELLSGPNRLKIRIDAMHGVVGPVKKILCEELGAPANSAVNCVPLEDFGGHHPDPNLTYADLVETMKSGEHDFGAADF
GDGDRNMIKGKHGFFV

>d3pmga3 c.84.1.1 (A:304-420) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

NPSDSVAIAANIFSIPYFQQTGVRGFARSMPGALDRVANATKIALYETPTGWKFFGNLMDASKLSCGEESFGTGSDDIREKDGLOWAVLAWLSIL
ATRKQSVEDILKDHWHKFG

>d1kfia1 c.84.1.1 (A:3-205) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

QVIPAPRVQTQPYAGQKPGTSLRKVSEATQPNEYENFVQSFNTLRKDELKPKNVLVGGDGRYFNQAIFSIIRLAYANDISEVHVQAGLMST
PASSHYIRKVNEEVNCIGGIILTASHNPGGKEHDFGIKFNVRTGAPAPEDFTDQIYTHTTKIKEYLTVDYEFEKHINLDQIGVYKFEGRLEKSHFEVK
VVDT

>d1kfia2 c.84.1.1 (A:206-323) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

VQDYTQLMQKLFDFDLLKGLFSNKDFSFRFDGMHGVAQPYAKHIFGTLGCSKESLLNCDPSEDFFGGHHPDPNLTYAHDIVELLDIHKKKDVGTPQ
FGAACDGDADRNMIILGRQFFF

>d1kfia3 c.84.1.1 (A:324-443) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

TPSDSLAVIAANANLIFKNGLGAARSMPGALDKVAAKNGIKLFETPTGWKFFGNLMDAGLINLCGEESFGTGSNHIREDGIWAVLAWLTIAHK
NKNTDHFTVTEEEIVTQYWQQFG

>d1k2yx1 c.84.1.1 (X:5-154) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

KAPTLPASIFRAYDIRGVVGDTLTAETAYWIGRAIGSES LAR GEPCVAVGRDGRLSGPVELVKQLIQGLVDCGCQVSDGMVPTVLYAANVLEGKSGV
MLTGAHNPPDYNGFKIVVAGETLANEQIQLRERIEKNDLASGVGSVEQVD

>d1k2yx2 c.84.1.1 (X:155-258) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

ILPRYFKQIRDDIAMAKPMKVVVDCGNVAGVIAPQLIEALGCSVPLYCEVDGNFPNHHDPGKPNLKDIAKVKAEADLGLAFDGDGRGVV
VTNTGTII

>d1k2yx3 c.84.1.1 (X:259-367) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

YPDRLLLMFAKDVSRNPGADIIFDVKCTRLLALISGYGGRPMWKTGHSLIKMKETGALLAGEMSGHVFKERWFGFDDGIYSARLLEILSQD
QRDSEHVFSAF

>d1k2yx4 c.84.1.1 (X:368-463) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

PSDISTPEINITVTEDSKFAIIEALQRDAQWGEGNITLDGVRVDYPKGWGLVRASNTTPVLRFEADTEEEELERIKTVFRNQLKAVDSSLVPVF

>d1fua2 c.85.1.1 (A:1-355) L-fucose isomerase, N-terminal and second domains {Escherichia coli}

MKKISLPKIGIRPVIDGRRMVGRESLEEQTMNMAKATAALLTEKLRHACGAAVECVISDTCIAGMAEAAACEEKFSSQNVLITVTPCWCGSETID

MDPTRPKAIWGFNGTERPGAVYAAALAAHSQKGIPAFSIYGHVDVQDADDSIPADVEEKLRFARAGLAVASMKGKSYLSGGVSMGIAGSIVDH
NFFESWLGMKVQAVDMTELRRRIDQKIYDEAELEMALAWADKNFRYGEDENNQYQRNAEQSRAVLRESLLMAMCIRDMMQGNSKLADIGRV
EESLGYNAYAAGFQGQRHWTDQYPNGDTAEAILNSSFDWNGVREPFVVATENDSLNGVAMLGHQLGT

>d1fw8a_c.86.1.1 (A:) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SKYSLAPVAKELQSLLGKDVTLNDCVGPEVEAAVKASAPGSVILLENLYHIEEGSRKVDGQKVAKSKEDVQKFRHELSSLADVYINDAFGTAHRAH
SSMVGFDLPQRAAGFLEKELEYFGKALENPTRPFLAILGGAKVADKIQNLIDNLLKVDIIGGGMAFTFKVLENTEIGDSIFDKAGAEIVPKLMEKA
KAKGVEVLPDFIIADAFSADANTKTVTDKEGIPAGWQGLDNGPESRKFAATVAKTIVWNGPPGVFEFEKFAAGTKALLDEVVKSSAAGNTVII
GGGDTATVAKKGVTDKISHVSTGGASLELEGKELPGVAFLSEKKSSKLSVQDLDLKDKRWFIRVDFNPLDGKKITSNQRIVAAALPTIKYVLEHHP
RYVVLASHLGRPNERN

>d1qpg_c.86.1.1 (-) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SLSSKLSVQDLDLKDKRWFIRVDFNPLDGKKITSNQRIVAAALPTIKYVLEHHPRYVVLASHLGRQPNERNEKYSLAPVAKELQSLLGKDVTLNDCVG
PEVEAAVKASAPGSVILLENLYHIEEGSRKVDGQKVAKSKEDVQKFRHELSSLADVYINDAFGTAHRAHSSMVGFDLPQRAAGFLEKELEYFGKA
LENPTRPFLAILGGAKVADKIQNLIDNLLKVDIIGGGMAFTFKVLENTEIGDSIFDKAGAEIVPKLMEKAKGVVEVLPDFIIADAFSADANTKTV
TDKEGIPAGWQGLDNGPESRKFAATVAKTIVWNGPPGVFEFEKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATVAKKGVTDKISHVSTGGGA
SELLEGKELPGVAFLSEKK

>d1php_c.86.1.1 (-) Phosphoglycerate kinase {Bacillus stearothermophilus}

MNKKTIRDVDRGKRVFCRVDFNVPMEQGAITDDTRIRALPTIRYLIHGAKVILASHLGRPKGKVEELRLDAVAKRLGELLERPVAKTNEAVGDE
VKAADVDRLEQGDVLLENVRFYPGEEKNDPELAFAELADLYVNDAFGAAAHRAHASTEGIAHYLPAVAGFLMEKELEVLGKALSNPDRPFTAIGGA
KVKDKIGVIDNLLEKVDNLIIGGLAYTFVKALGHDVGKSLLEEDIKELAKSFMEKAKEGVRFYMPDVVVADRFDANDANTKVVPIDAIPADWSALD
IGPKTRELYRDVIRESKLVVWNGPMGVFEMDAFAHGTKAIAEALAEALDTYSVIGGGDSAAAVEKFLADKMDHISTGGASLEFMEGKQLPGVVA
LEDK

>d1vpe_c.86.1.1 (-) Phosphoglycerate kinase {Thermotoga maritima}

EKMTIRDVDLKGKRVIMRVDFNVPVKDGVVQDDTRIRALPTIKYALEQGAKVILLSHLGRPKGEPSPFSLAPVAKRLSELLGKEVKFVPAVGDEVK
KAVEELKEGEVLLNTRFHGETKNDPELAFAKFWASLADIHVNDAFGTAHRAHASNVGIAQFIPSVAGFLMEKEIKFLSKVTYNPEKPYVVVLGGAKV
SDKIGVITNLMEKADRILIGGAMMFTFLKALGKEVGSSRVEEDKIDLAKEAKEKGVEILPVDAVIAQKIEPGVEKKVRIDDGIPEGWMGLDIG
PETIELFKQKLSDAKTVVWNGPMGVFEIDDAEGTKQVALAIALTEKGAIITVVGGSAAAVNKGLEDKFHVSTGGASLEFLEGKELPGIASMR
IKKA

>d16pk_c.86.1.1 (-) Phosphoglycerate kinase {Trypanosoma brucei}

EKKSINECDLKGKKVLRVDFNVPVKNGKITNDYRIRSLPLKKVLTGGSCVLMMSHLGRPKGIPMAQAGKIRSTGGVPGFQQKATLKPVAKRLSELL
RPVTFAPDCLNAADVVKSMSPGDVVLLENVRFYKEEGSKKAKDREAMAKILASYGDVYISDAFGTAHRSATMTGIPKILNGAAGYLMEKEISYFA
KVLGNPPRPLVAIVGGAKVSDKIQLLDNMLQRIDYLLIGGAMAYTFLKAQGYSIGKSCEESKLEFARSLLKKAEDRKVQVILPIDHVCHTEFKAVDSPLI
TEDQNIPEGHMALDIGPKTIEKYVQTIGCKSAIWNGPMGVFEMVPYSKGTFAIAKAMGRGTHEHGLMSIIGGGDSASAAELSGEAKRMSHVSTG
GGASLELEGKTLPGVTLDDK

>d1hdia_c.86.1.1 (A:) Phosphoglycerate kinase {Pig (Sus scrofa)}

NKLTLDKLNVKGKRVVMRVDFNVPMAAAQITNNARIKAAPVPSIKFCDDGAKSVVLMMSHLGRPDGSPMPDKYSLQPVAELKSALGKAVFLKDCV
GPAVEKACADPAAGSVILLENLRHVVEEGKGKDASGNKAAGEPAKIKAFRASLALGDVYVNDAFGTAHRAHSSMVGVNLPKKAGAFLMKKELNY
FAAAAESPPerPLAILGGAKVADKIQLINNMLQRIIDYLLIGGAMAYTFLKAQGYSIGKSCEESKLEFARSLLKKAEDRKVQVILPIDHVCHTEFKAVDSPLI
EQAKIGQATVASGIPAGWMLDCGPKSSAKYSEAVARAKQIVWNGPVGVFEWEAFAQGTAKLMDDEVVKATSRCITIIGGGDTATCCAKWNTED
NVSHVSTGGASLELEGKVLPGVDALSNV

>d1jixa_c.87.1.1 (A:) beta-Glucosyltransferase (DNA-modifying) {Bacteriophage T4}

MKIAIINMGNNVINFKTPSSETIYLFKVISEMGLNVDIISLNGVYTKSFDEVVDVNDYDRILVVNSSINFFGGKPNLAILSAQKFMKYKSKIYLFDTI
RLPFSQSWPNVKNRPWAYLYTEEELLIKSPIKVISQGINLDIAKAHHKKVDNVIEFEYFPIEQYKIHMNDFQLSKPTKTLVDVYGGSFRSGQRESKMF
FLFDTGLNIEFFGNAREKQFKNPKPWTKAPVFTGKIPMNMVSEKNSQIAALIIGDKNYNDNFITLRVWETMASDAVMLIDEEDTKHRIINDARF
YVNNRAELIDRVNELKHSVLRKEMLSIQHDLNKTRAKKAEWQDAFKKIDL

>d1f0ka_c.87.1.2 (A:) Peptidoglycan biosynthesys glycosyltransferase MurG {Escherichia coli}

KRLMVMAGGTGGHVFGLAVALAHHLMAQGWQVRWLGTADRMEDALVPKHGEIDFIRISGLRGKGKIALIAAPLRFNAWRQARAIMKAYKPDVV
LGMGGYVSGPGGLAAWSLGIPVVLHEQNGIAGLTNKWLAKIATKVMQAFPGAFPNAEVVGNPVRTDVLALPLPQQRLAGREGPVRVLVVGGSQG
ARILNQTMPQVAALKGDSVTIHQSGKGSSQSVEQAYAEAGQPQHKVTEFIDDMAAAYAWADVVCRSGALTVESEIAAGLPALFVFQHKDRQ
QYWNALPLEKAGAAKIIEQPQLSVDAVANTLAGWSRETLTMAERARAASIPDATERVANEVSRRVARAL

>d1f6da_c.87.1.3 (A:) UDP-N-acetylglucosamine 2-epimerase {Escherichia coli}

MKVLTVFGRPEAKMPLVHALAKDPFFEAHKCVTAQHREMLDQVLKLFISIVPDYDLNIMQPQGQLTEITCRILEGLKPILAEFKPDVVLVHGDTTT
LATSLAAFYQRIPVGHVEAGLRTGDLSPWPEEANRTLGHAMYHFSPTETSRQNLLRENVADSRIFITGNTVIDALLWVRDQVMSSDKLRSELAAN
YPFIDPDKKMILVTGHRRESFRGFFEEICHALADIATHQDIQIVPVHLNPVNREPVNRLGHVKNVILIDPQEYLPFWVLMNHAWLIITDSGGIQEE
APSLGKPVLVMDTTERPEAVTAGTVRLVGTDKQRIVEEVTRLLKDENEYQAMSRAHNPyGDGQACSRIEALKNNRISL

>d1iira_c.87.1.5 (A:) UDP-glucosyltransferase GtfB {Amycolatopsis orientalis}

MRVLLATCGSRGDTEPLVALAVRVRDLGADVRMCAPPDAERA
LAEVGVPHPVPGPSARAPIQRAKPLTAEDVRRFTTEAIATQFDEIPAAAEGCAAV
VTTGLAAAIGVRSVAEKGIPYFYAFHCPSPYPPPLGEPTQDTIDIPAQWERNNQSAYQRYGGLLNSHRDAIGLPPVEDIFTFGYTDHPWV
AADPVLAPLQPTDLDLVQTGAWILPDERPLSPELAFLDAGPPPVLGFGLSGAPADAVRAIDAIRAHGRRVILSRGWADLVLPPDGADCFAIGEV
NHQVLFGRVAAVIHHGGAGTTHVAARAGAPQILPQMADQPYYAGRVAELGVGVAHDGPIPTFDLSAALATALTPETHARATAVAGTI
RTDGAAV
AARLLDAVSRE

>d1em6a_c.87.1.4 (A:) Glycogen phosphorylase {Human (Homo sapiens)}

ENVAELKKFSNRHLHFTLVKDRNVATTRDYYFALAHTVDRDHVLGRWIRTQQHYYDKCPKRVYYSLEFYMGRTLQNTMINGLQNACDEAIYQLGLD
IEELEEEIEDAGLGNNGGLGLRAACFLDSMATLGLAAYGYGIRYEYGIFNQKIRDGWQVEADDWLRYGNPWEKSRPFMLPVHFYGVKEHTNTGTK
WIDTQVVLALPYDPDTPVPGYMNNVTNTMRLWSARAPNDFNLRDFNVGVDYIQAVALDRNLAENISRVLYPNDNFFEGKELRLKQEFYFVVAATLQDIIRR
FKASKFGSTRGAGTVFDAFPDQVIAQLNDTHPALAIPLEMRFV DIEKL PWSKA WELTQKTFAYTNHTVLPEALERWPVDLVEKLPRHLEIIYEINQKH
LDRIVALFPKDVKDRLRRMSLIEEGSKRINMAHLCIVGSHAVNGVAKIHS DIVKTKVFKDFSELEPDKFQNKNTNGITP RRLLLCNPGLAE LIAEKIGED
YVKDLSQLTKLHSFLGDDVFLRELAKVKQENKLKFSQFLETEYKVKINPSSMFDVQVKRIHEYKRQLLNCLHVITMYNRIKKDPKKLFVPTVII GGKAA
PGYHMAKMIKILITSVADVNNDPMVGSKLKVFLENRYRS LAEKVIPATDLSEQISTAGTEASGTGNMFKMLNGALTIGTMDGANVEMAEEAGEE
NLFIGMRIDDVAALDKKGYEAKYYEALPELKLVIDQIDNGFFSPKQPDLFKDIINMLFYHDRFKVFADYEAYVKCQDKVSQLYMNPKAWNTMVLK
NIAASGKFSSDRTIKEAQNIWNVEPS

>d1a8i__ c.87.1.4 (-) Glycogen phosphorylase {Rabbit (*Oryctolagus cuniculus*)}

QEKRKQISVRLAGVENVTELKKNFRHLHFTLVKDRNVATPRDYYFALAHTVRDHVLGRWIRTQQHYYEKDPKRIVYLSLEFYMGRTLQNTMVNL
ALENACDEATYQLGLDMEELLEEIEDAGLNGGLGRLAACFLDSMATGLAAYGYGIRYEFGINQKICGGWQMEEADDWLRYGNPWEKARPEFT
LPVFHYGRVEHTSQGAKWVDTQVVAMPYDTPVPGYRNNVVNTMRLWSAKAPNDFLKDFNVGGYIQAVLDRNLAENISRVLVLPNDNFFEGKEI
RLKQEYFVVAATLQDIIRRFKSSKGCRDPVRTNFDAFPDKVAIQLNDTHPSLAIPELMRVLDLERLDWDKAWEVTVKTCAYTNHTVPEALERWPV
HLLETLLPRHLQIYEINQRFLNRVAAAFPGDVDRLLRMSLVEEGAVKRINMAHLCIAGSHAVNGVARIHSEILKKTIFKDFYELEPHFKFQNKTNGITPR
RWLVLCNPGLAEIIAERIGEYISLDQLRKLLSYVDDEAFIRDVAKVQKENKLKFAAYLEREYKVHINPNSLFDVQVKRIHEYKRQLLNCLHVITLYNIK
KEPNKFVVPRTMIGGKAAPGYHMAKMIKLIKITAIGDVVNHDPPVGDRLRVIFLENYRVS LAEKVIPAAIDLSEQJSTAGETEASGTGNMKFMLNGALTI
GTMDGANVEMAEEAGEENFFIFGMRVEDVDRLDQRGYNQAQYYDRIPELRQIEQLSSGFFSPKQPDFKDIVNMLMHDRFKVFADYEYVKCQ
EVSAKYKNPREWTRMVIERNATSGKESSDRTIAQYAREIWGVEPSPQRQLP

>d1ygpa_c.87.1.4 (A:) Glycogen phosphorylase {Baker's yeast (*Saccharomyces cerevisiae*)}

TRRLTGFPLQEIKSIDIPTMIPLLSRALWNKHQVKKFNKAEDFQDRFIDHVETTLARSLYNCDDMVAYEAASMSIRDNLVIDWNKTTQQKFTTRDPKRVY
YLSLEFLMGRA LDNALINMKIEDPDPAA SKGKPREMIKGALDELGFKFLEDVLDQEPDA GLNGGGLGRLAACFVDSMATEGIPAWGYGLRYEYGIFA
QKIIJDGYQVETPDYWLNSGNPWEIERNEVQIPVTFYGYVDRPEGGKTTLSAQWIGGERVLAVAYDFPVPGFKTSVNVLRLWQARPTTEFDLNKF
NNGDYKNSVAQQQRAESITAVLYPNNDNFAQGKE LRLKQQYFWCAASLHDILRRFKSKRPWT EFPDQVAIQLNDTHPTLAIVELQRVVLDEKLDW
HEAWDIVTKTFAYTNHTVMQEALEKWP RRLFGHLLPRHLEIIYDINWF FLEDVAKKFPKDVL LSRSIIEENS PERQIRMAFLAIVGSHKVNGVVELH
SELIKTTIFKDFIKFYGPSKFVN TNGITPRRWLQ QANPSLAKLISETLNDPTEYLLDMAKLTQ LEKYVEDKEFLKKWNQVKLN NKIRLVLDLIKKENDGV
DIINREYLDLTD FDMOVKRIHEYKRQOLNVFGJIYRYLAMKNMLKNGASIEEVAR KYPRKVSIFGGKSAPGYYMAKLI LIKNCVADIVNNDESIEHLK

VVFVADYNVSKAELIIPASDLSEHISTAGTEASGTSNMKFMNGGLIIGTVGANVEITREIGEDNVFLFGNLSENVEELRYNHQYHPQDLPSSLDVLS
YIESGQFSPENPNEFKPLVDSIKYHGDDYLVSDDFESYLATHELVQEFHNQRSEWLKSVLSANVGFFSDRCIEEYSDTIWNVEPV

>d1qm5a_c.87.1.4 (A:) Maltodextrin phosphorylase (MALP) {Escherichia coli}

SQPIFNDKQFQEALSRQWQRYGLNSAAEMTPRQWWLAVSEALAEMLRAQPFAKPVANQRHVNYISMEFLIGRLTGNLLNLGWYQDVQDSLKA
YDINLTDLLEEEIDPALGGNGLGRLAACFLDSMATVGQSATGYGLFRQSFVDGKQVEAPDDWHRSNYPWRHNEALDVQVGIGGKVTKD
GRWEPEFTITGQAWDLPVVGYRNGVAQPLRLWQATHAHPFDLTKFDGFLRAEQQGINAEKLTKVLYPNNDNHTAGKKLRMQQYFQCACSVAD
ILRRHHLAGRKLHELADYEVIQLNDTHPTIAPELLRVLIDEHQMSWDDAWAITSKTFAYTNHTLMPEALERWDVKLVKGLLPRHMQIINEINTRFKTL
VEKTWPGDEKVWAKLAVVHDQVHMANLCVGGFAVNGVAALHSDLVVKDLFPEYHQLWPNKFHNTNGITPRRWIKQCNPALAALLDKSLQK
EWANDLDQLINLEKFADDKFRDQYREIQANKVRLAEVFKVRTGIEINPQAIFDIQIKRLHEYKRQHNLHILALYKEIRENPQADRVPRVFLFGAKA
APGYYLAKNIIFAINKVADVINNDPLVGDKLKVVFLPDYCVSAAEKLIAPAADISEQISTAGKEASGTGNMKLALNGALTVGTLGANVEIAEKVGEENIFI
FGHTVEQVKAILAKGYDPVKWRKKDKVLDALKESGKYSQDGDKHAFDQMLHSIGKQGGDPYLVMAFDAAYVEAQKQVDLYRDQEAWTRAAIL
NTARCGMFSSDRSIRDYQARIWQAKR

>d4ecaa_c.88.1.1 (A:) Asparaginase type II {Escherichia coli}

LPNITILATGGTIAGGGDSATKSNTVGVGVENLVNAVPLQKDIANVKGEQVNIGSQDMNDNVWTLAKKINTDCDKTDGFVITHGVDTMEETA
YFLDLTVCKDKPVMVGMARPSSTSADGPFLNLYNAVTAADKASANRGVLVMNDTVLDGRDVTKTNTTDVATFKSVNYGPLGIHNGKIDYQR
TPARKHTSDTPFDVSKLNELPKVGVIVNYANASDLPKALVDAGYDGIVSAGVGNGLYKSVFDTLATAAKTGTAVVRSRVPVTGATTQDAEVDDAKY
GFVASGTLNPQKARVLLQLALTQTKDPQQIQQIFNQY

>d1wsaa_c.88.1.1 (A:) Asparaginase type II {Wolinella succinogenes}

KPQVTILATGGTIAGSGESSVKSSYAGAVTVDKLLAAVPAINDLATIKGEQISSGSQEMTGKVWLKAKRVNELLAQKETEAVIITHGDTMEETAFFL
NLTVKSQKPVVLVGMARPGSSMSADGPMNLYNAVNIAKSTNKVVIVMNDEIHAAREATKLNTTAVNAFASPTNGKIGTVYYGKVEYFTQSV
RPHTLASEFDISKIEELPRVDILYAHPPDTDVLVNAALQAGAKGIIHAGMGNGNPFLTQNALEKAAKSGVVVARSSRVGSGSTTQEAEVDDKLGTV
ATESLNPQKARVLLMLALTKTSDREAIQKIFSTY

>d1jsra_c.88.1.1 (A:) Asparaginase type II {Erwinia chrysanthemi}

LPNIVILATGGTIAGSAATGTTGYKAGALGVDTLNAVPEVKKLANVKGEQFSNMASENMTGDDVVLKLSQRVNELLARDVDGVVITHGDTVEE
SAYFLHLTVKSDKPVVFAAMRPATAISADGPMNLLEAVRVAGDKQSRGRGVMVVINDRIGSARYITKTNASTLDTFRANEEGYLGVIIGNRIYYQNRI
DKLHTTRSVFDVRLGTLSPKVDILYQYQDDPEYLYDAAIQHGVKGIVYAGMGAGSVVRGIAGMRKALEKGVVVMRSTRGNGIVPPDEELPGLVSD
SLNPAHARILLMLALTRTSDPKVIQEYFHTY

>d1agx_c.88.1.1 (-) Glutaminase-asparaginase {Acinetobacter glutaminasificans}

KNNVVIVATGGTIAGAGASSTNSATYSAAKVPVDALIKAVPQVNDLANITGIQALQVASESITDKELLSLARQVNDLVKKPSVNGVITHGDTMEETA
FFLNLVHDKPIVLVGSMPSTALSADGMLNLYNAVALASSNEAKNKGVMVLMNDSIFAARDVTKGNIHAFVQSQWGALGTLVEGKPYWFRSSV
KKHTNNSEFNIEKIQGDALPGVQIVYGSNDNMMPDAYQAFAKAGVKAIIHAGTGNGSMANYLVPVERKLHDEQGLQIVRSSRVAQGFVLRNAEQPD
DKYGVIAAHDLNPQKARLLMALAKTNDAKEIQNMFWNY

>d4pgaa_c.88.1.1 (A:) Glutaminase-asparaginase {Pseudomonas sp., 7A}

KLANVVILATGGTIAGAGASAANSATYQAAKVGVDKLIAGVPELADLANVRGEQVMQIASESISITNDLLKGKRAELADSNDVDGIVITHGDTLEE
TAYFLNLVQKTDKPIVVVGSMRPGTAMSADGMLNLYNAVAVASNKDSRGKGVLVTMNDIQSGRDVSKSINIKEAFKSAWGPLGMVVEGKSYWF
RLPAKRHTVNSEFDIKQISSLQVQDIASYGNVTDTAYKALAQNQAKALIHAGTGNGSVSSRVPALQQLRKNGTQIIRSSHVNQGGFLRNAEQPDD
KNDWVVAHDLNPEKARILAMVAMTKTQDSKELQRIFWEY

>d1pfka_c.89.1.1 (A:) Phosphofructokinase {Escherichia coli}

MIKKIGVLTSGGDAPGMNAAIRGVVRSALEGEVIMGYDGYLGLYEDRMVQLDRYSVSDMINRGGTFLGSARFPEFRDENIRAVAIENLKKRGIDA
LVVIGGDGSYMGAMRLTEMGFCIGLPGTIDNDIKGTDTIGFTALSTVVAIDRLRDTSSHQRISVVEVMGRYCGDLTAAAIAGGCEFVVVPEV
EFSREDLVNEIKAGIAKGKKAIVAITEHMCVDDELAHFIEKETGRETRATVLGHIQRGSPVYDRILASRMGAYAIDLLAGYGGRCVGIQNEQLVH
HDIIDAIENMKRPFKGDWLCAKKLY

>d3pkf_c.89.1.1 (-) Phosphofructokinase {Bacillus stearothermophilus}

MKRIGVLTSGGDSPGMNAIRSVVRKAIYHGVEVYGVYHYAGLIAGNIKKLEVGDVGDIIHRRGGTILYTCPEFKTEEGQKKGIEQLKKHGQGLVV

IGGDGSYQGAKKLTEHGFCVGPGTIDNDIPGTDFTIGFTALNTVIDAIDKIRDTATSHERTYVIEVMGRHAGDIALWSGLAGGAETILPEADYDM
NDVIARLKRKGHERGKKHSIIVAEGVGSGVDFGRQIQEATGFETRVTVLGHVQRGGPTAFDRVLASRLGARAVELLLEGKGGRCVGIQNNQLVDHDI
AEALANKHTIDQRMYALSKEISI

>d1cbf__ c.90.1.1 (-) Cobalt precorrin-4 methyltransferase CbiF {Bacillus megaterium}

GLVPRGSHMKLYIIGAGPGDPDLITVKGLKLLQQADVVYADSLVSQDLIAKSCKPGAEVLKTAGMHLEEMVGTMLDRMREGKMWVRVHTGDPAMY
GAIMEQMVLKREGVDIEIVPGVTSVFAAAAAAEALTIPDLTQTIVLTRAEGRTPVPEFEKLTDLAKHKCTIALFLSSTLKKVMKEFINAGWSEDTV
VVVYKATWPDEKIVRTTVKLDAMRTNGIRKQAMILAGWALDP

>d1i74a_ c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase (family II) {Streptococcus mutans}

SKILVFGHQNPDSDAIGSSMAYAYLKRQLGVDAQAVALGNPNEETAFLDYFGIQAPPVKSQAEGAKQVILTDHNEFQQSIADIREEVVEVVDH
HRVANFETANPLYMRLEPGSASSIVYRLYKENGVAIPKEAGVMSGLISDTLLKSPTTHASDPAVAEDLAKIAGVLDQEYGLAMLKAGTNLASKTAA
QLVDIDAKTFELNGSQVRVAQVNTVDINEVLERQNEIEAKASQAANGYSDFVLMITDILNSNSEILALGNNTDKVEAAFNFVLENNHAFLAGAVSR
KKQVPQLTESFNG

>d1k20a_ c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase (family II) {Streptococcus gordonii}

SKILVFGHQNPDSDAIGSSYAFAYLAREAYGLTEAVALGEPEETAFLDYFGVAAPRVTSAKAEGAEQVILTDHNEFQQSVADIAEVEVYGVVDHH
RVANFETANPLYMRLEPGSASSIVYRMFKEHSVAVSKIEAGLMSGLISDTLLKSPTTHPTDKIAAPLAELAGVNLEEYGLAMLKAGTNLASKAEE
LIDIDAKTFELNGNNVRVAQVNTVDIAEVLERQAEIEAAIEKAIADNGYSDFVLMITDINSNSEILAIGSNMDKVEAAFNFVLENNHAFLAGAVSRKK
QVVPQLTESFNA

>d1k23a_ c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase (family II) {Bacillus subtilis}

MEKILIFGHQNPDTDTCSAIAYADLKNKLGNAEPVRLGQVNGETQYALDYFKQESPRLVETAANEVNGVILVDHNERQQSIKDIIEEVQVLEVIDHHR
IANFETAEPILYYRAEPVGCTATLNKMYKENVKIEKEIAGLMSAIISDLSLFFKSPTCTDDVAAKELAEIAGVDAEYGLNMLKAGADLSKKTVEELI
SLDAKEFTLGSKKVEIAQVNTVDIEDVKKRQAELEAVISKVAEKNLDFLLITDILENDSSLALAINEAALKAFNVTLENNALLGVVSRRKKQVVP
VLT DAM

>d1ayl_1 c.91.1.1 (228-540) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Escherichia coli}
IASMHCSANVGKGEKDVAVFFGLSGTGKTTLSTDPKRRLIGDDEHGWWDDGVNFEGGYAKTIKLSKAEPEIYNAIRRALLENTVREDGTIDFDD
GSKTENTRVSYPYHIDNIVKPVSKAGHATKVIFLTADAFLGVLPVSRLTADQTQYHFLSGFTAKLAGTERGITEPTPTFSACFGAAFLSLHPTQYAEVLVK
RMQAAGAQAYLVNTGWNGTGKRISIKDTRAIIDAILNGSLDNAETFTLPMFNLAIPTEPGVDTKILDPRNTYASPEQWQEKAETLAKLFIDNFDKYT
DTPAGAACLVAGPKL

>d1ii2a1 c.91.1.1 (A:201-523) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Trypanosoma cruzi}
HLCMHASANVGKQGDVTFFGLSGTGKTTLSDPHRNLLIGDDEHVWTDRGVFNIEGGCYAKAIGLNPKTEKDIYDAVRGAVAENCVLDKRTGEID
FYDESICKNTRVAYPLSHIEGALKIAIGHPKNVIFLTNDAGVMPVVARLTSQAQMFWFVMGYTANPGVEAGGTRTARPIFSSCFGGPFLVRHATF
YGEQLAEKMQKHNSRVWLNTGYAGGRADRGAKRMPLRVTRAIIDAIHDGTLDRTEYEYPGWGLHIPKYVAKVPEHLLNPRKAWKDVRQFNETS
KELVAMFQESFSRARFAAKASQEMKSAVPRYVEA

>d1khba1 c.91.1.1 (A:260-622) Cytosolic phosphoenolpyruvate carboxykinase (GTP-hydrolysing) {Human (Homo sapiens)}

WLAEHMLVLGITNPEGEKKYAAFPSACGKTNLAMMNPSLPGWKVECGDDIAWMKFDAQGHLRAINPENGFFGVAPGTSVKNPNAIKTIQK
NTIFTNVAETSDGGVYWEGLIDEPLASGVITSWKNKEWSSEDGEPCAHPNRFCTPASQCPIDAAWESPEGVPIEGIIFGGRRPAGVPLVYEALSWQ
HGVFGAAMRSEATAAEHKGKIIHDPFAMRPFFGYNFGKYLHWLSMAQHPAAKLPKIFHVNWFRKDKEGKFILWPGFGENSRVLEWMFNRI
DGKASTKLPIGYIPKEDALNLKGLGHINMMELFSISKEFWDKEVEDIEKYLVDQVNADLPCEIEREILALKQRISQM

>d1jb1a_ c.91.1.2 (A:) HPr kinase HprK C-terminal domain {Lactobacillus casei}

ERRSMHGVVLVDIYGLVLITGDSGVGKSETALELVQRGHRLIADDRDVYQQDEQTIVGAAPPILSHLLEIRGLIIDVMNLFGAGAVREDTTISLIVHL
ENWTPDKTFDRLGSGEQTQLIFDVPVPKITPVKVRNLAIIIEVAAMNFRAKSMGYDATKTFEKNLNHLIEH

>d1ayl_2 c.109.1.1 (1-227) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Escherichia coli}

MRVNNGLTPQELEYGISDVHDIVNPSYDLYQEELDPSLTGYERGVLTNLGAVAVDTGIFTGRSPKDKYIVRDDTRDTFWWADKGKGKNDNKPL
SPETWQHLKGLVTRQLSGKRLFVDAFCGANPDTRLSRVRFITEAWQAHFVKNMFIRPSDEELAGFKPDFIVMNGAKCTNPQWKEQGLNSENFVA
FNLTERMQLIGGTWYGGEMKKGMFSMMNYLLPLKG

>d1ii2a2 c.109.1.1 (A:2-200) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy-liase) {Trypanosoma cruzi}
PPTIHRNLLSPELVQWALKIEKDSRLTARGALAVMSYAKTGRSPLDKRIVDTDDVRENVDWGKVNMKLSEESFARVRKIAKEFLDTREHLFVVDCFAG
HDERYRLKVRVFTTRPYHALFMRDMLIVPTPEELATFGEPDYVIYNAGECKADPSIPGLTSTCVALNFKTREQVILGTEYAGEMKKGILTVMFELMPQ
MN

>d1khba2 c.109.1.1 (A:10-259) Cytosolic phosphoenolpyruvate carboxykinase (GTP-hydrolysing) {Human (Homo sapiens)}
NLSAKVVGSLSDLPAVREFLENNAECLCPDHICDGSEENGRLLGQMEEEGILRRLKKYDNCWLALTDPRDVARIESTVITQEQRDTVPPIK
TGLSQLGRWMSEEDFEKAFCNARFPGCMKGRTMYVIPFSMGPLGSPLSKIGIELDSPYVVASMRIMTRMGTVPLEALGDGEFKCLHSVGCPLPLQ
KPLVNNWPCNPELTIAHLPDRREIISFGSGYGGNSLLGKCFALRMASRLAKEEG

>d1doza_c.92.1.1 (A:) Ferrochelatase {Bacillus subtilis}
SRKKMGLLVAYGTPYKEEDIERYTHIRRGRKPEPEMLQDLKDRYEAIIGGISPLAQITEQQAHNL_EQHLNEIQDEITFKAYIGLKHIPEFIEDAVAEMH
KDGITEAVSIVLAPHFSTFSVQSYNKRAKEEAELGGLTITSVESWYDEPKFVTYVWDRVKETYASMPEDERENAMLI
VSAHSLPEKIKEFGDPYDQL
HESAKLIAEAGAGVSEYAVGWQSEGNTDPWLGPDVQDLTRDLFEQKGYQAFVYVPGFVADHLEVLYDNDYECKVTTDIGASYYRPEMPNAKPE
FIDALATVVLKKLGR

>d1hrka_c.92.1.1 (A:) Ferrochelatase {Human (Homo sapiens)}
RKPKTGILMNLNGGPTLGDVHDFLRLDRDLMTLPIQNKLAPFIKRTPKIQEQYRRIGGGSPIKIWTSKQGEGMVKLLDESPNTAPHKYIGF
RYVHPLTEAIEEMERDGLERAIAFTQYPQYSCSTTGSSLNAYRYYNQVGRKPTMKWSTIDRWPTHLLIQCFADHILKELDHFPLEKRSEVVILFAH
SLPMSSVNRGDPYQEVSVATVQKVMERLEYCNPYRLVWQSKVGPMPWLGPOQTDESIKGLCERGRKNILLVPIAFTSDHETLYE
LDIEYSQVLAKECG
VENIRRAESLNGNPLFSKALADLVHSIQSNELC SKQLTLSCPLCVNPVCRTKSFTSQQL

>d1qgoa_c.92.1.2 (A:) Cobalt chelatase CbiK {Salmonella typhimurium}
KKALLVVSFGTSYHDTCEKNIVACERDLAASCPCDRDLFRAFTSGMIIRKLQRQDGIDIDTPLQALQKAAQGYQDV
AICSLHIIINGDEYEKIVREVQLLR
PLFTRLTLGVPLSSHNDYVQLMQALRQQMPSLRQTEKVVFMGHGASHHAFAAYACLDHMMTAQRFPARVGA
VESYPEVDILIDSLRDEGVTVGH
LMPLMLVAGDHAINDMASDDGDSWKMRFAAGIPATPWLSGLGENPAIRAMFVA
HLHQALNM

>d1efdn_c.92.2.1 (N:) Periplasmic ferric siderophore binding protein FhuD {Escherichia coli}
GIDPNRIVALEWLPVELLLALGIVPYGVADTINYRLWVSEPLPDSVIDVGLRTEPNLELLTEMKPSFMVWSAGYGP
SPEMLARIAPGRGFNFSDGKQ
PLAMARKSLTEMADLLNLQSAETHLAQYEDFIRSMKPRFVKRGARPLLTLIDPRHMLVFGPNSLFQE
ILDEYGI
PNAWQGETNFWGSTA
SIDRL
AAVKDV
DVLCFHDNSKMDALMATPLWQAMPFVRAGR
FQVPAWWFYGATLSAMHFV
RVLDNAIG

>d1toaa_c.92.2.2 (A:) Periplasmic zinc binding protein TroA {Treponema pallidum}
GKPLVVTTIGMIADAVKNIQGDVHLKGLMGPVDPHYTATAGDVE
WLGNADLILYNGLET
KMGEVFSKLRGSRLV
VAVSETIPVSQRLSLEEAE
FDPHVWF
DVKLWSYSVKAVYESLCKLPGKT
REFTQRYQAYQQQLDKLDAYV
RRKAQSLPAERRV
LVT
AHDAFGYFSRAY
GFEVKGLQGV
STASEAS
AHDMQELA
AFIAQRKLPAIFI
ESSIPH
KNE
V
ALRDAV
QARGHV
VQIGGEL
FSDAMGDAGT
SEGT
YVGMV
THN
IDT
V
AALAR

>d1psza_c.92.2.2 (A:) Pneumococcal surface antigen PssA {Pneumococcus (Streptococcus pneumoniae)}
KKDTTSGQKLKV
VATNSIIADITKNIAGDKIDLHSIV
PIGQDPHE
YELP
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KKT
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>d1mioa_c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}
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>d1miob_c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}
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MFPDTSGVLDGPTTGEYKMYPEGGTIEDLKDGTNSDLTLSGSYASDLGAKTLEKKCKVPFKTLRPIGVSATDEFIMALSEATGKEVPASIEERGQLIDLMIDAQQYLQGKKVALLGDPDEIIALSKFIIELGAIPKYVTGTPGMKFQKEIDAMLAEGIESKVKVEGDFDVHQWIKNEGVDLLISNTYGKFIREENIPFVRGFPIMDRYGHYNNPKVGYKGAILRVEEITNVILDKIERECTEEDFEVVR

>d2mina_c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}

SREEVESLIQEVLLEVYPEKARKDRNKHLAVNDPAVTQSKCIISNKKSQPGLMTIRGCAYAGSKGVVWGPICKDMIHISHGPVGCGQYSRAGRRNYYIGTTGVNAFTMNFTSDFQEKDIFGGDKKLAKLIDEVETLFPLNKGISVQSECPIGLIGDDIESVKVKAELSHTIVPRCEGFRGVSQLGHHIANDARDWVLGKRDDETTFASTPYDVAIIGDYNIGGDAWSSRILLEEMGLRCVAQWSDGDSISEIELTPKVKLNLVHCYRSMMNYISRHMEEKYGIPWMEYNFFGPTKTIESLRAIAAKFDESIQKKCEEVIAKYKPEWEAVVAKYRPRLEGKRVMLYIGGLRPRHVIGAYEDLGMEVVTGYEFAHNDDYDRTMKEMGSTLLYDDVTGYEFEEFVFKRKPDLIGSGIKEKFIFQKMGIWFREMHSDYSGPYHGFDFAI FARDMDMTLNNPCWKKLQAPWE

>d2minb_c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}

SQQVDKIKASYPLFLQDQYKDMIAKLRDGFEKYPQDKIDEVFQWTTKEYQELNFQREALTVNPACQPLGAVLCALGFEKTMVHGSQGCVAYFRSYFNRFREPVCVSDSMTEAAVFGQQQNMDGLQNCATYKPMIAVSTTCMAEVIGDDLNAFINNSKEGFIPDEFPPVFAHTPSFVGSHVTGWDNMFEGIARYFTLKSMDKVVGSNNKINIVPGFETYLNFRVIRMLSEMVGVSLLSDPEEVLDTPADGQFRMYAGGTTQEEMKDAPNALNTVLLQPWHLEKTKFVEGTWKHEVPKLNIPMGLDWTDEFLMKVSEISGQPIPASLTKERGRLVDMMTDSHTWLHGKRFALWGDPDFVMGLVKFLLELGCEPVHILCHNGNKRWKAVDAILAASPYGNATVIGKDLWHLRSLVFTDKPDFMIGNSYGKFIQRDTLHKGKEFEVPLIRGFPIDRHHLHRSTTLGYEGAMQILTTLVNSILERLDEETRGMQATDYNHDLVR

>d1qgua_c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Klebsiella pneumoniae}

TNATGERNLALIQEVLEVFPETARKERRKHMMSDPKMKSVGKCIISNRKSQPGVMTVRGCAYAGSKGVVGPICKDMAISHGPVGCGQYSRAGRPNYYTGVSGVDSFGTLNFTSDFQERDIVFGGDKKLSKLIEMELLFPLTKGITIQSECPVGLIGDDISAVANASSKALDKPVIPVRCEGFRGVSQLGHHIANDVVRDWLNNREGQPFETTPYDVAIIGDYNIGGDAWASRILLEEMGLRVVAQWSDGTLVEMENTPFVKLNLVHCYRSMMNYIARHMEEKHQIPWMEYNFFGPTKIAESLRKIADQFDDTIRANAЕAVIARYEGQMAIIAKYRPRLEGKVLLYMGLRPRHVIGAYEDLGMEIIAGYEFAHNDDYDRTL PDLKEGTLLFDDASSYELEAFVALKPDLSGIGKEKYIFQKMGVPFRQMHSDYSGPYHGYDGFIAFARDMDMTLNNPAWNELTAPWL

>d1qgub_c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Klebsiella pneumoniae}

SQTIDKINSCYPLFEQDEYQELFRNKRQLEEAHDQAQRVQEWFATTTAEYEAUNFRREALTVDPAKACQPLGAVLCISLGFANTLPVHGSQGCVAYFRTYFNRHFKEPIACVSDSMTEAAVFGGNNNMNLGLQNASALYKPEIIAVSTTCMAEVIGDDLQAFIANAKKDFVDSIAPHAHTPSFIGSHVTGWDNMFEGFAKFTADYQGQPGKLPKLNLTGFETYLGNGFRVLKRMMEQMAVPCSSLSDPSEVLDTPADGHYRMYSGGTTQQEMKEAPDAIDTLLQWPWQLLKSKKVQEMWNQPAT EVAIPLGLAATDELLMTVSQLSGKPIADALTHERGRLVDMMLDSHTWLHGKKFLYGDPDFVMLTRFLLELGCEPTVILSHNANKRWQKAMNKMLDASPYGRDSEVFNCIDLWHRSLMFTRQPDFMIGNSYGKFIQRDTLAKGKAFEVPLIRLGFPFLDRHHLRQT TWGYEGAMNIVTTLNAVLEKLDSDTSQLGKTDYFDLVR

>d1jr2a_c.113.1.1 (A:) Uroporphyrinogen III synthase (U3S, HemD) {Human (Homo sapiens)}

MKVLLLKDAKEDDCGQDPYIRELGLYGLEATLIPVLSFEFLSPSFSEKLSHPEDYGGILIFTSPRAVEAAELCLEQNNKTEWERSLKEKVNNAKSVYVG NATASLVS KIGLDEGETCGNAEKLAEYICSRESSALPFLPCGNLKREILPKALKDKGIA MESITYQTVAHPGIQGNLNSYSSQQGPASITFFSPSGLYSLKHQELSGDNIDQIKFAAIGPTTARALAAQGLPVCTAESPTPQALATGIRKALQ

>d2dri_c.93.1.1 (-) D-ribose-binding protein {Escherichia coli, strain k-12}

KDTIALVVSTLNPNFFVSLKDGAKQEA KLGYNLVVLD SQNNPAKELANVQDLTVRGTKILLINPTSDAVGNAV KMANQANIPVITLDRQATKGEV VSHIASDNVLLGGKIA GDYIAK KAGEGAKVIELQGIAGTSAAREREGEGFQQVAAHKFNVLASQPD FDRIKGLNVMQNLLTAHPDVQAVFAQNDE MAL GALRALQTAGKSDVMVVGFDGTPGEKA VNDGKLAATIAQLPDQIGAKGVETADVLKGEVQAKYV DVLKLVVKQ

>d8abp_c.93.1.1 (-) L-arabinose-binding protein {Escherichia coli}

NLKLGF LVQPEEPWFQTEWKFADKAGKDLGFEV KIAVPDGEKTLNAIDS LAASGA KGFVICTPDPKLSAIVAKARGYDMKVI AVDDQFVN A KGK PMDTVPLV MLAATKIGERQGQELYKEMQKRGWDV KESAVMAITANE D TARRRTTGSM DALKAAGFPEKQIYQVPTKSNDIPGAFDAANSMLVQ HPEVKHWLIVGMNDSTVLGGV RATEGQGFKAADIIGINGVDAVSELSKAQATGFYGSLLPSPDVHGYKSSEMLYNWVAKDVEPPKFTEVTDVVLITRDNFKEEKKGLGGK

>d1rpja_c.93.1.1 (A:) D-allose-binding protein {Escherichia coli}

AAEYAVVLTLSNPFWVDMKKGIEDEAKTLGVSVDFASPSEGDFQS QLQLFEDLSNK NYKGIAFAPLSSVN L VMPVARAWKKGIYLVNLDEKIDMD

NLKKAGGNVEAFVTTDNVAVGAKGASFIIDKLGAEGBEAVIIEKGKAGNASGEARRNGATEAFKKASQJKLVASQPADWDRIKALDVATNVLQRNPNI
KAIYCANDTMAMGVAQAVANAGKTGKVLVVGTDGIPEARKMVEAGQMTATVAQNPADIGATGLKLMVDAEKGKVIPLDKAPEFKLVDISILVTQ
>d2gbp__ c.93.1.1 (-) Galactose/glucose-binding protein {Escherichia coli}
ADTRIGVTIYKYDDNFMSSVRKAIEQDAKAAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAINLVDPAAAGTVIEKARGQNVVFNFKEPS
RKALDSYDKAYVGTDKESGIIQGDLIAKHWAANQGWDLNKDGQIQFVLLKGEPGHPDAEARTTYVIKELNDKGIKTEQLQLDTAMWDTAQAKD
KMDAWLSGPNANKIEVVIANNDAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGALAGTVLNDANNQAKATFDLAKNLADGKAADGTN
WKIDNKVVVPYVGVDKDNLAESK
>d1gca__ c.93.1.1 (-) Galactose/glucose-binding protein {Salmonella typhimurium, strain lt2}
ADTRIGVTIYKYDDNFMSSVRKAIEKDGKSAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAINLVDPAAAGTVIEKARGQNVVFNFKEPSR
KALDSYDKAYVGTDKESGVIQGDLIAKHWAANQGWDLNKDGKIQYVLLKGEPGHPDAEARTTYVVKELNDKGIQTEQLALDTAMWDTAQAKD
KMDAWLSGPNANKIEVVIANNDAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGAMAGTVLNDANNQAKATFDLAKNLADGKAADGTS
WKIENKIVRVPYVGVDKDNLSEFTQK
>d1pea__ c.93.1.1 (-) Amide receptor/negative regulator of the amidase operon (AmiC) {Pseudomonas aeruginosa}
PLIGLLFSETGVTADIERSQRYGALLAVEQLNREGGVGGRPIETLSQDPGGDPDRYRLCAEDFIRNRGVRFLVGCYMSHTRKAVMPVVERADALLCYP
TPYEGFEYSPNIVYGGPAPQNQNSAPLAAYLIRHYGERVFIGSDYIYPRESNHVMRHLRQHGGTVLEEYIYIPLYSDDDLQRAVERIYQARADVVFSTV
VGTGTAELYRAIARRYGDGRPPIASLTTEAEVAKMESDVAEGQVVVAPYFSSIDTPSRAFVQACHGFPENATITAWAEAAYWQTLLGRAAQAA
GNWRVEDVQRHLYDIDIDAPQGPVRVERQNNHSRLSSRIAIDARGVFQVRWQSPEIRPDPYVVVHNLLDDW
>d1jx6a__ c.93.1.1 (A:) Quorum-sensing signal (autoinducer-2) binding protein LuxP {Vibrio harveyi}
GYWGYQEFLDEFPEQRNLTNALSEAVRAQPVPLSKPTQRPIKISVYPGQQVSDYWVRNIASFKEKLYKLNINYQLNQVFRPNADIQQQLSLSMEAL
KSKSDYLIFTLDTTRHRKFVEHVLDSNTKLILQNIITPVREWDKHQPFLYVGFDAEGRSRELATEFGKKFPKHTYYSVLYFSEGYISDVRGDTFIHQVNRR
DNNFELQSAYYTKATKQSGYDAAKASLAKHPDVDIFYACSTDVALGAVALAELGREDIMINGWGGSAELDAIQKGDDITVMRMNDTGIAMA
EAIKWDLEDKPVPTVYSGDFEIVTKADSPERIEALKRAFRYSD
>d1dbqa__ c.93.1.1 (A:) Purine repressor (PurR), C-terminal domain {Escherichia coli}
KSIGLLATSSEAAFAEIIAVEKNCFCQKGTYLILGNAWNNLKQRAYLSMMAQKRVGDLVMCSEYPEPELLAMLEEYRHIPMVVMDWGEAKADFT
DAVIDNAFEGGYMAGRYLIERGHREIGVIPGLERNTGAGFMKAMEEAMIKVPEWIVQGDFEPESGYRAMQQILSQPHRPTAVFCGGDIM
AMGALCAADEMGLRVPQDVSLSLGYDNVRNARYFTPALTTIHKQPKDSLGETAFNMLLDRIVNKREEPQSIEVHPRLIERRSVADGPFRDYRR
>d1jyea__ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}
LLIGVATSSLALHAPSQIVAAILSRADQLGASVVVSMVERSGVEACKTAVHNLLAQRVSGLIINYPLDDQDAIAVEAACTNVPALFLDVSQDQTPINSIIFS
HEDGTRLGVEHLVALGHQQIALLAGPLSSVSARLRLAGWHKYLTRNQIQPIAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMR
AITESGLRGADISVVGYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLPVSIVKRKTTLAPNTQTASRALADSLMQLARQV
SRL
>d1tlfa__ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}
SLLIGVATSSLALHAPSQIVAAIKSRADQLGASVVVSMVERSGVEACKA AVHNLLAQRVSGLIINYPLDDQDAIAVEAACTNVPALFLDVSQDQTPINSIIF
SHEDGTRLGVEHLVALGHQQIALLAGPLSSVSARLRLAGWHKYLTRNQIQPIAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAM
RAITESGLRGADISVVGYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNQLPVSIVKRKTTLAPNTQTASRALADSLMQLARQV
SRL
>d1byka__ c.93.1.1 (A:) Trehalose repressor, C-terminal domain {Escherichia coli}
SDKVVAIIVTRLDSLSENLAQTMILPAFYEQGYDPIMMESQFSPQLVAEHLGVLKRRNIDGVVLFGTGITEEMLAHWQSSLVLLARDAGFASVCYD
DEGAIKILMQRLYDQGHRNISYLGVPVHSVDVTGKRRHEAYLAFCKAHKLHPVAALPGLAMKQGYENVAKVITPETTALLCATDTLALGASKYLQEQR
DTLQLASVGNTPLMKFLHPEIVTVDPGYAEAGRQAACQLIAQVTGRSEPQQIIIPATL
>d2liv__ c.93.1.1 (-) Leucine-,isoleucine-,valine-binding (LIV) protein {Escherichia coli}
EDIKVAVVGAMSGPVAQYGDQEFTGAEQAVADINA KGGIKGNKLQIAKYDDACDPKQAVAVANKVNDGIKYVIGHLCSSSTQPASDIYEDEGILMI
TPAATAPELTARGYQLLRTTGLSDQGPTAAKYILEVKVPQRIAIVHDKQQYGEGLARAVQDGLKKGNANVVFFDGITAGEKDFSTLVARLKKE NIDFV
YYGGYHPEMGQILRQARAAGLKTQFMGPEGVANVLSNIAGESAEGLLVTPKKNYDQVPANKPIVDAIKAKKQDPSGAFVWTTYAA LQLQAGLN
QSDDPAEIAKYLKANSVDTVMGPLTWDEKGLKGFEFGVFDWHANGTADAK

>d2lbp__ c.93.1.1 (-) Leucine-binding protein {Escherichia coli}

DDIKVAVVGAMSGPIAQWGIMEFNGAEQAIKDINAKGGIKGDKLGVVEYDDACDPKQAVAVANKIVNDGIKYVIGHLCSSSTQPASDIYEDEGILMIS
PGATAPELTQRGYQHIMRTAGLDSSQGPTAAKYILETVKPQRIAIIHDKQQYGEGLARSVQDGLKAANANVVFFGITAGEKDFSALIARLKKENIDFV
YYGGYYPEMGQMRLQRARSVGLKTQFMGPEGVGNASLSNIAGDAAEGLMLVTMPKRYDQDPANQGIVDALKADKKDPSGPYVWITYAAVQLATA
LERTGSDEPLALVKDLKANGANTVIGPLNWDEKGDLKGDFGVFQWHADGSSTKAK

>d1dp4a_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Rat (Rattus norvegicus)}

SDLTVAVVPLNTSYPWSWARVGPAPVELALARVKARPDLPGWTVMVLGSSENAAGVCSDTAAPLAADLVWEHSPAVFLGPGCVYSAAPVGR
FTAHWRVPPLTAGAPALGIGVKDEYALTRTPSHVKLGDFVTALHRRLGWEHQALVLYADRLGDDRPCFFIVEGLYMRVRERLNITVNHQEFVEGDP
DHYPKLLRAVRRKGRVIYCSSPDAFRNLMILLALNAGLTGEDYVFFHLDVFGQSLKSAQGLVPQKPWERGDGQDRSARQAFQAALKITYKEPDNPNEY
LEFLKQLKLADKKFNFTVEDGLKNIIPASFHDGLLLYQAVTETLAQGGTVTDGENITQRMWNRSFQGVTGYLKIDRNGDRDTSFLWDMDPETG
AFRVVLYNNGTSQELMAVSEHKLYWPLGYPPDVPKCGF

>d1jdpa_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Human (Homo sapiens)}

EALPPQKIEVLVLPQDDSYLFLSLTRVRPAIEYALRSVEGNGTGRRLPPGTRFQVAYEDSDCGNRALFSLDRVAARGAKPDLILGPVCEYAAAPVAR
LASHWDLPMISAGALAAGFQHKDSEYSHLTRVAPAYAKMGEMLALFRHHHSRAALVYSDDKLERNCYFTLEGVHEVFQEEGLHTSIYFDET
DLDLEDIVRNQASERVVIMCASSDTIRSIMLVAHRHGMTSGDYAFFNIELFNSSSYGDGSWKRGDKHDFEAKQAYSSLQTVTLRTVKPEFEKFSME
VKSSVEKQGLNMEDYVNMFVEGFHDAILYVLALHEVLRAGYSKKDGKIIQQTWNRTFEGIAGQVSIDANGDRYGFDSVIAMTDVEAGTQEVID
YFGKEGRFEMRP

>d1ewka_ c.93.1.1 (A:) Metabotropic glutamate receptor subtype 1 {Rat (Rattus norvegicus)}

RSVARMDGDIVIGALFSVHHQPPAEKVKPERKC GEIREQYGIQRVEAMHTLDKINADPVLLPNITLGSEIRDSCWHSSVAEQSIEFIRDSLISIRDEKD
GLNRCYPDGTLPGRTKKPIAGVIGPGSSVAIQVQNLLQFDIPQIAYATSIDLSDKTLKYFLRVVPSDTLQARAML DIVKRYNWTYVSAVHTEG
NYGESGMADFKELAAGQEGLCIAHSKDIYSNAGEKSFDRLRKLRERLPKARVVCFCEGMTVRGLSAMRRLGVVGEFLIGSDGWADRDEVIEGYE
VEANGGITKLQSPPEVRSFDDYFLKLRLDTNTRNPWFPEFWQHRFQCLRGHLLENPNFKVCTGNESLEENYVQDSKMGFVINAIYAMAHLQNM
MHHALCPGHVGLCDAMKPIDGRKLDFLIKSSFVGVSCEEWFDEKGDAPGRYDIMNLQYTEANRYDYVHGTWHEGVLNIDDYKI

>d1jeta_ c.94.1.1 (A:) Oligo-peptide binding protein (OPPA) {Salmonella typhimurium}

ADVPAGVQLADKQTLCRRNNGEVQLDPHKIEGVPESNRDLFEGGLISDVEGHPSPGVAEKWENKDFKVWTFLRENAKWSDGTPVTAHDFVY
SWQRALDPNTASPASYLQYGHIANDDIIAGKKPATDGLVKALDDHTFEVTLSEPVPFYKLLVHPSVSPVPSAVEKFGDKWTQ PANIVTNGAYKL
NWVVNERIVLERNPQYWDNAKTVINQVTLPISEVTDNRYRSGEIDMTYNMPIELFQKLKEIPNEVRVDPYLCTYYEINNQKAPFNDVRVRT
ALKLALDRDIIVNKVKNQGDLPAYSTPPYTDGAKLVEPEWKWSQQKRNEEAKKLLAEAGFTADKPLTFDLYNTSDLHKKLAIAVASIWKKNLGVN
VNLENQEWTFLDTRHQGTFDVARAGWCADYNEPTSFLNTMSDSSNNTAHYKSPAFDKLIADTLVADDTQRSELYAKAEQQLDKDSAIVPVYYY
VNARLVKPWVGGYTGKDPLDNIYVKNLYIIKH

>d1pda_1 c.94.1.1 (3-219) Porphobilinogen deaminase (hydroxymethylbilane synthase), N-terminal domain {Escherichia coli}

DNVRLIATRQSPLALWQAHYVKDKLMASHPGLVVELPMVTRGDVILDPLAKVGGKGLVKELEVALLNRADIAVHSMKDVPVEFPQGLGLVTIC
EREPRDAFVSNNYDSLDALPAGSIVGTSSLRRQCQLAERRPDLIIRSLRGNVGTRLSKLDNGEYDIAILAVAGLKRLGLESRIRAALPPEISLPAVGQGA
VGIECRDSDRTRELLAAL

>d1lst_ c.94.1.1 (-) Lysine-,arginine-,ornithine-binding (LAO) protein {Salmonella typhimurium}

ALPQTVRIGTDITYAPFSSKDAKGEFIGFDIDLGNEMCKRMQVKCTWVASDFDALIPSALKAKKIDAISSLSITDKRQQEIAFSDKLYAADSLRIAAGGSPI
QPTLESLKGKHGVVLQGSTQEAYANDNWRTKGVDVAYANQDLIYSDLTAGRLDAALQDEVAASEGFLKQPGKEYAFAGPSVKDKYFGDGTGVG
LRKDDTELKAADFKAELTELQRDGTYDKMAKKYDFNJVYGD

>d1sbp_ c.94.1.1 (-) Sulphate-binding protein {Salmonella typhimurium}

KDIQLLNVSYDPTRELQYQYNKAFSAHWKQETGDNVVIDQSHGGSGKQATSVINGIEADTVTLALAYDVNAIAERGRIDKNWIKRLPDDSAPYTSTIV
FLVRKGNPQKIHWDNLDIKPGVSVITPNPKSSGGARWNYLAAWGYALHHNNNDQAKAEDFKALFKNVEVLDGARGSTNTFVERGIGDVLIWE
NEALLATNELGDKDFEIVTPSESILAEPTVSVDKVEKKDTKAVAECAYLYSPEGQEIAAKNFYRPRDADVAKYDDAFPKLKLFTIDEVFGGWAKA
QKDHFADGGTFDQISK

>d1ixh_ c.94.1.1 (-) Phosphate-binding protein {Escherichia coli}

EASLTGAGATFPAPVYAKWADTYQKETGNKVNYQGIGSSGGVKQIIANTVDFGASDAPLSDEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGELVLGK
TLDIYLGKIKKWDDEIAIKLNPGKLPSQNIAVRRADGSGTSVFTSYLAKVNEEWKNNGTGSTV/KWP1GLGGKNDGIAAFVQLRPGAIGYVE
YAYAKQNNLAYTKLISADGKPVSPTEENFANAAGKADWSKTFAQDLTNQKGEDAWPITSTTFILIHKDQKKPEQGTEVLKFFDWAYKTGAKQANDLD
YASLPDSVVEQVRAAWTKNIKDSGKPLY

>d3mbp_c.94.1.1 (-) D-maltodextrin-binding protein, MBP {Escherichia coli}

KIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIIFWAHDRFGGYAQSGLLAEITPDKA
FQDKLYPFTWDAVR
YNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEIPALDKELAKGKSA
MFNLQEPYFTWPLIA
DGGYAFKYENGKYDIKDVGDNAGAKAGLTLVD
LIK
NKHMNADTDYSIAEA
AFNKG
ETAMTINGP
WA
SNIDTSKV
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>d1elja_c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Pyrococcus furiosus}

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>d1eu8a_c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Thermococcus litoralis}

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>d3thia_c.94.1.1 (A:) Thiaminase I {Paenibacillus thiaminolyticus}

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PTVASLKGKRVGVLQGTTQETFGNEHWAPKGIEIVSYQQQDNIYSDLAGRIDAQFDEVAASEGFLQPGKDYKFGGPAVKDEKLFGVGTGMGL
RKEDNELREALNKAFAEMRADGTYEKLAKKYFDVDVYGG

>d1pot__ c.94.1.1 (-) Spermidine/putrescine-binding protein PotD {Escherichia coli}

NNTLFYNWTEYVPPGLEQFTKETGIKVYSTYESNETMYAKLKYKDAGAYDLVPSTYYVDKMRKEGMIQKIDKSCLTNFSNLDPDMLNKPDFDPNN
DYSIPIYGATAIGVNGDAVDPKSVTWADLWKPEYKGSLLTDDAREVFQMLRKLGYSGNTTDPEKEIAAYNELKKLMPNVAAFNSDNPANPYM
EGEVNLGMIWNGSAFVARQAGTPIDVWWPKEGGIFWMDSLAIPANAKNKEGALKLINFLRPDVAKQVAETIGYPTPNLAARKLLSPEVANDKTLYP
DAETIKNGEWQNDVGAASSIYEYYQKLKAG

>d1a99a_ c.94.1.1 (A:) Putrescine receptor (PotF) {Escherichia coli}

QKTLHIYNWSDYIAPDTVANFEKETGIKVYDVFDSNEVLEGKLMAGSTGFDFLVPSASFLERQLTAGVFQPLDKSKLPEWKNLDPELLKLVAKHDPD
NKFAMPYMWATTGIGYNVDVKAVLGENAPVDSWDLILKPENLEKLKSCGVSLDAPEEVFATVLNYLGKDPNSTKADDYTGPATDLLLKLRPNIRYF
HSSQYINDLANGDICVAIGWAGDVWQASNRAKEAKNGVNVSFSIPKEGAMAFFDVFAMPADAKNKEADYQFLNYLLRPDVVAHISDHVFYANAN
KAATPLVSAEVRENPGIYPPADVRAKLTFLKVQDPKIDRVRTRAWTKVKSG

>d1wdna_ c.94.1.1 (A:) Glutamine-binding protein {Escherichia coli}

KLVVATDTAFVPFEFKQGDLYVGFDVLWAAIAKELKLDYELKPMDFSGIIPALQTKNVDLALAGITITDERKKAIDFSDGYYKSGLLVMVKANNNDVK
SVKLDGKVVAKSGTGSVDYAKANIKTDLRFNIDNAYMELGTRNADAVLHDTPNILYFIKTAGNGQFKAVGDSLEAQQYGIAPKGSDELRDK
VNGALKTLRENGTYNEIYKKWFGTEPK

>d1ftka_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Rattus norvegicus}, GluR2

KTVVVTTILESPYVMMKKNHEMLEGNERYEGERVCDLAAEIAKHCDFKYLTKIVDGKYGARDADTKIWNMGVGEVYKADIAIAPIITLVREEVID
FSKPFMISLGIIMKPGTDGNPIESAEDLSKQTEIAYGTLDSGSTKEFFRSKIAVFDKMWTYMRSAEPSVFRRTAEGVARVRKSKGYAYLLESTMN
EYIEQRKPCDMKVGGLNLDKSGYGIATPKGSSLGNAVNLAVLKLNEQGLLDKLKNKWYDKGEC

>d1ii5a_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Synechocystis sp., GluR0}

GSAMALKVGVGVNPPVFYGEKGNAFTGISLDVWRAVAESQKWNSEYVRQNSISAGITAVAEGEGLILIGPISVTPERAIAEGITFTQPYFSSGIGLLI
PGTATPLFRSVGDLKNKEAVVRDTTAVDWANFYQADVRETNNLTAITLLQQVVEAVMFDRPALIYTRQNPNLNLEVTEIRVSLEPYGFVLKENS
PLQKTINVEMLNLLYSRVIAEFTERWLG

>d1amf__ c.94.1.1 (-) Molybdate-binding protein, ModA {Escherichia coli}

GKITVFAAASLTNAMEQDIATQFKKEKGVDVVFSSASSTLARQIEAGAPADLFISADQKWMYDVAVKKAIDTATRQTLGNSLVVVAPKASVQKDFTI
DSKTNWTSLLNGGRLAVGDPEHVPAGIYAKEALQKLGAWDTLSPKLAEDVRGALALVERNEAPLGVYGSNAVASKGVVVATFPEDSHKKVEYP
VAVVEGHNNATVKAFYDYLKGPGQAAEIFKRYGFTIK

>d1atg__ c.94.1.1 (-) Molybdate-binding protein, ModA {Azotobacter vinelandii}

ELKVVATNFLGTLTEQLAGQFAKQTGHAVVISSGSSGPVYQAQIVNGAPYVNFSADEKSPEKLDNQGFGALPGSRFTYAIGKLVLSAKPGLVDNQGKV
LAGNGWRHIAISNPQIAPYGLAGTQLVHLGLDKLTAQERIVEANSVGQAHQSQTASGAADLGVALAQIIQAAKIPGSHWFPPANYYEPIVQQAVI
TKSTAEKANAEQFMSWMKGPKAVAIKAAGYVLPQ

>d1al3__ c.94.1.1 (-) Cofactor-binding fragment of CysB {Klebsiella aerogenes}

TWPDKGSLYVATHTQARYALPGVIKGFIERYPRVSLHMHQGSPTQIAEVSKGNADFAIAATEALHYDDLVMPLCYHWNRSIVTPEHPLATKGSVSI
EELAQYPLVTYTFGFTGRSELDTAFNRAGLTPRIVFTAADVICKTVRLGLGVVIASMAVDPVSDPDVLVKLDANGIFSHSTTKIGFRRSTFLRSYMYDF
IQRFAPHLTDVVDTAVALRSNEDIEAMFKDIKLPEK

>d1i6aa_ c.94.1.1 (A:) Hydrogen peroxide-inducible genes activator OxyR, regulatory domain {Escherichia coli}

ETMSGPLHIGLIPTVGPYLLPHIIPMLHQTFPKLEMILHEAQTHQLLAQLDGKLDAMILVKESEAFIEVPLFDEPMILLAIYEDHPWANREAVPMAD
LAGEKLLMLEDGHCLRDQAMGFCFEAGADEDTHFRATSLETLRNMVAAGSGITLLPALAVPPerKRDGVVYLPAlKEPEPRRTIGLVYRPGSPLRSRYE
QLAEAIRARMDGHFD

>d1kwha_ c.94.1.1 (A:) Alginate-binding periplasmic protein AlgQ2 {Sphingomonas sp.}

KEATWVTDKPLTLKIHMHFRDKWWDENWPVAKESFRLTNVKLQSVANKAATNSSEQFNMMASGDLPDVVGGDNLKDKFIQYQGEAFVPL
NKLIDQYAPHIKAFFKSHPEVERAIKAPDGNIFYFIPYVPDGVVARGYFIREDWLKKLNKPPQNIDEYTVLKFKEKDPNGNGKADEVPFIDRHPDEV
FRLVNFWGARSSGSDNYMDFYIDNGRVKHPWAETAFRDGMKHVAQWYKEGLIDKEIFTRKAKAREQMFGGNLGGFTHDWFASTMTFNEGLAK

TVPGFKLIPPIAPPTNSKGQRWEEDSRQKVRPDGWAITVKKNPVEIKFFDFYFSRPGRDISNFGVPGVTYDIKNGKAVFKDSVLKSPQPVNQLYD
MGAQIPIGFWDYDYEWRQWTPEAQAGIDMYVKGKVMPGFEGVNMTREERAIYDKWADVRTYMYEMGQAWVMGTDVDTWDEYQRQ
LKLRLGLYQLQMMQQAYDRQYKN

>d1cb6a2 c.94.1.2 (A:1335-1691) Lactoferrin {Human (Homo sapiens)}

EEEAARRARVVCAVGEQEELRKCNQWSGLSEGSVTCSSASTTEDCIALVLKGEADAMSLDGGYVYTAKCGLVPVLAENYKSQQSSDPDPNCVD
RPVEGYLAVAVVRRSDTSLTWNSVKGKKSCHTAVDRTAGWNIPMGLLFNQTGSCKFDEYFSQSCAPGSDPRSNLCALCIGDEQGENKCPVNSNERY
YGYTGAFRCLAENAGDVAFVKDVTVLQNTDGNNEAWAKDLKLADFALLCLDGKRKPVTEARSCHLAMAPNHAVVSRMDKVERLKQVLLHQQA
KFGNRNGSDCPDKFCFLQSETKNLLFNDNTECLARLHGKTTYEKYLGPQYVAGITNLKKCSTSPLLEACEFLRK

>d1lct__ c.94.1.2 (-) Lactoferrin {Human (Homo sapiens)}

RSVQWCAVSNPPEATKCFQWQRNMRKVRGPPVSCIKRDSPIQCIAENRADAVTLDDGFIYEAGLAPYKLRVAAEVGTERQPRTHYYAVV
KGGSQLNELQGLKSCHTGLRRTAGWNVPIGTLRFLNWTGPPEPIEAAVARFFSASCVPGADKGQFPNLCRLCAGTGENKCAFSSQEPYFSYSGAF
KCLRDGAGDVAFIRESTVFEDLSDEAERDEYELLCPDNTRKPVDFKFDCHLARVPVSHAVVARSVNGKEDAIWNLRLRQAQEKFGKDKSPKFQFGSPS
GQKDLLFKDSAIGFSRVPPRIDSGLYLGSGYFTA

>d1lgbc_c.94.1.2 (C:) Lactoferrin {Human (Homo sapiens)}

HYYAVAVVKKGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLRFLNWTGPPEPIEAAVARFFSASCVPGADKGQFPNLCRLCAGTGENKCAFSSQE
PYFSYSGAFKCLKDAGDVAFIRESTVFEDLSDEAERDEYELLCPDNTRKPVDFKFDCHLAR

>d1ce2a1 c.94.1.2 (A:1-333) Lactoferrin {Domestic water buffalo (Bubalus arnee bubalis)}

APRKNRVRWCITSQPEWLKCHRWQWRMKLGAPSITCVRASVLECIRATEKADAVTLDDGMVFEAGRDPYKLRVAAEIYGTKESPQTHYYAVA
VVKKGSNFQLDQLQGRNSCHTGLGRSAGWNIPMGIILRPYLSWTELEPLQGAVAKFFSASCVPVDRQAYPNLCQLCKGEGENQCACSPREPYFGY
SGAFKCLQDGAGDVAFVKETTVFENLPKADRDQYELLCLNNTRAPVDAFKECHLAQVPSHAVVARSVDGKEDLIWKLLSKAQEKGKDKSPKFQFGSPS
FGSPPGQRDLLFKDSALGFLRIPSKVDSALYLGSRYLALKNLRE

>d1ce2a2 c.94.1.2 (A:334-689) Lactoferrin {Domestic water buffalo (Bubalus arnee bubalis)}

TAEEVQARRARVVCAVGPEEQKKCQQWSQQSGQIVTCATASTTDDCIALVLKGEADALSLDGGYVYTAKCGLVPVLAENRKSSKHSSLDCVLRPT
EGYLAVALVKKANEGLTWNSLKGKKSCHTAVDRTAGWNIPMGLIANQTGSCAFDEFFSQSCAPGADPKSRLCALCAGDDQGLDKCPVNSKEYYG
YTGAFRCLAEDVGDVAFVKNDTVWENTNGESTADWAKLNREDFRLLCLDGTRKPVTEAQSCHLAVAPNHAVVSLSERAAHVEQVLLHQQALFGE
NGKNCPDFKCLKSETKNLLFNDNTECLAKLGGRPTYEEYLGTEYVTAIANLKKCSTSPLLEACAFLTR

>d1b1xa1 c.94.1.2 (A:1-333) Lactoferrin {Horse (Equus caballus)}

APRKSVRWCITSPIAEAKCAFKQRNMKKVRGPSVCIKTSSEFICIAANKADA
VTLDDGLVYEAGLHPYKLRVAAEVYQTRGKPQTRYAVAVV
KKGSGFQLNQLQGVKSCHTGLGRSAGWNIPGILRPYLNWTGPPEPLQKAVANFFSASCVP
CADGKQYPNLCRLCAGTEADKCACSSQEPYFGY
AFKCLENGAGDVAFVKDSTVFENLPDEAERDKYELLCPDNTRKPVDAFKECHLARVPVSHAVVARSVDGRE
DLIWKLLHRAQEEFGRNKSSAFQLFGS
TPGEQDLLFKDSALGFRIPSKQIDSGLYLGANYLTATQNLR

>d1b1xa2 c.94.1.2 (A:334-689) Lactoferrin {Horse (Equus caballus)}

TAAEVAARRERVVCAVGPEEERKCKQWSVSNRKVACASASTTEECIALVLKGEADALNLDGGFIYVAGKGLVPVLAENQKSQNSNAPDCVHRP
PEGYLAVALVRSKSDADLTWNSLSGKKSCHTGVGRTA
AWNIPMGLLFNQTGSCKFDKFFSASCVP
CADGKQYPNLCRLCAGTEADKCACSSQEPYFGY
GYTGAFRCLAEGDVAFVKDVTVLQNTDGK
NSEPWAKDLQEDFELLCLDGTRKPV
VAAESCHLARAPNHAVVQS
SDRAQHLKKVFLQQDQFG
GNGPDCPGKCLKSETKNLLFNDNTECLAE
LQGKTTYEQYLGSEYV
TSITNLRCSSPLLEACAFLR

>d1dtza1 c.94.1.2 (A:1-333) Lactoferrin {Arabian camel (Camelus dromedarius)}

ASKKSVRWTTSPIAEKKCAQWQRMMKKVRGPSVTCVKKTSRFECIQ
AISTEKADAVTLDDGLVYDAGLDPYKLRPIAAEVG
TENQPTTHYYAVAI
AKKGTNFQLNQLQGLKSCHTGLGRSAGWNIPMGLL
RFLDWTGPPEPLQKAVAKFFSASCVP
CADGKQYPNLCRLCAGTGENK
CACSSQEPYFGY
GAFKCLQDGAGDVAFVKDSTVF
ESLPAKADRDQYELLCP
NNTRKPV
DAFQE
CHLARVP
SHAVV
ARSVNG
KEDLI
WKL
LVA
QEKG
RGK
PSAF
QLF
GSPAGQK
DLL
FKDS
ALGL
LIP
KKID
SGLY
LGS
NYIT
AIRGL
RE

>d1dtza2 c.94.1.2 (A:334-689) Lactoferrin {Arabian camel (Camelus dromedarius)}

TAEEVLRRAQVVCAVGSDEQLKQC
EWRSQSNQSV
CATASTT
EDCIALVLK
GEADAL
SLDGGY
VYAGK
GLVPV
LAESQQ
SP
ESS
GLDC
VHRP
KGY
LAVAL
VVR
KAND
KIT
WNSL
RGK
KSCH
TA
VDRT
AGWN
IPM
GPL
FKD
TD
SCR
FDE
FFS
QSC
APG
GSD
PRS
SKL
CALC
AG
NEE
QLK
CPN
SSER
LYG
YT

GAFRCLAENVGDVAFVKDVTVLNDNTDGKGTEQWAKDLKLGDFELLCLNGTRKPVTEAESCHLPVAPNHAVVSRIDKVAHLRQVLLRQQAHFGRNG
EDCPGKFCLFQSHTKNLLFNDNTECLAKLQKGKTTDEYLGPQYVTAIAKLRRCSTSPLLEACAFMLR

>d1dot_1 c.94.1.2 (1-334) Ovotransferrin {Duck (Anas platyrhynchos)}

APPKTTVRWCTISSAEKKCNSLKDHMQQERTLSCVQKATYLDCKAIANSNEADAISLDGGQVFEAGLAPYKLKPIAAEVYERSGGSTSYYAVAVVK
KGTDFAKDLRGKTSCHTGLRSAGWNIPIGTLIHREDIEWEGIESGISEQAVAKFFSASCVPGATIEQKLCRQCKGDAKTKCLRNGPYSGYSGAFQCL
KDGKGDVAFVKHTTVQENAEEKCNSLKDHMQQERTLSCVQKATYLDCKAIANSNEADAISLDGGQVFEAGLAPYKLKPIAAEVYERSGGSTSYYAVAVVK
VLKDLLFKDSAIMLKRVPELMDSQLYLGFEYYSAIQSLRK

>d1dot_2 c.94.1.2 (335-686) Ovotransferrin {Duck (Anas platyrhynchos)}

QLTVGPRENKIQWCAVGKDESKCDRWSVVSNGEVECTILDDNKDCIVKITKGEADAISLDGGFVYTAGVGLVPVVGESYEDETQCSKDEEQPAYY
FAAVVKKSSAITWNNLQGKKSCHAVGRTAGWNIPMGLIHNKTGSCDFDDYFSEGCAGPSPPNSRLCKLCQGSGENLLEKCVASSHEKYYGTGAL
RCLVEQGDVAFIKHSTVGENVSGSNKDDWAKGTRDDFELLCTNGKRAKTMDYKTCHLAKVPTHAVVARPEKANKIRELLEGQEKLFGHGTEKERF
MMFQSQTKDLLFKALTCLVKLQRQGITYKEFLGDEYYASVASLNTCNPSDPLLQVCTFLEDK

>d1gv8a_c.94.1.2 (A:) Ovotransferrin {Duck (Anas platyrhynchos)}

SYYAVAVVKKGTDFMIKDLRGKTSCHTGLRSAGWNIPIGTLIHRGDIEWEGIESGSVEQAVAKFFSASCVPGATTEQKLCRQCKGDAKTKCLRNAPY
SGYSGAFQCLKDGKGDVAFVKHTTVQENAEEKCNSLKDHMQQERTLSCVQKATYLDCKAIANSNEADAISLDGGQVFEAGLAPYKLKPIAAEVYEV
EHTEGSTSYYAVAVVKKGTEF

KSVIRWCTISSPEEKCCNNLRDLTQQERISLTCVQKATYLDCKAIANSNEADAISLDGGQVFEAGLAPYKLKPIAAEVYEV
EHTEGSTSYYAVAVVKKGTEF

TVNDLQGKTSCHTGLRSAGWNIPIGTLHNGRAIEWEGIESGSVEQAVAKFFSASCVPGATIEQKLCRQCKGDPKTKCARNAPYSGYSGAFHCLKG
KGDVAFVKHTTVNENAPDQKDEYELLCLDGSRQPVDNYKTCNWARVAAHAVVARDDNKVEDIWSFLSKAQSDFGVDTKSDFHFGPPGKKDPVL
KDLLFKDSAIMLKRVPSLMDSQLYLGFEYYSAIQSMR

>d1iq7a_c.94.1.2 (A:) Ovotransferrin {Chicken (Gallus gallus)}

RJQWCAGVKDESKCDRWSVVSNGDVECTVDETAKDCKIMKGEDAVALDGGLVYTAGVGLVPVMAERYDDESQCSKTDERPASYFAVAVARK
DSNVNWNNLKGKKSCHAVGRAGWVPMGLIHNRTGTCNFDEYFSEGCAGPSPPNSRLCQLCQGSGGIPPEKVASSHEKFYTGALRCLVEKG
DVAFIQHSTVEENTGGKNAWDWAKNLQMDDFELLCTGRRANVMDYRECNLAEVPTHAVVRPEKANKIRDLLERQEKRFGVNGSEKSFKMMF
ESQNKDLLFKDLTKCLFKVREGTTYKEFLGDKFYTVISSLKTCNPSDILQMCFSLEGK

>d1jnf1 c.94.1.2 (A:3-334) Transferrin {Rabbit (Oryctolagus cuniculus)}

EKTVRWCAVNDEASKCANFRDSMKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLADGLVHEAGLTPNNLKPVVAEFYGSKENPKTFYYAV
VKKGSNFDLNLQGKKSCHTGLRSAGWNIPIGLLCDLPKPLEKAVASFFSGSCVPCADGADFPQLCQLCPGCGCSSVQPYFGYSGAFKCLKD
GLGDVAFVKQETIFENLPSKDERDQYELLCLDNTRKPVDEYEQCHLARVPSHAVVARSVDGKEDLIWELLNQAQEHFHKDGSDFQLFSSPHGKNLL
FKDSAYGFFVPPRMDANLYLGFEYYTAVRNLREGICPD
F

>d1jnf2 c.94.1.2 (A:335-676) Transferrin {Rabbit (Oryctolagus cuniculus)}

LQDECKAVKWALGHHERLKCDEWSVTGGLIECESAETPEDCIKIMNGEADAMSLSGGYVIAGQCGLVPVLAENYESTDCKKAPEEGYLSAV
VKKSNPDINWNNLEGKKSCHAVDRTAGWNIPMGLLYNRINHCRFDEFFRQGCAGPSQKNSSLCELCVGPSCAPNNREGYYGTGAFRCLVEKG
DVAFKVKSQTVLQNTGGRNSEPWAKDLKEEDFELLCDGTRKPVSEAHNCHLAKPNHAVVSRDKAACVKQKLLDLQVEFGNTVADCSSKFCMFH
SKTKDLLFRDDTKCLVDRGKNTYEKYLGADYIKAVSNLRKCSTSRLLEACTFHKK

>d1tfd_c.94.1.2 (-) Transferrin {Rabbit (Oryctolagus cuniculus)}

VRWCAGVNDEASKCANFRDSMKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLADGLVHEAGLTPNNLKPVVAEFYGSKENPKTFYYAV
GSNFQLNLQGKKSCHTGLRSAGWNIPIGLLCDLPKPLEKAVASFFSGSCVPCADGADFPQLCQLCPGCGCSSVQPYFGYSGAFKCLKDGLGD
VAFVKQETIFENLPSKDERDQYELLCLDNTRKPVDEYEQCHLARVPSHAVVARSVDGKEDLIWELLNQAQEHFHKDGSDFQLFSSPHGKNLLFKDS
AYGFFK

>d1a8e_c.94.1.2 (-) Transferrin {Human (Homo sapiens)}

DKTVRWCAVSEHEATKQSF RDHMKSIPSDGPSVACKKASYLDCIKAIAAHEADAVTLADGLVDAYLAPNNLKPVVAEFYGSKEDPQTFFYAV
VKKDSGFQMNQLRGKKSCHTGLRSAGWNIPIGLLCDLPKPLEKAVANFFSGSCAPCADGTDFFPQLCQLCPGCGCSTLNQYFGYSGAFKCLKD
GAGDVAFKHSTIFENLANKADRQYELLCLDNTRKPVDEYEQCHLARVPSHTVVARSMDGGKEDLIWELLNQAQEHFHKDGSDFQLFSSPHGKD
L

LFKDSAHGFLKVPPRMDAKMYLGYEYVTAIRNLREGTC

>d1h76a1 c.94.1.2 (A:3-333) Transferrin {Pig (Sus scrofa)}

QKTVRWCTISNQEANKCSSFRENMSKAVKNGPLVSCVKSSYLDCAIKARDKEADAVTLADGLVFEAGLAPYNLPVVAEFYQKDNPQTHYYAVAV
VKKGSNFQWNQLQGKRSCHTGLGRSAGWIIPMGLLYDQLPEPRKPIEKAVASFFSSCVCPCADPVNFPKLCQQCAGKGAEKACSNHEPYFGYAGA
FNCLKEDAGDVAFKHSTVLENLPDKADRDQYELLCRDNTRRPVDDYENCYLAQVPSHAVVARSVDGQEDSIWELLNQAQEHFGRDKSPDFQLFS
SSHGKDLLFKDSANGFLKIPSKMDSSLYLGQYVTALRNLRREE

>d1h76a2 c.94.1.2 (A:342-687) Transferrin {Pig (Sus scrofa)}

ECKKVRWCAIGHEETQKCDAWSINSGGKIECVSAENTEDCIAKIVGEADAMSLSGGYYIAGKGLVPVLAENYKTEGENCVNTPEKGYLAVAVVKK
SSGPDLNWNNLKGKKSCHTAVIDRAGWNIPMGLLYNKNINSCKFDQFFGEGCAPGSQRNSSLCALCIGSERAPGRECLANNHERYYGTGAFRCLVE
KGDVAFKDQVQQNTDGKNKDDWAKDLQMDFELLQNGAREPVDNAENCHLARAPNHAVVARDKVTCAEELLQQAQFGRHVDCSSS
FCMFKSNTKDLLFRDDTQCLARVGKTTYESLGADYITAVANLRKSTSKLLEACTFHSA

>d1afwa1 c.95.1.1 (A:25-293) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

KNSLLEKRPEDVIVVAANRSAIGKGFKGAFKDVNTDLYNLFNEFIGRPFPLRADLNLLIEEVACGNVLNVGAGATEHRAACLASGIPYSTPVALNRQ
CSSGLTAVNDIANKIKVGQIDIGLALGVESMTNNYKNVNPLGMISSEELQKNREAKKCLIPMGITNENAANFKISRKDQDEFAANSYQKAYKAKNEG
LFEDEILPIKLPDGSCQSDEGPRPNVTAESLSSIRPAFKDRGTTAGNASQVSDGVAGVLLARRSVANQ

>d1afwa2 c.95.1.1 (A:294-417) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

LNLPVLGRYIDFQTVGVPPEIMGVGPAYAIPKYLEATGLQVQDIDIFEINEAFAAQALYCIHLGIDLNVNPRGGAIALGHPLGCTGARQVATIRLEKK
DQIGVVSMCIGTGMAAIFIKE

>d1qfla1 c.95.1.1 (A:4-268) Biosynthetic thiolase {Zoogloea ramigera}

SIVIASAARTAVGSFNGAFANTPAHELGATVISAVLERAGVAAGEVNEVLGQVLPAGEGQNPARQAAMKAGVPQEATAWMGNQLCGSLRAVAL
GMQQIATGDASIIVAGGMESMSMAPHCAHLRGGVKMDFKIMDTMIKGLTDAYGYHMFTAENVAKQWQLSRDEQDAFAVASQNKAEEA
QKDGRFKDEIVPFIVKGRKGDITVDAEYIRHGATLDSMAKLRAFDKEGTVTAGNASGLNDAAAALLMSEAEASRRG

>d1qfla2 c.95.1.1 (A:269-392) Biosynthetic thiolase {Zoogloea ramigera}

IQPLGRIVSWATVGVDPKVMGTGPIPASRKALERAGWKIGDLDLVEANEAAQACAVNKDLGWDPSONVNGGAIAGHPIGASGARILNTLLFE
MKRRGARKGLATLCIGGGMGVAMCIESL

>d1ek4a1 c.95.1.1 (A:1-253) Beta-ketoacyl-ACP synthase I {Escherichia coli}

MKRVVITGLGIVSSIGNNQQEVLASLREGRSGITFSQELKDSGMRSHW/WGNVKLDTTGLIDRKVVRFMSDASIYAFSMEQAIADAGLSPEAYQNNP
RVLGIAGSGGGSPRFQVFGADAMRGPRGLKAVGPVVTKAMASGVSACLATPFKIHGKVNYISSASATSACIGNAVEQIQLGKQDIV/FAGGGEELC
WEMACEFDAMGALSTKYNDTPEKASRTYDAHRDGFVIAGGGMVVVEELEHALARGAHI

>d1ek4a2 c.95.1.1 (A:254-406) Beta-ketoacyl-ACP synthase I {Escherichia coli}

YAEIVGYGATSDGADMVAPSSEGAVRCMKMAMHGVDTPIDYLNHGTVGDVKELAAIREVFGDKSPAISATKAMTGHSLGAAGVQEAIYSLL
MLEHGFIAPINSINIEELDEQAAGLINVTTTRELTTVMSNSFGGGTNATLVMRKLKD

>d1kas_1 c.95.1.1 (2-251) Beta-ketoacyl-ACP synthase II {Escherichia coli}

KRRVVVTGLMLSPVGNTVESTWKALLAGQSGISLIDHFDTSAYATKFAQLVKDFNCEDIISRKEQRKMDAFIQYGIVAGVQAMQDSGLEITEENATR
IGAAIGSGIGGLGLIEENHTSLMNGGPRKISPFFVPSTIVNMVAGHLTIMYGLRGPSSIATCTSGVHNIGHAARIAYGDADV MVAGGAEKASTPLG
VGGFGAARALSTRNDNPQAASRPWDKERDGFVLGDAGMLV/LEYEHAKKRG

>d1kas_2 c.95.1.1 (252-412) Beta-ketoacyl-ACP synthase II {Escherichia coli}

KIYAELVGFGMSSDAYHMTSPENGAGAALAMANRALDAGIEASQIGYVNAHGTPAGDKAEAQAQVKTIFGEAASRVLVSSTKSMTHLLGAAGA
VESIYSLALRDQAVPPTINLDNPDEGCDLDFVPHEARQVSGMEYTL CNSFGGGTNGSLIFKKI

>d1e5ma1 c.95.1.1 (A:6-255) Beta-ketoacyl-ACP synthase II {Synechocystis sp.}

KKRVVVTGLGATPIGNTLQDYWQGLMEGRNGIGPITRFDASDQACRGGEVKDFDATQFLDRKEAKRMDRFCHFAVCASQQAINDAKLVINELN
ADEIGVLIGTGIGGLKVLEDQQTILLDKGPSRCSPFMIPMMIANMASGLTAINLGAKGPNNCTVTACAAGSNAIGDAFRLVQNGYAKAMICGGTEAA
ITPLSYAGFASARALSFRNDDPLHASRPFKDRDGFVMGEGSGILILEELESALARGA

>d1e5ma2 c.95.1.1 (A:256-416) Beta-ketoacyl-ACP synthase II {Synechocystis sp.}

KIYGEMVGYAMTCDAYHITAPVPDGRGATRAIAWALKDSGLKPEMVSYINAHGTPANDVTETRAIKQALGNHAYNIAVSSTKSMTGHLLGGSGGI
EAVATVMAIAEDKVPPTINLENPDPECSDLVYVPGQSRALIVDVALNSFGFGGHNVTLAFKKYQ
>d1hnja1 c.95.1.1 (A:1-174) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}
MYTKIIGTGSYLPQVRNTADLEKMVDTSDIEWITRTGIRERHIAAPNETVSTMGFEAATRAIEMAGIEKDQIGLIVVATTSAHFPSAACQIQSML
GIKGCPAFDVAACAGFTYALSVDQYVKGAVKYALVVGSDVLARTCDPTDRGTIIIFGDGAGAAVLAASEEPGI
>d1hnja2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}
ISTHLHADGSYGEELLTPNADRVPENSIHLTMAGNEVFKVAVTELAHVDETLAANNLDRSQLDWLPHQANLRIISATAKKLGMSMDNVVTLDR
HGNTSAASVPCALDEAVRDGRIKPGQLVLEAFGGGFTWGSALVRF
>d1hzpa1 c.95.1.1 (A:10-174) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}
MTEIATTSGARSGVLLSVGAYRPERVTNDEICQHIDSSDEWIYTRTGKTRRFAADDSEAASMATEACRRALSNAGLSAADIDGVVTTNTHFLQTTP
AAPMVAAASLGAKGILGFDSLAGCAGFGYALGAAADMIRGGGAATMLVVGTEKLSPTIDYDRGNCIFADGAAAVVGETPFQGI
>d1hzpa2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}
GPTVAGSDGEQADAIRQDIDWITFAQNPSPGPRPFVRLGPVFRWAFAKMGDVGRRAAMDAGVRPDQIDFVPHQANSRINELLVKNLQLRPDA
VVANDIEHTGNTSAASIPLAMAELLTTGAAKPGDLALLIGYAGAGLSYAAQVVRM
>d1bi5a1 c.95.1.2 (A:1-235) Chalcone synthase {Alfalfa (Medicago sativa)}
MVSVSEIRKAQRAEGPATILAIGTANPANCVEQSTYPDFYFKITNSEHKTELKEFKQRMCDCDKSMIKRRYMYLTERKENPNVCEYMAPSLDARQDM
VVVEVPLRGKEAAVKAIKEWGQPKSKITHLIVCTSGVDMPGADYQLTKLLGLRPVVKRYMMYQQGAFAGGTVLRLAKDLAENNKGARVLVVCSEV
TAVTFRGPSDTHLDLSLVGQALFGDGAALIVGSDPVPEIEKP
>d1bi5a2 c.95.1.2 (A:236-389) Chalcone synthase {Alfalfa (Medicago sativa)}
IFEMVVWTAQTIAPDSEGAIDGHLREAGLTFHLLKDVGIVSKNITKALVEAFEPGLSISDYNISFWIAHPGGPAILDQVEQKLALKPEKMNATREVLSYEG
NMSSACVLFILDEMRRKSTQNGLKTTGEGLEWGVLFPGPLTIEVVLRSAI
>d1ee0a1 c.95.1.2 (A:20-235) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}
GLATILAIGTATPPNCVAQADYADYYFRVTKEHMVLDKEKFKRICEKTAIKKRYLALTEDYLQENPTMCEFMAPSLSNARQDLVVTGVPMLGKEAAVK
AIDEWGLPKSKITHLIFCTTAGVDMPGADYQLVKLLGLSPSVKRYMLYQQGAAAGGTVLRLAKDLAENNKGSRVLIVCSEITAILFHGPNEHHDSLVA
QALFGDGAALIVGSGPHL
>d1ee0a2 c.95.1.2 (A:236-395) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}
AVERPIFEIVSTDQTILPDTEKAMKLHLREGGLTFQLHRDVPLMVAKNIENAAEKALSPLGITDWNSVFWMVHPGGRAILDQVERKLNKEDKLRS
RHVLSEYGNLISACVLFIIDEVKRSMMAEGKSTTGEGLDCGVLFPGPGMTVETVVLRSVR
>d1feha1 c.96.1.1 (A:210-574) Fe-only hydrogenase, catalytic domain {Clostridium pasteurianum}
HMDRVKNALNAPEKHIVAMAPSVRASIGELFNMGFGVDVTGKIYTALRQLGFDKIFINFADMTIMEEATELVQRIENNGPFPMTSCCPGVW
RQAENYYPELLNNLSSAKSPQQIFTASKTYYPSISGLDPKNVFTVMPCTSKKFEADRPQMEKDGLRDIDAVITRELAKMIKDAKIPFAKLEDSEA
DPAMGEYSGAGAIFGATGGVMEAALRSAKDFAENAEELEDIEYKQVRLGNGIKEAEVEINNNKYNAVINGASNLFKFMKSGMINEKQYHFIEVMAC
HGGCVNGGGQPHVNPKDLEKVDIKKVRASVLYNQDEHLSKRKSHENTALVKMYQNYFGKPGGRAHEILHKYKK
>d1hfel1 c.96.1.1 (L:87-398) Fe-only hydrogenase larger subunit, C-domain {Desulfovibrio desulfuricans}
WVPEVEKKLDGKVCIAMPAPAVRYALGDAFGMPVGSVTGKMLAALQKLGFAHCWDTEFTADVTIWEEGSEFVERLTKSDMPLPQFTSCCPG
WQKYAETYYPELLPHFSTCKSPIGMNGALAKTYGAERMKYDPKQVYTSIMPCIAKKYEGLRPELKSSGMRIDATLTRELAYMIKKAGIDFAKLD
GKRDSLGMESTGGATIFGVTGGVMEAALRFAYEAVGKPKDSWDFKAVRGLDGKEATNVGGTDVKVAVVHGAKRFKQVCDVVKAGKSPYHFIE
YMACPGGCCVCGGGQPVMPGVLEAM
>d1aln_1 c.97.1.1 (1-150) Cytidine deaminase {Escherichia coli}
MHPRFQTAFAQLADNLQSALEPILADKYFPALLTGEQVSSLKSATGLDEDALAFALLPLAACARTPLSNFNGAIARGVSGTWYFGANMEFIGATM
QQTVHAEQSAISHAWLSGEKALAAITVNYTPCGHCRQFMNELNSGLDLRIHLP
>d1aln_2 c.97.1.1 (151-294) Cytidine deaminase {Escherichia coli}
GREAHALRDYLPAFGPKDLEIKTLLMDEQDHGYALTGDALSQAAIAANRSHMPYSKSPSGVALECKDGRIFSGSYAENAAFNPPLPQFQALILLN
LKGYDYPDIQRAVLAEKADAPIQWDATSLKALGCHSIDRVLL

>d1g8ma2 c.97.2.1 (A:201-593) AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC {Chicken (Gallus gallus)}

GVSQPLRGMNPHQSPAQLYTRPKLPLTVNGSPGFINLCDALNAWQLVKELKQALGIPAAASFHKVSPAGAAVGIPLEEEAQVMVHDLHKTLPPLASAYARSRGADMSSFGDFIALSDICDVPTAKIISREVSDGVVAPGYEEALKILSKKKNGGYCVLQMDPNYPEPDNEIRTLGLQLMQKRNNAVIDRSLFKNIVTKNKLPESAVRDLIVASIAVKYTQSNSVCYAKDGQVIGIGAGQQSRIHCTRLAGDKANSWLRHPRVLSMKFKAGVKRAEVNSAIDQYVTGTIGEDEDLVKWQAMFEVPAQLTEAEKKQWIAKLTAVSLSSDAFFPFRDNVDRAKRIGVQFIVAPSGSADEVVIEACNELGITLIHTNLRLFH

H

>d1rgea_d.1.1.1 (A:) RNase Sa {Streptomyces aureofaciens}

DVSGTVCLSLPPEATDTLNLIASDGPFPYSQDGVFQNRQESVLTQSYGYYHEYTVITPGARTGTRRIITGEATQEDYYTGDHYATFSLIDQTC

>d1fus__ d.1.1.1 (-) RNase F1 {Fusarium moniliforme}

ESATTGSTMNSASQVRAAANAACQYYQNDDTAGSSTYPHTYNNYEGDFPVDPYQEFPIKSGGVYTGGSPGADRVVINTNCEYAGAITHTGASGNNFVGCSGTN

>d1i0va_d.1.1.1 (A:) RNase T1 {Aspergillus oryzae}

ACDYTCGSNCSSDVSTAQAAGYKLHEDGETVGSNSYPHKYNNYEGDFSVSSPYEWPILSSGDVYSGGSPGADRVVFNENNQLAGVITHGTASGNNFVECT

>d1rtu__ d.1.1.1 (-) RNase U2 {Ustilago sphaerogena}

CDIPQSTNCGGNVYSNDDINTAIQGALDDVANGDRPDNYPHQYYXEASEDITLCGSGPWSEFPLVYNGPYSSRDNYVSPGPDRVIYQTNTGECATVHTGAASYDGFTQCS

>d1a2pa_d.1.1.1 (A:) Barnase/Binase {Bacillus amyloliquefaciens}

VINTFDGVADYLQTYHKLPDNYITKSEAQALGWVASKGNLADVAPGKSIGGDIFSNREGKLPGKSGRTWREADINYSGFRNSDRILYSSDWLIYKTTDHYQTFTKIR

>d1goua_d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}

AVINTFDGVADYLIRYKRLPDNYITKSQASALGWVASKGNLAEVAPGKSIGGDVFSNREGRLPSAGSRTWREADINYSGFRNADRLVYSSDWLIYKTTDHYATFTTRIR

>d2rbia_d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}

VINTFDGVADYLIRYKRLPDNYITKSQASALGWVASKGNLAEVAPGKSIGGDVFSNREGRLPSAGSRTWREADINYSGFRNADRLVYSSDWLIYKTTDNYATFTTRIR

>d1rds__ d.1.1.1 (-) RNase Ms {Molsin (Aspergillus saitoi)}

ESCEYTCGTCYWSSDVSAAKAKGYSLYESGDTIDDYPHEYHDYEGDFPVSGTYYEPIMSDYDVYTGSPGADRVIFNGDDELAVITHGTGASGDDFVACSSS

>d0rst__ d.1.1.1 (-) RNase St {Streptomyces erythreus}

QAPCGDTSGFEEVRLADLPPEATDTYELIEKGGPYYPEDGTVFENREGILPDCAEGYYHEYTVKTPSGDDRGARRFVVGDGGEYFYTEDHYESFRLTIVN

>d1aqza_d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus restrictus), restrictocin}

ATWTCINQQLNPKTNKEDKRLYSQAKAESNSHHAPLDGKTGSSYPHWFTNGYDGNGKLIKGRTPIKFGKACCDRPPKHSQNGMGKDDHYLL

EFPTFPDGHDYKFDSKKPKENPGPARVIYTPNKFVFCGIVAHQRGNQGDLRCSH

>d1de3a_d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus giganteus), alpha-Sarcin}

AVTWTCLNDQKNPKTNKYETKRLLYNQNKAESNSHHAPLDGKTGSSYPHWFTNGYDGNGKLIKGRTPIKFGKSDCDRPPKHSKDNGKTDHYLL

EFPTFPDGHDYKFDSKKPKENPGPARVIYTPNKFVFCGIIAHTKENQGELKLCSH

>d1cnfa_d.2.1.1 (A:) Plant class II chitinase {Barley (Hordeum vulgare)}

SVSSIVSRAQFDRMLLHRNDGACQAKGFYTYDAFVAAAAAFSGFTTGSADVQKREVAFLAQTSHETTGGWATAPDGAFAWGYCFKQERGASS

DYCTPSAQWPACPGKRYGRGPQLSHNMYGPAGRAIGV DLLANPDLVATDATVSFKTAMWFWMTAQPPKPSSHAVIVGQWSPSGADRAAGR

VPGFGVITNIINGGIECGHGQDSRVADRGFYKRYCDILGVGYGNLDCYSQRPFA

>d1dxja_d.2.1.1 (A:) Plant class II chitinase {Jack bean (Canavalia ensiformis)}

DVGVIDASLFDQLLKHRNDPACEGKGFSYNAFTAARSFGFGTTGDTNTRKREVAFLAQTSHETTGGAAGSPDPYAWGYCFTERDKSNKY
CDPGTPCPAGKSYYGRGPIQLTHNYAQAGRALGVDLINNPDLVARDAVISFKTAIWFWMTPQGNKPSCHDVITNRWTPSAADVAANRTPGFGV
ITNIINGGIECRGPSPASGDRIGFYKRYCVDLHLSYGPNLNCRDQRPGG
>d1sg_1 d.2.1.2 (1-144) Lysozyme {Chicken (Gallus gallus)}
MKVGRCELAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC
AKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRLQQHHLGGAKQAGDV
>d3lzt__ d.2.1.2 (-) Lysozyme {Chicken (Gallus gallus)}
KVFGRCLEAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC
KKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL
>d1jse__ d.2.1.2 (-) Lysozyme {Turkey (Meleagris gallopavo)}
KVYGRCELAAMKRLGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRTPGSKNLCNIPCSALQSSDITASVNC
KIASGGNGMNAWVAWRNRCKGTDVHAWIRGCRL
>d1hh1__ d.2.1.2 (-) Lysozyme {Guinea fowl (Numida meleagris)}
KVFGRCLEAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNSQATNRNTDGSTDYGVQLQINSRWWCNDGRTPGSRNLCNIPCSALQSSDITATANC
AKKIVSDGNGMNAWVAWRKHCKGTDVRVWIKGCRL
>d1ghla_ d.2.1.2 (A:) Lysozyme {Pheasant (Phasianus colchicus)}
GKIVGRCELAAMKRMGLDNYRGYSLGNWVCAAKFESNFNTGATNRNTDGSTDYGILQINSRWWCNDGRTPGSKNLCHIPCSALLSSDITASVNC
AKKIVSDGNGMNAWVAWRKHCKGTDVNWIRGCRL
>d1jsf__ d.2.1.2 (-) Lysozyme {Human (Homo sapiens)}
KVFERCELARTLKRGLMDGYRGISLANWMCLAKWESGYNTRATNYAGDRSTDYGFQINSRYWCNDGKTPGAVNACHLSCSALLQDNIADAVAC
AKRVRVRDPQGIRAWVAWRNRCQN RDVRQYVQGCGV
>d2eq1__ d.2.1.2 (-) Lysozyme {Horse (Equus caballus), milk}
KVFSKCELAHKLAQEMDGFGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWWCKDNKRSSNACNIMCSKLLDENIDDDIS
CAKRVVRDPKGMSAWKAWVKHCKDKDLSEYLASCNL
>d1qqya_ d.2.1.2 (A:) Lysozyme {Dog (Canis familiaris), milk}
MKIFSKCELARKLKSMDGMDFHGYSLANWVCMAEYESNFNTQAFNGRNSNGSSDYGFQLNSKWCKNSHSSANACNIMCSKFLDDNIDDDI
ACAKRVVKDPMNGMSAWVAWVKHCKGKDLSKYLASCNL
>d1jug__ d.2.1.2 (-) Lysozyme {Australian echidna (Tachyglossus aculeatus)}
KILKKQELCKNLVAQGMNGYQHITLPNWVCTAFHESSYNTRATNHNTDGSTDYGILQINSRYWCHDGKTPGSKNACNISCSKLLDDITDDLKA
KKA
IA GEAKGLTPWVAWSKCRGHDL SKFKC
>d1lmq__ d.2.1.2 (-) Lysozyme {Rainbow trout (Oncorhynchus mykiss)}
K VYDRCELARALKASGMDGYAGNSLPNVVCLVEHESSRDTSKTNRNGSKDYGLFQINDRYWCSKGASPGKDCNVKCSDLTDDITKA
AKCAKKIYKR
RVVLDPNGIGAWVAWRLHCQNQDLRSYVAGCGV
>d1gd6a_ d.2.1.2 (A:) Lysozyme {Silkworm (Bombyx mori)}
KTFTRCGLVHELRKHGFEENLMRNWVCLVEHESSRDTSKTNRNGSKDYGLFQINDKYWCSKGSTPGKDCNVTCSQLLTDDITVASTCA
KKIYKR
RFDAWYGWKNHCQGSLPDISSC
>d1iiza_ d.2.1.2 (A:) Lysozyme {Tasar silkworm (Antheraea mylitta)}
KRFTRCGLVNELRKQGFDENLMRDWVCLVENESARYTDKIANVNKNNGSRDYGLFQINDKYWCSKGSTPGKDCNVTCSQLLTDDITVASTCA
KKIYKR
TKFDAWSGWDNHCHNSNPDISSC
>d1alc__ d.2.1.2 (-) alpha-Lactalbumin {Baboon (Papio cynocephalus)}
KQFTKCELSQNLYIDGYGRIALPELICTMFHTSGYDTQAIVENDESTEYGLFQISNALWCKSSQSPQSRNICDITCDKFLLDDITDDIMCA
KKILDIKGI
DYWIAHKALCTEKLEQWLCEK
>d1b9oa_ d.2.1.2 (A:) alpha-Lactalbumin {Human (Homo sapiens)}
KQFTKCELSQLLKIDGYGGIALPELICTMFHTSGYDTQAIVENDESTEYGLFQISNKLWCKSSQVPQSRNICDISCDKFLLDDITDDIMCA
KKILDIKGI

DYWLAHKALCTEKLEQWLCEKL

>d1hfx__ d.2.1.2 (-) alpha-Lactalbumin {Guinea pig (Cavia porcellus)}

KQLTKCALSHELNDLAGYRDIRTLPWEWLICIFHISGYDTQAIVKNSDHKEYGLFQINDKDFCESSTVQSRNICDISCDKLLDDLTDDIMCVKKILDIKGID
YWLAHKPLCSDKLEQWYCEAQ

>d1fkqa_ d.2.1.2 (A:) alpha-Lactalbumin {Goat (Capra hircus)}

MEQLTKCEVFQKLKDLKYGGVSLPEWVCVAFHTSGYDTQAIVQNNNDSTEYGLFQINNKIWCCKDDQNPHSRNICNISCDKFLLDDLTDDIMCVKKILD
DKVGINYWLAHKALCSEKLDQWLCEKL

>d1f6ra_ d.2.1.2 (A:) alpha-Lactalbumin {Cow (Bos taurus)}

EQLTKCEVFRELKDLKGYGGVSLPEWVCTTFHTSGYDTQAIVQNNNDSTEYGLFQINNKIWCCKDDQNPHSSNICNISCDKFLLDDLTDDIMCVKKILD
VGINYWLAHKALCSEKLDQWLCEKL

>d1j8wa_ d.2.1.2 (A:) alpha-Lactalbumin {Mouse (Mus musculus)}

TELTCKKVSHAIKDMGDGYQQGISLLEWTCVLFHTSGYDSQAVVNDNGSTEYGLFQISERFWCKSSEFPESENICGISCDFKLLDDLEDDIVCAKKIVAIKG
IDYWKAYKPMCEKLEQWRCEKP

>d169la_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSDLDAVRRCALI
NMVFQMGETGVAGFTNSLRLMLQQKRWDAAAAAALAAAATPNAKRVITTFRTGTWDAYK

>d174la_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSDLDAVRRAA
LINMVFQMGETGVAGFTNSLRLMLQQKRWDAAVNLAKSRWYNQTPNRAKRVITTFRTGTWDAYKLN

>d176la_ d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRNCNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSDLDAVRRAAL
INMVFQMGETGVAGFTNSLRLMLQQKRWDAAVNLAKSRWYNQTPNRAKRVITTFRTGTWDAYKLN

>d189l_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNLFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPDLNVAKSELDKAIGRNCNGVITKDEAEKLFNQDVDAAVRGILRNPKLKPVYDSDLDAVRRCALI
NMVFQMGETGVAGFTNSLRLMLQQKRWDAAANLAKSRWYNQTPDRAKRVITTFRTGTWDAYKLN

>d191l_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRACAGAITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSDLDAVRRCALI
NMVFQMGETGVAGFTNSLRLMLQQKRWDAAAALAKSRWYNQTPNRAKRVITTFRTGTWDAYK

>d192l_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLAAKEELDKAIGRNTNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSDLDAVRRAALI
NMVFQMGETGVAGFTNSLRLMLQQKRWDAAVNLAKSRWYNQTPNRAKRVITTFRTGTWDAYK

>d217l_ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIDEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKEELDKAIGRNTNGVITKDEAEKLFNQDVDAAVRGILRNAKLKPVYDSDLDAVRRAALI
NMVFQMGETGVAGFTNSLRLMLQQKRWDAAVNLAKSRWYNQTPNRAKRVITTFRTGTWDAYK

>d1k28a3 d.2.1.3 (A:130-345) Tail-associated lysozyme gp5, catalytic domain {Bacteriophage T4}

NVLNQGGEVGYDSSSVIQDSNLDTAINPDDRPLSEIPTDDNPMSMAEMLRDEGLRLKVVWDTEGYPTIGIGHLIMKQPVRDMAQINKVLSKQ
VGREITGNPGSITMEEATTLFERDLADMQRDIKSHSKVGPVWQAVNRSRQMALENMAFQMGVGGVAKFNTMLTAMILAGDWEKAYKAGRDSL
WYQQTKGRASRVTMIIITGNLESYGVEVK

>d1am7a_ d.2.1.4 (A:) Lambda lysozyme {Bacteriophage lambda}

MVEINNQRKAFLDMLAWSEGTDNGRQKTRNHGYDVIVGGELFTDYSDHPRKLVTLPNPKLGAGRYQLLSWWDAYRKQLGLKDFSPKSQDAV
ALQQIKERGALPMIDRGDIRQAIDRCSNIWASLPGAGYQQFEHKADSLIAKFKEAGGTVR

>d153l_ d.2.1.5 (-) Lysozyme {Goose (Anser anser anser)}

RTDCYGNVRIDTTGASCKTAKPEGLSYCGVSASKKIAERDLQAMDRYKTIKKVGEKLCVEPAVIAGIISRESHAGKVLNGWGDRNGNGFLMQVD
KRSHPQGTWNGEVHITQGTTILINFIKTIQKKFPSWTKDQQQLKGGSAYNAGAGNVRSYARMDIGTHDDYANDVVARAQYYKQHGY

>d1qsaa2 d.2.1.6 (A:451-618) 70 kDa soluble lytic transglycosylase, SLT70 {Escherichia coli}

LAYNDLFKRYTSGKEIPQSYAMAIARQESAWNPVKSPVGASGLMQIMP GTATHTVKMFSIPGYSSPGQLLD PETNINIGTSYLQVYQQFGNNRIFS
SAAYNAGPGRVRTWLGN SAGRIDAVAFVESIPFSETRGYVKNV LAYDAYRYF MGDKPTLMSATEWGRRY

>d1qusa_d.2.1.6 (A:) 36 kDa soluble lytic transglycosylase, SLT35 {Escherichia coli}

MVEPQHNVMQMGGDFANNPNAQQFIDK MVNKHGFD RQQLQEILSQAKRLDSVRLMDNQAP TSVKPPSGPNGAWLRYRKKFITPDNVQNG
VVFWNQYEDALNRAWQVYGVPEIIVGIIGVETRWGRVMGKTRILDALATLSFNYP RRAEYFSGELETFL MARDEQDDPLNLKG SFAGAMGYGQ
FMPSSYKQYAVDFSGDGHINLWDPVDAIGS VANYFKAHGWVKG DQVA MANGQAP GLP NFG KTK YSI SQLAAAGLTPQQPLGNHQQASLLRD
VGTGYQYWGLPNFTITRYNHSTHYAMA VVQLGQ AVALRVQ

>d1chka_d.2.1.7 (A:) Endochitosanase {Streptomyces sp., strain N174}

AGAGLDDPHKKEIAM ELVSSAENSSL DWKAQYKYIEDIGDGRGYTGGIIGFCSGTGDMLELVQHYTDLEPGN ILAKYLPALKVNGSASHSGLGPFT
KD WATAAKDTVFQQAQN DERDRVYF DPAV SQAKADGLRAL QFAYYDAIVMHGPGNDPTSFGGIRKTAMKKARTPAQGGDETTLNGFLDARK
AAMILTEAAHDDTSRVDTEQRVFLKAGNLDLN PPLKWTYGD PYVINS

>d1qgia_d.2.1.7 (A:) Endochitosanase {Bacillus circulans}

ASPDDNFSPETLQFLRNNTGLDGEQWNINMKLINKPEQDDLNWIKYYGYCEDIEDERGYTIGLFGATTGSRDTHPDGPDLF KAYDAAKGASNPSA
DGALKRLGINGKMGSILEK DSEK VFCG KIKKLQN DAWRKAMWETFYVIRYSVEQARQGFTSAVTIGSFVDTALNQGATGGSDTLQG LLARS
GSSSNEKTFMKNFHAKRTLVDTN KYNKP PNGKNR V KQWDTLV DMGK MNLKNV DSEIAQV TDWEMK

>d1aec_d.3.1.1 (-) Actinidin {Chinese gooseberry or kiwifruit (Actinidia chinensis)}

LPSYVDWRSAGAVVDIKSQGECGGCWAF SAIATVEGINKIVTGV L ISLSEQELIDCGRTQNTRGCNGGYITDGFQFIINNGG INTEENPYTAQDGEC
NV DLQNEKYVTIDTYENV PYNNEW ALQTA VTYQP VSVAL DAAGDA FKQYSSGIFT GPCGT AIDH AVTIVGYGTEGGIDY WIVKNSWDTTWGEEGY
MRILRN VGGAGTCGIATMPSYPV KY

>d2act_d.3.1.1 (-) Actinidin {Chinese gooseberry or kiwifruit (Actinidia chinensis)}

LPSYVDWRSAGAVVDIKSQGECGGCWAF SAIATVEGINKITSGSLISLSEQELIDCGRTQNTRGCNGGYITDGFQFIINNGG INTEENPYTAQDGDC
DVALQDQKV TIDTYENV PYNNEW ALQTA VTYQP VSVAL DAAGDA FKQYSSGIFT GPCGT AIDH AVTIVGYGTEGGIDY WIVKNSWDTTWGEEGY
MRILRN VGGAGTCGIATMPSYPV KY

>d1ppn_d.3.1.1 (-) Papain {Papaya (Carica papaya)}

IPEYVDWRQKGAVTPVKNQGSCGSCWAF SAIATVEGINKITGKL VELSEQELVDCERRSHGCKGGYPPYALEYVAKNGIHLRSKPYKAKQGT C RAKQVGG
REKG PYAAKTDG V RQVQPY NEGALLY SIAN QPV SVV LEAG KDFQLY RGGIFVG PCGN KV DHA V AAVGYGP NYI LIKNSW GTGW GENG YIRIK RGT
GNSYVGCGLYTSSFPVKN

>d1pcia_d.3.1.1 (A:) Caricain (protease omega) {Papaya (Carica papaya)}

LTSTERLIQLFNSWMLNHNFYENVDEKLYRFEIFKDNLYIDETNKKNNSYWLGLNEFADLSNDEFNEKYVGLIDATIEQS YDEFIN EDIVNL PENV
DWRKKGA VTPVRHQGSCGSCWAF SAIATVEGINKIRTGKL VELSEQELVDCERRSHGCKGGYPPYALEYVAKNGIHLRSKPYKAKQGT C RAKQVGG
PIVK TSGV GRVQ PNNEG NLLN AIAK QPV SVV VESK GRPF QLYKGGIFEG PCGT KVDGA VTAVGYGKSGG KGYI LIKNSW GTAW GEKGYI RIKRAP GN
SPGVCGLYKSSYYPTKN

>d1ppo_d.3.1.1 (-) Caricain (protease omega) {Papaya (Carica papaya)}

LPENVDWRKKGA VTPVRHQGSCGSCWAF SAIATVEGINKIRTGKL VELSEQELVDCERRSHGCKGGYPPYALEYVAKNGIHLRSKPYKAKQGT C RAKQVGG
KQVGGPIVK TSGV GRVQ PNNEG NLLN AIAK QPV SVV VESK GRPF QLYKGGIFEG PCGT KVDGA VTAVGYGKSGG KGYI LIKNSW GTAW GEKGYI RIK
RAPGN SPGVCGLYKSSYYPTKN

>d1yal_d.3.1.1 (-) Chymopapain {Papaya (Carica papaya)}

YPQSIDWRAKGAVTPVKNQGACGSCWAF STIATVEGINKIVTGNL L ESEQELVDCDKHSYGC KGGYQTTSLQYVAN NGVHTSKV VPYQAKQYKCRA
TDKPGPKV KITGYK RVPSNC TFL GALAN QPLS VLVEAGG KPFQ LYKSGV FDGPCGT KLD HA VTAVGYGKSGG KGYI LIKNSW GTAW GEKGYI RIK
RQSGNSQGT CGVYKSSYYPTKN

>d1gece_d.3.1.1 (E:) Glycyl endopeptidase {Papaya (Carica papaya)}

LPESVDWRAKGAVTPVKH QGYC ESCW AF STIATVEGINKIKTGNL VELSEQELVDCD LQSYGC NRGYQSTS LQYVAQNGIHL RAKPYI AKQQTCRA
NQVGGPKVKTNGVGRVQSNNEG SLLN AIAH QPV SVV VESAGRDFQNYKGGIFEGSCGT KVDHA VTAVGYGKSGG KGYI LIKNSW GPGWG ENGYI

RIRRASGNSPGVCGVYRSSYYPIKN

>d1cqda_d.3.1.1 (A:) Proline-specific cysteine protease {Ginger rhizome (Zingiber officinale)}

LPDSIDWRENGAVVPVNQGGCGSCWAFSTVAAVEGINQIVTGLISLSEQQLVDCTTANHGRGGWMNPQFIVNNGGINSEETYRQGDGI
CNSTVNAPVVSIDSYENVPSHNEQLQAVANQPVSVTMDAAGRDFQLYRSGIFTGSCNISANHALTVGYGTENDKDFWIVKNSWGKNWGESG
YIRAERNIENPDGKGITRFASYPVKK

>d3gcb__ d.3.1.1 (-) Bleomycin hydrolase {Baker's yeast (Saccharomyces cerevisiae), Gal6}

AFQGAMASSIDISKINSWNKEFQSDLTHQLATTVLKNYNADDALLNKTRLQKQDNRVFNTVVSTDSTPVTNQKSSGRAWLFAATNQLRLNVSELN
LKEFELSQAYLFFYDKLEKANYFLDQIVSSADQDIDSRLVQYLLAAPTEDGGQYSMFLNLVKKYGLIPKDLYGLDPYSTTASRKWNSSLTTKLREFAETLR
TALKERSADDIIVTLREQMQRERIFRLMSLFMDIPPVQPNQEFTWEYVDKDKKIHTIKSTPLEFASKYAKLDPSTPVSLNDPRHPYGKLIKIDRLGNVLG
GDAVIYLNVDNETLSKLVVKRLQNNKAVFFGSHTPKFMDDKKTGVMDIELWNYPAINLPQQKASRIRYHESLMTHAMLITGCHVDETSKLPLRYRV
ENSWGKDGSKGDGLYMTQKYFEYCFQIVVDINELPKELASKFTSGKEEPVLPIDPMGALA

>d2cb5a_d.3.1.1 (A:) Bleomycin hydrolase {Human (Homo sapiens)}

SSGLNSEKVAALIQKLNSDPQFVLAQNVTHTHLDLICLKRAVTQRAQHVQFQHAVPQEGKPTINQKSSGRSWIFSCLNMRLPFMKLNIEEFES
QSYLFFWDKVERCYFFLSAFVDTAQRKEPEDGRLVQFLLMNPANDGGQWDMLVNIVEKYGVIPKKCFPESYTTEATRRMNDILNHKMREFCIRLN
LVHSATGEISATQDVMMEEIFRVRVVICLGNPPETFTWEYRDKDKNYEKGPITLEFYREHVKPLFNMEDKICLVNDPRPQKHKNKLYTVEYLSNM
VGGRKTLYNNQPIDFLKKMVAASIKDGEAVWFGCDVGKHFNSKGLSDMNLYDHELVFGVSLKNMNKAERLTFGESLMTHAMTFTAVSEKDDQD
GAFTKWRVENSWGEDHGHKGYLCMTDEWFSEYVYEVVDRKHVPPEEVLALEQEPIILPAWDPMGALA

>d1f2aa_d.3.1.1 (A:) Cruzain {Trypanosoma cruzi}

APAAVDWRARGAVTAVKDQGQCGSCWAFSAIGNVECQWFLAGHPLTNLSEQMLVSCDKTDGCGGGLMNNAFEWIVQENNGAVYTEDSYPYA
SGEGISPPCTTSGHTVGATITGHVELPQDEAQIAAWLAVNGPVAVAVDASSWMTYGGVMTSCVSELDHGVLVGYNDAAVPYWIINKSWTTQ
WGEEGYIRIAKGSNQCLVKEEASSAVVG

>d3pbh_d.3.1.1 (-) (Pro)cathepsin B {Human (Homo sapiens)}

MRSRPSFHPLSDELVNYVNKRNTTWQAGHNFYNVDMSYLKRCGTLGGPKPPQRMFTEDLKLPSFDAREQWPQCPTIKEIRDQGSCGSCWA
FGAVEAISDRICHTNAHSVEVSAEDLLTCCGSMCGDCNCNGGYPEAEAWNFWTRKGLVSGGLYESHVGRPYSIPPCEHHVNGSRPPCTGEGDTPK
CSKICEPGYSPTYKQDKHYGNSYSVSNSEKDIMAIEYKNGPVEGAFSVYSDFLYKSGVYQHVTGEMMMGGHAIRILGWGVENGTPYWLVANSWNT
DWGDNGFFKILRGQDHCGIESEVVGAPIRTD

>g1huc.1 d.3.1.1 (A;B;) (Pro)cathepsin B {Human (Homo sapiens)}

LPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICHTNXVSVEVSAEDLLTCCGSMCGDCNCNGGYPEAEAWNFWTRKGLVSGGLYESH
VGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYSPTYKQDKHYGNSYSVSNSEKDIMAIEYKNGPVEGAFSVYSDFLYKSGVYQHVTGEM
MMGHAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEVVGAPIRTD

>d1mira_d.3.1.1 (A;) (Pro)cathepsin B {Rat (Rattus norvegicus)}

SDDMINYINKQNTTWQAGRNFYNDISYLLKKCGTVLGGPKLPERVGFSEDINLPESFDAREQWSNCPTIAQIRDQGSCGSSWAFGAVEAMSDRIC
IHTNGRVNVEVSAEDLLTCCGIQCGDCNGGYPGAWNFWTRKGLVSGGVYNISHIGCLPYTIPPCEHHVNGARPPCTGEGDTPKCNKMCEAGYST
SYKEDKHYGTSYSVSDSEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDVMGGHAIRILGWGIENGVPYWLVANSWNADWDNGFFKIL
RGENHCGIESEIVAGIPRTQQYWGRF

>d1thea_d.3.1.1 (A;) (Pro)cathepsin B {Rat (Rattus norvegicus)}

LPESFDAREQWSNCPTIAQIRDQGSCGSCWAFGAVEAMSDRICHTNGRVNVEVSAEDLLTCCGIQCGDCNGGYPGAWNFWTRKGLVSGGVY
NSHIGCLPYTIPPCEHHVNGARPPCTGEGDTPKCNKMCEAGYSTSYKEDKHYGTSYSVSDSEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEA
GDVMGGHAIRILGWGIENGVPYWLVANSWNADWDNGFFKILRGENHCGIESEIVAGIPRT

>d1qdqa_d.3.1.1 (A;) (Pro)cathepsin B {Cow (Bos taurus)}

LPESFDAREQWPNCPTIKEIRDQGSCGSCWAFGAVEAISDRICIHSGRNVEVSAEDMLTCCGGECGDGCNGGEPSGAWNFWTRKGLVSGGLYN
SHVGCRPYSIPPCEHHVNGSRPPCTGEGDTPKCSKTCEPGYSPSYKEDKHFGBSSYVANNEKEIMAEIYKNGPVEGAFSVYSDFLYKSGVYQHVSG
EIMGGHAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQDHCGIESEIVAGMPCT

>d1cs8a_d.3.1.1 (A;) (Pro)cathepsin L {Human (Homo sapiens)}

SLTFDHSLEAQWTKWKAMHNRLYGMNEEGWRRAVWEKNMKIELHNQEYREGKHSFTMAMNAFGDMTSEEFRQMNGFQNRKPRKGKV
QEPLFYEAPRSVDWREKGYTPVKNQGQCGSCWAFSATGALEGQMFRKTGRLISLSEQNLVDCSGPQNEGCGGLMDYAFQVQDNGGLDSE
ESYPYEATEESCKYNPKYSVANDAGFVDIPKQEALKAVATVGPIVAIDAGHESFLYKEGIYFEPDCSSEDMDHGVLVGYGFESTESDNNKYWL
VKNSWGEWGMGGYVMAKDRRNHCIGIASASYPTV
>g1icf.1 d.3.1.1 (A.;B;) (Pro)cathepsin L {Human (Homo sapiens)}
APRSVDWREKGYTPVKNQGQCGSCWAFSATGALEGQMFRKTGRLISLSEQNLVDCSGPQNEGCGGLMDYAFQVQDNGGLDSEESYPYE
TEESCKYNPKYSVANDTGFVDIPKQEALKAVATVGPIVAIDAGHESFLYKEGIYFEPDCSSEDMDHGVLVGYGFESTXNNKYWLKNSWGE
WGMGGYVMAKDRRNHCIGIASASYPTV
>d1mem_a_d.3.1.1 (A;) (Pro)cathepsin K {Human (Homo sapiens)}
APDSVDYRKKGYTPVKNQGQCGSCWAFSSVGALEGQLKKKTGKLLNLSPQNLVDCVSENDGC GGYMTNAFQVQKNRGIDSEDAYPYVGQEE
SCMYNPTGKAACRGRYREIPEGNEKALKRAVARVGPVVAIDASLTSFQFYSKGVYYDESCNSDNLNAVLAVGYGIQKGNKHWIIKNSWGENWG
NKGYILMARNKNNACGIANLASFPKM
>d7pcka_d.3.1.1 (A;) (Pro)cathepsin K {Human (Homo sapiens)}
LYPEEILDTHWELWKKTHRQYNNKVDIERRLIWEKNLKYISIHNLEASLGVHTYELAMNHLDGDTSEEVVQKMTGLKVPLSHRSNDTLYIPEWE
GRAPDSVDYRKKGYTPVKNQGQCGSCWAFSSVGALEGQLKKKTGKLLNLSPQNLVDCVSENDGC GGYMTNAFQVQKNRGIDSEDAYPYVG
QEESCMYNPTGKAACRGRYREIPEGNEKALKRAVARVGPVVAIDASLTSFQFYSKGVYYDESCNSDNLNAVLAVGYGIQKGNKHWIIKNSWGEN
WGNKGYILMARNKNNACGIANLASFPKM
>d8pcha_d.3.1.1 (A;) (Pro)cathepsin K {Pig (Sus scrofa)}
YPPSMWDWKGNFVSPVKNQGSCGSCWTFSTTGALESAVAIATGKMLSLAEQQLVDCQAQNFFNNHGCQGLPSQAFEYIRYNKGIMGEDTYPYKG
QDDHCKFQPDKAIAFKDVANITMNDEEAMVEAVALYNPVSFAFEVTNDFLMYRKGISSSTSCHKTPDKVNHAVLAVGYGEENGIPYWIVKNSW
PQWGMNGYFLIERGKNMCGLAACASYPIPLV
>d1fh0a_d.3.1.1 (A;) (Pro)cathepsin V {Human (Homo sapiens)}
LPKSVWDWKKGYTPVKNQGQCGSCWAFSATGALEGQMFRKTGKLVSSEQNLVDCSRPQGNQGCNGGFMARAFQVVKENGGLDSEESYPVVA
VDEICKYRPENSVAQDTGFTVAPGKEALKAVATVGPIVAMDAGHSSFQFYKSGIYFEPDCSSKNLHDHGVLVGYFEGANSDNSKYWLVKNS
WGPEWGSNGYVIAKDKNNHCIGIATAASYPNV
>d1deua_d.3.1.1 (A;) (Pro)cathepsin X {Human (Homo sapiens)}
RGQTCYRPLRGDGLAPLGRRTYPRPHEYLSPADLPKSWDWRNVDGVNYASITRNQHIPQYCGSCWAHASTSAMADRINIKRGAWPSTLLSVQNV
IDCGNAGSCEGGNDLSVWDYAHQHGIPDETNNYQAKDQECDKFNCQCGTCNEFKECHAIRNTLWRVGDYGSLSGREKMMAEIYANGPISCGIM
ATERLANYTGGIYAELYQDTTYINHVSVAGWGISDGTEYWIVRNSWGEPWGERGLRIVTSTYKDGKGARYNLAIEEHCTFGDPIV
>d1ef7a_d.3.1.1 (A;) (Pro)cathepsin X {Human (Homo sapiens)}
LPKSWDWRNVDGVNYASITRNQHIPQYCGSCWAHASTSAMADRINIKRGAWPSTLLSVQNVIDCGNAGSCEGGNDLSVWDYAHQHGIPDET
NNYQAKDQECDKFNCQCGTCNEFKECHAIRNTLWRVGDYGSLSGREKMMAEIYANGPISCGIMATERLANYTGGIYAELYQDTTYINHVSVAGWG
ISDGTEYWIVRNSWGEPWGERGLRIVTSTYKDGKGARYNLAIEEHCTFGDPIV
>d1cv8_d.3.1.1 (-) Staphopain {Staphylococcus aureus}
NEQYVNKLENFKIRETQGNNGWCAGYTMSSLNATYNTNKYHAEAVMRFLHPNLQGQQFQFTGLTPREMIYFGQTQGRSPQLNNRMTTYNEVD
NLTKNNKGIAILGSRVESRNGMHAGHAMAVVGNAKLNNGQEVIIWNPWDNGFMFTAQIMKYHNYPNKGKLDTYTLSSNNPYFNHPKNLFAAISTRQYNNILPTYSGRESNVQKM
>d1dkia_d.3.1.1 (A;) Streptococcal pyrogenic exotoxin B {Streptococcus pyogenes}
LDKVNLLGGESGSNMVYVNIISTGGFIVSGDKRSPEILGYSTSGSFVDNGKENIASFMESYVEQIENKLDSTYAGTAEIKQPVVKSLDSKGJHYNQ
GNPNLNTPIEKVKPGEOQSFVGQHAATGSVATATAQIMKYHNYPNKGKLDTYTLSSNNPYFNHPKNLFAAISTRQYNNILPTYSGRESNVQKM
AISELMADVGISVDMYDGPSSGSAGSSRVQRALKENFGYNQSVHQINRGDFSKQDWEAQIDKELSQNQPVYYQGVGVGGHAFVIDGADGRNFY
HVNWGWWGGVSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVGIP
>d1qmya_d.3.1.2 (A;) FMDV leader protease {Foot-and-mouth disease virus}
MELTLYNGEKKTFSRPNHHDNAWLNAIQLFRYVEPFDWVYSSPENLTLEAIKQLEDLTGLELHEGGPPALVIWNKHLHTGIGTASRPSEVCVV
DGTDMSLADFHAGIFLGQEHAVFACVTNGWYAIADDDEFYPWTPDPSDVLVFVYD

>d1qola_d.3.1.2 (A:) FMDV leader protease {Foot-and-mouth disease virus}

MELTLYNGEKKTFYSRPNNHDAWLAILQLFRYVEEPFDWVYSSPENLTLEAIKQLEDLTGLELHEGGPPALVIWNKHLHTGIGTASRPSEVCVV
DGTDMCLADFAGIFLGKQEHAVFACVTSNGWYAIDDEDFYPWTPDPSDVLVFVYPDQEPLNGEWEKAKVQRKLK

>d1kf13 d.3.1.3 (L:2-355) Calpain large subunit, catalytic domain (domain II) {Human (Homo sapiens)}

AGIAAKLAKDREAAEGLGSHERAIKYLNQDYEARNECLEAGALFQDPSPALPSSLGKELGPYSSKTRGMWRKRPTEICADPQFIIGGATRTDICQG
ALGDCWLLAIAIASLTNEEILARVPLNQSFQENYAGIFHFQFWQYGEWVEVVVDDRLPTKDGEELLFVHSAGSEFWASALLEKAYAKINGCYEALSG
GATTEGFEDFTGGIAEWYELKPPPMLFKIIQKALQKGSLLGCSIDITSAADSEAITFQKLVKGHAYSVTGAEEVESNGSLQKLIRIRNPWGEVEWTGR
WNDNCPSWNTIDPEERERLRRHEDGEFWMSFSDFLRHYSRLEICNLTPDTLTSPTYKK

>d1df0a3 d.3.1.3 (A:2-355) Calpain large subunit, catalytic domain (domain II) {Rat (Rattus norvegicus)}

AGIAMKLAKDREAAEGLGSHERAIKYLNQDYETLRNECLEAGALFQDPSPALPSSLGKELGPYSSKTRGIEWKRPTEICADPQFIIGGATRTDICQGA
LGDSWLLAIAIASLTNEEILARVPLDQSFQENYAGIFHFQFWQYGEWVEVVVDDRLPTKDGEELLFVHSAGSEFWASALLEKAYAKINGCYEALSGGA
TTEGFEDFTGGIAEWYELRKPPPMLFKIIQKALEKGSLLGCSIDITSAADSEAVTYQKLVKGHAYSVTGAEEVESNGSLQKLIRIRNPWGEVEWTGKWN
DNCPSWNTVDPEVRANLTERQEDGEFWMSFSDFLRHYSRLEICNLTPDTLTCDSYKK

>d1f13a4 d.3.1.4 (A:191-515) Transglutaminase catalytic domain {Human (Homo sapiens)}

DAVYLDNEKEREYVLNDIVIYGEVNDIKTRSWSYGQFEDGILDTCYVMdraQMDSLGRGNPIKVSRCGSAMVNAKDEGVLVGSWDNIYAY
GVPPSAWTGSVDILLEYRSSENVPVRYGCWVFAGVNTFLRCLGIPARIVTNYFSAHNDNDANLQMDIFLEEDGNVNSKLTKDSVWNHYCWNEAW
MTRPDLPVGFGGWQAVDSTPQENSNDGMYRCGPASVQAIKHGVCFQFDAPFVFAEVNSDLIYITAKKDGTBVENVNDATHIGKLIVTKQIGGDG
MMDITDTYKFQEGQEEERLALETALMYGAKPLNTEGVMKSR

>d1g0da4 d.3.1.4 (A:141-461) Transglutaminase catalytic domain {Red sea bream (Chrysophrys major)}

DMVYLVPDESKLQEYVMNEDGVIYMGTDWYIYRSPWNYGQFEDYVMDICFEVLDNSPAALKNSEMIDIEHRSDPVYVGRTITAMVNSNGDRGVLTG
RWEEPYTDGVAPYRWTGSVPILQQWSKAGVRPVKGQCVVFAAVACTVLRCLGIPTRPITNFASAHDVNDGNLSVDLNERLESLSRQRSDSSW
NFHCWVESWMSREDLPPEGNDGWQVLDPTPQELSDFGECCGCPVAAIKEGNLGVKYDAPFVFAEVNADTIWIVQKDGQRRKITEDHASVGKNI
STKSVYGNIHREDVTLYKYPEGSQKEREVYKKAGRRT

>d1e2ta_d.3.1.5 (A:) Arylamine N-acetyltransferase {Salmonella typhimurium}

HMTSFLHAYFTRLHCQPLGVPTVEALRTLHahnCAIPFENLDVLLPREIQLDETAEEKLLYARRGGYCFLNGLFERALRDIGFNVRSLGRVILSHPA
SLPPRTHRLLLVDEDEQWIADVGFGQQTLTAPLRLQAEIAQQTPHGEYRLMQUEGSTWIQFRHHEHWQSAMYCFDLGVQQQSDHVMGNFWSA
HWPQSHFRHHLLMCRHLPDGKLTNFHTRYHQGHAVEQVNVPDVPSLYQLLQQQFLGVNDVKHGFTEAELAAVMAAF

>d1uch__ d.3.1.6 (-) Ubiquitin C-terminal hydrolase UCH-I3 {Human (Homo sapiens)}

RWLPLEANPEVTNQFLKQLGLHPNWQFDVYGMDELLSMVPRPVCAVLLFPITEKYEVFRTEEEKIKSQGQDVTSVYFMKQTISACGTIGLIH
AIANNKDKMHFESGSTLKKFLEESVMSPEERARYLENYDAIRVTHETSACHEGQTEAPSIDEKVDLHFIALVHVDGHLYELDGRKPFPINHGETSDTL
LEDAIEVCKKFMERDPDELRFNAIALSAA

>d1cmxa_d.3.1.6 (A:) Ubiquitin C-terminal hydrolase UCH-I3 {Synthetic, based on Saccharomyces cerevisiae sequence}

RAVPIESNPEVFTNFAHKGLKNEWAYFDIYSLTEPELLAFLPRPVKAIVLLFPINEDRKSTSQQITSSYDVIWFQSVKNACGLYAILHLSNNQSLLE
PGSDLNFLKSQSDTSSSNRNFDDVTTDQFLVNVIKENVQTFSTGQSEAPEATADTNLHYITYVEENGIFELDGRNLSGPLYLGKSDPTATDIEQELV
RVRVASYMEMANEEDVLFNFMGLGLPNA

>d1avpa_d.3.1.7 (A:) Human adenovirus 2 proteinase {Mastadenovirus H2}

MGSSEQELKAIVKDLGCGPYFLGYDKRFPGVSPHKLACAIVTAGRETGGVHWMAFAWNPRSKTCYLFEPMGFSQRLKQVYQFEYESLLRRSAI
ASSPDRCITLEKSTQSVQGPNSAACGLFCMFLHAFANWPQTPMDHNPTMNLITGVPNMSLNSPQVQPTLRRNQEQLYSFLERHSPYFRSHSAQI
RSATSFCHLKNM

>d1euva_d.3.1.7 (A:) Ulp1 protease C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

GSLVPELNEKDDQVQKALASRENTQLMNRDNIEITVDRFKTLAPRRWLNDTIEFFMKYIEKSTPNTVAFNSFFYTNLSERYQGVRRWMKRKKT
QIDKLDKIFTPINLNQSHWALGIIDLKKKIGYVDSLNGPNAMSFAILDLQKYMEESKHTIGEDFDLHLCPCQQPNGYDCGIYCMNTLYGSADA
PLDFDYKDAIRMRRFIAHLILTDALK

>d7ceib_d.4.1.1 (B:) DNase domain of colicin E7 {Escherichia coli}

RNKPGKATGKGKPVNNKWLNNAKGDLGSPVPDRIANKLKDKEFKSFDDFRKKFWEVS KDP ELSKQFSRNNNDRMKVGKAPKTRTQDVSGKRTS
FELHHEKPISQNGGVYDMDNISVVTPKRHIDIH

>d1emvb_d.4.1.1 (B:) DNase domain of colicin E9 {Escherichia coli}

MESKRNKGKATGKGKPVGDKWLDDAGKDSGAPIPDRIADKLDRKEFKSFDDFRKAVWEEVKDP ELSKNLNPNSKSSVSKGYSFTPKNQQVGG
RKVYELHHDKPISQGGEVYDMDNIRVTTPKRHIDIH

>d1ql0a_d.4.1.2 (A:) Sm endonuclease {Serratia marcescens}

SIDNCAVGCPGGSSKVSVRHAYTLNNNSTTKFANWVAYHITKDT PASGKTRNWKTDPALNPADTLAPADYTGANAAALKVDRGHQAPLASLAGVS
DWESLNLYLSNITPQKS DNLNQGAWARLEDQERKLIDRADISSVYVTGPLYERDMGKLP GTQKAHTIPSAYWKVIFINNSPAVNHYAFLFDQNTPKG
ADFCQFRVTVDIEKRTGLI WAGLPDDVQASLKS KPGVLPELMGCKN

>d1a73a_d.4.1.3 (A:) Intron-encoded homing endonuclease I-Ppol {Slime mold (Physarum polycephalum)}

ALTNAQILAVIDSWEETVGQFPVITHHVPLGGGLQGTLHCYEIPLAAPYGVGFAKNGPTRWQYKRTINQV VHRWGSHTVPFLLEPDNINGKTCTAS
HLCHNTRCHNPLHLCWESLDDNKG RNRWC PGPN GGCVHAVVCLRG PLYGP GATVAGPQQRGS HFVV

>d1e7la2 d.4.1.5 (A:1-103) Recombination endonuclease VII, C-terminal and dimerization domains {Bacteriophage T4}

MLLTGKLYKEEKQKFYDAQNGKCLICQRELPDVQANHLDHDHELNGPKAGKV RG LLCNLCDAAEGQM KHKFNRSGLKGQGV DYLEWLENLLTYL
KSDYTQNN

>d1dy5a_d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KETAAAKFERQHMDSSTAASSSNYCNCQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTNCYQS YSTMSITDCRETGSSKYPNC
AYKTTQANKHII VACEGSPYVPVHF DASV

>d1h8xa_d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KESAAAKFERQHMDSGNSPSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLDVQNVCFQE KVCKNGQGNCYKSNSSMHITDCRLTNGSRYP
NCAYRTSQKERHII VACEGSPYVPVHF DASVE

>d1rbd_d.5.1.1 (-) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

SSSNYCNCQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTNCYQS YSTMSITDCRETGSSKYPNCAYKTTQANKHII VACEGSPY
VPVHF DASV

>g1d5d.1 d.5.1.1 (A:,B:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KETAAAKMERQHLDXNYCNCQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTNCYQS YSTMSITDCRETGSSKYPNCAYKTTQ
ANKHII VACEGSPYVPVHF DASV

>d1e21a_d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Human (Homo sapiens), des1-7}

AFQRQHMDSDSSPSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLDVQNVCFQE KVCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRT
SPKERHII VACEGSPYVPVHF DASV

>d1rraa_d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Rat (Rattus norvegicus)}

AESSADKF KRQHM DTEGP SKSSPTYCNQMMK RQGM TKGSC KP VNTFVHEPLE DVQ AICS QGQV TCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRT
CDYTTT DSQKH IIIACDG NPYVPVHF DASV

>d1onc_d.5.1.1 (-) P-30 protein {Frog (Rana pipiens)}

EDWLT FQKKH ITNTR DVCD NIMST NL FHCK DKNTFI YSRPEPVKAICKGII ASK NVLT SEFY LSCN VT SRPC KYKL KK STNK FCVTC ENQAPVHF
GVGSC

>d1bc4_d.5.1.1 (-) Cytotoxic ribonuclease {Bullfrog (Rana catesbeiana)}

ENWATFQ QKHI INTPIINC NTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVIN MNVLSTTRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYP
VHFAGIGRC P

>d11bga_d.5.1.1 (A:) Seminal ribonuclelease {Cow (Bos taurus)}

KESAAAKFERQHMDSGNSPSSSNYCNCQMMKSRNLTKDRCKPVNTFVHESLADVKA VCSQKKVCKNGQTNCYQS KSTM RITDCRETGSSKYPN
CAYKTTQVEK HII VACGGKPS VPVHF DASV

>d1b6va_d.5.1.1 (A:) Hybrid between ribonuclease A and seminal ribonuclease {Cow (Bos taurus)}

KETAAAKFERQHMDSSTAASSSNYCNCQMMKSRNLTKDRCKPVNTFVHESLADVKA VCSQKKVCKNGQTNCYQS KSTM RITDCRETGSSKYPN

AYKTTQANKHIIIVACGGKPYVPVHFDSAV
>d1dyta_d.5.1.1 (A:) Eosinophil cationic protein (ECP), ribonuclease 3 {Human (Homo sapiens)}
RPPQFTRAQWFAIQHISLNPPRCTIAMRAINNYRWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCHRSPRVPLLHCDLINPGAQNI
RYADRPGRRFYVVACDNRDPRDSPRYPVPVHLDTTI
>d1hi2a_d.5.1.1 (A:) Eosinophil-derived neurotoxin (EDN) {Human (Homo sapiens)}
MKPPQFTWAQWFETQHINMTSQQCTNAMQVINNYQRRCKNQNTFLTTFANVVNVCGNPNTCPSNKTRKNCHHSGSQVPLIHCNLTPSPQ
NISNCRYAQQT PANMFYIVACDNRDQRRDPPQYPVPVHLDRII
>d1rnfa_d.5.1.1 (A:) Ribonuclease 4 {Human (Homo sapiens)}
MQDGMYQRFLRQHVPEETGGSDRYCNLMMQRKMTLYHCKRFNTFIHEDIWNIRSICSTTNIQCKNGKMNCHEGVVKVTDCRTGSSRAPNC
RYRAIASTRVVIACEGNPQVPVHFDG
>d1b1ia_d.5.1.1 (A:) Angiogenin {Human (Homo sapiens)}
EDNSRYTHFLTQHYDAKPQGRDDRYCESIMRRGLTSPCKDINTFIHGNKRSIKAICENKNGNPHRENLRISKSSFQVTTCKLHGGSPWPPCQYRATA
GFRNVVVACENGGLPVHLDQSIFRRP
>d1agi__d.5.1.1 (-) Angiogenin {Cow (Bos taurus)}
AQDDYRYIHFLTQHYDAKPQGRNDEYCFNMMKNRRLRPCDKDRNTFIHGNKNDIKAICEDRNGQPYRGDLRISKSEFQITICKHKGSSRPPCRYGA
TEDSRVIVVGCEGLPVHFDESFITPRH
>d1ag2__d.6.1.1 (-) Prion protein domain {Mouse (Mus musculus)}
GLGGYMLGSAMSRPMIHFGRNDWEDRYYRENMYRPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTKGENFTETDVKMMERVVEQMC
VTQYQKESQAYY
>d1b10a_d.6.1.1 (A:) Prion protein domain {Golden hamster (Mesocricetus auratus)}
LGGYMLGSAMSRPMMHFGNDWEDRYYRENMNRYPNQVYYRPVDQYSNQNNFVHDCVNITIKQHTVTTTKGENFTETDIKIMERVVEQMC
TQYQKESQAYYDG
>d1fo7a_d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}
LGGYMLGSAMSRPIIHFGRNDWEDRYYRENMRYPNQVYYRPDEYSNQNNFVHDCVNITIKQHTVTTTKGENFTETDVKMMERVVEQMC
ITQ
ERESQAYYQRGSS
>d1i4ma_d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}
GAVVGGYMLGSAMSRPIIHFGRNDWEDRYYRENMRYPNQVYYRPDEYSNQNNFVHDCVNITIKQHTVTTTKGENFTETDVKMMERVVE
QMC
ITQ
YERESQAYY
>d1dwya_d.6.1.1 (A:) Prion protein domain {Cow (Bos taurus)}
GLGGYMLGSAMSRPLIHFGRNDWEDRYYRENMRYPNQVYYRPDEYSNQNNFVHDCVNITVK
EHTVTTTKGENFTETDIKMMERVVEQMC
ITQ
YQRESQAYYQ
>d1i17a_d.6.1.1 (A:) Prion-like protein Doppel {Mouse (Mus musculus)}
RVAENRPGAFIKQGRKLIDFGAEGNRYAANYWQFPDGIYEGCSEANVTKEMLVTSCVNATQAANQAEFSREKQDSKLHQRVLWRLIKEICS
AK
HCDFWLERGAA
>d1e01a_d.7.1.1 (A:) Membrane-bound lytic murein transglycosylase D, MltD {Escherichia coli}
DSITYVRKGDSLSSIAKRHGVIKDVMRWNSDTANLQPGDKLTLFV
>d1hywa_d.186.1.1 (A:) Head-to-tail joining protein W, gpW {Bacteriophage lambda}
MTRQEELAAAARAALHDLMGKRVATVQKDGRVEFTATSVDLKKYIAELEVQ
TGMTQ
>d1ejra_d.8.1.1 (A:) Urease, gamma-subunit {Klebsiella aerogenes}
MELTPREKDKLLLTAALVAERRLARGLKLNPESVALISAFIMEGARDGKSASLMEEGRHVLREQVMEGVPEMIPDIQ
VEATFPDGSKLVTVHN
I
>d4ubpa_d.8.1.1 (A:) Urease, gamma-subunit {Bacillus pasteurii}
MHLNPAEKEKLQIFLASELLRRKARGLKLNPESVALISAFIMEGARDGKT
VAMLMEEGKHVLRDDVMEGVPEMIDDIQAEATFPDGTLVTVHN
PIS

>d1e9ya2 d.8.1.1 (A:1-105) Urease, gamma-subunit {Helicobacter pylori}
MKLTPKELDKMLHYAGELAKKRKEKGKLNVVEAVALISAHIMEEARAGKKAAELMQEGRTLLKPDDVMGVASMIHEVGIEAMFPDGTLVTV
HTPIEANGK
>d1qe6b_ d.9.1.1 (B:) Interleukin-8, IL-8 {Human (Homo sapiens)}
AKECRCQCICKTYSKPFHPKFIKERVIESGPHCANTEIIVKLSDGRECLDPKENWVQRVVEKFLKRAENS
>d3il8__ d.9.1.1 (-) Interleukin-8, IL-8 {Human (Homo sapiens)}
LRCQCICKTYSKPFHPKFIKERVIESGPHCANTEIIVKLSDGRECLDPKENWVQRVVEKFLKRAENS
>d1plfa_ d.9.1.1 (A:) Platelet factor 4, PF4 {Cow (Bos taurus)}
LQCVCVLTSGINPRHISSELEVAGLHCPSPLIATLKTGRKICLDDQQNPLYKKIIKRLLES
>d1pfma_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}
MSAKELRCQCVCVKTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNGRKICLDPASPIVKIIEKMLNSDKSN
>d1rhpa_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}
DLQCLCVKTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNGRKICLDPASPIVKIIEKMLNSDKSN
>d1mgsa_ d.9.1.1 (A:) Melanoma growth stimulating activity (MGSA) {Human (Homo sapiens)}
ASVATELRQCQLTQLQGIHPKNIQSVDVSPGPHCQAQTEVIATLKNGRKACLNPAPIVKIIEKMLNSDKSN
>d1roda_ d.9.1.1 (A:) IL-8/MGSA chimeric protein CIL-8M {Human (Homo sapiens)}
SAKELRCQCICKTYSKPFHPKFIKERVIESGPHCANTEIIVKLSDGRECLDPASPIVKIIEKMLNSDKSN
>d1huna_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens), 1-beta}
APMGSDPPTACCSYTAARKLPRNFVVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWWQEYVYDLELN
>d1b50a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens), 1-alpha}
SLAADTPTACCSYTSRQIPQNFIAYFETSSQCSKPGVIFLTKRSRQVCADPSEEWVQKYVSDLELSA
>d1ha6a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Mouse (Mus musculus), ccl20/mip-3a}
ASNYDCCLSYIQTPLPSRAIVGFTRQMADEACDINAIFIHTKRKSVCADPKQNWWKRAVNLLSLRVKKM
>d1cm9a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Kaposi's sarcoma herpes virus, VMIP-II}
SWHRPDCKCLGYQKRPLPVLLSWYPTSQLCSKPGVIFLTKRGKQVCADSKDWVKKLMQQLPVTAR
>d1b3aa_ d.9.1.1 (A:) RANTES (regulated upon activation, normal T-cell expressed and secreted) {Human (Homo sapiens)}
PYSSDTTPCCFAYIARPLPRAHIKEYFYTSKGSNCNPAAVVFTRKNRQVCANPEKKWVREYINSLEMS
>d1doka_ d.9.1.1 (A:) Monocyte chemoattractant protein-1 (MCP-1, MCAF) {Human (Homo sapiens)}
MQPDAINAPVTCCYNFTNRKISVQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKVWQDSMDHLKDQT
>d1esra_ d.9.1.1 (A:) Monocyte chemoattractant protein-2 (MCP-2) {Human (Homo sapiens)}
EPDSVISIPITCCFNVINRKIPIQRLEYTRITNIQCPKEAVIFKTQRGKEVCADPKERWVRDSMKHLDQIFQNLKP
>d1el0a_ d.9.1.1 (A:) CC chemokine I-309 {Human (Homo sapiens)}
SKSMQVPFSRCCFSFAEQEIPLRAILCYRNTSSICSNEGLIFKLKRGKEACALDTVGVWVQRHRKMLRHCPSKRK
>d1eot__ d.9.1.1 (-) Eotaxin {Human (Homo sapiens)}
GPASVPTTCCFNLANRKIPLQRLEYRRTSGKCPQKAVIFKTKLAKDICADPKKKWVQDSMKYLDQKSPTPKP
>d1eiha_ d.9.1.1 (A:) Eotaxin-2 {Human (Homo sapiens)}
VVIPSPCCMFVSKRIPENRVVSYQLSSRSTCLKAGVIFTKKGQQSCGDPKQEWVQRYMKNLDAKQKKASPR
>d1j9oa_ d.9.1.1 (A:) Lymphotactin {Human (Homo sapiens)}
VGSEVSDKRTCVSLTTQRLPVSRKTYTITEGSLRAVIFITKRLKVCADPQATWVRDVVRSMDRKSNTNNMIQTKPTGTQQSTNTAVTLG
>d1bo0__ d.9.1.1 (-) Monocyte chemoattractant protein-3 (MCP-3) {Human (Homo sapiens)}
QPVGINTSTTCCYRFINKKIPKQRLEYRRTSSHCPREAVIFKTKLDKEICADPTQKWVQDFMKHLDKKTQTPKL
>d1b2ta_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}
MQHHGVTKCNITCSKMTSKIPVALLIHYQQNQASCGRKAIILETRQHRLFCADPKEQWVKDAMQHLDROAAALTRNG
>d1f2la_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}

VTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAILETRQHRLFCADPKEQWVKDAMQHLDHQ
>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)}
DSSDLYAELRCLCIKTTSGIHPKNIQSLEVIGKGTHCNQVEVIATLKDGRKICLDPDAPRIKKIVQKKLAGD
>d1a15a_d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}
KPVLSYRCPCRFFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN
>d1a15b_d.9.1.1 (B:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}
RCPCRFFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEK
>d1qg7a_d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}
SYRPCRFFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN
>d1mi2a_d.9.1.1 (A:) Macrophage inflammatory protein-2 {Mouse (Mus musculus)}
AVVASELRCQCLKTLPRVDFKNIQSLSVTPPGPHCAQTEVIATLKGQQVKCLDPEAPLVQKIIQKILNKGKAN
>d2hcc_d.9.1.1 (-) Chemokine hcc-2 (macrophage inflammatory protein-5) {Human (Homo sapiens)}
HFAADCCTSYISQSPCSLMKSQYFETSSECSKPGVIFLTKKGRQVCAPSGPGVQDCMKKLPYSI
>d1qnka_d.9.1.1 (A:) Gro beta {Human (Homo sapiens)}
TELRCQCLQLQGQIHLKNIQSVVKVSPGPQHCAQTEVIATLNGQKACLNPASPMVKIIKMLKNGKSN
>d1g91a_d.9.1.1 (A:) Myeloid progenitor inhibitory factor-1 (MPIF-1) {Human (Homo sapiens)}
MDRFHATSADCCSYTPRSIPCSLLESYFETNSECSKPGVIFLTKKGRRFCANPSDKQVQVCMRMLKLDTRIKTRKN
>d1bf4a_d.9.2.1 (A:) DNA-binding protein {Archaeon Sulfolobus solfataricus, Sso7d}
ATVKFKYKGEEKEVDISKIKKVWRVGKMSFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK
>d1azpa_d.9.2.1 (A:) DNA-binding protein {Archaeon Sulfolobus acidocaldarius, Sac7d}
MVVKVKFKYKGEEKEVDTSKIKKVWRVGKMSFTYDDNGKTGRGAVSEKDAPKELLQMLARAEREKK
>d1ap0_d.9.2.2 (-) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}
HMVEEVLEEEEEEYVVEKVLDRVVKGKVEYLLWKGFSDEDNTWEPEENLDCPDLIAEFLQSQKTAHETDKS
>d1dz1a_d.9.2.2 (A:) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}
HMKEESEKPRGFARGLEPERIIGATDSSGELMFLMKWNSDEADLVAKEANVKCPQVVISFYERLTWH
>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)}
ISSPKQEEYEVERIVDEKLDRNGAVKLYRIRWLNYSSRSDTWEPPENLGCSAVLAEWKRRKRRLLGSNS
>d1bb8_d.10.1.1 (-) DNA-binding domain from tn916 integrase {Enterococcus faecalis}
EKRRDNRGRLIKTGESQRKDGRYLYKYIDSFGEPQFVYSWKLVATDRVAGRKDCISLREKIAELQKDIHD
>d1gcc_a_d.10.1.2 (A:) GCC-box binding domain {Mouse-ear cress (Arabidopsis thaliana)}
KHYRGVRQRPWGKFAAEIRDPAKNGARVWLGTFTAEDAALAYDRAAFMRGRSALLNFPLRV
>d1qk9a_d.10.1.3 (A:) Methyl-CpG-binding protein 2, MECP2 {Human (Homo sapiens)}
ASASPKQRRIIDRGPMYDDPTLPEGWTRKLQRKSGRSAGKYDVYLINPQGKAFRSKVELIAYFEKVGDTSLPDNDFDFTVTGRGSGSGC
>d1d9na_d.10.1.3 (A:) Methylation-dependent transcriptional repressor MBD1/PCM1 {Human (Homo sapiens)}
MAEDWLDCPALGPWGKRREVFRKSGATGRSDTYYQSPTGDRIRSKVELTRYLGPACDLTLFDFKQGILCYPARK
>d1k25a1_d.11.1.1 (A:632-692) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}
TESSYAMPSIKDISPGELEALRRNIVQPIVGTGKIKETSVEEGTNLAPNQQVLLSDK
>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}

QQSPYPMPSVKDISPGDLAEEELRRNLVQPIVVGTTKIKNSSAEEGKNLAPNQQVLILSDK
>d1qmea2 d.11.1.1 (A:693-750) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}
AEEVPDMYWTKETAETLAKWLNLIEFQSGSGTVQKQDVRANTAIKDIKKITLTGDD
>d1jj2r_ d.12.1.1 (R:) Ribosomal protein L23 {Archaeon Haloarcula marismortui}
SWDVKHPHVTEKAMNDMDFQNLQFAVDDRASKGEVADAVEEQYDVTVEQVNNTMDGEKKAVVRLSEDDDAQEVASRI
>d1ffki_ d.12.1.2 (I:) Ribosomal protein L15e {Archaeon Haloarcula marismortui}
MKSMYAYIREAWKRPYEGYVGELMWHLQKWRREPAVVIRPRTLDRARALGYKAKKGIIIVVRVIRRGGRRATRPNKGRSKMMVNRRPRK
KNLQWIAEERANRKYPNMEVLNSYVGEDGRYKWFEVILVDRDHPIAKSDPQLSWVSRTGRVYRGLTSAGRKARGLRRKGRGAEVRLPSLRANF
RKKR
>d1jj2l_ d.12.1.2 (L:) Ribosomal protein L15e {Archaeon Haloarcula marismortui}
ARSAYSYIREAWKRPKEGQIAELMWHRMQEWRNEPAVVRIERPTLDRARSLGYKAKQGIIIVRVAIRKGSSRTRFNKGRRSKMMVNRLTRKKN
IQRIAEERANRKFPNLRLVLSYVGEDGRHKWHEVILIDPDHPIAKSDDQLSWISRTRHRLRTFRGLTSAGRRCRGLRGQKGSEKVRLPSLRNGAKA
>d4rhn__ d.13.1.1 (-) Histidine triad nucleotide-binding protein (HINT) {Rabbit (Oryctolagus cuniculus)}
RPGGDTIFGKIIKEIPAKIIFEDDQCLAFHDISPOQAPTHFLVIPKKHISQISAAEADESLLGHLIVGKKCAADLGLKKGYRMVVNEGSDGGQSVYHV
HLHVLGGRQMWNPPG
>d1fit__ d.13.1.1 (-) FHIT (fragile histidine triad protein) {Human (Homo sapiens)}
SFRFGQHLIKPSVVFALKTELSFALVNRKPVPGHVLVCPLRPVERFDLRLPDEVADLFQTTQRVGTVEKFHGTSFTSMQDGPEAGQTVKHVHVH
VLPRKAGDFHRNDSIYEELQKHDKEFPASWRSEEEMAAEAAALRVYFQ
>d1kpf__ d.13.1.1 (-) Protein kinase C inhibitor-1, PKC-1 {Human (Homo sapiens)}
DTIFGKIIKEIPAKIIFEDDRCLAFHDISPOQAPTHFLVIPKKHISQISVAEDDDESLLGHLIVGKKCAADLGLNKGYRMVVNEGSDGGQSVYHVHLHV
LGGRQMHWPPG
>d1emsa1 d.13.1.1 (A:281-440) NIT-FHIT fusion protein, C-terminal domain {Nematode (Caenorhabditis elegans)}
RSDLYTLHINEKSSETGGLKARFNIPADHFYSTPHSFVFNLPVTDGHVLSPKRVVPRLTDLDAETADLFIVAKVQAMLEKHHNVTTTICVQD
GKDAGQTVPVHIIHLPRRAGDFGDNEIYQKLASHDKEPERKPRSNEQMAEEAVYRNLM
>d1guqa1 d.13.1.2 (A:2-177) Galactose-1-phosphate uridylyltransferase {Escherichia coli}
TQFNPVDPHRRYNPLTGQWILVSPHRAKRWPQGAQETPAKQVLPAPHDCFLCAGNVRTGDKNPDTGTYFTNDFAALMSDTPDAPESHDP
LMRCQSARGTSRVICFSPDHSKTLPELSVAALTEIVKTWQEQTAEGLKTPWVQVFENKGAAMGCSNPHPGQIWANSFLPN
>d1guqa2 d.13.1.2 (A:178-348) Galactose-1-phosphate uridylyltransferase {Escherichia coli}
EAEREDRLQKEYFAEQKSPMLVDYVQRELADGSRTVVETEHWLAVVPYAAWPFTLLLPAHVLRTDLTAQRSDLALALKLTSRYDNLFCQSF
PYSMGWHGAPFNGEENQHWQLHAHFYPLLRSATVRKFMVGYEMLAETQRDLTAEQAAERLRAVSDIHFRESGV
>d1jyaa_ d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}
YSFEQAITQLFQQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDEKETLLSHNIFSQDILKPILSWDEVGGHPVLWNRQPLNSLDNN
SLYTQLEMLVQGAERLQ
>d1k6za_ d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}
SFEQAITQLFQQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDEKETLLSHNIFSQDILKPILSWDEVGGHPVLWNRQPLNSLDNN
LYTQLEMLVQGAERLQ
>d1jyoa_ d.198.1.1 (A:) Virulence effector SptP secretion chaperone SicP {Salmonella typhimurium}
LQAHQDIIANIGEKLGLPLTFDDNNQCLLLSDIIFTSIEAKDDIWLNGMIILSPVCGDSIWRQIMVINGELAANNEGTLAYIDAAETLLIHAITDLT
NTYHIISQLESFVNQQEALKNILQEYAKV
>d1k3ea_ d.198.1.1 (A:) Secretion chaperone CesT {Escherichia coli}
MSSRSELLLEKFAEKIGIGSISFNENRLCSFAIDEIYYISLSDANDEYMMIYGVCGFPTDNSNFALEILNANLWFAENGGPYLCEAGAQSLLA
DDATPEKLENIEVVKSMEYLVLHNQGITLENEHMKIEISS
>d1k3sa_ d.198.1.1 (A:) Secretion chaperone SigE {Salmonella enterica}
MESLLNRLYDALGLDAPEDEPLIIDDGQVYFNESDHTLEMCCPFMPLPDDILTLQHFRLNYTSAVTIGADADNTALVALYRLPQTSTEEEALTGFELF

ISNVKQLKEHYA

>d1k8kf_d.198.2.1 (F:) ARPC4 (20 kDa subunit) {Cow (Bos taurus)}

TATLRLPYLSAVRATLQAALCLENFSSQVVERHNKPEVEVRSSKELLQPVTISRNEKEVKLIEGSINSVRVSIAVKQADEIEKILCHKFMRFMMRAENF
FIIRRKPVEGYDISFLITNFHTEQMYKHKLVDFVIHFMEIDKEISEMKLSVNARARIVAEELKNF

>d1k8kd1 d.198.2.1 (D:1-120) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

MILLEVNRIIEETLALKFENAAAGNKPEAVEVTADFVGVLYHISNPNGDKTKVMVSISLKFYKELOAQAHGADELLKRVYGSYLVNPESGYNVSLLYDLE
NLPASKDSIVHQAGMLKRC

>d1k8kd2 d.198.2.1 (D:121-284) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

FASVFEKYFQFQEEGKEGENRAVIHYRDDETMYVESKKDRVTVFSTVFKDDDDVVIGKVFMQEFGKFRASHTAPQVLFSHREPPLEKDTDAAV
GDNIGYITFVLFPRHTNASARDNTINLIHTFRDYLHYHIKCSKAIHTRMRAKTSDFLKVLNRARPDA

>d1kafa_d.199.1.1 (A:) DNA-binding C-terminal domain of the transcription factor MotA {Bacteriophage T4}

MEITSDMEEDKDMLKLKDNGFVLKKVEIYRSNYLAILEKRTNGIRNFEINNNGNMRFIFYKMMEEHIQKFTDIGMSCKIAKNGNVYLDIKRSAEN
IEAVITVASEL

>d1dar_3 d.14.1.1 (476-599) Elongation factor G (EF-G), domain IV {Thermus thermophilus}

VGKPQVAYRETITKPVDFEGKFIQTGGRGQYGHVKIKVEPLPRGSGFEVNAIVGGVIPKEYIPAVQKGIEAMQSGPLIGFPVVDIKVTLYDGSYHE
VDSSEMAFKIAGSMAIKEAVQKGDP

>d1pkp_1 d.14.1.1 (78-148) Ribosomal protein S5, C-terminal domain {Bacillus stearothermophilus}

GTTIPHEVIGHFGAGEIIKPKASEGTGVIAGGPARAVLELAGISDILSKSIGNSNTPINMVRATFDGLKQLK

>d1fge1 d.14.1.1 (E:74-154) Ribosomal protein S5, C-terminal domain {Thermus thermophilus}

GTIPHEIEVEFGASKIVLKPAAPGTGVIAGAVPRAILELAGVTIDLTKELGSRNPINAYATMEALRQLRTKADVERLRKG

>d1fjgi_d.14.1.1 (I:) Ribosomal protein S9 {Thermus thermophilus}

EQYYGTGRKKEAVARVFLRPGNGKVTVNGQDFNEYFQGLVRAVAALEPLRAVDALGRFDAYITVRGGGKSGQIDAICLGIARALVQYNPDYRAKLKP
LGFLTRDARVVERKKYGHKARRAPQYSKR

>d1a6f__d.14.1.2 (-) RNase P protein {Bacillus subtilis}

AHLKKRNRLKKNEDFQVKFHGTSVANRQFVLYTLDQPENDELRVGLSVKKIGNAVMRNRKRLIRQAFLEEKERLKEKDYIIARKPASQLTYEETKK
SLQHLFRKSSLYK

>d1d6ta_d.14.1.2 (A:) RNase P protein {Staphylococcus aureus}

MLLEKAYRIKKNADFQRIYKKGHSVANRQFVYTCNNKEIDHFRLGISVSKKLGNAVLRNKKRAIRENFKVHKSHILAKDIIIVIARQPAKDMTTLQIQNM
SLEHVLKIAKVFNKKIK

>d1b63a1 d.14.1.3 (A:217-331) DNA mismatch repair protein MutL {Escherichia coli}

GTAFLEQALAIIEWQHGDLTRLGVVADPNHTTPALAEIQCYVNGRMMRDRLINHAIRQACEDKLGADQQPAFVLYIEDPHQDVNVHPAKHEV
RFHQSRVLVHDFIYQGVLSVLQ

>d1h7sa1 d.14.1.3 (A:232-365) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}

GGKQLQSLIPFVQLPPSDSCEEYGLSCDALHNLFYISQCTHGVGRSSTDQFFFINRRPCDAVKCRLVNEVYHMYNRHQYPFVVLNISVDSE
CVDINVTPDKRQILLQEEKLLLAVLKTSLIGMFDS

>d1ei1a1 d.14.1.3 (A:221-392) DNA gyrase B {Escherichia coli}

GIKAFVEYLNKNKTPIHNPNIFYFSTEKDYGIGVEALQWNNDGFQENIYCFTNNIPQRDGTHLAGFRAAMTRTLNAYMDKEGYSKKAKVSATGDDAR
EGLIAVVSVVKVPDPKFSSQTSDKLVSSEVKSAAEQQQMNELLAEYLLNPTDAKIVVGKIIAADARAREAARRAREMT

>d1e3ha2 d.14.1.4 (A:3-151) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}

NETHYAEAVIDNGAFGTRTIRFETGRLRARQAAGSAVYLDDDTMVLATTASKNPKDQLDFPLTVDVEERMAYAAGKIPGSFFRREGRPSEDAILTCRL
IDRPLRPSFKGLRNEIQVVAATIMALNPDHLYDVVAINAASASTQLAGLP

>d1e3ha3 d.14.1.4 (A:346-482) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}

TDIRTLAAEVEAIPRVHGSALFERGETQILGVTTLNMLRMEQQQLDTLSPVTRKRYMHNYNFPPYSVGETGRVGSPKRREIGHGALAERAIVPVLPTRE
EFPYAIRQVSEALGSNGSTMSGVCASTMSLLNAGVPLK
>d1h72c1 d.14.1.5 (C:5-167) Homoserine kinase {Archaeon Methanococcus jannaschii}
MKVRVKAPCTSANLGVGFDFVFLCLKEPYDVIEVAIDDEIIIEVDDKNIPTDPDKNVAGIVAKMIDDFNIGKGVKITIKGVKAGSGLGSSAASSAG
TAYAINELFKLNLDKLKLVDYASGYELASSGAKHADNVAPAIFGGFTMVNTYEPLEVHLHIPID
>d1fi4a1 d.14.1.5 (A:3-190) Mevalonate 5-diphosphate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}
VYTASVTAPVNIAITLKYWGKRDTKLNLPTNSSISVTLSQDDLRTLSAATAPEFERDTLWLNGEPHSIDNERTQNCLRDLRQLRKEMESKDASLPTLSQ
WKLHIVSENNFPTAACGLASSAAGFAALVSAIAKLYQLPQSTSEISRIARKGSACRSLFGGYVAWEMGKAEDGHDSMAVQIADSSDWP
>d1c3ta_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
MQLFVKTLTGKLTVELEPSDTVNLKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDynLQESTIHLVLRLRGG
>d1gjza_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
GSMQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDynIQLKESTIHLVLRLRGG
>d1ubi_ d.15.1.1 (-) Ubiquitin {Human (Homo sapiens)}
MQIFVKTLTGKTITLEVEPSDTIENVKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDynIQLKESTIHLVLRLRGG
>d1ud7a_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
MQVFLKTGTVTIEVEPSDTVENFKAKIQDKEGIPPDQQRLIFAGKQLEDGRTLSDynIQLKESTIHLVLRLRGG
>d1a5r_ d.15.1.1 (-) SUMO-1 (smt3 homologue) {Human (Homo sapiens)}
GSMSDQEAKPSTEDLGDKKEGEYIKLVIGQDSSEIHFKVKMTTHLKKLKESYCQRQGVPMNSLRFLFEGQRIADNHTPKELGMEEEDVIEVYQEQT
GGHSTV
>d1euvb_ d.15.1.1 (B:) SUMO-1 (smt3 homologue) {Baker's yeast (Saccharomyces cerevisiae)}
PETHINLKVS DGSSEIFFKKTTPLRRLMEAFAKRQGKEMDSLRFLYDGIRIQADQTPEDLDMEDNDIIEAHREQIGG
>d1ndda_ d.15.1.1 (A:) Nedd8 {Human (Homo sapiens)}
MLIKVKTGTKEIEIDIEPTDKVERIKERVEEKEGIPPPQQQLIYSGKQMNDKTAADYKILGGSVLHLVLALR
>d1vcba_ d.15.1.1 (A:) Elongin B {Human (Homo sapiens)}
MDVFLMIRRHKTTIFTDAKESSTVFELKRIVEGILKRPPDEQRLYKDDQLDDGKTLGECGFTSQTARPQAPATVGLAFRADDTFEALCIEPFSSPPE
>d1bt0a_ d.15.1.1 (A:) Rub1 {Mouse-ear cress (Arabidopsis thaliana)}
MLIKVKTGTKEIEIDIEPTDTDIRKERVEEKEGIPPVQQQLIYAGKQLADDKTAKDYNIEGGSVLHLVLAL
>d1h8ca_ d.15.1.2 (A:) Fas-assosiated factor 1, Faf1 {Human (Homo sapiens)}
NAEPVSKLIRTPSGEFLERRFLASNKLQIVFDFVASKGFPWDEYKLLSTFPRRDVTQLDPNKSLEVKLFPQETLFLEAKE
>d1i42a_ d.15.1.2 (A:) p47 {Rat (Rattus norvegicus)}
KASSILINEAEPPTNIQIRLADGGRLVQKFNFHSHRISDIRLFIVDARPMAMAATSFVLMTFPNKELADENQTLKEANLLNAVIVQRLT
>d1eo6a_ d.15.1.3 (A:) Golgi-associated ATPase enhancer of 16 kD, Gate-16 {Cow (Bos taurus)}
MKWMFKEDHSLEHRCVESAKIRAKYPDRVPVIVEKVGSGQIVDIDKRKYLVPSDITVAQFMWIIRKRIQLPSEKAIFLFVDKTVQSSLTMGQLYEKEK
DEDGFLYVAYS GENTFG
>d1gnua_ d.15.1.3 (A:) GABA(A) receptor associated protein GABARAP {Human (Homo sapiens)}
MKFVYKEEH PFEKRRSEGEKIRKKYPDRVPVIVEKAPKARIGDLDKKYLVPSDLTVGQFYFLIRKRIHLRAEDALFFFVNNVIPPTSATMGQLYQEHH
EDFFFLYIAYSDESVYGL
>d1ef1a3 d.15.1.4 (A:4-87) Moezin {Human (Homo sapiens)}
TISVRVTTMDAELEFAIQPNTTGKQLFDQVVKTIGLREVWFFGLQYQDTKGFSTWLKLNKKVTAQDVRKESPLLFKFRKFYPE
>d1gc7a3 d.15.1.4 (A:1-87) Radixin {Mouse (Mus musculus)}
MPKPINVRVTTMDAELEFAIQPNTTGKQLFDQVVKTGVLREVWFFGLQYVDSKGYSTWLKLNKKVTTQDVKKENPLQFKFRKFYPE
>d1gg3a3 d.15.1.4 (A:1-81) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
MHCKVSLDDTVYECVVEKAKGQDLLKRVCEHNLLEEDYFGLAIWDNATSKTWLDSA KEIKKQVRGVPNFTFNVKFYP
>d1h4ra3 d.15.1.4 (A:20-103) Merlin {Human (Homo sapiens)}

KTFTVRIVTMADAEMEFNCEMKWKGKDLFDLVCRTLGLRETWFFGLQYTIKDTVAWLKMDKKVLHDVSKEEPVTFHFLAKFYPE
>d1c1yb_d.15.1.5 (B:) c-Raf1 RBD {Human (Homo sapiens)}
SNTIRVFLPNKQRTVVNRNGMSLHDCLMKALKVRLQPECCAVFRLLHEHKKKARLDWNTDAASLIGEELQVDFL
>d1fda_d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RalGDS {Rat (Rattus norvegicus)}
GDCCIIRVSLVDNGNMYKSIILVTSQDKAPTVRKAMDKHNLDDEPEDYELLQIISDHKLKIPENANVFYAMNSAANYDFILKKR
>d1raxa_d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RalGDS {Human (Homo sapiens)}
QQVGDCCIIRVSLVDNGNMYKSIILVTSQDKAPAVRKAMDKHNLEEEPEDYELLQILSDDRKLKIPENANVFYAMNSTANYDFVLKKRTFT
>d1rlf_d.15.1.5 (-) RalGDS-like factor, Rlf {Mouse (Mus musculus)}
GSSDCRIIRVQMELEDGSVYKSLVTSQDKAPSVISRLKKNNRDSAVASEFELVQLPGDRELTIHSANVFYAMDGASHDFLLRQRR
>d1ef5a_d.15.1.5 (A:) Rgl {Mouse (Mus musculus)}
EDTCIIRISVEDNNGNMYKSIILTSQDKTPAVIQRAMSCHKHNLESDPAEEYELVQVISEDDELVIPDSANVFYAMNSQVNFDIFLRKKN
>d1e8xa3_d.15.1.5 (A:142-321) Phoshoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}
AASEETLAFQRQLNALIGYDVTDSNVHDDLEFTRRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKITNNCVFIVIHRSTTSQTIKVASSD
TPGTILQSFFTAKMAKKSLMDIPESQNERDFVLRVCGRDEYLGETPIKNFQWVRQCLNGEEIHLVLDTPPDALDEVRKKE
>d1e8ya3_d.15.1.5 (A:143-322) Phoshoinositide 3-kinase (PI3K) {Human (Homo sapiens)}
MSEESQAFQRQLTALIGYDVTDSNVHDDLEFTRRLVTPRMAEVASRDPKLYAMHPWVTSKPLPEYLLWKKIANNCIFIVIHRSTTSQTIKVSPDDT
PGAILQSFFTAKMAKKSLMDIPESQSEQDFVLRVCGRDEYLGETPIKNFQWVRHCLKNGEEIHLVLDTPPDALDEVRKKE
>d1i35a_d.15.1.5 (A:) Protein kinase byr2 {Yest (Schizosaccharomyces pombe)}
CILRFIACNGQTRAVQSRGYQKTLAIALKKFSEDASKFIVCVSQSSRIKLIIEEEFKQJCFNSSSPERDRLLIVPKPCPSFEDLRRSWEIE
>d1d4ba_d.15.2.1 (A:) Cell death-inducing effector B (CIDE-B), N-terminal domain {Human (Homo sapiens)}
MEYLSALNPSDLLRSVSNISSFGRRVWTSAAPPQRPFRVCDHKRTIRKGLTAATRQELLAETLLLNGVLTGLEEDGTAVDSEDFFQLLEDDTCLM
VLQSGQSWSPTRSGVLHHHHHH
>d1c9fa_d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Mouse (Mus musculus)}
MCVALRQPCKVKLRALHSACKFGVAARSCQELLRGCVRFQLPMPGSRLCLYEDGTEVTDDCFPLPNDAELLLTAETWHGYVSD
>d1ibxa_d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Human (Homo sapiens)}
MLQKPKSVKLRLRSPRKFGVAGRSCQEVLKGCLRFQLPERGSRLCLYEDGTELTDYFPSVPDNAELVLLTGQAWQGH
>d1f2ri_d.15.2.1 (I:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Mouse (Mus musculus)}
MELSRGASAPDPDDVRPLKPCLLRRNHSRDQHGVAASSLEELRSKACCELLAIDKSLTPTILVLAEDGTIVDDDDYFLCLPSNTKFVALACNEKWTYND
D
>d1ibxb_d.15.2.1 (B:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Human (Homo sapiens)}
SGEIRTLKPCLRRNYSREQHGVAASCLEDRSKACDILAIDKSLTPTILVLAEDGTIVDDDDYFLCLPSNTKFVALASNEKWAYNNSD
>d1ip9a_d.15.2.2 (A:) Bud emergence mediator Bemp1 {Baker's yeast (Saccharomyces cerevisiae)}
GAMGSSTSGLTTKIKFYKKDDIFALMLKGDTTYKELRSKIAPRIDTDNFKLQTKLFDGSGEEIKTDSQVSNIQAKLKISVHD
>d1fm0d_d.15.3.1 (D:) Molybdopterin synthase subunit MoaD {Escherichia coli}
MIKVLFFAQVRELVGTDATEVAADFPTVEALRQHMAAQSDRWALALEDGKLLAAVNQTLVSDHPLTDGDEAFFPPVTGG
>d1f0za_d.15.3.2 (A:) Thiamin biosynthesis sulfur carrier protein ThiS {Escherichia coli}
MQILFNDQAMQCAAGQTVHELLEQLDQRQAGAALAINQQIVPREQWAQHIVQDGQILLFQVIAGG
>d1jsba_d.15.3.2 (A:) Hypothetical protein MTH1743 {Archaeon Methanobacterium thermoautotrophicum}
MVIGMKFTVITDDGKKILESGAPRRIKDVLGELIPIETVVVKKNGQIVIDEEIFDGDIIEVIRVIYGG
>d1czpa_d.15.4.1 (A:) 2Fe-2S ferredoxin {Cyanobacterium (Anabaena sp.), pcc 7119 and 7120}
ATFKVTLINEAEGTKHEIEVPDDEYILDAAEEQGYDLPFSCRAGACSTCAGKLVSGTVDDQSDQSFLDDQIEAGYVLTCVAYPTSDVVIQTHKEEDLY
>d1frd_d.15.4.1 (-) 2Fe-2S ferredoxin {Cyanobacterium (Anabaena sp.), pcc 7119 and 7120}
ASYQVRLINKQQIDTTIEDETTILDGAENGIELPFSCHSGSCSSCVGVVGEVDQSDQIFLDDEQMGKGFAALLCVTYPRSNCTIKTHQEPLYA
>d4fxc_d.15.4.1 (-) 2Fe-2S ferredoxin {Spirulina platensis}

ATYKVTLINEAEGINETIDCDDDTYILDAEEAGLDLPPSCRAGACSTCAGTITSGTIDQSDQSFLDDDQIEAGYVLTCVAYPTSDCTIKTHQEELGY
>d1fxia_d.15.4.1 (A:) 2Fe-2S ferredoxin {Cyanobacterium (Aphanothece sacrum)}

ASYKVTLKTPDGDNVITVPDDEYILDVAEEGLDLPSCRAMACSTCAGKLVSGPAPDEDQSFLDDDQIQAGYILTCVAYPTGDCVIETHKEEALY
>d1dox_d.15.4.1 (-) 2Fe-2S ferredoxin {Synechocystis sp., pcc 6803}

ASYTVKLITPDGEESIECSDDTYILDAEEAGLDLPPSCRAGACSTCAGKITAGSVQDQSDQSFLDDDQIEAGYVLTCVAYPTSDCTIETHKEEDLY
>d2cjn_d.15.4.1 (-) 2Fe-2S ferredoxin {Synechococcus elongatus}

ATYKVTLVPRDGSETTIDVPEDEYILDVAEEQGLDLPSCRAMACSTCAGKLLEGEVDQSDQSFLDDDQIEKGFLTCVAYPRSDCKILTNQEEELY
>d1awd_d.15.4.1 (-) 2Fe-2S ferredoxin {Chlorella fusca}

YKVTLKTPSGEETIECPEDTYILDAEEAGLDLPPSCRAGACSSCAGKVESGEVDQSDQSFLDDAQMGKGFVLTCVAYPTSDVTILTHQEALY
>d1frra_d.15.4.1 (A:) 2Fe-2S ferredoxin {Equisetum arvense}

AYKTVLKTPSGEFTLDVPEGTTILDAAEEAGYDLPSCRAMACSSCLGKVVSGSVDSEGSFLDDGQMEEGFVLTCIAIPESDLVIETHKEEELF
>d1doi_d.15.4.1 (-) 2Fe-2S ferredoxin {Archaeon Haloarcula marismortui}

PTVEYLNYEVVDDNGWDMYDDDVFGEASDMDDLDYGSLEVNEGEYILEAAEAQGYDWPFSCRAMACANCAAIVLEGIDMDMQQILSDEEV
EDKNVRRLTCIGSPDADEVKIVYNAKHLDYLQNRVI

>d1e0za_d.15.4.1 (A:) 2Fe-2S ferredoxin {Archaeon Halobacterium halobium}

PTVEYLNYETLDDQGWDMDDDDLFEKAADAGLDGEDYGTMEVAEGEYILEAAEAQGYDWPFSCRAMACANCAAIVLEGIDMDMQQILSDEEV
EEKDVRRLTCIGSPADEVKIVYNAKHLDYLQNRVI

>d1pf_d.15.4.1 (-) 2Fe-2S ferredoxin {Parsley (Petroselinum crispum)}

ATYNVKLITPDGEVEFKCDDDVYVLDQAEEEGIDLPSCRAMACSSCAGKLKTGSLNQDDQSFLDDDQIDEGWVLTCAAYPVSDVTIETHKEEELTA
>d1a70_d.15.4.1 (-) 2Fe-2S ferredoxin {Spinach (Spinacia oleracea)}

AAYKVTLVPTGNVEFQCPDDVYILDAEEEGIDLPSCRAMACSSCAGKLKTGSLNQDDQSFLDDDQIDEGWVLTCAAYPVSDVTIETHKEEELTA
>d1gaqb_d.15.4.1 (B:) 2Fe-2S ferredoxin {Maize (Zea mays)}

ATYNVKLITPGEVELQVPPDVYILDQAEEEDGIDLPSCRAMACSSCAGKVVSGSDQSYLDDGQIADGWVLTCHAYPTSDVVIEHTKEEELTG
>d1e9ma_d.15.4.1 (A:) Ferredoxin VI {Rhodobacter capsulatus}

AKIIFIEHNGTRHEVEAKPGTVMEAARDNGVPGIDACGGACACSTCHAYVDPAWVDKLPKALPTETDMIDFAYEPNPATSRLTCQIKVTSLLDGLV
VHLPEKQI

>d1put_d.15.4.1 (-) Putidaredoxin {Pseudomonas putida}

SKVVYVSHDGTRRQLDVADGVSLMQAAVNSNGYDIVGDCGGSASCATCHVYVNEAFTDKVPAANEREIGMLECVTAELKPNTRLCCQIMTPELDGI
VVDPVDRQW

>d1b9ra_d.15.4.1 (A:) Terpredoxin {Pseudomonas sp.}

PRVVFIDEQSGEYAVDAQDGQSLMEVATQNGVPGIVAECEGGSCVCATCRIEIEDAWVEIVGEANPDENDLQSTGEPMTAGTRLSCQVFDPSMDG
LIVRVPLPA

>d1ayfa_d.15.4.1 (A:) Adrenodoxin {Cow (Bos taurus)}

KITVHFINRDGETLTTKGKIGDSLLVVQNNLDIDGFGACEGTLACSTCHLIFEKLEAITDEENDMLDLAGLTDRSRLGCQICLTKAMDNM
VRVP

>d1feha2 d.15.4.2 (A:1-126) Fe-only hydrogenase, N-terminal domain {Clostridium pasteurianum}

MKTIIINGVQFNTDEDLTLKFKARDNNIDISALCFLNNCNNDINKCEICTVEVEGTGLTACDTLIEDGMIINTNSDAVNEKIKSRISQLDIHEFKCGPCN
RRENCEFLKLVKYKARASKPFLP

>d1hlra2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio gigas}

MIQKVITVNGIEQNLVDAEALLSDVLRQQQLGLTVKGCEQGQCGACSVILDGKVRACVTMCRVADGAQITTIEVG
>d1dgja2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio desulfuricans}

METKTLIVNGMARRLLSPNDLLDVLSQLQLTSVKVCGKGQCGACTVILDGKVRACIICKMSRVAENASVTLEG
>d1fo4a2 d.15.4.2 (A:3-92) Xanthine oxidase, N-terminal domain {Cow (Bos taurus)}

ADELVFFFVNGKKVVEKNADPETTLLAYLRRKLGRLGCKLGCCEGGCGACTVMLSXYDRLQDKIIFHSANACLA
PICTLHHVAVTTVEGIG

>d1jroa2 d.15.4.2 (A:1-84) Xanthine dehydrogenase chain A, N-terminal domain {Rhodobacter capsulatus}
MEIAFLNLGETRRVRIEDPTQSLLELLRAEGLTGTKEGCNEGDCGACTVMIRDAAGSRAVNACLMMLPQIAGKALRTIEGIAAP

>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}
KKIITNVNNGKAQEKAVERPTLLIHFLREELNLGTGAHIGCETSHCGACTVDIDGRSVKSCTHLAVQCDGSEVLTEGLA

>d2pia_3 d.15.4.2 (224-321) Phthalate dioxygenase reductase, C-terminal domain {Pseudomonas cepacia, db01}
SFGATNTNARENTPFTVRLSRSGTSFEIPANRSILEVRDANVRVPSSCESGTCGSCKTALCSGEADHRDMVLRDEKGTQIMVCVSRAKSAELVLDL

>d1fumb2 d.15.4.2 (B:1-105) Fumarate reductase iron-sulfur protein, N-terminal domain {Escherichia coli}
AEMKNLKIEVVRYNPENVDTAPHSAFYEVPYDATTSLDALGYIKDNLAPDLSYRWSCRMAICGSCGMMVNNPKLACKTFLRDYTDGMKVEALAN
FPIERDLVVD

>d1qlab2 d.15.4.2 (B:1-106) Fumarate reductase iron-sulfur protein, N-terminal domain {Wolinella succinogenes}
MGRMLTIRVKYDPQS AVSKPHFQEYKIEEAPSMTIFIVLN MIRETYDPDLNFDFVCRAGICGSCGMMINGRPSLACRTLKD FEDGVITLLPLPAFKLI
KDL SVD

>d1jq4a_d.15.4.2 (A:) Methane monooxygenase reductase N-terminal domain {Methylococcus capsulatus}
MQRVHTITAVTEDGESLRFECRSDEDVITAALRQNIFLMSSCREGGCATCKALCSEG DYDLKGCSVQALPPEEEEGL VLLCRTYPKT DLEI ELPYTH

>d1ssn__ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}
SSFDKGKYKKGDDASYFEP TGPYLMVNVTGVDSKGNE LSPHYVEFPIKPGTTLKEIYYVEWAL DATA YKEFRVVELPSAKIEV TYYDKNKKKE
TKSFPITEKG FVVPDLSEHIKNPGFNLITKVVIEKK

>d2sak__ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}
SYFEP TGPYLMVNVTGVDSKGNE LSPHYVEFPIKPGTTLKEIYYVEWAL DATA YKEFRVVELPSAKIEV TYYDKNKKKE
SEHIKNPGFNLITKVVIEKK

>d1bmlc1 d.15.5.1 (C:12-148) Streptokinase {Streptococcus equisimilis}
SVNNSQLV SVAGTV EGTNQDISLKFFEIDLTSRPAHGGKTEQGLSPKSKPFATDSGAM PHKLEADLLKAIQEQLIANVHSNDDYFEVIDFAS DATIT
DRNGKVYFADKDG SVTLPTQPVQEFLLSGHV RVR PYKE

>d1bmlc3 d.15.5.1 (C:285-372) Streptokinase {Streptococcus equisimilis}
DPFDRSHLKLFTIKYDV DNNTNELLKSEQLL TASERNLDFRDLYDPRDKAKL LYNNA DAFGIMDYLTGKVEDNHDDTRNIITV YM GKR

>d1c4pc_ d.15.5.1 (C:) Streptokinase {Streptococcus equisimilis}
KPIQNQAKSVD VEYTVQFTPLNPDDDFRPGLKLT KLLKLAIGDTITSQELLAQAQSILNKTHPGYTIYERDSSIVTHDNDIFRTILPMQEF TYHVKNR
EQAYEINKSGLNEEINNTDLISEKYYVLKKG

>d1qqra_ d.15.5.1 (A:) Streptokinase {Streptococcus equisimilis}
IQNQAKSVD VEYTVQFTPLNPDDDFRPGLKLT KLLKLAIGDTITSQELLAQAQSILNKTHPGYTIYERDSSIVTHDNDIFRTILPMQEF TYRVKNREQ
AYRINKSGLNEEINNTDLISEKYYVLKKG EKPYDPFD

>d1esfa2 d.15.6.1 (A:121-233) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}
EEKKVPINWL DGKQNTVPLETVKTNKKNVTQ QELDLQARRYLQE KYNLYNSDVF DGKVQR GLIVFH STEPSV NYDLFGAQGQYSN TLLRIYRD NK
TINSEN MHIDIYLYTS

>d1i4pa2 d.15.6.1 (A:121-239) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}
NHFDNGNLQNVLIRVYENKRNTISFEVQTDKKS VTAQELDIKARNFLINKKNLYEFNSSPYETGYIKFIENN GNTFWYDMMPAPGDKF DQSKYLM
YNDNKTVDSKS VKIEVHLTTKNG

>d3tss_2 d.15.6.1 (94-194) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}
LPTPIELPLKVHGKDPLKYWPKF DKKQLAISTLDFKIRHQLTQTHGLYRSSDKTGGYWKITMNDG STYQSDLSKKF EYNT EKPPINIDEIKTIEAEIN

>d1sebd2 d.15.6.1 (D:127-235) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
DKYRSITVRFEDGKNLLSF DVQT NKKVTAQELDYLTRHYLVKNKKLYETGYIKFIENENS FWYDMMPAPGDKF DQSKYLM MYNDNKMVDSKDV

KIEVYLT

>d3seb_2 d.15.6.1 (122-238) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

NGNQLDKYRSITVRVFEDGKNLLSFDVQTNKKVTAQELDYLTRHYLVKNKKLYEFNNSPYETGYIKFIENENSFWYDMMPAPGDKFDQSKYLMY
NDNKMVDSKDVKIEVYLTKK

>d1enfa2 d.15.6.1 (A:102-213) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}

EKLAQERVIGANVVWDGIQKETELIRTNKKNVTLQELDIKIRKILSDKYKYYKDSEISKGLIEFDMKTPRDSFDIYDLKGENDYEIDKIYEDNKLKSDDI
SHIDVNLYT

>d1an8_2 d.15.6.1 (96-208) Streptococcal superantigen Spe-C {Streptococcus pyogenes}

NKVNHKLLGNLFISGESQQNLNNKIILEKDIVTFQEIDFKIRKYLMDNYKIDATSPYSGRIEIGTKDGKHEQIDLFDSPNEGTRSDIFAKYKDNRINM
KNFSHFDIYLEK

>d1et9a2 d.15.6.1 (A:96-204) Streptococcal superantigen Spe-H {Streptococcus pyogenes}

EKKIEKVPVNWDKSKQQPPMFITVNPKVTAQEVDIJKRKLICKYDYNREQKYSKGTVTLDLNSGKDIVFDLYFGNGDFNSMLKIYSNNERIDS
TQFHVDVSIS

>d1eu3a2 d.15.6.1 (A:97-209) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}

TSIPKNIPVNWLWINGKQISVPYNEISTNKTIVTAQEIDLKVRKFLIAQHQLYSSGSSYKSGRLVFHTNDNSDKYSFDLFYVGYRDKESIFKVKYKDNRISFNID
KIGHLDIEIDS

>d1bxta2 d.15.6.1 (A:120-234) Streptococcal superantigen SSA {Streptococcus pyogenes}

QIEGKFPNITVKVYEDNENILSFDTTNKKQVTQELDCCTRILVSRKNLYEFNNSPYETGYIKFISSGDSFWYDMMPAPGAIFDQSKYLMYNDNK
TVSSSAIAIEVHLTKK

>d1fnua2 d.15.6.1 (A:108-221) Streptococcal pyrogenic exotoxin A1 {Streptococcus pyogenes}

GNHLEIPKKIVVKVSIDGIQSLSDIETNKKMVTAQELDYKVRKYIDNKQLYNGPSKYETGYIKFIPKNKESFWDFPPEFTQSKYLMYKDNETLD
NKTSQIEVYLTKK

>d1fcia_d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

TTFKLIINGKTLKGETTTEAVDAATAEKVFKQYINDNGIDGEWTYDDATKTVTVE

>d1fd6a_d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

MTTFKLIINGKTLKGETTTEAVDAATAEKVFKQYANDNGIDGEWTYDDATKTVTVE

>d1gb4__d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

MTTFKLIINGKTLKGETTIEAVDAAAEAEKFKQYANDNGIDGEWTYDDATKTVTVE

>d1pgb__d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

MTYKLILNGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTVTVE

>d1pgx__d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

ELPAVTTYKLVINGKTLKGETTTKAVDAETAEKFKQYANDNGVDGVWTYDDATKTVTEMVTEVPVA

>d1qkza_d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

VTTYKLVINGKTLKGETTTKAVDAATAEKVFKQYANDNGVDGEWTYDDATKTVTEK

>d2igd__d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

MTPAVTTYKLVINGKTLKGETTTKAVDAETAEKFKQYANDNGVDGVWTYDDATKTVTVE

>d2igg__d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}

LTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFKQYANDNGVDGEWTYDDATKTVTEKPE

>d1heze_d.15.7.1 (E:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

EVTIKVNIFADGKIQTAEFKGTTEEATAEAYRYADLLAKVNGEYTADLEDGGNHMNIKA

>d1hz6a_d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

HHAMEEVTKANLIFANGSTQAEFKGTFEKATSEAYAYADLKKDNGEWTVDVADKGYTLNIKFAG

>d1jmla_d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

MHHHHHHGMEEVTIKANLIFANGSTQAEFKGTFEKATSEAYAYADLKKDNGEWTVDVVPKAYTLNIKFAG

>d1k52a_d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}
MHHHHHHAMEEVTIKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVADGGYTLNIKFAG

>d1kh0a_d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}
EEVTIKANLIFANGSTQAEFKGTFEKALSEVLAYADTLKKDNGEWTIDKRVTNGVIILNIKFAG

>d2ptl_d.15.7.1 (-) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}
ENKEETPETPETDSEEETVIKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFAG

>d1tif_d.15.8.1 (-) Translation initiation factor IF3, N-terminal domain {Bacillus stearothermophilus}
KDFIINEQIRAREVRLIDQNGDQLGIKSQEAEIAARRNLDLVAPNAKPPVCRIMDYGKFRFEQQKKEEAR

>d1f52a1 d.15.9.1 (A:1-100) Glutamine synthetase, N-terminal domain {Salmonella typhimurium}
SAEHVLTMLNEHEVKFVDLRFTDTKGKEQHVTIPAHQVNAEFFEEGKMFDGSSIGGWKGINESDMVLMPDASTAVIDPFFADSTLIIRC DILEPGTLQ
GY

>d1coy_2 d.16.1.1 (319-450) Cholesterol oxidase {Brevibacterium sterolicum}
GNNGNIMVGRANHMWDATGSKQATIPTMGIDNWADPTAPIFAEIAPMPAGLETWVSLYLAITKNPERARFQFNSGTGKVDLTWAQSQNQKGIDM
AKKVFDFKINQKEGTIYRTDLFGVYYKTWGDDFTYHPLG

>d1ijha2 d.16.1.1 (A:319-450) Cholesterol oxidase {Streptomyces sp.}
GPNGNIMTARANHMWNPTGAHQSSIPALGIDAWNDNSDSSVFAEIAPMPAGLETWVSLYLAITKNPQRGTFVYDAATDRAKLNWTRDQNAPAVN
AAKALFDRINKANGTIYRYDLFGTQLKAFAADDFCYHPLG

>d1k0ia2 d.16.1.2 (A:174-275) p-Hydroxybenzoate hydroxylase (PHBH) {Pseudomonas aeruginosa}
LKVFERVYPFGWLGLADTPPVSHELIYANHPRGFALCSQRSATRSQYYVQVPLSEKVEDWSDERFWTELKARPSEVAEKLVTGPSLEKSIAPLSFVV
EP

>d1foha4 d.16.1.2 (A:241-341) Phenol hydroxylase {Soil-living yeast (Trichosporon cutaneum)}
GEQTDYIWGVLDAPASNFDIRSRCAIHSAESGSIMIIPRENNLVRFYVQLQARAEGGRVDRTKFTPEVVIANAKKIFHPYTFDVQQLDWFTAYHIG
QR

>d1an9a2 d.16.1.3 (A:195-287) D-amino acid oxidase {Pig (Sus scrofa)}
LQPGRGQIIVDAPWLKNFIITHDLERGIYNPSYIIPGLQAVTLGGTFQVGNWNEINNIQDHNTIWECCRLEPTLKDAKIVGEYTGFRPVPR

>d1c0pa2 d.16.1.3 (A:1194-1288) D-amino acid oxidase {Yeast (Rhodotorula gracilis)}
AEPIRGQTVLVKSPCKRCTMDSSDPASPAYIIPRGGEVICGGTYVGVDWDLNVNPETVQRILKHLRDPDISSDGTIEGIEVLRHNGLRPAR

>d1el8a2 d.16.1.3 (A:218-321) Sarcosine oxidase {Bacillus sp., strain b0618}
LQPYRQVVGFFESDESKYNSNDIFPGFMVEVPNGIYYGFPFGCGLKLGYHTFGQKIDPDTINREFGVYPEDESNLRAFLEEYMPGANGEKRGAV
CMYTKTL

>d1i8ta2 d.16.1.7 (A:245-313) UDP-galactopyranose mutases {Escherichia coli}
EYRSLSKFETERHEFPNFQGNAVINFTDANPVYTRIIIEHKHFDYVETKHTVVTKEYPLEWKVGDEPYYPV

>d1cf3a2 d.16.1.4 (A:325-520) Glucose oxidase {Aspergillus niger}
NLQDQTTATVRSRITSAGAGQGQAAWFATFNETFGDYSEKAHELLNTKLEQWAEEAVARGGFHNTTALLIQYENYRDWIVNHNVAYSELFMDTAGV
ASFVWDLLPFRGYVHILDKDPYLHHFAYDPQYFLNELDLLGQAAATQLARNISNSGAMQTYFAGETIPGDNLAYDADLSAWTEYIPIYHFRPNYHG
VGT

>d1gpea2 d.16.1.4 (A:329-524) Glucose oxidase {Penicillium amagasakiense}
NMQDQTTTVSSRASSAGAGQGQAVFFANFTETFGDYAPQARDLLNTKLDQWAETVARGGFHNTALKVQYENYRNWLLEDVAFAELFMDT
EGKINFDLWDLIPFTRGSVHILSSDPYLWQFANDPKFLNEFDLLGQAAASKLARDLTSQGAMKEYFAGETIPGYNLVQNATLSQWSDYVLQNFPRN
WHAVSS

>d1b5qa2 d.16.1.5 (A:294-405) Polyamine oxidase {Maize (Zea mays)}
DMAVYTKIFLKPRKFWPEGKGREFFLYASSRRGYYGVWQEFKQYPDANVLLVTDEESRRIEQQSDEQTKAEMQVLRKMFPGKDVPDATDILV
PRWWSDRFYKGTFSN

>d1f8ra2 d.16.1.5 (A:320-432) L-amino acid oxidase {Malayan pit viper (Calloselasma rhodostoma)}

HYRSGTKIFLTCTTFWEDDGIGHGGKTTDLPSRFIYYPNHNFTNGVGVIAYGIGDDANFFQALDFKDCADIVFNDLSLIHQLPKKDIQSFCYPSVIQK
WSLDKYAMGGITT

>d1gosa2 d.16.1.5 (A:290-401) Monoamine oxidase B {Human (Homo sapiens)}

PLGSVIKICIVYYKEFWRKKDYCGTMIDGEEAPVAYTLDKTPEGNYAAIMGFILAHKARKLARLTKEERLKKLCELYAKVLGSLEALEPVHYEKNWC
EEQYSGGCYTTY

>d1d5ta2 d.16.1.6 (A:292-388) Guanine nucleotide dissosiation inhibitor, GDI {Cow (Bos taurus)}

RKAGQVIRIIILSHPIKNTDANCQIIPQNQVNRSIDYVCMISYAHNVAAQGKYIAIASTTVETTDPEKEVEPALGLLEPIDQKFVAISDLYE

>d1mola_d.17.1.1 (A:) Monellin, B & A chains together {Serendipity berry (*Dioscoreophyllum cumminsii*)}

GEWEIIDIGPFTQNLGKFADVDEENKIGQYGRFLTNPVIRPCMKKTIYENEREIKGYEYQLYVYASDKLFRADISEDYKTRGRKLLRFNGPVP
PPP

>d1eqka_d.17.1.2 (A:) Phytocystatin {Japanese rice (*Oryza sativa*), subsp. *japonica*, oryzacystatin-I}

MSSDGGPVLGGEVPGNENDLHLVDLARFAVTEHNKKANSLEFEKLVSVKQQVVAGTLYYFTIEVKEGDAKKLYEAKVWEKPWMDFKELQEFP
KPV
DASANA

>d1cewi_d.17.1.2 (I:) Cystatin {Chicken (*Gallus gallus*)}

GAPVPVDENDEGLQRALQFAMAENRASNDKYSSRVVRVISAKRQLVSGIKYILQVEIGRTTCPKSSGDLQSCEFHDEPEMAKYTTCTFVVYSIPWLN
QIKLLESKCQ

>d1dvd_d.17.1.2 (-) Cystatin A (stefin A) {Human (Homo sapiens)}

MIPGGLSEAKPATPEIQEVVKVCPQLEEKTNETYGKLEAVQYKTQVVAAGTNYYIKVAGDNKYMHLKVFSLPGQNEDELVLTGYQVDKNKDDLTGF

>d1stfi_d.17.1.2 (I:) Cystatin B (stefin B) {Human (Homo sapiens)}

MMMSGAPSATQPATAETQHIADQVRSQLEEKYNKKFPVFKAVSFKSQVVAGTNYFIKVHVGDEFVHLRVFQSLPHENKPLTLSNYQTNKAKHDELTY
F

>d1g96a_d.17.1.2 (A:) Cystatin C {Human (Homo sapiens)}

VGGPMADASVEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNYFLDVELGRTTCTKTQPNLDNCPHDQPHLKRKAFCSFQIYAV
PWQGTMTLSKSTCQDA

>d1oaca2 d.17.2.1 (A:91-185) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

KRPHPNLALTADIEIKQAVEIVKASADFKPNTRFEISLPPDKEAVWAFALENKPVDQPRKADVIMLDGKHIEAVVDLQNNKLLSWQPIKDAHG

>d1oaca3 d.17.2.1 (A:186-300) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

MVLLDDFASVQNIINNSEEFAAAVKKRGITDAKKVITTPLTGYFDGKDGLKQDARLLKVISYLDVGDGNYWAHPIENLVAVVDEQKKIVKIEEGPV
PVPMTARPFDGRDRV
A

>d1ksia2 d.17.2.1 (A:6-98) Copper amine oxidase, domains 1 and 2 {Pea seedling (*Pisum sativum*)}

VQHPLDPLTKEEFLAVQTIVQNKPISNNRLAFHYIGLDDPEKDHVRYETHPTLVSIPRKIFVVAIINSQTHEILINLRIRSIVSDNIHNGY

>d1ksia3 d.17.2.1 (A:99-206) Copper amine oxidase, domains 1 and 2 {Pea seedling (*Pisum sativum*)}

GFPILSVEQSLAIKPLKYPFIDSVKRGLNLSEIVCSSFTMGWFGECKNVRTVRLDCFMKESTVNIYVRPITGITIVADLDMKIVEYHDRDIEAVPT
AENTEYQ

>d1av4_2 d.17.2.1 (9-96) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ASPFRLASAGEISEVQGILRTAGLLGPEKRIAYLGVLDPARGAGSEAEDRRFRVFIHDVSGARPQEVTSVTNGTVISAVELDTAATG

>d1av4_3 d.17.2.1 (97-211) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ELPVLEEEFVVEQLLATDERWLKALAARNLDVSKVRVAPLSAGVFNEYAEERGRRLGLAFVQDFPEDSAWAHPVDGLVAYDVVSKEVTRVIDTG
FPVPAEHGNYTDPELTG

>d1a2va2 d.17.2.1 (A:18-115) Copper amine oxidase, domains 1 and 2 {Yeast (*Hansenula polymorpha*)}

PARPAHPLDPLSTAEIKAATNTVKSYFAGKKISFNTVTLREPARAKAYIQWKEQGGPLPPRLAYYVILEAGKPGVKEGLVDSLSSLVETRALET
VQPI

>d1a2va3 d.17.2.1 (A:116-236) Copper amine oxidase, domains 1 and 2 {Yeast (*Hansenula polymorpha*)}

LTVEDLCSTEEVIRNDPAVIEQCVLSGIPANEMHKVYCDPWTIGYDERWGTGKRLQQALVYRSDEDDSQYSHPLDFCPIVDEKKVIFIDIPN
RRRK
VSKHKHANFYPKHMIEKGAMR

>d1eeja2 d.17.3.1 (A:1-60) Disulfide bond isomerase, DsbC, N-terminal domain {Escherichia coli}

DDAAIQQTAKMGIKSSDIQPAPVAGMKTVLTNSGVLYITDDGKHIIQGPMYDVSGTAPV
>d3stda_ d.17.4.1 (A:) Scytalone dehydratase {Fungus (*Magnaporthe grisea*)}
GEITFSDFYGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEFVGMSKQVLGDPTLRTQHFIGGTRWEKSEDEVIGH
QLRVPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKAGLKPDIRWGEGDFDRIFEDGRETFG
>d1ouna_ d.17.4.2 (A:) Nuclear transport factor-2 (NTF2) {Rat (*Rattus norvegicus*)}
GDKPIWEQIGSSFIQHYYQLFDNDRTQLGAIYIDASCLTWEGQQFQGKAAIVEKLSSLPFQKIQHSITAQDHQPTPDSCIISMVVGQLKADEDPIMGF
HQMFLLKNINDAWVCTNDMFRALHNF
>d1jkga_ d.17.4.2 (A:) NTF2-related export protein 1 (p15) {Human (*Homo sapiens*)}
ASVDFKTYVDQACRAAEFFVNVYTTMDKRRRLSRLYMGATLVWNGNAVGQESLSEFFMLPSSEFQISVDCQPVHDEATPSQTTVLVICGS
VKFEGNKQRDFNQNQFILTAQASPSNTVVKIASDCFQDWAS
>d1jkgb_ d.17.4.2 (B:) NTF2-like domain of Tip associating protein, TAP {Human (*Homo sapiens*)}
APPCKGYSYGTENLKSVLHLFLQQYYAIYDSGDRQGLDAYHDGACCSLSIPFIPQNPARSSLAEYFKDSRNVKKLKDPTLRFRLKHTRLNVVAFLNELP
KTQHDVNSFVVDSAQTSTLLCSVNGVFKEVDGKSRDSLRAFTRTFIAVPASNGLCIVNDELVRNASSEEIQRFAFAMPAPTP
>d1qjga_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Comamonas testosteroni and Pseudomonas testosteroni}
MNTPEHMTAVVQRYVAALNAGDLDGIVALFADDATVENPGSEPRSGTAAIREFYANSLKLPLAELTQEVRNAVANEEAAFAFIVSFYQGRKTVVAPI
DHFRFNGAGKVVSMSRALFGEKNIHAGA
>d1ea2a_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Pseudomonas putida}
NLPTAQEVQGLMARFIELDVVGDIIEAIVQMYADDATVEDPFGQPPIHREQIAAFYRQGLGGGVRACTGPVRASHNGCGAMPFRVEMVWNG
QPCALDVIDVMRFDHGRIQTMQAYWSEVNLSV
>d1eg9b_ d.17.4.4 (B:) Naphthalene 1,2-dioxygenase beta subunit {Pseudomonas putida}
MINIQEDKLVSAHDAEIELRFFNCNCHDSALQQEATLLTQEAHLLDIQAYRAWLEHCVGSEVQYQVISRELAASERRYKLNEAMNVYNENFQQLKVR
VEHQLDPQNWGNSPKLRFRFITNVQAAMDVNDKELLHIRSNVILHRARRGNQVDVFAAREDKWKRGEGGVRKLVQRFVDYPERILQTHNLMV
FL
>d1euic_ d.17.5.1 (C:) Uracil-DNA glycosylase inhibitor protein {Bacteriophage pbs2}
QLVIQESILMLPEEEVVEIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENIKML
>d1ugia_ d.17.5.1 (A:) Uracil-DNA glycosylase inhibitor protein {Bacteriophage pbs2}
TNLSDIIEKETGKQLVQESILMLPEEEVVEIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENIKML
>d1pcfa_ d.18.1.1 (A:) Transcriptional coactivator PC4 C-terminal domain {Human (*Homo sapiens*)}
AMFQIGKMRYSVSRDFKGKVLDIREYWMDPEGEMKPGRKGISLNPEQWSQLKEQISIDDDAVRKL
>d1jb0d_ d.187.1.1 (D:) Photosystem I subunit PsaD {Synechococcus elongatus}
TTLTGQPPLYGGSTGGLLAADTEEKYAITWTSPKEQVFEMPTAGAAVMREGENLVYFARKEQCLALAQQQLRPRKINDYKIYRIFPDGETVLIHPKDG
VFPEKVNKGREAENVSPRSIGQNPNSQLKFTGKKPYDP
>d3frua2 d.19.1.1 (A:1-178) Fc (IgG) receptor, alpha-1 and alpha-2 domains {Rat (*Rattus norvegicus*)}
AEPRPLPLMYHLAAVSDLSTGLPSFWATGWLGAQQYLTYNNLRQEADPCGAWIWENQVSWYWEKETDLKSKEQLFLEAIRTLENQINGTFTLQGLL
GCELDAPNSSLPTAVFALNGEEFMRFNPRTGNWSGEWPETDIVGNLWMKQPEAARKESEFLLSCPRLGHLERGRQNLEW
>d1cd1a2 d.19.1.1 (A:7-185) CD1, alpha-1 and alpha-2 domains {Mouse (*Mus musculus*)}
NYTFRCLQMSSFANRSWSRTDSVVWLGDLQTHRWSNDSATISFTKPWSQGKLSNQQWEKLQHMFQVYRVSFTRDIQELVKMMSPKEDYPIEIQI
SAGCEMPGNASESFLHVAFQGKYVVRFWGTSWQTVPGAPSWLDLPIKVLNADQGTSATVQMLLNDTCPLFVRGLLEAGKSDLEK
>d1hdma2 d.19.1.1 (A:13-93) MHC class II, N-terminal domains of alpha and beta chains {Human (*Homo sapiens*), HLA-DM}
LQNHTFLHTVYCQDGSPSGLSEAYDEDQLFFFDSQNTRPRLPEFADWAQEQQGDAILFDKEFCEWMQQIPKLDGKIPV
>d1hdmb2 d.19.1.1 (B:3-87) MHC class II, N-terminal domains of alpha and beta chains {Human (*Homo sapiens*), HLA-DM}
FVAHVESTCLDDAGTPKDFTCISFNKDLLCWDPEENKMAPCNSLANVLSQHLNQKDTLMQRLNGLQNCATHQPFWGSLTNR
>d1aqdb2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha and beta chains {Human (*Homo sapiens*), HLA-DR1}

RPRFLWQLKFECHFFNGTERVRLLERCIYNQEESVRFDSVGEGYRAVTELGRPDAEYWNSQKDLLEQRRAAVDTYCRHNYGVGESFTVQ
>d1bx2b2 d.19.1.1 (B:3-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}
TRPRFLWQPKRECHFFNGTERVRFLDRYFYNQEESVRFDSVGEGFRAVTELGRPDAEYWNSQKDLLEQRRAAVDTYCRHNYGVVESFTVQ
>d1fv1a2 d.19.1.1 (A:3-81) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}
EEHVIQAEFYLNPDQSGEFMFDGDEIFHVDMAKKETVWRLEFGRFASFAQGALANIAVDKANLEIMTKRSNYTP
>d1fv1b2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}
GDTRPRFLQQDKYECHEFFNGTERVRFLHLDIYNQEEQEDLRFDSVGEGYRAVTELGRPDAEYWNSQKDLLEQRRAAVDTYCRHNYGVGESFTVQ
>d1a6ab2 d.19.1.1 (B:5-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR3}
PRFLEYSTSECHFFNGTERVRYLDRFHNQEEENVRFDSVGEGFRAVTELGRPDAEYWNSQKDLLEQKGRRVNDYCRHNYGVVESFTVQ
>d1d5zb2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR4}
GDTRPRFLEQVKHECHFFNGTERVRFLDRYFYHQUEYVRFDSVGEGYRAVTELGRPDAEYWNSQKDLLEQKRAAVDTYCRHNYGVGESFTVQ
>d1jk8a2 d.19.1.1 (A:2-84) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}
VADHVASYGVNLYQSYGPQYSHEFDGDEEFYVDLERKETVWQLPLFRRRFPQFALTNIAVLKHNLNIVIKRSNSTAATN
>d1jk8b2 d.19.1.1 (B:3-94) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}
SPEDFVYQFKGMCYFTNGTERVRLTRYIYNREEYARFDSDVGVYRAVTPLGPPAAEYWNSQKEVLERTRAELDTVCRHNYQLELRTTLQR
>d1iaka2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}
IEADHVGSYGITVYQSPGDIGQYTFEDGDELFYVLDKKETVWMLPEFAQLRRFEPQGGLQNIATGKHNLIEILTKRSNSTP
>d1iakb2 d.19.1.1 (B:5-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}
GSFVHQFQPFCYFTNGTQRIRLVRYIYNREEYVRFDSVGEGYRAVTELGRPDAEYWNSQKYLERTRAELDTVCRHNYEKTEPTSLR
>d1fnga2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}
IKEEHTIIQAEFYLLPDKRGEFMFDGDEIFHV DIEKSETIWRLEEFKAFASFEAQGALANIAVDKANLDVMKERSNNTP
>d1fnbg2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}
RPWFLEYCKSECHFYNGTQRVRLVRYFYNLEENLRFDSDVGEGFRAVTELGRPDAENWNSQPEFLEQKRAEVDTVCRHNYEIFDNFLVP
>d1i3rb2 d.19.1.1 (B:1-120) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}
GKKVITAFNEGLKGSSVGGSGGGSRPWLFLEYCKSECHFYNGTQRVRLVRYFYNLEENLRFDSDVGEGFRAVTELGRPDAENWNSQPEFLEQ
KRAEVDTVCRHNYEIFDNFLVPRR
>d2iadb2 d.19.1.1 (B:5-93) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AD}
RHFVVQFKGECYYTNGTQRIRLVTRYIYNREEYVRYDSDVGEGYRAVTELGRPDAEYWNSQPEILERTRAEVDTACRHNYEGPETSTSLR
>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)}
DIEADHVGFYGTTVYQSPGDIGQYTHEFDGDELFYVLDKKKTWRLPEFGQLILFEPQGGLQNIAAKEHNLGILTFRSNFTPA
>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)}
RHFVHQFKGECYFTNGTQRIRLVTRYIYNREEYLRFDSDVGEGYRAVTELGRHSAEYYNKQYLERTRAELDTACRHNYEETEVPTSLR
>d1k8ia2 d.19.1.1 (A:11-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}
QNHTFRHTLCQDGIPNIGLSETYDEELFSFDFSQNTRVPLPDAEAQGQGDASIAFDKSFCEMLMREVSPKLEGQIP
>d1k8ib2 d.19.1.1 (B:1-94) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}
GFVAHVESTCVLNDAGTPQDFTYCVSFNKDLLACWDVDGKIVPCFGVLSRLAEIISNLNEQESLIHRLQNLQDCATHQPFWVLTHRTR
>d1i4fa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-A2.1}
GSHSMRYFTTSVRPGRGEPRFIAVGYVDDTQFVRFDSAASQRMEPAPWIEQEGPEYWDGETRKVKAHSQTHRVDLGLTRGYYNQSEAGSHT
VQRMYGCDEVGSDWRFLRGYHQYADGKDYLALKEDLRSWTADMAAQTTKHKWEAHVAEQLRAYLEGTCVEWLRRYLENGKETLQR
>d1hsaa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B2705}
GSHSMRYFHTSVSRPGRGEPRFITVGYVDDTLFVRFDSAASPREEPAPWIEQEGPEYWDRETQICKAKAQTDRDLRLLYYNQSEAGSHTLQ
NMYGCDVGPDRGRLRGYHQDAYDGKDYLALKEDLRSWTADMAAQTTKHKWEAHVAEQLRAYLEGECVEWLRRYLENGKETLQR
>d1hsba2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-AW68}
GSHSMRYFTTSVRPGRGEPRFIAVGYVDDTQFVRFDSAASQRMEPAPWIEQEGPEYWDRNTRNVKAQSQTDRVLDGLTRGYYNQSEAGSHT

IQMMYGCDVGSDFRFLRGYRQDAYDGKDYIALKEDLSWTAADMAAQTTKHWEAAHVAEQWRAYLEGTCVEWLRRYLENGKETLQR
>d1agda2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B0801}
GSHSMRYFTAMSRPGRGEPRFISVGYVDDTQFVRFDSAASPRPEPAPWIEQEGPEYWDRNTQIFKTNTQDRESLRNLRGYYNQSEAGSHTL
QSMYGCDVGPDRGRLRGHNQYADGKDYIALNEDLSWTAADTAACITQRKWEAARVAEQRDRAYLEGTCVEWLRRYLENGKDTLER
>d1a1na2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B*3501}
GSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSAASPRTEPRPPWIEQEGPEYWDRNTQIFKTNTQTYRESLRNLRGYYNQSEAGSHIIQ
RMYGCDLGPDRGRLRGHDQSAYDGKDYIALNEDLSSWTAADTAACITQRKWEAARVAEQLRAYLEGLCVEWLRRYLENGKETLQR
>d1e27a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B*5101}
GSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSAASPRTEPRAPWIEQEGPEYWDRNTQIFKTNTQTYRENLRIALRYYNQSEAGSHII
QTMYGCDVGPDRGRLRGHNQYADGKDYIALNEDLSSWTAADTAACITQRKWEAAREAEQLRAYLEGLCVEWLRRHYLENGKETLQR
>d1efxa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-CW3}
GSHSMRYFYTAVSRPGRGEPRFIAVGYVDDTQFVRFDSAASPRGEPRPAPWVEQEGPEYWDRETQKYKRQAQDRVSLRNLRGYYNQSEAGSHII
QRMYGCDVGPDRGRLRGYDQYADGKDYIALNEDLSWTAADTAACITQRKWEAAREAEQLRAYLEGLCVEWLRRYLNGKETLQR
>d1qqda2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-CW4}
SHSMRYFSTSWSVSPGRGEPRFIAVGYVDDTQFVRFDSAASPRGEPRPAPWVEQEGPEYWDRETQKYKRQAQDRVNLRLRGYYNQSEAGSHTL
QRMFGCDLGPDRGRLRGYNQFAYDGKDYIALNEDLSWTAADTAACITQRKWEAAREAEQRDRAYLEGTCVEWLRRYLENGKETLQR
>d1mhea2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-E}
SHSLKYFHHTSVSRPGRGEPRFISVGYVDDTQFVRFDSAASPRMVPRAPWMEQEGSEYWDRETRSAQIFRVNLRLRGYYNQSEAGSHTLQ
WMHGCELGPDRRFLRGYEQFAYDGKDYLTLNEDLSWTAVDAAQITQRKWEAAREAEHQRAYLEDTCVEWLHKYLEKGKETLLH
>d1de4a2 d.19.1.1 (A:4-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), hemochromatosis protein Hfe}
RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMWLQLSQSLKGWDHMFTVDFWTIMENHHNSKESHTLQ
VILGCEMQEDNSTEGYWKGYDGQDHLEFCPTDLWRAEPRAWPTKLEWERHKIRARQNRAYLERDCPAQLQQLELGRGVLD
>d1fzka2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2KB}
GPHSLRYFHTAVSRPGLGEPRYMEVGYVDDTEFVRFDSAENPRYEPRARWMEQEGPEYWERETQAKGNEQSFRVDLRTLLGYYNQSKGGSHTI
QVISGCEVGSDGRLRGYQQYADGCDYIALNEDLKTWTAAADMALITKHWEQAGAAEYYRAYLEGTCVEWLRRYLNGNATLLR
>d1jpfa2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2DB}
PHSMRYFETAVSRPGLGEPRYISVGYVDNKEFVRFDSAENPRYEPRAPWMEQEGPEYWERETQAKGQEWFRLRNLLGYYNQSAGGSHTL
QQMSGCDLGSDWRLRGYLQFAYEGRDYIALNEDLKTWTAAADMAAQITRRKWEQSGAAEHYKAYLEGECVEWLHRYLKGNATLLR
>d1mhca2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2M3}
GSHSLRYFHTAVSRPGRGEPRQYISVGYVDDQFQRCDSIEEIPRMEPRAPWMEKPERYEWKLKLKVKNIAQSARANLRTLLRYYNQSEGGSHILQ
WMVSCEVGPDMLLGAHYQAAYDGSDYITLNEDLSSWTAVDMVSQITKSRLESAGTAEYFRAYVEGECLLHRFLRNGKEIQLR
>d1ld9a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2LD}
GPHSMRYFETAVSRPGLGEPRYISVGYVDNKEFVRFDSAENPRYEPQAPWMEQEGPEYWERITQIAKGQEWFRLRNLLGYYNQSAGGTHTL
QWMYGCDVGSDFRRLRGYQFAYDGCDYIALNEDLKTWTAAADMAAQITRRKWEQAGAAEYYRAYLEGECVEWLHRYLKGNATLLR
>d1qo3a2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2DD}
SHSLRYFVTAVSRPGFGEPRYMEVGYVDTNFVRFDSAENPRYEPRARWIEQEGPEYWERETRRAKGNEQSFRVDLRTALRYYNQSKGGSHIQL
WMAGCDVESDGRLLRGYWQFAYDGCDYIALNEDLKTWTAAADMAAQITRRKWEQAGAAERDRAYLEGECVEWLRRYLNGNATLLR
>d1k8da2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), IB QA-2}
GQHSLQYFHTAVSRPGLGEPRWFISVGYVDDTQFVRFDSAENPRMEPRARWMEQEGPEYWERETQIAKGHEQSFRGSLRTAQSYNNQSKGGSHIQL
LQWMYGCDMGSDFRRLRGYQFAYEGRDYIALNEDLKTWTAAADMAAQITRRKWEQAGIAEKDQAYLEGTCMQLRRLYELGKETLLR
>d1ed3a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Rat (Rattus norvegicus), RT1-AA}
GSHSLRYFYTAVSRPGLGEPRFIAVGYVDDTEFVRFDSAENPRMEPRARWMEREGPEYWEQQTRIAKEWEQIYRVLRLRGYYNQSEGGSHTIQ
EMYGCDVGSDFGSLRGYRQDAYDGCDYIALNEDLKTWTAAADFAAQITRNKWERARYAERLRAYLEGTCVEWLSRYLELGKETLLR
>d1zaga2 d.19.1.1 (A:5-183) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}

DGRYSLTYIYTGLSKHVVEDVPAFQALGSINLDLQFFRYNSKDRKSQPMGLWRQVEGMEDWKQDSQLQKAREDIFMETLKDIVYYNDSNGSHVLQG
RFGCEIENNRSRGAFWKYYDGKDYIEFNKEIPAWPVFDPAAQITKQKWEAEPVYVQRAKAYLEECPATLRKYLKYSKNILDR
>d1hyrc2 d.19.1.1 (C:0-180) MHC I homolog {Human (Homo sapiens), Mic-a}
MEPHSLRYNLTVLSWDGSVQSGFLTEVHLDGQFLRCRDKCRAKPQGQWAEDVLGNKTWDRETRDLTNGKDRLMTLAHKDQKEGLHSLOEI
RVCEIHEDNSTRSSQHFYYDGELFLSQNLETKEWTPQQSSRAQTLMVRNFLKEDAMTKTHYHAMHADCLQELRRYLKSGVVLRR
>d1c16a2 d.19.1.1 (A:1-180) MHC I homolog {Mouse (Mus musculus), t22}
GSHSLRYFYTAWSRPGGLGEPWVGYVDDMQLVRFSKEETPRMAPWLEQEEADNWEQQTRIVTIQGQLSERNLMLTVHFYNKSMDDSHTLQW
LQGCDVEPDRHLCLWYNQLAYDSEDLPTLNENPSSCTVGNSTVPHISQDLKSHCSDLLQKYLEKGKERLL
>d1exua2 d.19.1.1 (A:4-176) Class I MHC-related Fc receptor {Human (Homo sapiens)}
HLSLLYHLTAVSSPAPGTPAFWVSGWLGPQQYLSNLRGEAEPGAWVVENQVSWYWEKETDLRIKEKLFLFLEAKFALKGGKPYTLQGLLGCELG
PDNTSVPTAKFALNGEEFMNFDLKQGTWGWDWPEALAIQRWQQDKAANKELTFLFSCPHRLREHLERGRGNLEW
>d1kcg_ d.19.1.1 (C:) Class I MHC-related molecule Ulbp3 {Human (Homo sapiens)}
DAHSLWYNFTIIHLPRHGQQWCEVQSVDQKNFLSYDCGSDKVLSMGHLEEQLYATDAWGKQLEMLREVGQRLRLEADTELEDFTPSGPLTLQV
RMSCECEADGYIRGSWQFSFDGRKFLLFDSNNRKWTVVHAGARRMKEKWEKDGLTFFKMVSMDCKSWLRDFLMHRKKRLE
>d1jfma_ d.19.1.1 (A:) NK cell ligand RAE-1 beta {Mouse (Mus musculus)}
DAHSRCNLTIKDPTPADPLWYEAKCFVGEILILHSNINKTMTSGDPGETANATEVKKCLTQPLKNLCQKLRNKVSNTKVDTHTKNTGYPHLQVTMIYP
QSQGRTPSATWEFNISDSYFFTFTENMSWRSANDEGVIMNWKDDGEFKVQLKFLIHECSQKMDEFLKQSKEK
>d2aak__ d.20.1.1 (-) Ubiquitin conjugating enzyme {Arabidopsis thaliana}
MSTPARKRLMRDFKRLQQDPAGISGAPQDNNIMLWNAVIFGPDDTPWDGGTFKLSLQFSEDYPNKPPTVRFVSRMFHPNIYADGSICLDILQNZ
WSPIYDVAAILTSIQSLLCDPNPNSPANSEAARMYSESKEYNRRVDRDVEEQSWT
>d1fzya_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc1}
SRAKRIMKEIQAQKDDPAAHITLEFVSESDIHHKGTFGLPPGTPYEGGFVVDIEVPMEYPFKPKMQFDTKVYHPNISSVTGAICLDILKNAWSPVI
TLKSALISLQALLQSPEPNPQDAEVAQHYLRDRESFNKTAALWTRLYAS
>d1ayza_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc2 (RAD6)}
STPARRRLMRDFKRMKEDAPPGVASPLPDNVMVWNAMIIGPADTPYEDGTFRLLLEFDEEYPNKPPhVKFLSEMFPNVYANGEICLDILQNRW
TPTYDVASILTSIQSLFNDPNPASPANVEAATLFKDHSQYVKRVKETVEKSWEDEMD
>d1qcqa_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc4}
MSSSKRIAKELSDSLDRDPPTSCSAGPVGDDLYHWQASIMGPADSPYAGGVFFLSIHFPDTYDFPKPPKISFTTKIYHPNINANGNICLDILKDQWSPALTL
SKVLLSICSLTDANPDDPLVPEIAHIYKTDPKYEATAREWTKKYAV
>d2ucz__ d.20.1.1 (-) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc7}
SKTAQKRLKELQQQLIKDSPPGIVAGPKSENNIFIWDLCLIQGPPDTPYADGVFNALKLEFPKDYLSPPLKFTPSILHPNIYPNGEVCVSILHSPGDDPNM
YELEARWSPVQSVEKILLVMSMSLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF
>d1jata_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc13}
AASLPKRIIKETEKLVSDPVGPGITAEPHDNRLRYFQVTIEGPEQSPYEDGIFELEYLPDDYPMEAPKVRFLTAKIYHPNIDRLGRICLDVLKTNWSPALQIR
TVLLSIQALLASPNDPLANDVAEDWIKNEQGAKAKAREWTKLYAKKKP
>d1j7db_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc13}
AGLPRIIKETQRLLAEPVPGIKAEPDESMARYFHVVIAGPQDSPFEGGTFKLELFPEEYPMMAAPKVRFMTKIYHPNVDKLGRICLDILKDQWSPALQI
RTVLLSIQALLSAPNPDDPLANDVAEQWKTNEAQIETARAWTRLYAMN
>d1jatb_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), mms2}
SKVPRNFRLLLEELEKGEKGFGPESCSYGLADSDDTMTKWNGTILGPPHSNHENRIYSLSIDCPNYPDSPPKVTFISKINLPCVNPTTGEVQTDFTLR
DWKRAYTMETLLDLRKEMATPANKKLRQPKEGETF
>d1j7da_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), mms2}
GVKVRPNFRLLLEELEGQKGVGDTVSWGLEDDEDMTLTRWTGMIIGPPRTNYENRIYSLKVECGPKYPEAPPSVRVTKINMNGINNSSGMVDA
RSIPVLAQWQNSYSIKVVLQELRLMMMSKENMKLPQPEGQTYNN

>d1c4zd_d.20.1.1 (D:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch7}
SRRLMKELEEIRKCGMKNFRNIQVDEANLLTWQGLIVPDNPYDKGAFRIEINFPAEYPFKPPKITFKTKIYHPNIDEKGQVCLPVISAENWKPATKTD
QVIQSLIALVNDPQPEHPLRADLAEYSKDRKKFCKNAEEFTKKY

>d1u9aa_d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc9}
LNMSGIALSRLAQRERKAWRKDHPFGFVAVPTKNPDGTMNLMNWCAIPGKKGTPWEGGLFKLRLMFKDDPSSPKCKFEPLLHVNVPSTV
CLSILEEDKDWRPAITIKQILLGIQELLNEPNIQDPAQAEAYTIYCQNRVEYEKRVRAQAKKFAPS

>d1i7ka_d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch10}
PVGKRLQQELMTLMMMSGDKGISAFPESNLFKWVGTIHGAAGTVYEDLRYKLSLEPPSGYPYNAPTVKFLPCYHPNVDTQGNISLDILKEKWSALY
DVRILLSIQSLLGEPEPNIDSPLNTHAAELWKNPTAFKKYLQETYSKQVT

>d2e2c_d.20.1.1 (-) Ubiquitin conjugating enzyme {Clam (Spisula solidissima), E-2C}
MTTSKERHSVSKRLQQELRTLLMSGDPGITAFPGDNLFKVVATLDGPKDTVYESLKVKLTLEFPSDYPYKPPVVFKFTPCWHPNVDQSGNICLDILK
ENWTASYDVRTILLSQLGEPEPNASPLNAQAADMWSNQTEYKKVLHEKYKTAQSDK

>d1bwza1_d.21.1.1 (A:1-130) Diaminopimelate epimerase {Haemophilus influenzae}
MQFSKMHGLGNDFVVVDGVTQNVFFPETIRRANRHCIGFDQLLIVEAPYDPELDFHYRIFNADGSEVSQCGNGARCFARFVTLKGLTNKKDISV
STQKGNMVLTVKDMNQIRVNMGEPIWEPAKIPF

>d1bwza2_d.21.1.1 (A:131-274) Diaminopimelate epimerase {Haemophilus influenzae}
TANKFEKNYILRTDIQTVLCGAVSMGNPHCVVQVDDIQTANVEQLGPLLESHERFPERVNAGFMQIINKEHIKLRVYERGAGETQACGSGACAAYAV
GIMQGQLNNNNVQVDLPGGSLMIEWNGVGHPLYMTGEATHIYDGFITL

>d1h6ra_d.22.1.1 (A:) Green fluorescent protein, GFP {Jellyfish (Aequorea victoria)}
SKGEELFTGVVPIVLDGDVNGHKFSVSGEGEGDATYGKLTLKFIVTTGKLPWPVTLTTFAYGLQCFARYPDHMKRHDFFKSAMPEGYVQERTIFF
KDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNNSHCYIVADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHY
HYLCYQSALS KDPNEKRDHMVLLEFVTAAGITH

>d2emd_d.22.1.1 (-) Green fluorescent protein, GFP {Jellyfish (Aequorea victoria)}
ELFTGVVPIVLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPWPVTLTTFAYGLQCFARYPDHMKRHDFFKSAMPEGYVQERTIFFKDD
GNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNNSHNVIIMADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHY
LSTQALS KDPNEKRDHMVLLEFVTAAGIT

>d1ggxa_d.22.1.1 (A:) Red fluorescent protein (fp583 or dsred(clontech)) {Coral (Discosoma sp.)}
VIKEFMRFKVRMEGTVGNGHEFEIEGEGRPYEHNTVKLKVTKGGPLPFAWDILSPQFQYGSKVVKH PADIPDYKKLSPEGFKWERVMNFEDG
GVVTVTQDSSLQDGCFIYKVFIGVNFP SDGPVMQKKTMGWEASTERLYPRDGVLKGEIHAKLKDGGHYLVEFKSIYMAKPVQLPGYYYDSKL
DITSHNEDTYTIVEQYERTEGRHHFL

>d1gl4a1_d.22.1.2 (A:399-631) Domain G2 of nidogen-1 {Mouse (Mus musculus)}
GSPQRVNGVKGRIFVGSSQVPVFENTDLHSYVVMNHGRSYTAISTIPETVGYSLLAPIGGIIIGWMFAEQDGFKNFSITGGFTRQAETFLG
HPGKLVKQQFSGIDEHGHLTISTELEGRVPQI PYGASVHIEPYTELYHYSSSVTSSSTREYTVMEPDQDGAAPSHTIYQWRQTITFQECAHDDARP
ALPSTQQQLSVDSVFLVLYNKEERILRYALSNSIGPVR

>d1c8za_d.23.1.1 (A:) Transcriptional factor tubby, C-terminal domain {Mouse (Mus musculus)}
GSVDIEVQDLEEFALRPAPQGITIKCRITRDKKGMDRGMFPTYFLHLDREDGKKVFLAGRKRKKSNTSNTSVDPTDLSRGGSYIGKLRNSLNGTK
FTVYDNGVNPQKASSSTLESGLRQELAACYETNVLGFKGPRKMSIVPGMNMVHERVCIRPRNEHETLLARWQNKTNTSIIELQNKTPTVWNDD
TQS VLN F HGRV TQASVKNFQIIHGNPDYIVM QFGRVAEDVFTMD NYPLCALQAF AIA LSS FD SKL ACE

>d2pil_d.24.1.1 (-) Pilin {Gc (Neisseria gonorrhoeae)}
FTLIELMIVIAIVGILAVALPAYQDYTARAQVSEAILAEGQKSAVTEYYLNHGKPENNTSAGVASPPSDIKGKYVKEEVKNGVVTATMLSSGVNN
EIKGKKLSLWARRENGSVKFCGQPVRTDDDTVADAKDGKEIDTKHLPSTCRDNFDAK

>d1hpwa_d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa}
ALEGTEFARAQLSEAMTASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKVTTGGTAAASGGCTIVATMKASDVATPLRGKTLTLLGNA
DKGSYTWA CTSNADNKYLPKTCQTATTTP

>d1dzoa_d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa, type IV pilin, pak pilin}
GTEFARSEGASALASVNPLKTTVEEALSRGWSVSGTGTEDATKKEVPLGVAADANKLGTIALKPDPADGTADITLTFTMGGAGPKNKGKIITLRTAA
DGLWKCTSDQDEQFIPKCSR

>d1p32a_d.25.1.1 (A:) Acidic mitochondrial matrix protein p32 {Human (Homo sapiens)}
MHTDGDKAFAVDFLSDEIKEERKIQKHKTLPKMSGGWELELNTEAKLVRKVAGEKITVTFNINNSIPPTFDGEEEPSSQGKVEEQEPELTSTPNFVVE
VIKNDDGKKALVLDCHYPEDEVGQEDEAEDIFSIREVSFQSTGESEWKDTNYTLNTDSLWALYDHLMDFLADRGVDNTFADELVELSTALEHQEYI
TFLEDLKSFKVKSQ

>d1blkf_d.26.1.1 (-) FK-506 binding protein (FKBP12), an immunophilin {Human (Homo sapiens)}
GVQVETISPGDGRTPKKGQTCVVHYTGMLEDGKKFDSSRDRNKPFKMLGKQEIRGWEVGVAQMSVGQRALKTISPDYAYGATGVPGIIPPHAT
LVFDVELLKLE

>d1c9ha_d.26.1.1 (A:) Calcineurin (FKBP12.6) {Human (Homo sapiens)}
GVEIETISPGDGRTPKKGQTCVVHYTGMLEDGKKFDSSRDRNKPFKFRIGKQEVIKGFEEGAQMSLGQRALKTCTPDVAYGATGHPGVIPPNATLI
FDVELLNLE

>d1yat_d.26.1.1 (-) Calcineurin (FKBP12.6) {Baker's yeast (Saccharomyces cerevisiae)}
SEVIEGNVKIDRISPGDGFATFPKTGDLTIHYTGTLENGQKFDSRDRNKPFKFRIGKQEVIKGFEEGAQMSLGQRALKTCTPDVAYGATGHPGVIPPNATLI
STLVFDVELLKVN

>d1pbk_d.26.1.1 (-) FKBP25 {Human (Homo sapiens)}
PKYTKSVLKKGDKTNFPKKGDVVHCWYTGTLQDGTVFDTNIQTSACKKKNAKPLSFKVGVGVKIRGWDEALLTMSKGEKARLEIEPEWAYGKKQPD
DAKIPPNAKLTFEVELVDID

>d1rot_d.26.1.1 (-) FKBP59-I, N-terminal domain {Rabbit (Oryctolagus cuniculus)}
GVDISPKQDEGVLKVIKREGTGTETPMIGDRVVFHYTGWLTDGKFDSSLDRDKFSFDLGKGEVIAWVIAVATMKVGECLCRITCKPEYAYGSAGSP
PKIPPNAATLVFEVELFEFKG

>d1pina2_d.26.1.1 (A:45-163) Mitotic rotamase PIN1, domain 2 {Human (Homo sapiens)}
GKNGQGEPARVRCSSHLLVKHSQSRRPSSWRQEKITRTKEEALELINGYIQKIKSGEEDFESLASQFSDCSSAKARGDLGAFSRGQMOKPFEDASFALR
TGEMSGPVFTDSGIHIIILRT

>d1eq3a_d.26.1.1 (A:) Parvulin {Human (Homo sapiens), hpar14}
NAVKVRHILCEKHGKIMEAMEKLKSGMRFNEVAAQYSEDKARQGGDLGWMTRGSMVGPFQEAALPVSGMDKPVFTDPPVTKFGYHIIIMVE
GRK

>d1fd9a_d.26.1.1 (A:) Macrophage infectivity potentiator protein (MIP) {Legionella pneumophila}
TDKDKLKSIGADLGKNFKNQGIDVNPEAMAKGMQDAMSGAQLALTEQQMKDVLNKFKQDKLMAKRTAEFNKKADENKVKGAEFLTENKNKPGV
VVLPSGLQYKVINSNGNVKPGKSDTVTEYTGRLIDGTVFDSSTEKTGKPATFQVSQVIPGWTTEALQLMPAGSTWEIYVPSGLAYGPRSVGGPIGPNET
LIFKIHLSVKKS

>d1grj_2_d.26.1.2 (80-158) GreA transcript cleavage factor, C-terminal domain {Escherichia coli}
MPNNNGRVIFGATVTVLNLDSEEEQTYRIVGDDAEFKQNLSVNSPIARGLIGKEEDVVVVIKTPGGEVEFEVIKVEYL

>d3eipa_d.26.2.1 (A:) Colicin E3 immunity protein {Escherichia coli}
GLKLDLTWFDKSTEDFKGEEYSKDFGDDGSVMESLGVPFKDNVNNGCFDVAEWPVLLQPYFNHQDISDNEYFVFSFYRDGDW

>d1edqa3_d.26.3.1 (A:444-516) Chitinase A {Serratia marcescens}
YGRGWTGVNGYQNNIPFTGTATGPVKGWTENGIVDYRQIAGQFMSEWQTYDATAEAPYVFKPSTGDLITFD

>d1goia3_d.26.3.1 (A:292-379) Chitinase B {Serratia marcescens}
YGRAFKGVSGGNGQQYSSHSTPGEDYPYSTDYWLGCEECVRDKDPRIASYRQLEQMLQGNGYQRLWNDKTTPLYHAQNGLFVTY

>d1d2ka2_d.26.3.1 (A:293-354) Chitinase 1 {Fungus (Coccidioides immitis)}
YGRAFASTDGIIGTSFNGVGGSWENGVWDYKDMPQQGAQVTELEDIAASYSYDKNKRILSY

>d1e9la2_d.26.3.1 (A:267-336) Chitinase-like lectin ym1 {Mouse (Mus musculus)}
YGHTFILSDPSKTGIGAPTISTGPPGKYTDSEGLLAYEVCTFLNEGATEVWDAPQEVPYAYQGNEWVGY

>d1fjgp_d.27.1.1 (P:) Ribosomal protein S16 {Thermus thermophilus}
MVKIRLARFGSKHNPHYRIVVTDARRKRDGYIEKIGYYDPRKTPDWLKVDVERARYWLSVGAQPTDTARRLLRQAGVFRQE

>d1fjgs_d.28.1.1 (S:) Ribosomal protein S19 {Thermus thermophilus}
PRSLKKGVFDDHLLEKVLELNALKGEKRLIKTWSRRSTIVPEMVGHTIAVYNGKQHVPVYITENMVGHKLGEFAPTRTYRGHGK

>d1qkha_d.28.1.1 (A:) Ribosomal protein S19 {Thermus thermophilus}
GVFVDDHLLEKVLELNALKGEKRLIKTWSRRSTIVPEMVGHTIAVYNGKQHVPVYITENMVGHKLGEFAPTRTY

>d1jj2w_d.29.1.1 (W:) Ribosomal protein L31e {Archaeon Haloarcula marismortui}
ERVVTIPLRDARAEPNKHRAKAMILIREHLAKHFSVDEDAVRLDPSINEAAWARGRANTPSKIRVRAARFEEGEAIVEAE

>d1b33n_d.30.1.1 (N:) Allophycocyanin linker chain (domain) {Mastigocladus laminosus}
GRLFKITACVPSQTRIRTQRELQNTYFTKLPYENWFREQQRIQKMGGKIVKVELATGKQGINTGLA

>d1qcsa2 d.31.1.1 (A:86-201) C-terminal domain of NSF-N, NSF-Nc {Hamster (Cricetus cricetus)}

DKAKQCIGTMTIEIDFLQKKNIDSNPYDTDKMAAEFIQQFNNQAFSVGQQQLVFSFNDKLFGLLVKDIEAMDPSILKGEPASGKRQKIEVGLVVGNSQV
AFEKAENSSLNLIGAKT

>d1cr5a2 d.31.1.1 (A:108-210) C-terminal domain of NSF-N, NSF-Nc {Baker's yeast (Saccharomyces cerevisiae), sec18p}
SGKQSYLGSIDISFRARGKAVSTVFDQDELAKQFVRCYESQIFSPQTQYLIMEFQGHFFDLKIRNVQAIDLGDIETSAVATGIETKGILTQQTQINFFKG
R

>d1cz4a2 d.31.1.1 (A:92-185) C-terminal domain of VAT-N, VAT-Nc {Archaeon Thermoplasma acidophilum}
TEIAKKVTLAPIRKDQRKLFGEGLIEEYVQRALIRRPMLEQDNISVPGTLLAGQTGLFKVVKTPSKVVPVEIGEETKIEIREEPASEVLEEGG

>d1e32a3 d.31.1.1 (A:107-200) Membrane fusion atpase p97 domain 2, P97-Nc {Mouse (Mus musculus)}
DVKYGKRIHVLPIDDTVEGITGNLFVYLPYFLEAYRPIRKGDIFLVRGGMRAVEFKVVETDPSPYCIVAPDTVIHCEGEPIKREDEEESLNE

>d1qipa_d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Human (Homo sapiens)}
GGLTDEAALSCSDADPSTKDFLQQTMLRVKDPKKSDFYTRVLGMTLIQKCDFPIMKFLYFLAYEDKNDIPKEKDEKIAWLSRKATLELTHNWGT
EDDETQSYYHNGNSDPRGFHIGIAVPDVSACKRFEELGVKFVKKPDDGKMKGLAFIQDPDGWIEILNPNKMATLM

>d1f9za_d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Escherichia coli}
MRLLHTMLRVGDLQRSIDFYTKVLGMKLLRTSENPEYKSLAFVGYPETEEAVIELTYNWGVDKYELGTAYGHIALSDNAEACEKIRQNNGNVTR
EAGPVKGTTVIAFVEDPDGYKIELIEEKDAGRGLGN

>d1qtoa_d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptomyces verticillus}
MVKFLGAVPVLTAVDV PANVSFWVDTLGFKEKDFGDRDFAGVRRGDIRLHISRTEHQIVADNTSAWIEVTDPDALHEEWARAVSTDYADTSGPAMTP
VGESPAGREFAVRDPAGNCVHFTAGE

>d1byla_d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptoalloteichus hindustanus}
FMAKLTSAVPVLTARDVAGAVEFWTDRLGFSRDFVEDDFAGVVRDDVTLFISAVQDQVVPDNTLAWWWVRGLDELYAEWSEVSTNFRDASGPA
MTEIGEQPWGREFALRDPAGNCVHFVAE

>d1ecsa_d.32.1.2 (A:) Bleomycin resistance protein, BRP {Klebsiella pneumoniae}
TDQATPNLPSRDFSTAAYERLFGFIVFRDAGWMILQRGDLMLEFFAHPLASWFSCCLRLDDLAEFYRQCKSVGIQETSSGYPRIHAPELQG
WGGTMAALVDPDGTLRLIQNEL

>d1jc4a_d.32.1.4 (A:) Methylmalonyl-CoA epimerase {Propionibacterium shermanii}
NEDLFICIDHVAYACPDADEASKYYQETFGWHELHREENPEQGVVEIMMAPAAKLTEHMTQVQVMAPLNDESTVAKWLAKHNGRAGLHHMAW
RVDDIDAVSATLRLERGVQLLYDEPKLGTGGNRINFMPKSGKGVLIELTQYPK

>d1gdga1 d.32.1.3 (A:1-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Pseudomonas sp.}
SIERLGYLGFAVKDVPAWDHFHFLTKSVGLMAAGSAGDAALYRADQRAWRIA VQPGELDDLAYAGLEVDDAAALERMA DKLRQAGVAFTRGDEALM
QQRKVMGLLCLQDPFGLPLEIYYGPAEIFHEPFLPSAP

>d1gdga2 d.32.1.3 (A:133-288) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Pseudomonas sp.}
VSGFVTGDDQGIGHFVRCVPDTAKAMAFYTEVLGFVLSIDIQMGPETSPVPAHFLHCNGRHHTIALAAFPKRIHHFMLQANTIDDVGYAFDRLDA
AGRITSLLGRHTNDQTLFYADTPSPMIEVEFGWGPRTVDSSWTVARHSRTAMWGHKS

>d1han_1 d.32.1.3 (2-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Burkholderia cepacia (formerly Pseudomonas cepacia)}

SIRSLGYMGFAVSDVAWRSLTQKGLIMEAGTTDNGDLFRIDSRAWRIAQQGEVDDLAFAFYEVADAAGLAQMADKLKQAGIAVTGDASLAR
RRGVTGLITFADPFGLPLEIYYGASEVFEKPFLPGA

>d1han_2 d.32.1.3 (133-289) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme) {Burkholderia cepacia (formerly Pseudomonas cepacia)}

AVSGFLTGEQGLGHFVRCVPDSKDALAFYTDVLGFQLSDVIDMKMGPDTVPAYFLHCNERHHTLAAFPPLPKRIHHFMLEVASLDDVGFAFDRVD
ADGLITSTLGRHTNDHMVSFYASTPSGVEVEYGWSARTVDRSWVVVRHDSPSMWGHKSVR

>d1mpya1 d.32.1.3 (A:1-145) Catechol 2,3-dioxygenase (metapycatechase) {Pseudomonas putida, mt2}

MNKGVMRPGHVQLRVLDMSKALEYVLLGLIEMDRDDQGRVYLKAWTEVDKFSVLREADEPGMDFMGFKVVDEDALRQLERDLMAYGCAV
EQLPAGELNCGRRVRFQAPSGHHFELYADKEYTGKWGLNDVNPEAWPRDLKG

>d1mpya2 d.32.1.3 (A:146-307) Catechol 2,3-dioxygenase (metapycatechase) {Pseudomonas putida, mt2}

MAAVRFDHALMYGDELPATYDLFTKVLGFYAEQVLDENGRVAQFSLSTKAHDVAIFIHHPEKGRHHVSFHLETWEDLLRAADLISMTDTSIDIGP
TRHGLTHGKTIYFFDPGNRNEVFCGGDYNYPDHKPVTWTTDQLGKAIFYHDRILNERFMTVLT

>d1cjxa1 d.32.1.3 (A:4-153) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas fluorescens}

YENPMGLMGFEFIEFASPTPGTLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILNNEPNSIASYFAAEHGPSVCGMAFRVKDSQKAYNRAELGAQPI
HIDTGPMENLPAIKGIGGAPLYLIDRFGEGLSSYIDIFVYLEGVERNPVG

>d1cjxa2 d.32.1.3 (A:154-356) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas fluorescens}

AGLKVIDHLTHNVYRGRMVYWWANFYEKLFNFREARYFDIKGEYTGLTSKAMSAPDMIRIPLNEESSKGAGQIEFLMQFNGEGIQHVAFLTDDLKV
TWDALKKGMRFMTAPPDTYYEMLEGRLPDHGEPVDQLQARGILLDGSSVEGDKRLLLQIFSETLMGPVFFEIQRKGDDGFEGNFKALFESIERD
QVRRGVLAT

>d1fx3a_d.33.1.1 (A:) Bacterial protein-export protein SecB {Haemophilus influenzae}

QPVLQIQRIVVKDVSFEAPNLPHIFQQEWPKPLGFDLSTETTQVGDDLYEVVLNISVETTLESDVAFICEVKQAGVFTISGEDVQMAHCLTSQCP
NMLFPYARELVSNLVNRGTFPALNLSPVNFDALFVEYMNRRQQAEN

>d1bm8_d.34.1.1 (-) DNA-binding domain of Mlu1-box binding protein MBP1 {Baker's yeast (Saccharomyces cerevisiae)}

QIYSARYSGVDVYEFIHSTGSIMRKKDDWVNATHILKAANFAKAKRTRILEKEVLKETHEKVQGGFGKYQGTWVPLNIAKQLAEKFSVYDQLKPLFD
F

>d1dk0a_d.35.1.1 (A:) Heme-binding protein A (HasA) {Serratia marcescens}

AFSVNYDSSFGGYSIHDLGQWASTFGDVNHTNGNVTDANSFFYGGSLGSQYAISSSTANQVTAFAVAGGNLTLYFNEPAHTLYGQLDSLSFGDGL
SGGDTSPSYIQVPDFVSFGGLNLSSLQAQGHGDBGVHVQVYGLMSGDTGALETALNGILDDYGLSVNSTFDQVAAATA

>d1eyqa_d.36.1.1 (A:) Chalcone isomerase {Alfalfa (Medicago sativa)}

SITAITVENLEYPAVTSPVTGKSYFLGGAGERGLTIEGNFIKFTAIGVYLEDIAVASLAAWKGSSEELLETLDFYRDIISGPFEKLIRGSKIRELSGPEYSR
KVMENCVAHLKSVGTYGDAEAEAMQKFAEFKPVNFPPGASFYRQSPDGILGLSFSPDTSIPEKEAALIENKAVSSAVLETMIGEHAVSPDLKRCLA
ARLPALLNE

>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)}

GFIITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLV

>d1jr1a3 d.37.1.1 (A:178-232) Type II inosine monophosphate dehydrogenase {Chinese hamster (Cricetulus griseus)}

IMTKREDLVVAPAGITLKANEILQRSKKGKLPVNENDELVIIARTDLKKNRD

>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}

MTSEHLVTAAVGTDLETAERILHEHRIEKLPLVDNSGRLSGLTIK DIEK VIEFPHA AKDEF

>d1bvqa_d.38.1.1 (A) 4-hydroxybenzoyl-CoA thioesterase {Pseudomonas sp., CBS-3}
ARSITMQQRIFGDCDPAGIVWYPNYHRWLDAASRNYFIKGLPPWRQTVVERGIVGTPIVSCASFVCTASYDDVLTIECIKEWRRKSFVQRHSV
SRTTPGGDVQLVMRADEIRVFAMNDGERLRAIEVPADYIELC

>d1mkaa_d.38.1.2 (A) beta-Hydroxydecanol thiol ester dehydrase {Escherichia coli}
VDKRESYTKEDLLASGRGEKGAKGPQLPAPNMLMMMDRVVKMTETGGNFDKGYVEAEILDINPDLWFFGCHFIGDPVMPGCLGLDAMWQLVGFY
LGWLGGEKGKRALGVGEVKFTGQLPTAKKVTYRIHFKRIVNRRILMGLADGEVLVDGRLIYTASDLKVGLFQDTSAF

>d1c8ua1_d.38.1.3 (A:2-115) Thioesterase II (TesB) {Escherichia coli}
SQALKNLLNLNEKIEEGLFRGQSEDLGLRQVF GGQVVGQALYAAKETVPEERLVHSFSYFLRPGDSKKPIYDVETLRDGNSFSARRVAIQNNGKPI
FYMTASFQAPEAGF

>d1c8ua2_d.38.1.3 (A:116-286) Thioesterase II (TesB) {Escherichia coli}
EHQKTMPSAPAPDGLPSETQIAQSLAHLLPPVLKDKFCIDRPLEVRPVEFHNPALKHVAEPHRQVVIRANGSVPDRLVHQYLLGYASDLNFLPVAL
QPHGIGFLEPGIQIATIDHSMWFHRPFNLNEWLLYSVESTSASSARGFVRGEFYTQDGVLVASTVQEVMRNHN

>d1cmia_d.39.1.1 (A) Dynein light chain 8 (DLC8) {Human (Homo sapiens)}
KAVIKNADMSEEMQQDSVECATAQALEKYNIEKDIAAHIKKEFDKKYNPTWHCIVGRNFGSYVTHETKHFIFYLGQVAILLFKSG

>d1csei_d.40.1.1 (I) Egl C {Leech (Hirudo medicinalis)}
KSFPEVVGKTVQDQAREYFTLHYPQYDVYFLPEGSPVTLDLRYNRVRVFYNPGTNVVNVPHVG

>d1egl_d.40.1.1 (-) Egl C {Leech (Hirudo medicinalis)}
TEFGSELKSPEVVGKTVQDQAREYFTLHYPQYDVYFLPEGSPVTLDLRYNRVRVFYNPGTNVVNVPHVG

>d1ypci_d.40.1.1 (I) Chymotrypsin inhibitor Cl-2 {Barley (Hordeum vulgare)}
MKTEWPELVGKSVEEAKKVLQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAQVPRVG

>d2snii_d.40.1.1 (I) Chymotrypsin inhibitor Cl-2 {Barley (Hordeum vulgare)}
LKTEWPELVGKSVEEAKKVLQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAEVPRVG

>g1cq4.1 d.40.1.1 (A;B) Chymotrypsin inhibitor Cl-2 {Barley (Hordeum vulgare)}
KTEWPELVGKSVEEAKKVLQDKPEAQIIVLPVGTIVXYRIDRVRLFVDKLDNIAQVPRVG

>d1tin_d.40.1.1 (-) Trypsin inhibitor V {Pumpkin (Cucurbita maxima)}
SSCPGKSSWPHLVGGGSVAKAIERQNPNVKAVIDEELGTPVTKDRCNRVRIWVNKRGLVVSPPRIG

>d1dwma_d.40.1.1 (A) Trypsin inhibitor LUTI {Flax (Linum usitatissimum)}
SRRCPGKNAWPELVGKSGNMAATVERENRNVHAIVLKEGSAMTKDFRCRDRVWVIVNDHGVVTSVPHIT

>d1jv2b3_d.200.1.1 (B:606-690) Integrin beta tail domain {Human (Homo sapiens)}
DACTFKKECKKFDRPYMTENTCNRYCRDEIESVKELKDTGKDAVNCTYKNEDDCVRFQYYEDSSGKSILYVVEEPECPKG

>d1hlra3_d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio gigas}
DYGADLGLKMPAGTLHLAMVQAKVSHANIKGIDTSEALTMPGVHSVITHKDVKGKNRITGLITFPTNKGDGWDRPILCDEKVFQYGDICIALVCADSE
ANARAAAEEKVKVDLEELPAY

>d1dgja3_d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio desulfuricans}
EFGADAALRMPENTLHLALAQAQKVSHALIKGIDTSEAEKMPGVYKVLTHKDVKGKNRITGLITFPTNKGDGWDRPILNDSKIFQYGDALAI CADSEA
NARAAAEEKVKFDLELLPEY

>d1fiqc1_d.41.1.1 (C:571-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}
DTVGRPLPHAAAMQASGEAVYCDDIPRYENELFLRLVTSTRAHAKIKSIDVSEAQKVPGFCFLSADDIPGSNETGLFNDETVFAKDTVTCVGHIIGA
VVADTPEHAERAHHVVKVTYEDLPA

>d1fo4a3_d.41.1.1 (A:537-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}
KLDPTYTSATLLFQKHPPANIQLFQEVPNGQSKEDTVGRPLPHAAAMQASGEAVYCDDIPRYENELFLRLVTSTRAHAKIKSIDVSEAQKVPGFCFL
SADDIPGSNETGLFNDETVFAKDTVTCVGHIIGA
>d1jrob1_d.41.1.1 (B:2-123) Xanthine dehydrogenase chain B, N-terminal domain {Rhodobacter capsulatus}
SVGKPLPHDSARAHVTGQARYLDDLPCPANTLHLAFLSTEASAAITGLDLEPVRESPGVIAVFTAADLPHNDASPAPSPEPVLATGEVHFVGQPFL

VAATSHRAARIAARKARTYAPR

>d1qj2b1 d.41.1.1 (B:10-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {Pseudomonas carboxydovorans}
TSAERAELQGMGCKRKVEDIRFTQGKGNVDDVKLPGMLFGDFRSSAHARIKSIDTSKAKALPGVFAVLTAADLKPLNLHYMPTLAGDVQAV
LADEKVLFQNQEVAFVAKDRYVAADAIELVEVDYELPVL

>d1ffvb1 d.41.1.1 (B:7-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {Hydrogenophaga pseudoflava}
DAEARELALAGMGASRLRKEDARFIQGKGNVDDIKMPGMLHMDIVRAPIAHGRIKKIHDKAALAMPGVHAVLTAEDLKPLKLHWMPMTLAGDVA
AVLADEKVHFQMQUEVAIVIADDYIAADAVEAVKVEYDELPPVIDP

>d1qapa2 d.41.2.1 (A:8-129) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Salmonella typhimurium}
DDRRDALLERINLDIPAAQAQALREDLGGEVDAGNDITAQLLPADTQAHATVITREDGVFCGKRWVEEVFIQLAGDDVRLTHVDDGDAIHANQTV
FELQGPARVLLTGERTALNFVQTL SG

>d1qpoa2 d.41.2.1 (A:2-116) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Mycobacterium tuberculosis}
GLSDWELAAARAIIARGLDEDLRYGPDTTLATVPASATTSLVTREAGVVAGLDVALLTNEVLGNTGYRVLDRVEDGARVPPGEALMTLEAQTR
GLLTAERTMLNLVGHLSG

>d2tpt_3 d.41.3.1 (336-440) Thymidine phosphorylase {Escherichia coli}
TAMLTKAVYADTEGFVSEMDTRALGMAVVAMGGRRQASDTIDSYGFTDMARLGQVQDGQRPLAVIHKDENNWQEAAKAVKAAIKLADKA
PESTPTVYRISE

>d1brwa3 d.41.3.1 (A:331-433) Pyrimidine nucleoside phosphorylase {Bacillus stearothermophilus}
KAAYTSTVAAADGYVAEMAADDIGTAAMWLGAAGRACKEDVIDLAVGIVLHKKIGDRVQKGEALATIHSNRPDVLDVKEKIEAAIRLSPQPVARPPLI
YETIV

>d1ffkf_d.41.4.1 (F:) Ribosomal protein L10e {Archaeon Haloarcula marismortui}
KPGAHFRNSIKPAYTRREYISGIPKGIAQFKMGNNGAGPTYPQAQVENVVEKPVQIRHNALEAARNAANRFVQNSGAAANYKFRIRKFPHVIREQ
DGDGMRAPFGKSGTAARSHGANHDFIAWVNPDPAVEFAWRRAYMKVTPTVNIDSSPAGNA

>d1jj2h_d.41.4.1 (H:) Ribosomal protein L10e {Archaeon Haloarcula marismortui}
KPGAMYRNSSKPAYTRREYISGIPGKKAQFDMGNNGAGPTYPQAQVELVVEKPVQIRHNALEAARVAANRYVQNSGAAANYKFRIRKFPHVIRENK
AAAAAAAAAADGMRAPFGKPVGTAARVHGANCHIFIAWVNPDPNVEEARRAKMVKTPTNIDSSPAGNA

>d1fm0e_d.41.5.1 (E:) Molybdopterin synthase subunit MoaE {Escherichia coli}
AETKIVVGQPFSVGEYPWLAERDEDGAVTFTGKVRNHNLGDSVNALTLEHYPGMTEKALAEIVDEARNRWPLGRVTIHRIGELWPGDEIVFV
GVTSAHSSAFEAGQFIMDYLKTRAPFWKREATPEGDRWVEARESDQQAAKRW

>d1buoa_d.42.1.1 (A:) Promyelocytic leukemia zinc finger (PLZF) protein BTB domain {Human (Homo sapiens)}
MGMIQLQNPSHPTGLLCKANQMRLAGTLCDVIMVDSQEFHAHRTVLACTSKMFEILFHRNSQHYLDFLSPKTFQQILEYAYTATLQAKAEDLDD
LLYAAEILEIYELEEQLKMKLETIQ

>d1vcbb_d.42.1.1 (B:) Elongin C {Human (Homo sapiens)}
MYVKLISSDGHEFIVKREHALTSGTIKAMILSPGQFAENETNEVNFRIPSHVLSKVCMDTYKVRTNTSSTEIPEFPIAPEIALELLMAANFLDC

>d1hv2a_d.42.1.1 (A:) Elongin C {Baker's yeast (Saccharomyces cerevisiae)}
MSQDFVTLVKDDKEYEISRSAAMISPTLKAMIEGPFRESKGRIELKQFD SHILEKAVEYLNYNLKYSGVSEDDDEIPEFEIPTEMSLELLAADYLSI

>d1a68_d.42.1.2 (-) Shaker potassium channel {California sea hare (Aplysia californica)}
ERVVINVSGLRFETQLKTLNQFPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGRLRRPVNVPLDVFSEEIKFYELGENAFERYREDEG
F

>d3kvt_d.42.1.2 (-) akv3.1 voltage-gated potassium channel {California sea hare (Aplysia californica)}
ENRVIINVGGIRHETYKATLKKIPATRLSRLEGMLNYDPVLNEYFFDRHPGVFAQIINYRSGKLHYPTDVCGPLFEELEFWGLDSNQVEPCCWMYT
TAHR

>d1exbe_d.42.1.2 (E:) KV1.1 {Rattus norvegicus}

CERVVINISGLRFETQLKTLAQFPNTLLGNPKKRMRYFDPLRNEYFFDRNRPSFDAILYQQSGGRLRRPVNVPLDMFSEEIKFYELGEA
>d1dsxa_d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}

ERVVINISGLRFEVQLKTLAQFPETLLGDPKKRMRYFDPLRNEYFFDRNRPSFDAILYQQSGGRLRRPVNVPLDIFSEEIRFYELG
>d1qdva_d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}

ERVVINISGLRFETQLKTLAQFPETLLGDPKKRMRYFDPLRNEYFFDRNRPSFDAILYQQSGGRLRRPVNVPLDIFSEEIRFYELGEEAMEMFREDEG
>d1fs1b2 d.42.1.2 (B:2-68) Cyclin A/CDK2-associated p45, Skp1 {Human (Homo sapiens)}

PSIKLQSSDGEIFEVDFVEIAKQSVTIKTMLEDLGMDPVLNVNAAILKKVIQWCTHHKDD
>d1efub2 d.43.1.1 (B:140-282) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}

DVLGSYQH GARIGVL VAAKG ADEEL V KHI AMHV AASKPEFI K P E D V S A E V V E K E Y Q V Q L D I A M Q S G K P K E I A E K M V E G R M K K F T G E V S L T G Q P F V M
EPSKTVGQLLKEHNAEVTFIRFEVGEGIEKVETDFAAEVAAMSKQS
>d1efub4 d.43.1.1 (B:55-139) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}

VAADGVIKTIDGNYGIILEVNCQTDVFVAKDAGFQAFADKVLDAAVAGKITDVEVLKAQFEEERVALVAKIGENINIRRALEG
>d1tfe_d.43.1.1 (-) Elongation factor Ts (EF-Ts), dimerisation domain {Thermus thermophilus}

AREGIIGHYIHHNQRGVVLVELNCETDFVARNELFQNLAKDLAMHIAMMNPRYVSAEEIPAELEKERQIYIQAALNEGKPQQIAEKIAEGRKKYLEE
VVLLEQPFVKDDKVKVKELIQQAIKIGENIVVRRFCRFELGA
>d1i0ha2 d.44.1.1 (A:91-205) Mn superoxide dismutase (MnSOD) {Escherichia coli}

GTTLQGDLKAAIERDFGSVDNFKAEEFEKAAASRGSGWAWLVLKGDKLAVVSTANQDSPLMGEAISGASGFPIMGLDVWEHAYFLKFQNRRPDYIK
EFWNVNVNWDEAAARFAAKK
>d1mnga2 d.44.1.1 (A:93-203) Mn superoxide dismutase (MnSOD) {Thermus thermophilus}

GGAKEPVGELKKAAIDEQFGGGFQALKELTQAAMGRFGSGWAWLVKDPFGKLHLSTPNQDNPVMEGFTPIVGIDVWEHAYYLKYQNRRADYLQA
IWNVLNWDVAAEFFKKA
>d1ap6a2 d.44.1.1 (A:84-198) Mn superoxide dismutase (MnSOD) {Human (Homo sapiens)}

NGGGEPKGELLEAIKRDFGSFDKFKEKLTAASVGVQGSGWGWLGFNIKERGHLQIAACPNQDPLQGTGLIPLLGIDVWEHAYYLQYKNVRPDYLKAI
WNVINWENVTERYMACKK
>d1kkca2 d.44.1.1 (A:98-213) Mn superoxide dismutase (MnSOD) {Aspergillus fumigatus}

EKSGGGKIDQAPVLKAAIEQRWGSFDKFKEEFTKTSVGTFGSGWGWLVKADGSLALASTIGAGCPLTIDTPLTCDVWEHAYYIDYRNLRPKYVEAFWNL
AKGIWNVINWAEAENRYIAGDK
>d1dt0a2 d.44.1.1 (A:84-197) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}

AGGQPTGALADAINAAFGSFDFKKEEFTKTSVGTFGSGWGWLVKADGSLALCSTIGAGAPLTSQDTPLLCDVWEHAYYIDYRNLRPKYVEAFWNL
VNWAFVAEQFEGKTYKV
>d3sdpa2 d.44.1.1 (A:84-190) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}

DAGGQPTGALADAINAAFGSFDFKKEEFTKTSVGTFGSGWAWLVKADGSLALCSTIGAGAPLTSQDTPLLCDVWEHAYYIDYRNLRPKYVEAFWNL
VNWAFVAEEG
>d1isaa2 d.44.1.1 (A:83-192) Fe superoxide dismutase (FeSOD) {Escherichia coli}

NAGGEPTGKVAEIAASFADFKAAQFTDAIKNFGSGWTWLKVNSDGKLAIVSTSAGTPTTDATPLLTVDVWEHAYYIDYRNARPGYLEHFW
ALVNWEFVAKNLAA
>d1idsa2 d.44.1.1 (A:86-199) Fe superoxide dismutase (FeSOD) {Mycobacterium tuberculosis}

NGGDKPTGELAAAIAAFGSFDKFRAQFHAAATTVGSGWAALGWDTLGNKLLIFQVYDHQTNFPLGIVPLLLDMWEHAFYLQYKNVKVDFAKA
FWNVNWADVQSRYAAATS
>d1coja2 d.44.1.1 (A:91-212) Fe superoxide dismutase (FeSOD) {Aequifex pyrophilus}

GGKGEPEALKKIEEDIGGLACTNELKAAAMAFRGWAILGLDIFSGLRVNGLDAHNVNLTLGLIPLIVIDTYEHAYYVDYKNKRPPYIDAFFKNIN
WDVVNERFEKAMKAYEALKDFIK
>d1sssa2 d.44.1.1 (A:93-208) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus solfataricus}

PSGKGGGKPGGALADLINKQYGSFDRFKQVFTETANSPLPGTGWAFLYYDTESGNLQIMTFENHFQNHIAEIPIIILDEFEHAYYLQYKNKRADYVNA

WWNVVNWDAAEKKLQKYL

>d1b06a2 d.44.1.1 (A:93-210) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus acidocaldarius}

PAGKGGKGPGGALADLIDKQYGSFDRFKQVFSESANSLPGSGWTVLYYDNEGNLQIMTVENHFMNHIAELPVILIVDEFEHAYYLQYKNKRGDYLN
AWWNVNVNWDDAEKRQLQKYLNK

>d1bsma2 d.44.1.1 (A:87-201) Cambialistic superoxide dismutase {Propionibacterium shermanii}

SAPERPTDELGAAIDEFFGSFDNMKAQFTAAATGIQGSGWASLVWDPLGKRINTLQFYDHQNNLPAGSIPLQLDMWEHAFYLQYKNVKGDYVKS
WWNVNVNWDDVALRFSEARVA

>d1qnna2 d.44.1.1 (A:85-191) Cambialistic superoxide dismutase {Porphyromonas gingivalis}

KGGAPKGKLGEAIDKQFGSFEKFKEEFTAGTTLFGSGWVWLASDANGKLSIEKEPNAGNPVRKGLNPLLGFDVWEHAYYLTYQNRRADHLKDLWS
IVWDWDIVESRY

>d1ctf__ d.45.1.1 (-) Ribosomal protein L7/12, C-terminal domain {Escherichia coli}

EFDVILKAAGANKVAVIKAVRGATGLKEAKDLVESAPAALKEGVSKDDAEALKALEEAGAEVEVK

>d1dd3a2 d.45.1.1 (A:58-128) Ribosomal protein L7/12, C-terminal domain {Thermotoga maritima}

EFDVVLKSFQNKIQVIVKVVREITGLKEAKDLVEKAGSPDAVIKSGVSKEEAEEIKKLEEAGAEVELK

>d1ekta_ d.46.1.1 (A:) Transcription-state regulator AbrB, the N-terminal DNA recognition domain {Bacillus subtilis}

MKSTGIVRKVDELGRVVIPIELRRTLGIAEKDALEIYVDEKEIILKKYKPNMT

>d1mmsa2 d.47.1.1 (A:8-70) Ribosomal protein L11, N-terminal domain {Thermotoga maritima}

QIKLQLPAGKATPAPPVGPAQHGQHGVNIIMEFCRFAETADKAGMILPVVITVYEDKSFTII

>d2reb_2 d.48.1.1 (269-328) RecA protein, C-terminal domain {Escherichia coli}

NFYGELVDLGVKEKLIKEKAGAWYSYKGEKIGQGKANATAWLKDNPETAKEIEKKVRELLL

>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)}

PQYQTWEFSRAAEKLYLADPMKARVVLKYRHSQDGNCVKTDDLVCLVYKTDQAQDVKKIEKFHSQLMRLMVA

>d1e8ob_ d.49.1.1 (B:) Signal recognition particle alu RNA binding heterodimer, SRP9/14 {Human (Homo sapiens)}

VILLESEQFLTELTRLFQKCRSSGSVFTLKKYDGRTPKIPRKSSVEGLEPAENKCLLRATDGKRKISTVSSKEVNKFQMASNLRLANMDGLKRDKK

>d1914__ d.49.1.1 (-) Signal recognition particle alu RNA binding heterodimer, SRP9/14 {Mouse (Mus musculus)}

MVLLESEQFLTELTRLFQKCRSSGSVFTLKKYDGRTPKIPRKSSVEGLEPAENKCLLRATDGKRKISTVSSKEVNKFQMASNLRLANMDGLKRDKK
NKSKKSKPAQGGEQKLISEEDDSAGSPMPQFQTWEESRAAEKLYLADPMKVRVVLKYRHVDGNLCIKVTDDLVCVYRTDQAQDVKKIEKFHSQ
MRLMVAKESRNV

>d1di2a_ d.50.1.1 (A:) Double-stranded RNA-binding protein A, second dsRBD {Xenopus laevis}

MPVGLSLOELAVQKGWRLPEYTVAQESGPPHKREFITCRVETFVETGSGTSKQVAKRVAEEKLTKFKT

>d1ekza_ d.50.1.1 (A:) Staufen, domain III {Fruit fly (Drosophila melanogaster)}

MDEGDKKSPISQVHEIGIKRNMTVHFVLRREEGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAEKMLVELQKL

>d1stu__ d.50.1.1 (-) Staufen, domain III {Fruit fly (Drosophila melanogaster)}

PISQVHEIGIKRNMTVHFVLRREEGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAEKMLVELQKL

>d1qu6a1 d.50.1.1 (A:1-90) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}

GSHMEMAGDLSAGFFMEELNTYRQKQGVVLKYQELPNSGPPHDRRFTFQVIIDGREPGEGRSKKEAKNAAAKLAIVEILNKEKKAVSPL

>d1qu6a2 d.50.1.1 (A:91-179) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}

LTTTNSEGLSMGNYIGLNLRIAQQKRLTVNYEQCAGSVHGPEGFHYCKCMGQKEYSIGTGSTKQEAKQLAAKLAYLQILSEETGSGC

>d1pkp_2 d.50.1.2 (4-77) Ribosomal S5 protein, N-terminal domain {Bacillus stearothermophilus}

INPNKLELERVVAVNRAVKVKGGRRLRFSALVVGDKNHGFGFTGKAQEVPPEARAKIAEDAKNLIEVPIV

>d1fjge2 d.50.1.2 (E:5-73) Ribosomal S5 protein, N-terminal domain {Thermus thermophilus}

DFEEKMILIRRRTARMQAGGRRFRFGALVVVGDRQGRVGLGFGKAPEVPLAVQKAGYYARRNMVEVPLQN

>d1ah5_2 d.50.2.1 (220-313) Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}
NHHETALRVTAAERAMNTRLEGGCQVPIGSYAEILDGEIWLALVGAPDGSQIRGERRGAPQDAEQMGISLAEELLNNNGAREILAEVYNGDAPA

>d1pda_2 d.50.2.1 (220-307) Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}
NHHETALRVTAAERAMNTRLEGACQVPIGSYAEILDGEIWLRLGVGAPDGSQIRGERRGAPQDAEQMGISLAEELLNNNGAREILAEVY

>d1dq3a2 d.50.3.1 (A:336-414) PI-Pfui intein middle domain {Archaeon Pyrococcus furiosus}
GNFGLPLNLFNAFKEWASEYGVEFKTNGSQTIAIINDERISLGQWHTRNRVSKAFLVKMLRKLYEATKDEEVKRMLHLIE

>d1jida_d.201.1.1 (A:) SRP19 {Human (Homo sapiens)}
AARSPADQDRFICIYPAYLNNKKTIAEGRRIPIKAVENPTATEIQDVCSAVGLNVFLEKNKMYREWNRDVQYRGRVRVQLQEDGSLCLVQFPSRKS
VMLYAAEMIPKLKTR

>d1dt4a_d.51.1.1 (A:) Neuro-oncological ventral antigen 1, nova-1, KH3 {Human (Homo sapiens)}
MKDVVEIAVPENLVGAILGKGGKTLVEYQELTGCRISKKGEFLPGTRNRKVITGTPAATQAAQYLITQRI

>d1dtja_d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}
MKELVEMAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGEFLPGTRNRVTITGSPAATQAAQYLISQRVT

>d1ec6a_d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}
MKELVEMAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGEFLPGTRNRVTITGSPAATQAAQYLISQRVTYEQGVGRASNPQKV

>d1vig_d.51.1.1 (-) Vigilin, KH6 {Human (Homo sapiens)}
INRMDYVEINIDHKFHRHLIGKSGANIRIKDQYKVSVRIPPSEKSNLIRIEGDPQGVQQAKRELLELAS

>d2fmr_d.51.1.1 (-) Fragile X protein, KH1 {Human (Homo sapiens)}
ASRFHEQFIVREDLMGLAIGTHGANIQQARKVPGVTAIDLDEDCTFHIYGEDQDAVKKARSFLE

>d1khma_d.51.1.1 (A:) HnRNP K, KH3 {Human (Homo sapiens)}
GSPNSYGDGGPIITTQVTPKDLARSIIGKGGQRIKQIRHESGASIKIDEPLEGSEDRIITITGTQDQIQNAQYLLQNSVKQYSKGKF

>d1k1ga_d.51.1.1 (A:) RNA splicing factor 1 {Human (Homo sapiens)}
TRVSDKVMIPQDEYPEINFVGLIGPRGNTLKNIEKECNACKIMIRGKGSVKEGVGRKDQMLPGEDEPLHALVTANTMENVKAVEQIRNILKQGI
ETPEDQNDLRKMQLRELARLNGLTR

>d2proc1 d.52.1.1 (C:18-85) Alpha-lytic protease prodomain {Lysobacter enzymogenes}
IFPTQLPQYLQTEKLARTQAAAIERFGAQFAGSWIERNEDGSFKLVAATSGARKSSTLGGVEVRNVR

>d3proc1 d.52.1.1 (C:6-85) Alpha-lytic protease prodomain {Lysobacter enzymogenes}
PQLKFAMQRDLGIFPTQLPQYLQTEKLARTQAAAIERFGAQFAGSWIERNEDGSFKLVAATSGARKSSTLGGVEVRNVR

>d3proc2 d.52.1.1 (C:86-163) Alpha-lytic protease prodomain {Lysobacter enzymogenes}
YSLKQLQSAMEQLDAGANARVKGVSKPLDGVQSWYVDPRSNAVVKVDDGATDAGVDFVALSGADSAQVRIESSPGKL

>d1gpm a3 d.52.2.1 (A:405-525) GMP synthetase, C-terminal, dimerisation domain {Escherichia coli}
GPGLGVRVLGEVKKEYCDLLRRADAIFIELRKADLYDKVSQAFTVFLPVRSVGMGDRKYDWVSLRAVETIDFMTAHWAHPYDFLGRVSNRII
NEVNGISRVVYDISGKPPATIEWE

>d1fgc1 d.52.3.1 (C:2-106) Ribosomal protein S3 N-terminal domain {Thermus thermophilus}
GNKIHPIGFRLGITRDWESRWYAGKKQYRHLLEDQRIRGLLEKELYASGLARVDIERAADNVAVTVHVAKPGVVIGRGERIRVLREELAKLTGKNVA
LNVQE

>d1egaa2 d.52.3.1 (A:183-295) GTPase Era C-terminal domain {Escherichia coli}
DYITDRSQRFMASEIIREKLMRFLGAELPYSVTVEIERFVSNERGGYDINGLILVEREGQKKMVIGNKGAKIKTIGIEARKDMQEMFEAPVHLELWVKV
KSGWADDERALRSL

>d1hh2p2 d.52.3.1 (P:199-276) Transcription factor NusA, C-terminal domains {Thermotoga maritima}
RVPEFVIGLMKLEIPEVENGIVEIKAIAREPGVRTKAVASNDPNVDPIGACIGEGGSRIAIIKELGEKLDVLKWS

>d1hh2p3 d.52.3.1 (P:277-344) Transcription factor NusA, C-terminal domains {Thermotoga maritima}
DDPKQLIANALAPATVIEVLDKENKAARVLVPPTQLSLAIGKGGQNARLAALKTGWKIDIKPIMNL

>d1k0ra2 d.52.3.1 (A:184-262) Transcription factor NusA, C-terminal domains {Mycobacterium tuberculosis}

THPNLVRKLFLEVPEIADGSVEIVAVAREAGHRSKIAVRSNVAGLNAKGACIGPMGQRVRNVMSLSGEKIDIIDYDD
>d1k0ra3 d.52.3.1 (A:263-329) Transcription factor NusA, C-terminal domains {Mycobacterium tuberculosis}
DPARFANALSPAKVVSVSVIDQTARAARVVVPDFQLSLAIGKEGQNARLAARLTGWRIDIRGDAPP
>d1e3ha4 d.52.3.1 (A:579-632) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 6
{Streptomyces antibioticus}
APRIITVKIPVDKIGEVIGPKRQMINQIQEDTGAETIEDDTIYIGAADGPAA
>d1fjgc2 d.53.1.1 (C:107-207) Ribosomal protein S3 C-terminal domain {Thermus thermophilus}
QNPNLSPPLVAQRVAEQIERRFAVRRAIKQAVQRVMESGAKGAKVIVSGRIGGAEQARTEWAAQGRVPLHTLRANIDYGFALARTTYGVLGVKAYIF
LGEV
>d1hh2p4 d.202.1.1 (P:1-126) Transcription factor NusA, N-terminal domain {Thermotoga maritima}
MNIGLLEALDQLEEKGISKEEVIPILEKALVSAYRKNGNSKNVEVVIDRNTGNIKVYQLLEVVEEVEDPATQISLEEAKKIDPLAEVGSIKKELNVKNF
GRIAATQAKQVLIQRIRELEKEQ
>d1k0ra4 d.202.1.1 (A:-4-99) Transcription factor NusA, N-terminal domain {Mycobacterium tuberculosis}
VSRRHMNIDMAALHAIENVDRGISVNELLTIKSALLTAYRHTQGHQTDARIEIDRKTGVVRVIARETDEAGNLISEWDDTPEGFGRIAATTARQVMLQ
RFRDAE
>d1onea2 d.54.1.1 (A:1-141) Enolase {Baker's yeast (Saccharomyces cerevisiae)}
AVSKVYARSVYDSRGNPTVEVELTTEKGFRSIVPSGASTGVHEALEMRDGDKSKWMGKVLHAVKNVNDVIAPAFVKANIDVKDQKAVDDFLISL
DTANKSKLGANAILGVSLAASRAAAEKNVPLYKHLADLSKSKT
>d1pdz_2 d.54.1.1 (1-139) Enolase {Lobster (Homarus vulgaris)}
SITKVFARTIFDSRGNPTVEVDLYTSKGLFRAAVPSGASTGVHEALEMRDGDKSKYHGKSVFNAVKNVNDVIVPEIIKSLKVTQQKECDEFMCKLDG
TENKSSLGANAILGVSLAICKAGAAELGIPLYRHIANLANY
>d1e9ia2 d.54.1.1 (A:1-139) Enolase {Escherichia coli}
SKIVKIIGREIIDSRGNPTVEAEVHLEGGFVGMAAAPSGASTGSREALERDGDKSRLGKGVTKAVAANGPIAQALIGKDAKDQAGIDKIMIDLDT
ENKSKGFGANAILAVSLANAKAAAAGMPLYEHIAELNGT
>d1bqg_2 d.54.1.1 (12-143) D-glucarate dehydratase {Pseudomonas putida}
GAPVITDLKVVPGAGHDMSMLNLSGAHGPLTRNILITDSSGHVGVEVPGGEGIRKTLEDARHLLINQSIGNYQSLLNKVRNAFADRDVGGRGLQT
FDLRIAVHAVTAVESALDLLGQHLQVPAALLG
>d1ec7a2 d.54.1.1 (A:5-137) D-glucarate dehydratase {Escherichia coli}
FTTPVVTMQUEVAGHDSMLNLSGAHAPFFTRNIVIKDNSGHTGVGEIPGGEKIRKTLEDAIPLVVGKTLGEYKNVLTVRNTFADRDAGGRGLQ
TFDLRTTIHVVTGIEAMLDLLGQHLGVNVASLLG
>d1fhua2 d.54.1.1 (A:1-99) O-succinylbenzoate synthase {Escherichia coli}
MRSAQVYRWQIPMDAGVVLDRRLKTRDGLYVCLREGEREGWGEISPLPGFSQETWEEAQSVLLAWVNNLAGDCELPQMPSVAFGVSCALAE
LTDTLP
>d1muca2 d.54.1.1 (A:4-130) Muconate-lactonizing enzyme (cis muconate cycloisomerase) {Pseudomonas putida}
ALIERIDAIIVDLPTIRPHKLAMHTMQQQLVLRVRCSDGVEGIGEATTIGGLAYGYESPEGIKANIDAHLAPALIGLAADNINAAMLKLDKLAKGNTF
AKSGIESALLDAQGKRLGLPVSELLGG
>d2mnr_2 d.54.1.1 (3-132) Mandelate racemase {Pseudomonas putida}
EVLTGLRTRAVNPLAYPVHTAVGTVGTAPLVLDLATASAGVVGHSYLFAYTPVALKSLKQLDDMAAMIVNEPLAPVSLEAMILAKRFCLAGYTGLIR
MAAAGIDMAAWDALGKVHETPLVKLLGANAR
>d2chr_2 d.54.1.1 (1-126) Chloroformate cycloisomerase {Alcaligenes eutrophus}
MKIDAIEAVIVDVPTKRPIQMSITTVHQSYIVRVYSEGLVGVEGGSGVGGPVWSAECATIKIIVERYLAPHLLTDAFNVGALQTMARAVTGNA
SAKAADVEMALLDLKARALGVSIAELLGG
>d1jpdx2 d.54.1.1 (X:-2-113) L-Ala-D/L-Glu epimerase {Escherichia coli}
GSHMRTVKVFEEAWPLHTPFVIARGSRSEARVVVELEEEGIGKTGECTPYPRYGESDASVMAQIMSVVPQLEKGLTREELQKILPAGAARNALDCA

LWDLAARRQQQSLADLIGI

>d1jpm2 d.54.1.1 (A:1-125) L-Ala-D/L-Glu epimerase {Bacillus subtilis}

MKIIRIETSRIAVPLTKPKTALRTVTYTAESIVRITYDLSGAVGWGEAPPTLVITGDSMDIESAIHHVLKPALLGKSLAGYEAILHDIQHLLTGNMSAKAA
VEMALYDGWAQMCGLPLYQMLGG

>d1kcza2 d.54.1.1 (A:1-160) beta-Methylaspartase {Clostridium tetanomorphum}

MKIVDVLCPTGLTFYFDDQRAIKKGAGHDGFTYTGSTVTGFTQVRQKGESISVLLVEDGQVAHGDCAAVQYSGAGGRDPLFLAKDFIPVIEKEIA
PKLIGREITNFKPMAEEFDKMTVNGNRLHTAIRYGITQAILEDVAKTRKVTMAEVIRDEYNP

>d1kkoa2 d.54.1.1 (A:1-160) beta-Methylaspartase {Citrobacter amalonaticus}

MKIKQALFTAGYSSFYFDDQQAIKNGAGHDGFIYTGDPVTPGFTSVRQAGECVSVQLILENGAVAVGDCAAVQYSGAGGRDPLFLAEHFIPFLNDHI
KPLLEGRDVDAFLPNARFFDKLRIDGNLLHTAVRYGLSQALLDATAASGRLKTEVCDEWQL

>d1bxe_a_d.55.1.1 (A:) Ribosomal protein L22 {Thermus aquaticus, subsp. Thermus thermophilus}

MEAKAIARYVRISPRKVRLVVDLIRGKSLEARNILRYTNKRGAYFVAKVLESAAAANAVNNHDMILEDRLYVKAAYVDEGPALKRVLPRARGRADIKKR
TSHITVILGEK

>d1jj2q_d.55.1.1 (Q:) Ribosomal protein L22 {Archaeon Haloarcula marismortui}

GISYSVEADPDTTAKAMLRERQMSFKHSKAIAREIKGKTAGEAVDYLEAVIEGDQPVPFKQHNSGVGHKSVDGWDAGRYPEKASKAFDLLEN
GNADHQGFDGEAMTIKHVAHKVGEQQGRKPRAMGRASAWNSPQVDVELILEEP

>d1gd8a_d.188.1.1 (A:) Prokaryotic ribosomal protein L17 {Thermus thermophilus}

SSHRLALYRNQAKSLLTHGRITTVPKAKELRGFVDHLIHLAKRGDLHARRLVLRLQDVKLVRKLFDEIAPRYRDRQGGYTRLKLAERRRGDGAPLA
LVELVE

>d1oela3 d.56.1.1 (A:137-190,A:367-409) GroEL {Escherichia coli}

PCSDSKAIAQVGTISANSDETVGKLLAEMDKVGKEGVITVEDGTGLQDELDVXXERVAKLAGGVAVIKVGAATEVEMKEKKARVEDALHATRAAVE
E

>d1ioka3 d.56.1.1 (A:137-190,A:367-409) GroEL {Paracoccus denitrificans}

PVNDSSEVAQVGTISANGESFIGQQIAEAMQRVGNEGVTVEENKGMETEVEVVXERVAKLAGGVAVIRVGGMTEIEVKERKDRVDDALNATRAA
VQE

>d1a6da3 d.56.1.2 (A:146-214,A:368-403) Thermosome {Archaeon Thermoplasma acidophilum}

TDDATLRKIALTSGKNTGLSNDFLADLVVKAVNAVAEVRDGKIVDTANIKVDKKNNGSVNDTQFISAVSILIRGGTDHVSEVERALNDARVVAI
TKEDGK

>d1a6db3 d.56.1.2 (B:145-215,B:368-403) Thermosome {Archaeon Thermoplasma acidophilum}

GADEKALLKMAQTSLSNSKSASVAKDKLAEISYEAVKSVAELRDGKYVDFDNIQVVKQGGAIDDTQLINXKAVSILVRGETEHVVDEMERSITDSH
VVASALEDG

>d1h6ha_d.189.1.1 (A:) p40phox NADPH oxidase {Human (Homo sapiens)}

AVAQQLRAESDFEQLPDDVAISANIA DIEEKRGFTSHFVFVIEVKTKGGSKYLIYRRYRQFH ALQS KLEERFG PDSKSSA LACTLPTLPAK VYVGKQEA
EMRIPALNAYMKSLLSPVVWVLMDEDVRIFLYQSPYDSEQVP

>d1gd5a_d.189.1.1 (A:) p47phox NADPH oxidase {Human (Homo sapiens)}

GSMGDTFIRHIALLGFEKRFVPSQHYVYMFVWKWQDLSEKVVYRRFTIEYEFHKTLEMFPIEAGAINPENRIIPHLPAPKWFDGQRAAENRQGT
YCSTLMSLPTKISRCPHLLDFFKVRPDDLKP

>d1ji8a_d.203.1.1 (A:) DsrC, the gamma subunit of dissimilatory sulfite reductase {Archaeon Pyrobaculum aerophilum}

MPVKCPGEYQVDGKKVILDEDCFMQNPEDWDEKVAEWLARELEGIQKMTEEHWKLVKYLREYWETFGTCPIKMTKETGFSLEKIYQLFPSGP
HGACKVAGAPKPTGCV

>d1ghha_d.57.1.1 (A:) DNA damage-inducible protein DinI {Escherichia coli}

MRIEVTIAKTSPLPAGAIDALAGELSRRIQYAFPDNEGHVSVRYAAANNLSVIGATKEDKQRISIEILQETWESADDWFVSE

>d1fxd_d.58.1.1 (-) Ferredoxin II {Desulfovibrio gigas}

PIEVNDDCMACEACVEICPDVFEMNEEGDKAVVINPDSLDCEEEAIDSCPAEAIVRS

>d1dura_d.58.1.1 (A:) Ferredoxin II {Peptostreptococcus asaccharolyticus}
AYVINDSCIACGACKPECPVNQIPEGSIYAIADSCIDCGSCASCPVGAPNPED

>d1fca_d.58.1.1 (-) Ferredoxin II {Clostridium acidi-urici}
AYVINEACISCGACEPECVPDAISQGGSRVIDADTCIDCGACAGVCPVDAPVQA

>d2fdn_d.58.1.1 (-) Ferredoxin II {Clostridium acidi-urici}
AYVINEACISCGACEPECVNAISSGDDRYVIDADTCIDCGACAGVCPVDAPVQA

>d1clf_d.58.1.1 (-) Ferredoxin II {Clostridium pasteurianum}
AYKIADSCVSCGACASECPVNAISQGDSIFVIDADTCIDCGNCANCPVGAPVQE

>d1blu_d.58.1.1 (-) Ferredoxin II {Chromatium vinosum}
ALMITDECINCDVCEPECPNGAISQGDETYVIEPSLCTECVGHYETSQCVECPVDCIIKDP SHEETEDELRAKYERITG

>d7fd1a_d.58.1.2 (A:) Ferredoxin {Azotobacter vinelandii}
AFVVTNDNICKYTDCVECPVDCFYEGPNFLVIPHDECIDCALCEPECAPAQAI FSEDEV PEDMQEFIQLNAELAEVWP NITEKKDPLPDAEDWDGV
KGKLQHLER

>d1bc6_d.58.1.2 (-) Ferredoxin {Bacillus schlegelii}
AYVITEPCIGTKDASCVECPVDCIHEGEDQYYIDPDVCIDCGACEAVCPVSAIYHEDFVPEEWKS YIQKNRDFKK

>d1h98a_d.58.1.2 (A:) Ferredoxin {Thermus thermophilus}
PHVICEPCIGVKDQSCVECPVECIYDGDDQFYIHPEECIDCGACVPACPVNAIYPEEDVPEQWKS YIEKNRKL AGL

>d1xer_d.58.1.3 (-) Ferredoxin {Archaeon Sulfolobus sp.}
GIDPNYRTNRQVVGEHSGHKVYGPVEPPKVLGIHGTVGVDFDLCIADGSCINACPVN VFQWYDTPGHPASEKKADPVNEQACIFCMACVNCPV
AAIDVKPP

>d1vjq_d.58.1.4 (-) Ferredoxin {Thermotoga maritima}
MKVRVDADACIGCGVCENLCPDVFQLGDDGKAKVLQPETDLPCA KDAADSCPTGAISVE

>d1fxra_d.58.1.4 (A:) Ferredoxin I {Sulfate-reducing bacteria (Desulfovibrio africanus)}
ARKFYVDQDECIACESC VIEAPGAFAMDPEIEKAYVKDVEGASQEEV EAMTCPVQCIHW EDE

>d1iqza_d.58.1.4 (A:) Ferredoxin {Bacillus thermoproteolyticus}
PKY TIVDKETCIACGAC GAAA PDIYDYDEDGIA YVTLDNNQGIVE VPDI LIDDMMDA FEGCPTDSIKVA DEPF DGNKFE

>d1jb0c_d.58.1.4 (C:) Photosystem I iron-sulfur protein PsaC {Synechococcus elongatus}
AHTVKIYDT CIGCT QCV RACPTD VLEM PWDGCKAGQIA SPRT EDCVGCKRCETACPTD FLSIRVY LGAE T RSMGLAY

>d1feha3_d.58.1.5 (A:127-209) Fe-only hydrogenase, second domain {Clostridium pasteurianum}
KDKE TYV DERSKSL TVDR TKCLL CGRC VNAC GKT NT ETYAM KFLNK NGK TII GA EDE KCF DDTN CLLC GQ CIAC PVA ALSE KS

>d1hfel2_d.58.1.5 (L:2-86) Fe-only hydrogenase larger subunit, N-domain {Desulfovibrio desulfuricans}
SRTVMERIEYEMHTDPKADPDKLHFVQIDEAKCIGCDTCSQYCPTAAIFGEMGEPSI PHIEACINCGQCLTHCPENAIYE AQS

>d1keka5_d.58.1.5 (A:669-785) Pyruvate-ferredoxin oxidoreductase, PFOR, domain V {Desulfovibrio africanus}
TSQFEKRGVAINVPQWV PENCIQCNQCAFVCPHSAILPVLAKEEELVGAPANFTALEAKGKELGYKFRIQINTLDCMCGNCADICPPKEKALVMQ
PLDTQRDAQVPNLEYAARIP

>d1h7wa5_d.58.1.5 (A:845-1017) Dihydropyrimidine dehydrogenase, C-terminal domain {Pig (Sus scrofa)}
ELQGWGDQSPGTESHQKGKP VPRIAELMGKKLPNFGPYLEQRKKIIAE EKMRLKEQNAAFPLLERKPFIPKKPIPAIKDVIGKALQYL GTF GELS NIEQ
VVAVIDEEMCINCGKCYMT CND SGYQAIQFDPELHPLPTVTDCTGCTLCSVCP I IDCIRMV SRTTPYEPKRGL

>d1jnr_b_d.58.1.5 (B:) Adenylylsulfate reductase B subunit {Archaeon Archaeoglobus fulgidus}
PSFVNPEKCDGCKALERTACEYICPNDLMTLDKEKMKAYNREPDMCWECYSCV KMCPQGAIDV RGYVDYSPLGGACVPMRGTS DIMWTVKYRN
GKVLRFKFAIRTT PWGSIQP FEGFPEPTEALKSELLAGEPEIIGTSEFPQVKKKA

>d1d09b1_d.58.2.1 (B:1-100) Aspartate carbamoyltransferase {Escherichia coli}
MTHDNKLQV EA IKRGTV IDH IPA QIGFKLLSLFKLTETDQR ITIGLNLP GEMGRKDLI KENTFLSEDQV DQLALYAPQATVN RIDNYEVVGKSRPSL P

>d2atcb1_d.58.2.1 (B:1-100) Aspartate carbamoyltransferase {Escherichia coli}

MTHNDKLQVAEIKRGTVINHIPAEIGFKLSSLFKLTETQDRITIGLNLPSEMGRKDLIKIENTFLSEDEVDELALYAPQATVNRINDYEVVGKSRPSLP
>d1pca_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Pig (Sus scrofa)}
KEFVGHQVLRISVDEAQVQKVKELEDLEHLQLDFWRGPARGFPIDVRVPFPSIQAVKFLEAHGIRYTIMIEDVQLLDEEQEQQMFASQGR
>d1pyta_d.58.3.1 (A:) Procarboxypeptidase A {Cow (Bos taurus)}
KEFVGHQVLRITAADAEAVQTVKELEDLEHLQLDFWRGPQPGSPIDVRVPFPSIQAVKFLEAHGIRYRIMIEDVQSLLDEEQEQQMFASQSR
>d1aye_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Human (Homo sapiens)}
LETFGDQVLEIVPSNEEQIKNLLQLEAQEHLQLDFWKSPPTPGETAHVRVPFNQAVKFLESQGIAYSIMIEDVQVLLDKENEEMLFNRRR
>d1nsa_2 d.58.3.1 (7A-95A) Procarboxypeptidase B {Pig (Sus scrofa)}
FEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSTVQIKPHSTVDFRVKAEDILAVEDFLEQNELQYEVLINNLRSVLEAQFDSVR
>d1pba_d.58.3.1 (-) Procarboxypeptidase B {Pig (Sus scrofa)}
HHSGEHFEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSTVQIKPHSTVDFRVKAEDILAVEDFLEQNELQYEVLINN
>d1spbp_d.58.3.2 (P:) Subtilisin prosegment {Bacillus amyloliquefaciens}
EKKYIVGFQTMSTMSAAKKKDVISQGGKVEKQFKYVNAAAATLDEKAVKELKKDPGVAYVEEDHIAHEY
>d1scjb_d.58.3.2 (B:) Subtilisin prosegment {Bacillus subtilis}
EKKYIVGFQTMSTMSAAKKKDVISQGGKVEKQFKYVNAAAATLDEKAVKELKKDPGVAYVEEDHIAHEY
>d1itpa_d.58.3.2 (A:) Proteinase A inhibitor 1, POIA1 {Oyster mushroom (Pleurotus ostreatus)}
GSAGKFIVIFKNDVSEDKIRETKDEVIAEGGTITNEYNMMPGMKGFAELTPQSLTKFQGLQGDLIDSIEEDGIVTTQ
>d1mli_d.58.4.1 (-) Muconalactone isomerase {Pseudomonas putida}
MLFHVKMTVKLPVDMMDPAKATQLKADEKELAQRQLQREGTWRHLWRIAGHYANYSVFDVPSVEALHTLMQLPLFPYMDIEVDGLCRHPSSIHD
DR
>d2pii_d.58.5.1 (-) PII (product of glnB) {Escherichia coli}
MKKIDAIKPKLDDVREALAEVGITGMTVTEVKGFGRKHGTELYRGAEMYVDFLPKVIEIVVPDDIVDTCDTIIRTAQTGKIGDGKIFVFDVARVI
RIRTGEEDDAI
>d1gnka_d.58.5.1 (A:) PII-homolog GlnK {Escherichia coli}
MKLVTVIKPKLEDVREALSSIGIQGLTVTEVKGFGRKHGAEYRGAESVNFLPKVKIDVIAADDQLDEVIDIVSKAATGKIGDGKIFVFDVARVI
RTGEADEAAI
>d1nuea_d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo sapiens)}
ANLERTFIAKPDGVQRGLVGEIIKRFEQKGFRVAMKFLRASEEHLKQHYIDLKDRPFFPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPA
DSKPGTIRGDFCIQVGRNIIHGSDSVKAKEISLWFKPEELDYKSCAHDWVYE
>d1ehwa_d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo sapiens), NDK4}
HMGTRERTLVAVKPDGVQRRLVGDVIQRFERRGFTLVGMKMLQAPESVLAEHYQDLRRKPFYPALIRYMSGPVVAMVWEGLNVVKTGRVMLGETNPA
TDSAEAAPGTIRGDFS VHISRNVIHASDSVEGAQREIQLWFQSSELVSW
>d1be4a_d.58.6.1 (A:) Nucleoside diphosphate kinases {Cow (Bos taurus)}
ANSERTFIAKPDGVQRGLMGEIIKRFEQKGFRVAMKFMRASEDLLKEHYIDLKDRPFFAGLVKYMHS GPVVAMVWEGLNVVKTGRVMLGETNPA
ADSKPGTIRGDFCIQVGRNIIHGSDSVESA EKIALWFPEELVNYKS CAQNWIYE
>d1hlwa_d.58.6.1 (A:) Nucleoside diphosphate kinases {Dictyostelium discoideum}
VNKERTFLAVKPDGVARGLVGEIIARYEKKGFLVGLQLVPTKDLAESHYAEHKERPF FGLVSFITSGPVVAMVFEKGKVVASARLMIGVTNPLASA
PGSIRGDFGVDRGRNIIAGSDSVE SANREIALWFKPEELLTVKPNP NLYE
>d1nsqa_d.58.6.1 (A:) Nucleoside diphosphate kinases {Drosophila melanogaster}
AANKERTFIMVKPDGVQRGLVGKIIERFEQKGFKLVALKFTWASKELLEHYADLSARPFFPGLVN YMNSGPV VPMVWEGLNVVKTGRQMLGATN
PADSLPGTIRGDFCIQVGRNIIHGSDAVESAEKIALWFNEKE LVTWT PAAKDWIYE
>d1nhkl_d.58.6.1 (L:) Nucleoside diphosphate kinases {Myxococcus xanthus}
AIERTLSIIKPDGLEKGVIGKIISRFEEKGLKPV A IRLQHLSQA QAE GFYAVHKARPFFKDLVQFMISGPV VLMVLEGENA V LANRD IMGATNP AQAAE
GTIRKDFATSIDKNTVHGSDSLENAKIEIAYFFRETEIH SYPYQ

>d1ha1_1 d.58.7.1 (8-92) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
EPEQLRKLFIGGLSFETTDESLRHFEQWGTLDCCVVMRDPNTKRSRGFGFTYATVEEVDAAMNARPHKDGRVVEPKRAVSRE
>d1ha1_2 d.58.7.1 (99-180) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
AHLTVKKIFVGGIKEDTEEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAVTFDDHDSVDKIVIQKYHTVNGHNCEVRKAL
>d2up1a2 d.58.7.1 (A:99-190) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
GAHLTVKKIFVGGIKEDTEEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAVTFDDHDSVDKIVIQKYHTVNGHNCEVRKALSQEMASAS
>d1fht__ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}
AVPETRPNHTIYINNLNEKIKKDELKKSLYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSATNALRSMQGFPFYDKPMRIQYAKTDSDIIAKMKGTFV
ERDRKREKRKPKSQE
>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)}
AVPETRPNHTIYINNLNEKIKKDELKKSLLHAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSSATNALRSMQGFPFYDKPMRIQYAKTDSDIIAKM
>d2u1a__ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}
MAPAQPLSENPPNHILFLTNLPEETNELMSMLFNQFPGFKEVRVLPGRHIAFVEFDNEVQAGAARDALQGFKITQNNAMKISFAKK
>d1a9nb_ d.58.7.1 (B:) Splicing factor U2B" {Human (Homo sapiens)}
IRPNHTIYINNMNDKIKKEELKRSLYALFSQFGHVVDIVALKTMKMRGQAFVIFKELGSSTNALRQLQGFPFYGKPMRIQYAKTDSDIIKMRG
>d1u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}
ARRLYVGNIPFGITEEAMMDFFNAQMRLGGLTQAPGNPVLAQINQDKNFALEFRSVDETTQAMAFDGIIFQGQSLKIRRPHDYQPLPG
>d2u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}
AHKLFIGGLPNYLNDDQVKELLTSGPLKAFNLVKDSATGLSKGYAFCEYDINVTDQAIAGLNGMQLGDKLLVQRASVGAKNA
>d1b7fa1 d.58.7.1 (A:123-204) Sex-lethal protein {Drosophila melanogaster}
SNTNLIVNYLPQDMTDRELYALFRAIGPINTCRIMRDYKTGYSYGAVIDFTSEMDSQRAIKV LNGITVRNKRKLVSYARPG
>d1b7fa2 d.58.7.1 (A:205-289) Sex-lethal protein {Drosophila melanogaster}
GESIKDTNLYVTNLPRTITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRYNKREEAQEAISALNNVIPEGGSQPLSVRLAEEHGK
>d1sxl__ d.58.7.1 (-) Sex-lethal protein {Drosophila melanogaster}
MSYARPGGESIKDTNLYVTNLPRTITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRYNKREEAQEAISALNNVIPEGGSQPLSVRLAEEHGK
>d1d8za_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}
MDSKTNLIVNYLPQNMTQDEFKSLFGSIGDIESCKLVRDKITGQSLGYGFVNYSDPNDADKAINTLNGLKLQTKTIVSYARPSSASIR
>d1d9aa_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}
DANLYVSGLPKTMSQKEMEQLFSQYGRITSRILLDQATGVSRGVGFIRFDKRIEAAAIGLNGQKPLGAAEPITVKFANNPSQ
>d1fxla1 d.58.7.1 (A:37-118) Hu antigen D (Hud) {Human (Homo sapiens)}
SKTNLIVNYLPQNMTQEERSLFGSIGEIESCKLVRDKITGQSLGYGFVNIDPKDAEKAIINTLNGLRLQTKTIVSYARPS
>d1fxla2 d.58.7.1 (A:119-203) Hu antigen D (Hud) {Human (Homo sapiens)}
SASIRDANLYVSGLPKTMTQKELEQLFSQYGRITSRILVDQVTGVSRGVGFIRFDKRIEAAAIGLNGQKPSGATEPITVKFA
>d1hd1a_ d.58.7.1 (A:) Heterogeneous nuclear ribonucleoprotein d0 {Human (Homo sapiens)}
KMFIGGLSWDTTKKDLKDYFSKFGEVVDFCTLKDPITGRSRGFGVLFKESESVDKVMMDQKEHKLNGKVIDPKRA
>d2msta_ d.58.7.1 (A:) Neural RNA-binding protein Musashi-1 {Mouse (Mus musculus)}
KIFVGGGLSVNTTVEDVKHYFEQFGKVDDAMLMDKTTNRHRGFGFTFESEDIVEKVCIEHFHEINNKMVVECKKA
>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)}
PSLRKSGVGNIFIKNLDKSIDNKALYDTFSAGGNILSCKVVCDENGSKGYGFVHFETQEAAERAIEKMNGMILLNDRKVFGRFKSRKER
>d1qm9a1 d.58.7.1 (A:1-110) Polypyrimidine tract-binding protein {Human (Homo sapiens)}

MGNSVLLS NLNPERVTPQSLFILFGVYGDVQRVKILFNKKENALVQ MADGNQAQLAMSHLNGHKLHGKPIRITSKHQNQLPREGQEDQGLTK
DYGNSPLH RFKKPGS

>d1qm9a2 d.58.7.1 (A:111-198) Polypyrimidine tract-binding protein {Human (Homo sapiens)}

KNFQNIFPPSATLHSNI PPSVSEEDLKVL FSSNGGVVKGF KFFQKDRKMA LIQMGS VEEAVQ ALIDLHNHD LGENHHL RVSFSKSTI

>d1fj7a_d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}

GSHMLED PVEGSE STTPFNLFIGNLNP NKSVAELKVAI SELFAKNDLA VDV RTGTNRKFGYVDFESAED LEKALELTGLKV FGNEIKLEKP KGRDGTR
GC

>d1fjca_d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}

SHMLED PCTS KK VRAART LLA KNLS FNI TEDELKEV FEDALEIR LV SQDGKSKGIAYIEFKSEADA EKNLEE KQGA EIDGRSV SLYTGEKGGTRG

>d1fjeb1 d.58.7.1 (B:1-91) Nucleolin {Golden hamster (Mesocricetus auratus)}

GSHMVEGSE STTPFNLFIGNLNP NKSVAELKVAI SELFAKNDLA VDV RTGTNRKFGYVDFESAED LEKALELTGLKV FGNEIKLEKP KGR

>d1fjeb2 d.58.7.1 (B:92-175) Nucleolin {Golden hamster (Mesocricetus auratus)}

DSKKVRAART LLA KNLS FNI TEDELKEV FEDALEIR LV SQDGKSKGIAYIEFKSEADA EKNLEE KQGA EIDGRSV SLYTGEKG

>d1h6kx_d.58.7.1 (X:) CBP20, 20KDa nuclear cap-binding protein {Human (Homo sapiens)}

KSCT LYVG NLSFY TTEE QIYELFSKSGDI KKIIMGLDKMTAC GFCFVE YS RADA ENAM RYING TRL DDI IRTD W DAG

>d1fo1a2 d.58.7.2 (A:123-191) mRNA export factor tap {Human (Homo sapiens)}

TIPYGRKYDKAWLLSMIQSKCSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRISII

>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)}

SQTIALLNIYRNPNQNSQSADGLRS AVSDVEMQEHYDEFFEEVFTEMEEKYGEVEEMNVCDNLGDHLVGNVYVKFRREEDA EKAVIDLN NRWFNG
QPIAELSP

>d1dbda_d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}

RTTNTDGF HLLKAGGSCF ALISGTANQVKCYRFRVKKNHRHRYENCTTWFTVADNGAERQGQAQILITFGSPSQRQDFLKHVPLPPGMNISGFTA
SLDF

>d2bopa_d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}

SCF ALISGTANQVKCYRFRVKKNHRHRYENCTTWFTVADNGAERQGQAQILITFGSPSQRQDFLKHVPLPPGMNISGFTA SLDF

>d1a7ge_d.58.8.1 (E:) Papillomavirus-1 E2 protein {Human papillomavirus type 31}

ATTP IIHLKG DANI LKCLRYRLSKYKQLYEQVSSTWHWTCTDGKH KNAIVTLTYISTSQRDDFLNTVVIPNTVS VSTGYMTI

>d1by9_d.58.8.1 (-) Papillomavirus-1 E2 protein {Human papillomavirus type 16}

TTPIVHLKG DANTL KCLRYRFKKHCTL YTA VSSTWHWTGH NVKHKSAIVTLTYDSEWQRDQFLSQVKIPKTITVSTGFMS

>d1f9fa_d.58.8.1 (A:) Papillomavirus-1 E2 protein {Human papillomavirus type 18}

HMTPIIHLKGDRNSLKCLRYRLKHSDHYRDISSTWHWTGAGNEKTGILT VTYHSETQRTKFLNTVAIPDSVQILVGYMTM

>d1b3ta_d.58.8.1 (A:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}

KGGWFGKHRGQGGSNPKFENIAEGLR ALLARSHVERTDEGTWVAGVFVYGGSKTSLYNLR GTALAIPQCRLTPLSRLPFGMAPGP GPQGPLRE
SIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPA PTCNIRTVCSFDDGV DLP

>d1vhib_d.58.8.1 (B:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}

PKFENIAEGLR ALLARSHVERTDEGTWVAGVFVYGGSKTSLYNLR GTALAIPQCRLTPLSRLPFGMAPGP GPQGPLRESIVCYFMVFLQTHIFAEV
LKDAIKDLVMTKPA PTCNIRTVCSFDDGV DLP

>d3r ubl2 d.58.9.1 (L:22-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish}

samsun}

LTYYTPEYQTKDILAAFRVTPQPGVPPEAGAAVAESSTGTWTTVWTGLTSDRYKGRCYRIERVGEKDQYIAYVAPLDLFEEGSVTNMFTSI
VGNVFGFKALRALRLEDLRIPPAYVKT

>d1bura2 d.58.9.1 (A:12-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (*Spinacia oleracea*)}

EFKAGVKDYKLTYTPEYETLTDILAAFRVSPQPGVPPEAGAAVAESSTGTWTTVWTGLTNLDRYKGRCYHIEPVAGEENQYICYVAYPLDLFEE
GSVTNMFTSIVGNVFGFKALRALRLEDLRIPVAYVKT

>d1bwva2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

RIKNSRYESGVIPYAKMGYWNPDYQVKDTDVLALFRVTPQPGVPDPIEAAA VAGESSTATWTVVWTDLTAADLYRAKAYKVDQVPPNNPEQYFAYI
AYELDLFEEGSIANLTASIIGNVFGFKAVKALRLEDMLRPLAYLKTFQ

>d1gk8a2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}

TKAGAGFKAGVKDYRLTYTPDYVVRDTDILAAFRMTPQPGVPPECGAAVAEA SSTGTWTTVWTGLTSDRYKGRCYDIEPVPGEDNQYIAYVAY
PIDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDLRIPVAYVKT

>d1bxna2 d.58.9.1 (A:22-150) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}

YKMGYWDGDYVPKDTDLLALFRITPQDGVPDPVEAAA VAGESSTATWTVVWTDLTACDMYRAKAYRVDPVPPNNPEQFFCYVAYDLSLFEEGSIA
NLTAIIIGNVFSFKPIKAARLEDMLRFPVAVVKT

>d1rbla2 d.58.9.1 (A:9-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}

SAAGYKAGVKDYKLTYTPDYTPKDTDLAAFRFSPQPGVPADEAGAAIAAE SSTGTWTTVWTDLTMDRKGKCYHIEPVAGEENSYFAFIAYPLD
LFEEGSVTNILTSIVGNVFGFKAIRSLRLEDIRFPVALVKT

>d5ruba2 d.58.9.1 (A:2-137) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Rhodospirillum rubrum}

DQSSRYVNALKEEDLIAGGEHVLCAYIMKPKAGYGYVATAAHFAAESSTGTWTTVWTDLTDDTRGVDALVYEVDEARELT KIAYPVAFDRNITDGKA
MIASFLTLTMGNQNQGMGDVEYAKMHDFYVPEAYRALFD

>d1geha2 d.58.9.1 (A:12-136) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Archaeon *Thermococcus kodakaraensis*}

YVDKGYEPSKKRDIIAVFRVTPAEGYTIEQAGAVAAE SSTGTWTTLPWYEQERWADLSAKAYDFHDMGDGSWIVRIAYPFHAFEEANLPGLLASIA
GNIFGMKRVKGLRLEDLYFPEKLIREF

>d2acy_ d.58.10.1 (-) Acylphosphatase {Cow (*Bos taurus*)}

AEGDTLISV DYEIFGKVQGVFFRKYTQAEGKKLGLVGWVQNTDQGTVQGQLQGPASKVRHMQEWELETKGSPKSHIDASFHNEKVIVKLDYTDFQI
VK

>d1aps_ d.58.10.1 (-) Acylphosphatase {Horse (*Equus caballus*)}

STARPLKSV DYEVFGRVQGVCFRMYAEDEARKIGVVGWVKNTSKGTVTGQVQGPEEKVNSMKWSLSKVGSPSSRIDRTNFSNEKTISKLEYNSFSV
Y

>d1i1ga2 d.58.37.1 (A:62-141) LprA {Archaeon *Pyrococcus furiosus*}

YSLVTITGVDTKPEKLFVEAKLKEYDFVKELYLSSGDHMIMAVIWAKDGEDLAEIISNKIGKIEGVTKVCPCAIILEKLK

>d1dar_4 d.58.11.1 (600-689) Elongation factor G (EF-G), domains III and V {*Thermus thermophilus*}

VILEPIMRVEVTTPEEYMGDVIGDLNARRGQILGMEPRGNAQVIRAFVPLAEMFGYATDLRSKTQGRGSFVMFFDHYQEVPKQVQEKLK

>d1fnma4 d.58.11.1 (A:404-482) Elongation factor G (EF-G), domains III and V {*Thermus thermophilus*}

VPEPVIDVAIEPPTKADQEQLSQLALARLAEEDPTFRVSTHPETGQTIIISGMGELHLEIIVDRLKREFKVDANVGKPQVA

>d1b64_ d.58.12.1 (-) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Human (*Homo sapiens*)}

MLVAKSSILLDVKPWDDETDMAKLECVRSIQADGLVVGSSKLVPVGYGIKKLQIQCVVEDDKVGTDMLEEQTAFEDYVQSMDVAFNKI

>d1f60b_ d.58.12.1 (B:) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Baker's yeast (*Saccharomyces cerevisiae*)}

PAAKSIVTLDVKWPWDDETNLEEMVANVKAIEMEGLTWGAHQFIPIGFGIKKLQINCVVEDDKVSLDDLQQSIEEDEDHVQSTDIAAMQKL

>d1gh8a_ d.58.12.1 (A:) aEF-1beta {Archaeon *Methanobacterium thermoautotrophicum*}

MGDVVATIKVMPESPVDVLEALKKEIQRPEGTELHKIDEPIAFGLVALNVMVVGDAEGGTEAAEESLSGIEGVSNIEVTDRRLM

>d1b7yb4 d.58.13.1 (B:682-775) Phenylalanyl-tRNA synthetase {*Thermus thermophilus* (*Thermus aquaticus*)}

LAFQDPSRHPAAFRDLAVVVPAPTPYGEVEALVREAAGPYLESALFDLYQGPPLPEGHKSLAFHLRFRHPKRTLDEEVEEAVSRVAEALRAR
>d1jjcb4 d.58.13.1 (B:682-785) Phenylalanyl-tRNA synthetase {Thermus thermophilus (Thermus aquaticus)}

LAFQDPSRHPAAFRDLAVVVPAPTPYGEVEALVREAAGPYLESALFDLYQGPPLPEGHKSLAFHLRFRHPKRTLDEEVEEAVSRVAEALRARGFGLR
GLDTP

>d1loua_d.58.14.1 (A:) Ribosomal protein S6 {Thermus thermophilus}

MRRYEVNIVLPNLDQSQLALEKEIIQRAAENYARVEKVEELGLRLAYPIAKDPQGYFLWYQVEMPEDRVNDLARELRIRDNVRRVMVVKSQEP
F

>d1qjha_d.58.14.1 (A:) Ribosomal protein S6 {Thermus thermophilus}

MRRYEVNIVLPNLDQSQLALEKEIIQRALENYARVEKVALGLMVLAYPIAKDPQGYFLWYQVEMPEDRVNDLARELRIRDNVRRVMVVKS

>d1fjgj_d.58.15.1 (J:) Ribosomal protein S10 {Thermus thermophilus}

KIRKLRGFDHKTLDAASKIVEAARRSGAQVSGPIPLTRVRRTFTVIRGPFKHKSREHFELRTHNRLVDIINPNRKTIQLMTLDLPTGVEIEIKT

>d1fa0a1 d.58.16.1 (A:352-523) Poly(A) polymerase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

NDFFFRYKFYLEITAYTRGSDEQHLKWSGLVESKVRLVMKLEVLAGIKIAHPFTKPFESSYCCPTEDDYEMIQDKYGSHTETALNALKLVTDENKEES

IKDAPKAYLSTMIGLDFNIENKKEKVDIHIPCTEFVNLCRSFNEDYGDHKVFNLALRFVKGYDLPDEVFD

>d1f5aa1 d.58.16.1 (A:365-498) Poly(A) polymerase, C-terminal domain {Cow (Bos taurus)}

PNFFQKYKHYIVLLASAPTEKQRLEWVGLVESKIRILVGSEKNEFITLAHVNPQSFAPKENPDKEEFTMWVIGLVFKKTENSENLSVDTYDIQSFT
DTVYRQAINSCKMFEVDMKIAAMHVKRKQLHQQLP

>d1afj_d.58.17.1 (-) Mercuric ion binding protein MerP {Shigella flexneri}

ATQTVTLAVPGMTCAACPITVKKALKVGTCDISLTNECQVTDNEVTADSIKEIIECGFDCEILRDS

>d1fvqa_d.58.17.1 (A:) Copper transporter domain ccc2a {Baker's yeast (Saccharomyces cerevisiae)}

AREVILAVHGMTCSACTNTINTQLRALKVTKCDISLTNECQVTDNEVTADSIKEIIECGFDCEILRDS

>d1aw0_d.58.17.1 (-) Menkes copper-transporting ATPase {Human (Homo sapiens)}

LTQETVINIDGMTCNSCVQISIEGVISKPGVKSLVSLANSNGTVEYDPLLTSPETLRGAIEDMGFDATLSD

>d1cc8a_d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Baker's yeast (Saccharomyces cerevisiae)}

AEIKHYQFNVMTCGCSGAVNKVLTKLEPDVSKIDISLEKQLVDVYTTLPYDFILEKIKKTGKEVRSGKQL

>d1fe0a_d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Human (Homo sapiens), HAH1}

PKHEFSVDMTCGGCAEAVSRVLNLGGVKYDIDLPNKKVCISEHSMDTLLATLKKTGKTVSYLGL

>d1cpza_d.58.17.1 (A:) Copper chaperone {Enterococcus hirae}

AQEFSVKGMSCNHCVARIEEAVGRISGVKKVKVQLKEKAVV/KFDEANVQATEICQAINELGYQAECI

>d1k0va_d.58.17.1 (A:) Copper chaperone {Bacillus subtilis, CopZ}

MEQKTLQVEGMSCQHCVKAVETSVGELDGSAHVNLLEAGKVDVSFDADKVSVDIADAIEDQGYDVAKIEGR

>d1qupa2 d.58.17.1 (A:2-73) Copper chaperone for superoxide dismutase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

TTNDTYEATYAIPMHENCVCNDIKACLNVPGINSLNFDIEQQIMSVESSVAPSTIINTLRNCGKDAAIRGA

>d1gmua2 d.58.38.1 (A:71-138) Urease metallochaperone UreE, C-terminal domain {Klebsiella aerogenes}

DEEVSVVRCDDPFMLAKACYALGNRHVPLQIMPGELEYHHDHVLDMLRQFGLTVFGQLPFEPEAGA

>d1eara2 d.58.38.1 (A:75-142) Urease metallochaperone UreE, C-terminal domain {Bacillus pasteurii}

LEKVVVIKPQTMQEMGKMAFEIGNRHTMCIIEDDEILVRYDKTLEKLIDEVGVSYEQSERRFKEPKY

>d1psda3 d.58.18.1 (A:327-410) Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain {Escherichia coli}

FPEVSLPLHGGRRLMHIHENRPGVLTAALKFAEQGVNIAAQYLQTSQMGGYVVVIDIEADEDVAEKALQAMKAIPGTRARLLY

>d1tdj_2 d.58.18.2 (336-423) Allosteric threonine deaminase C-terminal domain {Escherichia coli}

QREALLAVTIPEEKGSFLKCQLLGRSVEFNYRFADAKNACIFVGVRSLRGLEERKEILQMLNDGGYSVVDLSDDEMAKLHVRYMV

>d1tdj_3 d.58.18.2 (424-514) Allosteric threonine deaminase C-terminal domain {Escherichia coli}

GGRPSHPLQERLYSFEFPESPGLLNLGTYWNISLFHYRSHGTDYGRVLAFFELGDHEPDFETRLNELGYDCHDETNNPAFRFLAG

>d1phza1 d.58.18.3 (A:19-115) Phenylalanine hydroxylase N-terminal domain {Rat (Rattus norvegicus)}

GQETSYIEDNSNQNGAISLIFSLKEEVGALAKVRLFEENDINLTHIESRPSRLNKDEYFFTYLDKRTKPVLGSIIKSLRNDIGATVHELSRDKEK

>d1cg2a2 d.58.19.1 (A:214-326) Carboxypeptidase G2, dimerisation domain {Pseudomonas sp., strain rs-16}

SGIAYVQVNITGKASHAGAAPELVNALVEASDLVRLTMNIDDKAKNLRFNWTIAKAGNVSNIPASATLNADVRYARNEDFDAAMKTLEERAQQK
KLPEADVKVIVTRGRPA

>d1dqaa1 d.58.20.1 (A:587-703) NAD-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

GMTRGPVVRPLRACDSAEVKALETSEGFAVIKEAFDSTSFRARLQLHTSIAGRNLYIRFQSRSGDAMGMNMISKTEKALSKLHEYFPEMQILAV
SGNYCTDKPAAINWIEGRG

>d1qaxa1 d.58.20.1 (A:111-220) NAD-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

LMHAQVQIVGIQDPLNARLSLLRKDEIELANRKDQLLNSLGGGCRDIEVHTFADTPRGPMVAHLIVDVRDAMGANTVNTMAEAVAPLMEAITG
GQVRLRILSNLADL

>d1ekra_d.58.21.1 (A:) Molybdenum cofactor biosynthesis protein C, MoaC {Escherichia coli}

GEAHMVDVSAAKETVREARAEEFVTMRSETLAMIIDGRHHKGDFVATARIAQIAAKRTWDLIPLCHPLMLSKEVNLQAEPHNVRRIETLCRLTG
KTGVEMEALTAASVAALTYDMCKAVQKDMVIGPVRLAKSGGKSGDFK

>d1f3va_d.58.22.1 (A:) TRADD, N-terminal domain {Human (Homo sapiens)}

HEEWVGSAVLVFESSLDKVVLSDAYAHPPQQKVAVYRALQAALESGGSPDVQMLKIHRSDPQLIVQLRFCGRQPCGRFLRAYREGALRAALQRSLA
AALAQHSVPLQLELRAGAERLALLADEERCLSCILAQQPDLRDEELAELEDALRNLLCG

>d1mla_2 d.58.23.1 (128-197) Probable ACP-binding domain of malonyl-CoA ACP transacylase {Escherichia coli}

GTGAMAAIIGLDDASIAKACEEEAEGQVSPVNFNSPGQVVIAGHKEAVERAGAACAKRALPLPV

>d1ffgb_d.58.24.1 (B:) CheY-binding domain of CheA {Escherichia coli}

PRIILSRLKAGEVDLLEELGHLTTLTDVVKGADSLSAILPGDIAEDDITAVLCVIEADQITFETV

>d1kp6a_d.58.25.1 (A:) Killer toxin KP6 alpha-subunit {Smut fungus (Ustilago maydis)}

NNAFCAGFGLSCKWECWCTAHGTGNERYATAAGCGDHLSKSYYDARAGHCLFSDDLRLNQFYSHCSSLNNNMSCRSLSK

>d1h72c2 d.58.26.1 (C:168-300) Homoserine kinase, C-terminal domain {Archaeon Methanococcus jannaschii}

FKLDILIAIPNISINTKEAREILPKAVGLKDLVNNVGKACGMVYALYNKDKSLFGRYMMMSDKVIEPVRGKLIPNYFKIKEEVKDKVYGITISGSGPSIIAFPK
EEFIDEVENILRDYYENTIRTEVGKGVVEV

>d1fi4a2 d.58.26.2 (A:191-393) Mevalonate 5-diphosphate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

QMKAICLVVSDIKKDVSTQGMQLTVATSELFKERIEHVVPKRFEVMRKAIVEKDFATFAKETMMDNSFATCLDSFPPIFYMNDTSKRIISWCHTI
NQFYGETIVAYTFDAGPNNAVLYLAENESKLFAFIYKLFGSVPGWDKKFTTEQLEAFNHQFESSNFTARELDLELQKDVARVILTQVGSGPQETNESLID
AKTGL

>d1regx_d.58.27.1 (X:) Translational regulator protein regA {Bacteriophage T4}

MIEITLKKPEDFLKVKETLTRMGIANNKDKVLYQSCHILQKGLYYIVHFKEMLRMDGRQVEMTEDEVRRDSIAWLLEDWGLIEIVPGQRTFMKDLT
NNFRVISFKQKHEWKLVPKYTIGN

>d1fvga_d.58.28.1 (A:) Peptide methionine sulfoxide reductase {Cow (Bos taurus)}

KIVSPQEALPGRKEPLVVAAKHHVNGNRTVEPFPEGTQMAVFGMCFWGAERKFVTLKGVYSTQVGAGGYTPNPTYKEVCSGKTGHAEVRRVV
FQPEHISFEELLKVFWENHDPTQGMRQGNDHGSQYRSAIYPTSAEHVGAALKSKEDYQKVLEHGFGLITTDIREGQTFYYAEDYHQQYLSKDPDGY
C

>d1ff3a_d.58.28.1 (A:) Peptide methionine sulfoxide reductase {Escherichia coli}

SLFDKKHLVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMEIAIFAMGCFWGVERLFWQLPGVYSTAAGYTGGYTPNPTYREVCSDGTGHAE
AVRIVYDPSVISYEQLLQFWENHDPAQGMRQGNDHGTQYRSAIYPLTPEQDAARASLERFQAAMLAADDRHITTEIANATPFYYAEDDHQQYLHK
LHKNPYGYCGIGGIGVCLPPEA

>d1ff3c_d.58.28.1 (C:) Peptide methionine sulfoxide reductase {Escherichia coli}

LVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMEIAIFAMGCFWGVERLFWQLPGVYSTAAGYTGGYTPNPTYREVCSDGTGHAEAVRIVYD
PSVISYEQLLQFWENHDPAQGMRQGNDHGTQYRSAIYPLTPEQDAARASLERFQAAMLAADDRHITTEIANATPFYYAEDDHQQYLHK

>d1azsa_d.58.29.1 (A:) Adenylyl cyclase VC1, domain C1a {Dog (Canis familiaris)}

DMMFHKIYIQKHDNVSLFADIEGFTSLASQCTAQELVMTLNELARFDKLAENHCLRIKILGDCYYCSDLPEARADHAHCCVEMGMDMIEAISLV
REMTGVNVNMRVGIHSGRVHCGLRKWQFDVWSNDVTANHMEAGGAKAGRIHITKATLSYNGDYVEPGCGGERNAYLKEHSIETFLIL

>d1azsb_d.58.29.1 (B:) Adenylyl cyclase IIC1, domain C2a {Rat (Rattus norvegicus)}

HQSYDCVCVMFASIPDFKEFYTESDVNKEGLECLRLLNEIIADFDDLLSKPKFSGVEKIKTIGSTYMAATGLSAIPSQEHAQEPEHQYMHIGTMVEFAYA
LVGKLDAINKHSFNDFKLRVGINHGPVIAGVIGAQPQYDIWGNTVNVASRMDSTGVLDKIQLQVTEETSLILQTLGYTCRGIINVKGKDLKTYFVNT

>d1fx2a_d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma brucei), different isoform}

NNNRAPKEPTDPVTILIFTDIESSTALWAAHPDLMPDAVAAHHRMVRSLIGRYKCYEVKTVGDSFMIASKPFAAVQLAQELQLCFLHHDWGTNALD
DSYREFEEQRAGECEYTPPTAHMDPEVYSRLWNLRLRVGIHTGLCDIRHDEVTKGYDYYGRTSNMAARTESVANGQQVLMTHAAYMSLSAEDR
KQIDVTALGVALRGVSDPVKMYQLNTVPSRNFAALRLDREYFD

>d1fx4a_d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma brucei), different isoform}

DNDsapKEPTGPVTLIFTDIESSTALWAAHPDLMPDAVATHHRLIRSLITYECYEVKTVGDSFMIASKPFAAVQLAQELQLCFLRLDWETNAVDESY
REFEEQRAGECEYTPPTASLDPEVYSRLWNLRLRVGIHTGLCDIRHDEVTKGYDYYGRTSNMAARTESVANGQQVLMTHAAYMSLSGEDRNQL
DVTTLGATVLRGVPEPVRMYQLNAVPGRNFAALRLDR

>d1eqoa_d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK {Escherichia coli}

TVAYIAIGSNLASPLEQVNAAALKALGDIPESHILTSSFYRTPPLGPQDQPDYLNAAVALETSLAPEELLNHTQRIELQQGRVRKAERWGPRTLDDIML
FGNEVINTERLTVPHYDMKNRGFMLWPLFEIAPELVPDGEMLRQILHTRAFDKLNKWF

>d1cbka_d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase, HPPK {Haemophilus influenzae}

MITAYIALGSNLNTPVEQLHAALKAIQLSNTHLTTSSFYKSPLGPQDQPDYVNAVAKIETELSPKLDELQRIENEQGRVRLRRWGERTLDDILY
GNEIIQNERTLIPHDMHNREFVIVPLFEIASDLVLPNSQIITELVKQFADHKMIKLNPF

>d1gpja3 d.58.39.1 (A:1-143) Glutamyl tRNA-reductase catalytic, N-terminal domain {Archaeon Methanopyrus kandleri}

MEDLVSVGITHKEAEVEELEKARFESDEAVRDIVESFGLSGSVLLQTSNRVEVYASGARDRAEELGDLIHDDAWVKRGSEAVRHLFRVASGLESMMV
GEQEILRQVKKAYDRAARLGLTDEALKIVFRRAINLGKRAREETRI

>d1hbnc_d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanobacterium thermoautotrophicum}

AQYYPGTTKVAQNRRNFCNPEYELEKLRISDEDVVKILGHRAPGEEYPSVHPPLEEMDEPEDAIREMVEPIDGAKAGDRVRYIQFTDSYFAPAQPM
YVRSRAYLCRYRGADAGTLSGRQIETRERDLEKISKELETEFFDPARSGVRGKSVGHSLRLEDGMMFDMLRRQIYNKDTGRVEMVKNQIGDEL
DEPVDLGEPLETLMEKTTIYRVDGEAYRDDVEAVEIMQRIHVLSQGGFN

>d1e6vc_d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanopyrus kandleri}

FYYPGETDVAENRRKYMNPNEYELKKLREIPDEDIVRLMGHREPGEEYPSVHPPLEEMEEPECPIRELVEPTEGAKAGDRIRYIQFTDSYFAPIHPYIRAM
RMYMWRYRGVDTGSLSGRQIIEVRERDLEKIAKELLETIEFDPARSGVRGATVGHALRLDENGLMLHALRRYRLNEETGEVEYVKDQVGIELDEPIP
VGAPADEDLKERTTIYRIDLGYPREDEELLQVQVQRIHELRTLAGYRPEE

>d1e6yc_d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanoscincus barkeri}

AYERQYYPGATSAANRRKHMMSGKLEKLREISDEDLTAVLGHRAPGSDYPSTHPPLAEMGEpacstrenvaatpgaaagdrvryiqfadsmynapat
PYFRSYFAAINFRGVDPGTLSGRQIVEARERDMEQCAKVQMETEITDHAGVRGATVHGHSVRLQEDGVMFDMLRRRENGTIIMDKDQVAIP
LDRKVDLGKPMSSSEAARKTTIYRVDNVAFRDDAEVVEWVHRIFDQRTKFGFQPK

>d1hbna2_d.58.31.2 (A:2-269) Alpha chain {Archaeon Methanobacterium thermoautotrophicum}

ADKLFINALKKFEESPEEKTTFTLGGWKQSERKTEFVNAGKEVAKRGIPQYNPDIGTPLGQRVLMPYQVSTTDYVEGDDLHFVNNAAMQQMW
MWDDIRRTVIVGLNHAHAVIEKRLGKEVTPETITHYLETVNHAMPAAVQEHMVETHPALVADSYVKVFTGNDEIADEIDPAFVIDINKQFPEDQ
AETLKAEVGDDGIWQVVRIPITVSRTCAGTTSRWSAMQIGMSMISAKQAAGEATGDFAYAAKHAEVIMGTLPV

>d1e6va2_d.58.31.2 (A:8-272) Alpha chain {Archaeon Methanopyrus kandleri}

LFMKALKEKFEESPEEKYTKYIFGGWKQSERKKEFWADKIVEERGVPHYNPDIGVPLGQRKLMQVSGTDVFVEGDDLTNFVNNAAMQQMW
DDIRRTVIVGMFTAHRVLERRLGKEVTPETINEYMETLNHALPGGAVVQEHMVIEHPLTWDCYAKIITGDELADEIDDKFLDIEKLFPEEQAEQLIK
AIGNRTYQVCRMPTIVGHVCDGATMYRWAAMQIAMSIFICAYKIAAGEAAVSDFAFASKHAEVINMGEMLP

>d1e6ya2_d.58.31.2 (A:1002-1283) Alpha chain {Archaeon Methanoscincus barkeri}

AADIFSKFKKDMEVKFAQEFGSNKQTGGDITDKTAKFLRLGPEQDPRKVEMIKAGKEIAEKRGIAFYNPMMHSGAPLGQRAITPYTISGTDIVCEPDD
LHYVNNAAMQQMWDDIRTCIVGLDMAHETLEKRLGKEVTPETINHYLEVNHAMPGAAVVQEMMVETHPALVDDCYVKVFTGDDALADEIDK
QFLIDINKEFSEEQAAQIKASIGKTWSQAIHIPTIVSRRTDGAQTSRWAAMQIGMSFISAYAMCAGEAAVADLSFAAKHAALVSMGEMLPA
>d1hbzb2 d.58.31.2 (B:2-188) Beta chain {Archaeon Methanobacterium thermoautotrophicum}
AKFEDKVDLYDDRRGNLVEEQVPLEALSPLRNPAIKSIVQGIKRTVAVNLEGENALKTAKVGGPACKIMGRELDLIVGNAESIAAAKEMIQVTEDDD
TNVELLGGGKRALVQVPSARFDVAEYSAAPLTATAFVQAIINEFDVSMYDANMVKAALVGRYPQSVEYMGANIATMLDIPQKLEG
>d1e6vb2 d.58.31.2 (B:7-189) Beta chain {Archaeon Methanopyrus kandleri}
DTVVDLYDDRGNCVAEEVPIEVLSMRNEAIQSIVNDIKRTVAVDLEGINALQNATVGGKGMKIPGREMDVDIVDNAEAIADEIEKMRVYQDDDTN
VEPMYDGKRLLVLPSERVKMADPVSGTLQAGMAVHAIIDVCEVDMWDANMVKAAVFGRYPQTIDYFGGNVASMLDVPMKQEGV
>d1e6yb2 d.58.31.2 (B:2002-2185) Beta chain {Archaeon Methanosaeca barkeri}
SDTVDIYDDRGKLLESNVDIMSLAPTRNAAIQSIIIMDTKRSVAVNLAGIQGALASGKMGKGRLQILGRGLNYDIVGNADAIAENVKKLVQVDEGDDT
NVIKVGGKSLLIQSPKSRIIAGADFMSATTVGAAAVTQTIMDMFGTDPYDAPIVKSAVWGSYPQTMDLMGGQVQGILSIPQNNNEGL
>d1e8ga1 d.58.32.1 (A:274-560) Vanillyl-alcohol oxidase {Fungus (Penicillium simplicissimum)}
GGYQSYLITPLPKDGLKQAVDIIRPLRLGMALQNVPTIRHILDAAVLGDKRSYSSRTEPLSDEELDKIAKQLNLGRWNFYGALYGPPIRRLWETIKD
AFSAIPGVKFYFPEDTPENSVLVRDKTMQGIPTYDELKWIDWLPGNGAHFFSPIAKVSGEDAMMQYAVTKKRCQEAGLFIGTFTVGMREMHHI
VCIVFNKKDLIQKRKVQWLMRTLIDDCAANGWGEYRTHLAFMDQIMETYNNNSFLRFNEVLKNAVDPNGIIAPGKSGVWPSQYSHVTWKL
>d1dqa1 d.58.32.1 (A:243-521) Flavoprotein subunit of p-cresol methylhydroxylase {Pseudomonas putida}
PVFKPFEVIFEDAEATIVEIVDALPLRMSNTIPNSVVIASLWEAGSAHLTRAQYTTEPGHTPDVKQMQKDTGMGAWNLYAALYGTQEQQDVNW
KIVTDVFKKLGKGRIVTQEEAGDTQPFKYRAQLMSGVPNLQEFGLYNWRGGGGSMWFAPVSEARGSECKQAAMAKRVLHKYGLDYVAEFIVAPR
DMHHVIDVLYDRTNPEETKRADACFNLDEFEKEGYAVYRVNTRFQDRVAQSYGPVKRKLEHAIKRAVDPNNILAPGRSGIDLNNDF
>d1f0xa1 d.58.32.2 (A:274-567) D-lactate dehydrogenase {Escherichia coli}
KNQQVFIYGTNQPEVLTEIRRHLANFENLPVAGEYMHARDIYDIAEKYGKDFTLMIIDKLGTDKMPFFNLKRTDAMLEVKKFRPHFTDRAMQKFG
HLPFSHLPPRMKNWRDKYEHHLKKMAGDGVGEAKSWLVDFKQAEGLFFVCTPEEGSKAFLHRFAAAGAACIRYQAVHSDEVEDIALDIALRRND
TEWYEHPPEIDSQVLVHKLYGHFMCYVFHQDYIVKKGVDVHALKEQMILELLQQRGAQYPAEHNVGHLYKAPETLQKFYRENDDPTNSMNPNGIKT
SKRKNW
>d1i19a1 d.58.32.3 (A:274-613) Cholesterol oxidase {Brevibacterium sterolicum}
FRQRCQSYTDIPWRELFAPKGADGRTFEKVAESGGAEIWYPFTEKPWMKVWTSPTKPDSSNEVGLSAGSLVGKPPQAREVSGPYNYIFSDN
LPEPITDMIGAINAGNPGIAPLFGPAMYEITKGLAATNANDIWGWSKDVQFYIKATTLLTEGGGAVVTSRANIAVINDTEWFHERIEFYRAKGEF
PLNGPVEIRCCGLDQAADVVKVPSVGPPTISATRPRPDHPDWVAIWLNLGVPGTPGMFEFYREMEQWMRSHYNNDDATFRPEWSKGWAFGP
DPYTDNDIVTNKMRATYIEGVPTTENWDTARARYNQIDPHRVTNGFMDKLL
>d1ftra1 d.58.33.1 (A:1-148) Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon Methanopyrus kandleri}
MEINGVEIEDTFAEAFAEKMARVLITAASHKWAMIAVKEATGFGTSVIMCPAEAGIDCGYVPPEETDGRPGVTIMIGHNDEDELKEQLDRIGQCV
MTAPTAASFADAMPEAKEDEDRVGYKLSFFGDGYQEEDELGRKVWVW
>d1ftra2 d.58.33.1 (A:149-296) Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon Methanopyrus kandleri}
EGEFIVEDSFGITTGVAGGNFYIMAESQPAGLQAAEAAVDAIKGVVEGAYAPFPGGIVASASKVGSQYDFLPASTNDAYCPTVEDNELPEGVKCVYEIV
INGLNEEAVKEAMRVGIEAACQQPGVVKISAGNFGGKLGQYEIHLHDLF
>d1qd1a1 d.58.34.1 (A:2-180) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}
SQLVECPNFSEGKNQEVIDAISRAVAQTPGCVLLVDSPGPNRTVYTFGRPEDVVEGALNAARAAYQLIDMSRHGEHPRMGALDVCPIPVR
GVTMDECVRCAQAFGQRRAEELGVPVLYGEAARTAGRQSLPALRAGEYEALPEKLQAEWAPDFGPSAFVPSWGATVAGARK
>d1qd1a2 d.58.34.1 (A:181-326) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}
FLLAFNINLLSTREQAHRIALDLREQGRGKDQPGPRLKKVQAIGWYLDEKNLAQVSTNLLDFEVTLHVTFEETCREAQELSPLVVGSQLVGLVPLKALL
DAAAFYCEKENLFLLQDEHRIRLVLVNRGLDSLAPFKPKERIIYLV

>d1djoa1 d.58.35.1 (A:7-114) Pseudouridine synthase I {Escherichia coli}
PPVYKIALGIEYDGSKYYGWQRQNEVRSVQEKEKALSQVANEPIVFCAGRTDAGVHGTGQVVFETTALRKDAAWTLGVNANLPGDIARWVK
TVPDDFHARFSAT

>d1djoa2 d.58.35.1 (A:115-270) Pseudouridine synthase I {Escherichia coli}
ARRYRYIIYNHRLRPAVLSKGVTHFYEPLDAERMHRAAQCLLGENDFTSFRAVCQCSRTPWRNVMHINVTRHGPYVVVDIKANAFVHHMVRNIVG
SLMEVGAHNQPESWIAELLAAKDRTLAAATAKAEGLYLVAVDYPDRYDLPKPPMGPLFLAD

>d1k8wa1 d.58.35.2 (A:9-73) Pseudouridine synthase II TruB {Escherichia coli}
MDINGVLLDKPQGMSSNDALQKVRIYNANRAGHTGALDPLATGMLPICLGEATKFSQYLLSD

>d1k8wa2 d.58.35.2 (A:74-312) Pseudouridine synthase II TruB {Escherichia coli}
KRYRVIARLGQRTDTSADGQIVEERPVTFAEQLAAALDTFRGDIEQIPSMYSALKYQGKKLYEYARQGIEVPREARPITVYELLFIRHEGNELEIHC
SKGTYIIRTIIDLGKLGCGAHVIYLRLRAVSKPVERMVTLERHLRELVEQAEEQQDIPAAELLDPLMPMDSPASDYPVVLNLPTSSVYFKNGNPVRTS
GAPLEGLVRVTEGENGKFIGMGEIDDEGRVAPRRLVVEY

>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}
IGWVKGIDDNWHLTFIENGRILDYPARPLKTGLLEIAKIHKDFRITANQNLIAGVPESEKAKIEKIAKESGLMNAVT

>d1bxya_ d.59.1.1 (A:) Prokaryotic ribosomal protein L30 {Thermus thermophilus}
MPRLKVKLVKSPIGYPKDQKAALKALGLRLQQERVLEDTPAIRGNVEVAHLVRVEVVE

>d1jj2v_ d.59.1.1 (V:) Archaeal L30 (L30a) {Archaeon Haloarcula marismortui}
MHALVQLRGEVNHMHTDIDQDTLEMLNIHHVNHC TLV PETDAYRGMVAKVNDVAFGEPSQETLETVLATRAEPLEGGDADVDEWVAEHTDYDDIS
GLAFALLSEETTLREQGLSPTLRLHPPRGGHGDGVKHPVKEGGQLGKHDT EGIDDLLEAMR

>d1fw9a_ d.190.1.1 (A:) Chorismate lyase {Escherichia coli}
SHPALTQLRALRYSKEIPALDPQLLDWLLEDSTMKRFEQQGKTVSVMIREGFVEQNEIPEELPLPKESRYWLREILLSADGEPWLAGRTVVSTL
SGPELALQKLKGKTPLGRYLFSTSSTLDRFIEGRDAGLWGRRSRLRSGKPLLTELFLPASPLY

>d1bowa_ d.60.1.1 (A:) Multidrug-binding domain of transcription activator BmrR {Bacillus subtilis}
RLGEVFVLDEEEIRIIQTEAEGIPENVLNASYSKLKKFIESADGFTNNSYGATFSQPYTSIDEMTYRHIFTVLTNKQISSITPDMEITTPKGRYACIAYN
FSPEHYFLNLQKLKYIADRQLTVVSDVYELIIPIHYSPPKQEEYRVEMKIRL

>d1d5ya3 d.60.1.2 (A:122-294) Rob transcription factor, C-terminal domain {Escherichia coli}
EFTMPEHKFVTLEDTPLIGVTQSICLQISDFRHEMRYQFWHDFLGNAPTIPPVYGLNETRPSQDKDDEQEVFYTALAQDQADGYVLTGHPV
MLQGGEYVMFTYEGLGTGVQEFLTVYGTCPMLNLRKGQDIERYYPAEDAKAGDRPINLCELLPIRRKLA

>d1jh6a_ d.61.1.1 (A:) tRNA splicing product Appr>p cyclic nucleotide phosphodiesterase {Thale cress (Arabidopsis thaliana)}
MEEVKKDVSVALPDESEPRFKKLMEALRSEFTGPRFVPHVTAVSAYLTADAEKKMFESACDGLKAYTATDRVSTGFFQCVFLLLQTTPPEVM
EAGEHCKNHFNCTTYPMPHLSLLYAELEEEKKNAQEKA YTLSSLGDSFLNRALCKTDTEDKTLETWETVAVCNLNP

>d1f32a_ d.62.1.1 (A:) Pepsin inhibitor-3 {Pig roundworm (Ascaris suum)}
FLFSMSTGPFICTVKDNQVFVANLPWTMLEGDDIQVGKEFAARVEDCTNVKHDMAPTCTKPPFCGPQDMKMFNFVGCSVLGNKLFIDQKYVRD
LTAKDHAEVQTFREKIAAFEEQQENQPPSSGMPHGA PAGGLSPPPPSFCTV

>d1d8ia_ d.63.1.1 (A:) mRNA triphosphatase CET1 {Baker's yeast (Saccharomyces cerevisiae)}
HMYRNVPWAQWKPTIKALQSIINVKDLKIDPSFLNIPDDDLTKSVQDWYATIYISAPELRSFIELEMKFGVIIDAKGPDRVNPPVSSQCVFTELDAH
LTPNIDASLFKELSKYIRGISEVTENTGKFSIIESQTRDSVYRVLSTQRPRFLRMSTDIKTRGVGQFIEKRHVAQLLLYSPKDSYDVKISLNLELPVDNDP
PEKYKSQSPISERTKDRVSYIHNDSCTRIDITKVENHNQNSRSQSETTHEVELEINTPALLNAFDNITNDSKEYASLIRFLNNGTIIRRKLSSLY

>d2if1_ d.64.1.1 (-) Eukaryotic translation initiation factor eIF-1 (SUI1) {Human (Homo sapiens)}
MRGSHHHHHTDPMSSAIQNLHSFDPFADASKGDDLLPAGTEDYIHIRIQQQRNGRKLT TVQGIADDYDKKKLVCAFKKFACNGTVIEHPEYGEVIQ
LQGDQRKNICQFLVEIGLAKDDQLKVHGF

>d1d1ra_ d.64.1.1 (A:) YciH {Escherichia coli}

KGDGVVRIQRQTSGRKKGKVCLITGVDLDDAELTKLAAELKKCGCGAVKDGVICEIQGDKRDLKSLEAKGMKVLAGGLE
>d1lbu_2 d.65.1.1 (84-213) Zn²⁺ DD-carboxypeptidase, C-terminal, catalytic domain {Streptomyces albus G}
VNFTYAELNRCNSDWGGKVSAAATARANALVTMWKLQAMRHGDKPITVNGGFRSVCNSVGGASNSRHMYGHAADLGAGSQGFCALAQA
AARNHGFTEILGPYPGPHNDHTHVAGGDGRFWSAPSCGI
>d1vhb__ d.65.1.2 (-) Sonic hedgehog {Mouse (Mus musculus)}
KLTPPLAYKQFIPNVAEKTGLASGRYEGKITRNSERFKELTPNYPDIIFKDEENTGADRLMTQRCKDKLNALAVISVMNQWPGVKLRVTEGWDEDGH
SEESLHYEGRADVDTTSRDRSKYGMILARLAVEAGFDWVYYYESKAHIHCSVKAENSVAAK
>d1qf6a2 d.66.1.1 (A:2-62) Threonyl-tRNA synthetase (ThrRS), N-terminal 'additional' domain {Escherichia coli}
PVITLPDGSQRHYDHAVSPMDVALDIGPLAKACIAGRNGELVDACDLIENDAQLSIIA
>d1fjgd_ d.66.1.2 (D:) Ribosomal protein S4 {Thermus thermophilus}
GRYIGPVCRLCRREGVKLYLKGERCYS PKCAMERRPPGQHGQKRARRPSDYAVRLREKQKLRIYGISERQFRNLFEASKKGVTGSVFLGLLESRL
DNVVYRLGFAVSRQRQARQLVRHGHTVNGRRVDPYRVRPGDEIAVAEKSRNLEIRQNLEAMKGRKVGPWLSLDVEGMKGKFLRPLDREDLALP
VQENLVIEFYSR
>d1c06a_ d.66.1.2 (A:) Ribosomal protein S4 {Bacillus stearothermophilus}
MKLSEYGLQLQEKKQKLRHMYGVNERQFRKTTEEAGKMPGKHGENFMILLESRLDNLVRLGLARTRRQARQLVTHGHILVDGSRVNIPSYRVKPGQ
TIAVREKSRLNQVIKEALEANNYIPDLSFDPEKMEGYTRLPERSELPAEINEALIVEFYSR
>d1dm9a_ d.66.1.3 (A:) Heat shock protein 15 kD {Escherichia coli}
PAVEVRLDKWLWAARFYKTRALAREMIEGGKVHYNGQRSKPSKIVELNATLTLRQGNDERTVIVKAITEQRRPASEAALLYETAESVEKREKMALAR
KLNALT
>d1qf6a3 d.67.1.1 (A:63-241) Threonyl-tRNA synthetase (ThrRS), second 'additional' domain {Escherichia coli}
KDEEGLEIIRHSCAHLGHAIKQLWPHTKMAIGPVIDNGFYYDVLDLRTLTQEDVEALEKRMHELAEKNYDVIKKVSWEARETFANRGESYKVSI
DENIAHDDKPGLYFHEEYDMCRGPHVNMRFCHHFKLMKTAGAYWRGDSNNKMLQRIYGTAWADKKNALNQRLEEA
>d1f7ua3 d.67.2.1 (A:2-135) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Baker's yeast (Saccharomyces cerevisiae)}
ASTANMISQLKKLSIAEPAVAKDSHPDVNIVDLMRNYISQELSKISGVDSLIFPALEWTNTMERGDLIPIPRRIKGANPKDLAVQWAEKFCGDFLE
KVEANGPFIQFFFNPQFLAKLVIPDILTRKEDY
>d1iq0a3 d.67.2.1 (A:1-96) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Thermus thermophilus}
MLRRALEEIAQALKEMGVPMVRLKVARAPKDCKPGDYGVPLFALAKELRKPPQAIQELKDRPLPEFVEEAVPVGGYLNFRLRTEALLREALRPKA
>d1dd5a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermotoga maritima}
VNPFIFIKEAKEKMKRTLEKIEDERLKMRTGKPSPAILEEIKV DYYGVPTPVNLATISISEERTLVIKPWDKSVLSIEKAINASDLGLNPINDGNVIRLFPS
PTTEQREKWVKKAKEIIVEEGKIAIRNIRREILKKIKEDQKEGLIPEDDAKRLNEIQLTDEFIEKLDEVFEIKKEIMEF
>d1eh1a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermus thermophilus}
MTLKELYAETRSHMQKSLEVLEHNLAGLRTGRANPALLHLKVEYYGAHVPLNQIATVAPDPRTLTVQSWDQNALKAIKAIRDSDLGLNPNPSNKGD
ALYNIPPLTEERRKDLVRAVRQYAEGRVAIRNIRREALDKLKLAKELHLSEDET KRAEAEI QKITDEFIAKADQLAEKKEQEILG
>d1ek8a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Escherichia coli}
MISDIRKDAEV RMDKCVC EAFKTQISKIRTGRASPSSLGIVVEYYGTPTLRQLASV TVE DSR TLKINVFDRSMSPAVEKAIMASDLGLNPNSAGSDIR
VPLPPLTEERRKDLTKIVRGEAEQARVAVRNVRDANDKVKALLKDKEISEDDDRSQQDVQKLTDAIKKIEAALADKEAELMQF
>d1ge9a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Aequifex aeolicus}
MIKELEDIFKEAEKDMKKAVEYYKNEIAGLRTSRASTALVEEIKVEYYGSKVP IKQLGTISVPEHNQIVIQVWDQNAVPAIEKAI REELNLNP TVQGNVIR
VTLPPLTEERRREL VRLLHKITEEARVRVRNRREAKEMIELEGISEDEKKRALERLQKLTDKYIDEINKLMEA KEKEIMSV
>d1j98a_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Bacillus subtilis}
VESFELDHNAV VAPYV RHCGVHKVG TDGVVNKFDIRFCQPNKQAMKPD TIHTLELLAFTIRSHA EKYDHFDI IDIS PMGC QTGYLVVSGETTSAE
VDLLED TMK EAVEITEIPAANEKQCGQAKLHDLEGAKRLMRFWLSQDKEELLKVFG
>d1inna_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Deinococcus radiodurans}

NVESFDLDHTKVKAPYVRLAGVKTPKGDQISKYDLRFLQPNQGAIDPAAIHTLEHLLAGYMRDHLEGVVDSPMGCRTGMYMAVIGEPDEQGV
MKAFEAALKDTAGHDQPIPVGSELECGNYRDHDLAAARQHARDVLDQGLKVQETILL
>d1j6wa_d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Haemophilus influenzae}
LLDSFKVDHTKMNAPAVRIAKTMLTPKGDNITVFDLRCIPNKEILSPKGIHTLEHLFAGFMRDHNGDSIEIIDSPMGCRTGFYMSLIGTPNEQKVSE
AWLASMQDVLGVQDQASIPELNIYQCGSYTEHSLEDAHEIAKNIARGIGVNKNEDLSLDN
>d1j6xa_d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Helicobacter pylori}
MKMNVESFNLDHTKVKAPYVRIADRKKGVNGDLIVKYDVRFKQPNRDHMDMPSLHSLEHLVAEIRNHANYVWDWSPMCQTGFYLTVLNHDN
YTEILEVLEKTMQDVLAKEVPASNEKQCGWAANHTLEGAQNLARAFLDKRAEWSEVG
>d1hr6b1 d.185.1.1 (B:24-245) Mitochondrial processing peptidase (MPP) beta chain {Baker's yeast (Saccharomyces cerevisiae)}
PGTRTSKLPGNLTIAYEIPNTSSATVGIFV DAGSRAENVKNNGTAHFLEHLAFKGQTQRPQQGIELEIENIGSHLNAYTSRENTVYYAKSLQEDIPKAV
DILSDILTKSVDNSAIEERDVIRESSEEVDKMYDEVVFDHLHEITYKDQPLGRTILGPIKNIKSITRTDLKDYITKNYKGDRMVLAGAGAVDHEKLVQYA
QKYFGHVPKSESPVPLGSPR
>d1hr6b2 d.185.1.1 (B:246-462) Mitochondrial processing peptidase (MPP) beta chain {Baker's yeast (Saccharomyces cerevisiae)}
GPLPVFCRGERFIKENTLPTTHIAIALEGWSAPDYFVALATQAIVGNWDRAIGTGTNSPSPLAVAASQNGSLANSYMSFSTSYADSGLWGMYIVT
DSNEHNVRILVNEILKEWKRIKSGKISDAEVNRKAQLKAQLLSDGSTAIVEDIGRQVTTGKRLSPEEVFEQVDKITKDDIIWMANYRLQNKPV
MVALGNTSTVPNVSYIEEKLQNQ
>d1hr6a1 d.185.1.1 (A:14-233) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}
ARTDNFKLSSLANGLKVATNTPGHFSALGLYIDAGSRFEGRNLKGC THILDRLAFKSTEHVEGRAMAETLELLGGNYQCTSSRENLMYQASVFNQD
VGKMLQLMSETVRFPKITEQEQLSAEYEIDEVWMKPELVLPELLHTAAYSGETLGSPLICPRGLIPSISKYLLDYRNKFYT PENTVAAFVGVPHE
KALETGKYLGDWQSTHPPITKK
>d1hr6a2 d.185.1.1 (A:234-470) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}
VAQYTGGESCIAPPVFGNLPELFHIQIGFEGLPIDHPDIYALATLQTLGGGGFSAGGPKGKMYRSLYTHVLNQYYFVENCVAFNHSYSDSGIFGISM
SCIPQAAPQADEVIAQQMINTFANKDLRLTEDEVSRAKNQLKSSLMNLESKLVELEDMGRQVLMHGRKIPVNEMISKIEDLKPD DISRVAEMIFTG
NVNNAGNGKGRATVVMQGDRGSFGDVENVLKAYGLGNSS
>d1be3a1 d.185.1.1 (A:1-233) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}
TATYAQALQSVPETQVSQLDNGLRVASEQSSQPTCTGVVWIDAGSRYESEKNNNGAGYFVEHLAFKGTKNRPNALEKEVESMGAHLNAYSTREHTA
YYIKALSKDLPKAVELLADIVQNCSELDQSIEKERDVLQELQENDTSMRDVVFNYLHATAFQGTPLAQSVEGPSENVRKLSRADLTEYLSRHYKAPRM
VLAAAGGLEHRQLLDLAQKHFGSGSGTYDEDAVPTLSP
>d1be3a2 d.185.1.1 (A:234-446) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}
CRFTGSQICHREDGLPLAHVIAVEGPGWAHPDNVALQVANAIIGHYDCTYGGGAHLSPLASIAATNKLCSQSFQTFNICYADTGLGAHFVCDHMS
IDDMMFVLQGQWMRLCTSATESEVLRGKNNLRNALVSHLDGTPVCEDIGRSLLTYGRRIPLAEWESRIAEV DARV VREVC SKYFYDQCPAVAGFGP
IEQLPDYNRIRSGMFWLRF
>d1bcc a1 d.185.1.1 (A:4-232) Cytochrome bc1 core subunit 1 {Chicken (Gallus gallus)}
YAQALQSVPETQVSQLDNGVRVASEQSSQPTCTGVVWIDAGSRYESEKNNNGAGYFLEHLAFKGTKNRPQNALEKEVESMGAHLNAYSSREHTAYI
KALSKDVPKAVELLADIVQNCSELDQSIEKERDVI VRELQENDTSMREVVFNYLHATAFQGTGLAQSVEGPSENIRKLSRADLTEYLSTHYTAPRMVLA
AAGGVEHQQLLELAQKHFGGPFTYDDDAVPTL
>d1bcc a2 d.185.1.1 (A:233-445) Cytochrome bc1 core subunit 1 {Chicken (Gallus gallus)}
KCRFTGSQIRHREDGLPLAHVIAVEGPGWAHPDLVALQVANAIIGHYDCTYGGGLHSSPLASIAVTNKLCSQSFQTFNICYSETGLGFYFVCDRMSI
DDMMFVLQGQWMRLCTSISESEVLRGKNNLRNALVSHLDGTPVCEDIGRELLTYGRRIPLEWEERLAEVDARMVREVC SKYIYDQCPAVAGPGPI
EQLPDYNRIRSGMFWLRF
>d1ezva1 d.185.1.1 (A:27-239) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}
AEVTQLSNGIVVATEHNPAHTASVGVVFSGAANENPYNNGVSNLWNKIFLSKENS AAK EGLALSSNISRDFQSYIVSSLPGSTD KSLDFLNQSFQI
QKANLSSSNFEATKKSVLKQVQDFEDNDHPNRVLEHLHSTA FQNTPLS LPTRG TLESLENLVVADLESFANNHFLNSNAV VGTGNIKHEDLVNSIES
KNLSQLQTGTKPVLKK

>d1ezva2 d.185.1.1 (A:240-456) Cytochrome bc1 core subunit 1 {Baker's yeast (*Saccharomyces cerevisiae*)}
KAAFLGSEVRLRDTLPKAWISLAVEGEPVNSPNYFVAKLAQIFGSYNAFEPASRLQGIKLLDNIQEYQLCDNFNHFSLSYKDSGLWGFSTATRNVT
MIDDLIHTLKQWNRLTISVTDTEVERAKSLLKLQLGQLYESGNPVNDANLLGAEVLIKGSKLSLGEAFKKIDAITVKDVKAAGKRLWDQDIAIGTG
QIEGLLDYMRIRSDMSMMRW

>d1be3b1 d.185.1.1 (B:21-235) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}
PQDLEFTRLPNGLVIASLENYPASRIGLFIKAGSRYENSNNLGTSHLLRASSLTTKGASSFKITRGIEAVGGKLSVTSTRENMAYTVECLRDDVILMEF
LLNVTTAPEFRRWEVAALQPQLRIDKAVALQNPQAHVIENLHAAAYRNALANSLYCPDYRIGKVTVELHDYVQNHTSARMALIGLGVSHPVLKQV
AEQFLNIRGGGLGLSGA

>d1be3b2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}
KAKYHGGEIREQNGDSLVHAALVAESAIGSAEANAFSVLQHV LGAGPHVKRGSNATSSLYQAVAKGVHQPF DVS AFN ASY SDG LFG FYT ISQ AAS
AGDVIKAAYNQVKTIAQGNLNSPDVQAAKNKLKAGYLMSVESSEGFLDEVGSQALAAGSYT P STV LQQ IDA VAD A DV IN A AKK FV SGR KSMAAS
GNLGHTPFIDEL

>d1bccb1 d.185.1.1 (B:18-235) Cytochrome bc1 core subunit 2 {Chicken (Gallus gallus)}
PPHPQDLEITKLPNGLVIASLEN YSPG STIGV FIKAGSRYEN SSNL GTSH LLRASS LTTKGASS FKIT RGIEAV GGK LSV ESTREN MAYT VECL RDDV EIL
MEFLNNTTAP EFRPWEVADLQPQLKIDKAVAF QNPQ THV IENL HAAAYRN ALAD SLYCP DYRIG KVT SVELHDFVQ NHFTSAR MALV GLGV SHP VL
KNVAEQLLNIRGGGLGLSGA

>d1bccb2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Chicken (Gallus gallus)}
KAKYRGGEIREQNGDSLVHAAIVAESAII GAEANAFSVLQHV LGAGPHVKRG LNATSSLYQAVAKGVHQPF DVS AFN ASY SDG LFG FYT ISQ AAY
AGQVIKAAYNQVKTIAQGNVSNENVQAAKNKLKAKYLMVESSEGFL FEEVG SQALAAGSYN P STV LQQ IDA VAD A DV IN A AKK FV S RQ KSMAAS
GNLGHTPFVDEL

>d1ezvb1 d.185.1.1 (B:17-218) Cytochrome bc1 core subunit 2 {Baker's yeast (*Saccharomyces cerevisiae*)}
LTVSARDAPTKISTLAVKVHGGSRYATKDGVAHLLNRNFQNTNTRSAKLVRESELLGGTFKSTLDREYITLKATFLKDDLPYYVNALADVLYKTA FKP H
ELTESVLP AARYDYVA AEQCPV KSAEDQ LYAITFRKGLGNPL YDGVERVSLQD IKDFADK VYTKENLEVSGEN VVEADLKRFVDE SLLSTLPAGKSLV SK
>d1ezvb2 d.185.1.1 (B:219-368) Cytochrome bc1 core subunit 2 {Baker's yeast (*Saccharomyces cerevisiae*)}
SEPKFFLGEENRVFIGDSVAAIGIPVN KASLAQYEV LAN LTSA SELS GLISSAKLDKFTDGGLFTLVRDQDSA VVSSNIKIVADLKKGD LSPAIN Y
TKLKN AVQNESVSSPIELNFD AVKDFKL GFNYVAVGDVSNLPYLD E

>d1tig__ d.68.1.1 (-) Translation initiation factor IF3, C-terminal domain {Bacillus stearothermophilus}
INVKEVRLSPTIEEHDFNTKLRNARKFLEKGDKV KATIRFKGRAITHKEIGQRVLDRLSEACADIAVVETAPKMDGRNMFLV LAPKND

>d2ifea_ d.68.1.1 (A:) Translation initiation factor IF3, C-terminal domain {Escherichia coli}
VIQVKEIKFRPGTDEGDYQVKLRSLIRFLEEGDKAKITLRFGRGREMAHQ QIGMEV LNRVKDDLQELAVVESFPTKIEGRQMIMV LAPKKQ

>d196v_ d.68.1.1 (V:) Translation initiation factor IF3, C-terminal domain {Thermus thermophilus}
EVKS IKFRV KIDEHDYQTKL GHIKRFLQEGHKV KV TIMFRG RGEVAHPELGERILNRV TEDLK DLAVVEMKPEM ILGRDM NMFLV LAPVK

>d1dcja_ d.68.3.1 (A:) SirA {Escherichia coli}
MTDLFSSPDHTLDALGLRCPEPVMMVRKTVRNMQPGETLIIADDPAT TRDIPG FCTFMEHELVAKETDGLPYRYLIRKG G

>d1jdqa_ d.68.3.2 (A:) Hypothetical protein TM0983 {Thermotoga maritima}
GSSHHHHHHSGLVPRGSHMAKYQVTKTL D VRGEVCPVDPVETKRALQNMKPGEILEVWIDYPM SKERI PETVKKLGHEV LEIEVGPSEWKIYIKV
K

>d1qmha2 d.68.2.1 (A:5-184,A:280-338) RNA 3'-terminal phosphate cyclase, RPTC {Escherichia coli}
MIALDGAQGEGGGQILRSALSLSMITGQPTITSIRAGR A KPG L RQH LTAVKAATEICGAT VEGAELGSQRL FRPG T VRGGDYRFAIGSAGS CTLV
QT VLPALWFADGPSRVEVSGG TDNPSAPPAD FIRV LEP LLA KIGIHQ QT LLR HG FYPAGGGVVATEVSPV ASFN TQLG XAVGEYLA DQLV LPMA L
AGAGEFTVAHPSCHLLT NI AVERFLPVRFS LIETDG VTRV SI

>d1uae__ d.68.2.2 (-) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT, MurA, MurZ) {Escherichia coli}
MDKFRVQGPTKLQGEVTISGAKNAALPILFA ALLAE PVEIQN VP KLKD VDTSMKLLSQLGAKVERNGS VHID ARDV NVFCAP YDLV KTM RASI WAL
GPLVARFGQQVSLPGGCTIGARPVDL HISGLEQLGATIKLEEGYVKA SVD GRLKG AHIVMDK VSVG ATV TIMCAATLAEGTTI ENA AREPEI VDTAN

FLITLGAKISGQGTDRIVIEGVERLGGGVYRVLPDRIETGTFVAAAISRGKIIICRNAQPDTLDAVLAKLRDAGADIEVGEDWISLDMHGKRPKAVNVR
TAPHPAFPTDMQAQFTLLNLVAEGTGFITETVFENRFMHVPELSRMGAHAEIESNTVICHGVEKLSGAQVMATDLRASASLVLAGCIAEGTTVVDR
YHIDRGYERIEDKLRALGANIERVKG
>d1ejda_d.68.2.2 (A:) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT, MurA, MurZ) {Enterobacter cloacae}
MDKFRVQGPTRLQGEVTISGAKNAALPILAALLAEEPVEIQNVPKLKDIDTTMKLLTQLGTKVERXGSVVIDASNNFSAPYDLVKTMRASIWL
GPLVARFGQQVSLPGGCAIGARPVDLHIFGLEKLGAIEKLEEGYVKASVNGRLKGAHIVMDKVSVGATVIMSAATLAEGTTIENAREPEIVDTAN
FLVALGAKISGQGTDRITIEGVERLGGGVYRVLPDRIETGTFVAAAISGGKIVCRNAQPDTLDAVLKREAGADIEGEDWISLDMHGKRPKAVTVR
TAPHPAFPTDMQAQFTLLNLVAEGTGVITETIFENRFMHVPELIRMGAHAEIESNTVICHGVEKLSGAQVMATDLRASASLVLAGCIAEGTTVVDR
HIDRGYERIEDKLRALGANIERVKG
>d1g6sa_d.68.2.2 (A:) 5-enol-pyruvyl shikimate-3-phosphate(EPSP) synthase {Escherichia coli}
MESLTLPPIARVDTINLPGSKSVNRALLAALAHLGKTVLNTNLLSDDRHMLNALTALGVSYTLSADRTRCEIINGNGPLHAEGALELFLGNAGTA
MRPLAAACLGSNDIVLTGEPRMKERPIGHLDALRLGGAKITYLEQENYPPLRLQGGFTGGNVVDGSVSSQFLTALLMTAPLAPEDTVIRKGDLS
KPYIDITNLNMKTFGVEIENQHYQQFVKGGSYQSPGTYLVEGDASSASYFLAAAIIKGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDYI
SCTRGEELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKETDRLFAMATELRKVGAEEVEEGHDYIRTPPEKLNFAEIATYNDHRMAMC
FSLVALSDTPVTILDPKTAKTFPDYFEQLARISQAA
>d1imua_d.204.1.1 (A:) Ribosome binding protein Y (HI0257, YfiA homologue) {Haemophilus influenzae}
MTLNITSKQMDITPAIREHLEERLAKLGKWTQLISPHTVLFNKVPNGFSVEASIGTPLGNLLASATSDDMYKAINEVEEKLERQLNKLQHKSESRRADE
RLKDSFEN
>d1tola2_d.69.1.1 (A:125-216) C-terminal domain of TolA {Escherichia coli}
SGADINNYAGQIKSAIESKFYDASSYAGKTCTLRIK LAPDGMLDIKPEGGDPALCQAA ALAAKLA KIPKPPSQAVYEVFKNAPLDFKPA
>d1kpta_d.70.1.1 (A:) Virally encoded KP4 toxin {Ustilago maydis, P4 strain}
LGINCRCGSSQCGLGGNLMVRIRDQACGNQGQTWC PGERRAKVC GTGNSISAYQSTNNCISGTEACRHTNLVNHGCRVCGSDPLYAGNDVSRG
QLTVNYVN
>g1kve_1.d.70.1.2 (A;B;) SMK toxin {Halotolerant yeast (Pichia farinosa)}
WSLRWRMOKSTTIAAIAGCSAATFGGLAGGIVGCIAAGILAILQGFVNWHNGGGDRSNPVXGEATTIWGVGADEAIDKGTPSKNDLQNSMA
DLAKNGFKHQGVACSTVKDGNKD VYMIKFLSLAGGSNDPGGSPCSDD
>d1ev0a_d.71.1.1 (A:) Cell division protein MinE topological specificity domain {Escherichia coli}
RSDAEPhYLPLQRKDILEVICKYVQIDPEMVTQVLEQKQGDISILENVTLP EAEELK
>d1dw9a2_d.72.1.1 (A:87-156) Cyanase C-terminal domain {Escherichia coli}
RIPTDPTMYRFYEMILQVYGTTLKALVHEKFGDGII SAINFKLDVKKVADPEGGERAVITLDGKYLPTKPF
>d3rubs_d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}
MQVWPPIGKKYETLSYLPPLTEQLLAEVNYLLVNNWIPCLEFEVKDGFVYREHLKSPGYYDGRYWTMWKLMFGCTDATQVLAEEAKKAYP
QAWIRIIGFDNVRQVQCISFIAYKPEGY
>d1burs_d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}
MQVWPILGKKYETLSYLPPLTDQLARQV DYLNNKWWPCLEFETDHGFVYREHHNSPGYYDGRYWTMWKLMFGCTDPAQVLNEECKKEY
DAFIRIIGFDNKRQVQCISFIAYKPGY
>d8ruci_d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}
MQVWPILNLKKYETLSYLPPLTDQLARQV DYLNNKWWPCLEFETDHGFVYREHHNSPGYYDGRYWTMWKLMFGCTDPAQVLNEECKKEY
PNAFIRIIGFDNSNREVQCISFIAYKPGY
>d1bwvs_d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}
VRITQGTFSLPDLTDEQIKKQIDYMISKKLAIGIEYTNDIHPRNAYWEIWGLPLFDVTDPAAVLFEINACRKARSNFYIKVVGFSVRGIESTIISFIVNRP
KHEPGFNLMRQEDKSRSIKYIHSYESYKPEDERY
>d1gk8i_d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}
MVWTPVNNKMFETFSYLPPLTDEQIAAQVDYIVANGWIPCLEFAEADKAYVSNESAIRFGSVSCLYYDNRYWTMWKLMFGCRDPMQVLREIVAC

TKAFPDAYVRLVAFDNQKQVQIMGFLVQRP

>d1bxni_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}

MRITQGTFSFLPELTDEQITKQLEYCLNQGWAVGLEYDDPHPRNTYWEMFGLPMFDLRDAAGILMEINNARNTFPNHYIRVTAFDSTHTVESVV
MSFIVNRPADEPGFRLVRQEEPGRTLRYSIESYA

>d1rblm_ d.73.1.1 (M:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}

SMKTPKERRFETFSYLPLSLDRQIAAQIEYMIEQGFHPLIEFNEHSNPEEFYWTMWKLPLFACAAPQQVLDEVRECRSEYGD CYIRVAGFDNIKECQ
TSSFIVHRPGR

>d1dcpa_ d.74.1.1 (A:) Pterin-4a-carbinolamine dehydratase (PCD)/dimerization cofactor of HNF1 (DCoH) {Rat (Rattus norvegicus)}

HRLSAEERDQLLPNLRAVGWNELEGRDAIFKQFHFKDFNRAFGFMTRVALQAEKLDHHPEWFNVYNKVHITLSTHECAGLSERDINLASFIEQVAVS
MT

>d1xxaa_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Escherichia coli}

LKNLVLDIDYNDAVVIHTSPGAAQLIARRLLSLGKAEGILGTIAGDDTIFTTPANGFTVKDLYEAILELF

>d1b4ba_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Bacillus stearothermophilus}

ALVDVFILDGTLGNLLVRLPGLNAHAIGVLLNDWDEIVGTCGDDTCLIICRTPKDAKKVSNQLLSML

>d1f9na2 d.74.2.1 (A:79-149) C-terminal domain of arginine repressor {Bacillus subtilis}

ALMDAFVKIDSASHMIVLKTMMPGNAQAIGALMDNLDWDEMMGTCGDDTILICRTPEDTEGVKNRLLELL

>d1i50k_ d.74.3.2 (K:) RPB11 {Baker's yeast (Saccharomyces cerevisiae)}

MNAPDRFELFLLGEGESKLKIDPDTKAPNAVITFEKEDHTLGNLIRAELLNDRKVLFAAYKVEHPFFARFKLRIQTTEGYDPKDALKNACNSIINKLGAL
KTNFETEWNLQTL

>d1bdfa1 d.74.3.1 (A:2-52,A:179-232) RNA polymerase alpha {Escherichia coli}

QGSVTEFLKPRLVIEQVSSTHAKVTLEPLERGFHTLGNPLRRILLSSIPXPVRRVAFQVEDTRLGQRTDLKLT RIWTGSVTPLEALNQAVAILKEHLNYFAN
LEAFV

>d1i6va1 d.74.3.1 (A:6-49,A:173-229) RNA polymerase alpha {Thermus aquaticus}

LKAPVFTATTQGDHYGEFVLEPLERGFVTLGNPLRRILLSSIPXPVRRVAFQVEDTRLGQRTDLKLT RIWTGSVTPLEALNQAVAILKEHLNYFAN
PE

>d1i50c1 d.74.3.1 (C:3-41,C:173-268) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

EEGPQVKIREASKDNVDFILSNVDLAMANSLRRVMIAEIXAAAIEFYDPWNKLKHTDYWEQDSAKEWPQSKNCYE DPPNEGDPFDYKAQADT
FYMNVESVGSI PVQDV VRGIDL TQKKVASILLALTQMDQD

>d1c0aa2 d.74.4.1 (A:288-420) Prokaryotic AspRS, insert domain {Escherichia coli}

NPMELTDVADLLKSVEFAVFAFPANDPKGRVAALRVPGGASLTKQIDEYGNFVKIYGAKGLAYIKVNERAKGLEINSPVAKFLNAEI EDILDRTAAQ
DGDMIFFGADNKKIVADAMGALRKVGKDLGLT

>d1g51a2 d.74.4.1 (A:295-414) Prokaryotic AspRS, insert domain {Thermus thermophilus}

FGLELKEVGPLFRQSGFRVQEAE SVKALALPKSRKEA EEEVAKRHKAQGLAWARVEEGGS GGVAKFLEPVREALQATEARP GDTLLFVAGP
RKVAATALGAVRLRAADLLGLK

>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}

MEGMLKGEGPGPLPPLLQQYVELRDQPYDYL LFQVGDFYECFGEDAERLARALGLVLTHKTSKDFTPMAGIPLRAFEAYAERLLKMGFRLAVADQ
VEPAEEAEGLVRREV TQLLPGT

>d1e3ma4 d.75.2.1 (A:2-116) DNA repair protein MutS, domain I {Escherichia coli}

SAIENFDAHTPMQM QYRLKAQHPEILLFYRMGDFYELFYDDAKRASQLL DISLKRGASAGEPIPMAGIPYHAVENYLAKLVNQGESVAICEQIGDP
ATSKGPVERKVVRI VTP

>d1e3mb4 d.75.2.1 (B:14-116) DNA repair protein MutS, domain I {Escherichia coli}

MQQYLRKAAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKGASAGEPIPMAGIPYHAVENYLAKLVNQGESVAICEQIGDPATSKGPVERKVV
RIVTP

>d1gyfa_d.76.1.1 (A:) GYF domain from cd2bp2 protein {Human (Homo sapiens)}

DVMWEYKWENTGDAELYGPFTSAQMQTWVSEGYFPDGVYCRKLDPGGQFYNSKRIDFDLYT

>d1jg5a_d.205.1.1 (A:) GTP cyclohydrolase I feedback regulatory protein, GFRP {Rat (Rattus norvegicus)}

PYLLISTQIRMEVGPTMVGDEHSDPELMQQLGASKRVLGNNFYEYYVNPPRIVLDKLECRGFRVLSMTGVGQTLWWCLHKE

>d1iq4a_d.77.1.1 (A:) Ribosomal protein L5 {Bacillus stearothermophilus}

MNRLKEKYLNNEVVPALMSKFNYKSIMQVPKIEKIVINMGVGDAVQNPKAQSAVEELTLIAGQRPVVTRAKKSIAGFRLRQGMPIGAKVTLRGERM
YEFLDKLISVSLPRARDFRGSKKSFDRGNYTLGIKEQLIFPEIDYDKVNKVRGMIDIVTTANTDEEARELLALLGMPFQK

>d1jj2d_d.77.1.1 (D:) Ribosomal protein L5 {Archaeon Haloarcula marismortui}

FHEMREPRIEKVVVHMGIGHGGRDLANAEDILGEITGQMPVRTKAKRTVGEFDIREGDPIGAKVTLRDEMAEEFLQTALPLAELATSQFDDTGNSF
GVEEHTEFPSQEYDPSIGYGLDVTVNLVRPGYRVAKRDKASRSIPTKHRLNPADAVAFIESTYDVE

>d1eika_d.78.1.1 (A:) RNA polymerase subunit RBP5 (RNA polymerase subunit H) {Archaeon Methanobacterium thermoautotrophicum}

MKREILKHQLVPEHVILNESEAKRVLKELDAHPEQLPKIKTTDPVAKAIGAKRGDIVKIRKSPTAEEFVTYRLVQD

>d1hmja_d.78.1.1 (A:) RNA polymerase subunit RBP5 (RNA polymerase subunit H) {Archaeon Methanococcus jannaschii}

PKHEIVPKEEEILKRYNIKIQQLPKIYEDDPVIQEIGAKEGDVVRVIRKSPTAGVSIAYRLVKRI

>d1dzf2_d.78.1.1 (A:144-215) Eukaryotic RPB5 C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

ITHHELVPKHIRLSSDEKRELLKRYRLKESQLPRIQRADPVALYLGLKRGEVVKIRKSETSGRYASYRICM

>d1qkla_d.78.1.2 (A:) RPB6 {Human (Homo sapiens)}

MSDNEDNFDGDDFDDVEEDEGLDDLENAAEEGQENVEILPSGERPQANQKRITTPYMTKYERARVLGTRALQIAMCAPVMVELEGEDPLLIAMK
ELKARKIPIIRRYPDGSYEDWGVDELITD

>d1i50f_d.78.1.2 (F:) RPB6 {Baker's yeast (Saccharomyces cerevisiae)}

KAIPKDQRATT PYMTKYERARILGTRALQISMNAPVFVDLEGEDPLRIAMKELAEKKIPLVIRRYPDGFSFEDWSVEELIVDL

>d1qu9a_d.79.1.1 (A:) Conserved 'hypothetical' protein YjgF {Escherichia coli}

SKTIATENAPAAIGPYVQGVLDGNMIITSGQIPVNPKTGEVPADVAQQARQSLDNVKAIVEAAGLKVGDIVKTTFVKDLNDATVNATYEAFFTEHN
ATFPARSCVEVARLPKDVKIEIAIAVRR

>d1qd9a_d.79.1.1 (A:) Purine regulatory protein YabJ {Bacillus subtilis}

TKAVHTKHAPAAIGPYSQIIVNNMFYSSGQIPLTPSGEMVNGDIKEQTHQVFSNLKAVLEEAGASFETVVKATVFIADMEQFAEVNEVYQYFDTH
KPARSCVEVARLPKDALKLVEIEVIALVK

>d1jd1a_d.79.1.1 (A:) Highdosage growth inhibitor YER057cp (YE07_YEAST) {Baker's yeast (Saccharomyces cerevisiae)}

TTLTPVICESAPAAAASYSHAMKVNNLIFLSGQIPVTPDNKLVEGSIADKAEQVIQNIKNVLEASNSSLDRVVKVNIFLADINHFAEFNSVYAKYFNTHK
PARSCVAVAALPLGVDMEMEAIAAER

>d1dbfa_d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}

MMIRGIRGATTVERDTEEEILQKTQLLEKIIENHTKPEDVVQMLLSATPDLHAVFPAKAVRELSGWQYVPVTCMQEMDVTGGLKKCIRVMMTVQ
TDVPQDQIRHVYLEKAVVLRPDLSLTKNTL

>d1fnja_d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}

MIRGIRGATTVERDTEEEILQKTQLLEKIIENHTKPEDVVQMLLSATPDLHAVFPAKAVRELSGWQYVPVTCMQEMDVTGGLKKCIRVMMTVQT
DVPQDQIRHVYLEKAVVLR

>d1jy8a_d.79.5.1 (A:) 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF {Escherichia coli}

MRIGHGFDVHAFGGEGPIIIGGVIRPYEKGLLAHSDGDVALHALTDALLGAAALGDIGKLFPDTDPFKGADSRELLREAWRRIQAKGYTLGNVDVTII
AQAPKMLPHIPQMRRVIAEDLGCHMDDVNVKATTTEKLGFTGRGEGIACEAVALLI

>d1fsz_2_d.79.2.1 (232-356) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}

INVDFADVKA VMNNNGGLAMIGIGESDSEKRAKEAVSMALNSPLLDVDIDGATGATGALIHVMGPEDLTLEEAREVVATVSSRLDPNATIIGATIDENLE

NTVRVLLVITGVQSRIEFTDTGLKRKKL

>d1tuba2 d.79.2.1 (A:246-440) Tubulin alpha-subunit {Pig (Sus scrofa)}

GALNVDLTETQTNLVPYPRGHFPLATYAPVISAEGKAYHEQLSVAEITNACFE PANQMVKCDPRHGKYM ACCLLYRGD VPKDVNAIAITKRTIQF
VDWCPTGFVKVGINYEPPTVPGDLAKVQRAVCMLSNTTAIEAWARLDHKFDL MYAKRAFVHWYVGEGMEEGFSEAREDMAALEKDYEEVG
VDSV

>d1tubb2 d.79.2.1 (B:246-437) Tubulin beta-subunit {Pig (Sus scrofa)}

GQLNADLRKLAVNMVPPRHLFFMPGAPLTSRGSQQYRALTVPELTQQMFDAKNMMAACDPRHGRYLTVAAVFRGRMSMKEVDEQMLNVQ
NKNSSYFVEWIPNNVKTAVCDIPPRGLKMSATFIGNSTAIQELFKRISEQFTAMFRRKAFLHWYTGEGMDEM EFTAEESNMNDLVSEYQQYQD

>d1ck9a_d.79.3.1 (A:) Eukaryotic ribosomal protein L30 (L30e) {Baker's yeast (Saccharomyces cerevisiae)}

APVKSQESINQKLALVIKGKTYLGYKSTVKS LRQGKSKLIIAANTPVLRKSELEYYAMLSKTKVYYFQGGNNELGTAVGKLFRVGVVSILEAGDSDILTT
LA

>d1jj2f_d.79.3.1 (F:) Ribosomal protein L7ae {Archaeon Haloarcula marismortui}

PVYVDFDVPADLEDDALEALEVARDTGAVKKGTNETT KSIERGSAELVFAEDVQPEEIVMHIPELADEKGVPFIFVEQQDDLGH AAGLEVGSAAA AV
TDAGAAATVLEEIADKVEELR

>d1e7ka_d.79.3.1 (A:) Spliceosomal 15.5kd protein {Human (Homo sapiens)}

ADVNP KAYPLADAHLKKLLDVQQSCNYKQLRK GANEATKTLNRGISEFIVMAADAEPLEIILHPLL CEDKNVPYVFVR SKQALGRACGVSRPVIAC
SVTIKEGSQLKQQIQSIQQSIERLLV

>d1dt9a2 d.79.3.2 (A:277-422) C-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 {Human (Homo sapiens)}

NVKFIQEKKLIGRYFDEISQDTGKYCFGVEDTLKALEMGA VEILIVYENLDIMRYVLHCQGTEEEKILYLTPEQE KDKSHFTDKETGQEHE LIESMPLLE
WFANNYKKFGAT LEIVTDKS QEGSQFVKFGGGIGGILRYRVDFQGM

>d1clia1 d.79.4.1 (A:5-170) Aminoimidazole ribonucleotide synthetase (PurM) N-terminal domain {Escherichia coli}

TSLSYKDAGVDIDAGNALVGRIKG VVKTRPEVMGG LGGF GALCALPQKYREPVLVSGTDGVGTKLRLAMD LKRHD TIGIDL VAMCVNDLVQGA
EPLFLDYYATGKLDV DTASAVISGIAEGCLQSGCSLVGGETAEMPGMYHG EDYDVAGFCVG VVEKSEII

>d1cib1 d.79.4.1 (B:1021-1170) Aminoimidazole ribonucleotide synthetase (PurM) N-terminal domain {Escherichia coli}

ALVGRIKG VVKTRPEVMGG LGGF GALCALPQKYREPVLVSGTDGVGTKLRLAMD LKRHD TIGIDL VAMCVNDLVQGA EPLFLDYYATGKLDV
DTASAVISGIAEGCLQSGCSLVGGETAEMPGMYHG EDYDVAGFCVG VVEKSEII

>d1otfa_d.80.1.1 (A:) 4-oxalocrotonate tautomerase {Pseudomonas sp., Dm pI}

PIAQLYII EGR TDEQKETLIRQVSEAMANSLDAPLERVRV LITEMPK NHFGIGGEPASK

>d1bjpa_d.80.1.1 (A:) 4-oxalocrotonate tautomerase {Pseudomonas putida, XylH}

PIAQIHILEGR SDEQKETLIREVSE AISRSLDAPL TS VRV IITEMAKGHFGIGGELASKVRR

>d1otga_d.80.1.2 (A:) 5-carboxymethyl-2-hydroxymuconate isomerase (CHMI) {Escherichia coli}

PHFIVECSDNIREEADLPG LFAKVNP TL AATGIFPLAGIR SRVHWVDTWQMADGQHDYAFVHMTLKIGA GR SLES RQQAGEMLFELIKTHFA ALME
SRLL ALSF EI ELHPTLNFKQNNVHALFK

>d1gd0a_d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Human (Homo sapiens)}

PMFIVNTNVPRASV P DGF LSEL TQQLA QTGK P P QYIA VH VP DQL MFTSGT SDPCALCSLHSIGKIGGAQNRNSKLLCGLLS DR LHISPDRV YIN YY
DMNAANVGWNNSTFALEHH

>d1fim_d.80.1.3 (-) Microphage migration inhibition factor (MIF) {Rat (Rattus norvegicus)}

PAFIVNTNVPRASV PEGFLSEL TQQLA QTGK P A QYIA VH VP DQL MFTSGT SDPCALCSLHSIGKIGGAQNRNSKLLCGLLS DR LHISPDRV YIN YY
DANA

>d1mfia_d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Mouse (Mus musculus)}

PMFIVNTNVPRASV PEGFLSEL TQQLA QTGK P A QYIA VH VP DQL MFTSGT SDPCALCSLHSIGKIGGAQNRNSKLLCGLLS DR LHISPDRV YIN YY
DMNAANVGWNNGSTFA

>d1hfoa_d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Trichina (Trichinella spiralis)}

PIFTLNTNIKATDVPSDFLSSTSALVGNILSKPGSYAVAHINTDQQLSFGGSTNPAAGTLMISIGGIEPSNRDHSAKLFDLNTKLGIPKNRMYIHFVN
LNGDDVGWNGTTF
>d1dpta_d.80.1.3 (A:) D-dopachrome tautomerase {Human (Homo sapiens)}
PFLELDTNLPANRVPAGLEKRLCAAASILGPADRVNVTVRPGLAMALSGSTEPCAOQLSISSIGVVGTAEEDNRSHSAHFFFLTKELALGQDRILIRFFF
LESWQIGKIGTVMTFL
>d1gad02 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Escherichia coli}
CTTNCLAPLAKVINDNFGIIEGLMTTVHATTATQKTDGSPHKDWRRGGGRASQNIIPSTGAAKAVGKVLPELNGKLTGMAFRVPTPNVSVDLTVR
LEKAATYEQIKAALKAAEAEKGVLGYTEDDVSTDFNGEVCTSVDKAGIALNDNFVKLVSWYD
>d1gd1o2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Bacillus stearothermophilus, nca 1503}
CTTNCLAPFAKVLHEQFGIVRGMMTTVHSYTNDQRILDLPHKDLRRARAAAESIPTTGAAKAVALVPELKGKLNMGAMRVPTPNVSVDLVAEL
EKEVTEEVNAALKAAEAEKGILAYSEEPLVSDYNGSTVSSTIDALSTMVIDGKMKVVKVSWYD
>d1cer02 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermus aquaticus}
CTTNSLAPVMKVLEAFGVEKALMTTVHSYTNDQRLLDPLPHKDLRRARAAAENIIPSTTGAAKAVALVPEVKGKLDGMAIRVPTPDGSITDLTVKRE
VTAEEVNAALKAAEAEKGILAYSEEPLVSDYNGSTVSSTIDALSTMVIDGKMKVVKVSWYD
>d1hdg02 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermotoga maritima}
CTTNSIAPIVKLHEKFGIVSGMLTTVHSYTNDQRVLDPLPHKDLRRARAAAENIIPSTTGAAKAVALVPEVKGKLDGMAIRVPTPDGSITDLTVKRE
ETTVEEVNAVMKEATEGRLKGIIIGYNDEPIVSSDIIGTTFSGIFDATITNVIGGKLVKVASWYD
>d1b7go2 d.81.1.1 (O:139-300) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Sulfolobus solfataricus}
CNTTALLRTICTVNKVKVSRVTRRAADQKEVKKGPINSVDPATVPSHHAKDVNSVIRNLIDATMAVIAPTTLMHMHFINITLKDVKVEKKDILS
VLENTPRIVLISSKYDAEATAELVEARDLKRDRNDIPEVMIFSDSIYVKDDEVMLMYAVHQ
>d1cf2o2 d.81.1.1 (O:139-303) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Methanothermus fervidus}
SCNTTGLCRTLKPLHDSFGIKKVRAVIVRRGADPAQVSKGPINAIIPPKLPSHHGPDVKVLDINIDTMIAVIVPTTLMHQHNVMVEETPTVDDII
DVFEDTPRVLISAEDGLTSTAEIMEYAKELGRSRNDLFEIPVWRESITVVVDNEIYMQAVHQESD
>d1gaa2 d.81.1.1 (A:165-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Trypanosoma brucei, glyosome}
CTTNCLAPLVHVLVKEFGISTGLMTTVHSYTATQKTDGVSVKDWRRGGRAAAALNIIIPSTTGAAKAVGMVIPSTQGKLTGMAFRVPTADSVVDLTF
IATRDTISIKEIDAALKRASKTYMKNILGYTDEELVSADFISDSRSSIYDSKATLQNNLPNERRFFKIVSWYD
>d1i32a2 d.81.1.1 (A:166-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Leishmania mexicana}
CTTNCLAPIVHVLTKENFGIETGLMTTIHSYTATQKTDGVSVKDWRRGGRAAAQNIIPSTTGAAKAVGMVIPSTQGKLTGMSFRVPTPDVSVDLTFR
ATRDTSIQEIDKAIKAAQTYMKGILGFTDEELVSADFINDNRSSVYDSKATLQNNLPGEKRFKVVSWYD
>d1dssg2 d.81.1.1 (G:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Lobster (Palinurus versicolor)}
CTTNCLAPVAKVLHENFEIVEGLMTTVHAVATQKTDGPSAKDWRRGGRAAQNIIPSTTGAAKAVGMVIPSTQGKLTGMAFRVPTPNVSVDLTV
RLGKECSYDDIKAAMKAASEGPLQGVLGYTEDDVVSCDFTGDNRSIFDAKAGIQLSKTFVKVSWYD
>d3gpdg2 d.81.1.1 (G:151-314) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Human (Homo sapiens)}
CTTNCLAPLAKVIHDHFGIVEGLMTTVHAITATQKTDPSGKWLWRGGRAAQNLIPASTGAAKAVGKVIPELDGKLTGMAFRVPTANVSVDLTCRL
EKPAKYDDIKVVKEASEGPLKGILGYTEDEVVSDDFNGSNHSSIFDAGAGIELNDTFVKLVSWYD
>d1jn0a2 d.81.1.1 (A:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Spinach (Spinacia oleracea)}
CTTNCLAPFKVLDQKFGIICKGTTTHTHSYTGDQRLLDASHDLRRARAACLNIVPTSTGAAKAVALVPLQLKGKLNGLARVPTPNVSVDLTVQVS
KKTFAEEVNAAFRESADQELKGILSVCDEPLSIDFRCTDSSTIDSSLTMVGMDDMVKVIWAYD
>d1gl3a2 d.81.1.1 (A:134-354) Aspartate beta-semialdehyde dehydrogenase {Escherichia coli}
NCTVSLMLMSLGGFANDLVDWVSVATYQAASGGGARHMRELLTQMGHLYGHVADELATPSSAILEDERKVTLTRSGELPVDNFGVPLAGSLIPWI
DKQLDNGQSREEWKGQAETNKILNTSSIPVDSLICRCHSQAFITKLKDVSIPTVEELLAHHNPWAKVVPNDREITMRELTPAAVTGTLTP
VGRLRKLNIMGPEFLSAFTVGDQLLWG
>d1ebfa2 d.81.1.2 (A:151-340) Homoserine dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}
PIISFLREIIQGTGDEVEKIEGIFSGTLSYIFNEFSTSQANDVKFSDVVVKVAKKLGYTEPDPRDDNLGVDVARKVTIVGRISGVEVESPTSFPVQSLPKPLESV

KSADEFLEKLSDYDKDLTQLKKEAATENKVLRFIGKVDATKSVVGIEKYDYSHPFASLKGSDNVISIKTKRYTNPVIQGAGAG
>d1e5qa2 d.81.1.2 (A:125-391) Saccharopine reductase {Rice blast fungus (*Magnaporthe grisea*)}
LDPGIDHLYAIKTIIEVHAAGGKIKTFLSYCGGLPAPESSDNPLGYKFWSRGVLALARNAASFYKDGKVTNVAGPELMATAKPYFIYPGFAFVAPNR
DSTPYKERYQIPEADNIVRGLRYQGFPQFIKVLDIGFLSDEEQPFLKEAIPWKEATQKIVKASSASEQDIVSTIVSNATFESTEEQKRIVAGLKWLGS
DKKITPRGNALDTLCATLEEMQMFEGERDLVMLQHKFEIENKDSRETRTSSLCEYGAPIGS
>d1f06a2 d.81.1.3 (A:119-268) Diaminopimelic acid dehydrogenase (DAPDH) {Corynebacterium glutamicum}
WDPGMFSINRVYAAVLAEHQQHTFWPGPLSQGHSDALRRIPGVQAVQYTLPSADEALEKARRGEAGDLTGKQTHKRQCFVVADAADHERIEND
IRTMPDYFVGYEVENVFIDEATFDSEHTGMPHGGHVITTDGGFNHTVEYLKD
>d1dih_2 d.81.1.3 (131-240) Dihydrodipicolinate reductase {Escherichia coli}
VGVNVMLLKEAKVMGDYTDIEIIAEHRHKVDAPSGTALAMGEAIAHALDKDLKDCAVSREGHTGERVPGTIGFATVRAGDIVGEHTAMFAD
IGERLEITHKASSR
>d1k5ha3 d.81.1.3 (A:126-274) 1-deoxy-D-xylulose-5-phosphate reductoisomerase {Escherichia coli}
ESLTCGRLFMDAVKQSKAQLLPVDEHNAIFQSLPQPIQHNLGYADLEQNGVVSILLTSGGGFRETPLRDLATMTPDQACRHPNWSMGRKISVD
SATMMNKGLEYIEARWLFNASASQMEVLIHPQSVIHSMVRYQDGSQLAQLGEP
>d1gcua2 d.81.1.4 (A:129-246) Biliverdin reductase {Rat (*Rattus norvegicus*)}
MEEFEFLRREVLGKELLKGLSLRTASPLEERFGPAFSGISRLTWLVSLFGEISLISATLEERKEDQYMKMTVQLETQNKGLLSWIEEKGPLKRNRYV
NFQFTSGSLEEVPSVGVN
>d1h6da2 d.81.1.5 (A:213-374) Glucose-fructose oxidoreductase {Zymomonas mobilis}
DPMNRAAVKLIRENQLGKLGMVTTDNSVMDQNDPAQQWRLRRELAGGGSLMDIGIYGLNGTRYLLGEEPIEVRAYTSDPNDERFVEVEDRIIW
QMRFRSGALSHGASSYSTTSRSFSVQGDKAVLLMDPATGYYQNLISVQTPGHANQSMMQPQFIMPAN
>d1dpga2 d.81.1.5 (A:182-412,A:427-485) Glucose 6-phosphate dehydrogenase {Leuconostoc mesenteroides}
KEMVQNIAALRFGNPIDAAWNKDYIKNVQVTLSEVLGVEERAGYDTAGALLDIMIQNHTMQIVGWLAMEKPESTDKDIRAAKNAAFNALKIYD
EAEVNKYFVRAQYQAGDSADFKPYLEELDPADSKNNTFIAGELQFDLPRWEGVPFYVRSGKRLAAKQTRDIVFKAGTFNFGSEQEAQEAVLSIID
PKGAIELKLNAAKSVEDAFNRTIDLGWTVDSEDKKNTPXGSNFADWNGVSIAWKFVDAISAVYTADKAPLETYKSGSMGPEASDKLLAANGDAWVF
KG
>d1qkia2 d.81.1.5 (A:200-434,A:450-511) Glucose 6-phosphate dehydrogenase {Human (*Homo sapiens*)}
DHYLGKEMVQNLMLVRFANRIFGPIWNRDNIACVLTKEPFGTEGRGGYFDEFGIIRDVMQNHLQMLCLVAMEKPESTNSDDVRDEKVVLCKI
SEVQANNVVLGQYVGPNPGEGEATKGYLDLPTVPRGSTTATFAAVVLYVENERWDGVPFILRCGKALNERKAEVRLQFHDVAGDIFHQCKRNEV
IRVQPNEAVYTKMMTCKPGMFFNPEEELDLTYGNRYKNVKLPXMHFVRSDLEAWRIFTPLLHQIELEKPKPIPVIYGSRGPTADELMKRVGFQY
EGTYKWVN
>d1oaca4 d.82.1.1 (A:5-90) Copper amine oxidase, domain N {Escherichia coli}
AHMVPMDKTLKEFGADVQWDDYAQQLFTLIKDGAYVKVPGQAQTAIVNGQPLALQVPPVMKDNKAWVSDTFINDVFQSGLDQTFQVE
>d1ekga_d.82.2.1 (A:) C-terminal domain of frataxin {Human (*Homo sapiens*)}
LDETTYERLAEETLDSLAEFFEDLADKPYTFEDYDVSGSGVLTVKLGGLGTYVINKQTPNKQIWLSPPSSGPKRYDWTGKNWVYSHDGVSLHELLA
AELTKALKTKLDLSSLAGSG
>d1ew4a_d.82.2.1 (A:) CyaY {Escherichia coli}
MNDSEFHRLADQLWLTIERLDDWDGDSIDCEINGVLTITFENGSKIINRQEPLHQVWLATQGGYHFDLGKDEWICDRSGETFWDLLEQAAT
QQAGETVSFR
>d1ewfa1 d.83.1.1 (A:1-217) Bactericidal permeability-increasing protein, BPI {Human (*Homo sapiens*)}
VNPGVVVRSQKGLDYASQQGTAALQKELKRIKIPDYSDFKIKHLGKGHYSMSMDIREQLPSSQISMVPNVGLKFSISNANIKISGKWAQKRFK
MSGNFDSLIEGMSISADLKLGSNPTEGKPTITCSSCSSHINSVHVHISKSKVGWLQFLHKKIESALRNKMNSQVCEKVTNSSELQPYFQTLPVMTK
IDSVAGINYGLVAPPATTA
>d1ewfa2 d.83.1.1 (A:218-456) Bactericidal permeability-increasing protein, BPI {Human (*Homo sapiens*)}
ETLDVQMKGEFYSENHHNPPPAPPVMEFPAAHDRVYLGSDYFFNTAGLVYQEAGVLKMTLRDDMIPKESKFRLLTKFFGTFLPEVAKKFPNMK

IQIHVSASTPPHLSVQPTGLTFYPAVDVQAFALPNSALASLFLIGMHTTGSMEVAESNRLVGELKLDRLLELKHSNIGPFPVELLQDIMNYIVPILVL
PRVNEKLQKGFLPLTPARVQLYNVLQPHQNLLFGADVVYK
>d1ihra_d.191.1.1 (A:) Dimeric C-terminal domain of membrane protein TonB {Escherichia coli}
ARAQALRIEGQVKVKFDVTDPGRVDNVQILSAKPNMFEREVKNAMRRWRYEPGKPGSGIVVNILFKINGTTE
>d2sici_d.84.1.1 (I:) Subtilisin inhibitor {Streptomyces albogriseolus, s-3253}
YAPSALVLTVGKGSATTAAPERAVTLCAPPGSGTHPAAGSACADLAvggDNLALTRGEDVMCPMVDPVLLTVGVWQGKRVSYERVFSNECE
MNAHGSSVFAF
>d1e6ta_d.85.1.1 (A:) MS2 virus coat protein {Bacteriophage MS2}
ASNFTQFVLVDNGGTGDVTWAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQNRKYTIKVEVPKVATQTVGGVELPVAAWRSYLNMELTIPFAT
NSDCELIVKAMQGLLKDGNNPIPSAIAANSGIY
>d1unaa_d.85.1.1 (A:) GA coat protein {Bacteriophage GA}
ATLHSFVLVDNGGTGNVTWVPSNANGVAEWLSNNRSRSQAYRVTASYRASGADKRKYTIKLEVPKIVTQVVNGVELPVAWKAYASIDLTIPIAATD
DVTVISKSITGLFKVGNPIAEAISSQSGFYA
>d1frsa_d.85.1.1 (A:) fr coat protein {Bacteriophage FR}
ASNFEFVFLVDNGGTGDVKVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSANNRKYTIVKVEVPKVATQVQGGVELPVAAWRSYMNMELTIPVF
ATNDDCALIVKALQGTFKTNPIATAIAANSGIY
>d1qbea_d.85.1.1 (A:) Qbeta coat protein {Bacteriophage Qbeta}
AKLETVTIGNIGKDGKQTIVLNPRGVNPNTNGVASLSQAGAVPALEKRTVSVSQPSRNRKNYKVQVKIQNPTACTANGSCDPSVTRQAYADVTSFT
QYSTDEERAFAVTRTEAALLASPLLIDAIDQLNPAY
>d1dwna_d.85.1.1 (A:) PP7 coat protein {Bacteriophage PP7}
SKTIVLSVGEATRTLIEIQSTADRQIFEEKVGPLVGRRLTASLRQNGAKTAYRVNLKLDQADVDCSTSVCGELPKVRYTQVWSHDVTIVANSTEASRK
SLYDLTKSLVATSQVEDLVVNLVPLGR
>d1ej1a_d.86.1.1 (A:) Translation initiation factor eIF4e {Mouse (Mus musculus)}
KHPLQNRWALWFFKNDKSKTWQANLRLISKFDTVEDFWALYNIQLSSNLMPGCDYSLFKDGIEPMWEDENKRGGRWLITLNKQQRRSDLDRF
WLETLLCLIGESFDDYSDDVCGAVNVRAKGDKIAIWTTCECENRDAVTHIGRVYKERLGLPPKIVIGYQSHADTAKSGSTTKNRFVV
>d1ap8_d.86.1.1 (-) Translation initiation factor eIF4e {Baker's yeast (Saccharomyces cerevisiae)}
MSVEEVSKKFEENVSVDDTTATPKTVLSDAHFDVKHPLNTKWTLYTKPAVDKSESWSDLLRPVTSQFTVEEFWAIQNIPEPHPLKSDYHVFRN
DVRPEWEDEANAKGGKWSFQLRGKGADIDELWLRTLLAVIGETIDEDEDSQINGVVLIRKGNNKFALWTKSEDKEPLLRIIGGKFKQVLKLTDDGHLE
FFPHSSANGRHPQPSITL
>d3grs_3_d.87.1.1 (364-478) Glutathione reductase {Human (Homo sapiens)}
YNNIPTVVFSHPIGTVGLTEDEAIHKYGIENVKTSTSFTPMLHNIISGSTYKKFMVRIVTNHADGEVLGVHMLGDSSPEIIQSVAICLKMGAKISDFY
FDNTVVAIHPTAEEFVTMR
>d1gesa3_d.87.1.1 (A:336-450) Glutathione reductase {Escherichia coli}
YSNIPTVVFSHPIGTVGLTEPQAREQYQDDQVKVYKSSFTAMYTAVTTHRQCRMKLCVGSEEKIVGIHGIGFGMDEMILQGFAVALKMGTAKKD
FDNTVVAIHPTAEEFVTMR
>d1feca3_d.87.1.1 (A:358-485) Trypanothione reductase {Crithidia fasciculata}
HTKVACAVFSIPPMSGVCGYVEEDAACKYDQVAVYESSFTPLMHNISGSTYKKFMVRIVTNHADGEVLGVHMLGDSSPEIIQSVAICLKMGAKISDFY
NTIGVHPTSAEELCSMRTPAYFYEKGRVEK
>d1aoga3_d.87.1.1 (A:358-487) Trypanothione reductase {Trypanosoma cruzi}
DHTRVASAVFSIPPMSGVCGYEVVAVYESSFTPLMHKVGSKYKTFVAKIITNHSDGTVLGVHLLGDNAPEIIQGIGICLKLNAKISDFYNTIGV
HPTSAEELCSMRTPSYYVKGEKMEK
>d1h6va3_d.87.1.1 (A:367-499) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}
YDNVPTTVFTPLEYGCCGLSEEKAVERKFGREENIEVYHSFWPLEWTVPSRDNNCYAKVICNLKDNERVVGHVLGPNAGEVTQGFAALKCGLTKQ
QLDSTIGIHPVCAEIFTTLSTKRSGGDILQSGCCG

>d1nhp_3 d.87.1.1 (322-447) NADH peroxidase {Enterococcus faecalis}
GVQGSSGLAVFDYKFASTGINEVMAQKLKGKETKAVTVVEDYLMDFNPDKQKAWFKLVDPETTQILGAQLMSKADLTANINAISLAIQAKMTIEDLA
YADFFFQPAFDKPWNIINTAALEAVKQER

>d1d7ya3 d.87.1.1 (A:309-405) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}
TAPGYAELPWYWSDQGALRIQVAGLASGDEEIVRGEVSLDAPKFTLIELQKGRIVGATCVNNARDFAPLRLLLAVGAKPDRAALADPATDLRKAAA

>d1lv1_3 d.87.1.1 (336-458) Dihydrolipoamide dehydrogenase {Pseudomonas putida}
PAAIAAVCFDPEVVVGKTPEQASQQGLDCIVAQFPFAANGRAMSLESKSGFVRVVARRDNHLILGWQAVGVAVSELSTAFQAQSLEMGACLEDVA
GTIHAHPTLGEAVQEAALRALGHALHI

>d1lpfa3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}
YDLIPSVIYTHPEIAWVGKTEQTLKAEGVEVNVTGPFAASGRAMAANDTGLVKVIADAKTDRVLGVHVIGPSAAELVQQGAIGMFGTSaedLG
MMVFSHPTLSEALHEAALAVNGHAIHIA

>d3lada3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}
YDLIPAVIYTHPEIAGVGKTEQALKAEVAINVGVPFAASGRAMAANDTAGFKVIADAKTDRVLGVHVIGPSAAELVQQGAIAMEFGTSaedLG
MVFAHPALSEALHEAALAVSGHAIHVA

>d1ebda3 d.87.1.1 (A:347-461) Dihydrolipoamide dehydrogenase {Bacillus stearothermophilus}
AIPAVVFSDEPCASVGYFEQQAKDEGIDVIAAKFPFAANGRALALNDTGFKLVVRKEDGVIIGAQIIGPNASDMIAELGLAIEAGMTAEDIALTIH
PTLGEIAMEAAEVAL

>d1ojt_3 d.87.1.1 (471-598) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}
ARVIPGVAYTSPEAVVGETELSAKASARKITKANFPWAASGRAIANGCDKPFTKLIFDAETGRIIGGGIVGPNGGDMIGEVCLAIEMGCDAA
DICKT IHPHPTLGE SIGMAAEVALGCTDLPPQQK

>d1jeha3 d.87.1.1 (A:356-478) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}
YNNIPSVMYSHPEAVVGKTEEQLKEAGIDYKIGKFPFAANSRAKTNQDTEGFVKILIDS KTERILGAHIIGPNAGEMIAEAGLALEYGASAEDVARVC
HAHPTLSEAFKEANMAAYDKAIHC

>d1dxla3 d.87.1.1 (A:348-470) Dihydrolipoamide dehydrogenase {Garden pea (Pisum sativum)}
YDKVPGVVTNPEVASVGKTEEQVKETGVEYRVGKPFMANSRAKADNAEGLVKIIAEKETDKILGVHIMAPNAGELIHEAAIALQYDASSEDIARVC
HAHPTMSEAIKEAAMATYDKPIHI

>d1fcda3 d.87.1.1 (A:328-401) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (Chromatium vinosum)}

PGTPSYLNTCSILAPAYGISVAAIYRPNADGSAIESVPDSGGVTPVDAPDWVLEREVQYAYSWYNNIVHDTFG

>d1qj2c1 d.87.2.1 (C:178-285) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal domain {Pseudomonas carboxydovorans}
GHGYAYEKLKRKIGDYATAAAAVVLTMSGGKCVTASIGLTNVANTPLWAEEAGKVLVGTALDKPALDKAVALAEAITAPASDGRGPAEYRTKMAGVM
LRRAYERAKAR

>d1ffvc1 d.87.2.1 (C:178-287) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal domain {Hydrogenophaga pseudoflava}
GTGWAYEKLKRKTGDWATAGCAVVMRKGNTVSHIRIALTNVAPTA
RAEEAAALLGKAFTKEAVQAAADAAIAICEPAEDLRGDADYKTAMAGQ
MVKR ALNAAWARCA

>d1fo4a4 d.87.2.1 (A:415-531) Xanthine oxidase, domain 4 (?) {Cow (Bos taurus)}
DEFFSAFKQASRREDDIAKVTGMRVLFQPGSMQVKELALCYGGMADRTISALKTQKQLSKFWNEKLLQDV
CAGLAEELSLSPDAPGGMIEFRRT
LTLSFFFKFYLTVLKKLGKDS

>d1jroa3 d.87.2.1 (A:346-462) Xanthine dehydrogenase chain A, domain 4 {Rhodobacter capsulatus}
PGLRCYKLSKRFQFDQDISAVCGCLNLTGSK IETARIAF GGMAGVPKRAA
FEAALIGQDFREDTIAALPLLAQDFTPLSDMRASAAYRMNAAQAM
ALRYVRELSEAVAVLEVMP

>d1rsa_d.88.1.1 (A:) Serum response factor (SRF) core {Human (Homo sapiens)}

>d1mnma_d.88.1.1 (A:) MCM1 transcriptional regulator {Baker's yeast (*Saccharomyces cerevisiae*)}

QKERRKIEIKFIENKTRRHVTFSKRKGIMKKAFESVLTGTVLQQVSETGLVYTSTPKFEPIVTQQEGRNLIQACLNAPDD

>d1egwa_d.88.1.1 (A:) Mef2a core {Human (*Homo sapiens*)}

GRKKIQTIRMDERNRQVTFTKRKGIMKKAFESVLTGTVLQQVSETGLVYTSTPKFEPIVTQQEGRNLIQACLNAPDD

>d1tbd_d.89.1.1 (-) The origin DNA-binding domain of SV40 T-antigen {Simian virus 40}

GSKVEDPKDFPSELLSFLSHAVFSNRTLACFAITYTKEKAALLYKKIMEKYSVTISRHNSYNHNILFFLTPHRHRSAINNYAQKLCTFSFLICKGVNKEYL

MYSALTRDPFSVIESLPGGLKEHDFNPESS

>d1f08a_d.89.1.2 (A:) Replication initiation protein E1 {Bovine papillomavirus}

GSRATVFKLGLFKSLFLCSFHDITRLFKNDKTTNQQWVLAVGLAEVFEASFELLKKQCSFLQMQRSHEGGTCAVYLICFNTAKSRETVRNLMANM

LNVREECLMLQPPKIRGLSAALFWFKSSLSPATLKHGALPEWIRAQTLN

>d1nox_d.90.1.1 (-) NADH oxidase {Thermus thermophilus, HB8}

PVLDAKTAALKRRSIRRYRKDPVPEGLLREILEAALRAPSAWNLPWVVVRDPATKRALREAAGQAHVEEAPVVLVYADLEDALAHLDDEVIPG

VQGERREAQKQAIQRAFAAMGQEARKAWASGQSYYLLGYLLLLEAYGLGSVPMLGFDPERVRAILGLPSRAAIPALVALGYPAAEGYPHSRLPLERVV

LWR

>d1bkja_d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio harveyi}

NNTIETILAHRSIRKFTAVPITDEQRQTIQAGLAASSSSMLQVSVIRVTDSEKRNELAQFAGNQAYVESAAEFLVFCIDYQRHATINPDVQADFTELTLI

GAVDSGIMAQNCLAAESMGLGGVYIGGLRNSAAQVDELLGPENSAVLFGMCLGHPDQNPEVKPRPAHVHHENQYQELNLDDIQSYDQTM

QAYYASRTSNQKLSTWSQEVTKLAGESRPHILPYLNKGLAKR

>d1vfra_d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio fischeri}

THPIIHDLENRYTSKKYDPSKKVSQEDLAVLLEALRLSASSINSQPWFKIVIESDAAKQRMHDHSFANMHQFNQPHIKACSHVILFANKLSYTRDDYDVV

LSKAVADKRITEEQKEAAFASFVFELNCDENGEHKAWTKPQAYLALGNALHTLARLNIDSTMEGIDPELLSEIFADELKGYECHVALAIGYHHPSED

YNASLPKSRKAFEDVITIL

>d1kqba_d.90.1.1 (A:) Nitroreductase {Enterobacter cloacae}

DIISVALKRHSTKAFDASKKLTAEEAKITLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGTYVFNERKMLDASHVVFCAKTAMDDAWLERVV

DQEEADGRFNTPEAKAANHKGRTYFADMHRVDLKDDQWMAKQVYLNVGNFLLGVAALGLDAPIEGFDAAILDEFGLKEKGFTSLVVVPG

HHSVEDFNATLPKSLRPLSTIVTEC

>d1icra_d.90.1.1 (A:) Nitroreductase {Escherichia coli, minor form}

DIISVALKRHSTKAFDASKKLTAEEAKITLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNYVFNERKMLDASHVVFCAKTAMDDVWLKV

VDQEDADGRFATPEAKAANDKGRKFADMHRKDLHDDAEWMAKQVYLNVGNFLLGVAALGLDAPIEGFDAAILDEFGLKEKGFTSLVVVPG

HHSVEDFNATLPKSLRPLQINITLVE

>d1f5va_d.90.1.1 (A:) Nitroreductase {Escherichia coli, oxygen-insensitive form}

MTPTIELIGHRSIRHFTDEPISEAQREAIINSARATSSSFLQCSSIIIRTDKALREELVLTGGQKHVAQAAEFWVFCADFNRHLQICPDAQLGLAEQLL

LGVVDTAMMAQNALIAAESLGLGGVYIGGLRNNIEAVTLLKLPOHVLPFLGLCLGPADNPDLKPRLPASILVHENSYQPLDKGALAQYDEQLAEYY

LTRGSNNRRTWSDHIRRTIIESRPFILDYLHKQGWATR

>d1dt9a3_d.91.1.1 (A:5-142) N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 {Human (*Homo sapiens*)}

PSAADRNVEIWKIKKLIKSLEAARGNGTSMISLIIPPKDQISRVAKMLAEGFTASNIKSRVNRLSVLGAITSVQQRLKLYNKVPPNGLVVYCGTIVTEEG

KEKKVNIDFEPFKPINTSLYLCDNKFHTEALTALLSD

>d1c7ka_d.92.1.1 (A:) Zinc protease {Streptomyces caespitosus}

TVTVTYDPSNAPSQQEIANAQIWNSVRNVQLRAGGNADFSYYEGNDSRGSYAQTDGHGRGYIFLDYQQNQQYDSTRVTAHETGHVLGLPDH

YQGPCSELMSGGGPGPSCPNTYPNAQERSRVNALWANG

>d1g12a_d.92.1.12 (A:) Fungal zinc peptidase {Grifola frondosa}

TYNGCSSSEQSALAAAASAQSYVAEISLYQLOHTAATPRYTTWFGSISSRHSTVLQHYDMNSNDFSSYFDCTCTAAGTFAYVYPNRGTVYLCG

AFWKAPTTGTDQSAGTLVHESSHFRNGGTKDYAGQAAAKSLATMDPDKAVMNADNHEYFSENNPAQS

>d1eb6a_d.92.1.12 (A:) Fungal zinc peptidase {Aspergillus oryzae, deuterolysin}

TEVTDCKGDAESSLTALSNAAKLANQAEEAESGDESKFEEYFKTTDQQTRTTVAERLRAVAKEAGSTSGGTTYHCNDPYGYCEPNVLAYTLP SKN
EIANCDIYYSELPPLAQKCHAQDQATTLHEFTHAPGVYQPGTEDLGYGYDAATQLSAQDALNNADSYALYANAIELKC

>d1ezm_d.92.1.2 (-) Elastase {Pseudomonas aeruginosa}

AEAGGPGENQKIGKYTYGSDYGPLIVNDRCMDDGNVITDMNSSTDSKTPFRACPTNTYKQVNGAYSPLNDAHFFGGVVFKLYRDWFGTSP
LTHKLYMKVHYGRSVENAYWDGTAMLFGDGATMFYPLVSLDVAHEVSHGFTEQNSGLIYRGQSGGMNEAFSDMAGEAAEFYMRGKNDFLIGY
DIKKGSGALRYMDQPSRDRSIDNASQYYNGIDVHHSSGVYNRAFYLLANSPGWDRKAFEVFVDANRYWTATSNYNSGACGVIRSAQNRNSA
ADVTRAFSTVGVTCP

>d8tlne_d.92.1.2 (E:) Thermolysin {Bacillus thermoproteolyticus}

ITGTSTVGVGRGVLDQKNINTTYSTYYLQDNTRGDGIFTYDAKYRTTLPGLWADADNQFFASYDAPAVDAHYAGVTYDYYKNVHNRLSYDGN
NAAIRSSVHYSQGYNNAFWNGSEMIVYGDGDGQTFIPLSGGIDVVVAHELTHAVTDYTAGLIYQNESGAINEAISDIFGTLVEFYANKNPDWEIGEDVV
TPGISGDSLRSMSDPAKYGDPDHYSKRTGTQDNGGVHINSGIINKAAYLISQGGTHYGVSVVGIQRDKLGKIFYRALTQYLPTSNFSQLRAAVQSA
TDLYGSTSQEVASVKQAFDAVGVK

>d1npc_d.92.1.2 (-) Neutral protease {Bacillus cereus, strain dsm 3101}

VTGTNKVGTGKVLGDTKSLNTLSSGYYLQDNTRGATIFTYDAKNRSTLPGTLWADADNVFNAAYDAAAVIDAHYAGKTYDYYKATFNRNSIND
AGAPLKSTVHGSVNNNAFWNGSQMVYGDGDGVTFSLSGGIDVIGHELTHAVTENSSNLIYQNESGALNEAISDIFGTLVEFYDNRNPDWEIGEDI
YTPGKAGDALRSMSDPTKYGDPDHYSKRTGTQDNGGVHINSGIINKQAYLLANGGTHYGVTVTGTGKDKLGAIYRANTQYFTQSTTFSQARAGA
VQAAADLYGANSAAVAVKQSFSAVGVN

>d1bqba_d.92.1.2 (A:) Aureolysin {Staphylococcus aureus}

AAATGTGKVLGDTKDININSIDGGSLEDLTHQGKLSAYNFNDQTGQATLTNEDENFKDDQRAGVDANYAKQTYDYYKNTFGRESYDNHGPI
VSLTHVNHGGQDNRNNAAWIGDKMIYGDGDGRTFTNLSGANDVVAEITHGVQQTANLEYKDQSGALNESFDVFGYFVDDDFLMGEDVV
TPGKEGDALRSMSNPEQFGQPSHMKDYVYTEKDNGGVHTNSGIPNKAAYNVQAIQSKSEQIYRALTETLTSNSFKDLKDALYQAAKDLYEQQT
AEQVYEAWNEVGVE

>d1hs6a3_d.92.1.13 (A:209-460) Leukotriene A4 hydrolase catalytic domain {Human (Homo sapiens)}

LESRQIGPRTLVWESEKEQVEKSAYEFSETESMLKIAEDLGGPVVWQYDLLVPPSFYGGMENPCLTFVTPTLAGDKSLNVIAHEISHSWTGNLVT
NKTWDHFWLNEGHTVYLERHICGRLFGEKFRHFNALGGWGELQNSVKTGETHPFTKLVVDLTDIDPDVAYSSVPYEGFALLFYLEQLLGGPEIFLG
FLKAYVEKFSYKSITTDWKDFLYSYFKDKDVVLNQVDNAWLSPGLPPIKPNY

>d1dmta_d.92.1.4 (A:) Neutral endopeptidase (neprilysin) {Human (Homo sapiens)}

GICKSSDCIKAARLIQNMDATTEPCDFFKYACGGWLKRNVIPETSSRYGNFIDLRLDELEVVLKDVQLQEPKTEDIVAVQKAKALYRSCINESAIDSRRGG
EPPLLKLLPDIYGWPVATENWEQKYGASVTAEKIAQLNSKYGKV/LINLFVGTDKNSVNHWIHDQPRGLPSRDYECTGIYKEACTAYVDFMISVA
RLIRQEERLPIDENQLALEMNKVMLEKEIANATAKPEDRNDPMILYNKMTLAQIQNNFSLEINGKPFWSLNFTNEIMSTVNISITNEEDVVVYAPEY
LTKLKPILTKYSARDLQNLMSWRFIMDLVSSLSRTYKESRNAFRKALYGTSETATWRCANYVNGNMENAVGRLYVEAAFAGESKHVEDLIAQIRE
VFIQTLDDLWMDAETKKRAEEKKALAIKERIGYPDDIVSNDNKLNNYELELNYKEDEFYENIIQNLKFQSQSKQLKLREVKDKDEWISGAAVVNAFYSS
GRNQIVFPAGILQPFFSAQQNSLNYGGIGMVIGHEITHGFDDNGRNFNKGDLVWWTTQQSASFKEQSQCMVYQYGNFSWDLAGGQHLN
GINTLGENIADNGGLGQAYRAYQNYIKKNGEEKLLPGLDLNHKQLFLNFAQVWCGBTYRPEYAVNSIKTDVHSPGNFRIIGTLQNSAEFSEAHCRKN
SYMNPEKKCRVW

>d1i1ip_d.92.1.5 (P:) Neurolysin (endopeptidase 24.16) {Rat (Rattus norvegicus)}

MSSYTAAGRNVLRWDLSP_EQIKTRTEQLIAQTKQVYDTVTGIALKEVTYENCLQLADIEVTYIVERTMLDFPQHVSSDREVRAAESTADKKLSRF DIE
MSMREDVFQRIVHLQETCDLEKIKPEARRYLEKSIMKGKRNGLHLSEHIRNEIKSMKRMSELCIDFNKNLNEDDTSLVFSKAELGALPDDFIDSLEKT
DEDKYKVTLYPHYFPVMKKCCVPETRRKMEMAFHTRCKQENTAILQQLLPLRAQVAKLLGYNTHADFVLELN TAKSTS RVAFLDDLSQKLKPLGE
AEREFILESLKKKECEERGFYDGKINAWDLHYYMTQTEELKYSVDQESLKEYFPIEVVTEGLLSIYQELLGLSFEQVPAHVVWNKSVSLYTVKDKATGEV
LGQFYLDLYPREGKYNHAACFGLQPGCLLPGDSRMMMSVAALVNFSPQVAGRPSLLRHDEVRTYFHEFGHVMHQICAQTD FARFSGTNVETDFVE
VPSQMLENWWVDVDSLRLSKHYKDGHPIITDELLEKLVASRLVNTGLLRLQIVLSKVDQSLHTNATLDAASEYAKYCTEILGVAATPGTNMPATFGH

LAGGYDGQYYGYLWSEVFSMDMFHSCFKKEGMNPEVGMKVRNLILKPGGSLGMDMLQNFLQREPNQKAFLMSRGL
>d1j7na1 d.92.1.14 (A:27-263) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}
ERNKQTQEEHLKEIMKHIVKIEVKGEAAKLLKEVKPDSVLEMYKAIGGGKYIVDGDITKHSLEALSEDKKKDIYGDALLHEHYVYAKEGYEPV
LVIQSSEDYVENTEKALNVYYEIGKILSRDILSKINQPYQKFIDVLNTIKNASDSQDQLFTNQLKEHPTDFSVFLEQNSNEVQEVFAKAFAYYIEPQH
RDVLQLYAPEAFNYMDKFNQEINLSLEELKDQR
>d1j7na2 d.92.1.14 (A:551-773) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}
PKSKIDTKIQEAQLNINQEWNKALGLPKYTKLITFNVHNRYASNIVESAYLILNEWKNNIQSDLKVTNYLDGNRFTDITLPNIAEQYTHQDEIY
EQVHSKGLYVPESRSILLHGPKGVELRNDSSEGFIHEFGHAVDDYAGYLLDKNQSDLVTNSKKFIDIFKEEGSNLTSYGRTEAEFFAEARLMHSTDHA
ERLKVKQKNAPKTQFQFINDQIKFI
>d1lml__ d.92.1.3 (-) Leishmanolysin {Leishmania major}
VVRDVNWGALRIAVENTEDLTDPAYHCARVGQHVVDHAGAIVTCTAEDILTNEKRDILVKHLIPQAVQLHTERLKVQQVQGKWVTDMDVGDIGDF
KVPQAHITEGSNTDFVMYVASVPSEEGVLAWATTCTQTFSDGHPAVGVINIPAANIASRYDQLVTRVVTHEMAHALGFSGPFFEDARIANVPNVR
GKNFDVPVINSSTAVAKAREQYGCDTLEYLEVEDQGGAGSAGSHIKMRNAQDELMAPAAAAGYTALTMAIFQDLFYQADFSKAEVMPWGQN
AGCAFLTNKCMQSVTQWPAMFCNESDAIRCPTSRLSLGACGVTRHPGLPPWQYFTDPSLAGVSAFMDCPVVVPYSDGSCTQRASEAHASLL
PFNFVSDAARCIDGAFRPKATDGVKSAGLCANVQCDTATRTYSVQVHGSNDNTCPGLRVELSTSNAFEGGGYITCPYVEVCQGNVQAAKD
>d1kapp2 d.92.1.6 (P:1-246) Metallo protease, catalytic (N-terminal) domain {Pseudomonas aeruginosa, alkaline protease}
GRSDAYTQVDNFLHAYARGGDELVNGHPSYTVQAAEQILREQASWQKAPGDSVLTLSYSFLTPNTPWKYVSDIYSLGKFSAFSAQQQAQA
KLSLQSWSVTNIHFVDAGQGDQGDLTFGNFSSVGAAFAFLPDVVDALKQGSWYLINSSYANVNPAANGNYGRQLTHEIGHTLGLSHPGDYN
AGEGDPTYADATYAEDTRAYSVMSYWEEQNTGQDFKGAYSSAPLDDIAAIQKLY
>d1sat_2 d.92.1.6 (4-246) Metallo protease, catalytic (N-terminal) domain {Serratia marcescens}
TGYDAVDDLHYHERNGNQINGKDSFSNEQAGLFITRENQTWNGYKVFGQPVKLTSFPDYKFSSTINVAGDTGLSKFSAEQQQQAKLSLQSADV
ANITFTVEAGQKANITFGNYSQDRPGHYDYGTYQAYALPNTIWQGQDLGGWTWNVQNSNVKHPATEDYGRQFTTHEIGHALGLSHPGDYNAG
EGDPTYADVTYADETRQFSLMSYWSETNTGGDNGGHYAAAPLDDIAAIQHLY
>d3btaa3 d.92.1.7 (A:1-546) Botulinum neurotoxin {Clostridium botulinum, serotype A}
PFVNQFNQYKDPVNGVDIAYIKIPNVGQMOPVKAFKIHNIWVIPERDTFTNPEEGDLNPPEAKQVPVSYYDSTYLDNEKDNYLGVTKLFERIY
STDLGRMLLTSIVRGIPFWGGSTDTELKVIDTNCINVIQPDGSYRSEELNLVIIIGPSADIQFECKSGFGEVNLNLRNGYGSTQYIRFSPDFTFGFEESLEV
DTNPLLGAGKFAUTPAVTLAHELIHAGHRLYGAINPNRPFVNTNAYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNNFKFDIASTLNKA
IVGTTASLQYMKNVFKEKYLLEDTSGKFSVDKLFKDLYKMLTEIYTEDNFVFKFKVLNRKTYLNFDKAVFKINIVPKVNYTIYDGFNLRTNLAANFN
GQNTEINNMNFTKLKNFTGLFEFYKLLCVRGIITSKTSKLDKGYNKALNDLICKVNNWDLFFSPEDNFTNDLNKGEETSDNIEAAEENISLDLIQY
YLTFNFDNEPENISIENLSSDIIGQLELMPNIERFPNGKKYELDK
>d1epwa3 d.92.1.7 (A:1-533) Botulinum neurotoxin {Clostridium botulinum, serotype B}
PVTINNFNYNDPIDNNNIIMMEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCEYDPDYLNTNDKKNIFLQTMKLFNRRIKS
KPLGEKLEMIIINGIPYLGDRRVPLEEFNTNIASVTVNKLISNPGEVERKKGIFANLIIFGPVNLNETIDIGIQNHFASREGFGGIMQMFKCPEYVSV
FNNVQENKGASIFNRRGYFSDPALILMHELIHLHGLYGIKVKDDLPVPNEKKFFMQSTDIAQAEELYTFGGQDPSIITPSTDKSIYDKVLQNFRGIVDR
LNKVLVCISDPNININIYKNKFKDKYKFVDEDSEGKYSIDVESFDKLYKSLMFGFTETNIAENYKIKTRASYFSDSLPPVKIKNLLDNEIYTIEEGFNISDKDM
EKEYRGQNKAINKQAYEISKEHLAGVYKIQMCKSVKAPGICIDVDNEDLFFIADKNSFDDLSKNERIEYNTQNSYIENDFPINELILDTLISKIELPSENT
ESLTDNFNDVDPVYEKQPAIKKIFTDE
>d1f83a_ d.92.1.7 (A:) Botulinum neurotoxin {Clostridium botulinum, serotype B}
PVTINNFNYNDPIDNNNIIMMEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCEYDPDYLNTNDKKNIFLQTMKLFNRRIKS
KPLGEKLEMIIINGIPYLGDRRVPLEEFNTNIASVTVNKLISNPGEVERKKGIFANLIIFGPVNLNETIDIGIQNHFASREGFGGIMQMFKCPEYVSV
FNNVQENKGASIFNRRGYFSDPALILMHELIHLHGLYGIKVKDDLPVPNEKKFFMQSTDIAQAEELYTFGGQDPSIITPSTDKSIYDKVLQNFRGIVDR
LNKVLVCISDPNININIYKNKFKDKYKFVDEDSEGKYSIDVESFDKLYKSLMFGFTETNIAENYKIKTRASYFSDSLPPVKIKNLLDNEIYTIEEGFNISDKDM
EKEYRGQNKAINKQAYEISK
>d1ast__ d.92.1.8 (-) Astacin {European fresh water crayfish (Astacus astacus)}

AAILGDEYLWSGGVIPYTFAGVSGADQSAILSGMQUEEKTICRFVPRTTESDYVEIFTSGSGCWSYGRISGAQQVSLQANGCVYHGTIIHELMHAI
GFYHEHTRMDRDNYVTINYQNVDPMSMTSNFDIDTYSRYVGEDYQYYSIMHYGKYSFSIQWGVLETIVPLQNGIDLTDPYDKAHMLQTDANQINNLY
TNECSL

>d4aig__ d.92.1.9 (-) Snake venom metalloprotease {Eastern diamondback rattlesnake (*Crotalus adamanteus*), adamalysin II}
NLPQRYIELVVVADRRVFMKYNSDLNIIRTRVHEIVNIINEFYRSLSNRVSLTDLEIWSGQDFITIQSSSNTLNSFGEWRERVLLTRKRHDNAQLTAINF
EGKIIGKAYTSSMCNPRSSVGIVKDHSPINLLAVTMAHELGHNLGMEHDGKDCLRGASLCIMRPGLTGRSYEFSDDSMGYYQKFLNQYKPQCILN
KP

>d1atla_d.92.1.9 (A:) Snake venom metalloprotease {Western diamondback rattlesnake (*Crotalus atrox*), atrolysin C}
LPQRYIELVVVADHRVFMKYNSDLNTIRTRVHEIVNFINGFYRSLSNIHVS LTDLEIWSNEDQINIQSASSTLNAFAEWRETDLNRKSHDNAQLTAIE
LDEETGLAPLGTMCDPKLSIGIVQDHSPINLLMGVTMAHELGHNLGMEHDGKDCLRGASLCIMRPGLTGRSYEFSDDSMHYYERFLKQYKPQCILN
NKP

>d1buda_d.92.1.9 (A:) Snake venom metalloprotease {Five-pace snake (*Agkistrodon acutus*), acutolysin A}
FQRYMEIVVVDHSMVKYNGDSDSIKAWVYEMINTITESYSLKIDISLSGLEIWSGKDLIDVEASAGNTLKSFGEWRAKDLIHRISHDNAQLLATDF
DGATIGLAYVASMCNPKRSVGVIQDHSSVNRLVAITLAHEMAHNLGVSHDEGSCSCGGKSCIMSPSISDETIKYFSDCSIQCRDYISKENPPCILN
>d1qua_a_d.92.1.9 (A:) Snake venom metalloprotease {Chinese five-pace snake (*Agkistrodon acutus*), acutolysin C}
PAPQTSEIHLFLVDHSMYAKYNSNSSKTTLKARVNIMMAIYSSNLVITSGIEMWSAADLITVQSSSNTLKFASWRETDLLKRTSDNAQLLTATN
FNGNTVGLAYLKTMCNKSYVGLIQDHSAPILLMAVTMAHELGHNLGMNHGDAGCSCATCIMAPVLSSGPAKSFSDCSKHDYQSFTIHKPQCLLN

>d1bkca_d.92.1.10 (A:) TNF-alpha converting enzyme, TACE, catalytic domain {Human (*Homo sapiens*)}
DPMKNTCKLKVADHRFYRYMGRGEESTTNYLIELIDRVDDIYRNTAWDNAGFKGYGIQEIRLKSPQEVKPGEKHYNMAKSYPNEEKDAWDVK
MILLEQFSFDIAEEASKVCLAHLFYQDFDMGTLGLAYVSPRANSHGGVCPKAYYSPVGKKNIYLNGLTSTKNYGKILTKEADLVTTHELGHNFGAE
HDPDGLAECAPNEDQGGKYVMYPIAVSGDHENNKMFSCSKQSIYKTIESKAQECFQER

>d1cgla_d.92.1.11 (A:) Fibroblast collagenase (MMP-1) {Human (*Homo sapiens*)}
VLTENGNPRWEQTHLRYRIENYTPDLPRADVDHAIEKAFQLWSVTPLFTKVSEGQADIMISFVRGDHRDNSPDFGPGGNLAHAFDPGPGIGGDA
HFDEDERWTNNFRYENLHRVAAHELGHSLGHSTDIGALMPSYTFSGDVQLAQDDIDGIQAIYGRSQNPVQ

>d1hfc__ d.92.1.11 (-) Fibroblast collagenase (MMP-1) {Human (*Homo sapiens*)}
PRWEQTHLTYRIENYTPDLPRADVDHAIEKAFQLWSVTPLFTKVSEGQADIMISFVRGDHRDNSPDFGPGGNLAHAFQPGPGIGGDAHFDEDE
RWTNNFRYENLHRVAAHELGHSLGHSTDIGALMPSYTFSGDVQLAQDDIDGIQAIYGRS

>d1fbl_2 d.92.1.11 (100-271) Fibroblast collagenase (MMP-1) {Pig (*Sus scrofa*)}
FVLTPGNPRWENTHILTYRIENYTPDLSREDVDRAIEKAFQLWSNVPLFTKVSEGQADIMISFVRGDHRDNSPDFGPGGNLAHAFQPGPGIGGDA
HFDEDERWTKNFRDYNLYRVAHELGHSLGHSTDIGALMPSYIYTGDVQLSQDDIDGIQAIYGPSENPVQPSG

>d1hova_d.92.1.11 (A:) MMP-2 {Human (*Homo sapiens*)}
MYNFFPRPKWDKNQITYRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRIHDGEADIMINFGRWEHGDGYPFDGKDGLLAHAFAPGTGVGG
DSHFDDDELWTNTSANSLFLVAAHEFGHAMGLEHSQDPGALMAPIYTAKNFRLSQDDIKGIQELYG

>d1i76a_d.92.1.11 (A:) Neutrophil collagenase (MMP-8) {Human (*Homo sapiens*)}
MLTPGNPKWERTNLTYRIRNYTPQLSEAVERAIKDAFELWSVASPLIFTRISQGEADINIAFYQRDHGDNSPFDGPGNILAHAQPGQGIGGDAHF
DAEETWTNTSANSLFLVAAHEFGHAMGLEHSQDPGALMAPIYTAKNFRLSQDDIKGIQELYG

>d1qiba_d.92.1.11 (A:) Gelatinase A {Human (*Homo sapiens*)}
RKPKWDKNQITYRIIGYTPDLDPETVDDAFARAFQVWSDVTPLRFSRIHDGEADIMINFGRWEHGDGYPFDGKDGLLAHAFAPGTGVGGDSHFDD
DELWSLGKGVGYSFLVAAHEFGHAMGLEHSQDPGALMAPIYTAKNFRLSQDDIKGIQELYGASP

>d1hy7a_d.92.1.11 (A:) Stromelysin-1 (MMP-3) {Human (*Homo sapiens*), fibroblast}
FRTFPGIPKWRKTHILTYRIVNYTPDLPKDAVDSAVEKALKVWEETPLTSRLEYGEADIMISFAVREHGDFYPFDGPGNLAHAYAPGPGINGDAHF
DDDEQWTKDTTGTNLFLVAAHEIGHSLGLFHSANTEALMYPLYHSLTDLTFRLSQDDINGIQSLYGPPP

>d1mmq_d.92.1.11 (-) Matrilysin (MMP-9) {Human (*Homo sapiens*)}
YSLFPNSPKWTSKVVTYRIVSYTRDLPHITVDRLVSKALNMWGKEIPLHFRKVVWGTADIMIGFARGAHGDSYFPDGPNTLAHAFAPGTGLGGDA

HFDEDERWTDGSSLGINFLYAA~~THE~~LGHSLGMGHSSDPNAVMYPTYGNGDPQNFKLSQDDIKGIQKLYGK
>d1hv5a_d.92.1.11 (A:) Stromelysin-3 (MMP-11) {Mouse (Mus musculus)}
MFVLSGGRWEKTDLTYRILRFPWQLVREQVRQTVAEALQVSEVTPLTFTEVHEGRADIMDFARYWHGDNLPDFGPGGILAHAFFPKTHREGDV
HFDYDETWTIGDNQGTDLQVAHEFGHVGLQHTTAAKALMSPFYTFRPLSLSPPDRRGIQHLYG
>d1jk3a_d.92.1.11 (A:) Macrophage elastase (MMP-12) {Human (Homo sapiens)}
GPVWRKHITYRINNYTPDMNREDVDYAIRKA~~F~~QVWSNVTPLKF~~S~~KINTGMADILVVFARGAHGDFHAFDGKGGILAHA~~F~~GPGSGIGGDAHFDED
EFWTTHSGGTNLFLTA~~V~~HAI~~G~~HSLGLGHSSDKAVMFPT~~Y~~KYVDINTFRLSADDIRGIQSLYG
>d830ca_d.92.1.11 (A:) Collagenase-3 (MMP-13) {Human (Homo sapiens)}
YNVF~~P~~RTLKWSKMNLTYRIVN~~Y~~TPDMT~~H~~SEVEKA~~R~~KA~~F~~KVWS~~D~~V~~T~~PLNFTRLHDG~~I~~ADIMISFGIKEHGDFYPFDGPSGLLA~~A~~F~~P~~PGPNYGGDA
HFDDDETWTSSSKGYNLFLVA~~A~~HEFGHSLGLDHSKDPGALMFPIYT~~T~~GKSHFM~~L~~PD~~D~~VQGIQSLY~~G~~PGDE
>d1cxva_d.92.1.11 (A:) Collagenase-3 (MMP-13) {Mouse (Mus musculus)}
YNVF~~P~~RTLKWSQTNLTYRIVN~~Y~~TPDM~~H~~SEVEKA~~R~~KA~~F~~KVWS~~D~~V~~T~~PLNFTRIYDG~~T~~ADIMISFGTKEHGDFYPFDGPSGLLA~~A~~F~~P~~PGPNYGGDA
HFDDDETWTSSSKGYNLFLVA~~A~~HEFGHSLGLDHSKDPGALMFPIYT~~T~~GKSHFM~~L~~PD~~D~~VQGIQFLYG
>d1bqqm_d.92.1.11 (M:) Membrane-type matrix metalloproteinase (CDMT1-MMP) {Human (Homo sapiens)}
IQGLKWQHNEITFCIQNYTPKVGEYATYEAIRKA~~R~~FRVWE~~S~~ATPLRFREV~~P~~Y~~A~~IREGHEKQADIMIFFAEGFHGD~~S~~TPFDGEGGFLA~~H~~AYFPGPNIGGD
THFDAEPWTVRNEDLN~~G~~NDIFLVAVHELGH~~A~~GLEHSSDPSAIMAPFYQWM~~T~~ENFVL~~P~~DDRRGIQQLYGGES
>d1qba_4 d.92.2.1 (201-337) Bacterial chitobiase, Domain 2 {Serratia marcescens}
SNADLQTL~~P~~AGALRGKIVPTPMQVKVHAQDADLRKGVALDLSTLV~~K~~PAADVVSQR~~F~~ALLGV~~P~~VQ~~T~~NGYPIKTDI~~Q~~PGFKGAMA~~V~~SGAYELKIGKKE
AQVIGFDQAGV~~F~~YGLQSILS~~V~~PSDGSGKIA~~T~~LDASDAPR
>d1jaka2 d.92.2.1 (A:8-150) beta-N-acetylhexosaminidase, N-terminal domain {Streptomyces plicatus}
DRKAPVRPTPLDRVIPAPASVDPGGAPYR~~I~~TRGTHIRVDD~~S~~REARRVG~~D~~YLADLLRPATGYRLPVTAHG~~H~~GGIRLRLAGGPYGDEGYRLDSGPAGVTI
TARKAAGLFHG~~V~~QTLRQLL~~P~~AVEKD~~S~~AQPGP~~W~~L~~V~~AGG~~T~~IDTPR
>d1cwdl_d.93.1.1 (L:) p56-lck tyrosine kinase {Human (Homo sapiens)}
GSWFFKNLSRKDAERQLLAPGNTHGSFLIRESE~~T~~AGSF~~S~~LSVRDFDQNQGEV~~V~~KHYKIRNLDNGGFY~~I~~SPRITF~~P~~GL~~H~~ELVRHYTNASDGLCTRLRS
>d1lkka_d.93.1.1 (A:) p56-lck tyrosine kinase {Human (Homo sapiens)}
LEPEPWFFKNLSRKDAERQLLAPGNTHGSFLIRESE~~T~~AGSF~~S~~LSVRDFDQNQGEV~~V~~KHYKIRNLDNGGFY~~I~~SPRITF~~P~~GL~~H~~ELVRHYTNASDGLCTRL
SRPCQT
>d1bkl_d.93.1.1 (-) v-src tyrosine kinase {Rous sarcoma virus, Schmidt-ruppin strain a}
EEWYFGKITR~~R~~ESE~~LL~~N~~P~~ENPRGTFLVRESETTKGAYCLS~~S~~DFNA~~K~~GLNV~~K~~HYKIRKLDSGGFYITSRTQ~~F~~SSLQQLVAYYSKHA~~D~~GLCHRLTNVC
PTSKEFIVTD
>d1shaa_d.93.1.1 (A:) v-src tyrosine kinase {Rous sarcoma virus, Schmidt-ruppin strain a}
AEEWYFGKITR~~R~~RESER~~LL~~N~~P~~ENPRGTFLVRESETTKGAYCLS~~S~~DFNA~~K~~GLNV~~K~~HYKIRKLDSGGFYITSRTQ~~F~~SSLQQLVAYYSKHA~~D~~GLCHRLTNV
CPT
>d1a09a_d.93.1.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}
DSIQAEWYFGKITR~~R~~RESER~~LL~~NAENPRGTFLVRESETTKGAYCLS~~S~~DFNA~~K~~GLNV~~K~~HYKIRKLDSGGFYITSRTQ~~F~~NSLQQLVAYYSKHA~~D~~GLCHR
LTTVCP
>d1g83a2 d.93.1.1 (A:142-245) Tyrosine kinase Fyn {Human (Homo sapiens)}
DSIQAEWYFGK~~L~~GRKDAERQLLSFGNPRGTFLIRESETTKGAY~~S~~LSIRDWDDMKGDHV~~K~~HYKIRKLDSGGYYITTRAQFETLQQLVQHYSERAGLS
SRLVVP
>d1ayaa_d.93.1.1 (A:) Tyrosine phosphatase Syp {Mouse (Mus musculus)}
MRRWFHPNITGVEAENLLTRGV~~D~~GSFLARPSKS~~N~~PGDF~~T~~LSVRRNGAVTHIKIQNTGDYYDLYGGEKFATLAE~~V~~QYYMEHHGQLKEKNGDVIELK
YPLN
>d1fhs_d.93.1.1 (-) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo sapiens)}
GIEMKPHPWFFGKIPRAKEEMLS~~K~~QRHDGAFLIRESESAPGDF~~S~~LSV~~K~~FGNDVQHFKVLRDGAGKYFLWVV~~K~~FN~~S~~LN~~E~~LV~~D~~YHRSTS~~V~~SRNQQI~~F~~

RDIEQVPQQPTYVQA

>d1zfp_e_d.93.1.1 (E:) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo sapiens)}

KPHPWFFGKIPRAKEEMLSQRHDGAFLIRESESAPGDFSLVKFGNDVQHFKVLRDGAGKYFLWVV/KFNSLNELV/DYHRSTS/VRNQQIFLRDIE
Q

>d1qcfa2 d.93.1.1 (A:146-248) Hemopoetic cell kinase Hck {Human (Homo sapiens)}

EEWFFKGISRKDAERQLLAPGNMLGSFMIRDSETTKGSYSLVRDYDPRQGDTVKHYKIRTLNGGFYISPRSTFSTLQELVDHYKKGNGLCQKLSV
PCMSS

>d1mil__ d.93.1.1 (-) Shc adaptor protein {Human (Homo sapiens)}

GSQRLRGEWFHGKLSRREAALLQLNGDFLVRETTTPGQYVLTGLQSGQPKHLLVDPEGVVRTKDHRFESVSHLISYHMDNHLPIISAGSELCLQQ
PVERKL

>d1qada_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Cow (Bos taurus)}

EDLPHHDEKTWNVGSSNRNAENLLRGKRDGTFLVRESSKQGCYACSVVVGEVKHCVINKTATGYGFAEPYNLYSSLKELVLHYQHTSLVQHNDSL
NVTLAYPVYA

>d1pica_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Human (Homo sapiens)}

GSPIPHDEKTWNVGSSNRNAENLLRGKRDGTFLVRESSKQGCYACSVVVGEVKHCVINKTATGYGFAEPYNLYSSLKELVLHYQHTSLVQHNDSL
NVTLAYPVYAQQRR

>d1fu6a_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Rat (Rattus norvegicus)}

GMNNNMSLQDAEWYWGDISREEVNEKLRDTADGTFVRDASTKMHGDTLRLKGNNNSIKIFHRDGKYGFSPLTFNSVVELINHYRNESLAQ
YNPKLDVKLLYPVSKY

>d1ab2__ d.93.1.1 (-) Proto-oncogen tyrosine kinase {Human (Homo sapiens)}

GSGNSLEKHSWYHGPVSRNAEYLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLYVSSESRFNTLAEVHHHSTVADGLITLHYP
APKRGIIHRD

>d1a81a1 d.93.1.1 (A:9-137) Syk tyrosine kinase {Human (Homo sapiens)}

SANHLPFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSAHGRKAHHYTIERELNGTYIAGGRTHASPADLCHYHSQESDGLVCLLKP
FNRPQGVQPKTGPFEDLKENLIREYVKQTWN

>d1a81a2 d.93.1.1 (A:138-262) Syk tyrosine kinase {Human (Homo sapiens)}

LQGQALEQAIISQKPQLEKLIATTAEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNNGSYALCLLHEGKVLHYRIDDKTGKLSIPEGKKFDTL
WQLVEHYSYKADGLLRLTVPCQKI

>d1a81e1 d.93.1.1 (E:9-117) Syk tyrosine kinase {Human (Homo sapiens)}

SANHLPFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSAHGRKAHHYTIERELNGTYIAGGRTHASPADLCHYHSQESDGLVCLLKP
FNRPQGVQPKT

>d1a81e2 d.93.1.1 (E:152-262) Syk tyrosine kinase {Human (Homo sapiens)}

PQLEKLIATTAEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNNGSYALCLLHEGKVLHYRIDDKTGKLSIPEGKKFDTLWQLVEHYSYKADGL
LRVLTVPCQKIGTQ

>d1csya_ d.93.1.1 (A:) Syk tyrosine kinase {Human (Homo sapiens)}

GSRRASVGSHKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNNGSYALCLLHEGKVLHYRIDDKTGKLSIPEGKKFDTLWQLVEHYSYKADGL
RVLTVPCQKIGTQ

>d2plda_ d.93.1.1 (A:) Phospholipase C-gamma-1 {Cow (Bos taurus)}

GSPGIHESKEWYHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYAFRAEGKIKHCRVQQEGQTVMLGNSEFDSLVDLISYYEKHPLYRKMKLRY
PINEENSS

>d1blk__ d.93.1.1 (-) P55 Blk protein tyrosine kinase {Mouse (Mus musculus)}

GSVAPVETLEVKEWFFRTISRKDAERQLLAPMNKAGSFLIRESESNKGAFSLVKDITTQGEVVKHYKIRSLDNGGGYIISPRITFPTLQALVQHYSKKGD
GLCQKLTLPVCVNLA

>d2abl_2 d.93.1.1 (140-237) Ab1 tyrosine kinase {Human (Homo sapiens)}

SLEKHSWYHGPVRNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLYVSSESRFNTLAELVHHSTVADGLITLHYPAP
>d1jwoa_d.93.1.1 (A:) Csk homologous kinase Chk {Human (Homo sapiens)}
LSLMPWFHGKISGQEAVQQLQPEDGLFLVRESARHPGDYVLCVSFGRDVHRYVLHRDGHLTIDEAVFFCNLMDMVEHYSKDKGAICTKLRPKRK
K
>d1bf5a3 d.93.1.1 (A:569-710) STAT-1 {Human (Homo sapiens)}
LLPLWNDGCIMGFISKERERALLKDQQPGTFLLRFSESSREGAITFTWVERSQNGGEPDFHAVEPYTKKELSAVTFPDIIRNYKVMAAENIPENPLKYL
YPNIDKDHAFGKYYSRGYIKTELISVS
>d1bg1a3 d.93.1.1 (A:576-716) STAT3b {Mouse (Mus musculus)}
ILALWNEGYIMGFISKERERAILSTKPPGTFLRFSESSKEGGVTFTWVEKDISGSTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNLVSPLVLYPDI
PKEEAFGKYCRPESQEHPPEADPGSAAPYLTKFICVTPF
>d2cbla3 d.93.1.1 (A:264-351) Cbl {Human (Homo sapiens)}
THPGYMAFLTYDEVKARLQFIHKPGSYIFRLSCTRLGQWAIGYVTADGNILQTIPHNKPLFQALIDGFREGFYLPDGRRNQNPDLTG
>d2shpa2 d.93.1.1 (A:2-110) Tyrosine phoshatase shp-2 {Human (Homo sapiens)}
KSRRWFHPNITGVEAENLLTRGVDGSLARPSKSNPGLTLSVRRNGAVTHIKIQNTGDYYDLYGGEKFATLAEVQYYMEHHGQLKEKNGDVIELK
YPLNCADPTSE
>d2shpa3 d.93.1.1 (A:111-218) Tyrosine phoshatase shp-2 {Human (Homo sapiens)}
RWFHGHLSGKEAEKLLTEKGKHGSFLVRESQSHPGDFVLSVRTGDDKGESNDGSKVTHVMIRCQELKYDVGGGERFDSDLVEHYKKNPMVETL
GTVLQLKQPLNT
>d1d4ta_d.93.1.1 (A:) The Xlp protein Sap {Human (Homo sapiens)}
MDAVAVYHGKISRETGEKLLLATGLDSYLLRDSESVPGVYCLCVLYHGVIYTYRSQTELGSWSAETAPGVHKRYFRKIKNLISAFQKPDQGIVIPLQY
PVEK
>d1spha_d.94.1.1 (A:) Histidine-containing phosphocarrier protein (HPr) {Bacillus subtilis}
AQKTFKVTADSGIHARPATVLVQTASKYDADVNLLEYNGKTVNLKDIMGVMSLGIAKGAEITISAGADENDALNAEETMKSEGLGE
>d1ptf_d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Enterococcus faecalis}
MEKKEFHIVAETGIHARPATLLVQTASKFNSDINLEYKGKSVNLKSIMGVMSLGVGQGSDVTITVDGADEAEGMAIVETLQKEGLA
>d1opd_d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Escherichia coli}
MFEQEVTITAPNGLHTRPAQFVKEAKGFTSEITVTSNGKSASAKDLFKLQLTQLGTVVTISAEGEDEQKAVEHLVKLMAELE
>d1pch_d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Mycoplasma capricolum}
AKFSAIITDKVGLHARPASVLAKEASKFSSNITIIANEKQGNLKSIMNVMAMAIKTGTEITIQAQDGNDAQAIQAIQTMIDTALIQG
>d1zer_d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Staphylococcus aureus}
MEQNSYVIIDETGIHARPATMLVQTASKFDSDIQLENGKKVNLKSIMGVMSLGVGKDAEITIYADGSDESDAIQAIQTMIDTALIQG
>d1qr5a_d.94.1.1 (A:) Histidine-containing phosphocarrier protein (HPr) {Staphylococcus carnosus}
MEQQSYTIIDETGIHARPATMLVQTASKFDSDIQLENGKKVNLKSIMGVMSLGVGKDAEITIYADGSDEADAQAIQAITDVLSK EGLTE
>d1k1ca_d.94.1.1 (A:) Crh, catabolite repression HPr-like protein {Bacillus subtilis}
VQQKVEVRLKTGLQARPAALVQEANRFTSDVFLEKDGKKVNAKSIMGLMSLAVSTGTEVTLIAQGEDEQEALEKLAAYVQEEV
>d1jrma_d.206.1.1 (A:) Hypothetical protein MTH637 {Archaeon Methanobacterium thermoautotrophicum}
VITMDCLREVGDDLLVNIEVSPASGKFGIPSYNEWRKRIEVKIHSPPQKGKANREIIKEFSETFGRDVEIVSGQKSRQKTIRIQQGMGRDLFLKLVSEKGL
EIP
>d1iba_d.95.1.1 (-) Glucose permease domain IIB {Escherichia coli}
MAPALVAFAFGGKENITNLDACITRLRVSVADVSVDQAGLKKLGAAAGVVVAGSGVQAFGKTSNDLNKTEMDEYIRNFG
>d1af5_d.95.2.1 (-) DNA endonuclease I-Crel {Chlamydomonas reinhardtii}
KYNKEFLYLAGFVDGDGSIAQIKPNQSYKFKHQLSLTFQVTQKTRRWFLGKLVDEIGVGVYDRGSVSDYILSEIKPLHNFLTQLQFPLKLKQKQAN
LVLKIIEQQLPLEVCTWVDQIAALNDS
>d1g9za_d.95.2.1 (A:) DNA endonuclease I-Crel {Chlamydomonas reinhardtii}

NTKYNKEFLLYLAGFVDGDGSIIAQIKPNQSYKFHKQLSLTFQVTQKTQRRWFSDKLVDEIGVGYVRDRGSVSDYILSEIKPLHNFLTQLQPFLKLKQKQ
ANLVLKIIEQLPSAKESPDKFLEVCTWVDQIAALNDSKTRKTTSETRAVLD
>d1b24a1 d.95.2.1 (A:7-99) I-dmol {Archaeon Desulfurococcus mobilis}
VSGISAYLLGLIIGDGGGLYKLKYKGNRSEYRVVITQKSENLIKQHAPILMQFLIDELNVKSQIQVKGDTRYELRVSSKKLYYYFANMLERIR
>d1b24a2 d.95.2.1 (A:100-179) I-dmol {Archaeon Desulfurococcus mobilis}
LFNMREQIAFIKGLYVAEGDKTLKRLRIWNKNKALLEIVSRWLNNLGVRNTIHDDHRHGKVVLNISLRDIRKFVHTILS
>d1dfa2 d.95.2.2 (A:181-298) PI-Scel {Baker's yeast (Saccharomyces cerevisiae)}
PILYENDHFFDYMQKSKFHLTIEGPKVLAYLLGLWIGDGSLDRATFSVDSRDTSLMERVTEYAEKLNCAEYKDRKEPVAKTVNLYSKVRGNGIRNN
LNTENPLWDAIVGLGFLKD
>d1dfa3 d.95.2.2 (A:299-415) PI-Scel {Baker's yeast (Saccharomyces cerevisiae)}
GVKNIPSFSTDNIGTRETFLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGLVSLARSLGLVVSNAEPAKVDMMNGTKHHKISYAIMMSGDVLLNVLSKC
AGSKKKRPPAPAAFARE
>d1dq3a3 d.95.2.2 (A:129-226) PI-Pfui intein {Archaeon Pyrococcus furiosus}
PDGEDYKFIFDYWLAGFIAGDGFCKYHSHVKHGHEYIYDRRLIYDYRIETFEIINDYLEKTFGRKYSIQKDRNIYYIDIKARNITSHYLKLEGIDNG
>d1dq3a4 d.95.2.2 (A:227-335) PI-Pfui intein {Archaeon Pyrococcus furiosus}
IPPPQILKEGKNAVLSFIAGLFDAGHVSNKPGIELGMVNKRILEDVTHYLNALGIKARIKEKLKDGDYVLHVEYSSLLRFYELIGKNLQNEEKREKLEK
VLSNHKG
>d1a8ra_d.96.1.1 (A:) GTP cyclohydrolase I {Escherichia coli}
PSLSKEAALVHEALVARGLTPLRPPVHEMDNETRKSLIAGHMTEIMQLLNLDADDLMEPHRIAKMYVDEIFSGLDYANFPKITLIENKMKVDE
MVTVRDITLTSTCESHFVTIDGKATVAYIPKDSVIGLSKINRIVQFFAQRPVQERLTQQJLIALQTLGTTNNVAVIDAVHYCVKARGIRDATSATTTSL
GGLFKSSQNTRHEFLRAVRHHN
>d1is8a_d.96.1.1 (A:) GTP cyclohydrolase I {Rat (Rattus norvegicus)}
PRPSEEDNELNLPNLAAYSSILRSLGEDPQRQGLLTPWRAATAMQFFTKGYQETISDVLNDAIFDEDHDEMIVVKDIDMFSMCEHHLPFVGRV
HIGYLPNKQVQLGLSKLARIVEIYSRRLQVQERLTQKQIAVAITEALQPAGVGVVIEATHMCMVMRGVQKMNSKTVTSTMLGVFREDPKTREELTLIRS
>d1b66a_d.96.1.2 (A:) 6-pyruvoyl tetrahydropterin synthase {Rat (Rattus norvegicus)}
LRRRARLSLVSFSASHRLHSPSLSAEENLKVGKCNPNHGHNKYKVVVTIHEIDPVGMVMNLTDLKEYMEEAIMKPLDHKNLDDVPYFADV
VSTTENVAVYIWENLQRLLPVGALYKVKVYETDNNIVVYKGE
>d1dhm_d.96.1.3 (-) 7,8-dihidroneopterin aldolase {Staphylococcus aureus}
MQDTIFLKGMRFYGYHGALSAENEIGQIFKVDVTLKVDLSEAGRTDNVIDTVHYGEVFEEVKSIMEGKAVNLLEHLAERIANRINSQYNRVMETKVRI
TKENPPPIPQHYDGVGIEIVRENK
>d1b9la_d.96.1.3 (A:) 7,8-dihidroneopterin triphosphate epimerase {Escherichia coli}
AQPAAIIRIKNLRLRTFIGIKEEINNRQDIVNVTIHYPADKARTSEDINDALNYRTVTKNIIQHVENNRSLEKLTQDVLIDIAREHHWVTYAEVEIDKL
HALRYADSVSMTLSWQR
>d1uox_1 d.96.1.4 (1-136) Urate oxidase (uricase) {Aspergillus flavus}
SAVKAARYGKDNVRVYKVKDEKTGVQTVYEMTCVLLEGEIETSYTAKDNVIVATDSIKNTIYITAKQNPVTPPELFGSILGTHFIEKYNHIHAHVNV
IVCHRWTMRMDIDGKPHFSFIRDSEEKRNQVQDVVE
>d1uox_2 d.96.1.4 (137-295) Urate oxidase (uricase) {Aspergillus flavus}
GKGIDIKSSLSGLTVLKSTNSQFWGFLRDEYTLKETWDRILSTDVDAWQWKNFSGLQEVRSHVPKFDATWATAREVTLKTAEDNSASVQATMYK
MAEQILARQQLIETVEYSLPNKHYFEIDLSPWHKGLONTGKNAEVFAPQSDPGLIKCTVGRS
>d1puc_d.97.1.1 (-) suc1 {Fission yeast (Schizosaccharomyces pombe)}
SKSGVPRLLTASERERLEPFIDQIHYSRUYADDEYEYRHVMLPKAMLKAIPTDYFNPETGTLRILQEEEWRGLGITQSLGWEMYEVHVPEPHILLFKREK
D
>d1qb3a_d.97.1.1 (A:) cks1 {Baker's yeast (Saccharomyces cerevisiae)}
HAFQGRKLTDQERARVLEFQDSIHYSRYSDDNNEYRHVMLPKAMLKVIPSDYFNSEVGLRILQEEEWRGLGITQSLGWEMYEVHVPEPHILLFKRP

SIGIHVEKSWGLGRIVTEIFEEVAEAHLIQPTFITEYPAEVSPARRNDVNPEITDRFEFFIGGREIGNGFSELNDAEDQAQRFLDQVAAKDAGDDEAM
FYDEDYVTALEHGLPPTAGLGIGIDRMVMLFTNSHTIRDVILFPAMRP

>d1kmma2 d.104.1.1 (A:4-325) Histidyl-tRNA synthetase (HisRS) {Escherichia coli}

NIQAIRGMNDYLPGETAIWQRIEGTLNVLSGYSEIRLPIVEQTPLFKRAIGEVTDVVEKEMYTFEDRNGDSLRLPEGTAGCVRAGIEHGLYNQE
QRLWYIYGPMFRHERPQKGRYRQFHQLGCEVFGLQGPIDAEALIMITARWWRALGISEHVTLENSIGLEARANYRDALVAFLEQHKEKLDedCKR
RMYTNPLRVLD SKNPEVQALLNDAPALGDYLDEESREHFAGLCKLLESAGIAYTVNQRLVRLGLDYYNRTVFEWVTNSLGSQGTVCAGGRYDGLVEQL
GGRATPAVGFMGLERLVLLVQAVNPEFA

>d1qe0a2 d.104.1.1 (A:1-325) Histidyl-tRNA synthetase (HisRS) {Staphylococcus aureus}

MIKIPRGQTQDILPEDSKWRYIENQLDELMFTFYNYKEIRTPFESTDLFARGVGDDSTDVVQKEMYTFKDKGDRSITLRPEGTAAVVRSYIEHKMKGNP
NQPIKLYNGPMFRYERKQKGRYRQFNQFGVAAIGAENPSVDAEV LAMVMHIYQSFGLKHLKLVINSVGDMASRKEYNEALVKH FEPVIHEFCSDC
QSRLHTDPMRILDCKVDRDKEAKTAPRITDFLNEESKAYYEQVKAYLDDLGIPYTEDPNLVRGLDYYTHTAFELMMMDNPYDGAITLGGGRYNGL
LELLDGPS ETGIGFALSIERLLAEEEGIELD

>d1h4vb2 d.104.1.1 (B:2-325) Histidyl-tRNA synthetase (HisRS) {Thermus thermophilus}

TARAVRGTKDLFGKELRMHQ RIVATARKVLEAGALELVTPIFEETQVFEKGVGAATD VRKEMFTQD RGRSLTRPEGTAAMVRA LEHGMKV
WPQPVRWLWMAGPMFRAERPQKGRYRQFHQV NYE ALGSEN PILD AEV VLLY ECL KELG LRR LKV KLS VGD PED RARY NAY LREV LSPH REA LSED
SKERLEENPMRILD SKSERD QALL KELG VRPML DFLGE EEAR AHL KEVER HLER LSV PYE LPA LV RGL DYY VRTA FEV HHEE IGA QSAL GGG GRYD GLS
ELLGGPRVPGVGFAGVERVALALEAEGFGLPE

>d1atia2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}

AASSLDELVALCKRRGFIFO SSEIYGGLQGVYDYGPLGVELKNNLQAWWRRNVYERDDMEGLDASVLTHRLVLHSGHEATFADPMVDNRITKKR
YRLDHLLKEQPEEV LKRLYRAMEVEEENIHLVQAMMQAPERAGGAMTAAGVLD PASGE PGDWTPPRYFNM MFQDLRGPRGGRGLLAYLRPET
AQGIFVNFKNVLDATSRKLGFIAQIGKA FRNEITPRNFIFRVREFEQMIEIYFVRPGEDEYWHRYWVEERLKW WQEMGLSRENLV PYQQPPESSA
HYAKATDV DILYRFPHGSLELEGIAQRTDFDLSHTKDQE ALGITARVLNEHSTQRLAYRD PETGKWFV PYVIEPSAGVDRGV LALLAE AFTREELPNG
EERIVLKLKP

>d1b76a2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}

AASSLDELVALCKRRGFIFO SSEIYGGLQGVYDYGPLGVELKNNLQAWWRRNVYERDDMEGLDASVLTHRLVLHSGHEATFADPMVDNAKARY
WTPPR YFNMMMFQDLRGPRGGRL LAYLRPETAQGIFVNFKNVLDATSRKLGFIAQIGKA FRNEITPRNFIFRVREFEQMIEIYFVRPGEDEYWHRY
WVEERLKW WQEMGLSRENLV PYQQPPESSAHYAKATV DILYRFPHGSLELEGIAQRTDFDLSHTKDQE ALGITARVLNEHSTQRLAYRD PETGK
WFV PYVIEPSAGVDRGV LALLAE AFTREELPNG EERIVLKLKP

>d1qf6a4 d.104.1.1 (A:242-532) Threonyl-tRNA synthetase (ThrRS) {Escherichia coli}

RDHRKIGKQLDLYHMQEEAPGMVFWHNDGWTIFRELEV FVR SKL KEYQYQEVKGPFMMDRV LW EKTGHWDNYKDAMFTTSENREYCIKPMN
CPGHVQIFQNQGLKS YRDLPLRMAEFGSCHRNEPSGSLHGLMRVRGFTQDDAHIFCTEEQIRDEVNGCIRLVDMYSTFGFEKIVV KLSTRPEKRIGSD
EMWDRAEADLA VALEENNIPFEYQLGEGAFYGP KIEFTLYDCLDRAWQC GTVQLDFSLPSRLSASYVG EDNERKVPVMIHRAILGSMERFIGILTEEF
AGF

>d1eova2 d.104.1.1 (A:205-557) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}

PILLEDASRSEAEAA GLPVVNLDTRL DYLRTV TNQAI FRIQAGV CEL FREY LATKKF TEV HTPKLLGAPSEGGS VFEV TYFKG KAYLAQSPQFN
KQQLIVAD FERV YEIGPV FRAENS NT HRHM TEFT GLD MEMA FEEHY HEV LDTL SELF VFI SELPK RFAHEI ELVR KQYP VEE FKPD KGM VR LT K
GIEM LRAAGKEIGD FEDL STENEKFLGKL VR DKYD TDFY ILDKF PLEIR PFT MPDP ANPK YNSY DFFMR GEEILSGA QRHD HALL QERMKA HGLSP
EDPGLKD YCDGFSYGC PPHAGGGIGLERV VMF YLD KNIR RASL FPR DP KR LRP

>d1b8aa2 d.104.1.1 (A:104-438) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus kodakaraensis}

PLPLDPTGKVKAELDTRLNNRFMDLRRPEVMAIFKIRSSVFKAVRDFHENG FIEIHTPKIIATATEGGTEL FPMKY FEEDAFLAESPQLYKEIMMASGL
DRVYEIAPIFRAEEHNTTRHLNEAWSIDSEMAFIEDEEEVMSFLERLVAHAINYVREHNAKELDILNFELEEPKLPFPRVSYDKALEILGDLGKEIPWGE
DIDTEGERLLGKYM MENENAPLYFLYQYPSEAKPFYIMK YDNKPEICRAFDLEYRG VEISSGGQREHRHDILVEQIKEGLNPES FEFY LKA FRYGMPP
HGGFGLGAERLIKQMLDPNIREVILFPRDRRLT

>d1c0aa3 d.104.1.1 (A:107-287,A:421-585) Aspartyl-tRNA synthetase (AspRS) {Escherichia coli}

VLPLDSNHVNTEEARLKRYYLDLRRPEMAQRKLKTRAKITSVRRFMDDHGFLDIETPMLTKATPEGARDYLVPSRVHKGKFYALPQSPQLFKQLLMM
SGFDTRYQIVKCFRDEDLRADRQPEFTQIDVETSMTAPQVREVMEALVRHLWLEVKGVDLGFVPMFTAEEERRGSDKPDLRXDESWAPLWVI
DFPMFEDDGEGLTAMHHPTSPKDMTAELKAAPENAVANAYDMVINGYEVGGGSVRIHNGDMQQTVFGILGINEEEQREKFGFLDALKYGT
PPHAGLAFGLDRITMLTGTDNIRDVIAFPKTTAAACLMTEAPSFAAPNTALAELSIQVVK
>d1g51a3 d.104.1.1 (A:105-294,A:415-580) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}
TPPFVDAWRGEEEKEASEERLKYRYLDLRRRMQENLRLRHRVIKAIWDFLDREGFVQVETPFLKSTPEGARDFLVPRHEPGLFYALPQSPQL
FKQMLMVAGLDRYFQIARCFRDEDLRADRQPDFTQLDLEMSFVEVEDVLELNERLMAHVFRALGVELPLPFPRLSYEEAMERYGSDKPDLRXREG
FRFLWVVDPLLEDEEEAWTYMHPFTSPHPEDPLLEKDPGRVRALAYDLVLNGVEVGGSIRIHDPLQARVFRLLGIGEEEQREKFGFFLEAL
EYGAPPHGGIAWGLDRLLALMTGPSIREVIAFPKNKEGKDPLTGAPSPVPEEQLRELGLMVVRP
>d1jjca_d.104.1.1 (A:) Phenyl-tRNA synthetase (PheRS) alpha subunit, PheS {Thermus thermophilus and (Thermus aquaticus)}
RVDVSLPGASLFSGGHPITLIMERELVEIFRALGYQAEGPEVESEFFNFNDALNIPEHHPARMDMWDTFWLTGEGFRLEGPLGEEVEGRLLLRTHTSPM
QVRYMYVAHTPPFRIVVPGRVFRFEQTDAHEAVFHQLEGLVVGEGIAMAHLGAIYELAQALFGPDSKVRFQPVYFPFVEPGAQFAWWPEGGK
WLELGGAGMVHPKVFQAVDAYRERLGLPPAYRGVTGFAFLGLVERLAMLRYGIPDIRYFFGGLKFLEQFKGVL
>d1jjcb5 d.104.1.1 (B:475-681) Phenyl-tRNA synthetase (PheRS) beta subunit, PheT, central domain {Thermus thermophilus
(Thermus aquaticus)}
ALPAFFPAPDNRGVEAPYRKERRQLREVLSGLGFQEVTYSFMDPEDARRFLDPPRLLLNLPAPEKAALRTHLFPGLVRLKENLDLDRPERALLFEV
GRVFREREETHLAGLLFGEVGGLPWAKERLSGYFLLKGYLEALFARLGLAFRVEAQAFPLHPGVSGRVLVEGEEVGFLGALHPEIAQELELPPVHLFEL
RLPLPDK
>d1hc7a2 d.104.1.1 (A:5-276) Prolyl-tRNA synthetase (ProRS) {Thermus thermophilus}
KGLTPQSQDFSEWYLEVQKAEADYGPVRGTIVVRPYGYAIWENIQQVLDRMFKETGHQNAFYPLFIPMSFLRKEAEHVEGFSPELVTHAGGEE
LEEPLAVRPTSETVIGYMWSKWIRSWRDLPQLLNQWGNVVRWEMRTRPFLRTSEFLWQEGHTAHATREEAEVEVRRMISIYARLAREYAAIPVIEG
LKTEKEKFAGAVYTTIEALMKDGKALQAGTSHYLGENDAFARFDIKFQDRDLQVKYVHTTSWGLSWRFIGAIIMTHGDD
>d1g5ha2 d.104.1.1 (A:41-330) The aaRS-like accessory subunit of mitochondrial polymerase gamma, N-terminal domain {Mouse
(Mus musculus)}
EALVDLCCRHHFLSGTPQQQLSTAALLSGCHARGPLGVELRKNLASQWWSSMVFREQVFAVDSLHQEPGSSQPRDSAFLVSPESIREILQDREPSK
EQLVAFLENLLKTSKLRATLLHGALEYHNCLDLVNRKLPGLAQIGVCFHPVSNSNQTPSSVTRVGEKTEASLVWFTPTRTSSQWLDFWLRHRLWW
WRKFAMSPSNFSSADCQDELGRKGSKLYSFPGKEPIETLWNLGDQELLHTYPGNVSTIQRDGRKNVPCVLSVGDVDLGTAYLDSFQL
>d12asa_d.104.1.1 (A:) Asparagine synthetase {Escherichia coli}
AYIAKQRQISFVKSHFSRQLERLGLIEVQAPILSRVGDTQDNLSGAEKAVQVKVAKLPDAQFEVHSLAKWKRQTLGQHDFSAGEGLYTHMKALR
PDEDRLSPLHSVYVQWDWVERVMGDGERQFSTLKVTEAIWAGIKATEAAVSEEFGLAPFLPDQIHVFHSQELLSRPDLDAGRERAIAKDLGAVF
LVGIGGKLSDGHRHDVRAPDYDDWSTPSELGHAGLNGDILVNPVLEDAFELSSMGIRVDADTLKHQLALTGDEDRLLEWHQALLRGEMPQTIG
GGIGQSRLTMQLQLPHIGQVQAGVWPAAVRESVPSLL
>d1bia_3 d.104.1.2 (64-270) Biotin repressor/biotin holoenzyme synthetase, catalytic (central) domain {Escherichia coli}
IQLNAKQIQLGQLDGGSVAVLPVIDSTNQYLLDRIGELKSGDACIAEYQQAGRGRGRWFSPFGANLYLSMFWRLEQGPAAAIGLSLVIGIVMAEV
RKLGADKVRVKWPNDLYLQDRKLAGILVELTGTKDAAQIVGAGINMAMRRVEESVNQGWITLQEAGINLDRNTLAAMLIRELRAALELFEQEGL
APYLSRWEKLDN
>d1qtsa2 d.105.1.1 (A:825-938) Alpa-adaptin AP2, C-terminal subdomain {Mouse (Mus musculus)}
FFQPTEMASQDFFQRWKQLSNPQQEVQNIFAKHPMDTEITKAKIIGFSALLEEVDPNPANFVGAGIIHTKTQIGCLLREPNLQAQMYRTLRTS
KDTVSQRLECELLSEQF
>d1e42a2 d.105.1.1 (A:825-937) Beta2-adaptin AP2, C-terminal subdomain {Human (Homo sapiens)}
LFVEDGKMERQVFLATWKDIPNEELQFQIKECHLNADTVSSKLQNNNVYTIAKRNVEGQDMILYQSQLKTNGIWILAELRIQPGNPNTSLKRAP
EVSQYIYQVYDSILKN
>d1c44a_d.106.1.1 (A:) Sterol carrier protein 2 (SCP2) {Rabbit (Oryctolagus cuniculus)}
SSAGDGFKANLVFKEIEKKLEEGERQFVKKIGGIFAFVKVKGPGGKEATWVVDVKNGKGSVLPNSDKADCTITMADSDLLALMTGKMNPQSAFFQ

GKLKITGNMGLAMKLQNLQLQPGKAKL
>d1ikta_d.106.1.1 (A:) SCP2-like domain of MFE-2 {Human (Homo sapiens)}
LQSTFVFEIGRRKDIDGPEVVKKNAVFEWHITKGGNIGAKWTIDLKGSGSKVYQGPAKGAADTTIILSDEFMEVVLGKLPQKAFFSRLKARGN
IMLSQKLQMLKDYAKL
>d1eq6a_d.107.1.1 (A:) Ran-binding protein mog1p {Baker's yeast (Saccharomyces cerevisiae)}
SMNNKEVELYGGAITTVVPPGFIDASTLREVPTQEYVNSRDEEEFEDGLATNESIVDLLETVDKSDLKEAWQFHVEDLTELNNTKWEALQEDT
VQQGTGFTGLVMEAVNKWGPDLAQTVVIGVALIRLTQFDTDVVISINVPLKEEASQASNKELPARCHAVYQLQEMVRKFHVVDTSLF
>d1b87a_d.108.1.1 (A:) Aminoglycoside 6'-N-acetyltransferase {Enterococcus faecium}
MIISEFDRNNPVLKDQLSDLLRTWPEEYGDSSAEVEEMMNPERIAVAADVQDDELVGFIGAIPQYGITGWELHPLVVESSRRKNQIGTRLVNYLEKE
VASRGGITIYLGTDDLDHGTTLSQTDLYEHTFDKVASIQNLREHPYEFYELGYKIVGVLNPANGWDKPDIMAKTIIPRDS
>d1bo4a_d.108.1.1 (A:) Aminoglycoside 3-N-acetyltransferase {Serratia marcescens}
GIIRTCLGPDVQKSMRAALDFGREFGDVATYSQHQPSDYLGNLRSKTFIALAAFQEAvgalaayVLPKFEQPRSEIYIYDLAVSGEHRQQGIA
TALINLLKHEANALGAYVIYQADYGDDPAVALYTKLG
>d1cm0a_d.108.1.1 (A:) Histone acetyltransferase domain of P300/CBP associating factor, PCAF {Human (Homo sapiens)}
KVIEFHVGNSLNQPKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTALIKDGRVIGGICFRMFPSQGFTEVFCAVTSNEQVKGYGTHL
MNHKEYHIKHDILNFLTYADEYAIGYFKKQGFSKEIKIPKTKYVGYIKDYEGATLMGCELNPRI
>d1ygha_d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Baker's yeast (Saccharomyces cerevisiae)}
KIEFRVVNNNDNTKENMMVLTGLKNIFQKQLPKMPKEYIARLVDRSHLSMAVIRKPLTVVGGITYRPFDKREFAEIVFCASSTEQVRGYGAHLMNHL
KDYVRNTSNIKYFLTYADNYAIGYFKKQGFTKEITLDKSIWMGYIKDYEGGTLMQCSMLPRIRYLD
>d1qsta_d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Tetrahymena thermophila}
LDFDILTNDGTHRNMKLLIDLKNIFSRQLPKMPKEYIVKLFDRRHESMVILKNKQKVIGGICFRQYKPKQRFAEVAFLAVTANEQVRGYGTRLMNKFK
DHMQKQNIEYLTYADNFAIGYFKKQGFTKEHRMPQEKWKGYIKDYDGGLMECYIHPYVDY
>d1qsma_d.108.1.1 (A:) Histone acetyltransferase HPA2 {Baker's yeast (Saccharomyces cerevisiae)}
DNITVRVTENDKEGWQRLWKSQYQDFYEVSPDDDDNFGRFLDPNIKMWAAVAVERSSSEKIIGMINFFNHMTTWFKDKEYINDLYDENSRVK
GAGGKLIQFVYDEADKLGTPSVWCTDESNHRAQLLYKVGYKAPKILYKRKGY
>d1bob_d.108.1.1 (-) Histone acetyltransferase HAT1 {Baker's yeast (Saccharomyces cerevisiae)}
FKPETWTSSANEALRVSVGENAVQFSPLFTPIYGDSEKIYGYKDIIHLAFDSVTFKPVNVKYSAKLGDDNIVDVEKLLSFLPKDDVIRDEAKWV
DCFAERKTHNLSDFVEKVSLEYSLNGEEFVYKSSLVDDFARRMHRRVQIFSLLFIEANYIDETDPSWQIYWLNNKTKELIGFVTYKYWHLGAKS
FDEDIDKKFRAKISQFLFPPYQNKGHSCLYEAIQSWEDEKSITEITVEDPNEAFDDLDRNDIQQLRKLYDAVFQKHSDLSDEFLESSRKSLSKLEER
QFNRLVEMLLLNNNS
>d1fy7a_d.108.1.1 (A:) Histone acetyltransferase ESA1 {Baker's yeast (Saccharomyces cerevisiae)}
ARVRNLNRRIIMGKYEIEPWYFSPYPIELTDEDIFYIDDFTLQYFGSKKQYERYRKKCTLRHPGNEIYRDDYVSFFEIDGRKQRTWCRNLCLSKLFLDHK
TLYYDVPFLFYCMTRRDELGHHLVGYFSKEKESADGYNVACILTPQYQRMGYGKLLIESYELSKKENKVGSPKPLSDLGLLSYRAYWSDTLITLLVE
HQKEITIDEISSMTSTTIDILHTAKTLNIRYYKGQHIFLNEDILDYRNRLKAKKRRTIDPNRLIWKPP
>d1cjwa_d.108.1.1 (A:) Serotonin N-acetyltransferase {Sheep (Ovis aries)}
HTLPANEFRCLTPEDAAGVFEIEREAFISVSGNCPLNLDVQHFLLCPESLGLWFVEGRVLVAFIIGSLWDEERLTQESLAHRPRGHS AHLHALAVHRS
FRQQGKGGSVLLWRYLHVGAQPAVRRALMCEDALVPFYQRFGFHPAGPCAIVVGSLTTEMHCSC
>d1i12a_d.108.1.1 (A:) Glucosamine-phosphate N-acetyltransferase GNA1 {Baker's yeast (Saccharomyces cerevisiae)}
LPDGFYIRRMEEGDLEQVTETLKVLTTVGTITPESFCKLIKYWNEATVWNDNEDKKIMQYNPMVIVDKRTETVAATGNIIIERKIIHEGLCGHIEDIAV
NSKYQGQQGLGKLLIDQLVTIGFDYGCYKIIIDCDEKVNFKFYEKCGFSNAGVEMQIRK
>d1iica1_d.108.1.2 (A:34-218) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces cerevisiae)}
AMKDHKFWRTQPVKDFDEKVEEGPIDKPPTPEDISKPLPLSSFEWCSDVDNKKQLEDVFVLLNENYVEDRDAGFRFNYTKEFFNWALKSPGW
KKDWHIGVRVKEIQKLVAFISAIPVTLGVRGKQVPSVEINFLCVHKQLRSKRLTPVLIKEITRRVNKCDIWHALYTAGIVLPAPVSTCR
>d1iica2_d.108.1.2 (A:219-455) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces cerevisiae)}

YTHRPLNWKKLYEVDFTGLPDGHTEEDMIAENALPAKTKAGRLKKEDIDQVFELFKRYQSRFELIQIFTKEEFHNFIGEESLPLDKQVIFSYYVEQP
DGKITDFFSFYSLPFTILNNNTKYKDLGIGLYYYYATDAFQFKDRDPKATKALKTRLCELIYDACILAKNANMDVFNALTSDQDNTLFDDLKFGPGDGFL
NFYLFNYRAKPTGGLNPDNSNDIKRRSNVGVVML

>d1nmta1 d.108.1.2 (A:60-224) N-myristoyl transferase, NMT {Yeast (*Candida albicans*)}

EGPIDKLKTPEDVPNDPLPLISDFEWSTLDIDDNQLQDLYKLLDNYVEDIDATFRFKYSHEFFQWALKPPGWRKDWHVGVRVKSTGKLAFIAATPV
TFKLNKSNKVIDSVEINFLCIHKKLRNKRLAPVLIKEITRRVNQNIWQALYTGGSILPTPLTTCR

>d1nmta2 d.108.1.2 (A:225-451) N-myristoyl transferase, NMT {Yeast (*Candida albicans*)}

YQHRPINWSKLHDVGFSHLPPNQTKSSMVASYTLPNPKLKGRLPMTGKDVTLSLLYKYQERFDIVQLFTEEFKHWMLGHDENSDSNVVKSYV
VEDENGIITDYFSYLLPFTVLDNAQHDELGIAYLFYYASDSFEKPNEYKRNELITDALITSKKFGVDVFNCCLTCQDNTYFLKDCFGSGDGFLNYYLFN
YRTFPMDGGIDKKTKEVVEDQTSGIGVVLL

>d2vik__ d.109.1.1 (-) Villin, domain 1 (res. 1-126) {Chicken (*Gallus gallus*)}

VELSKKVTGKLDKTPGQIWRRIENMEMVPVPTKSYGNFYEGDCYLLSTRKTGSGFSYNIHYWLGNSSQDEQGAAIYTQMDEYLGSAVQHR
EVQGHESETFRAYFKQGLIYKQGGVASGMK

>d1svy__ d.109.1.1 (-) Severin, domain 2 {Dictyostelium discoideum}

EYKPRLLHISGDKNAKVAEVPLATSSLNGDCFLLDAGLTIFYQFNGSKSSPQEKNKAAEVARAIDAERKGLPKVEFCETSDSDIPAEFWKLGGKGAIAA
KH

>d1d0na2 d.109.1.1 (A:153-262) Gelsolin {Horse (*Equus caballus*)}

VPNEVVVQRLLQVKGRVVVRATEVPVSWEFNNGDCFILDGNNIYQWCGSKSNRFERLKATQVSKGIRDNERSGRAQVSFEEGAPEAMLQLV
GPKPTLPEATEDTVK

>d1d0na3 d.109.1.1 (A:263-383) Gelsolin {Horse (*Equus caballus*)}

EDAANRKLAKEYVSNGAGPMVVSLVADENPFAQGALARSEDCFILDHGKDGFIVWKGKQANMEERKAALKTASDFISKMDYPKQTQSVLPEGG
ETPLFRQFFKNWRDPDQTEGLGLAYL

>d1d0na4 d.109.1.1 (A:384-532) Gelsolin {Horse (*Equus caballus*)}

SSHIAHVERVPFDAATLHTSTAMAAQHGMDDDGQKQJWRVEGSKVPPATYQFQYGGDSIILYNYRHGSRQGQIIYNWQGAQSTQDEVA
ASAIALTAQLDEELGGTPVQSRVVQGKEPAHMSLFGGKPMIVYKGTSREGGQTA

>d1d0na5 d.109.1.1 (A:533-628) Gelsolin {Horse (*Equus caballus*)}

PASTRLFQVRASSSGATRAVEIIPKAGALNSNDAFLKTPSAAYLWVGAGASEAEKTGAQELLRLRAQPVQVAEGSEPSFWEALGGKATYRTSP

>d1d0na6 d.109.1.1 (A:629-755) Gelsolin {Horse (*Equus caballus*)}

RLKDKKMDAHPPRLFACSNKIGRFVIEVPGEFMQEDLATDDVMLLTDWDQVFVWVGKDSQDEEKTEALTSAKRYIDTPAHRDRRTPTVV/KQG
FEPPSFVGVFLGWDDSYWSVDPLDRAELAA

>d1d4xg_ d.109.1.1 (G:) Gelsolin {Human (*Homo sapiens*)}

VEHPEFLKAGKEPGLQIWRVEKFDLVPVPTNLGYDFFTGDAYVILKTVQLRNGNLQYDLHYWLGNECSQDESGAAAIFTVQLDDYLNGRAVQHREV
QGFESATFLGYFKSGLKYYKGGVASGFK

>d1db0b1 d.109.1.1 (B:412-532) Gelsolin {Human (*Homo sapiens*)}

MDDDGTTGQKQIWRIEGSNKVPPATYQFQYGGDSIILYNYRHGRQGQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSRVVQGKEPA
HLMSLFGGKPMIIYKGTSREGGQTA

>d1db0b3 d.109.1.1 (B:629-742) Gelsolin {Human (*Homo sapiens*)}

RLKDKKMDAHPPRLFACSNKIGRFVIEVPGEFMQEDLATDDVMLLTDWDQVFVWVGKDSQDEEKTEALTSAKRYIDTPANRDRRTPTVV/KQGFF
EPPSFVGVFLGWDDSYWS

>d1kcqa_ d.109.1.1 (A:) Gelsolin {Human (*Homo sapiens*)}

VVQRLFQVKGRVVVRATEVPVSWEFNNGDCFILDGNNIHQWCGSNSNRYERLKATQVSKGIRDNERSGRARHVSEEGTEPEAMLQVLGPKA
LPAGTEDTA

>d1f7sa_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Plant (*Arabidopsis thaliana*), ADF1}

ASGMAVHDDCKLRFELKAKRTHRFIVYKIEEKQKQVVVEKGQPIQTYEEFAACLPADECRAIYDFDFVTAENCQKSIFIWCPDIAKVRSKMIYA

SSKDRFKRELDGIQV реверсия

>d1cfya_d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Baker's yeast (Saccharomyces cerevisiae)}

VAVADESLTAFNDLKGKKYKFILFGLNDAKTEIVVKETSTDPSYDAFLEKLPENDCLYAIYDFEYEINGNEGKRSKIVFFTSPDTAPVRSKMVYASSKD
ALRRALNGVSTDVQGTDSESYDSVLERVSR

>d1cnua_d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Amoeba (Acanthamoeba castellanii), actophorin}

GIAVSDDCVQKFNELKLGHQHRYVTFKMNASNTEVVVEHVGPNATYEDFKSQLPERDCRYAIFDYEFQVDGGQRNKITFILWAPDSAPIKSMMY
TSTKDSIKKKLVGIQVEVQATDAAEISEDAVERAKKD

>d1hqz1_d.109.1.2 (1:) Cofilin-like domain of actin-binding protein abp1p {Baker's yeast (Saccharomyces cerevisiae)}

LEPIDYTTHSREIDAЕYLKIVRGSDPDТWLIISPNAKKEYEPESTGSSFHDFLQLFDETКVQYGLARVSPPGSDVEKIIIGWCPDSAPLKTRASFAANFA
AVANNLFKGYHVQVTARDEDLLDENELLMKISNAAGA

>d1ak7_d.109.1.2 (-) Destrin {Human and pig (Homo sapiens) and (Sus scrofa)}

TMITPSSGNASGVQVADEVCRIFYDMKVRKCSTPEEIKRKKAВIФCLSADKKCIIVEEGKEILVGДVGVTITDPFKHFVGMLPEKDCRYALYDASFETK
ESRKEELMFFLWAPELAPLKSКMIYASSKDAIKKKFQGИKHECQANGPEDLNRCACIAEKLGGSLIVAFEGCPV

>d1pne_d.110.1.1 (-) Profilin (actin-binding protein) {Cow (Bos taurus)}

AGWNAYIDNLMADGTСQDAAIVGYKDSPSVWAAVPGKTFVNITPAEVГVLVGKDRSSFYVNGLTGGQKCSVIRDSSLQDGEFTMDLRTKSTGGAP
TFNITVTMTAKTLVLLMGKEGVHGGMINKKCYEMASHLRRSQY

>d1fil_d.110.1.1 (-) Profilin (actin-binding protein) {Human (Homo sapiens), isoform I}

AGWNAYIDNLMADGTСQDAAIVGYKDSPSVWAAVPGKTFVNITPAEVГVLVGKDRSSFYVNGLTGGQKCSVIRDSSLQDGEFTMDLRTKSTGGА
PTFNVTVTKTDKTLVLLMGKEGVHGGLINKCYEMASHLRRSQY

>d1d1ja_d.110.1.1 (A:) Profilin (actin-binding protein) {Human (Homo sapiens), isoform II}

AGWQSYVDNLМCDGCCQЕAAIVGYCDAKVWAATAGGVFQSITPIЕIDMIVGKDREGFFNGLTGAKKCSVIRDSSLQDGEFSMDLRTKSTGGP
TYNVAVGAGRALVIMGKEGVHGGTLNKKAYELALYLRRSD

>d1acf_d.110.1.1 (-) Profilin (actin-binding protein) {Acanthamoeba castellanii}

SWQTYVDTNLVGTGAVTQAAIIGHDGNTWATSAGFAVTPAQGTTLAGAFNNADAIRAGGFДLAGVHYVTLRADDRSIYGRKKGSSGVITVKTSKAILV
GVYNEKIQPGTAANVVEKLADYLIGQGF

>d1f2ka_d.110.1.1 (A:) Profilin (actin-binding protein) {Acanthamoeba castellanii}

SWQTYVDTNLVGTGAVTQAAIIGHDGNTWATSAGFAVSPANGAALANAFKDATAIRNGFELAGTRYVTIRADDRSVYGRKKGSSGVITVKTSKAILIG
VYNEKIQPGTAANVVEKLADYLIGQGF

>d1ypra_d.110.1.1 (A:) Profilin (actin-binding protein) {Baker's yeast (Saccharomyces cerevisiae)}

SWQAYTDNЛIГTГVDKV реверсия

SWQAYTDNЛIГTГVDKV реверсия

SWQAYTDNЛIГTГVDKV реверсия

>d1cqa_d.110.1.1 (-) Profilin (actin-binding protein) {Birch (Betula verrucosa)}

SWQTYVDEHLMCIDGQGEELAASAIVGHDSVWAQSSFPQFKPQEITGIMKDFEEPGLAPТGLHLGGIКYMVIQGEAGAVIRGKKGSGGITIK
KTGQALVFGFYIYEPVTPGQCNMVVERLDYLDQGL

>d3nul_d.110.1.1 (-) Profilin (actin-binding protein) {Mouse-ear cress (Arabidopsis thaliana)}

SWQSYVDDHLMCDVЕGNHLTAAAILGQDGСVWAQSAKFPQLKPQEIDGИKKDFEEPGLAPТGLHLGGIКYMVIQGEAGAVIRGKKGSGGITIK

TNQALVFGFYIYEPVTPGQCNMVVERLDYLDQGL

>d1g5ua_d.110.1.1 (A:) Profilin (actin-binding protein) {Para rubber tree (Hevea brasiliensis), hevb8}

SWQTYVDDHLMCDIDGHLTAAAILGQDGСVWAQSSFPQFKSDEVAAMKDFDEPGSLAPТGLHLGGIКYMVIQGEAGAVIRGKKGSGGITVKR
TGQALIIGIYDEPLTPGQCNMVVERLDYLDQGL

>d1f5ma_d.110.2.1 (A:) Hypothetical protein ykl069wp {Baker's yeast (Saccharomyces cerevisiae)}

STGFHHADHVNYSSNLNKEEILEQLLSYEGLSDGQVNWVCNLSNASSLIWHAYKSLAVDINWAGFYVTQASEENTLILGPFQGKVACQMIQFGK
VCGTAASTKETQIVPDVNKYPGHIACDGETKSEIVVPIISNDGKTLGVIDIDCLDYEGFDHVДKEFLEKLAKLINKSCV

>d3pyp_d.110.3.1 (-) Photoactive yellow protein, PYP {Ectothiorhodospira halophila}

MEHVAFGSEDIENTLAKMDDGQLDGLAFGAIQLGDGNILQYNAEAEITGRDPKQVIGKNFFKDVPCTDSPEFYGKFKEGVASGNLNTMFYTF
DYQMTPTKVKVHMKKALSGDSYWVFVKRV

>d1ew0a_d.110.3.2 (A:) Histidine kinase FixL heme domain {Rhizobium meliloti}

GSHMLETEDVVRARDAHLSILDTPDATVVSATDGTIVSFNAAAVRQFGYAEVEVIGQNLRILMPEPYRHEHDGYLQRYMATGEKRIIGIDRVVSG
QRKDGSTFPMKLAvgemRSGGERFFTGFIRDLT

>d1dp6a_d.110.3.2 (A:) Histidine kinase FixL heme domain {Bradyrhizobium japonicum}

DAMIVIDGHGIIQLFSTAERLFGWSELEAIGQNVNILMPEPDRSRHDSYISRYRTTSDPHIIGIGRIVTGKRRDGTTFPMHLSIGEMQSGGEPYFTGF
VRDLTEHQQTQARLQEL

>d1bywa_d.110.3.3 (A:) Erg potassium channel, N-terminal domain {Human (Homo sapiens)}

SRKFIIANARVENCAVIYCNDGFCELCGYSRAEVMQRPCTCDFLHGPTQRRAAAQIAQALLGAERKVEIAFYRKDGSCFLCLVDVVPVKNEDGAVI
MFILNFEVVMEK

>d1g28a_d.110.3.4 (A:) Photoreceptor phy3 flavin-binding domain, lov2 {Maidenhair fern (Adiantum capillus-veneris)}

KSFVITDPRLPDNPIIFASDRFLELTETYTREEVLGNNCRFQGRGTDRKAVQLDAVKEQRDVTVQVLNYTKGRAFWNLFLQVMRDENGDVQYF
IGVQQEM

>d1ifqa_d.110.4.1 (A:) Sec22b {Mouse (Mus musculus)}

SVLLTMIARVADGLPLAASMQEDEQSGRDLQQYQSQAQLFRKLNEQSPTRCTLEAGAMTFHYIIEQGVCYLVCEAAFPKKLAFAYLEDLHSEFDEQ
HGKKVPTVSRPYSFIEFDTFIQKTKLYI

>d1h8ma_d.110.4.1 (A:) Synaptobrevin homolog 1 ykt6 {Baker's yeast (Saccharomyces cerevisiae)}

MRIYYIGVFRSGGKALELSEVKDSLQFGFFERSSVGQFMFTAETVASRTGAGERQSIEEGNYIGHVYARSEGICGVLIITDKQYPVRPAYTLNKILDEY
LVAHPKEEWADVTETNDALKMKQLDTISKYQDPSQADA

>d1cfe_d.111.1.1 (-) Pathogenesis-related protein 1 (PR1) {Tomato (Lycopersicon esculentum), P14a}

QNSPQDYLVHNDARACQVGVPMSWDANLASRAQNYANSRAGDCNLIHSGAGENLAKGGDFTGRAAVQLWVSERPSNYATNQCVGGKKC
RHYTQVWRNSVRLGCRARCNNWWFISCNYDPVGNWIGQRPY

>d1qnxa_d.111.1.1 (A:) Insect allergen 5 (AG5) {Yellow jacket (Vespa vulgaris), Ves v 5}

AEAEFNNYCKIKCLKGGVHTACKYGSKPNCGNKVVSYGLTKQEKDILKEHNDFRQKIARGLETRGNPGPQPPAKNMKNLVWNDLAYVAQVW
ANQCQYGHDTCRDVAKYQVGQNVALTGSTAAYDDPVKLVKMWEDEVKDYNPKKKFSNFLKTGHYTQMVWANTKEVGCISIYIQEKWHK
HYLVCNYGPSGNFKNEELYQT

>d1a6ja_d.112.1.1 (A:) Nitrogen regulatory bacterial protein Ila-ntr {Escherichia coli}

LQLSSVLNRECTRSRVHCQSKKRALEIISELAQQLSLPPQVFEAILTREKGSTGIGNGIAIPHGLEEDTLRAVGVFVQLETPIAFDAIDNQPVDLLF
ALLVPADQTKTHLHTSLVAKRLADKTICRRLRAAQSDDEELYQIITDTE

>d1a3aa_d.112.1.1 (A:) Phosphotransferase Ila-mannitol {Escherichia coli}

LFKLGAENIFGRKAATKEEAIRFAGEQLVKGGYVEPEYVQAMLDREKLPTYLGESIAVPHGTVEAKDRVLTGVVFCQYPEGVRFGEEDDIARLVIG
IAARNNEHIQVITSLTNALDDESVIERLAHTTSVDEVLELLAGRK

>d1hypn_d.112.1.2 (P:) Erythrocyte membrane Band 3 {Human (Homo sapiens)}

KVYVELQELVMDEKNQELRWMEAARWVQLEENLGENGAWRPHLSHLTWSLLELRRVFTKGTVLLDQETSLAGVANQLDRIFEDQIRPQDR
EELLRALLKHSHAGELEALGGVKPAVLTRSGDPSQPLPQHSSLETQLFCEQGDGGTEGHSPSGILEKIPPSEATLVLVGRADFLEQPVLGFVRLQEA
AELEAELPVPIRFLVLLGPEAPHIDYTQLGRAAATLMSERVFRIDAYMAQSRGELLHSLEGFLDCSLVLPPTDAPSEQALLSLPVQRELLRRYQ

>d1mut_d.113.1.1 (-) Nucleoside triphosphate pyrophosphorylase (MutT) {Escherichia coli}

MKKLQIAVGIIRNENNEIFTRRAADAHMANKLEFPGGKIEMGETPEQAVVRELQEEVGITPQHFSLEKLEYEFPDRHITLWFWLVERWEGEPWGK
EGQPGEWMSLGLNADDFFPANEPIAKLKRL

>d1g0sa_d.113.1.1 (A:) ADP-ribose pyrophosphatase {Escherichia coli}

MLKPDNLPTFGKNDVEIIARETLYRGFFSLDLYRFRHRLFNGQMSHEVRREIFERGHAAVLLPDPVRDEVVIEQIRIAAYDTSETPWLLEMVAGMI
EEGESVEDVARREAIEEAGLIVKRTKPVLFLASPGGTSSIMVGEVDATTASGIHGLADENEDIRVHVVREQAYQWVEEGKIDNAASVIALQWL
QLHHQALKNEWA

>d1jkna_d.113.1.1 (A:) Diadenosine tetraphosphate hydrolase {Narrow-leaved blue lupine (*Lupinus angustifolius*)}
GPLGSMDSPEGYRRNVICLMNNKKIFAASRLDIPDAWQMPQGGIDEGEDPRNAIRELREETGVTSAEVIAEVPYWLTYDFPPKVREKLNQWGSDWKGQAQKWFLKFTGQDQEINLLGDGSEKPEFGESWVTPEQLIDLTVEFKKPVYKEVLSVFAPHL
>d1hx3a_d.113.1.2 (A:) Isopentenyl diphosphate isomerase {Escherichia coli}
EHVILLNAQGVPTGTLEYKAAHTADTRLHLAFSSWLFNAKGQLLVTRRALSKKAWPGVWTNSVAGHPQLGESNEDAVIRRCRYELGVEITPPESIYPDFRYRATDPSGIVENEVCVFAARTTSA
FRYRATDPSGIVENEVCVFAARTTSA
>d1hzta_d.113.1.2 (A:) Isopentenyl diphosphate isomerase {Escherichia coli}
LHLAFSSWLFNAKGQLLVTRRALSKKAWPGVWTNSVCGHPQLGESNEDAVIRRCRYELGVEITPPESIYPDFRYRATDPSGIVENEVCVFAARTTSA
LQINDEVMDYQWCCLADVLHGIDATPWAFSPWMVMQATNREARKRLSAFTQLKL
>d1ush_1 d.114.1.1 (363-550) 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain {Escherichia coli}
KIGETNGRLEGDRDKVRFVQTNMGRLLAAQMDRTGADFAVMSGGGIRDIESAGDISYKNVLKVQPGNVVVYADMTGKEVIDYLTAQAQMKPDS
GAYPQFANVSFVAKDGKLNLDLKIKGEPVDPAKTYRMATLNFNATGGDGYPRLDNKPGVNTGFIDAELKAYIQKSSPLDVSVYEPKGEVSWQ
>d1hrua_d.115.1.1 (A:) Hypothetical protein YrdC {Escherichia coli}
NNLQRDAIAAAIDVLNEERVIAYPTEAVFGVGCDPSETAVMRLLELKQRPVDKGLILIAANYEQLPKYIDDTMLTDVQRETIFSRWPGPVTFVFPAPA
TTPRWLTGRFDLSLAVRTDHPLVVALCQAYGKPLVTSANSLGLPPCRTDEVRAQFGAAFPVVPGETGGRNLPSEIRDALTGELFR
>d1g57a_d.115.1.2 (A:) 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB {Escherichia coli}
LLSFGTPFERVERNALAALREGRGVMVLDDEDRENEGDMIFPAETMTVEQMALTIHGSGIVCLCITEDRRKQLDPMMVENNTSAYGTGFTVIEA
AEGVTTGVSAADRITTVRAAIADGAKPSDLNRPGHVFPRLAQAGGVLTRGGHTEATIDLMTLAGFKPAGVLCELTNDGTMARAPCIEFANKHN
MALVTIEDLVAYRQAHE
>d1dbxa_d.116.1.1 (A:) Hypothetical protein HI1434 (YbaK homologue) {Haemophilus influenzae}
TPAIDLLKKQKIPFILHTYDHDPNNQHFGDEAAEKLGIDPNRSFKTLLVAENGDKKKLACFVLATANMLNLKKAASKSIGVKKVEMADKAAQKSTGYLVGGISPLGQKKRKVTVINSTALEFETIYVSGGKRGLSVEIAPQDLAKVLGAETFDIVDE
>d1qqqa_d.117.1.1 (A:) Thymidylate synthase {Escherichia coli}
MKQYLELMQKVLDGFTQKNDRTGTGTLISFGHQMRFDNLQDGFLVTTKCHRLSIIHELLWFLQGDTNIAYLHENNTIWDEWADENGDLPVYGKQWRAWPTPDGRHIDQITVNLQLKDPSRIIVSAWNVGELDKMALAPCHAFFQFYVADGKLSCLYQRSCDVFLGLPFNIASYALLVHMMAOQCDELGVDFVWTGGDTHLYSNHMDQTHLQLSREPRPLPKLIKRKPESIFDYRFEDFEIEGYDSHPGIKAPVAI
>d1tsy__d.117.1.1 (-) Thymidylate synthase {Lactobacillus casei}
MLEQPYLDLAKVLDGEHFKPDFRTHTGTYSIFGHQMRFDLSKGFPPLTTKVPFGLIKSELLWFHGDTNIRFLQHRNHIWDEWAFEKWVKSDHEYHGPDMTDGFHRSQKDPEFAAVYHEEMAKFDDRVLHDDAAKYGDLGLVYGSQRAWHTSKGDTIDQLGDVIEQIKTHPYSRKLIVSAWPEDVPTMALPPCHTLYQFYVNDGKLSLQLYQRSADIFLGVPFNIASYALLTHLVAHECGLEVGEFIHTFGDAHYVNHDQIKEQLSRTPRPAPTLQLNPDKHDFDFDMKDIKLLNYDPYPAIKAPVAV
>d1bkpa_d.117.1.1 (A:) Thymidylate synthase {Bacillus subtilis}
TQFDKQYNSIIKDIINNGISDEEFDVRTKWDSDGTPAHTLSVISQMRFDNSEVPILTTKVAWKTAIKELLWIWQLSNDVNDLNMMGVHIWDQWKQEDGTIGHAYGFQLGKKNRSLNGEKVDQVSYLLHQLKNNPSSRRHITMLWNPDELDAMALTPCVYETQWYVKHGKLHLEVRARSNDMALGNPNFNVFQYNVLQRMIAQVTGYELGEYIFNIGDCHVYTRHIDNLKIQMEREQFEAPELWINPEVKDFYDFTIDDFKLINYKHGDKLLFEAV
>d1tis__d.117.1.1 (-) Thymidylate synthase {Bacteriophage T4}
MKQYQDLIKDIFENGYETDDRTGTGTIALFGSKLRWDLTKGFPATVTTKLAWKACIAELIWFLSGSTNVNDLRLIQHDSLIQGKTVWDENYENQAKD LGYHSGELGPIYGKQWRDFGGVDQIIEVIDRIKKLPNDRRQIVSAWNPAELKYMALPPCHMFYQFNVRNGYLDLQWYQRSPVDFLGLPFNIASYATLVHIVAKMCNLIPGDLIFSGGNTHIYMNHVEQCKEILRREPKECELVISGLPYKFRLSTKEQLKYVLKLRPKDFVLNNYVSHPPIKGKMAV
>d1f28a_d.117.1.1 (A:) Thymidylate synthase {Pneumocystis carinii}
NAEEQQYLNVLQYIINHGEDRPDRTGTGTLVFAPSPLKFSLRNKTFLPLTTKRVFIRGVIEELLWFIRGETDSLKLREKNIHIWDANGSREYLDIGLTKRQEGDLGPIYGFQWRHFGAEYIDCKTNYIGQGVSQLANIQQKIRTSPYDRLILSAWNPADEKMALPPCHMFQFYVHIPSNNHRPELSCQLYQRSCDMGLGVPFNIASYALLTCMIAHVCDLDPGDFIHVMGDCHIYKDHIEALQQQLTRSPPFPTLSNRSITDIEDFTLDDFNIQNYHPYETIKMKMSI
>d2tsra_d.117.1.1 (A:) Thymidylate synthase {Rat (*Rattus norvegicus*)}

QHGELQYLRQVEHIMRCGFKKEDRTGTGTLVFGMQARYSLRDEFPLTTKRVFWKGVLELLWFIGSTNAKE_LSSKGVR_IWDANGSRDFLDLGF
SARQEGLGPVYGFQWRHFGADYKDMDSYSGQGVQLQKVIDTIKTNPDDR_RIIMCAWNPKDPLMALPPCHALCQFYVN_GE_LSCQLYQRSG
DMGLGV_PFN_IAS_ALLTYMIAHITGLQPGDFVHTLGDAI_HLNHIEPLK_IQLQREPRPFPKLRLRK_VETIDDFKVEDFQIEGYNPHPTI
>d1hvy_a_d.117.1.1 (A:) Thymidylate synthase {Human (*Homo sapiens*)}
PPHGE_LQYLGQIQHILRCGV_RKDDRTGTGTLVFGMQARYSLRDEFPLTTKRVFWKGVLELLWFIGSTNAKE_LSSKGVR_IWDANGSRDFLDLGF
STREEGD_LGPVYGFQWRHFGAEYRDMESDYSQGVQLQRV_IDTIKTNPDDR_RIIMCAWNPRDPLMALPPCHALCQFYVN_GE_LSCQLYQRSGD
MGLGV_PFN_IAS_ALLTYMIAHITGLKPGDFIHTLGDAI_HLNHIEPLK_IQLQREPRPFPKLRLRK_VE_KIDDFKAEDFQIEGYNPHPTIKMEMAV
>d1b5ea_d.117.1.1 (A:) dCMP hydroxymethylase {Bacteriophage T4}
MISDSMTV_EEEIRLHLGLALKEKDFVV_DKTVK_TII_GASFVADEPFIFGALN_DEYIQRELEWY_KSKSLFVKDIPGETPKIWQQVASSKGEINSNYGWAI
WSEDNYAQYDMCLAE_GQNPD_SRRGIMYTRPSMQFDYNKDGM_SDFMCTNTVQYLIRD_KKINAVVNMR_SNDV_VFGFRNDYAWQKYVLDKLVS
DLNAGDSTRQYKAGSIIWNVGS_LHVSRHFYLVDHWWKTGETHISKKDY
>d1kq4a_d.207.1.1 (A:) Thy1 homologue {Thermotoga maritima, TM0449}
HM_KID_IDKGFVELDV_MGNDLSA_VRAARV_SFDMGLKDEERDRH_LIEYLMK_HGHETPFEHIVFTFH_VKAPIFVARQWFRHRIASYNELSGRYSKLSY
EFYIPS_PERLEGYKTTIPPERVTEKISEIVDKAYRTYLEIESGV_PREVARIVLPLNLYTRFFWTVN_ARS_MNFLNL_RADSHAQWEIQQYALAIARIFKEKCP
WT_FEAFLKYAYKG_DI_L
>d1lba_d.118.1.1 (-) Bacteriophage T7 lysozyme (Zn amidase) {Bacteriophage T7}
AKQRESTDAIFVHCSATKPSQN_VGVREIRQWHKEQGWLDVG_YHFI_IKRDGT_VAGRDEM_AVGS_HAKGYNHNSIGVCLGGIDD_KFDAN_FPAQ
MQSLRSLLVTLLAKYEGAVLRAHHEVAPKACPSFDLKRW_WE_KNELVTS_DRG
>d1cyo_d.120.1.1 (-) Cytochrome b5 {Cow (*Bos taurus*)}
SKAVYYTLEEIQKHNN_SKSTWL_LH_YKV_DLT_KF_LEEHPG_GEEVLREQAGG_DATENFEDV_GHSTDARELS_KTFIIGELHP_DRS_KIT
>d1f03a_d.120.1.1 (A:) Cytochrome b5 {Cow (*Bos taurus*)}
AVKY_YTLEEIQKHNN_SKSTWL_LH_YKV_DLT_KF_LEEHPG_GEEVLREQAGG_DATENFEDV_GHSTDARELS_KTYIIGELHP_DRS_KIA
>d1aqa_d.120.1.1 (-) Cytochrome b5 {Rat (*Rattus norvegicus*)}
KYYTLEEIQKH_DSK_STWL_VI_LH_HKV_DLT_KF_LEEHPG_GEEVLREQAGG_DATENFEDV_GHSTDARELS_KTYIIGELHP_DRS_KIA
>d1axx_d.120.1.1 (-) Cytochrome b5 {Rat (*Rattus norvegicus*)}
DKDVYYTLEEIQKH_DSK_STWL_VI_LH_HKV_DLT_KF_LEEHPG_GEEVLREQAGG_DATENFEDV_GHSTDARELS_KTYIIGELHP_DRS_KIAKPSETL
>d1euea_d.120.1.1 (A:) Cytochrome b5 {Rat (*Rattus norvegicus*)}
DPAVTY_YR_EEVAKRN_TAEETWMVIHGRVYD_ITRFLSEHPG_GEEVLREQAG_ADATESFEDIGHSPDAREMLKQYYIGDVHPNDLKPK
>d1icca_d.120.1.1 (A:) Cytochrome b5 {Rat (*Rattus norvegicus*)}
DPAVTY_YR_EEVAKRN_TSEETWMVIHGRVYD_ITRFLSEHPG_GEEVLREQAG_ADATESFEDV_GHSPDAREMLKQYYIGDVHPNDLKPK
>d1do9a_d.120.1.1 (A:) Cytochrome b5 {Rabbit (*Oryctolagus cuniculus*)}
DKDVYYTLEEIKHNHS_KSTWL_LH_HKV_DLT_KF_LEEHPG_GEEVLREQAGG_DATENFEDV_GHSTDARELS_KTFIIGELHP_DRS_KL_SKPMETL
>d1cxya_d.120.1.1 (A:) Cytochrome b558 {Ectothiorhodospira vacuolata}
TLPVFTLEQVAEH_HSPDC_CWMAIH_GKV_DLT_PY_VP_NH_PG_GAG_MMLV_WCGQESTE_AWETKS_YGE_HSSLA_AR_LLQ_RY_LIGTL
>d1ltda2_d.120.1.1 (A:10-97) Flavocytochrome b2, N-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}
KISPAEVAKHNKP_DDC_WW_VW_VINGYVYD_LTRFLPN_HPG_GQDV_IK_FNAGKD_VTA_IF_EPLH_AP_NV_ID_KYI_APEKKLG_LQ_GSM_PPEL_VCPPY
>d1soxa2_d.120.1.1 (A:3-93) Sulfite oxidase, N-terminal domain {Chicken (*Gallus gallus*)}
SYPEYTREEVGRHRSPEER_VV_WTHGTDVF_DT_VEL_HPG_GPD_KILLAAGGA_EPF_WALYAV_HGE_PH_VLE_LQQYKV_GEL_SP_DE_APAAPDA
>d1vcc_d.121.1.1 (-) Vaccinia DNA topoisomerase I, 9 kDa N-terminal fragment {Vaccinia virus, strain WR}
MRALFYKD_GKL_FDNNFLNP_VSDDNP_AYEV_LQ_HV_KIP_TH_LTDVV_VYEQ_TWEE_ATRL_IF_VG_SDS_KRRQYFY_GKM_H
>d1amw_d.122.1.1 (-) HSP90 {Baker's yeast (*Saccharomyces cerevisiae*)}
ASETFEFQAEITQLMSL_IINTVYSN_KE_IFLREL_ISNASDALD_KIRY_KSLSD_PKQLE_EPD_LF_IRT_PKPEQ_KV_LIRD_SGIGMT_KAEL_INNLGT_IAKSGTKAFM
EALSAGADV_SMIGQFGVG_FYSLFLV_ADRV_QV_IS_KN_DEQY_IWE_NAGGS_FTV_LDEV_NER_IGR_GT_IRLFLK_DDQLEY_LE_EKRI_EVIKRHSEF_VAYPI
QLVVTKEVE

>d1byqa_d.122.1.1 (A:) HSP90 {Human (Homo sapiens)}

PMEEEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIRYETLTDPSKLDGKELHINLIPNKQDRTLTIVDTGIGMTKADLINNLGTIAKS
GTKAFMEALQAGADISMIGQFGVGFYSAYLVAEKVTITKHNDDEQYAWESSAGGSFTVRTDTGEPMGRGKVLHLKEDQTEYLEERRIKEIVKKHS
QFIGYPITLFVE

>d1ei1a2 d.122.1.2 (A:2-220) DNA gyrase B {Escherichia coli}

SNSSDSSSIKVKGDAVRKRPGMYIGDTDDGTGLHHMVFEVVDNAIDEALAGHCIEIITIHADNSVSQDDGRGIPTGIHPEEGVSAEVIMTVL
HAGGKFDDNSYKVSGGLHGVGVSVNALSQKLELVIQREGKIHRQIYEHGPQAPLAVTGETKTGTMVRFWPSLETFNTVTEFEYEILAKRLRELSE
LDSGVSIIRLDKRDGKEDHFHYEG

>d1b63a2 d.122.1.2 (A:-2-216) DNA mismatch repair protein MutL {Escherichia coli}

SHMPIQVLPPQLANQIAAGEVVERPASVVKELVENSLAGATRIDIDIERGGAKLIRIRDNGCGIKKDELALALARHATSKIASLDDLEAIISLGFRGEAL
ASISSVSRLTLSRTAEQQEAWQAYAEGRDMNVTVKPAAHPVGTTLEVLDLFYNTPARRKFLRTEKTEFNHIDEIIRRIALARFDVTINLSHNGKIVRQY
RAVPEGGQKERRLGAIC

>d1bkna2 d.122.1.2 (A:20-216) DNA mismatch repair protein MutL {Escherichia coli}

VERPASVVKELVENSLAGATRIDIDIERGGAKLIRIRDNGCGIKKDELALALARHATSKIASLDDLEAIISLGFRGEALASISSVSRLTLSRTAEQQEAWQ
AYAEGRDMNVTVKPAAHPVGTTLEVLDLFYNTPARRKFLRTEKTEFNHIDEIIRRIALARFDVTINLSHNGKIVRQYRAVPEGGQKERRLGAIC

>d1h7sa2 d.122.1.2 (A:29-231) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}

GQVVLSSLAVKELVENSLAGATNIDLKLKDYGVDIEVSDNGCGVEEENFEGLTLKHTTSKIQEFADLTQVETFGFRGEALSSLCALSDVTISTCHASA
KVGTRLMFDHNGKIIQKTPYPRPRGTTVSQQLFSTLPVRHKEFQRNIKEYAKMVQLHAYCIISAGIRVSCTNQLGQGKRQPVCTGGSPSIKENI
GSVF

>d1bxda_d.122.1.3 (A:) Histidine kinase domain of the osmosensor EnvZ {Escherichia coli}

TGQEMPMEMADLNAVLGEVIAAESGYEREIETALYPGSIEVKMHPLSIKRAVANMVNAARYGNGWIKVSSGTEPNRAWFQVEDDGGPIAPEQR
KHLFQPFVRGDSARTISGTGLGLAIVQRIVDNHNGMЛЕГЛTSERGGLSIRAWLPVPVTRAQGTTKEG

>d1i58a_d.122.1.3 (A:) Histidine kinase CheA {Thermotoga maritima}

GSHMVPISFVNFRPVRMVRDLAKKMNEVNFMIRGEDTELDRTFVEEIGEPLLHLLRNAIDHGIPEKKEERIAKGKPIGTLILSARHEGNVVIEWEDD
GRGIDKEKIIRKAIEKGLIDESKAATLSDQEILNFLVPGFSTKEVSEVSGRGVGMDVVKNVVESLNGSISIESEKDGTKVTLRPLT

>d1id0a_d.122.1.3 (A:) Histidine kinase PhoQ domain {Escherichia coli}

RELHPVAPL LDNLTSALNKVYQRKGVNISLDISPEISFVGEQNDFVEVMGNVLDNACKYCLEFVEISARQTDEHLYIVVEDDGGPIPLSKREVIFDRGQR
VDTLRPGQGVGLAVAREITEQYEGKIVAGESMLGGARMEVIFGRQH

>d1gkza2 d.122.1.4 (A:186-378) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK) {Rat (Rattus norvegicus)}

DFVGIICTRLSPKKIEKWVDFARRCEHKYGNAPRVRINGHVAARFPFIPMPLDYLPELLKNAKRATMESHLDPYNPDVVITIANNDVLIIRISD
RGGGIAHKDLDRVMDYHFTTAEASTQDPRISPLFGHLDMHSGGQSGPMHGFGFLPTSRAYAEYLGGLQLQLQGIGTDVYLRHIDGREE

>d1jm6a2 d.122.1.4 (A:1177-1366) Pyruvate dehydrogenase kinase {Rat (Rattus norvegicus), isozyme 2}

PKHIGSIDPNCSVSDVVKDAYDMAKLLCDKYYMASPDLEIQEVNATNATQPIHMVYVPSLYHMLFELFKNAKRATVESHESSLTPPIKIMVALGEE
DLSIKMSDRGGGVPLRKIERLFSYMYSTAPTPQPGTGGTPLAGFGYGLPISRLYAKYFQGDLQLFSMEFGFTDAVYLKALSTDVERLPVY

>d1ixma_d.123.1.1 (A:) Sporulation response regulatory protein SpoOB {Bacillus subtilis}

SDTALTNEIHLGHRSRHDWMNKLQLIKGNLSQLKYDRVFE MIEEMVIDAKHESKLSNLKTPHLAFDFTFNWKTHYMTLEYVLGEIKDLSAYDQKL
AKLMRKLFLFDQAVSRESENHTVSLQTDHPDRQLILYLFHGFADPSAFDDIRQNGYEDVDIMRFEITSHECLIEIGL

>d1bola_d.124.1.1 (A:) Ribonuclease Rh {Rhizopus niveus}

SSCSSTALSCNSANSDTCCSPEYGLVVLNMQWAPGYGP DNAFTLHGLWPDKCSGAYAPSGCDSNRASSIASVIKSKDSSLNSMLTYWPSNQG
NNNVFW SHEWSKGTCVSTYDPDCYDNYEEGEDIVDYFQKAMDLRSQYNVYKAFSSNGITPGGTYTATEMQSAIESYFGAKAKIDCSSGTLSDVAL
YFYVRGRDTYVITDALSTGSCSGDVEYPTK

>d1bk7a_d.124.1.1 (A:) Ribonuclease MC1 {Bitter gourd (Momordica charantia)}

FDSFWFVQQWPPAVCSFQKSGCPGSGLRTFTIHLWLPQQSGTSLTNCGPSFDITKISHLQS LNTLWPVNVL RANNQQFWSHEWTKHGT CEST
FNQAAYFKLAVDMRNNYDIIGALRP HAAGPNGRTKSROAIGFLKAKFGKFPGLRCRTDPQTKVSYLVQV VACFAQDGSTLIDCTR DTCGANFIF

>d1dixa_d.124.1.1 (A:) RNase LE {Tomatoes (*Lycopersicon esculentum*)}
ASGSKDFDFYFVQQWPGSYCDTKQSCCYPTTGKPAADFGIHGLWPNNNDGTPSNCDPNSPYDQSQISDLISSMQQNWPTLACPSGSGSTFW
HEWEKHGTCAESVLTNQHAYFKKALDLKNQIDLLSILQGADIHPGESYDLVNIRNAIKSAIGYTPWIQCNCVDQSGNSQLYQVYICVDGSGSSLIECPI
FPGGKCGTSIEFPTF

>d1iqqa_d.124.1.1 (A:) S3-RNase {Japanese pear (*Pyrus pyrifolia*)}
YDYFQFTQQYQLAVCNSNRTLCKDPDKLFTVHGLWPSNMVGPDPSKCPINKRKEKLLEHQLEIWPNVFDRTKNNLFWDKEWMKHGSCGYPT
IDNENHYFETVIKMYISKQQNVSRLSKAKIEPDGKKRALLDIENAIRNGADNKKPKLKCKKGTTTELVEITLCSDKSGEHFIDCPHPFEPISPHYCPTN
NIKY

>d1g2ra_d.192.1.1 (A:) Hypothetical cytosolic protein SP0554 {Streptococcus pneumoniae}
RKIPLRKSVSNEVIDKRDLLRIVKNKEGQVFIDPTGKANGRGAYIKLDNAEALEAKKKVFNRFSMVEESFYDELIAYVDHKVKRRELGE

>d1c4ka3_d.125.1.1 (A:570-730) Ornithine decarboxylase C-terminal domain {Lactobacillus sp., strain 30a}
APLKQVLPISYAANEERYNGYTIRELCQELHDYFKNNNNTFYQKRLFREFFPEQGMLPYEARQE FIRNHNKLVPLNIEGEIALEGALPYPPGVFCVAP
GEKWSSETAVKYFTILQDGINNFPGFAPEIQGVYFKQEGDKVVAYGEVYDAEVAKNDRYNN

>d1g61a_d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Archaeon *Methanococcus jannaschii*}
MIIRKYFSGIPTIGVIALTTEITLLPIFLDKDDVNEVSEVLETKCLQTNIKGSSLVGSLSVANKYGLLPKIVEDEELRIKNFLKENNLNVEIJKSNTAL
GNLILTNDKGALISPELKDFKKDIEDSLNVEVEIGTIAELPTVGSNAVVTNGCCLTHPLVEDDELEFLKSLKVEYIGKTANKTTSVGACIANSKGAVV
GGDTTGPELLIIEDALGL

>d1g62a_d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Baker's yeast (*Saccharomyces cerevisiae*)}
MATRTQFENSNEIGVFSKLTNTYCLVAVGGSENFYSAFEAEGLDAIPIVHTTIAGTRIIGRMTAGNRRGLLVTQTTDQELQHLRNSLPDSVKIQRVEER
LSALGNVICCNDYVALVHPPIDRETEELISDVLGVEVFRQTISGNILVGSYCSLSNQGGLVHPQTSVQDQEELSSLQVPLVAGTVNRGSSVGAGMV
VNDYLAVTGLDTAPELSVIESIFRL

>d1jdw_d.126.1.2 (-) L-arginine: glycine amidinotransferase {Human (*Homo sapiens*)}
CPVSSYNEWDPLEEVIVGRAENACVPPFTIEVKANTYEKYWPFYQKQGGHYFPKDHLKKAVALIEEMCNILKTEGVTVRRPDPIDWSLKVKTPDFEST
GLYSAMPRDILIVVGNEIIEAPMAWRSRFFEYRAYRSIIKDYFHRAKWTAPKPTMADELYNQDPIHSVEDRHKLAAQGKFVTTEFPCFDAADFI
RAGRDIFAQRSQVTNYLGIEWMRRHLAPDYRVHISFKDPNPMHIDATFNIIGPGIVLSNPDRPCHQIDLFKKAGWTIITPPTPIIPDDHPLWMSSKW
LSMNVLMLDEKRMVMDANEVPIQKMFKEKGITTKVNIRNANSLGGFHWCVDVRRGTLQSYLD

>d1bwda_d.126.1.2 (A:) L-arginine: inosamine-phosphate amidinotransferase {Streptomyces griseus}
RSLVSVHNEWDPLEEVIVGTAVGARVPTADRSVFAVEYAGDYESQEIQPSGAYPDRVLKETEEELHVLAELTKLGVTVRPGPRDHSALIKTPDWET
DGFHDYCPRDGLLSGQTIIETPMALRSRFLESAYKDLLEYFASGSRWLSAPKPRLTDDSYAPQAPAGERLTDEEPVFDAANVLRFTDLYLVSDSG
NELGAKWLQSAVGDTYTVHPCRKLYASTHVDSTIVPLRPGVLTNPSRVNDENMPDFLRSWENITCPELVDIGFTGDKPHCSVWIGMNLLVRPDLA
VVDRRQTALIRLLEKGMMNVPLQLTHSRTLGGGFHATLDVVRTGALEYQF

>d1h70a_d.126.1.3 (A:) Dimethylarginine dimethylaminohydrolase DDAH {Pseudomonas aeruginosa}
FMFKHIIARTPARSLVDGLTSHLGKPDYAKALEQHNAYIRALQTCVDITLLPPDERFPDSVVEDPVLCTSRAIITRPGAESRRGETIIEETVQRFYP
GKVERIEAPGTVEAGDIMMVGDHFYIGESARTNAEGARQMIALEKHGLSGSVRLEKVLHLKTGLAYLEHNNLLAAGEFVSKPEFQDFNIIIEPEEES
YAANCIWVNERNVIMPAGYPRTREKIALGYRVIEWDTSEYRKIDGGVSSMSLRF

>d1chma2_d.127.1.1 (A:157-402) Creatinase, catalytic (C-terminal) domain {Pseudomonas putida}
MIKSAEEHVMIRHGARIADIGGAAVVEALGDQVPEYEVALHATQAMVRAIADTFEDVELMDTWTFQSGINTDGAHNPVTRKVNKGDILSLNC
FPMIAGYYTALERLTLFDHCSDDHRLWQVNVEVHEAGLKLICKPGARCSDIARELNEIFLKHDVLQYRTFGYGHSGFTLSHYGREAGLELRREDITVLE
PGMIVVSMEPMIMLPEGLPAGGYREHDILIVNENGAENITKFPYGPEKNIIR

>d1c22a_d.127.1.1 (A:) Methionine aminopeptidase {Escherichia coli}
AISIKTPEDIKMVRAGRLAAEVLEMIEPYVKPGVSTGELDRICNDYIVNEQHAVAACLGYHGPKSVCISINEVVCHGIPDDAKLLKDGDIVNIDVTVIK
DGFHGDTSKMFIVGKPTIMERLCRITQESLYLALRMVKPGINLREIGAAIQKFVEAEGFSVVREYCGHIGQGFHEEPQLVHYSRETNVVLKPGM
TFTIEPMVNAGKKEIRTMKGWTVKTKDRSLSAQYEHTIVTDNGCEILTRKDDTIPAIISHD

>d1xgsa2_d.127.1.1 (A:1-194,A:272-295) Methionine aminopeptidase {Archaeon *Pyrococcus furiosus*}

MDTEKLMKAGEIAKKVREKAIKLARPGMLLEAESIEKMMELGGKPAFPVNLSINEIAAHYTPYKGDTTVLKEGDYLKIDVGVLHIDGFIADTAVTR
VGMEEDELMEAACEALNAASVARAGVEIKELGKAIENEIRKRGFKPIVNLSGHKIERYKLHAGISIPNIYRPHDNYVLKEGDVFAIEPFATIGAXRNGIV
AQFEHTIIVEKDSVITTE

>d1b6a_2 d.127.1.1 (110-374,449-478) Methionine aminopeptidase {Human (Homo sapiens)}

KVQTDPSPVPCIDLYPVGFPKGQEYPPQTDGRATAWRTSEEKKALDQASEEIWNDFREAAEAHRQVRKYMSWIKPGMTMIEICEKLEDCSR
KLIKENGLNAGLAGPTGCSLNCAHYTPNAGDTTVLQYDDICKIDFGTHISGRIIDCAFTVTNPKYDTLLKAVKDATNTGICAGIDVRLCDVGEAIQ
EVMESYEVEIDGKTYQVKPIRNLNGHSIGQYRIHAGKTVPIVKGEATRMEEGEVYAIETFGSTGKGVVXDIKGSYTAQFEHTILLRPTCKEVVSRGDD
Y

>d1az9_2 d.127.1.1 (177-440) Aminopeptidase P, C-terminal domain {Escherichia coli}

SPEEIAVLRRAGEITAMAHTRAMEKCRPGMFYHELEGIEHHFNRHGARYPSYNTIVSGENGCLHYTENECEMRDGLVLIDAGCEYKGYAGDIT
RTFPVNKGFTQAQREIYDIVLESLETSLRLYRPGTSILEVTGEVVRIMVSGLVKGILKGVDDELIAQNAHRPFFMHGLSHWLGLDVHDVGVYQDRS
RILEPGMVLTVEPGLYIAPDAEVPEQYRIGIRIEDDIVITETGNENLTASVKKPEEIEALMVAARKQ

>d1f52a2 d.128.1.1 (A:101-468) Glutamine synthetase, C-terminal domain {Salmonella typhimurium}

DRDPRSIKRAEDYL RATGIADTVLFGPEPEFFLFD DIRFGASISGSHVAID DIEGAWNSSTKYEGGNKGHRPGVKGGYFPVPPVDSAQDIRSEMCLV
MEQMGLVVEAHHHEVATAGQNEVATRFNTMTKKADEIQIYKVVHNVAHREFGKTATFMPKPMFGDNGSGMHCHMSLAKNGTNLFSGDKYAGL
SEQALYYIGGVVIKHAKAINALANPTTNSYKRLVPGYEAPVMLAYSARNRSASIRPVVASPKARRIEVRFPDPAANPYLCFAALLMAGLDGIKNKIHPGE
PMDKNLYDLPPEEAKEIPQVAGSLEEALNALDLDREFLKAGGVFTDEAIDAYIALRREEDDRVRMTPHPVEFELYSV

>d1crka2 d.128.1.2 (A:99-380) Creatine kinase, C-terminal domain {Chicken (Gallus gallus), mitochondria}

TMKHTDLDASKITHGQFDERYVLSSRVRTGRSIRGLSLPPACRSAERREVENVVVTALAGLKGDLSGKYYSLTNMSERDQQQLIDDHFDFKPVSP
LTCAGMARDWPDARGIWHNNNDKTFLVWINEEDHTRVISMEKGNNMKRVFERFCRGLKEVERLIKERGWEFMWNERLGYVLTCPSNLGTGLRAG
VHVKLPLRSKDPFRPKILENLRLQKRGTVGGVDTAAADVYDISNLD RMGRSEVELQVIDGVNYLVDCEKKLEKGQDIKVPPPLPQFGRK

>d1qh4a2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Chicken (Gallus gallus), brain-type}

TDEHKTDLNADNLQGGDDLDPNYVLSSRVRTGRSIRGFCLPPHCSRERRAIEKLSVEALGSLGGDLKGKYYALRNMTDAEQQQQLIDDHFDFKPV
PLLASGMARDWPDARGIWHNDNKTFLVWINEEDHLRVISMQKGGMKMEVFRFCRGLKEVERLIQERGWEFMWNERLGYVLTCPNLGTGLRAG
VHIKLPNLGKHEKFGEVLKRLRLQKRGTVGGVDTAAVGGVFDVSNADRLGFSEVELQMVVDGVKLLIMEKRLKGQSIDDLMPAQK

>d1qk1a2 d.128.1.2 (A:103-379) Creatine kinase, C-terminal domain {Human (Homo sapiens), mitochondria}

TTDLDASKIRSGYFDERYVLSSRVRTGRSIRGLSLPPACTRAERREVERVVVDALSGLKGDLAGRYYRLSEMTEAEQQQLIDDHFDFKPVSP
MARDWPDARGIWHNNEKSFLIVVNEEDHTRVISMEKGNNMKRVFERFCRGLKEVERLIQERGWEFMWNERLGYVLTCPNLGTGLRAGVHIKLP
LLSKDSRFPKILENLRLQKRGTVGGVDTAAAGGVFDISNLDRLKGSEVELVQLVIDGVNYLIDCERRLERGQDIRIPTPVIHTKH

>d2crka2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Rabbit (Oryctolagus cuniculus)}

TDKHTDLNHENLKGDDLDPHYVLSSRVRTGRSIRGFCLPPHCSRERRAIEKLSVEALNSLTGEFKGKYYPLKSMTEEQQQQLIDDHFDFKPVSP
LLASGMARDWPDARGIWHNDNKSFLVWVNEEDHLRVISMQKGGMKMEVFRFCRGLQKIEIFKKAGHPFMWNEHLGYVLTCPNLGTGLRAG
GVHVVKLAHLSKHPKFEELTRLRLQKRGTSVFDAAVGSVFDISNADRLGSSEVEQVQLVVDGVKLMVEMEKKLEKGQSIDDMIPAQK

>d1g0wa2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Cow (Bos taurus), retinal isoform}

TDEHKTDLNQGGDDLDPNYVLSSRVRTGRSIRGFCLPPHCSRERRAIEKLA VEALSSLDGLAGRYYALKSMTEAEQQQLIDDHFDFKPVSP
LLASGMARDWPDARGIWHNDNKTFLVWINEEDHLRVISMQKGGMKMEVFRFCRGLQKIEIFKKAGHPFMWNEHLGYVLTCPNLGTGLRAGV
HIKLPHLGKHEKFSEVLKRLRLQKRGTVGGVDTAAVGGVFDVSNADRLGFSEVELQMVVDGVKLLIMEQRLEQQQAIDDLMPAQK

>d1bg0_2 d.128.1.2 (96-357) Arginine kinase {Horseshoe crab (Limulus polyphemus)}

TDKHPKQWGDINTLVGLDPAGQFIISTRVRCGRSLQGYPFNPCLTAEQYKEMEEKVSSSTLSSMEDELKGTYPLTGM SKATQQQLIDDHFDFK
FLQTANACRYWPTGRGIFHNDAKTFLVWWVNEEDHLRIISMQKGGMKMEVFRFCRGLQKIEIFKKAGHPFMWNEHLGYVLTCPNLGTGLRAGV
KDRKVLEDIASKFNLQVRGTRGEHTESEGGVYDISNKRRRLGTEYQAVREMQDGILEMIKMEKAAA

>d1cdwa1 d.129.1.1 (A:155-252) TATA-box binding protein (TBP), C-terminal domain {Human (Homo sapiens)}

SGIVPQLQNIVSTVNLGCKLDTIALRARNAEYNPKRFAAVIMRIREPRTTALIFSSGKMVCTGAKSEENSRLAARKYARVVKLGFPACKLDFKIQ

>d1cdwa2 d.129.1.1 (A:253-333) TATA-box binding protein (TBP), C-terminal domain {Human (Homo sapiens)}

NMVGSCDVFKPIRLEGLVLTHQQFSSYEPELFPGLIYRMKPRIVLLIFSGKVLTGAKVRAEIYEAFENIYPILKGFRK
>d1qnaa1 d.129.1.1 (A:17-115) TATA-box binding protein (TBP), C-terminal domain {Arabidopsis thaliana}
HPSGIVPTLQNIVSTVNLDCKLDLKAIALQARNAEYNPKRFAAVIMRIREPKTTALIFASGKVMVCTGAKSEDFSCKMAARKYARIVQKLGPAFKDFKI
>d1qnaa2 d.129.1.1 (A:116-198) TATA-box binding protein (TBP), C-terminal domain {Arabidopsis thaliana}
QNIVGSCDVFKPIRLEGLAYSHAFFSSYEPELFPGLIYRMKVPKIVLLIFSGKIVITGAKMRDETYKAFENIYPVLSEFRKI
>d1ytba1 d.129.1.1 (A:61-155) TATA-box binding protein (TBP), C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
SGIVPTLQNIVATVTLGCRDLKTVLHARNAEYNPKRFAAVIMRIREPKTTALIFASGKVMVGTGAKSEDDSKLASRKYARIQKIGFAAKFTDF
>d1ytba2 d.129.1.1 (A:156-240) TATA-box binding protein (TBP), C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
KIQNIVGSCDVFKPIRLEGLAFSHGTSSYEPELFPGLIYRMVVKPKIVLLIFSGKIVLTGAKQREEIYQAFEAIPVLSFRKM
>d1aisa1 d.129.1.1 (A:1-92) TATA-box binding protein (TBP), C-terminal domain {Archaeon Pyrococcus woesei}
MVDMMSVKLRIENIVASVDSLFAQLDLEKVLDCPNSKYNPEEFPGIICHDDPKVALLIFSSGKLVVTGAKSVQDIERAVAKLAQKLKSIGV
>d1aisa2 d.129.1.1 (A:93-181) TATA-box binding protein (TBP), C-terminal domain {Archaeon Pyrococcus woesei}
KFKRAPQIDVQNMVFSGDIGREFNLDVVALTPNCEYEPEQFPGVIYRVKEPKSVILLFSSGKIVCSGAKSEADAWEAVRKLLRELDKY
>d1mpga2 d.129.1.2 (A:1-99) 3-Methyladenine DNA glycosylase II (gene alkA or aidA) {Escherichia coli}
MYTLNWQPPYDWWSMLGFLAARAVSSVETVADSYYARSLAVGEYRGVVTAPIRHTLHINLSAGLEPVAAECLAKMSRLFDLQCNPQIVNGALG
RLG
>d1ko9a2 d.129.1.2 (A:12-135) 8-oxoguanine glycosylase {Human (Homo sapiens)}
GHRTLASTPALWASIPCPRSELRLDLVLPQGSFRWREQSPAHWSGVLADQVWTLTQTEEQLHCTVYRGDKSQASRPTDELEAVRKYFQLDVTLA
QLYHHWGSDSHFQEVAQKFQGVRLLRQ
>d1f46a_d.129.4.1 (A:) Cell-division protein ZipA, C-terminal domain {Escherichia coli}
RKEAVIIMNVAAHHGSELNGELLNISIQAGFIFGDMNIYHRHLSPDGSGPALFSANMVKPGTFDPEMKDFTTGVTFMQVPSYGDELQLFKLM
LQSQAQHIADEVGGVLLDDQRMMTPOQKLREYQDIIREVKDANA
>d3pmga4 d.129.2.1 (A:421-561) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}
RNFFTRYDYEEVEAEGATKMMKDLEALMFDRSFGKQFSANDKVTVEKADNFYHDPVDGSVSKNQGLRLIFADGSRIIFRLSGTGSAGATIRLYID
SYEKDNAKINQDPQVMLAPLISIALKVSQQLQERTGRTAPTVIT
>d1kfia4 d.129.2.1 (A:444-572) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}
RNYYSRYDYEQVDSAGANKMMEHLKTKFQYFEQLKQGNKADIYDYVDPVDQSVSKNQGVRFVFGDGSRIIFRLSGTGSVGATIRIYFEQFEQQQIQ
HETATALANIILGLEISDIAQFTGRNEPTVIT
>d1bv1_d.129.3.1 (-) Major tree pollen allergen {White birch (Betula verrucosa), Bet v 1}
GVFNEYETETTSVIPAARLFKAFLDGDNLFPKAVPQAISVENIEGGPGTIKKISFPEGPLPKYVKDRVDEVDTNFKYNYSVIEGGPIGDTLEKISNEI
KIVATPDGGSILKISNKYHTKGDHEVKAEQVKASKEMGETLLRAVESYLLAHSDAYN
>d1e09a_d.129.3.1 (A:) Major tree pollen allergen {Sweet cherry (Prunus avium), pru av 1}
GVFTYESEFTSEIPPPRLKAFVLDADNLVPKIAPQAIKHSEILEGDDGGPGTIKKITFGEQGSQYGYVKHKIDSIDKENYSYSYTLIEDALGDTLEKISYETKL
VASPSGGSIKSTSHYHTKGNVEIKEHVKAGKEKASNLFKLIETYLKGHPDAYN
>d1em2a_d.129.3.2 (A:) Lipid transport domain of Mln64 {Human (Homo sapiens)}
SFSAQEREYIRQGKEATAVVDQILAQEENWKFEKNNEYGDTVYTIEVPFHGKTFILKFLPCPAELVYQEVLQPERMVLWNKTVTACQILQRVEDNTL
ISYDVSAGAAGGVSPRDFVNVRRIERRDRYLSSGIATSHSAKPPTHKYVRGENGPMMIVLKSASNPRVCTFWIILNTDLKGRPLPRYLIHQSLAAT
MFEFAFHRLQRRISELGA
>d1fvza_d.129.3.4 (A:) Phoshatidylinositol transfer protein, PITP {Rat (Rattus norvegicus)}
VLLKEYRVILPVSVDEYQVGQLYSVAEASKNETGGGEGEVLVNEPYEKDDGEKGQYTHKLYHLQSKVPTFVRMLAPEGALNIHEKAWNAPYCRTVI
TNEYMKEDFLIKIETWHKPDLGTQENVHKEPEAWKHVEVIYIDIADRSQVLSKDYKAEDPAFKSIKTGRGPLGPNWQELVNQKDCPYMCAYKL
VTVKFKWWGLQNKVENFIHKQEKRLTNFHRQLFCWLKDVKVDTMDDIRMEEETRQLDEMROKDPVKGMTAD
>d1eg9a2 d.129.3.3 (A:155-447) Naphthalene 1,2-dioxygenase alpha subunit, C-domain {Pseudomonas putida}
EAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGS

GMGVLDGYSGVHSADLPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTFPNNMSLTCSGVFKVWNPIDANTTEVWTYAIKEKDMPEDLKR
RLADSVQRTFGPAGFWESDDNDNMETASQNGKKYQSRSDLLSNLGFEDVYGDAVPGVVGKSAIGETSYRGFYRAYQAHVSSNWAEFEHASS
TWHTELTKTT

>d1mxa_1 d.130.1.1 (1-102) S-adenosylmethionine synthetase {Escherichia coli}

AKHLFTSESVSEGHPDKIADQISDAVLDAILEQDPKARVACETYVKTGMVLVGGEITTSAWVDIEEIRNTVREIGYVHSDMGFDANSCAVLSAIGKQS
PDI

>d1mxa_2 d.130.1.1 (108-231) S-adenosylmethionine synthetase {Escherichia coli}

RADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHRLVQRQAEVRKNGTLPWLRPAKSQVTFQYDDGKIVGIDAVVLSTQHSEEIDQKSLQEAV
MEEIIKPILPAEWLTSATKFFINPTGRFV

>d1mxa_3 d.130.1.1 (232-383) S-adenosylmethionine synthetase {Escherichia coli}

IGGPMGDCGLTRKIIIVDTYGGMARHGGGAFSGKDPSKVDRSAAYAARYVAKNIVAAGLADRCEIQSYAIGVAEPTSIMVETFGTEKVPSEQTLVV
REFFDLRLPYGLIQLQMLDHPIYKETAAYGHFGREHFPWEKTDKAQLLRDAAGLK

>d1qm4a1 d.130.1.1 (A:17-116) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}

GAFMFTSESVGEGHPDKICDQISDAVLDAHLKQDPNAKVACETVCKTMVLLCGEITSMAMIDYQRVRDTHIGHYDDSAKGDFKTCNVLVALE
QQSP

>d1qm4a2 d.130.1.1 (A:129-252) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}

EDVGAGDQGLMFGYATDETEECMPLTIVLAHKLNTRMADLRRSGVLPWLRPDSKTQTVQYVQDNGAVIPVRVHTIVSQHNEDITLEAMREAL
KEQVIKAVVPAKYLDDETDIYHLQPSGRFV

>d1qm4a3 d.130.1.1 (A:253-396) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}

IGGPQGDAGVTGRKIIIVDTYGGWGAHGGGAFSGKDYTKVDRSAAYAARWVAKSLVKAGLCRRVLVQVSYAIGVAEPLSISIFTYGTSSKKTERELLEV
NKNFDLPGVIVRDLKLKPIYQKTACYGHFGRSEFPWEVPKKLVF

>d2pola1 d.131.1.1 (A:1-122) DNA polymerase III, beta subunit {Escherichia coli}

MKFTVEREHLKPLQQVSGPLGGRPTLPIGNLLLQVADGTLSTGTDEMEMVARVALQPHEPGATTVPARKFFDICRGLPEGAEIAVQLEGERML
VRSGRSRFSLSTLPAADFPNLDDW

>d2pola2 d.131.1.1 (A:123-244) DNA polymerase III, beta subunit {Escherichia coli}

QSEVEFTLPQATMKRLIEATQFSMAHQDVRYYLNGMLFETEGEELRTVATDGHLAVCSMPIQSLPSHSVIVPRKGVIELMRMLDGGDNPLRVQI
GSNNIRAHVGDFIFTSKLVDGRFPDY

>d2pola3 d.131.1.1 (A:245-366) DNA polymerase III, beta subunit {Escherichia coli}

RRVLPKNPDKHLEAGCDLLQAFARAIALSNEKFRGVRLYVSENQLKITANNPEQEEAEILDVTYSGAEMEIGFNVSYVLDVLNALKCENVRMMLTD
SVSSVQJEDAASQSAAYVVMPPMRL

>d1b77a1 d.131.1.2 (A:1-110) gp45 sliding clamp {Bacteriophage RB69}

MKLSKDTIAILKNFASINSILLSQGKFIMTRAVNGTTYAEANISDEIDFDVALYDLNSFLSILSLSDDAEISMHTDGNIKIADTRSTVYWPAADKSTIVF
PNKPIQFP

>d1b77a2 d.131.1.2 (A:111-228) gp45 sliding clamp {Bacteriophage RB69}

VASVITEIKAEDLQQLLRVSRLQLQIDTIAITNKDGKIVINGYNKVEDSGLTRPKYSLTLDYDGSNNNFVINMANMKIOPGNYKVMLWGAGDKVAAK
FESSQVSYVIAMEADSTHDF

>d1czda1 d.131.1.2 (A:1001-1110) gp45 sliding clamp {Bacteriophage T4}

MKLSKDTTALLKNFATINSGIMLKSGQFIMTRAVNGTTYAEANISDVIDFDVAIYDLNGFLGILSLVNDDAEISQSEDGNIKIADARSTIFWPAADPSTV
VAPNKPIPFP

>d1czda2 d.131.1.2 (A:1111-1228) gp45 sliding clamp {Bacteriophage T4}

VASAVTEIKAEDLQQLLRVSRLQLQIDTIAITVKEGKIVINGFNKVEDSALTRVKYSLTLDYDGENTFNFIINMANMKMOPGNYKLLLWAKGKQGAAK
FEGEHANYVVALEADSTHDF

>d1dmla1 d.131.1.2 (A:29-169) UL42 {Human herpes virus type 1}

APCQVVLQGAELNGILQAFAPLRTSLLDSLLVMGDRGILIHNTIFGEQVFLPLEHSQFSRYWRGPTAAFLSLVDQKRSLLSVFRANQYPDLRRVELAIT

GQAPFRTLVQRIWTTSDGEAVELASETLMKRELTSFVVLV
>d1dmla2 d.131.1.2 (A:170-319) UL42 {Human herpes virus type 1}
PQGTPDVQLRQLTKVLNATGADSATPTTFELGVNGKFSVTTSTCTFAAREGVSSSTSTQVQILSNALTAKGQAAANAKTVYGENTHRTFSV
VVDDCSMRAVLRLQVGGGTKLFFLTPVPSCVTATGPNAVASVFLKPQK
>d1plq_1 d.131.1.2 (1-126) Proliferating cell nuclear antigen (PCNA) {Baker's yeast (Saccharomyces cerevisiae)}
MLEAKFEEASLFKRIIDGFKDCVQLVNPFQCKEDGIIAQAVDDSRVLLSLEIGVEAFQEYRCDPVTGMDLTSKILRCGNNTDTLTIADNTPDSIILL
FEDTKKDRIAESLKLMDIDADFL
>d1plq_2 d.131.1.2 (127-258) Proliferating cell nuclear antigen (PCNA) {Baker's yeast (Saccharomyces cerevisiae)}
KIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSVIIPFVDMEHPPETSIKLEMIDQPVDLTFGAKYLLDIKGSSLDRVGIRLSS
EAPALFQFDLKSGFLQFFLAPKFNDEE
>d1axca1 d.131.1.2 (A:1-126) Proliferating cell nuclear antigen (PCNA) {Human (Homo sapiens)}
MFEARLVQGSILKKVLEALKDLINEACWDISSSGVNLQSMDSHVSLVQLTLRSEGFDTYRCDRNLAMGVNLTSMSKILKCAGNEDIITLRAEDNADT
LALVFEAPNQEKVSDYEMKLMQLDVEQL
>d1axca2 d.131.1.2 (A:127-255) Proliferating cell nuclear antigen (PCNA) {Human (Homo sapiens)}
GIPQEYSCVVKMPSGEFARICRDLSHIGDAVVSCAKDGVKFSASGEGLGNIGNIKLSQTNSVDKEEAVTIEMNEPVQLTFALRYLNFFTAKTPLSSTVT
LSMSADVPLVVEYKIADMGHLKYYLAPKI
>d1ge8a1 d.131.1.2 (A:2-117) Proliferating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}
PFEARVFEGAKEFAQLDTASKLIDEAAFKVTEDGISMRAAMDPSRVVLDLNLPSIFSKEYEVVEPETIGVNLDHLKKILRGKAQDTLILKGEENFLEITIQ
GTATRTFRVPLID
>d1ge8a2 d.131.1.2 (A:126-247) Proliferating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}
PELPFTA KV VV LG E V L K D A V K D A S L V S D S I K F I A R E N E F I M K A E G E T Q E V E I K L T L E D E G L L D I E V Q E E T K S A Y G V S Y L S D M V K G L K A D E V T I K F G N E M
PMQMEYYIRDEGRLTFLAPRV
>d1hra4 d.133.1.1 (A:311-907) Aldehyde oxidoreductase {Desulfovibrio gigas}
MSGPAAAAEDAIEIHPGTPNVYFEQPIVKGEDTGPIFASADVTGDFYVGRQPHMPIEPDVAFAYMGDDGKCYIHKSIGVHLHYMIAPGVGLEP
DQLVLVANPMGGTFGYKFSPTSEALAVAAMATGRPVLHLYNQQQQYTGKRSPWEMNVKFAAKDGTLLAMESDWLVDHGPYSEFGDLLTR
GAQFIGAGYNNIPNIRGLRTVATNHVWGSARFGYGAQPSMFASECLMDMLAEKLGMDPLELRYKNAYRPGDTNPTQGEPEVFSLPDMIDQLRPKY
QAALEKAQKESTATHKKVGVisGIVGSGLDGPDAESEAWEALNADGTITVHTAWEDHGQGADIGCVTAHEALRPMGVAPEKIKFTWPNTATTPN
SGPSGSREQVMTGNAIRVACENLLKACEKPGGGYYTYDELKAADKPKITGNWTASGATHCDAVTLGKPFVVYMYGVFMAEVTVDVATGQTTV
DGMTLMADLGLSLCNQLATDGQIYGGLAQGIGLALSEDFFEDIKKHATLGAGFPFIKQIPDKLDIVVNHPRPDGPGASGVGELPLSPHAAIINA
ATGVRIYRLPAYPEKVLEALK
>d1dgja4 d.133.1.1 (A:311-906) Aldehyde oxidoreductase {Desulfovibrio desulfuricans}
MSAPEAMAPDAIEIHPGTPNVYDQLEEKGEDTVPFFNDPANVVAEGSYYTQRQPHMPIEPDVFGYGYINEQGQVVIHSKSVAIHLHALMIAPGLGLE
FPKDLVLVQNTTGGTFGYKFSPTMEALGVAVMATGRPCHLRNYEQQQNYTGKRSPFWTTMRYAADRQGKILAMETDWSVDHGPYSEFGDLLT
LRGAQYIGAGYGYIANIRGTGRTVATNHCGAAFRGYGAPESEFPSEVLMDELAEGKLGMDPFELRALNCYREGDTSSGQIPEVMSLPEMFDKMRP
YYEESKKRKVERSTAEIKRGVGVALGVYAGLDGPDTSEAWVELNDDGSVTLGNSWEDHGQGADAGSLGTAHEALRPLGITPENIHLVMNTSKTP
NSGPAGGSRSQVVTGNAIRVACEMIIEGMRKPGGGFFTPAEMKAERGRPMRYDGKWTAPAKDCDAKGQGSPFACMYGLFLTEVAVEVATGKATV
EKMVCVADIGKICNKLVVDGQIYGGLAQGVGLALSEDYEDLKKHSTMGGAGIPSIMIPDDIEIVYVETPRKDGPFGASGVGEMPLTAPHAIIINGIY
NACGARVRHLPARPEKVLEAMP
>d1fo4a5 d.133.1.1 (A:695-1332) Xanthine oxidase, C-terminal domain {Cow (Bos taurus)}
IITIEDAIKNNSFYGSELKIEKGDLKGFSEADNVVSGELYIGGQDHFYLETHCTIAIPKGEEGEMELFVSTQNAMKTQSFVAKMLGVPNRILRVKRM
GGGGGGKETRSTLVSVALAAYKTGHPVRCMLDRNEDMLITGGRHPFLARYKVGFMKTGTIVALEVDHYSAGNSRDLHSIMERALFHMDNCY
KIPNIRGTGRLCKTNLSSNTAFRGFGGPQALFIAENWMSEAVTCGLPAEEVRWKNMYKEGDLTHFNQRLEGFSVRCWDECLKSSQYYARKSEVD
KFNKENCWKKRGLCIIPKFGISFTVPLNQAGALIHVYTDGSVLVSHGGTEMGQGLHKTMVQASKALKIPISKIYISETSTNTVNPSSPTAASVSTD
YQQAVYEACQTILRKLEPFKKKNPDGSWEDWVMAAYQDRVSLSTGFYRTPNGLGSFETNSGNAFHFTYGVACSEVEIDCLTDHKNLRTDIVMD

VGSSLNPAIDIGQVEGAFVQGLGLFTLEELHYSPEGSLHTRGPSTYKIPAFGSIPTEFRVSLRDCPNKKAIYASKAVGEPPFLGASVFFAIKDAIRARA
QHTNNNTKELFRLDSPATPEKIRNACVDKFTTLCVTGAPGNCKPWSLRV

>d1jrob2 d.133.1.1 (B:124-777) Xanthine dehydrogenase chain B, C-terminal domain {Rhodobacter capsulatus}

PAILTLQALAADSRFEGGPVIWARGDVETALAGAAHLAEGCFEIGGQEHFYLEGQAALPALAEGGVVIHCSSQHPSEIQHKVAHALGLAFHDVRVE
MRRMGGGGKESQGNHLAIACAVAARATGRPKMRYDRDDDMVITGKRHDFRIRYRIGADASGKLLGADFVHLARCGWSADSLPVCDRAML
HADGSYFVPALRIESHRLRTNTQSNTAFRGFGGPQGALGMERAIEHLARGMGRDPAELRALNFYDPPERGGLSAPPSPPEIATKKTQTHYQQEVA
DCVLGELVTRLQKSANFTTAAWNSTNRTLARGIALSPVKFGISFTLHNQAGALVQIYTDGSVALNHGTEMGQGLHAKMVQVAAVLGI
DPVQRITATDTSKVPNTSATAASSGADMNGMAVKDACETLRGRLAGFVAAREGCAARDVIFDAGQVQASGKSWRFAEIVAAAYMARISLSATGY
ATPKLSWDRLRGQGRPFYFAYGAIAEVVIDRLTGENRILRDTILHDAGASLPALDIGQIEGAYVQGAGWLTTEELVWDHCGRMLTHAPSTYKIPAF
SDRPRIFNVALWDQPNEETIFRSKAVGEPPFLLGISAFLALHDACAACGPHWPDLQAPATPEAVLAARRAEGRA

>d1qj2b2 d.133.1.1 (B:147-809) Carbon monoxide (CO) dehydrogenase molybdoprotein {Pseudomonas carboxydovorans}

VDPFKAMEPDAPLLREDIKDKMTGAHGARKHHNHIFRWEIGDKEGTDATFAKAEVVS KDMFTYHRVHPSPLETCQCVA SMDKIKGE LT WGT FQA
PHVIRTVVSLISGLPEHKIHVIAPD IGGGFGNKGAYSGYVCAVVASIVLGPVWKVEDRMENLSTS FARDYHMT TELAATKD GKI LAM RCH VLA
HGAFD ACADPSKWPAGFMNICTGSYDMPVAHLAVDGVTNKA SGGVAYRXSFRVTEAVY AIERAIETLAQRLEMD SADL RIKNFI QPEQFPYMAPL
GWEYDSGN YPLAMKKAMDTVG YHQLRAEQKAKQEA FKGETREIMGIGSFT EIVGAGPSKNC DILGVSMFD SAEIRI HPTGS V IARMG TKS QGQ
GHETTYAQIATELGIPADDIMIEGNTDAPYGLTYGSRSTPTAGAATAVAARKIKAKAQMIAAHMLEVHEGDLEWDVDRFRVKGLPEKF KTM KEL
AWASYN SPPP NLEPGLEAVNYDPPNM TYPFGAYFCIM DIDIDTGVAKTRFYAL DDCGTRINPMIIEGQVHGGL TEAF AVAMGQE IRYDEQGNVL
GAS FMDFFLPTA VETPKWETDYTVTPSPHHPIGAKGVGESPHVGGVPCFSNAVN DAYAFLNAGHIQMPHD AWRLW KVGEQLGLHV

>d1ffvb2 d.133.1.1 (B:147-803) Carbon monoxide (CO) dehydrogenase molybdoprotein {Hydrogenophaga pseudoflava}

IDALKPDAPV LREDLAGTKTSGA HGPREHHN HIFTWGAGDKA TDAV FANAP VT VSQHMYYPRVH PCPLETCGCVA SFDP IKGD LTT YITSQ APHV
RTVVSMLSGIPESKVRIVSPD IGGGFGNKG YIPGYVCAIVASIVLGPVWKVEDRV ENISTTA FARDYHMDGELAATPDG KILGLRVNVVADHG AF
ACADPTKFPAGLFHICSGSYDIPRAHCSV/KGVTNKA PGGVAYRCSFRVTEAVY LIER MVDLAQKLNMDKAEIRAKN FIRKEQFPYTTQFGF EYD SG
DYHTALKVLD AVDYPALRAEQAARRADPNSPTLMG IGLVTFTEVVGAGPSKMC DILGVGMFDSC EIRI HPTGS IARMGT ITQGQGHQTT YAQI A
TEL GIPSEVIQVEEGDT STAPYGLTYGSRSTPVAGAAIA ALAARKI HA KARKIA AAHM LEVNEND LDWEVDRFKVKGDDSKF KTMADI AWQAYHQ PP
AGLEPGLEAVHYYDPPNFTYPFGIYLCVVDIDRATGETKVRRFYAL DDCGTRINPMIIEGQI HGGL TEGYAVAMGQQMPFDAQGNLLGNTLMDYFLP
TAVETPHWETDHTVTPSPHHPIGAKGVAESPHVGSIPTFTAAVVD AFAHVGV THLDM PHTS YRV/WKSLKEHNLAL

>d1aop_3 d.134.1.1 (149-345) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4 {Escherichia coli}

NDMRNRNVLCTSNPYSQLHAEAYEWAKKISEHLLPRTRAYAEIWL DQE KVATT DEEPI LGQT YLPRKFTT VVIPPQN DIDLH AND MNF VAI AENGK
LVGFNLLVGGGLSIEHGNKKT YARTASEFGY LP LEHT LAVA EAVV TT QRDWGNRT DRKNAK TKT LERV G VET FKA E VERRAGIK FEP IRPYE FT GRGD
R

>d1aop_4 d.134.1.1 (426-570) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4 {Escherichia coli}

PQRENSMACVS FPTCPLAMA EAERFLPSFIDN IDNLMAK HGVSDEHIVM RVTGCPNGC GRAM LAEV GLVG KAPGRY NLHGG NRIGTRIP RMYK
ENITEPEI LASLDELIG RWAKEREAGE GFGDFT VRAG IIRPV LD PAR DLW D

>d1klqa_d.135.1.1 (A:) The spindle assembly checkpoint protein mad2 {Human (Homo sapiens)}

GSITL RGSAEIVAEFFSFGINSILYQRGIYPS ETFRVQ KYGL TLV TDLE LIKY LNNV VEQL KDWLY KCSV QKL VVVISNIESGEVLERW QFDIECDK TAK
DDSAPREKSQKAIQDEIRSVRQITATVTFPLLEVSCSF DLIYTDKDLV PKEE SGPFITNSEE VRLRSFTT IHKV NSMV KIPV ND

>d1byra_d.136.1.1 (A:) Nuclease Nuc {Salmonella typhimurium}

EPSVQVG SPEG SARVL VLSA IDS AKTSI RMM MAYSFT A P D IM KALV AAK KRG DV KIVIDER GNT GRASIA AM NYI ANS G I PLRT DS NF PI Q HDK V IIV
DNVT VETGSF NFT KAA ET KNS E NAVV I WNM PKLA E S FLEHW QDRW NQGRD YRS

>d1f0ia1 d.136.1.2 (A:6-263) Phospholipase D {Streptomyces sp.}

AATPHLDAVEQTLRQVSPGLE GDVWERTSGNKLDGSAADPSDWLLQTPGCWGDDK CADRV GTKRLA KMTE NIGNA TRVDI STLAPF PNGA FQ
DAIVAGL KESA AKGNSL KVRL VGAAPV YHMNGIPS K YRD KLA LGK AA ENITL NVAS MTT SKA FSW NH SKI LVV DGQ SALT GG IN SWK DDY LD T
HPVSDV DLA L TGP AAGS AGRY LDTL WTWT CKN KSNI ASVW FAAS GNAG CMPT MHKD TNPKA SPAT G

>d1f0ia2 d.136.1.2 (A:264-514) Phospholipase D {Streptomyces sp.}

NVPVIAVGGLGVGIKDVKDPKSTFRPDPTASDTKCVVGLHDNTNADRDYDTVNPEESALRALVASAKGHIEISQQDLNATCPPLPRYDIRLYDALAAK
MAAGVKVRIVVSDPANRGAVGSGGYSQIKSLSEISDTLRNRLANITGGQQAAKTAMCSNLQLATFRSSPNGKWADGHPYAQHHKLVSVDSTSFTYIG
SKNLYPSWILQDFGYIVESPEAKQLDAKLLDPQWKYSQETATVDYARGICGA

>d1jy1a1 d.136.1.3 (A:145-350) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}

LEDPGEGQDIWDMILDKGNPQFYLTRSGVKPKYNSGALHIKDILSPLFGTLVSSAQFNFCDFDVWLKVQYPFRKKPILLVHGDKREAKAHLHAQ
AKPYENISLCQAKLDIAFGTHHTKMMLLYEGLRVVIHTSNLIADWHQKTQGIWSPLYPRIADGTHKSGESPTHKFANLISYLTAYNAPSLKEWID
VIHKHDLSET

>d1jy1a2 d.136.1.3 (A:351-608) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}

NVYLIBSTPGRFQGSQKDNWGHFRKKLKDASSMPNAESWPVVGQFSSVGSGLADESKWLCEKFESMILTGKESKTPGKSSVPLYLIYPSVENV
RTSLEGYPAGGSPLPSIQTAEKQNWLHSYFKWSAETSGRSNAMPHIKTYMRPSPDFSKIWFVTSANLSKAAWGALEKNGTQLMIRSYELGVFL
PSALGLDSFKVKQKFFAGSQEPMATFPVYDLPPELYGSKDRPWIWNIPYVKAPDTHGNMWVPS

>d1ckv__ d.137.1.1 (-) Soluble methane monooxygenase regulatory protein B {Escherichia coli}

MSVNSNAYDAGIMGLKGKDFADQFFADENQVHVESDTVVLVKKSDIEINTFEEILLTDYKKNVNPTVNVEDRAGYWWIKANGKIEVDCDEISELLG
RQFNVYDFLVDSSTIGRAYTGNKFTITSELMLGDRKLEDYHA

>d2moba_ d.137.1.1 (A:) Soluble methane monooxygenase regulatory protein B {Methylosinus trichosporium}

SNAVVLVLMKSDEIDAIEDIVLKGKAKNPSIVVEDKAGFWWIKADGAEIDAAEAGEELLGKPFVYDLLINVSSTVGRAYTLGKFTITSEL

>d1g10a_ d.137.1.1 (A:) Toluene-4-monooxygenase catalytic effector protein {Pseudomonas mendocina}

STLADQALHNNNVGPIIRAGDLVEPVIAETEIDNPGKEITVEDRRAYVRIAEGELILTRKLEELQLGRPFNMQELEINLASFAGQIQADEDQIRFYFDKT
M

>d1hqj__ d.137.1.1 (-) Phenol hydroxylase P2 protein {Pseudomonas sp., CF600}

MSSLVYIAFQDNDNARYVVEAIQDNPHAVVQHHPAMIRIEAEKRLEIRRETVEENLGRAWDVQEMLVDVITIGGNVDEDDDRFVLEWKN

>d1jjcb6 d.138.1.1 (B:191-399) B3/B4 domain of PheRS, PheT {Thermus thermophilus (Thermus aquaticus)}

LKAELPLPFALKVEDPEGAPHFTLGYAFGLRVAPSPLWMQRALFAAGMRPINNVDVTNYVMLERAQPMHAFDLRFVGEIAVRRAREGERLKTL
DGVERTLHPEDLVIAGWRGEESPLLAGVMGGAESERVDETEIAALEVACFDPVSIRKTARRHGLTEASHRFERGVDPGLQVPAQRRLSLLQAL
AGARVAEALLEAGSPK

>d1clia2 d.139.1.1 (A:171-345) Aminoimidazole ribonucleotide synthetase (PurM) C-terminal domain {Escherichia coli}

DGSKVSDGDLIALGSSGPHSNGYSLRKILEVSGCDPQTTELGDKPLADHLLAPTRIYKSVLELIEKVDHIAHLTGGFWENIPRVLPDNTQAVI
DESSWQWPEVFNWLTAGNVEHHEMYRTFCNCVGMIIALPAPEVDKALALLNANGENAWKIGIIKASDSEQRVVIE

>d1hw7a_ d.193.1.1 (A:) Heat shock protein 33, Hsp33 {Escherichia coli}

HDQLHRYLFENFAVRGELTVSETLQQILENHDPQPVKNVLAELLVATSLTATKFDGDIRVQLQGDGPMNLAVINGNNNQQMRGVARVQGEIP
ENADLKTIVGNGYVITTPSEGERYQGVVGLEGDTLAACLEDYFMRSEQLPTRLFIITGDVDGKPAAGGMILLQVMPAQNAQQDDFDHLATLTETIK
TEELTLTANEVLWRLYHEEEVTVYDPQDVEFKCTC

>d1jw3a_ d.208.1.1 (A:) Hypothetical protein MTH1598 {Archaeon Methanobacterium thermoautotrophicum}

MKGFEFFDVTADAGFWAYGHDLLEVFENAALMFEVMTDSLVEAAEERRVEITSEDVRSLLYDWLDELLFIHDTEFILSKFKVKIDEKDDGLHLTGT
AMGEEIKEGHERRDEVKAVTFHMMIEILDEDGLIKARVILDL

>d1dl5a2 d.197.1.1 (A:214-317) Protein-L-isoaspartyl O-methyltransferase, C-terminal domain {Thermotoga maritima}

NLLERNRKLLREFPNREILVRSHIFVELV DLLTRRLTEIDGTFYYAGPNGVVEFLDDRMRIYGDAPEIENLLTQWESCGYRSFEYMLHVGYNASFHIS
CSI

>d1seia_ d.140.1.1 (A:) Ribosomal protein S8 {Bacillus stearothermophilus}

VMTDPIADMLTAIRNANMVRHEKLEPVASKIKREIAEILKREGFIRDYEYIEDNKQGILRFLKYGPNERVITGLKRISKPGLRVYVKAHEVPRVLNGLIA
ILSTSQGVLTDKEARQKGTGGEIIAYVI

>d1an7a_ d.140.1.1 (A:) Ribosomal protein S8 {Thermus thermophilus}

TDPIADMLTRIRNATRVYKESTDPASRFKEEILRILAREGFIKGYERVDGKPYLRVLYKGPRRQGPDRPEQVIHHIRRISKPGRRVVGVKEIPRV
RRGLGIAILSTSKGVLTDREARKLGVGELICEVW

>d1i94h_d.140.1.1 (H:) Ribosomal protein S8 {Thermus thermophilus}
MLTDPIADMTRIRNATRVYKESTEVPASRFKEEILKILAREGFIKYERVEVDGKPYLRHLKYGPRRQGPDRPEQVIKHIRRISRPGRVVGVKEIPR
VRRGLGIAILSTPKGVLTDREARKLGVGELICEVV
>d1i6ua_d.140.1.1 (A:) Ribosomal protein S8 {Archaeon Methanococcus jannaschii}
SLMDPLANLNHISNCERVGKKVYIKPASKLIGRVLKVMQDNGYIGEFEFIEDGRAGIFKVELIGKINKCGAIKPRFPVKFGYEKFKEKRYLPARDFGILI
VSTTQGVMSHEEAKKRGLGGRLAYVV
>d1rl6a1 d.141.1.1 (A:7-81) Ribosomal protein L6 {Bacillus stearothermophilus}
PIEIPAGVTVTNGNTVTVKGPKGELTRTFHPDMTITVEGNVITVTRPSDEKHHRALHGTRSSLANMVEGVSKG
>d1rl6a2 d.141.1.1 (A:82-170) Ribosomal protein L6 {Bacillus stearothermophilus}
YEKALELVGVGYRASKQGKKLVLGVYSHPVIEPEEGLEIEVPSQTKIIVKGADKQRVGELAANIRAVRPPEPYKGKGIRYEGELVRL
>d1jj2e1 d.141.1.1 (E:1-79) Ribosomal protein L6 {Archaeon Haloarcula marismortui}
PRVELEIPDVDAEQDHLDITVEGDNGSVTRRLWYPDIDVSDGDTVIESDEDNAKTMSTIGTFQSHIENMFHGVTEG
>d1jj2e2 d.141.1.1 (E:80-172) Ribosomal protein L6 {Archaeon Haloarcula marismortui}
WEYGMEVFYSHFPMQVNVEGDEVVIENFLGEKAPRTTIHGDTDVEIDGEELTVSGPDIEAVGQTAADIEQLTRINDKDRVVFQDGVYITRKP
>d1gsa_2 d.142.1.1 (123-314) Glutathione synthetase {Escherichia coli}
NEKLFTAWFSDLPTLVTRNKAQLKAFWEKHSDIILKPLDMGGASIFRVEGDPNLGVIAETLTEHGTRYCMAQNYLPAIKDGDKRVLVVDGEPVP
YCLARIPQGETRGNLAAGGRGEPRPLTESDWKiarQIGPTLKEKGLIFVGLDIIGDRLTEINVTSPTCIREIEAEFPVSITGMLMDAIEARLQ
>d1iow_2 d.142.1.1 (97-306) D-ala-D-ala ligase {Escherichia coli, gene ddlB}
KLRSKLLWQGAGLPVAPWVALTRAEEFKGLSDKLAEISALGLPIVVKPSREGSSVGMSKVVAENALQDALRLAFQHDEEVVIEKWLSGPEFTVAILGE
EILPSIRIQPSGTFYDYEAKFLSDETQYFCPAGEASQEANLQALVLKAWTTLGCKGWRIDVMLSDGQFYLLANTSPGMTSHSLVPMARQAG
MSFSQLVVRILEAD
>d1ehia2 d.142.1.1 (A:135-362) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}
DKALTKELETVNGIRNTKYIVDPESANNWSWDKIVAEGLNIVFVKAANQGSSVGISRVTNAAEYTEALSDSFQYDYKVLIIEAVNGARELEVGVIGN
DQPLVSEIGAHTVPNQGSGDGYDYNNKFDNSAVHFQIPAQLSPEVTKEVKQMALDAYKVVLNRGEARMDFLLDENNVYLGEPNTPGFTNM
SLFKRLWDYSDINNAKLVDMIIDYGFEDFAQNKKLS
>d1e4ea2 d.142.1.1 (A:132-342) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}
DKSLTYIVAKNAGIATPAFWVINKDDRPVAATFTYPVFVKPARSGSSFGVKKVNSADELDYAIESAQRQDSKILIEQAVSGCEVGCAVLGNSAALVVGEV
DQIRLQYGFRIHQVEPEKGSENNAVITYPADLSAERGRRIQETVKKIYKTLGCRGLARVDMFLQDNGRIVLNEVNTLPGFTSYSRYPRMMAAAGISLP
ELIDRLIVLALK
>d1dv1a3 d.142.1.2 (A:115-330) Biotin carboxylase subunit of acetyl-CoA carboxylase {Escherichia coli}
DKVSAIAAMKKAGVPCVPGSDGPLGDDMDKNRAIAKRIGYPVIKASGGGGGRGMRVVRGDAELAQISMTRAEAKAAFSNDMVYMEKYLENP
RHVEIQVLADGQGNAYLAERDCSMQRHHQKVVEEAPAPGITPELRRYIGERCAKACVDIGYRGAGTFEFLFENGFYFIEMNTRIQVEHPVTEMIT
GVDLIKEQLRIAAGQPLSIKQEEVHV
>d1gsoa3 d.142.1.2 (A:104-327) Glyceramide ribonucleotide synthetase (GAR-syn) {Escherichia coli}
SKAFTKDFLARHKIPTAEYQNFTVEPALAYLREKGAPIVIKADGLAAGKGVIVAMTLEEAAVHDMLAGNAFGDAGHRIVIEFLGEEASFIVMV
DGEHVLPMATSQDHKRVGDKDTGPNNTGGMGAYSPAPVTTDDVHQRTMERIIWPTVKGMAAEGNTYTGFLYAGLIMDKQGNPKVIEFNCRGDL
ETQPIMLRMKSDLVELCLAAACESKLDEKTSEWD
>d1b6ra3 d.142.1.2 (A:79-276) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}
DRLTQKQLFDKLHLPTAPWQLLAERSEWPVAFDRLGELAIVKRRTGGYDGRGQWRLRANETEQLPAECYGECIVEQGINFSGEVSLVGARGFDGSTV
FYPLTHNLHQDGILRTSVAFPQANAQQQARAEEMLSAIMQELGYVGVMAMECFVTPQGLLINEAPRVHNSGHWTQNGASISQFELHLRAITDLP
LPQPVV
>d1eyza3 d.142.1.2 (A:113-318) Glyceramide ribonucleotide transformylase PurT {Escherichia coli}
NREGIRRLAAEELQLPTSTYRFADSESLFREAVIDGYPCIVKPVMSGGKQTFIRSAEQLAQAWKYAQGGGRAGAGRIVVEGVVKFDIEITLLTVA
VDGVHFCAPVGHRCEDGYRESWPQQMSPLALERAEQEIARKVVLALGGYGLFGVELFCGDEVIFSEVSPRPHDTGMVTLISQDLSEFALHVRAF

LGLPVGGGIRQY

>d1a9xa5 d.142.1.2 (A:128-402) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

DRRRFDVAMKKIGLETARSGIAHTMEEALAVAADVGFFCIIRPSFTMGSGGGIAYNREFEEICARGLDLSPTKELLIIDESLIGWKEYEMEVVRDKNDNCIIVCSIENFDAMGIHTGDSITVAPAQTLDKEYQIMRNASMAVLREIGVETGGSNVQFAVNPKNGRLLIVIEMNPRVSRSSALASKATGFPIAKVAAKLA
VGYTLDELMNDITGGRTPASEFESIDYVVTIKIPRFNFEKFAGANDRLLTQMKSVEVMAIGRTQQESLQKALRGL

>d1a9xa6 d.142.1.2 (A:677-935) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

RFQHAVERLKLKQPANATVTAIEMAVEKAKEIGYPLVVRAAMEIVYDEADLRRYFQTAVLDHFLDDAVEVDVDAICDGEMLIGGIMEHIEQAGVHSGDSACSLPAYTLSQEIQDVMRQQVQLAFELQVRGLMNQVFAVKNNEVYLIEVNPRARTVPFVKATGVPLAKVAARVMAGKSLAEQGVTKEVIPYY
SVKEVVLVPNKFPGVDPILLGPEMRSTGEVMGVGRTFAEAFAKAQLGS

>d1auva2 d.142.1.3 (A:214-417) Synapsin Ia, C-terminal domain {Cow (Bos taurus)}

NSLHSVYNFCDKPWVFAQMVRHLKKLGTEEFPLINQTYPNPKEMLSSTTYPVVVKMGAHSGMGKVVDNQHDFQDIASVVALTKTYATTEPFIDAKYDVRIKQIGQNYKAYMRTS VSGNWKTNTGSAMLEQIAMS DRYKLWVDTCEIFGGLDICAVEALHGKDGRDHII
EVVGSSMPLIGDHQDEDKQLIVEVNNKMAQA

>d1jkjb2 d.142.1.4 (B:1-238) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Escherichia coli}

MNLHEYQAKQLFARYGLPAPVGACTTPREAAA SKIGAGPWWVKCQVHAGGRGKAGGVKVVNSKEDIRAF AENWL GKR LV TYQTDANGQPVN QIL
VEAATDIAKELYLGAVVDRSSRRVVFMASTE GGVEIEKVAEETPHLHKVALDPLTGPM PYQGREL AFKLGLEGKLVQQFTKIFMGLATIFERDLAL
IEINPLVITKQGD LICLDGKGADGNALFRQPD LREM RDQSQE

>d1eucb2 d.142.1.4 (B:0-245) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Pig (Sus scrofa)}

MVNLQEYQSKKMSDNGVKVQRFFVADTANEALEAKRLNAKEIVLKAQILAGGRGKGVSSGLKGGVHLTKDPEVVGQLAKQMIGYNLATKQTP
KEGVVKVNKMVAEALDISRETYLAILMDRSCNGPV LGSPQGGV DIEEVAASNP E LIFKEQIDII EGIKDSQA QRMAENLGFLGPLQNQAADQJKKLY
NLFLKIDATQVEVNPFGTPEGQVCFDAKINFDDNAEFRQKDIFAMDDKSEN

>d1kbla3 d.142.1.5 (A:2-376) Pyruvate phosphate dikinase, N-terminal domain {Clostridium symbiosum}

AKWVYKFEENASMRNLLGGKGNCNAEMTILGMPIPQGFTVTEACTEYYNSGKQITQEIQDQIFEAITWLEELNGKKG DTEDPLLVSRSGARAS
MPGMMDTILNGLNDVAEGFAKKTGNP RFA YDSYRRIQMYSDVVMEVPKSHFEKIIDAMKEEKGVHF DTLTADDLKELAEKF KAVYKEAMNG
EEFPQEPKDQLMGAVKAVFRSWDNPRAIVYRMMNDIPGDWGTAVNVQTMVFGNKG ETS GTVA FTRNPSTGEKGIYGEYLINAQGEDVVAGVR
TPQPITQLENDMPDCYKQFMDLAMKLEKHFRDMQDM EFTIEEGKLYFLQTRNGKRTAP AALQIACDLVDEGMITEEEAVVRIEAKSLDQL

>d2hgsa2 d.142.1.6 (A:304-474) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

TKVQQELSRPGM L EMLLPQPEAVARL RATAF GLYSL DVGE EG DQ AIAE ALAAPS RFV LKPQ REGG GN NLY GEEM VQALK QL KDSE ERASY ILM
KIEPEPFENCLLRPGSPARV VQCISELGIFGVY VRQEK TLVMNKHVGHLL RTKAIE HADGGV AAGV AVLDNPYPV

>d2hgsa3 d.142.1.6 (A:3-201) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

TNWGSLLQDKQQLEELARQAVDRA LAEGVLLRTSQE PTSSEV VSYAPFTL FPSL VPS ALLEQAYA VQMD FNLL DAVSQNA AFLEQ TLS STIK QDDFT
ARLFDIHKQLKEGIAQTVFLGLNRSDYM FQRSADGSPALKQIEINTISAFGGLASRTPAVHRVLSKTK EAGKILSNNPSKGLALGI AKAWELYG
S

>d1a0i_2 d.142.2.1 (2-240) ATP-dependent DNA ligase, N-terminal domain {Bacteriophage T7}

VNIKTNPKAVSFVESA IKKALDNAGYLIAEIKYDGVRGNICVDNTANSY WLSRVSKTIPALEHLNGFDVRWKRLN DRCFYKDGFM LDGELMVKG
VDFNTGSGLLRKWTDTKQNQFHEELFVEPIRKDKV PFKLHTGHLHIKLYA ILPLHIVESGEDCDVMTLLMQEHVKNMPLLQ EYFPEI EWQAAESY
EVYDMV ELQQLYEQKRAEGHEGLIVKDPMCYKRGKKSGWWKMK

>d1fvia2 d.142.2.1 (A:2-189) ATP-dependent DNA ligase, N-terminal domain {Chlorella virus, PBCV-1}

AITKPLLA TLENIEDVQFPCLATPKIAGIRS VKQTQML SRTFKP IRNS VMN RLTE LLPEG SDGE ISIEG ATF QD TTS AVMTGHK M YNA KFS YYW FDYV
TDDPLKKYI DRV EMD MKN YI TVPHILE HAQV KIPL IPV EINN ITELL QYER DVLS KG FEG V MIR KPDG KYK FGR STL KEG ILL MKQ

>d1b04a_d.142.2.2 (A:) Adenylation domain of NAD+-dependent DNA ligase {Bacillus stearothermophilus}

DRQQAERRAAELRELLNRYGYEYYVLD RPSVP DA EYDRLM QELIAIEQYPEL KTS DSPT QRIGG PPLEAF RKVA HRV PMMSL ANA FGEG DLR DFDR
RVRQEVGEA YVCEA IDGLA VSV RYEDGYF VQGAT RDGTT GEDI TNL KTIRSLPLR LKE PV SLEARGE AFMP KASFL RLNEER KARGE ELFAN PRN
AAAGSLRQLDPKVAASRQLD LFVYGLADAE ALG IASH SEAL DYLQ ALG FKVN PERR CANIDE VIA FVSE WHD KRPL QP YEID GIVIK VDS FAQQ RAL

GATAKSPRWAIAKYKPAE

>d1dgsa3 d.142.2.2 (A:1-314) Adenylation domain of NAD⁺-dependent DNA ligase {Thermus filiformis}

MTREREARRINERLDLIRYHNRYRYVVLADPEISDAEYDRLRELKELEERFPFKSPDSPTEQVGARPLEPTFRPVRHPTRMYSLDNAFTYEEVLAFER
LEREAEAPSILYTVEHKVDGLSVLYEEGVWSTGSGDGEVGEEVTQNLITIPIRRLKGVPDRLEVRGEVYMPIEAFLRNNEELEERGEKVFKNPRNAA
AGSLRQKDPRVAKRGLRATFYALGLGLLEESGLKSQYELLWLKEKGFPVEHCYEKALGAEGVEEVYRRGLAQRHALPFEADGVVLKLDDLTWGE
LGYTARAPRFLAYKFP

>d1ckma2 d.142.2.3 (A:11-238) RNA guanylyltransferase (mRNA capping enzyme), N-terminal domain {Chlorella virus, PBCV-1}

NITTERAVLTNLGLQIKLHKVVGESRDDIVAKMKDLAMDDHKPRLPGPNPVSIERKDFEKLQNKYVVSEKTDGIRFMFFTRVFGFKVCTIIDRA
MTVYLLPFKNIPRVLFQGSIFDGECLCVDIVEKKFAFVLFDAVVSGVTVSQMDLASRFFAMKRSLKEFKNVLPEDPAILRYKEWIPLEHPTIIKDHKKAN
AIYHTDGLIIMSVDEPVYGRNFNLKLPKG

>d1a48__ d.143.1.1 (-) SAICAR synthase {Baker's yeast (Saccharomyces cerevisiae)}

SITKTELDGILPLVARGKVRDIYEVDAAGTLLFVATDRISAYDVIMENSYPEKGILLTKLSEFWFKFLSNDVRNHLDIAPGKTIFDYLPAKLSEPKYKTQLED
RSLLVHKHKLIPLEVIVRGYITGSAWKEYVKTGTGHQLKQPQGLKESQEFPPEPIFTPSTKAEGQEHDENISPQAQAAELVGEDLSRRVAELAVKLYSKCKDY
AKEKGIIIADETKFEFGIDEKTNEIILVDEVLPDSSRFWNGASYKVGESQDSYDKQFLRDWLTANKLNGVNGVKMPQDIVDRTRAKYIEAYETLTGSKW
SH

>d1bo1a_ d.143.1.2 (A:) Phosphatidylinositol phosphate kinase IIbeta, PIPK IIbeta {Human (Homo sapiens)}

KLFRASEPILSVLMWGVNHTINELSNVPVPMLMPDDFKAYSKIKVDNHLFNKENLPSRFKFKEYCPMVFRNLRERFGIDDQDYQNSVTRSAPINS
SQGRCGTRFLTYDRRFVIKTVSSVEDVAEMHNILKKYHQFIVECHGNTLLPQFLGMYRLLTVDGVETYMVVTRNVFSHRLTVHRKYDLKGSTVAREAS
DKEKAKDLPTFKDNDFLNEGQKLVGEESKKNFKLEKLKRDVEFLAQKIMDYSLLVGHDVDRAEQEEMEVEERADEECENDGVGGNLLCSYGTTP
DSPGNLLSFPRFFGPGEFDPSVDVYAMKSHESSPKVEVFMAIIDLPTDKKAAHAAKTVKHGAGAEISTVNPEQYSKRFNEFMSNILT

>d1blxa_ d.144.1.1 (A:) Cyclin-dependent PK (CDK, different isoforms) {Human (Homo sapiens)}

GLCRADQQYECVAEIGEGAYGKVKARDLKNGGRFVALKRVVQTGEEGMPLSTIREAVLRLHETFEHPNVVRLFDVCTSRTDRETKLTLVFEHVD
QDLITYLDKVEPEGVPTETIKDMMFQLLRGLDFLHSHRVVHRDLKPQNILVTSSGQIKLADFGLARIYSFQMALTSSVVTLWYRAPEVLLQSSYATPV
DLWSVGCIAFMRRKPLFRGSSVDQLGKILDVIGLGEEDWPRDVALPRQAFHSKSAQPIEKFTIDELGKDLLKCLTFNPNAKRISAYSALSHPYF
QDLERCKEN

>d1jvpp_ d.144.1.1 (P:) Cyclin-dependent PK (CDK, different isoforms) {Human (Homo sapiens)}

MENFQKVEKIGEGTYGVVKARNKLTGEVVALKKIRLDTETEGVPTAIREISLLKELNHPNIVKLLDVITENKLYLVFEFLHQDLKKFMDASALTGIPLP
LIKSYLFQLLQLGAFCHSHRVLHRDLKPQNLINTEGAIKLADEGLARAFGVPTVYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGCIAEMVTRRAL
FPGDSEIDQLFRIFRTLGPDEVVWPGBTSMPDFYKPSFPKWARQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPPFDVTKPVPHRL

>d1apme_ d.144.1.1 (E:) cAMP-dependent PK, catalytic subunit {Mouse (Mus musculus)}

SEQESVKEFLAKAKEDFLKKWETPSQNTAQLDQFDRIKTLGTGSFGRVMILVKHESGNHYAMKILDQKVVVLKQIEHTLNEKRILQAVNFPFLVKLE
FSFKDNSNLYMVMMEYVAGGEMFSHLRRIGRFAEPHARFYAAQIVLTFEYLHSDLIYRDLKPENLLIDQQGYIQVTDGFAKRVKGRTWLCGTPPEYLA
PEIILSKGYNKAVDWALGVLIYEMAAGYPPFFADQPIQIYEKIVSGKVRFPSHSSLKDLLRNLLQVDTKRGNLKNGVNDIKHWFATTDWIAI
YQRKVEAPFIPKFKPGPDTSNFDDYEEEIRVSINEKCGKEFTEF

>d1fota_ d.144.1.1 (A:) cAMP-dependent PK, catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

YSLQDFQILRTLGTGSFGRVHLIRSRHNGRYYAMKVLKKEIVVRLKQVHEHTNDERLMLSIVTHPIIIRMWGTFQDAQQIFMIMDYIEGGELFSLLRK
QRFPNPVAKFYAAEVCLALEYLHSKDIYRDLKPENILDKNGHKITDFGFAKYVPDVTLCGTPDYIAPEVVSTKPYNKSIDWWWSFGILYEMLAGYT
PFYDSNTMKTYEKILNAELRFPPFFNEDVKDLSRLITRDLSQLGNLQNGTEDVKNHPWFKEVWEKLLSRNIETPYEPPIQQGQGDTSQFDKYPEE
DINYGVQGEDPYADLFRDF

>d1a06__ d.144.1.1 (-) Calmodulin-dependent protein kinase {Rat (Rattus norvegicus)}

WKQAEDIRDYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAVLHKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEK
GFYTERDASRLIFQVLDAVKYLHDLGIVHndlKPENLYYSLDEDKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYIL
LCGYPPFYDENDAKLFEQILKAELYFDSPYWDDISDSAKDFIRHLMEKDPEKRTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKSKWKQAFN
ATAVVRHM

>d1ia8a_d.144.1.1 (A:) Cell cycle checkpoint kinase chk1 {Human (Homo sapiens)}

AVPFVEDWDLVQTGEGAYGEVQLAVNRVTEEAVAKIVDMKRAVDCPENIKKEICINKMLNHENVKFYGRREGNIQYLLEYCSGGELFDRIEP
DIGHMPEPDQAQRFFHQLMAGVVYLHGIGITHRDIKPENLLDERDNLKISDFGLATVFRYNNRERLLNKMCGLPYVAPELLKRREFHAEPVDVSCG
IVLTAMILAGELPWDPQSDSCQEYSDWKEKKTYLPWKIDSAPALLHKILVENPSARITIPDIKKDRWYNKPLKGAKRP

>d1phk_d.144.1.1 (-) gamma-subunit of glycogen phosphorylase kinase (Phk) {Rabbit (Oryctolagus cuniculus)}

FYENYEPKEILGRGVSSVRRCIHKPTCKEYAVKIIDVTGGGSFAEEVQELREATLKEVDILRKVSGHPNIIQLKDTYETNTFFFVFDMKKGELFDYLTE
KVTLSEKTRKIMRALLEVICALHKLNIVHDLKPKENILDDDMNIKLTDFGFSCLDPGEKLREVCGTPSYLAPEIIECSMNDNHPGYGKEVDMWST
GVIMYTLLAGSPPFWHRKQMLMLRMIMSGNYQFGSPEWDDYSDTVKDLVSRLFVVPQPKRYTAEEALAHPFFQQV

>d1h8fa_d.144.1.1 (A:) Glycogen synthase kinase-3 beta (Gsk3b) {Human (Homo sapiens)}

SKVTTVVATPGQGPDRPQEVSYTDTKVIGNGSFGVVYQAKLCDSGELVAIKVLQGKAFKNRELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYLNVL
DYVPETVYRVARHYSRAKQTLPVIYVLYMYQLFRSLAYIHSFGICHDRDIKPQNLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDY
TSSIDVWSAGCVALELLGQPPIPGDGSVQDQLVEIIKVLGTPTRREQIREMNPNEYTEFAFPQIAHPWTKVFRPRTPPEAIALCSRLLYEPTPTARLTPLEAC
AHSFFDELRDPNVKLPNGRDTPALFNFTTQELSSNPPLATILIPPHARIQA

>d1tkia_d.144.1.1 (A:) Titin, kinase domain {Human (Homo sapiens)}

KELYEKYMIAEDLGRGEFGIVHRCVETSSKKTYMAFKFVKVKGTDQVLVKEISILNIARHRNLHLHESFESMEELVMIEFFISGLDIFERINTSAFLNER
EIVSYVHQVCEALQFLHSHNIGHFDIRPENIYQTRSSTIKIEFGQARQLKPGDNFLLFTAPEYYAPEVHQHDVVSTATDMWSLGTLYVLLSGINPP
LAETNQQIENIMNAEYTFDEEAFCISIEAMDFVDRLLVKERKSRTMASEALQHPWLKQKIERVSTKVRTLKHHRRYYHTLIKDLNMVVAARISCG
GAIRSQKGVSVAKVVASI

>d1koba_d.144.1.1 (A:) Twitchin, kinase domain {California sea hare (Aplysia californica), twk43}

INDYDKFYEDIWKYYVPPQVEVKQGSVYDYYDILEELGSGAFGVHRCVEATGRVFVAKFINTPYPLDKYTVKNEISIMNQLHHPKLNILHDAFEDKY
EMVLILEFLSGGELFDRIAEDYKMSEAEVINYMRQACEGLKHMHEHSIVHLDIKPENIMCETKKASSVKIIDFGLATKLPDEIVKVTATAEFAAPEI
VDREPVGFTDMWAIGVGLGVLLSGLSPFAGEDDLETQNVKRCDFWEDEDAFSSVSPEAKDFIKNLLQKEPRKRLTVHDALEHPWLKGDHNSLTSR
IPSSRYNKIRQKIKEKYADWPAPQPAIGRANFSSLRKHRPQEYQIYDSYFDRKEAV

>d1koa_2_d.144.1.1 (5915-6264) Twitchin, kinase domain {Caenorhabditis elegans, pjk4}

YDNYVFDIWKQYPQPVEIKHDHVLDHYDIHEELGTGAFGVHVRTERATGNNFAAKFVMTPHESDKETVRKEIQTMSVLRHPTLVNLHDAFEDD
NEMVMIYEFMSGGELFEKVADEHNKMSDEAVEYMRQVCKGLCHMHENNYVHLDLKPKENIMFTTCSRNLKIDFGLTAHDPKQSVKVTGTAE
FAAPEVAEGKPVGYYDMWSVGVLSYILLSGLSPFGENDDETLRNVKSCDWNMDDSAFGISEDGKDFIRKLLADPNTRMTIHQALEHPWLTPG
NAPGRDSQIPSSRYTKIRDTSKTYDAWPEPLPLGLRISNYSSLRKHRPQEYISIRDAFWDRSE

>d1p38_d.144.1.1 (-) MAP kinase p38 {Mouse (Mus musculus)}

ERPTFYRQELNKTIWEVPERYQNLSPVGSGAYGSVCAFDKTGAKVAKKLYRPFQSELFAKRAYRELRLKHMVKHENVIGLLDVFTPDETLDDFTDV
YLVTHLMGADLNNIVKCQKLTDDHVQFLYQILRGLKYIHSADIIRDLKPSNLAVNEDCELKIDFGLARHTDEMTGYVATRWYRAPEIMLNWMH
YNQTVDIWSVGCIMAELLTGRTLFPGTDIDQLKLRLVGTPGAELLKPKISSESARNYIQLAQMPKMINFANVFIGANPLAVDLLEKMLVLDSDKRIT
AAQALAHAYFAQYHDPDDEPVADPYDQSFSERDILLIDEWKSLSYDEVISFVPPPLD

>d1cm8a_d.144.1.1 (A:) MAP kinase p38-gamma {Human (Homo sapiens)}

RSGFYRQEVTATAEVRAVYRDLQPVGSGAYGAVCSAVDGRGAKVAKKLYRPFQSELFAKRAYRELRLKHMVKHENVIGLLDVFTPDETLDDFTDV
YLVMPFMGTDLGKLMKHEKLGEDRIQFLVYQMLKGLRYIHAAGIIHDLKPGNLAVNEDCELKIDFGLARHQADSEMTGYVVTWYRAPEVILNW
MRYTQTVDIWSVGCIMAEMITGKTLKGSDHLDQLKEIMKVTGTPPAEFVQRLQSDEAKNYMKGLPELEKKDFASILTNASPLAVNLLEKMLVLD
QRVTAGEALAHPYFESLHDTEDEPQVQKYDDSFDDVDRTLDEWKRVTYKEVLSFKP

>d1pme_d.144.1.1 (-) MAP kinase Erk2 {Human (Homo sapiens)}

GQVFDVGPRTNLSYIGEGAYGMVCSAYDNVNKVRVAIKKISPFEHQTYCQRTLREIKILLRFRHENIIGINDIIRAPTIEQMKDVLVTHLMGADLYKLL
KTQHLSNDHICYFLYQILRGLKYIHSANVLHDLKPSNLLNTTCDLKICDFGLARVADPDHDHTGFLTEVATRWYRAPEIMLNSKGYTKSIDIWSVGC
ILAEMLSNRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINLKARNYLLSPHKNVWNRLFPNADSKALDLDKMLTFNPHKRIEVEQALAHPYLEQ
YYDPSDEPIAEAPFKFDMELDDLPKEKLKELIFEETARFQPGYRS

>d1jnk_d.144.1.1 (-) c-jun N-terminal kinase (jnk3s) {Human (Homo sapiens)}

DNQFYSVEGDESTFTVLKRYQNLPIGSGAQGIVCAAYDAVLDRNVAIKLSPRFQNQTHAKRAYRELVLMKCVNHKNIISLLNVFTPQKTLEEFQDV
YLVMEMLMDANLCQVIQMELDHERMSYLQYQMLCGIKHLHSAGIIHDLKPSNIVVKSCTLKILDGLARTAGTSFMMPYVVTRYYRAPEVILGMG
YKENVDIWSVGCGEMVRHKILFPGRDYIDQWNKVICLQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHNKLKASQARDLL
SKMLVIDPAKRISVDDALQHPYINVWYDPAEVEAPPOIYDKQLDEREHTIEEWKELEYKEVMN

>d1ckia_d.144.1.1 (A:) Casein kinase-1, CK1 {Rat (*Rattus norvegicus*)}

MELRVGNRYRLGRKIGSGSGFDIYLGTDIAAGEEVAIKLECVTKHPQLHIESKIYKMMQGGVGIPTIRWCGAEGDYNVMVMELLGPSLEDLFNFCS
RKFLSLKTVLLADQMISRIEYIHSKNFIDRDKPDLNGLGKGNLVYIIDFGLAKKYRDARTHQHIPYRENKNLTGARYASINTHLGIEQSRRDDLES
LGYVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKGYPSEFATYLNFCRSLRFDDKPDYSYLRQLFRNLFRQGFSYDYVFDWNMLKFG
ASR

>d1csn_d.144.1.1 (-) Casein kinase-1, CK1 {Fission yeast (*Schizosaccharomyces pombe*)}

NVVGVHYKVGRRIEGEFGVIFEGTNLLNNQQVAIKFEPRRSDAPQLRDERTYKLLAGCTGIPNVYYFGQEGLHNVLVIDLLGPSLEDLLDCGRKFS
VKTVAMAQMLARVQSIHEKSLVYRDIKPDNFLIGRPN SKNANMIYVVDFGMVKFYRDPVTQKHIPYREKKNLSGTARYMSINTLGREQSRRDD
LEALGHVFMYFLRGSLPWQGLKAATNKQKYERIKEKKQSTPLRELCA GFPEEFYKYMHYARNLAFDATPDYDYLQGLFSKVLERLNTTEDENFDWNL
L

>d1a6o_d.144.1.1 (-) Protein kinase CK2, alpha subunit {Maize (*Zea mays*)}

SKARVYADVNVLRPKEYWDYEALTVQWGEQDDYEVVRKVRGKYSEVFEGINVNNNEKCIKILKPVKKKKIREI KILQNLCGGPNVKLLDIVRDQH
SKTPSLIFEYVNNTDFKVLYPTLTDYDIRYYIYELLKALDYCHSQGIMHRDVKPHNVMDHELRLKRLIDWGLAEFYHPGKEYNRVASRYFKGPELLVD
LQDYDYSLSLDMWSLGCMFAGMIFRKPEFFYGHNDHQDLVKIAKVLGTDGLNVLNKYRIELDPQLEALVGRHSRKPWLFMNA DNQHLSPEAIDF
LDKLLRYDHQERLTALEMTHPYFQQVRAAENS

>d1b6cb_d.144.1.1 (B:) Type I TGF-beta receptor R4 {Human (*Homo sapiens*)}

TTLKDLIYDMTTSGSGSGLPLLVRQTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKFSSREERSWFREAEIYQTVMLRHENILGIAADNKDNGT
WTQLWLVSODYHEHGSLFYLNRYTVTVEGMIKALSTASGLAHLHMEIVGTQGKPAIAHDLKSKNIVKKNGTCCIADLGLAVRHDSATDTIDIAPN
HRVGTKRYMAPEVLDDSNMKHFESFKRADIYAMGLVFWEIARRCSIGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRV
MAKIMRECWYANGAARLTALRIKKTLSQQQE

>d1f3mc_d.144.1.1 (C:) pak1 {Human (*Homo sapiens*)}

SDEEILEKLRSIVSGDPKKYTRFEKIGQGASGTVYTAMDVATGQEV AIRQMNLLQQPKKELIINEILMRENKNPNIVNYLDSYLVGDELWVVM
LAGGS LTDVVTETCMDEGQIAAVCRECLQALEFLHSNQVIHRDIKSDNILLGMDGSVKLDFGCAQTPEQSKRSTMVGTPYWMAPEVVTRKAYG
PKVDIWSLGIMAIEMIEGEPPYLNNPLRALYLIATNGTPELQNPEKLSAIFRDFLNRCMDV EKRGSAKELLHQFLKIAPLSSLTPLIAAAKEATK

>d1howa_d.144.1.1 (A:) Sky1p {Baker's yeast (*Saccharomyces cerevisiae*)}

HFPAFKGEPYKDARYILVRKLGWGHFSTVWLA KDMVNNTVAMKIVRGDKVYTEAAEDEIKLLQRVNDADNTKEDSMGANHILKLLDFHNHKGP
NGVHVVMVFEV LGENLLALIKYEHRIPIYVKQISKQLLGLDYMHRRCGIIHTDIK PENVLMEIVD SPENLIQKIA DLGNACWYDEHYTNSIQTRE
YRSPEVLLGAPWCGADIWSTA CLIFELITGDFLFEPDEGH SYTKDDDHI A QIIELLGEPSYLLRNGKYTRTFNSRGLRNISKLFWP LEDVTEKYKF
SKDEAKEISDFLSPMLQLDPRKRADAGGLVNHPWLKD LGMEEIRVPDRELYGSGSDIPGW FEEVR

>d1qcfa3_d.144.1.2 (A:249-531) Haemopoetic cell kinase Hck {Human (*Homo sapiens*)}

KPQKPWEKDAWEIPRESLKLEKKLGAGQFGEVWMATYNKHTKAVKTMKPGSMSVEAFLAEANVMKTLQHDKLVLHAVVTKEPIIITEFMAKG
SLLDFLKSDEGSKQPLKLI DFSAQIAEGMAFIEQRNYIHRDLRAANILV SALS VCKIADFG LARVIEDNEYTAREGAKFPIKWTAPEAINFGSFTIKSDV
WSFGILLMEIVTYGRIPY PGMSNPEVIRALERGYRMPR PENCPEELY NIMMRCWKNRPEERTF EYIQSVLDDFTATESQYEEIP

>d1qpca_d.144.1.2 (A:) Lymphocyte kinase (lck) {Human (*Homo sapiens*)}

KPWWED EWEVPRE TLKVERLGAGQFGEVWMGY YNGHTKAVVSKLQGSMSPDAFLAEANLMKQLQHQR LVRLYAVV TQEPIIITEY MENGS
VDFLKTPSGIKLTINKL DMAA QIAEGMAFIEERNYIHRDLRAANILVSDTLSCKIADFG LARVIEDNEYTAREGAKFPIKWTAPEAINFGSFTIKSDV
FGILLTEIVTHGRIPY PGMTNPEV IQNLERGYRMVRPDNCPEELYQLMRLCWKERPEDRPTFDYLSVLEDFFTATE

>d1fmk_3_d.144.1.2 (249-533) c-src tyrosine kinase {Human (*Homo sapiens*)}

KPQTQGLAKDAWEIPRESLRLEV KLGQGCFGEVWMGTWNGTTRVAIKTLKPGTMSPE AFLQEAQVMKKLRHEKLVQLYAVVSEPIIYIVTEYMSKG
SLLDFLKG ETGKYLRLPQLDMAAQIASGMAYVERM NYVH RDLRAANILVGENLVCKVADFG LARVIEDNEYTARQAKFPIKWTAPEA ALYGRFTIK

SDVWSFGILLTEKKRGPYPGMVNREVDQVERGYRMPCPPECPESLHDLMCQCWRKEPEERPTFEYLQAFLEDYFTSTEPQYQPGENL
>d1fgka_d.144.1.2 (A:) Fibroblast growth factor receptor 1 {Human (Homo sapiens)}
ELPEDPRWELPRDRLVLGKPLGEGAFGQVVAEAGLDKDPNRTKAVKMLKSDATEKDLSLDISEMEMMKMIGKHKNIINLLGACTQDGPLYVI
VEYASKGNLREYLQARRPPGLEYSYNPSHNPEEQLSSKDLVSCAYQVARMEYLASKKCIHRDLAARNVLVTDNVMIADFGLARDIHIDYYKKTT
NGRLPVKWMAPAEALFDRIYTHQSDVWSFGVLLWEITLGGSPYGPVVEELFKLLKEHRMDKPSNCTNELYMMMRDCWHAVPSQRPTFKQLVE
DLDRIVALTS
>d1vr2a_d.144.1.2 (A:) Vascular endothelial growth factor receptor 2 (kdr) {Human (Homo sapiens)}
LPYDASKWEFPRDRKLKGKPLGRGAEGQVIEADFGIDKTATCRTAVAKMLKEGATHSEHRALMSELKILIHGHHLNVNLLGACTKPGGPLMVIVE
FCKFGNLSTYLSRKNEFPYKVAPEDLYKDFLTLEHLCYSFQVAKGMELASRKCIHRDLAARNILLSEKNVVKICDFGLARDIYKDPDYVRKG达尔P
LKWMAPETIFDRVTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHGNLL
QANA
>d1ir3a_d.144.1.2 (A:) Insulin receptor {Human (Homo sapiens)}
SSVFPDEWEVSREKITLLRELGQGSFGMVYEGNARDIIKGEAETRAVAKTVNESASLRERIEFLNEASVMKGFTCHHVVRLLGVSKGQPTLVVME
MAHGDLKSYLRSRPEAENNPGRPPTLQEMIQMAAEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLP
VRWMAPESLKDGVFVFTSSDMWSFGVLLWEITSLAEQPYQGLSNEQVLKFVMDGGYLDQPDNCPERVTDLMRMCWQFNPKMRPTFLEIVNLLK
DDLHPSPFPEVSFFHSEENK
>d1k3aa_d.144.1.2 (A:) Insulin-like growth factor 1 receptor {Human (Homo sapiens)}
VPDEWEWAREKITMSRELQGSFGMVYEGVAKGVVKDEPETRAVAKTVNEAASMRERIEFLNEASVMKEFNCHHVVRLLGVVSQGQPTLVIMELM
TRGDLKSYLRSRPEMENNPNLAPPSSKMIQMAGEIADGMAYLNAKKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGGKGLLPVR
WMSPESLKDGVFVFTTSDVWSFGVLLWEITLAEQPYQGLSNEQVLRFVMEGGLLDKPDNCPDMLLELMRMWCWQYNPKMRPSFLEISSIKEEME
PGFREVSFYSEENK
>d1byga_d.144.1.2 (A:) C-terminal src kinase (csk) {Human (Homo sapiens)}
GWALNMKELKLLQTIGKGEFGDVMLGDYRGNKAVAKC1KNDATAQAFLAEASVMTQLRHSNLVQLLGIVEEKGGLYVTEYMAKGSVDYLRSGRGR
SVLGGDCLLKFSLDVCEAMEYLEGNNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVWTAPEALREKKSTKSDVWSFGILLWEIYS
FGRVPYPRIPLKDVVPRVEKGYKMDAPDGCPPAVYEVMKNCWHLDAAMRPSFLQLREQLEHIKTHEL
>d1iepa_d.144.1.2 (A:) Abelson tyrosine kinase (abl) {Mouse (Mus musculus)}
MDPSSPNYDKWEMERTDITMKHKLGGGQYGEVYEGVWKKYSLTVAVKTLKEDTMEVEEFLKEAAVMKEIKHPNLVQLLGVC TREPPFYIITEFMTY
GNLLDYLRECRNQEVSADVLLYMATQISSAMEYLEKKNFVHRDLAARNCLVGENHLVKADFGLSRLMTGDTYTAHAGAKFPIWTAPESLAYNKSI
KSDVWAFGVLLWEIATYGMSPYGPIDLSQLVYELLEKDYRMERPEGCPEKVYELMRACWQWNPSDRPSFAEIHQAFETMFQ
>d1jpaa_d.144.1.2 (A:) ephb2 receptor tyrosine kinase {Mouse (Mus musculus)}
KIFIDPFTFEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHKLPGKREIFVAIKTLKSGYTEKQRRDFLSEASIMQGFDHPNVIHLEGVVTKSTPV
MIITEFMENGSLDSFLRQNDGQFTVIQLVGMRLGIAAGMKYLADMNYVHRDLAARNILVNSNLVCKVSDFGLSRFLEDDTS DPTYTSALGGKIPIRW
TAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYWDMTNQDVINAIEQDYLPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMI
RNPNPLKA
>d1fvra_d.144.1.2 (A:) Tie2 kinase {Human (Homo sapiens)}
PTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVCLKLGHHPNIINLLGACEHRYLYLAIEYAPHGNL
LDFLRKSRVLETDPAFIANSTASTLSSQQLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSRGQEVYVKKTMGRLPVRWMAIE
SLNSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKLPGQYRLEKPLNCDDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNT
TLYEKFTYAGIDCSAE
>d1cjaa_d.144.1.3 (A:) Actin-fragmin kinase, catalytic domain {Slime mold (Physarum polycephalum)}
AGALWEIEKEELFTKLPAPSSAINSHLQPAKPKVPKKPSKWDPPAEFKVDSLAVSYNDIDINWKNLQQFKGIERSEKGTEGLFFVETESGVFIVKRST
NIESETFCSSLCCMRLGLHAPKRVVSSNSEEGTNMLECLAAIDKSFRVITTLANQANILLMELVRGITLNKLTTSAPENVLTKSTMQQQLGSLMALDVIVN
NSDRLPIAWTNEGNDNIMLSERGATVVPIDSKIIPLDASHPHGERVRELLRTLIAHPGHESSQFHSIRDIIYTGYDVGTEGSISMQEGFLATVRECAS
FDLDAFERELLSWQESLQKCHNLSISPQAIPFILRMLRIFH

>d1ia9a_d.144.1.5 (A:) Trp Ca-channel kinase domain {Mouse (*Mus musculus*)}
YYSAVERNNNLMRSLQSIPFVPPRGEPTVYRLEESSPSILNNSMSSWSQLGLCAKIEFLSKEEMGGGLRAVKVLCTWSEHDILKGHLYIICKFLP
EVINTWSSIYKEDTVLHLCLREIQQQRAAQKLTFAFNQMKPKSIPYSPRFLEVFLYCHSAGQWFAVEECMTGEFRKYNNNNGDEIIPNTLEEIMLAF
SHWTYEYTRGELLVLDLQGVGENLTDPVIKAEEKRSCDMVFGPANLGEDAIIKNFRAKHHCNCCRKLKPDLKRNDYT

>d1e8xa4 d.144.1.4 (A:726-1092) Phosphoinositide 3-kinase (PI3K), catalytic domain {Pig (*Sus scrofa*)}
TAMLHDFTQQVQVIDMLQKVTDIKSLAEKYDVSSQVISQLKQKLENLQNLNPQSFRVPYDPLKAGALVIEKCKVMASKKPLWLEFKADPTAL
SNETIGIIFKHGDDLRQDMILQILRIMESIWETESDLCLLPYGCISTGDKIGMIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQA
ERFVYSCAGYCAGVATFVLGIGDRHNDNIMISETGNLFHIDFGHILGNYKSFGLINKERVPFVTPDFLVFMGTSGKTSLFHQKFQDVCKAYLALRHHT
NLLIILFSMMLMTGMPQLTSKEDIEYIRDALTVGKSEEDAKKYFLDQIEVCRDKGWTVQFNWFLHVL

>d1j7la_d.144.1.6 (A:) Type IIIa 3',5'-aminoglycoside phosphotransferase {Enterococcus faecalis}
AKMRISPELKKLIEKYRCVKDTEGMSPAKVYKLVGENENLYLKMTDSRYKTTDVEREKDMMLWLEGKLPVKVLHFERHDGWSNLLMSEADGV
LCSEEEYDEQSPKEIIEYLACIRLFHSIDISDCPYTNSDLRSLAELDLYNNDLADVDCENWEEDTPFKDPRELYDFLKTEKPEEELVFSHGDLGDSNIFVK
DGKVSGFIDLGRSGRADKWKYDIAFCVRSIREDIGEEQYVELFFDLLGIKPDWEKIKYYILLDEF

>d1e8ga2 d.145.1.1 (A:6-273) Vanillyl-alcohol oxidase {Fungus (*Penicillium simplicissimum*)}
EFRPLTLPKSLSDNFEDIQDIIRVGSENVEISSKDQIVDGSYMKPTHDPHTVMDQDFLASAIVAPRNADVQSIVGLANKFSPLWPISIGNR
SGYGGAAPRVSGSVVLDMGKNMNRVLEVNVSEGAYCVVEPGVTYHDLHNYLEANNLRDKLWLDPDLGGGSVLGNAVERGVGYTPYGDHWMM
HSGMEVLANGELLRTGMGALPDKRPTMGLKPEDQPWSKIAHLPYGFGPYIDGLFSQSNSMGIVTKIGIWLMPNP

>d1diqa2 d.145.1.1 (A:7-242) Flavoprotein subunit of p-cresol methylhydroxylase {Pseudomonas putida}
AVLPKGVTQGEFNKAVQKFRALLGDDNVLVESDQLVPYNKIMMPVENAAHAPSAAVTATTVEQVQGVVKICNEHKIPWTISTGRNFGYGSAPVQ
RGQVILDLMNKIIKIDPEMEMCYALVEPGVTFGQMYDYIQENNLPMVMSFAPSIAGPVGNTRGVGYTPYGEHFMMQCGMEVLANGDVYR
TGMGGVPGSNTWQIFKWGYGPTLDGMFTQANYGICTKMGFWLMPKP

>d1f0xa2 d.145.1.1 (A:9-273) D-lactate dehydrogenase {Escherichia coli}
NKAFLNELARLVGSSHLLTDAKTRYKGFSGQGDALAVVPGSLLELWRVLKACVTADKIIILMQAANTGLTEGSTPNGNDYDRDVIISTRLDKL
HVLGKGEQVLAGPTTLYSLEKALKPLGREPHSVIGSSCIGASVIGGICNNSSGSLVQRGPAYTEMISLAFARINEDGKLTNVHLGIDLGETPEQILSKLDD
DRIKDDDVHRDGRHAHDYDYVHRVRDIEADTPARYNADPDRLFESSGCAGKLAFAVRLDTFEAE

>d1i19a2 d.145.1.1 (A:57-273) Cholesterol oxidase {Brevibacterium sterolicum}
VAPLPTPPNFPNDIALFQQAYQNWSKEIMLDATWVCSPKTPQDVRLANWAHEHDYKIRPRGAMHGWTPLTVEKGANVEKVILADTMTHLNGIT
VNTGGPVATVAGAGASIEAVTELQKHDLGWANLPAPGVLSIGGALVNAHGAALPAVGQTTLPGHTYGSLSNLVTELTAVVWNNGTTYALETYQRN
DPRITPLLTNLGRCLTSVMTMQAGPN

>d1uxy_1 d.145.1.2 (3-200) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Escherichia coli}
HSLKPWNTFGIDHNAQHIVCAEDEQQLNAWQYATAEGQPVLILGEGSNVLFLEDYRGTVIINRIKGIEIHDEPDWYLHVGAGENWHRLVKYTLQE
GMPGLENLALIPCGVSSPIQNIGAYGVELQRVCAYDSVELATGKQVRLTAKECRFGYRDSIFKHEYQDRFAIVAVGLRLPKEWQPVLTYGDLTRLDP
TT

>d1hska1 d.145.1.2 (A:15-208) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Staphylococcus aureus}
NKDIYQALQQLIPNEKIVDEPLKRYTYKTGGNADFYTPTKNEEVQAVVKYAYQNEIPVTLNGNSNIIREGGIRGIVISLLSDHIEVSDDAIAGSGA
AIIIDVSRVARDYALTGLEFACGIPGSIGGAVYMNAGAYGGEVVKDCIDYALCVNEQGSLIKLTTKELELDYRNSIIQKEHLVLEAAFTLAP

>d1qj2c2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal domain {Pseudomonas carboxydovorans}
MIPGSFDYHRPKSIADAVALTKGEDARPLAGGHSLIPIMKTRLATPEHLVLDLRDIGDLVGIREEGTDVVIGAMTTQHALIGSDFLAAKLPIRETSLLIA
DPQIRYMGITIGNAANGDPGNDMPALMQCLGAAYELTGPPEGARIVAARDYYQGAYFTAIEPGELLTAIRIPVPPPT

>d1ffvc2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal domain {Hydrogenophaga pseudoflava}

MIPPRFEYHAPKSVGAEAVALLGQLGSDAKLLAGGHSSLLPMMKLRFAQPEHLIDINRIPELRGIREEGSTVIGAMTVENDLISSPIVQARLPLAEEAKL
IADPQVRNRGTTGGDIAHGDPGNDHPALSIAVEAHFVLEGPNGRRTVPADGFFLGTYMLLEENEVMVEIRVPAFAQ

>d1fiqb2 d.145.1.3 (B:224-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}

PKQLRFEGERTVTIQASTLKELLDLKAQHPEAKLVGNTEIGIEMFKFNQLFPMIICPAWIPELNAVEHGPEGISFGAACACALSSVEKTLEAVAKLPTQK
TEVFRGVLEQLRWFAKGQVKSVASLGGNIITASPISDLNPVFMASGTKLIVSRGTRRTVPMMDHTFFPSYRKTLGPEEILLSIEIPYSRE

>d1fo4a6 d.145.1.3 (A:192-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}

SPSLFNPEEFMPLDPTQEPIFPPELLRLKDVPKQLRFEGERVTWIQASTLKELLDLKAQHPEAKLVGNTEIGIEMFKFNQLFPMIICPAWIPELNAVE
HGPEGISFGAACACALSSVEKTLEAVAKLPTQKTEVFRGVLEQLRWFAKGQVKSVASLGGNIITASPISDLNPVFMASGTKLIVSRGTRRTVPMMDHTFF
PSYRKTLGPEEILLSIEIPYSRE

>d1jroa4 d.145.1.3 (A:179-345) Xanthine dehydrogenase chain A, domain 3 {Rhodobacter capsulatus}

PAFLPETSDALADWYLAHPEATLIAGGTDVSLWVTKALRDLPEAVFLSHCKDLAQIRETPDGYGIGAGVTIAALRAFAEGPHPALAGLRRFASEQVRQ
VATIGGNIANGSPIGDGPALIAMGASLTERRGQERRRMPLEDFFLERYRKQDRRPGEFVESVTPKSA

>d1uxy_2 d.146.1.1 (201-342) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
{Escherichia coli}

VTPQQVFNAVCHMRTTKLPDPKVNGNAGAFFKNPVSAETAKALLSQFTAPNYPQADGSVKLAAGWLIDQCQLKGMQIGGAHVHRQQALVLIN
EDNAKSEDVVQLAHHVRQKVGEKFNVVLEPEVRFIGASGEVSAETIS

>d1hska2 d.146.1.1 (A:209-317) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
{Staphylococcus aureus}

GKMTEIQAKMDDLTERRESKQPLEYPSCGSVQRPPGHFAGKLIQDSNLQGHRIGGVEVSTKHAGFMVNVDNGTATDYENLIHYVQKTVKEKFGIE
LNREVRIIGEHPK

>d1qlma_d.147.1.1 (A:) Methenyltetrahydromethanopterin cyclohydrolase {Archaeon Methanopyrus kandleri}

MVSVNENALPLVERMIERAELLNVEVQLENGTTVIDCGVEAAGGFEAGLLSEVCMGGLATVELTEFHDGLCLPAVQVTTDHPAVSTLAAQKAG
WQVQVGDYFAMGSGPARALALKPKETYEEIDYEDDAVAILCLESSELPDEDVAEHVADECGVDPENLYLLVAPTASIVGSVQVSARVVEETGLYKLEV
LEYDVTRVYATGTAPIAVADDGEAMGRNTDCILYGGTVLYVEGDDDELPEVVEELPSEASEDYGKPFMKIFEEADYDFYKIDPGVFAPARVVND
LSTGKTYTAGEINVSDLKESFSL

>d1c4za_d.148.1.1 (A:) Ubiquitin-protein ligase E3a, Hect catalytic domain (E6ap) {Human (Homo sapiens)}

NPYLRKVRRDHIDDALVRLEMIAHENPADLKKQLYVEFEQEQQVDEGGVSKEFFQLVVEIFNPDIGMFTYDESTKLFWFNPSSFETEGQFTLIGIV
LGLAIYNNCILDVHFPMVVYRKLMGKKGTFRDLGDSHPVLYQSLKDLLEYEGNVEDDMMITFQJISQTLFGNPMMYDLKENGDKIPITNENRKEFV
NLYSDYILNKSVEKQFKAFRRGFHMVTNESPLKYLFRPEEIELLICGSRNLDQALEETTEYDGGYTRDSVLIREFWEIVHSFTDEQKRLFLQFTTGTDRA
PVGGLGKLKMIIAKNGPDTERLPTSHTCFNVLLPEYSSKEKLKERLLKAITYA

>d2ahja_d.149.1.1 (A:) Nitrile hydratase alpha chain {Rhodococcus erythropolis}

IDHTTENAAPAQAPVSDRAWALFRALDGKGLVPDGYVEGWKKTFEEDSPRRGAEVARAWTDPEFRQLLTDGTAAVAQYGYLGPQGEYIVAVED
TPTLKNIVCSLASCTAWPILGPPTWYKSFEYRARVVERPRKVLSMGTEIASDIEIRVYDTTAETRYMVLQPQPGATEGWSQEQLQEIVTKDCLIGV
AIPQV

>d1f7la_d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS {Bacillus subtilis}

GIYGIGLDITELKRIASMAGRQKRFAERILTRSELDQYYELSEKRKNEFLAGRFAAKEAFSKAFGTGIGRQLSFQDIEIRKDQNGKPYIICKLSPAABHVIS
THTKEYAAAQVVIER

>d1ftha_d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS {Streptococcus pneumoniae}

MIVGHGIDIEELASIESAVTRHEGFAKRVITALEMERFTSLKGRQQIEYLAGRWSAKEAFSKAMGTGISKLGFQDLEVNNERGAPYFSQAPFSGKIWL
SISHTDQFVTASVILEEN

>d1qr0a1 d.150.1.1 (A:1-101) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

MKIYGIYMDRPLSQEENERFMTFISPEKREKCRFYHKEDAHTLLGDVLVRSVISRQYQLDKSDIRFSTQEYGKPCIPDLPDAHFNISHSGRWVIGAF
DS

>d1qr0a2 d.150.1.1 (A:102-228) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

QPIGIDIEKTPISLEIAKRFFSKTEYSDLLAKDKDEQTDYFYHLWSMKESFIKQEGKGLSLPLDSFSVRLHQDGQVSIELPDSHSPCYIKTYEVDPGYKM
AVCAAHPDFPEDITMVSYEELLRAAA

>d1ako__ d.151.1.1 (-) DNA-repair enzyme exonuclease III {Escherichia coli}

MKFVFSNINGLRARPHQLEAIVEKHQPDVIGLQETKVHDDMFPLEEVALGYNVFYHGQKGHYGVALLTKEPIAVRRGPGDDEEAQRRIIMAEIP
SLLGNVTVINGYFPQGESRDHPKPAKAQFYQNQLQNYLETELKRDNPVLIMGDMNISPTLDIGEENRKRWLRTGKCSFLPEEREWMDRLMSW
GLVDTFRHANPQTADRFSWFDYRSKGFFDNRGLRIDLLASQPLAECCTGIDYEIRSMEKPSDHAPVWATFRR

>d1hd7a_ d.151.1.1 (A:) DNA repair endonuclease Hap1 {Human (Homo sapiens)}

LYEDPPDQKTSPSGKPATLKICSWNVDGLRAWIKKGLDWVKEAPDILCLQETKCSENKLPAELQELPLSHQYWSAPSDKEGYSGVGLLSRQCPLK
VSYGIGDEEHQEGRVIVAEFDSFVLTVTAYVPNAGRGLVRLEYRQRWDEAFRKFLKGASRKPLVLCGDLNVAHEEIDLRLNPKGNNKAGFTPQERQ
GFGELLQAVPLADSFRHLYPNTPYAYTFWTYMMNARSKNVGRWLDFLLSHSLLPALCDSKIRSKALGSDHCPITLYAL

>d2dnja_ d.151.1.1 (A:) Deoxyribonuclease I {Cow (Bos taurus)}

LKIAAFNIRTGETKMSNATLASYIVRIVRRYDIVLIQEVRDSHLVAVGKLLDYLNQDDPNTYHYVVSEPLGRNSYKERYLFLFRPNKVSVLDTYQYDDG
CESCGNDSFSREPAVVKFSSHSTKVKEFAIVALHSAPDAVEAINSPLYDVLQQKWHLNDVMLMGDFNADC SYVTSSQWSSIRLRTSSTFQWLIP
DSADTTATSTNCAYDRIVVAGSLLQSSVPGSAAPPDFQAAAGLSNEMALAISDHYPVEVTLT

>d1i9za_ d.151.1.2 (A:) Synaptojanin, IPP5C domain {Yeast (Schizosaccharomyces pombe)}

YDPIHEYVNHELRKRENEFSEHKNVKIFVASYNLNGCSATTKLENWLFPENTPLADIYVVGQFQEVQLTPQQVISADPAKREWESCVKRLLNGKCTS
GPGYVQLRSGQLVGTALMIFCKESCLPSIKNVEGTVKKTGLGGVSGNKGAVAIRFDYEDTGLCFITSHLAAGYTNYDERDHDYRTIASGLRFRRRGRSIF
NHDYVVVFGDFNYRISLTYYEEVPCIAQGKLSYLFEYDQLNKQMLTGKVFPPFSELPTFPPTYKFDIGTDIYDTSKHRVPAWTDRLYRGELVPHSYQ
SVPLYYSDHRPIYATYEANIVKVDREKKKLFEEELYNQRKQEVRDASQ

>d1aora2 d.152.1.1 (A:1-210) Aldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

MYGNWGRFIRVNLTGDIKVEEYDEELAKKWLSRGLAIYLLLKEMDPVTDPSPENKLIIAGPLTGTSAPTGGRYNVVTKSPLTGFITMANSGGYF
GAEALKFAGYDAIVVEGKAEPVYIYIKDEHIEIRDASHIWGKKVSETEATIRKEVGSEKVKIASIGPAGENLVKFAAIMNDGHRAAGRGGVGAVMGSK
NLKAIAVEGSKTV

>d1b25a2 d.152.1.1 (A:1-210) Formaldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

MYGWWGRILRVNLTTGEVKVQEYYPEEVAKKFIGGRGLAAWILWNEARGVEPLSPENKLIFAAGPFNGLPTSGKLVVAKSPLTGGYGDGNLGT
MASVHLLRAGYDALVVEGKAKKPVYIYIEDDNTSILSAEGLWGKTTFETERELKEIHGKNVGVLTGPAGENLVKYAVVISQEGRAAGRPGMGAVMG
SKKLKAVVIRGTKEIPVA

>d1gdoa_ d.153.1.1 (A:) Glucosamine 6-phosphate synthase, N-terminal domain {Escherichia coli}

CGIVGAIAQRDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTRLRLGVQMLAQAAEEHPLHGGTIAHTRWATHGEPESEVNAHPVSEHIVV
VHNGIIENHEPLREELKARYTFVSETDTEVIAHLVNWELQKQGGLREAVLRAIPQLRGAYGTIVMDSRHPDTLLAARSGSPLVIGLGMGENFIASDQL
ALLPVTRRFIFLEEGDIAETRRSVNIFDKTGAEVKRQDIESNL

>d1gph12 d.153.1.1 (1:1-234) Glutamine PRPP amidotransferase, N-terminal domain {Bacillus subtilis}

CGVFGIWGHEEAPQITYGLHSLQHRGQEGAGIVATDGEKLTAKGQQLITEVFQNGELSKVKGKAIGHVRYATAGGGGYENVQPLLFRSQNNNGS
LALAHNGNLTQNLVQKQLENQGSIFQTSSDTEVLAHLIKRSGHFTLKDQIKNSLSMLKGAYAFLIMTETEMIVALDPNGLRPLSIGMMGDAYVVASE
TCAFDVVGATYLREVEPGEMLIINDEGMKSERFSMNINRS

>d1ecfa2 d.153.1.1 (A:1-249) Glutamine PRPP amidotransferase, N-terminal domain {Escherichia coli}

CGIVGIAGVMPVNQSIYDALTVLQHRGQDAAGIITIDANNCFRLRKANGLVSDFEARHMQRQLGNMGIGHVRYPTAGSSASEAQPFYVNSPYGI
TLAHCNGNLTNAHELKKLFEEKRKHINTTSDEIILLNIFASELDNFRHYPLEADNIFAAIAATNRLIRGAYACVAMIIGHGMVAFRDPNGIRPLVLGKRD
DENRTEYMVASESVALTLGFDLIRDVAPGEAIYITEEGQLFTRQCADNPVS

>d1ct9a2 d.153.1.1 (A:1-192) Asparagine synthetase B, N-terminal domain {Escherichia coli}

ASIFGVFDIKTDAVELRKKALESRLMRHRGPDWSGIYASDNAILAHERLSIVDVNAGAQPLYNQQKTHVLAVNGEIYNHQALRAEYGDYQFQTGS
DCEVILALYQEKGPEFLDDLQGMFAFALYDSEKDAYLIGRDHLGIIPLYMGYDEHGQLYVASEMKALVPVCRTIKEFPAGSYLWSQDGEIRSYYH

>d1jgt2 d.153.1.1 (A:4-209) beta-Lactam synthetase {Streptomyces clavuligerus}

PVLPAAFGLASARTGGGRAPGPVFATRGSHIDTPQGERSLAATLVHAPSVAPEVARSLTGAPTTAVLAGEIYNRDELLSVLPAGPAPEGDAELV

LRLLEYDLHAFRLVNGRFATVVRTGDRVLLATDHAGSVPLYTCVAPGEVRASTEAKALAAHRDPKGFLADARRVAGLTGVYQVPAGAVMDIDLGS

GTAVTHRTWT

>d1ea0a3 d.153.1.1 (A:1-422) Alpha subunit of glutamate synthase, N-terminal domain {Azospirillum brasilense}

CGVGFIAIDGKPRRSVVEKGIEALKAVVHRGAVDADGKTGDGAGIHAVPQKFFKDHVKGIGHRAPDNKLAVGQVFLPRIQLDAQEACRCIVETEILAFGYYIYGWRQVPINVDIIGEKANATRPEIEQIIVGNNKGSDEQFELDLYIIRRRIEAKVGKGEQINDFYICLSARSIIYKGMLAEQLTTFPDLDERFESDFAIYHQRYSTNTFTPWPLAQPFRMLAHNGEINTVKGNVNWMKAHETRMEHPAFTGTHMQDLKPVIGVGLSDSGSLDTVFEVMVRAGRTAPMVKMMMLVPQALTSSQTTPDHNKALIQYCNSVMEPWDPGAALAMTDGRWVVGMDRNGLRPMRYTITTDGLIIGGSETGMVKIDETQVIEKGRLPGEMIAVDLQSGKLYRDRELKDHLATLPWDKWVN

>g1gk9.1 d.153.1.2 (A;B:) Penicillin acylase {Escherichia coli}

QSSSEIKIVRDEYGMPIHYANDTWHLYGYGYVVAQDRLFQMEMARRSTQGTVAEVLGKDFVKFDKDIRRNYPDAIRQAQIAALSPEDMSILQGYADMGMNAWIDKVNTNPETLLPKQFNTFGFTPKRWEFPDVAMIFVGTMANRFSdstSEIDNLALLTALKDKYGVSQGMMAVFNQLKWLNVNPSAPTTIAVQESNYPLKFQNQQNSQTAKSNSMWVIGKSKAQDAKAIMVNGPQFGWYAPAYTYIGLHGAGYDVTGNTPFAYPGLVFGHNGVISWGSTAGFGDDVDIFAERLSAEPKGYYLHNGKWWKMLSREETITVKNGQAETFTWRTVHGNILQTDQTTQAYAKSRAWDGKEVASLLAWTHQMKAKNWQEWTQQAQKALTINWYYADVNGNIGYVHTGAYPDRQSGHDPRLPVPGTGKWDWKGLPFEMNPVKVYNPQSGYIANWNNSPQKDYPASDLFAFLWGGADRVTEDRLLEQKPRLTADQAWDVRQTSRQDNLRLFLPTLQAATSGLTQSDPRRQLVETLWDGINLLNDDGKTWQQPGSAILNVWLTSMKRTVVAAVPMPFDWKYSASGYETTQDGPTGSLNISVGAKILYEAVQGDKSIPQAVDLAGPKPQQEVVLAALDTWETLSKRYGNNSNWKTPAMA LTFRANNFFGPVQAAAEETRHQAEQYQNRTENDMIVFSPTTSDRPVLAWDVVAPGQSGFIAPDGTVDKYEDQLKMYENFGRKSLWTKQDVEAHKESQEVLVHQR

>g1cp9.1 d.153.1.2 (A;B:) Penicillin acylase {Providencia rettgeri}

ESTQIKIERDNYGVPHIYANDTYSFYGYGYAVAQDRLFQMEMAKRSTQGTVEVFGKDYISFDKEIRNNYWPSIHKQJNQLPSQECDILRGYADGMNAWIKQINTKPDDLMPKQFIDYDFLPSQWTSFDVAMIMVGTLANRFSDMNSEIDNLALLTALKDKYGEQLGVEFFNQJNWLNNPNAPTTISEEFTYSDXSXNVWLVGKTKASAKAILNGPCQFGWFNPAYTYIGLHGAGFNIVGNTPFAYPAILFGHNGHVSWGSTAGFGDGVDFAEQVSPEDPNSYHQGQWKKMLSRQETLNVGEQPITFEIYRTVHGNVVKRDKTHTAYSKARAWDGKELTSLMAWVKQGQAQNWWQWLDQANQALTINWYYADKDGNIYVHTGHYPDRQINHDPRLPVSGTGEWDWKGIQPFANNPKVYNPQSGYIANWNNSPAKNYPASDLFAFLWGSADRVKEIDNRIEAYDKLTADDMWAILQQTSRVDLNHRLFTPFLTQATQGLPSNDNSVKLVSMILQQWDGINQLSSDGKHYIHPGSAILDIWLKEMLKATLGQTVAPFDKWYLASGYETTQEPTGSLNISTGAKLLYESLLEDKSPISQSIDLFSQGPQNDVIRKTLNTTYQKMIIEKGDN PANWQTPATALETFRENFFGIPQALPQENFHQNEYHNRGTENDLIVFTEEGVSAWDVVAPGQSGFISPQGKPSPHYQDQLSLYQQFGKKPLWLNSEDVAPIESTETLIIER

>g1fm2.1 d.153.1.2 (A;B:) Cephalosporin acylase {Brevundimonas diminuta}

QAPIAAYKPRSNEILWDGYGVPHIYGVDAVPSAFYGYGWAQARSHGDNILRLYGEARGKGAEYWGPDYEQTTVWLLTNGVPERAQQWYAQQSPDFRANLDAFAAGINAYAQQNPPDISPEVRQVLPVSGADVVVAHRLMNFLYVASPGRGLXNSWAVPGKTANGNALLQNP HLSWTTDYFTYYEAHVTPDFEIYGATQIGLPVIRFAFNQRMGITNTVNGMVGATNYRLLQDGGLYLDGQVRPFERRQASYRLRQADGSTVDKPLEIRSSVHGPVFERADGTAVAVRAGLDRPGMLEQYFDMITAHSFDDYEAMARMQVPTNFNIVYADREGTINYSFNGVAPKRAEGDIAFWQGNVPGDSSRYLWTETHPLDILPRVTNPPGGFVQNSNDPPWPTWPVTPYCPANHPSYLAPQTPHSLRAQQSVRLMSENDDLTLERFMALQFSHRAVMADRTLPLIPAALIDPDP EVQAAARLLAAWDRDFTSDSRAALLFEEWARLFAGQNAFATPWSLDKPVSTPYGVRDPKAVDQLRTAIANTKRKYGAIDRPFGDASRMILNDVNPGAAAGYGNLGSFRVFTWSDPDENGIRTpvHGETWVAMIEFSTPVRAYGLMSYGNRSRQPGTTHYSDQIERVSRADFRELLRREQVEAAQERTPNF

>d2pvaa_d.153.1.3 (A;) Penicillin V acylase {Bacillus sphaericus}

CSSLSIRTTDDKSLFARTMDFTMEPD SKVII VPRNYGIRLLEKENV V INNSYAFV GMGSTDITSPVLYDGVNEKTYADEPKKG TGLMGAMLYYATFATYADEPKKGTTGINPVYVVISQVLGNCVTVDDVIEKLTSYLLNEANII LGFAPP LHYTFTDASGESIVIEPD KTGITI HRK TIGVMTNSPGYEWHQTNLRAYIGVTPNPPQD IMM GDL DTPFGQGAGGLGLPGDFTPSARFLRVAYWKKY TEKAKNETEGVTNLFHILSSV NIPKG VVLTNEGKTDYI TSAMCAQSKNYYFKLYD NSRISAVSLMAENLNSQDLITFEWDRKQDIQLNQVN

>d1pma1_d.153.1.4 (1;) Proteasome beta subunit (catalytic) {Archaeon Thermoplasma acidophilum}

TTVGITLKDAVIMATERRVTMENFIMHKGKKLFQIDTYGMIAGLVGDAQVLRVYMKA ELEYRLQRRVNMPIEAVATLSSNMLNQVKYMPY MVQLLVGGIDTAPHVFSIDAAGGSVEDIYASTGSGSPFVYGVLESQYSEKMTVDEGVDLVIRAIASAOKRDSASGGMIDVAVITRKDGYVQLPTDQIE

SRIRKGLIL

>d1ryp1_d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

QFNPYGDDNGGTILGIAGEDFAVLAGDTRNITDYSINSRYEPKVFDGDNIVMSANGFAADGDAL/KRKFNSVKWYHFDNDKKLSINSAARNIQHLL
YGKRFFPYVHTIIAGLDEDKGAVYSFDPVGSYEREQCRAAGGAASLIMPFLDNQVNFKNQYEPGTNGKVKPLKYLVEEVIKLVRDSFTSATERHI
QVGDGLEILIVTKDGVRFKEFYELRK

>d1ryp2_d.153.1.4 (2:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TQQPIVTGTSVISMKYDNGVIAADNLGSYGSLLRFNGVERLIPVGDNVVGISGDISDMQHIERLLKDLVTENAYDNPLADAEEALEPSYIFEYLATVM
YQRRSKMNPLWNAAIVAGVQSNGDQFLRYVNLLGVTYSSPLATGFGAHMANPLLRKVVDRRESDIPKTTVQVAEEAIVNAMRVLYYRDARSSRNFS
LAIIDKNTGLTFKKNLQVENMKWDFAKDIKGYGTQKI

>d1ryph_d.153.1.4 (H:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

LKKGEVSLGASIMAVTFKDGVILGADSRTTGAYIANRVTDKLTRVHDKIWCCRSQSAADTQAIADIVQYHLELYTSQYQTPSTETAASVFKELEYENKD
NLTAIIIVAGYDDKNKGEVYTIPGGSVHKLPYAIAGSGSTFIYGYCDKNFRENMSKEETVDFIKHSLSQAIKWGDSSGGVIRMVVLTAAVERLIFYPD
EYEQL

>d1rypi_d.153.1.4 (I:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTIVGVKFNNGVIAADTRSTQGPIVADKNCALKHRISPCKWCAGAGTAADTEAVTQLIGSIELHSLYTSREPRVVSALQMLQHLFQYQGHIGAYLI
VAGVDPTGSHLFSIHAGSTDVYYLSLGSGLAAMAVLESHWKQDLTKEEAIKLASDAIQAGIWNDLGSNSNDVCVMEIGKDAEYLRLNYLTPNV
REEKQKSYKFPRGTTAVLKESIVNICD

>d1rypj_d.153.1.4 (J:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

SDPSSINGIVVAMTGDCAVIACDLRLGSQSLGVSNKFEKIFHYGHVFLGITGLATDVTLNEMFRYKTNLYKLKEERAIEPETFTQLVSSLYERRFGP
YFVGPPVAGINSKSGKPFIAFGFDLIGCIDEAKDFIVSGTASDQLFGMCESLYEPNLEPEDLFETISQALLNAADRDAWSGWGAVVYIJKDEVVKRYLKM
RQD

>d1rypk_d.153.1.4 (K:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MDIILGIRVQDSVILASSKAVTRGIVSLKDSDDKTRQLSPHTLMSFAGEAGDTVQFAEYIQANIQLYSIREDYELSPQAVSSFVRQELAKSIRSRRPYQVN
VLIGGYDKKKNPPELYQIDYLGTKVELPYGAHGSGFYTSLLDHYRPDMTEEGLDLLKLCVQELEKRMMPDFKGIVKIVDKDGIRQVDDFQAQ

>d1rypl_d.153.1.4 (L:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTTLAFRFQGGIIVAVDSRATAGNWVASQTVKRVIEINPFLGTMAGGAADCQFWETWLGSQCRHLERKERISVAAASKILSNLVYQKGAGLSM
GTMICGYTRKEGPTIYYVSDGTRLKGDFICVGSGQTFAVGVLDSNYKWDLSEDALYLGKRSILAAAHRDAYSGGSVNLYHVTEDGWYHGNHDVG
ELFWKVKEEEGSFNNVIG

>d1pmaa_d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Archaeon Thermoplasma acidophilum}

TVFSPDGRFLQVEYAREAVKKGSTALGMKFANGVLLISDKKVRSLIEQNSIEKIQLIDDYVAATSGLVADARLVDFARISAQQEKVTYGSVNIENLV
KRVADQMQQYTQYGGVRPYGVSLIFAGIDQIGPRLFDPCDPAGTINEYKATAIGSGKDAVVSFLEREYKENLPEKEAVTIGIKALKSLEEGERKAPEIAS
ITVGNKYRIYDQEEVKKFL

>d1rypa_d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

AGYDRHITIFSPEGRLYQVEYAFKATNQTINSLAVRGKDCTVVISQKKVPDKLLDPTTWSYIFCISRTIGMVNGPIPDAARALRAKEAAEFRYKYG
YDMPCDVLAKRMANLSQIYTQRAYMRPLGVILTFVSVDIELGPSIYKTDPAQYYVGYKATATGPKQQEITNLENHFKSKIDHINEESWEKVEFAIT
HMIDALGTEFSKNDLEVGVATDKFFTLSAENIEERLVAIAEQD

>d1rypb_d.153.1.4 (B:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MTDYRSFLTFSPSGKLGQIDYALTAVKQGVTSLSGKATNGVVIATEKSSSPLAMSETLSKVSLLTPDIGAVYSGMGPDYRVLVDKSRKVAHTSYKRIY
GEYPPTKLLVSEVAKIMQEATQSGGVRPGVSLIAGHDEFNGFSLYQVDPGSYFPWKATAIGKGSVAAKTFLEKRWNDELEDAIHIALTLKESVE
GEFNGDTIELAIIGDENPDLLGTYGPIPTDKGPRFRKLTSQEINDRLEA

>d1rypc_d.153.1.4 (C:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GSRRYDSRTTIFSPEGRLYQVEYALESHAGTAIGIMASDGIVLAAERKVSTLLEQDTSTEKLYKLNDKIAVAVAGLTADAELINTARIHAQNYLKYNE
DIPVEILVRRRLSDIKQGQYQHGGLRPFGVFSIYAGYDDRYGYQLYTSNPGSNTGWAISVGANTSAATLQMDYKDDMKVDDAIELALKTLSKTTD
SSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILVKTGIT

>d1rypd_d.153.1.4 (D:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GYDRALSIFSPDGHIFQVEYALEAVKRGTCAVGVKGKNCVVLGCERRSTLKLQDTRITPSKVKIDSJVLSFGLNADSRLIEKARVEAQSHRLTLEDP
VTVEYLTRYVAGVQQRYTQSRRPFGVSTLIAQFDPRDDEPKLYQTEPSGIYSSWSAQTGRNSKTVREFLEKNYDRKEPPATVEECVKTVRSLLEV
QTGAKNIEITVVVPDSDIVSSEEINQYVTQIEQEKEQQE

>d1rype_d.153.1.4 (E:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

DRGVSTFSPEGRLFQVEYSLEAIKGSTAIGIATKEGVVLGVEKRATSPLESIEKIVEIDRHIGCAMSGLTADARSMIEHARTAAVTHNLYYDEDINVE
SLTQSVCSDLALRFGEGASGEERLMSRPFVGALLAGHDADDGYQLFHAEPSTFYRYNAKAIGSGSEGAQAEELLNEWHSSLTLKEAELVLKILKQVM
EEKLDENNAQLSCITKQDGFKIYDNEKTAELIKEKEAAE

>d1rypf_d.153.1.4 (F:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

FRNNYDGDVTFSPTGRLFQVEYALEAIKQGSVTVGLRSNTHAVLVALKRNADELSSYQKKIIKCDEHMGLSLAGLAPDARVLSNYLRQQCNYSSLVF
NRKLAVERAGHLLCDKAQKNTQSYYGRPYGVGLIIGYDKSGAHLLFQPSGNVTELYGTAIGARSQGAKTYLERTLDTFIKIDGNPDELIKAGVEAISQ
SLRDESLTVNLNSIAIVGKDTPFTIYDGEAVAKYI

>d1rypg_d.153.1.4 (G:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GTGYDLSNSVSPDGRNFQVEYAVKAVENGTSIGIKCNDGVVFAVEKLITSKLLPVQKNVKIQVVDRHIGCVYGLPDRHLVNRGREEAASFKKLY
KTPIPIPAFADRLGQYVQAHTLYNSVRPFGVSTIFGGVDKNGAHLYMLEPGSYWGYKGAATGKGRQSAKAELEKLVDDHHPEGLSAREAVKQAAKIIY
LAHEDNKEKDFFELEISWCSELSETNGLHKFKVKGDLQEAIDFAQKEIN

>d1ht1a_d.153.1.4 (A:) HsIV (ClpQ) protease {Escherichia coli}

TTIVSVRRNGHVIAGDGQATLGNTVMKGNVKVRRYNDKVIAGFAGGTADAFTLFLFERKLEMHQGHVLKAAVELAKDWRTDRMLRKLEALL
AVADETASLIITGNGDVVQPENDLIAIGSGGPYAQAAARALLENTELSAREIAEKALDIAGDICITYNHFTIEELSYK

>d1jjwa_d.153.1.4 (A:) HsIV (ClpQ) protease {Haemophilus influenzae}

TTIVSVRRNGQVVGGDGQVSLGNTVMKGNARKVRRYNGKVLAGFAGGTADAFTLFLFERKLEMHQGHLLKSAVEAKDWRTDRALRKLEAM
LIVADEKESLIITGIGDVVQPEEQDQILAIGSGGNYALSAARALVENTELSAHEIVEKSLRIAGDICVFTNTNFTIEELP

>g1apy.1 d.153.1.5 (A;;B;) Glycosylasparaginase (aspartylglucosaminidase, AGA) {Human (Homo sapiens)}

SPPLLVNTWPFKNATEAAWRALASGGSALEVGACMERCQCDGSVGFGGSPDELGETTLDAMIMDGTTMDVAVGDLRRKNAIGVARKV
LEHTTHLLGESATTFAQSMGFINEDLSTSASQALHSDWLARNCPNYWRNVIPPSKYCGPYKPPXTIGMVIHKTGHIAAGTSTNGIKFKIHGR
VGDSPIPGAGAYADDTAGAAAATGNGDILMRFLPSYQAVEYMRRGEDPTIACQKVISRQKHFPEFFGAVICANVTGSYGAACNLSTFTQFSFMVY
NSEKNQPTEEKVDCI

>g2gac.1 d.153.1.5 (A;;B;) Glycosylasparaginase (aspartylglucosaminidase, AGA) {Flavobacterium meningosepticum}

NKPIVLSTWNFGHANVEAWKVLSKGGKALDAVEKGVRILVEDDPTERSVGYGGRPDRDGRVTLDACIMDENYNGSVACMEHIKNPISVARAVME
KTPHVMVLVGDALEFALSQGFKKENLLTAESEKEWKEWLTXCIGMIALDAQGNLSGACTSGMAYKMHGRVGDSPIIGAGLFVDNEIGAATATGH
GEEVIRTGTHLVELMNQGRTPQQACKEAVERIVKIVNRRGKNLKDQVGFIALNKGEYGAYCIQDGDNFAVHDQKGNRLETP

>d1b65a_d.154.1.1 (A:) L-aminopeptidase D-Ala-esterase/amidase {Ochrobactrum anthropi}

KPRARDLGLPFTGVTGPYNAITDVGVGFGQTIIENEPRPGRKRPARSGBTAILPHMQSETPVPVYAGVHRFNGNGEMTGTHWIEDGGYFLGPVV
ITNTHGIGMAHHATVRWMVDRYASTYQTDLWIMPVAETYDGalNDINGFPTEADVRKALDNVASGPVQEGNCGGGTGMITYGFKGGTGT
ASRVVEFGGRSFTIGALVQANHGQRDWLTIAGVPVGQHMRDGTSQLQERGSIIIVLATDPLMPHQQLKRLARRASIGIRNGTPGGNNSGDIFI
AFSTANQRPMQHRSAPFLDVEMVNDEPLDTVYLAADVSDVEAVVNAMIAAEDMGGTPFDRLVQAIIDHERLRAVRLRQYGRRA

>g1pya.1 d.155.1.1 (A;;B;) Histidine decarboxylase {Lactobacillus sp., strain 30a}

SELDALKNLGVDRDRIAISPYKQWTRGYMEPGGNNGYVTGLKVDAGRDKSDDVLDGIVSYDRAETKNAYIGQINMTTASXFTGVQGRVIGYDILR
SPEVDKAKPLFTETQWDGSELPIYDAKPLQDALVEYFGTEQDRRHYPAPGSFIVCANKVTAERPKNDADMKPGQQGYVWSAIAISFAKDPTKDSS
MFVEDAGVWETPNEDELLEYLEGRRKAMAKSIAECGQDAHASFESSWIGFAYTMMEPGQIGNAITVAPYVSLPIDSPGGSILTPDKMEIMENLT
MPEWLEKMGYKSLSANNAALKY

>d1jl0a_d.156.1.1 (A:) S-adenosylmethionine decarboxylase {Human (Homo sapiens)}

HFFEGTEKLLLEVWFSRQQPDANQGSGDLRTIPRSEWDILLKDVQCSIISVTKTQDQEAYVLESESSMFVSKRRFILKTCGTTLLKALVPLLKLARDYSGF
DSIQSFFYSRKNMKPSHQQGYPHRNFQEEIEFLNAIFPNGAGYCMGRMNSDCWYLYTLDFPESRVISQPDQTLIELMSELDPAVMDDQFYMKDGV

AKDVTRESGIRDILPGSVIDATMFNPGSMNGMKSDGTWTIAITPEPEFSYVSFETNLSQTSYDDLIRKVVEVFKPGKFVTTLFVNQSSKCRTVLAS
PKIEGFKRLDCQSAMFNDYNFVFTSFAKKQ

>d2bc2a_d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacillus cereus}

TVIKNETGTISISQLNKNVVWVTELGSFNGEAVPSNGLVNTSKGLVLVDSWDDKLTKELIEMVEKKFQKRVTDVIITHAHADRIGGIKTLKERGIKAH
STALTAELAKKNGYEEPLGLDLQTVNLKGFMNKVETFYPGKGHTEDNIVVWLPQYNILVGGALVKSTSAKDLGNVADAYVNEWSTSIENVLKRYRN
NAVVPGHGEVGDKGLLHTLDLK

>d1a7ta_d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacteroides fragilis}

SVKISDDISITQLSDKVYTYSLAEIEGMVPSNGMIVINNHQAALLTPINDAQTEMILVNWVTDLSHAKVTFIPNHWGDCIGGLGYLQRKGV
QSYANQMTIDLAKEKGLPVPEHGFTDSLTVSLDGMPLQCYYLGGGHATDNIVVWLPTENILFGGCMILKDQNQTTSIGNISADVTAWPKTLDVKAK
FPSARYVPGHGNYGGTEIEHTKQIVNQYESTS

>d1smla_d.157.1.1 (A:) Zn metallo-beta-lactamase {Xanthomonas maltophilia}

EVPLPQLRAYTVDASWLPQMAPLQIADHTWQIGTEDLTALLVQTPDGAVLLDGGMPQMASHLLDNMKARGVTPRDLRLILLSHAHADHAGPVAE
LKRRTGAKVAANAESA VLLARGGSDDLHFBDGITYPPANADRIVMDGEVITVGGIVFTA HFMAGHTPGSTAWTWTDTRNGKPVRIA YADSL SAPGY
QLQGNPRYPHLIEDYRRSFATVRALPCDVLLTPHPGASNWDYAGARAGAKALTCKAYADAAEQKFDGQLAKETAG

>d1jjea_d.157.1.1 (A:) Zn metallo-beta-lactamase {Pseudomonas aeruginosa, IMP-1}

SLPDLKIEKLDEGVYVHTSFEVNGWGVVKHGLVVLVNAEAYLIDTPFTAKDTEKLTVFVERGYKIKGSISSHFHS D STGGIEWLNSRSIPTYASELT
NELLKKDGKVQATNSFSGVNYWL VKNKIEVYFPGP GHTPDNVVW LPERKILFGGCIFKPYGLGNLG DANIEAPKSAKLLSKYKAKLVVPSHSE
VGDASLLKLTLEQAVKGLNESKK

>d1qh5a_d.157.1.2 (A:) Glyoxalase II (hydroxyacylglutathione hydrolase) {Human (Homo sapiens)}

MKVVEVLPALTDNYMYLVIDDETKEAAIVDPVQPQKVVAARKHGVKLTVLTTHHWDHAGGNEKLVKLESGLKVYGGDRIGALTHKITHLSTLQ
VGSLNVKCLATPCHTSGHICYFVKPGGSEPPAVFTGDTLVAGCGKFYEGTADEMCKALLEVLGRLPDTRVYCGHEYTINNLKFARHVEPGNAIRE
KLA WAKEKYSIGEPTV P STLAEEFTYNP FMVR REKTVQQHAGETDPVTTMRAVRREKDQFKMP RD

>d1e5da2 d.157.1.3 (A:2-250) Rubredoxin oxygen:oxidoreductase (ROO), N-terminal domain {Desulfovibrio gigas}

QATKIIDGFHLVGAIDWNSRDFHGYTLSPMGTTYNAYLVEDEKTLFDTVKAEYKGELLCGIASVIDPKKIDYLVIQHLEDHAGALPALIEACQPEKIFT
SSLGQKAMESHFHYKDWPVQVVKHGETSLGKRTVTFYETRMLHW PDSMV SWFADEKVLISNDIFGQNIAASERFSDQIPVHTLERAMREYYANI
VNPyAPQTLKAIETLVGAGVAPEFICPDHGVIFRGADQCTFAVQKYVEYAEQK

>d1a6q_d.158.1.1 (-) Protein serine/threonine phosphatase 2C {Human (Homo sapiens)}

GAFLDKPKMEKHNAQGQGNGLRYGLSSMQGWRVEMEDAHTAVI GLPSGLESWSFFAVYDGHAGSQVAKYCCEHLLDHITNNQDFKGSAGAPS V
ENVKNGIRTGFLEIDEHMRVMSEKKHGADRGSTAVGVLI SPQHTYFINCGDSRGLLCNRKVHFTQDHKPSNPLEKERIQNAGGSVMIQRVNG S
LA VSR ALGDFDYKCVHKGK PTEQLVSP EPEVHDIERSEEDDQFIIACDGIWDMGNEELCDFVRSRLEV TDDLEKVCNEVDTCLYKGSRD NMSVIL
ICFPNAPKVSPEAVKKEAELKYLECRVEI IKKQGEGV PDLHV MRTLAS ENIPSLP PGGELASKRN VIEAVY NR LN P Y

>d4kbpa2 d.159.1.1 (A:121-432) Plant purple acid phosphatase, catalytic domain {Kidney bean (Phaseolus vulgaris)}

QTGLDVPYT FGLIGDLGQSFDSNTL SHYELSPKKGQTVLFVG DLSYAD RYPNHDNVRWDTWGRFTERSVAYQPWIWTAGNHEIEFAPEINETEPFK
PF SYRYHVP YEAS QSTPFW YSIK RASA HII VLSSY SAYGRGTPQ YTWL KKL R KV RSET PWL VLMHSP LYNSY HHFME GEA MRTK FEA WFV KYK
V D VV FAGHV HAYER SERV SNI AYKITD GLC TPVKD QSA PVYITIG DAG NYG VID S NM IQP QPE YSAF REAS FG HGM FDI KNR THA HF SW NRN QDGV
AVEADSVWFFNRHWYV PDDST

>d1qhwa_d.159.1.1 (A:) Mammalian purple acid phosphatase {Rat (Rattus norvegicus)}

STLRFVAVGDWGGVPNAPFHTAREMANAKEIARTVQIMGADFIMSLGDNFYFTGVHDANDKRFQETFEDVFS DRALRNIPWVLAGNHDH LGN
VSAQIAYS KISK RWNFPSPYRLRFK VPRS NITVA IFMLDTV MLC GN SDDF VSQQPEM PRD LGV ART QLSW LKQ LAAK EDYV LVAGHPI WSIAE
HGPTRCLVKNLRP LLAAYGVTAYLCGHDHNLQY LQDENG VGYV LSGAGNFMDPS VRHQRK VPNGYLRFHYGSEDSLGGFTY VEIGSKEMSITY VEA
SGKSLFKTSLP RRP

>d1utea_d.159.1.1 (A:) Mammalian purple acid phosphatase {Pig (Sus scrofa)}

PTPILRFVAVGDWGGVPNAPFHTAREMANAKIA TTVK TLGADF ILSL GDNF YFTGVHD A KDR FQETFEDVFS DP SLRN VPW HVLAGNHDH LGN
VSAQIAYS KISK RWNFPSPYRLRFKIPRS NVSVA IFMLDTV LCG NSDDF VSQQ PER PRN LAL ART QL AWIK KQ LAAK EDYV LVAGHYPV WSIAE

GPTHCLVKQQLPLLTTHKVTAYLCGHDHNLQYLQDENGLGFVLSGAGNFMDPSKKHLRKVPNGYLRFHGAENSLGGFAYVEITPKEMSVTYIEASGK
SLFKTKLPRRA

>d1ii7a_d.159.1.4 (A:) Mre11 {Archaeon Pyrococcus furiosus}

MKFAHLADIHLGYEQFHKPQREEEFAEFKNALEIAVQENVDFILAGDLFHSSRPSPGTLLKAIALLQIPKEHSIPVFAIEGNHDRTQRGPSVLNLED
GLVYVIGMRKEKVENEYLTSERLGNGEYLVKGVYKDLEIHGMKYMSSAWFEANKEIKRLFRPTDNAILMLHQGVREVSEARGEDYFEIGLGDLPEGY
LYYALGHIHKRYETSYSGSPVVPGSLERWDFGDYEVRYEWDGIFKERYGVNKGYIVEDFKPRFVEIKVRFIDVKIGSEEIRKAIKRLIPLPKNAYV
RLNIGWRKPFDLTEIKEELLNEVYLKIDTWRI

>d1ush_2 d.159.1.2 (26-362) 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal domain {Escherichia coli}

YEQDKTYKITVLHTNDHHGHFWRNEYGEYGLAAQKTLVDGIRKEVAEEGSVLLSGGDINTGPESDLQDAEPDFRGMLVGYDAMAIGNHEFD
NPLTVLRQQEKWAKFPLLSANIYQKSTGERLFKPWALFKRQDLKIAVIGLTTDDAKIGNPEYFTDIEFRKPADEAKLVIQELQQTEKPDIIAATHMGHY
DNGEHGSNAPGDVEMARALPAGSLAMIVGGHSQDPVCMAAENKKQVVDYVPGTPCKPDQQNGIWIVQAHEWGKYVGRADFEFRNGEMKMV
NYQLIPVNLLKKVWTWEDGKSERVLYTPEIAENQQMISLLSPFQNKGKAQLEV

>d1jk7a_d.159.1.3 (A:) Protein phosphatase-1 (PP-1) {Human (Homo sapiens)}

KLNIDSIIQRLLERVRSKPGKNVQLQENEIRGLCLKSREIFLSQPILLEAPLICGDIHGQYYDLLRFEYGGFPESNYLFLGDYVDRGKQSLETICLLA
YKIKYPENFLLRGNHECASINRIYGFYDECKERYNIKLWKTFTDCFNCLPIAAIVDEKIFCCHGGLSPDLQSMEQIRRIMRPTDVPDQGLLCDLLWSDP

DKDVLGWGENDRGVSFTFGAEVVAFLKHDLICRAHQVVEDGYEFFAKRQLVTLFSAPNYCGEFDNAGAMMSVDETLMCFSQILKPA

>d1tcoa_d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Cow (Bos taurus)}

VVFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEETVALRIITEGASILRQEKNLLIDAPVTVCVDIHGQFFDLMKLFEVGGSPANTRYLFLGDY
VDRGYFSIECVLYLWALKILYKPTLFLRGHNHECRHLTEYFTFKQECKIKYSERVYDACMDAFCPLAALMNQQFLCVHGLSPEINTLDIRKLDRFK
EPPAYGPMCDILWSDPLEDFGNEKTQEHTHNTVRGCSYFYSYPAVCEFLQHNNLLSILRAHEAQDAGYRMYRKSQTGFPSSLITIFSPAPNYLDVYNN
KAAVLKYENNVMNIQFNCSHPYWLPNFMDVFTWSLPVGEKVTEMLVNVLNIC

>d1auia_d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Human (Homo sapiens)}

TDRVVKAVPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALRIITEGASILRQEKNLLIDAPVTVCVDIHGQFFDLMKLFEVGGSPANTR
YLFLGDYVDRGYFSIECVLYLWALKILYKPTLFLRGHNHECRHLTEYFTFKQECKIKYSERVYDACMDAFCPLAALMNQQFLCVHGLSPEINTLDDR
KLDRFKEPPAYGPMCDILWSDPLEDFGNEKTQEHTHNTVRGCSYFYSYPAVCEFLQHNNLLSILRAHEAQDAGYRMYRKSQTGFPSSLITIFSPAPNYL
DVYNNKAAVLKYYENNVMNIQFNCSHPYWLPNFMDVFTWSLPVGEKVTEMLVNVLNICSDDELGESEEDGFDGATAARKEVIRNKIRAIKGMA
RVFSVLREESESVTLKGLPTGMLPSGVLSGGKQLQSATVEAIEADEAIKGFPQHKITSFEEAKGLDRINERMPPR

>d1g5ba_d.159.1.3 (A:) lambda ser/thr protein phosphatase {Bacteriophage lambda}

MRYYEKIDGSKYRNIVVGDHLGCYTNLMNKLDTIGFDNKKDLISVGLVDRGAENVECLEITFPWFRAVRGNHEQMMIDGLSERGNVNHWL
LNGGGWFFNLDYDKEILAKALAHKADELPLIIELVSKDKKYVICHADYPFDEYEFGKPVDHQQVIWNRRERISNSQNGIVKEIKGADTFIFGHTPAVKPL
KFANQMYIDTGAFFCGNLTQVQGA

>d1emsa2 d.160.1.1 (A:10-280) NIT-FHIT fusion protein, N-terminal domain {Nematode (Caenorhabditis elegans)}

MATGRHFIAVCQMTSDNDLEKNFQAAKNMIERAGEKKCEMVFLPECFDFIGLNKNEQIDLAMATDCEYMEKYRELARKHNIWLSLGLHHKDPSD
AAHPWNTHLIIDS DGVTRA EYNKLHLFDIIPGKVRMLMESEFSKAGTEMIPPVDTPIGRGLSICYDVRFPELWLNRKRGQAQLSFPSAFTLNTGLAH
WETLLRARAIENQCYVAAAQTGAHNPKRQSYGHSMVDPWGA VVACQSERVDMCFAEIDL SYVDTLREMQPVFSHR

>d1f89a_d.160.1.1 (A:) hypothetical protein yl85 {Baker's yeast (Saccharomyces cerevisiae)}

SASKILSQKIKVALVQLSGSSPDKMANLQRAATFIERAMIKEQPDTKLVVLPECFNSPYSTDQFRKYSEVINPKEPSTS VQFLSNLANKFKIILVG GTIPEL
DPKTDKIYNTSII FNEGDGKLIK DHRKVHLFDIPNGISFHESETLSPGEKSTTIDTKYKGKFGVGICYDMRFP E LAMSARKGAFAMIYPSAFNTVTGPL
HWHLLARSRAVDNQVYVYMLCSPARNLQSSYHAGHSIVDPRGKIVAEAGEGEEIIYAELDPEVIESFRQAVPLTKQRFF

>d1erza_d.160.1.2 (A:) N-carbamoyl-D-aminoacid amidohydrolase {Agrobacterium sp.}

TRQMILAVGQQGPIARAETREQVVVRLDMLTKAASRGANFIVFPELATTFFPRWHFTDEAELDSFYETEMP GPVVRPLFEKAAELGIGFNLGYAEL
VVEGGVKRKFNTSILVKSGKIVGK YRKIHLPGHKEYA YRPFQHLEKRYFEPGDLGFPVYDVAAKMGMFICNDRWPEAWRVMGLRGAEIICGG
YNTPTHNPPVVPQHDHLTSFHLLSMQAGSYQNGAWSAAAGKVGMEENCMLLGHSCIVAPTGEIVALTTLEDEVITA AVDLDRCRELREHIFNFKQ
HRQPQHYGLIAEL

>d1hq0a_d.194.1.1 (A:) Type 1 cytotoxic necrotizing factor, catalytic domain {Escherichia coli}

SIESTSKSNFQKLSRGNIDVLKGRGSISSTRQRAIYPYFEAAANADEQQPLFFYIKKDRFDNHGYDQYFYDNTVGPNIGIPLNTYTGEIPSDSLSSLGSTYW
KKYNLTNETSIIRVSNSARGANGIKIALEEVQEKGKVIITSGNLSGCTTIVARKEGYIYKVHTGTTKSLAGFTSTGVKKADEVLELLTKEPIPRVEGIMSND
FLVDYLSENFEDSLITYSSEKKPDSQTIIIRDNVSVFPYFLDNIPEHFGTSATVLVRVDGNVVRSLESYSLNADASEISVLKVFSKKF

>d1qdla_d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase subunit, TrpE {Archaeon Sulfolobus solfataricus}

AMEVHPISEFASPFEVKCIERDFKVAGLLESIGGPQYKARYSVAIYSTNGYLKIHDDPVNLNGYLKDLKLADIPGLFKGGMIGYISYDAVRFWEKIRD
LKPAAEWDWYAEFFPDNIIYDHNEGKVVNADLSSVGGCGDIGEFKVSFYDESLNKNSYERIVSESLEYIRSGYIFQVVLRFYRYIFSGDPLRIYYNLR
RINPSPYMFYLKFDEKYLIGSSPELLFRVQDNIVETYPIAGTRPRGADQEEDLKLELEMNSEKDKAHEHMLVLDARNDLGKVCVPGTVKVPELMYVE
KYSHVQHIVSKVIGTLKKYNALNVLSATFPAGTVSGAPKPMAMNIIETLEEYKRGPYAGAVGFISADGNAEFAIAIRTAFLNKELLRIHAGAGIVYDSN
PESEYFETEHKLKALKTAIGVR

>d1i1qa_d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase subunit, TrpE {Salmonella typhimurium}
KPTLELLTCDAAYRENPTALFHQVCGRPATLLESADIDSKDDLKSLLVDSALRITALGDTVTIQALSDNGASLLPLLDTALPAGVENDVLPAGRVLRFP
PVSPLLDENARLCLSVFDARLQLQGVVNIPQTQEREAMFFGLFAYDLVAGFEALPHLEAGNNCPDYCFYLAETLMVIDHQKKSTRIQASLFTASDREK
QRNLNARLAYSQLTQPAPPVTPVPPDMRCECNQSDAFAGVVRQLQKAIRAGEIFQVVPSSRFLPCPSPLAAYVLLKSNPSPYMFFMQDNDF
TLFGASPESSLKYDAASRQEIEYPIAGTRPRGRRADGTLRDLDSRIELDMRTDHKESELSEHMLVLDARNDLARICTPGSRYVADLTKVDRYSYVMHLV
SRVVGELRHLDALHAYRACMNMGTLSGAPKVRAMQLIADAEGQRGSYGGAVGYFTAHGDLTCIVIRSALENVIATVQAGAGIVLDSVPQSE
ADETRNKARAVLRAIATAHHAA

>d1i7qa_d.161.1.1 (A:) Anthranilate synthase aminodeoxyisochorismate synthase/lyase subunit, TrpE {Serratia marcescens}

TKPQLTLLVKQASYRGDPPTLHFQLCGARPATLLESAINDKQNLQSLLVIDSALRITALGHTVSQALTANGPALLPLDEALPPEVRNQARPNGRELT
FPAIDAVQDEDARLRLSLSVFDALRTILTVSPADEREAVMLGGLFAYDLVAGFENLPALRQDQRCDFCFYLAETLLVLDHQRGSRQLQASFSEQASE
AQRLQHRLERLQAELOQQPPQPIPHQKLENMQLSCNCQSDEEYGAVVSELQEAIRQGEIFQVVPSSRFLPCPAPLGPYQTLKDNNPSPYMFFMQDD
DFTLFGASPEALKYDAGNRQEIEYPIAGTRPRGRRADGSLDDLSRIELEMRTDHKELAEHLMLVLDARNDLARICQAGSRYVADLTKVDRYSFVM
HLVSRVVGTLRADLDVLHAYQACMNMGTLSGAPKVRAMQLIAALRSTRRGSYGGRVGYFTAVRNLDTCIVIRSAVEDGHRTVQAGAGVVQDSIPE
READETRNKARAVLRAIATAHHAKEVF

>d1k0ga_d.161.1.1 (A:) P-aminobenzoate synthase component I {Escherichia coli}

MKTLSPAVITLLWRQDAAEFYFSRLSHLPWAMLLHSGYADHPYSRFDIVVAEPICTLTTFGKETVSESEKRTTTDDPLQLVQQVLDRADIRPTHNED
LPFQGGALGLFGYDLGRRFESLPEIAEQDIVLPDMAVGIVYDWALIVDHQRHTVSLLSHNDVNARRAWLESQQFSPQEDFTLTSWDWSNMTREQYG
EKFRQVQEYLHSGDCYQVNLAQRFHATYSGDEWQAFLQLNQANRAPFSALRLEQGAILSLSPERFILCDNSEIQTPIKGLPRLPDPQEDSKQAVK
LANSAKDRAENLMIVDLMRNDIGRVAAGSVKVPFELVVEPFPAVHVLTITAQLPEQLHASDLLRAFPGGSITGAPKVRAMEIIDELEPQRRNA
WCGSIGYLSFCGNMDTSITRTLTAINGQIFCSAGGGIVADSQEEAEYQETFDKVNRILKQLEK

>d1mla2 d.162.1.1 (A:145-313) Malate dehydrogenase {Pig (Sus scrofa)}

VTTLDIVRANAFVAELKGGLPARVSVPIVGGHAGKTIPLISQCTPKVDFPQDQLSTLTGRIQEAGTEVVKAKAGAGSATLSMAYAGARFVSLVDAM
NGKEGVVECSFKSQETDCPYFSTPLLGKKGIEKNLIGKISPFEKMKIAEAIPELKASIKGEEFVKNM

>d5mdha2 d.162.1.1 (A:155-333) Malate dehydrogenase {Pig (Sus scrofa)}

TRLHDHNRAKAQIALKLGVTSSDVKNVIIWGNHSSTQYPDVNHAKVKLQAKEVGVYEAVKDDSWLKGEFITTQQRGAAVIKARKLSSAMSAAKAIC
DHVRDIWFGTPEGEFVSMGIISDGNSYGVPPDLYSFPTIKDKTWKIVEGLPINDFSREKMDLTAKELAEEKETAFFLSSA

>d7mdha2 d.162.1.1 (A:198-385) Malate dehydrogenase {Sorghum (Sorghum vulgare), chloroplast}

TRLDENRAKCQLALKAGFYDVKVSNVTIWGNHSTTQVPDFLNAKIDGRPVKEIKRTKWLEEFTITVQKRGGALIQKWGRSSAASTAVSIADAISL
VTPTPEGDWTFSTGVYTTGNPYGIAEDIVFSMPCRSKGDGDYELATDVSNDDFLWERIKKSEAELLAEKKCAHLTGEGNAYCDLPEDTMLPGEM

>d1civa2 d.162.1.1 (A:194-385) Malate dehydrogenase {Flaveria bidentis, chloroplast}

TRLDENRAKCQLALKAGFYDVKVSNVTIWGNHSTTQVPDFLNAKIDGRPVKEIKRTKWLEEFTITVQKRGGALIQKWGRSSAASTAVSIADAISL
LVTPTEGDFWFSTGVYTNGNPYGIAEDIVFSMPCRSKGDGDYEFVKDVFDDYLSKKIKKSEDELLAEKKCAHLTGEGIAVCDLPEDTMLPGEM

>d2cmd_2 d.162.1.1 (146-312) Malate dehydrogenase {Escherichia coli}

VTTLDIIRSNTVAELKGKQPGEVEVPVIGGHSGVTILPLSQVPGVSFTEQEADLTKRIQNAGTEVVEAKAGGGSATLSMGQAAARFGLSLVRALQ
GEQGVVECAYVEGDGQYARFFSQPLLKGNGVEERKSIGTSLSAFEQNALEGMLDTLKDI ALGQEFVNK
>d1bdma2 d.162.1.1 (A:155-332) Malate dehydrogenase {Thermus flavus}
TRLDHNRRAKAQLAKKTGTGVDRIRRMVVGNHSSIMFPDLHAEVDGRPALELVDMEWYEKVFPI TVAQRGAIIQARGASSAASAANAAIEHIR
DWALGTPEGDWVMSAVPSQGEYGIPEGIVYSFPVTAKDGAYRVVEGLEINEFARKRMEITAQELLDEMEQVKALGLI
>d2hlp a2 d.162.1.1 (A:163-330) Malate dehydrogenase {Archaeon Haloarcula marismortui}
FGGRRLDSARFRYVLSEEFDAPVQNVEGTLGEHGDQA QPVFSKVRDGTDPFSGDEKEQLLGD LQESAMD VIERKGATEWPARGVAHMVEAILH
DTGRVLPASVKLEGEGHEDTAFGVPVRLGSNGVEEIVEWLDDYEQDLMADA EKLSDQYDKIS
>d1b8pa2 d.162.1.1 (A:159-329) Malate dehydrogenase {Aquaspirillum arcticum}
LRLDHNRALSQIAAKTGKPSSIEKLFWGNHSPTMYADYRYAQIDGASVKDMINDDAWNRDTFLPTVGKRGAAIIDARGVSSAASAANAAIDHIH
DWVLGTAGWKTTMGIPSDGSYGIPEGVIFGPVTTENGEYKIVQGLSIDA FSQERINVNL NELEEQNGVQHLLG
>d1guya2 d.162.1.1 (A:144-306) Malate dehydrogenase {Chloroflexus aurantiacus}
AGVLDAARYRTFIAMEAGVSVEDVQAMLMGGHGDEMPLPRFSTISIPVSEFIAPDRLAQI VERTRKGGGEIVNLLKTGSAYYAPAAATAQMVEAV
LKD KKRVM PVA AYL TGQ YGLNDI YFG VPV ILG AGG VE KILE PLN EEM ALL N ASA K VRAT LDTL
>d1gv0a2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium tepidum}
AGVLD SARFRSFIAMELG VSMQDV TACVL GGHDAM VPV VKYTTVAGIPV ADLISAER IELVERTRGGAEIVNHLKQGS AFYSPAT SVV EMVESIV
LDRKRVLTCAVSLDGQYQIDGTFVGVVPVKGKNGVEHIYEIKLDQSDL LQKSAKIVDENCKML
>d1guza2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium vibrioforme}
AGVLDAARFRSFIAMELG VSMQDINACVL GGHDAM VPV VKYTTVAGIPV ADLISAER IELVERTRGGAEIVNHLKQGS AFYAPASSV VEMVESIV
LDRKRVLP CAVGLE GQY QIDKTFVGVVPVKGKNGVEHIYEIKLDQSDL LQKSAKIVDENCKML
>d1hyha2 d.162.1.1 (A:167-329) L-2-hydroxyisocapronate dehydrogenase, L-HICDH {Lactobacillus confusus}
GTLLDTARMQRAVGEAF DLD PRS VSGY NLGEH GNSQ FVA STV RVM GQPI VTLAD AGD IDLA IEE EARKGGFTV LNG KGY TSYGV AT SAI RIKA V
MADAHAELVSNRRDDMG MYLSYPAI GRDG VLAETT LDLT DEQ EKLL QSRDY IQ QRF DEI VDTL
>d9ldta2 d.162.1.1 (A:163-331) Lactate dehydrogenase {Pig (Sus scrofa)}
SGCNLDSARFRYLMGERLGVHPLSCHGWILGEHGDSV PVWSGVNVAGVSLKNLHPEL GTDADKEHWKA VHKEV VDSAYEV IKLKG YT SWAIGL
VADLAESIMKNLRRVHPISTMIKGLYGIKENVFLSVCPCILGQNGISD VVKV TLPEEEAH LKKSADTLWGIQKELQF
>d1i0za2 d.162.1.1 (A:161-332) Lactate dehydrogenase {Human (Homo sapiens), heart isoform (H chain)}
SGCNLDSARFRYLMGERLGVHPLSCHGWILGEHGDSV PVWSGMNVAGVSLKTLHPEL GTDADKEHWKA VHKEV VDSAYEV IKLKG YT SWAIGL
SVADLIESMLKNLRSIHPVSTMVKGMYGIENEVFLSPCILNARGLTSVINQKLK DDEVAQLKKSADTLWDI QKDLKD
>d1i10a2 d.162.1.1 (A:160-331) Lactate dehydrogenase {Human (Homo sapiens), muscle isoform (M chain)}
SGCNLDSARFRYLMGERLGVHPLSCHGWILGEHGDSV PVWSGMNVAGVSLKTLHPEL GTDADKEHWKA VHKEV VDSAYEV IKLKG YT SWAIGL
SVADLAESIMKNLRRVHPVSTMVKDFYGIKDDVFLSVCPCILGQNGISD LVKV TLPEEEAH LKKSADTLWGIQKELQF
>d2Idx_2 d.162.1.1 (160-331) Lactate dehydrogenase {Mouse (Mus musculus)}
SGCNLDSARFRYLMGERLGVHSCSCHGWVGEHGDSV PSVWSGMNVASIKLHPLDGTNKDKQDWKKLHKDV VDSAYEV IKLKG YT SWAIGL
SVTDLARSILKNLKR VHPV TTVLKG FHGIKEEVFLSIPC VLGE SGITDFV KVNM TAEE EGLKKSADTLWNM QK NLE
>d1ldm_2 d.162.1.1 (161-329) Lactate dehydrogenase {Dogfish (Squalus acanthias)}
SGCNLDSARFRYLMGERLGVHSCSCHGWVGEHGDSV PSVWSGMNVASIKLHPLDGTNKDKQDWKKLHKDV VDSAYEV IKLKG YT SWAIGL
D LAETIMK NLCRVHPV STMVKDFYGIKDNVFLSVCPLN DHDG ISNIVK M KLPNEE QQ LQKS ATT LW DIQ KDLKF
>d1ceqa2 d.162.1.1 (A:164-329) Lactate dehydrogenase {Malaria parasite (Plasmodium falciparum)}
GGVLDTSRLKYYISQKLNVCPRDVNAHVGAHGNK MVLLKRYITVGGIPLQEF INNKLISDAELEAIF DRTVNTALEIVNLHASP VYAPAAIIEMAESYL
KDLKKVLICSTLLEGQYGHSDIFGGTPV LGANGVEQVIELQLNSEEKAKFDEAIAETKRMKALA
>d1ldna2 d.162.1.1 (A:163-330) Lactate dehydrogenase {Bacillus stearothermophilus}
TI LDTARFRFLLGEYFSVAPQNVHAYIIGEHDTEPVWSQAYIGVMPIRKLVESKGEEAQKDLERIFVNVRDAAYQIEKKGATYYG IAMGLARVTRAIL
HNENAILTVSAYLDGLYGERDVYIGVPAVINRNGIREVIELN DDEKNRFHSAATLKS VLAFT

>d1llc_2 d.162.1.1 (165-334) Lactate dehydrogenase {Lactobacillus casei}

TSLDTARFRQSIAEMVNVDARSVHAYIMGEHGDEFPVSHANIGVTIAEWVKAHPEIKEDKLVKMFEDVRDAAYEIIKLKGATFYGIATALARISK
AILNDENAVLPVLSPYMDGQYGINFLYIGTPAVINRNGIQNILEIPLTDHEEESMQKSASQLKVLDAFAKNID

>d1ez4a2 d.162.1.1 (A:163-334) Lactate dehydrogenase {Lactobacillus pentosus}

TSLDSSRLRVALGKQFNVDPRSVDAYIMGEHGDFEAAYSTATIGTRPVDRVAKEQGVSDDLAKLEDGVRNKAYDIINLKGTIFYGIGTALMRISKAIL
RDENAVLPVGAYMDGQYGLNDIYIGTPAIIGGTGLKQIIESPLSADELKKMQDSAATLKKVLNDGLAELEN

>d1llda2 d.162.1.1 (A:150-319) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}

TNLDSARLRFLIAQQTGVNVKNVHAYIAGEHGDSEVPLWESATIGGVPMWDTPPLPGHDPLADKREEIHQEVKNAAYKIINGKGATNYAIGMSGV
DIIAEVLHDTNRILPVSSMLKDFHGSDICMSVPTLLNRQGVNNNTINTPVSDEKELAALKRSAETLKETAACQFGF

>d1a5z_2 d.162.1.1 (164-333) Lactate dehydrogenase {Thermotoga maritima}

GTVDLTLARLTLIAQHCGFSRPSRVHVYVIGEHGDSEPVWSGAMIGGIPLQNMCQVCQKCDSKILENFAEKTKRAAYEIIERKGATHYAIALAVADIVE
SIFFDEKRVLTLSVYLEDYLGVKDLCISVPVTLGHGVERILENLNNEEELEAFRKSASILKNAINEITAEEN

>d1hyea2 d.162.1.1 (A:146-313) MJ0490, lactate/malate dehydrogenase {Archaeon Methanococcus jannaschii}

LGTHLDLSRFKVAIAKFFGVHIDEVRTRIIGEHGDSMVPLSATSIIGGIPIQKFERFKELPIDEIIEDVTKGEQIIRLKGSEFGPAAILNVVRCIVNNEKR
LLTLSAYVDGEFDGIRDVCIPVKIGRDGIEEVVSIELDKDEIIAFRKSAEIIKKYCEEVKNL

>d1aiha_d.163.1.1 (A:) Integrase {Bacteriophage HP1}

ETELAFLYERDIYRLAECDNSRNPDLGLIVRCLATGARWSEATLTQSQVMPYKITFTNTSKKNRTVPISELFDMPLKKRGRLFNDAYESFENAVL
RAEIELPKGQLTHVLRHTFASHFMMNGGNILVLKEILGHSTIEMTMRYAHFAPSHLESAVKFNPNSPAQ

>d1ae9a_d.163.1.1 (A:) Integrase (Int) {Bacteriophage lambda}

RSRLTADEYLKIYQAAESSPCWLRLAMELVVTGQRVGDLCEMKWSDIVDGLYVEQSCTGVKIAIPTALHIDLGISMKETLDKCKEILGGETIIASTR
REPLSSGTVSRYFMRARKASGLSFEGDPPTFHELRLSLSARLYEKQISDKFAQHLLGHKSDTMASQFRDRGREWDKIEI

>d1f44a2 d.163.1.1 (A:130-343) Cre recombinase {Bacteriophage P1}

RAKQALAFERTDFDQVRSLMENSRCQDIRNLAFLGIAYNTLLRIAEIARIVKDISRTDGGRMLIHIGRTKTLVSTAGVEKALSLGVTKLVERWISVSG
VADDPPNNYLFCRVRKNGVAAPSATSQLSTRALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGGWTVNVNIVMN
FIRNLDSETGAMVRLEDGD

>d5crxb2 d.163.1.1 (B:130-314) Cre recombinase {Bacteriophage P1}

RAKQALAFERTDFDQVRSLMENSRCQDIRNLAFLGIAYNTLLRIAEIARIVKDISRTDGGRMLIHIGRTKTLVSTAGVEKALSLGVTKLVERWISVSG
VADDPPNNYLFCRVRKNGVAAPSATSQLSTRALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQAGG

>d1a0p_2 d.163.1.1 (111-292) Recombinase XerD {Escherichia coli}

KDLSEAQVERLLQAPLQDQPLELRDKAMLEVLYATGLRSELVGLTMSDISLRQGVVRVIGKGNKERLVLPLGEEAVWLETYEHGRPWLNGVSIDVL
FPSQRQQMTRQTFWHRIKYAVLAGIDSEKLSPHVLRHAFATHLLNHGADLRVQMLLGHSDLSTTQIYTHVATERLRLHQ

>d1floa2 d.163.1.1 (A:135-423) Flp recombinase {Baker's yeast (Saccharomyces cerevisiae)}

KGNSHSKKMLKALLSEGESIWEITEKILNSFEYTSRFTKTLYQFLFLATFINCGRFSDIKNVDPKSFKLVQNKLQYLGVIQCLVTETKTSVRHIYFFSARGR
IDPLVYLDLFLRNSEPVLKRVNRTGNSSNKQEYQLLKDNLVRSYNKKNAPYSIFAIKNGPKSHIGRHLMTSFLSMKGLTELTNVGNWSDKRASA
VARTTYTHQITAIPDHYFALVSRRYYADPISKEIALKDETNPPIEWWQHIEQLKGSAEGSIRYPAWNGIISQEVLQYLDYLSYINRRI

>d1a31a1 d.163.1.2 (A:431-626,A:720-765) Eukaryotic DNA topoisomerase I, catalytic core {Human (Homo sapiens)}

PSSRIKGEKDQWQYETARRLKKCVDKIRNQYREDWKSKEVKVRQRAVALYFIDKLALRAGNEKEEGETADTVGCCSRVEHINLHPEDGQEVYVVF
DFLQKDSIRYYNKVPKVPEKVKFLQLFMENKQPEDDLFDRLLNTGILNKLQDLMEGLTAKVFRNTNASITLQQQLKELTAPDENIPAKILSYRNARAV
XKLNLYLDPRITVAWCKKWGVPIEKIYNKTQREKFAWAIDMADEDYEF

>d1a41_d.163.1.2 (-) Eukaryotic DNA topoisomerase I, catalytic core {Vaccinia virus}

NAKRDRIFRVYNVMKRINCFINKNIKKSSTDNSYQLAVFMLMETMFFIRFGKMKYLKENETVGLTLKNKHIEISPDEIVIKFVGKDKVSHEFVVHKS
NRLYKPLLKLTDDSSPEEFLFNKLSERKVYECIKQFGIRKDLRTYGVNYTFLYNFWTNVKISPLPSPKKLIALTQAEVVGHTPSISKRAYMATTILEMV
KDKNFDLUVSKTTDEFLSIVVDHVKS

>d1mhda_d.164.1.1 (A:) SMAD MH1 domain {Human (Homo sapiens)}

PIVKRLLGWKGEQNGQECKEAVKSLVKKLKTGQLDELEKAITTQNVNTKCITIPRSLDGRLQVSHRKGLPHVYICRLWRWPDLHSHHELRAM
ELCEFAFMKKDEVCPNPYHYQRVET

>d1hufa_d.195.1.1 (A:) YopH tyrosine phosphatase N-terminal domain {Yersinia pestis}

LSSLSDLHRQVSRLVQQESGDCTGKLGNVAANKETTFQGLTIASGARESEKVFAQTVLSHVANVLTQEDTAKLLQSTVKHNLNNYDLRSVGNGNSV
LVSLRSDQMTLQDAKVLLEAALRQES

>d1mrj_d.165.1.1 (-) alpha-Trichosanthin {Mongolian snake gourd (Trichosanthes kirilowii maxim)}

DVSFRLSGATSSSYGVFISNLRKALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADETISVAIDVTNVYIMGYRAGDTSYFFNEASATEAAKYVFKDAMR
KVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTLYYNANSAAASALMVLIQSTSEAARYKFIEQQIGKRVDKTFLPSLAIISLENSWSALSQIQIAST
NNGQFESPVVLINAQNQRVTITNVDAVGVTTSNIALLNRNNMA

>d1bryy_d.165.1.1 (Y:) Bryodin {Red briony (Bryonia dioica)}

DVSFRLSGATTTSYGVFIKNLREALPYERKVNIPLLSSISGSGRYTLLHHTNYADETISVAIDVTNVYIMGYLAGDVSYFFNEASATEAAKFVFKDAKK
VTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTLYYTASSAASALLVLIQSTAESARYKFIEQQIGKRVDKTFLPSLATISLENNWSALSQIQIASTNN
GQFESPVVLIDGNNQRVSITNASARVVTTSNIALLNRNNIA

>d1mrg_d.165.1.1 (-) alpha-Momorcharin (momordin) {Bitter gourd (Momordica charantia)}

DVSFRLSGADPRSYYGMFIKDLRNALPFREKVNIPLLPSVSGAGRYLLMHLFNRDGKTIVAVDVTNVYIMGYLADTTSYFFNEPAELASQYVFRDA
RRKITLPYSGDYERLQIAAGKPREKIPIGLPALESAISTLHYDSTAAGALLVLIQTTAEARFKYIEQQIWERAYRDEVPSLATISLENSWSGLSKQIQIASTNN
QGNNGIFRTPIVLVDNKGNRVQITNVTSKVVTTSNIQLLNTRNI

>d1cf5a_d.165.1.1 (A:) Beta-momorcharin {Bitter gourd (Momordica charantia)}

DVNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDRFILLNLTSYAYETISVAIDVTNVYVVAYRTRDVSYFFKESPEAYNILFKGTRKITLPY
GNYENLQTAAHKIRENIDGLPALSSAITLFYNAQSAPSALLVLIQTTAEARFKYIERHVAKYVATNFKPNAIISLENQWSALSQJFLAQNQGGKF
RNPVDLIKPTGQRFQVTNVDSVVKGNIKLLLNSRASTADEN

>d1ce7a_d.165.1.1 (A:) Mistletoe lectin I A-chain {European mistletoe (Viscum album)}

YERGDLVTAQTTGAGYFSFITLLRDYVSSGSFSNAIPLLSQSGGGGEAGRFLVELNSGGDITVAIDVTNLVVAYQAGSQSYFLSGPGGRHGFTG
TTRSLPFNGSYPDLEQYGGQRKQIPLGIQDQLIQSVTALKFGSTRTGARSILILIQMISEAARFNPIWRARQYINSGASFLPDVYMLELETSWGQQST
QVQHSTDGVFNNPIALADPGGGVTLTNVRDVIASLAIMLFVC

>d1abra_d.165.1.1 (A:) Abrin A-chain {Abrus precatorius}

EDRPIKFSTEGATSQSYKQFIEALRERLGGIHDIPVLPDPTTLQERNRYITVELNSDTEIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSADYLFTGT
DQHSLPYGYTDLERWAHQSRQQIPLGLQALTHGISFFRGNDNEEKARTLIVIIQMVAEAARFRYISNRVRVSIQGTAFQPDAAAMISLENNWD
NLSRGVQESVQDTFPNQVTLNIRNEPVIVDSLHPTVAVLALMLFVCNPPN

>d1apa_d.165.1.1 (-) Pokeweed antiviral protein alpha {Pokeweed (Phytolacca americana)}

INTITFDVGNATINKYATFMKSIIHNQAKDPTLKCYGIPMLPNTNLTPKYLVLTLQDSSLKTTLMLKRNNLYVMGYADTYNGKCRYHIFKDISNTTERND
VMTTLCNPSSRVGKNIYDSSYPALEKKVGRPRSQVQLGIQILNSGIGKIYGVDSFTEKTEAEFLVIAIQMVSEAARFKYIENQVKTNFNRAFPNAK
VLNLEESWGKISTAIHNAKNGALTSPLELKANGSKWIVLRVDDIEPDVGLKYVNGTCQAT

>d1d6aa_d.165.1.1 (A:) Pokeweed antiviral protein alpha {Pokeweed (Phytolacca americana)}

VNTIIYNVGTTISKYATFLNDLRNEAKDPSLKCYGIPMLPNTNTPKYVVELQGSNKKTITLMRRNNLYVMGYSDFETNKCRYHIFNDISGTERQ
DVETTLCPNANSRVSKNINFDSRYPTELESKAGVKSRSQVQLGIQILDNSIGKISGVMSFTEKTEAEFLVIAIQMVSEAARFKYIENQVKTNFNRAFPNP
PKVNLQETWGKISTAIHDAKNGVLPKPLEVDASGAKWIVLRVDEIKPDVALLNYVGGSQTT

>d1qi7a_d.165.1.1 (A:) Saporin So6 {Common soapwort (Saponaria officinalis)}

VTSITLDLVNPAGQYSSFVDKIRNNVKDPNLKYGGTDIAVGPSSKEKFLRINFQSSRGTVSLGLKRDNLVVAYLAMDNTNVNRAYFKSEITSALTA
LFPEATTANQKALEYTEDYQSIKNAQTQGDKSRKELGLGIDLLTFMEAVNKKARVVKNEARFLIAIQMTAEVARFRYIQLVTKNFPNKFDSNDK
VIQFEVSWRKISTAIYGDAKNGVFNKDYDFGFGKVRQVKDLQMGLLMYLGKPK

>d1ift_d.165.1.1 (-) Ricin A-chain {Castor bean (Ricinus communis)}

YPIINFTTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFLVLESNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAET
HLFTDVQNRYTFAFGNNYDRLEQLAGNLRENIELGNGPLEEAIASALYYSTGGTQLPLTARFSIICIQMISEAARFKYIEGEMRTRIRYNNRRSAPDPSVIT

LENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPP

>d1hwma_d.165.1.1 (A:) Ebulin A-chain {Sambucus ebulus}

IDYPSVSNLAGAKSTTYRDFLKNLRDVRATGTYEVGLPVLRRERESEVQVKNRFLVRLTNYNGDTVTSAVDVTNLYLVAFSANGNSYFFKDATELQKS
NLFLGTTQHTLSFTGNYDNLETAAGTRRESIELGPNPLDGAITSWLWYDGGVARSLVLIQMVPPEARFRYIEQEVRRLSQQLTSFTPNALMSMENN
WSSMSLEVQLSGDNVSPFSGTVQLQNYDHPTPLVDNFEEELYKITGIAILLFRCVA

>d1dm0a_d.165.1.2 (A:) Shiga toxin, A-chain {Shigella dysenteriae}

KEFTLDFSTAKTYVDSLNVIRSAIGTPLQTISGGTSLLMIDSGTGDNLFAVDVRGIDPEEGRFNNRLIVERNNLYVTGFVNRTNNVFYRFADFSHVT
PGTTAVTLDGDSSYTLQRVAGISRTGMQINRHSLTTSYLDLMSHSGTSLQSVARAMLRFVTVAEALRFRQIQRGFRLLDDLSGRSYVMTAEDVD
LTLNWGRLSSLPDYHGQDSRVGRISFGSINAILGSVALILNCHHHASRVARMASDEFPSMCPADGRVRGITHNKILWDSSLGAIM

>g1ts.1 d.166.1.1 (A;C:) Heat-labile toxin, A-chain {Escherichia coli, type IB}

RLYRADSRPDEIKRSGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSRSAHLAGQSILGYSTYYIYVIATAPNMFNNDV
LGVYSPHPYEQEV SALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYRNLNIAPAEDGYRLAGFPFDHQAWREEPWIHHAPQCGXGDTCTNE
ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRI

>g1tii.1 d.166.1.1 (A;C:) Heat-labile toxin, A-chain {Escherichia coli, type IIB}

NDYFRADSRTPDEVRRSGGLIPRGQDEAYERGTPININLYDHARGTATGNTRYNDGYVSTTTLRQAHLLGQNMLGGYNEYIYVVAAPNLFDVN
GVLGRYSPYPSENEYAALGGIPLSQIIGWYRVSGAIEGGMHRNRDYRDLFRGLSAAPNEDGYRIAGFPDGPAWEVPWREFAPNSCLPXTTCAS
LTNKLSQHDLADFKKYIKRKFTLMTLLSINN

>d1f0la2 d.166.1.1 (A:1-187) Diphtheria toxin, N-terminal domain {Corynebacterium diphtheriae}

GADDVVDSKSFMENFSSYHGTPGYVDSIQKGIQKPKSGTQGNYDDDWFQYSTDNKYDAAGYSVDNENPLSGKAGGVVKVTPGLTKVLALK
VDNAETIKKELGLSLTEPLMEQVGTEEFIKRGDGASRVVSLPFAEGSSVEYINNWEQAKALSVELEINFETRGKRGQDAMYEYMAQACA

>d1ikpa2 d.166.1.1 (A:395-606) Exotoxin A, C-terminal domain {Pseudomonas aeruginosa}

PTGAELGDDGDSVFSRGTQNWTVERLQQHRLQLEERYVFGYHGTLEAAQSIVFGGVRARSQLDLAIWRGFYIAGDPALAYGYAQDQEPDA
RGRIRNGALLRVYPRSSLPGFYRTSLAAPEAAGEVERLIGHPLPLRLAITGPEEEGGRLETILGWPLAERTVVIPSIAPTDPRNVGGDLPSSIPDK
EQAISALPDYASQPGK

>d1prta_d.166.1.1 (A:) Pertussis toxin, S1 subunit {Bordetella pertussis}

DPPATVYRYDSRPPEDVFQNGFTAWGNNDNVLEHLTGRSCQVGSSNSAFVSTSSRRTYEVYLEHRMQEAEAERAGRGTGHFIGIYEVRADNNF
YGAASSYFEYVDTYGDNAGRILAGALATYQSEYLAHRRIIPPENIRRTRVYHNGITGETTTEYSNARYVSQQTRANPNPYTSRRVASIVGTLVRMAP
VVGACMARQAESSEAMAASERAGEAMEVLVYYESIASF

>g1xtc.1 d.166.1.1 (A;C:) Cholera toxin {Vibrio cholerae}

NNDKLYRADSRPDEIKQSGGLMPRGQSEYFDRGTQMNINLYDHARGTQTGFVRHDDGYVSTSLSRSAHVGQTILSGHSTYYLYVLATAPNMFN
NDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHFGVLDEQLHRNRGDRYYSNLIDIAAADGYLAGFPPEHRAWREEPWIHHAPPGENAPR
XSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL

>d1qs1a1 d.166.1.1 (A:60-264) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}

TDKVEDFKEDKEAKEWGKEKEWKLTAKEGKMNFLDNKNDIKTNYEITFSMAGSFEDIEKDLKEIDKMFDTNLSNSIITYKNVEPTTIGFNKS
LTEGNTINS DAMAQFKEQFLDRDIKFDSYLDTHLTAQQVSSKERVLKVTPSGKGSTPTKAGVILNNSEYKMLIDNGYMVHVDKVSJVKKGVECL
QIEGLTKK

>d1qs1a2 d.166.1.1 (A:265-461) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}

SLDFKNDINAHEHSWMKNYEEWAKDLDSQREALDGYARQDYKEINNYLRNQGGSGNEKLDAQKNIISDALGKKPIPENITVYRWCGMPEFGYQ
ISDPLPSLKDFFEQFLNTIKEDKGYMSTSLSERLAAFGSRKIIIRLQVPKGSTGAYLSAIGGFASEKEIILDKDSKYHIDKVTEVIKGVKRYVVDATLLT

>d1g24a_d.166.1.1 (A:) Exoenzyme c3 {Clostridium botulinum}

AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNLIKQVELLDKSFNKMTPENIMLFRGDDPAYLGTEF
QNTLLNSNGTINKTAFEKAKFLNKDRLEYGYISTLMNVSQAGRPIITFKVAKGSKAGYIDPISAFAGQLEMLPRHSTYHIDDMLRSSDGKQIIIT
ATMMGTAINPK

>d1j7na3 d.166.1.1 (A:264-550) Anthrax toxin lethal factor, middle domain {Bacillus anthracis}

MLSRYEKWEKIKQHYQHWSDSLSEEGRGLLKKLQIPIEPKKDDIIHSLSQEEKELLKRIQIDSSDFLSTEEKEFLKKLQIDIRDSLSEEKEELLNRIQVDSSN
PLSEKEKEFLKKLKLQDIPYDINQLQDTGLIDSPSINLDVRKQYKRDQNIDALLHQSIGSTLYNKIYENMNIINNLATLGADLVSTDNTKINRGIF
NEFKKNFKYSISNSYMINVDINERPALDNERLKWRIQLSPDRAGYLENGKLILQRNIGLEIKDVQIICKSEKEYIRIDAKV
>d1a26_2 d.166.1.2 (797-1012) Poly(ADP-ribose) polymerase, C-terminal domain {Chicken (Gallus gallus)}
LRTDIKVVDKDSEEAKIQQYVKNTAATHNAYDLKVVIFREREGESQRYKPKQLHNQRLLWHSRTTNFAGILSQLRIAPPEAPVTGYMFGKG
YFADMVSKSANYCHTSQADPIGLILLGEVALGNMYELKNASHITKLPKGKHSVGLKTAPDPTATTLGVVEPLNGNISTGINDTCLLYNEYIVYDVA
QVNLYKLKLFNYKTS
>d1g2aa_d.167.1.1 (A:) Peptide deformylase {Escherichia coli}
SVLQLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSENRDERLVLINPELLEKSGETGIEEGCLSIPEQRALVPR
AEVKVIRALDRDGKPFELADGLAICIQHEMDHLVGKLFMDYLSPLKQQRIRQKVEKLDRL
>d2def_d.167.1.1 (-) Peptide deformylase {Escherichia coli}
VLQLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSENRDERLVLINPELLEKSGETGIEEGCLSIPEQRALVPR
AEVKVIRALDRDGKPFELADGLAICIQHEMDHLVGKLFMDYLS
>d1jbia_d.209.1.1 (A:) Cochlin {Human (Homo sapiens)}
TAPIAITCFTRGLDIRKEKADVLCPGGCPLEFSVYGNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVTLE
>d1chu3 d.168.1.1 (A:238-353) L-aspartate oxidase {Escherichia coli}
LEFNQFHPTALYHPQARNFLTEALRGEGLKRPDGTRMPDFDERGELAPRDIVARAIDHEMKRLGACMFLDISHKPADFIRQHFPMIYEKLLGL
GIDLTDQEPVPIVPAAHYT
>d1fuma3 d.168.1.1 (A:226-357) Fumarate reductase flavoprotein subunit {Escherichia coli}
MEFVQYHPTGLPGSGILMTEGCRGEGGLVNKNGYRYLQDYGMGPETPLGEPKNQYMELGPRDKVSQAFWHEWRKGNTISTRGDVYVYDLRHL
GEKKLHERLPFICELAKAYVGDPVKEPIPVRPTAHYT
>d1qlaa3 d.168.1.1 (A:251-371) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}
MEAVQFHPTPLPSGILTEGCRGDDGILRDVDGHRFMPDYEPEKKELASRDVVSRRMIEHIRKGKGVQSPYQHVLWDISILGRKHETNLRDVQE
CEYFAGIDPAEKWAPVLPMQHYS
>d1e39a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}
QYIQAAPTLSVKGGVMVTEAVRGNGAILVNREGKRVNEITTRDKASAAILAQTGKSAYLIFDDSVRKSLSKIDKYIGLGVAPTADSLVKLGKMEGID
KALTETVARYNSLVSSGKDTEFERNPLPRALNEGNYIAEVTPGVHH
>d1qo8a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}
HPTVGKDSRILSETVRGVGAVMVNKDGDNRFISELTTRDKASDAILKQPGQFAWIIFDNQLYKKAKMVRGYDHLEMILYKGDTVEQLAKSTGMKVAD
LAKTVSDYNGYVASGKDTAFGRADMPLMTQSPYYAVKVAPGIHHTMGGV
>d1d4ca3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella putrefaciens}
YIQAHPYSPAGGMITEAVRGNGAIVVNREGNRMNEITTRDKASAAILQQKGESAYLVFDDSIRKSLKAIEGYVHLNIVKEGKIEELAKQIDVPAAE
LAKTVTAYNGFVKSGKDAQFERPDLPRELVVPFYALEIAPAVHHT
>d1jnra3 d.168.1.1 (A:257-401) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}
FEHRFIPFRFKDGYGPVGAWFLFKCKAKNAYGEYIKTRAEELEKYKPYGAAQPIPTPLRNHQVMLEIMDGNQPIYMHTEEALELAGGDKKKLKHI
YEEAFEDFLDMTWSQALLWACQNIIDPQEQQSEAAPEPYIMGSHSGE
>d1lit_d.169.1.1 (-) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}
CPEGTNAYRSYCYYFNEDRETWVDADLYCQNMNSGNLVSILTQAEGAFVASLIKESGTDDFNWIGLHDPPKKNRWHWSSGSLVSYKSWGIGAPS
SVNPGYCVSLSSTGFQWKDVPCEDKFSFVCKFKN
>d1qdda_d.169.1.1 (A:) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}
QEAQTELQPQARISCPEGTNAYRSYCYYFNEDRETWVDADLYCQNMNSGNLVSILTQAEGAFVASLIKESGTDDFNWIGLHDPPKKNRWHWSSGS
LVSYKSWGIGAPSSVNPYCVSLSSTGFQWKDVPCEDKFSFVCKFKN
>d1b6e_d.169.1.1 (-) CD94 {Human (Homo sapiens)}
CSCQEKKWVGYRCNCYFISSEQTKWNESRHLCASQKSSLQLQNTDELFMSSSQFYWIGLSYSEEHTAWLWENGALSQYLFPSFETFNTKNCIAY

NPNGNALDESCEDKNRYICKQQLI

>d1e87a_d.169.1.1 (A:) CD69 {Human (Homo sapiens)}

SSCSEDWVGYQRKYFISTVKRSWTSACQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWVGLKEPGHPWKWSNGKEFNNWFNVTGSDKCVFL
KNTEVSSMECEKNLYWICNKPYK

>d1hq8a_d.169.1.1 (A:) NK cell-activating receptor nkg2d {Mouse (Mus musculus)}

GYCGPCPNWICHRRNNCYQFFNEEKTNQSASCLSQNSLLKIYSKEEQDFLKLVSYHWMGLVQIPANGSWQWEDGSSL SYNQLTVEIPKGS
CAVGSSFKAYTEDCANLNTYICMKRAV

>d1hyra_d.169.1.1 (A:) NK cell-activating receptor nkg2d {Human (Homo sapiens)}

ESYCGPCPKNWICYKNNCYQFFDESKNWWYESQASCMSQNASLLKVSKEDQDLLKLVSYHWMGLVHIPTNGSWQWEDGSILSPNLTIEMQKG
DCALYASSFKGYIENCSTPNTYICMQRTV

>d1egia_d.169.1.1 (A:) Macrophage mannose receptor, CRD4 {Human (Homo sapiens)}

CPEDWGASSRTSLCFKLYAKGKHEKKTWESRDFCRALGGDLASINNKEEQQTIWRLITASGSYHKLFWLGLTYGSPSEGFTWSDGSPVSYENWAYG
EPNNYQNVEYCGELKGDPMTMSWNDINCEHLNNWICQIQ

>d1bj3a_d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis)}

DCPSGWSSYEGHCYKPFKLYKTWDDAERFCTEQAKGGHLVSIESAGEADFVAQLVTQNMKRLDFYIWIGLRVQGKVQCNEWSDGSSVSYENWIE
AESKTCGLEKETGFRKWVNIIYCGQQNPVCEA

>d1ixxa_d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis)}

DCLSGWSSYEGHCYKAFEKYKTWEDAERVCTEQAKGAHLVISSGEADFVAQLVTQNMKRLDFYIWIGLRVQGKVQCNEWSDGSSVSYENWI
EAESKTCGLEKETDFRKWVNIIYCGQQNPVCEA

>d1ixxb_d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis)}

DCPSDWSSYEGHCYKPFSEPKNWADAENFCTQQHAGGHLVSFSSEEADFVVKLAQTFGHSIFWMGLSNVWNQCNWQWSNAAMLRYKAW
AEESYCVYFKSTNNKWRSRACRMMAQFVCEFQA

>d1c3aa_d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis), flavocetin-A}

DFDCIPGWSAYDRYCYQAFSKPKNWEDAESFCCEEGVKTSHLVSISSGEADFVAQLVAEKIKTSFQYVWIGLRIQNKEQQCRSEWSDASSVNYENLVK
QFSKKCYALKKGTELRTWFNVYCGTENPEVCKYTPEC

>d1c3ab_d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis), flavocetin-A}

GFCCPLGWSSYDEHCYQVFQQKMNWEDAEEKFTQQHKGSHLVSFSSEEVDFTSKTFPILKYDFVWIGLSNVWNNECTKEWSDGTKLDYKAWSG
GSDCIVSKTTDNQWLSMDCSSKKYYVCKFQA

>d1fvua_d.169.1.1 (A:) Snake coagglutinin {Snake (Bothrops jararaca), botrocetin}

DCPSGWSSYEGNCYKFFQQKMNWADAERFCSEQAKGGHLVSIKIYSKEKDFVGDLVTKNIQSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENV
ERTVKKCFALEKDLGFVLWINLYCAQKNPFVCKSPPP

>d1fvub_d.169.1.1 (B:) Snake coagglutinin {Snake (Bothrops jararaca), botrocetin}

DCPPDWSSYEGHCYRFFKEWMHWDDAEEFCTEQQTGAHLVSFSKEEADFVRSLTSEMKGDVWIGLSDVWNKRFEWTDGMEDYDDYYLI
AEYECVASKPTNNKWWIIPCTRKFNFVCEFQA

>d1ioda_d.169.1.1 (A:) Snake coagglutinin {Sharp-nosed viper (Deinagkistrodon acutus)}

DCSSGWSSYEGHCYKVKQSHTWADAESFCRKVNGGHLVSISSGEADFGVQLIAQKIKSAIHVVIGLRAQNKEKQCSIEWSDGSSISYENWIEEE
SKKCLGVHETGFHKWENFYCEQQDPFVCEA

>d1iodb_d.169.1.1 (B:) Snake coagglutinin {Sharp-nosed viper (Deinagkistrodon acutus)}

DCPSDWSSYEGHCYKPFNEPKNWADAENFCTQQHTGSHLVSFSQSTEADFVVKLAQTFDYGIFWMGLSKIWNQCNWQWSNAAMLKYTDWA
EESYCVYFKSTNNKWRSRITCRMIANFVCEFQA

>d1jwia_d.169.1.1 (A:) Snake coagglutinin {Puff adder (Bitis arietans), bitiscetin}

CLPDWSSYKGHCYKVKVKGWTEDAEKFCVENSGLASIDSKEEADFVTKLASQTLTKFVYDAWIGLRDESKTQQCSPQWTGSSVYENVDEPTK
CFG LDVHTEYRTWDLPCGEKNPICKS

>d1jwib_d.169.1.1 (B:) Snake coagglutinin {Puff adder (Bitis arietans), bitiscetin}

GCLPDWSSYKGHCYKVFKEKTWADAECFKELVNGGHLMSVNSREEGEFISKLALEKMRIVLVWIGLSHFWRICPLRWTGDARLDYRALSDEPICF
VAESFHNKWIQWTCNRKKSFVKYRV

>d2afpa_d.169.1.1 (A:) Type II antifreeze protein {Sea raven (Hemitripterus americanus)}

QRAGPNCAGWQPLGDRCIYYETTAMTWALAETNCMKLGGHLASIHSQEEHSFIQLNAGVVWIGGSACLOQAGAWTSDGTPMNFRSWCSTK
PDDVLAACCMQMATAADQCWDDLPCASHKSVCAMTF

>d1h8ua_d.169.1.1 (A:) Eosinophil major basic protein {Human (Homo sapiens)}

RYLLVRSLSQTFSQAWFTCRRCYRGNLVSIHNFNINYRIQCSVALNQGQQWIGGRITGSGRCRRFQWVDGSRWNFAYWAHQPSRGGHCVALC
TRGGYWRRRAHCLRLPFICSY

>d1qo3c_d.169.1.1 (C:) NK cell receptor ly49a {Mouse (Mus musculus)}

STVLDSLQHTGRGDKVYFCYGMKCYYFVMDRKTWSGCKQTCSLSSLLKIDDEDELKFLQLVPSDSCWGLSYDNKKDWAWIDNRPSKLAL
NTRKYNIRDGGCMLLSKTRLNDNGNCDCQVFICIGKRLDK

>d1qo3d_d.169.1.1 (D:) NK cell receptor ly49a {Mouse (Mus musculus)}

DKVYWF CYGMKCYYFVMDRKTWSGCKQTCSLSSLLKIDDEDELKFLQLVPSDSCWGLSYDNKKDWAWIDNRPSKLALNTRKYNIRDGGC
MLLSKTRLNDNGNCDCQVFICIGKRLDK

>d1dv8a_d.169.1.1 (A:) H1 subunit of the asialoglycoprotein receptor {Human (Homo sapiens)}

CPVNWVEHERSCYWFSRSGKAWADADNYCRLEDAHLVVVTSWEEQKFVQHHIGPVNTWMGLHDQNGPWKWDGTDYETGFKNWRPEQPD
DWYGHGLGGGEDCAHFTDDGRWNDVCQRPYRWVCETEL

>d1k9ia_d.169.1.1 (A:) DC-SIGN (dendritic cell-specific ICAM-3 grabbing nonintegrin) {Human (Homo sapiens)}

PCPWEWTFQGNCYFMSNSQRNWHDSDTACKEVGAQLVVIKSAEEQNFLQLQSSRSNRFTWMGLSDLNQEGTWQWVDGSPLLPSFKQYWNR
GEPNNVGEEDCAEFGNGWNDKCNLAKFWICKKSAA

>d1k9ja_d.169.1.1 (A:) DC-SIGNR (DC-SIGN related receptor) {Human (Homo sapiens)}

CRHCPKDWTFFQGNCYFMSNSQRNWHDSDTACKEVGAQLVVIKTAEEQNFLQLQTSRSNRFSWMGLSDLNQEGTWQWVDGSPLLPSFKQYWNR
NSGEPNNSGNEDCAEFGSGWNDRCDVDNYWICKKPAA

>d1g1sa1_d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}

WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVLPPYSSYYWIGIRKNNKTWTWVGTKKALTNEAENWADNEPNKRNNEDCVEIYIK
SPSAPGKWNEDEHCLKKHALCY

>d1g1ta1_d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}

WSYNTSTEAMYDEASAYCQQRYTHLVAIQNKKEEYLNSILSYSPSYWIGIRKVNNTWWVGTLQPLTEAKNWAPGEPNRQKDEDCCVEIYIK
EKDVGMWNDERCSKKKLALCY

>d1hup_1_d.169.1.1 (112-228) Mannose-binding protein A, lectin domain {Human (Homo sapiens)}

KQVGNKFFLTNGEIMTFEKVKALCVKFOASVATPRNAEANGAIQNLKEEAFGLITDEKTEGQFVDLTGNRLTYTNWNEGEPNNAGSDEDCCVLLKN
GQWNDVPCSTSHLAVCEFPI

>d1fifa1_d.169.1.1 (A:105-226) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}

KKSGKKFFVTNHERMPFSKVKALCSELRGTVAPIRNAEENKAIQEVAKTS AFLGITDEVTEGQFMYVTGGRLTYSNWKKDQPDDWYGHGLGGED
CVHIVDNGLWNDSCQRPYTAVCEFPA

>d1rdl1_d.169.1.1 (1:) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}

KYFMSSVRRMPLNRAKALCSELQGTVATPRNAEENRAIQNVAKDVAFLGITDQRTENVFEDLTGNRVRYTNWNEGEPNNVSGGENCVLLNGK
WNDVPCSDSFLVCEFS

>d2msba_d.169.1.1 (A:) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}

KKFFVTNHERMPFSKVKALCSELRGTVAPIRNAEENKAIQEVAKTS AFLGITDEVTEGQFMYVTGGRLTYSNWKKDQPDDWYGHGLGGED
NDISQCQASHTAVCEFPI

>d1b08a1_d.169.1.1 (A:235-355) Surfactant protein, lectin domain {Human (Homo sapiens), SP-D}

PNGQSVGEKIFKTAGFVKPFTEAQLLCTQAGGQLASPRSAENAALQQLVVAKNEAAFLSMTDSKTEGKFTYPTGESLVSNWAPGEPNDDGGSED
CVEIFTNGKWNDRACGEKRLVCEFS

>d1byfa_d.169.1.1 (A:) Lectin TC14 {Tunicate (Polyandrocarpa misakiensis)}

DYEILFSDETMNYADAGTYCQSRGMALVSSAMRDSTMVKAILAFTEVKGHDYWVGADNLQDGAYNFLWNGVSLPTSDLWSPNEPSNPQSW
QLCVQIWSKYNLLDDVGCGGARRVICEKELD

>d1tn3__ d.169.1.1 (-) Tetranectin {Human (Homo sapiens)}

ALQTVCULKTKVHMKCFLAFTQTKTFHEASEDCISRGGTLSPTQTSSENDALYELRQSVGNNEAEIWGLNDMAAEGTWVDMTGARIAYKNWETEI
TAQPDGGKTENCAVLSGAANGKWFDFKRCRDQLPYICQFGIV

>d1prtb2 d.169.1.2 (B:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain {Bordetella pertussis}

GIVIPPQEQTQHGSPYGRCAKTRALTVaelRGSGDLQEYLRHVTRGWSIFALYDGTLYGGEYGGVIKDGTPGGAFDLKTTFCIM

>d1prt2 d.169.1.2 (C:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain {Bordetella pertussis}

GIVIPPKALFTQQGGAYGRCPNGTRALTVAelRGNAELQTYLRQITPGWSIYGLYDGTLYLGQAYGGIIKDAPPAGIFIYRETFCIT

>d1prea1 d.169.1.2 (A:2-84) Proaerolysin, N-terminal domain {Aeromonas hydrophila}

EPVYDPQLRLFSLGQGVCGDKYRPVNREEAQS VKS NIVGMMGQWQISGLANGWVIMGP GYNGEIKPGTASNTWCYPTNPVTGE

>d1f00i3 d.169.1.3 (I:842-939) Intimin {Escherichia coli}

LIVPNMSKRVTYNDAVNTCKNFGGKLPSQNELENVFKA WGAANKYEYYKSSQTISWVQQTAQDAKSGVASTYDLVKQNPLNNIKASESNAYATC
VK

>d1cwva5 d.169.1.3 (A:887-986) Invasin {Yersinia pseudotuberculosis}

NRWIYDGGRSLVSSLEASRQCQGSDMSA VLESSRATNGTRAPDTLWGEWSLTAYSSDWQSGEYVVKKTSTDFTMNM DGTALQPGPAYLAFF
LCALSI

>d1tsg__ d.169.1.4 (-) TSG-6, Link module {Human (Homo sapiens)}

GVYHREARSGKYKLTYAEAKAVCEFE GGHLATYKQLEAARKIGFH VCAAGWMAKGRVGYPIVKPGPNCFGKTGIIDY GIRL NR SERWDAYCYNPHAK

>d1bnla_ d.169.1.5 (A:) Endostatin {Human (Homo sapiens)}

HSHRDFQPVLHLVALNAPLSGGMRGIRGADFQCFQQARA VGLAGTFR AFLSSRLQDLYSIVRRADRAAVPIVNLKDELFPSWEALFSGSEGPKPG
ARIFSFDGKDVLRHPTWPQKVWHGSDPNGRRLLTESYCETWRTEAPSATGQASSLLGGRLLGQSAASCHHAYIVLCIENS F

>d1koe__ d.169.1.5 (-) Endostatin {Mouse (Mus musculus)}

QPVLHLVALNTPLSGGMRGIRGADFQCFQQARAAGLSTFRAFLSSHLDLSTV RKAERFGLPIVNLKGQVLFNNWDSIFSGDGGQFNTHIPIYSFDGRDV
MTDPSWPQKVWHGSNPHGVRLVDKYCEAWRTTDMAVTGFASPLSTGKILDQKAYSCANRLIVLCIENS F

>d1dy2a_ d.169.1.5 (A:) Endostatin domain of collagen alpha1(xv) {Mouse (Mus musculus)}

RPVLHLVALNTPVAGDIRADFQCFQQARAAGLSTFRAFLSSHLDLSTV RKAERFGLPIVNLKGQVLFNNWDSIFSGDGGQFNTHIPIYSFDGRDV
MTDPSWPQKVWHGSNPHGVRLVDKYCEAWRTTDMAVTGFASPLSTGKILDQKAYSCANRLIVLCIENS F

>d1by2__ d.170.1.1 (-) M2BP {Human (Homo sapiens)}

AVNDGDMRLLADGGATNQGRVEIFYRGQWGTCDNLWDLTDASV CRALGFENATQALGRAAFGQGSGPIMLDEVQCTGTEASLADCKSLGWLK
SNCRHERDAGVVCTNETRSTHTL

>d1mwpa_ d.170.2.1 (A:) N-terminal domain of the amyloid precursor protein {Human (Homo sapiens)}

LLAEPQIAMFCGRLNMHMNVQNGKWSDPSGT KTCIDTKEGILQYQCEVYPELQITNVVEANQPV TIQNWCKRGRKQCKTHPHFVIPYRCLVGEF
V

>d1fid__ d.171.1.1 (-) Fibrinogen C-terminal domains {Human (Homo sapiens), gamma}

QIHDTGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWTVFQKRLGSVDFKKNNWIQYKEFGFHLSPGTTEFWLGNEKIHLISTQS
AIPYALRVELEDWNGRTSTADYAMFKVGPEADKYR LTYAYFAGGDAGDAFDGFDFGDDPSDKFTSHNGMQFSTWDNDNDKFEGNCAEQDGSG
WWMNKCHAGHLNGVYYQGGTYSKASTPNGYDNGIIWATWKTRWYSMKT TMK IIPFNRLTIGEGQQHH

>d1fzcb1 d.171.1.1 (B:200-458) Fibrinogen C-terminal domains {Human (Homo sapiens), beta}

SCNIPVVSGKECEEIRKGGETSEMYLIQPDSSVKPYRVYCDMINTENGWTVIQNRQDG SVDFGRKWD PYKQGFGNVATNTDGKNYCGLPGEYW
LGNDKISQLTRMGPTELLIEDWKGDKVKAHYGGFTVQNEANKYQISVNKYRGTAGNALMDGASQLMGENRTMTIHNMGFFSTYDRNDGW
LTSDPRKQCSKEDGGGWWYNRCHAANPNGRYYWGQYT WDMAKHTDDGVVV MNWKG SWYSMRKMSM KIRPFF

>d1fzda_d.171.1.1 (A:) Fibrinogen C-terminal domains {Human (*Homo sapiens*), fibrinogen-420, alpha-E}
GGWLLIQQRMDGSLNFNRTWQDYKRGFGLNDEGEFEGFWLGNLYHLLTQRGSVLRVELEDWAGNEAYAEYHFRVGSEAEGYALQVSSYEGTAG
DALIEGSVEEGAETSHNNMQFSTFDRDADQWEENCAEVYGGGWYNNCQAANLNGIYYPGGSYDPRNNSPYEIENGVVVSFRGADYSLRA
VRMKIRPLVTQ

>d1jfec1 d.171.1.1 (C:142-393) Fibrinogen C-terminal domains {Chicken (*Gallus gallus*), gamma}
TAEIQETTGRDCQDIANKGARKSGLYFIKPQAKQSFLVCEIDTYGNGWTVLQRRDGSEDFRRNWVQYKEFGFHLSPPDTTEFWLGNEKIHLITT
QSTLPYALRIELEDWSGKKGTDAYAVFKVGETEDKYRLTYAYFIGGEAGDAFDGFNFGDDPSDKSYTYHNGMRFSTFDNDNDNFEGNCAEQDGSG
WWMNRCAGHLNGPYIGGVYSRDTGTNSYDNGIIVATWRDRWYSMKTTMKIIPFNRLS

>d1jfeb1 d.171.1.1 (B:200-464) Fibrinogen C-terminal domains {Chicken (*Gallus gallus*), beta}
SPCVASCNIPVVGRECEDIYRKGGTSEMYIIQDPFTPYRVCDMETDNGGWTLIQNRQDGSVNFRAWDEYKRGFGNIAKSGGKKYCDTPGE
YWLGNDKISQLTKIGPTKVLIEDEWNGDKVSALYGGFTIHNEGNKYQLSVSNYKNAGNALMEGASQLYGENRTMTIHGMYFSTYDRDNDG
WLTTDPRKQCSKEDGGGWYNRCHAANPNGRYYWGGTYSWDMAKHGTDDGIVWMNWKGWYSMCKMSMKIPYFPD

>d1jc9a_d.171.1.1 (A:) Tachylectin 5a {Japanese horseshoe crab (*Tachylepus tridentatus*)}
DPTDCADILNGYRSSGGYRIWPKSWMVTGTLNVYCDMETDGGGWTVIQRGNYGNPSDYFYKPWKNYKLGFGNIEKDFWLGNDRIFALTNQR
NYMIRFDLKDENDTRYAIQDFWIENEDYLYCLHIGNYSGDAGNSGRHNGHFSTIDKDHDTETHCAQTYKGGWWYDRCHESNLNGLYLNGE
HNSYADGIEWRAWKGHYSLPQVEMKIRPVEF

>d1g9mg_d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type 1}
EVVLNVNTENFMWKNMDMVEQMHDIIISLDQSLKPCVKLTPLCVGAGSCNTSVITQACPKVSFEPPIHYCAPAGFAILKCNNTFNGTGPCTNV
TVQCTHGIRPVVSTQLLNGSLAEEEVIRSVNFTDNAKTIVQLNTSVEINCTGAGHCNISRAKWNNTLKQIASKLREQFGNNKTIIFKQSSGGDPEIV
THSFNCGGEFFYCNSTQLNSTWFNSTWSTEGLNTTEGSDTILPCRICKQIINMWQKVKGAMYAPPISGQJRCSSNITGLLTRDGGSNNSEEIFRP
GGGDMRDNRSELKYKVVKIE

>d1g9ng_d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type 1}
LENVTENFMWKNMDMVEQMHDIIISLDQSLKPCVKLTPLCVGAGSCNTSVITQACPKVSFEPPIHYCAPAGFAILKCNDFNGTGPCTNVST
QCTHGIRPVVSTQLLNGSLAEEEVIRSENFTNNAKTIVQLNESVVINCTGAGHCNLSKTQWENTLEQIAIKLKEQFGNNKTIIFNPSSGGDPEIVTHS
FNCGGEFFYCNSTQLFTWNDTRKLNNTGRNITLPCRICKQIINMWQEVGKAMYAPPIRGQIRCSSNITGLLTRDGKDTNGTEIFRPGGDMRD
WRSELKYKVVKIE

>d1msk_d.173.1.1 (-) Methionine synthase (activation domain) {Escherichia coli}
TPPVTLAARDNDFAFDWQAYTPPVAVHRLGVQEVEASIETLRNYIDWTPFFMTWSLAGKYPRILEDEVVGVEAQRLKDANDMLDKLSAEKTLNPR
GVVGLFPANRVGDDIEIYRDETTRTHVINVSHHLRQQTEKTGFANYCLADFVAPKLSGKADYIGAFAVTGLEEDALADAFEAQHDDYNKIMVKALAD
RLAEAAEYLHERVRKVYWGAYAPNENLSNEELIRENYQGIRPAPGPACPEHTEKATIWELLEVEKHTGMKLTESFAMWPGASVSGWYFSPDSKYY
AVAQIQRDQVEDYARRKGMSVTEVERWLAPNLGYDAD

>d1jwka_d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Mouse (*Mus musculus*)}
QYVRIKNWGSGEILHDTLHHKATSCFTCKSKSCLGSIMNPKSLTRGPRDKPTPLEELLPHAIIFINQYYGSFKEAKIEELARLEAVTKEIETTGTYQLT
DELIFATKMAWRNAPRCIGRIQWSNLQVFNDARNCSTAQEMFQHICRHILYATNNNGNIRSAITVFPQRSRGKHDFRLWNSQLRYAGYQMPDGTIRG
DAATLEFTQLCIDLGWKPYGRFDVLPLVLQADGQDPVFEIPPDLVLEVTMEHPKYEWFQELGLKWLPAVANMLLEVGGLEFPACPFNGWYM
GTEIGVRDFCDTQRYNILEEVGRRMGLEHTLASLWKDRAVTEINVAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRARGGCPADWIALVPPVS
GSITPVFHQEMLNYVLSFYQQIEPWKTHIWQNN

>d1nos_d.174.1.1 (-) Nitric oxide (NO) synthase oxygenase domain {Mouse (*Mus musculus*)}
NPKSLTRGPRDKPTPLELLPHAIIFINQYYGSFKEAKIEELARLEAVTKEIETTGTYQLTDELIFATKMAWRNAPRCIGRIQWSNLQVFNDARNCSTA
QEMFQHICRHILYATNNNGNIRSAITVFPQRSRGKHDFRLWNSQLRYAGYQMPDGTIRGDAATLEFTQLCIDLGWKPYGRFDVLPLVLQADGQDP
VFEIPPDLVLEVTMEHPKYEWFQELGLKWLPAVANMLLEVGGLEFPACPFNGWYMGTIEIGVRDFCDTQRYNILEEVGRRMGLEHTLASLWK
RAVTEINVAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRARGGCPADWIALVPPVS
HH

>d3nosa_d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Human (*Homo sapiens*)}

KFPRVKNWEVGSITYDTLSAQAAQGDGCTPRRCLGLVFPRKLQGRPSGPAPAEQLSQARDFINQQYSSIKRSGSQAHEQRLQEVEAEVAATGTYQLRESELVFGAKQAWRNAAPRCVGRIQWGLQFDARDCRSAQEMFTYICNHKYATNRGNLRSAITVFPQRCPGRDFRIWNSQLVRYAGYRQQDGSVRGDPANVEITELCIQHGWTPGNGRFDVLPLLLQAPDEPPELFLLPPELVLEHPTLEWFAALGLRWYALPAVSNMLLEIGGLEFPAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMULDRTTSSLWKDKAAVEINAVLHSYQLAKVTIVDHHAATASFMKHLENEQKARGGCPADWAIVPPI

SGSLTPVFHQEMVNYFLSPAFLYQPDWP

>d4nosa_d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Human (Homo sapiens)}

RHVRIKNWGSGMTFQDTLHHKAKGILCRSKSCLGSIMTPKSLTRGPRDKPTPPDELLPQAIENVNQYGSFKEAKIEHLARVEAVTKEIETTGTYQLTGDELIFATKQAWRNAAPRCIGRIQWSNLQVFDARSCSTAREMFEHICRHVRYSTNNGNIRSAITVFPQRSDGKHDFRVWNAQLIRYAGYQMPDGSIRGDPANVEFTQLCIDLGWPKYGRFDVVPLVLQANGRDPELFEIPPDLLEVAMEHPKYEWFFRELELKWLPAVANMLLEVGGLEFPGCPFNGWMGTEIGVRDFCDVQRYNILEEVGRRMGLETHKLASLWKDQAVVEINIAVIHSFKQNVTIMDHHSAAESFMKYMQMNEYRSRGCPADWIWVPPMSGSLTPVFHQEMLNLYVLPFYQVEAWKTHVWQD

>d1d0ca_d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Cow (Bos taurus)}

GPKFPRVKNWELGSITYDTLCAQSQQDGPCTPRRCLGLSVLPRKLQTRSPGPPPAEQLLSQARDFINQQYSSIKRSGSQAHEERLQEVEAEVASTGYHLRESELVFGAKQAWRNAAPRCVGRIQWGLQFDARDCSSAQEMFTYICNHKYATNRGNLRSAITVFPQRAPGRDFRIWNSQLVRYAGYRQQDGSRGDPANVEITELCIQHGWTPGNGRFDVLPLLLQAPDEAELFVLPPELVLEVMEHPTLEWFAALGLRWYALPAVSNMLLEIGGLEFSAAPFSGWYMSTEIGTRNLCDPHRYNILEDVAVCMULDRTTSSLWKDKAAVEINLAVLHSFQLAKVTIVDHHAATVSFMKHLDEQKARGGCPADWAIVPPI

PISGSLTPVFHQEMVNYILSPAFLYQPDWP

>d1k25a3 d.175.1.1 (A:67-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}

QITRTVPAKRGTIYDRNGVPIADEDATSYNVAYVIDKYYKSATGKILYVEDAQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGSKGNITYANMM

AIKKELETAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRVGNIVPGTELVSQQTVDGKDVTY

>d1qmea3 d.175.1.1 (A:71-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}

TVPAKRGTIYDRNGVPIADEDATSYNVAYVIDKYYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNLKQVSFGAKGNITYANMMSIKK

ELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGMESSLNSILAGTDGIITYEKDRLGNIVPGTEQVSQRTMDGKDVTY

>d1soxa3 d.176.1.1 (A:94-343) Sulfite oxidase, middle catalytic domain {Chicken (Gallus gallus)}

QDPFAGDPPRHPGLRVNSQKPFNAEPPAELLAERFLTPNELFFTRNHLPVAEPSSYRLVDGPGGGTLSLSAELRSRFPKHEVTATLQCAGNRRSE

MSRVRPVKGLPWDIGAISTARWGGARLIRDVLLHAGFPEELQGEWHVCFEGLDADPGGAPYGAISIPYGRALSPAADVLLAYEMNGTELPRDHGFV

RVVPGVVGARSVKWLRRAVSPDESPSHWQQNDYKGFSPCVWDWDTVDYRTAPAIQ

>d1hyoa2 d.177.1.1 (A:119-416) Fumarylacetate hydrolase, FAH, C-terminal domain {Mouse (Mus musculus)}

ATIGDYTFYSSRQHATNVGIMFRGKENALLPNWLHLPVGYHGRASSIVSGTPIRRPMQMRPDNSKPPVYGACRLLDMELEMAFFVGPGNRF

GEPIPIKAHEHIFGMVLMDWSARDIQQWEYVPLGFLGKSGFTTISPWVVPMDALMPFVVPNPKQDPKPLPYLCHSQPYTFDINLSVSLKGEG

MSQAATICRSNFKHMYWTMLQQLTHHSVNGCNLRPGDLLASGTISGSDPESFGSMILESWKGTKAIDVGQQQRTFLDGDEVITGHCGQGDGYR

VGFGQCAGKVLPA

>d1i7oa1 d.177.1.1 (A:1-213) 4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase HpcE {Escherichia coli}

MKGTFIAVALNHRSQLDAWQEAFQQSPYKAPPKTAVVWFKPRNTVIGCEPIPFPQGEKVLSGATVALVGKTATKVREEDAAEYIAGYALANDVSLP

EESFYRPAIKAKCRDGFCPIGETVALSNVDNLTIYTEINGRPADHWNTADLQRNAQQLSALSEFATLNGDAILLGTPQARVEIQPGDRVRVLAEGFP

PLENPVVDEREVTTRK

>d1i7oa2 d.177.1.1 (A:214-429) 4-hydroxyphenylacetate degradation bifunctional isomerase/decarboxylase HpcE {Escherichia coli}

SFPTLPHPHGTLFALGLNYADHASELEFKPPEEPLVFLKAPNTLTGDNQTSVRPNNIEYMHYEALVVVIGKQARNVSEADAMDYVAGYTVCNDYAIR

DYLENYYRPNLRLVKSRDGLTPMLSTIVPKEAIPDPHNLTLLRTFVNGELRQQGTTADLIFSVPLIAYLSEFMTLNPGDMIATGTPKGLSDVPGDEVVV

EVEGVGRLVNRISEETAK

>d1toh_d.178.1.1 (-) Tyrosine hydroxylase {Rat (Rattus norvegicus)}

KVPWFPRKVESELDKCHHLVTKFDPDLDHPGFSQVYRQRRKIAEIAFQYKHGEPIPHVEYTAEEIATWKEVYVTLKGYATHACREHLEGFQLLER

YCGYREDSPQLEDVSRLKERTGFLRPVAGLLSARDFLASLAFRVFQCTQYIRHASSPMHSPEPDCCHELLGHVPMILADRTFAQFSQDGLASLGAS

DEEIEKLSTVWFTVEGLCKQNGELKAYGAGLSSYGEHLSEEPEVRAFDPTAAVQPYQDQTYQPVYFVSESFNDAKDCLRNYASRIQRPFSVK
FDPTYLAIDVLDSPHTIQRSLEGVQDELHTLAHLSAIS

>d3pah__ d.178.1.1 (-) Phenylalanine hydroxylase {Human (Homo sapiens)}

TPWPFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNRYHGQPIPRVEYMEEKKTWGTVFKTLKSLYKTHACYEYNHIFPLLE
KYCGFHEDNIPQLEDVSQFLQTCTGFLRVPAGLSSRDFLGGAFRHFCTQYIRHGSKPMYTPEDPICHLLGHVPLSDRSFAQFSQEIGLASLGAP
DEYIEKLATIYWFTVEGLCKQGDSIKAYGAGLSSFGELQYCLSEKPKLLPLELEKTAIQNYTVTEFQPLYVAESFNDAKEKVRNFAATIPRPFVRYDPY
TQRIEVL

>d1phza2 d.178.1.1 (A:116-427) Phenylalanine hydroxylase {Rat (Rattus norvegicus)}

NTVPWFPPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNRYHGQPIPRVEYTEEKQTWGTVFRTLKALYKTHACYEHNHIFPLL
EKYCGFREDNIPQLEDVSQFLQTCTGFLRVPAGLSSRDFLGGAFRHFCTQYIRHGSKPMYTPEDPICHLLGHVPLSDRSFAQFSQEIGLASLGA
PDEYIEKLATIYWFTVEGLCKEGDSIKAYGAGLSSFGELQYCLSDKPKLLPLELEKTAQCQEYSVTEFQPLYVAESFSDAKEKVRTFAATIPRPFVRYDP
YTQRVEVLDTN

>d1dqa4 d.179.1.1 (A:462-586,A:704-870) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

LSDAEIIQLVNAKHIPAYKLETLIETHERGSIRRQLLSSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCL
VASTNRGCRAIGLGGGASSRVLADXSVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNHAANIVTAIYIACGQDAAQNVGSS
NCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALAAGHLVKSHMIHN

>d1hw8a2 d.179.1.1 (A:441-586,A:704-861) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

EPRPNEECLQILGNAEKGAFLSDAEIIQLVNAKHIPAYKLETLIETHERGSIRRQLLSSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGV
GPLCLDEKEFQVPMATTEGCLVASTNRGCRAIGLGGGASSRVLADXSVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNHAAA
NIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGE
LSLMAALAAGH

>d1hw8c2 d.179.1.1 (C:488-586,C:704-860) Substrate-binding domain of HMG-CoA reductase {Human (Homo sapiens)}

HERGVSIRRQLLSSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRGCRAIGLGGGASSRVLA
DXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNHAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPS
IEIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALAAG

>d1qaxa2 d.179.1.1 (A:4-110,A:221-428) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLLANAGALPMIDIANGMIENVIGTFELPYAVASNQINGRDVLVPLVVEEPSIVAAASYMAKLARANG
GFTTSSSAPXRLLARAQVRITPQQLETAEFSGEAVIEGILDAYAFAAVDPYRAATHNKIGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGSLLTWE
KDNNNGHLVGTLLEMPMPVGLVGGATKTHPLAQSLRILGVKTAQALAEIAVAVGLAQNLGAMRALATEGIQRGHMALHARNIAVVAGARGDEVDW
VARQLVEYHDVRADRAVALLKQKRGQ

>d1qaxb2 d.179.1.1 (B:504-610,B:721-875) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLLANAGALPMIDIANGMIENVIGTFELPYAVASNQINGRDVLVPLVVEEPSIVAAASYMAKLARANG
GFTTSSSAPXRLLARAQVRITPQQLETAEFSGEAVIEGILDAYAFAAVDPYRAATHNKIGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGSLLTWE
KDNNNGHLVGTLLEMPMPVGLVGGATKTHPLAQSLRILGVKTAQALAEIAVAVGLAQNLGAMRALATE

>d1k92a2 d.210.1.1 (A:189-444) Argininosuccinate synthetase, C-terminal domain {Escherichia coli}

AYSTDNSMLGATHEAKDLEYLNSSVKIVNPIMGVKFWDENVKIPAEETVRFEQGHPVALNGKTFSDDVEMMLEANRIGGRHGLGMSDQIENRIIE
AKSRGIYEAPGMALLHIAYERLLTGIGHNEDTIEQYHAHGRQLGRLLYQGRWFDSQALMLRDSLQRWVASQITGEVTLELRGNDYSILNTVSENLYK
PERLTMEKGDSVFSPDDRIGQLTMRNLDITDTREKLFGYAKTGLSSSAASGPVQVENLENK

>d16vpa_ d.180.1.1 (A:) Conserved core of transcriptional regulatory protein vp16 {Herpes simplex virus type 1}

SRMPSPPMPVPPAALFNRLDDLGFSAGPALCTMLDTWNEDLFSALPTNADLYRECKFLSTLPSDVVEWGDAYVPERTQDIRAHGDVAFPTLPATR
DGLGLYYEALSRRFFHAELRAREESYRTVLANFCASLYRYLARASVRQLHRQAHMRGRDRDLGEMLRAТИADРYYRETARLARVLFHLYLFLTREILWAAY
AEQMMRDPDFCLCCDLESWRQLAGLFQPMFVNGALTVRGVPIEARRLRELNHIREHNLPLVRSAAATEEPGAPLTPPTLHGNQARASGYFMVL
IRAKLDSYSSFTTSPSEAVMREHAYSRAPTKNNYGSTIEGLLDPLDDDAPEEAGLAAPRLSFL

>d1bdfa2 d.181.1.1 (A:53-178) RNA polymerase alpha subunit {Escherichia coli}

GCAVTEVEIDGVLHEYSTKEGVQEDILEIILNLKGLAVRVQGKDEVILNKSGIGPVTAADITHDGDVEIVKPQHVICHTDENASISMRIKVQRGRGY
VPASTRIHSEEDERPIGRLVDACYS

>d1i6va2 d.181.1.1 (A:50-172) RNA polymerase alpha subunit {Thermus aquaticus}

GTAVTSVYIEDVLHEFSTIPGVKEDVVEIIINLKELVVRFLDPKMASTTLIRAEGPKEVRAVDFTPSADVEIMNPDLHIATLEGGKLYMEVRVDRGVG
YVPAERHGIKDRINAIPVDAIFS

>d1i50c2 d.181.1.1 (C:42-172) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

PTLAIDSVEVETNTTVLADEFIAHRLGLPQLSMDIEQLEYSRDCFCEDHCDKCSVVTLQAFGESESTTNVYSKDLIVSNLMGRNIGHPIIQDKEGNG
VLIICKLRKGQELKLTCVAKKGIAKEHAKWGP

>d1el6a_ d.182.1.1 (A:) Baseplate structural protein gp11 {Bacteriophage T4}

SRLADFLGFRPKTGDIDVMNRQSVGSVTISQLAKGFYEPNIESAINDVHNFSIKDVTIITNKTGVSPEGVSQTDYWAFSGTVTDDSLPPGSPITVLVF
GLPVSAATTGMTAIEFVAKVRALQEAIASFATINSYKDHDPTDSKLEVTYLDNNQKHVLSTYSTYGITISQEIISESKGPGYGTWNLLGAQTVLDNQQPT
VFYHFERTA

>d1fh6a_ d.183.1.1 (A:) Major capsid protein gp5 {Bacteriophage HK97}

SLGSDADSAGSLIQPMQIPGIIMPGRLRTIRDLLAQGRTSSNALEYVREEVFTNNADVVAEKALKPESDITFSKQTANVKTIAHWVQASRQVMDDA
PMIQLSYINNRLMYGLAKEEGQLLNGDTGDNLEGLNKVATAYDTSLNATGDTRADIIAHAIYQVTESEFSASGIVLNPRDWHNIALLKDNEGRYIFG
GPQAFTSNIMWGLPVVPTKAQAAGTFTVGGFDMASQVWDRMDATVEVSREDRDNFVKNMILTILCEERLALAHYRPTAIKGTFS

>d1fn9a_ d.196.1.1 (A:) Outer capsid protein sigma 3 {Reovirus}

MEVCLPNHGQVVDLINNAFEGRVSIYSAQEGWDKTISAQPDMMVCGGAVVCMHCLGVVGLQRKLKHLPHHRCNQQIRHQDYVDFVQFADRVTA
AHWKRGMLSFAQMHEMMNDVSPDDLDRVRTEGGLVVELNWLQVDPNSMFRSHSSWTPLQVVDDLTKLDDQYWTALNLMIDSSDLIPNF
MMRDPSHAFNGVKLGGSARQTQFSRTFDSRSSLEWGVMVYDYSELEHDPSKGRAYRKELVTAPRDGFHFGLSHYSRATTPILGKMPAVFSGMLTG
NCKMYPFIKGAKLTVRKLEAVNHAWGVEKIRYALGPGGMTGWYNRTMQQAPIVTPAALTMFPTIKFGDLNYPVMIGDPMILG

>d1qgwa_ d.184.1.1 (A:) Phycoerythrin 545 alpha-subunits {Cryptophyte (Rhodomonas sp.), cs24}

AMDKSAKAPQITIFDHRCRAPKESTGGKAGGQDDEMMVKVASTKTVSESDAAKKLQEFIGEKGIDGPFTSKN

>d1qgwb_ d.184.1.1 (B:) Phycoerythrin 545 alpha-subunits {Cryptophyte (Rhodomonas sp.), cs24}

AMDKSAKAPVITIFDHRCRAPKEYTGAKAGGKDDEMMVKAQSVKIEVSTGTAEGVLATSLAKMTK

>d1jyoe_ d.184.1.2 (E:) Virulence effector SptP domain {Salmonella typhimurium}

DKAYVAPEKFSSKVLTLGKMPFLKNTEVVQKHTENIRVQDQKILQTFHALTEKYGETAVNDALLMSRINMNKPLTQRLAVQITECVKAADEGFINLK
IKSK

>g1hle.1 e.1.1.1 (A:,B:) Elastase inhibitor {Horse (Equus caballus)}

MEQLSTANTHFAVDLFRALNESDPTGNFISPLSISSALAMIFLGRGNTAAQVSKALYFDTVEDIHSRFQSLNADINKPGAPYILKLANRLYGEKTYNFL
ADFLASTQKMYGAE LASVDFQQAPEDARKEINEWVKGQTEGKIPELLVKGMVDNMTKLVNVNAIFKGNWQQKFMKEATRDAPFRLNKKDTKTV
KMMYQKKFPYNYIEDLKRVLLELPYQGKELSMIILLPDDEDESTGLEKIEKQLTLDKREWTKPENLYLAEVNVHLPFKLEESYDLTSHLARLGVQDL
FNRGKADLSGMSGARDLFVSKIIHKSFDLNEEGTEAAAATAGTILLAXEENFNADHPFIFFIRHNPSENILFLGRFSSP

>d1ovaa_ e.1.1.1 (A:) Ovalbumin {Hen (Gallus gallus)}

GSIGAASMEFCDFVKELKVHHANENIFYCPIAIMSALAMVYLGAKDSTRQINKVVRFDKLPFGDSIEACQGTSVN VHSSLRIDL NQITKPNDVYS
FSLASRLYAEERYPILPEYLQCVKELYRGGLEPINFQTAADQARELINSWVESQNTGIIRNVLQPSSVDSQTAMVLVNAIFKGLWEAKFKDEDTQAMP
FRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPFASGTMMSMLVLPDEVSGLEQLESIINFELTEWTSSNVMEEERKIKVYLP RMKMEEKYNLT
SVLMAMGITDVFSSSANLSGIISSAESLKISQAVHAAHAEINEAGREVVGSAEAGVDAASVSEEFRADHPFLFCIKHIATNAVLFFGRCVSP

>g1as4.1 e.1.1.1 (A:,B:) Antichymotrypsin, alpha-1 {Human (Homo sapiens)}

GLASANVDFAFSLYKQLVLKAPDKNVIFSPPLSISTALAFSLGAHNTTLEILKGLKFLNLTESEAEIHQS FQHLLRTLNQSSDELQLSMGNAMFVKEQLS
LLDRFTEDAKRLY GSEAFTDFQDSAAKKLINDYVKNGTRGKITDLIKDLSQTMMVLVNYIFFKAKWEMPFD PQDTHQS RFYLSKKWVMVPM
MSLHHLTIPYFRDEELSTVVELKYTGNA SALFILPDQDKMEEVEAMLLP ETLKRWRD SLEFREIGELYLPKFSISRDYNLNDILLQLGIEAFTSKADLSG
ITGARNLAVSQVVKHAKL DV FEEGTEASRATAVKITLLXGTIVRFNRFLMIIVPTDTQN IFFMSKV TNPKQ

>d1qlpa_ e.1.1.1 (A:) Antitrypsin, alpha-1 {Human (Homo sapiens)}

FNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGL
KLVDKFLEDVKKLYHSEAFTVNFGDTEEAKQINDYVEKGQTGKIVDLVKELDRDTVFALVNYIFFKGKWERPFEVKDTEEDFHVDQTTVKVPMM
KRLGMFNIQHCKLSSWVLLMKYLGNTAIFFLPDEGKQLQHLENELTHDIITKFLENEDRRSASLHLPLKSITGTYDLKSVLGQLGITKVFSNGADLSGV
TEEAPLKLASKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFLMIEQNTKSPLFMGKVVNPNTQK

>d1atta_e.1.1.1 (A:) Antithrombin {Cow (Bos taurus)}

VEDVCTAKPRDIPVNPMCIYRATEGGQSEQKIPGATNRRWELSKANSHFATAFYQHLADSKNNNDNIFLSPSISTAFAMTKLGACNNLTQLMEV
FKFDTISEKTSQDHFFFAKLNCRLYRKANKSSSELVSANRLFGDKSITFNETYQDISEVVGAKLQPLDFKGNAEQSRLTINQWISNKTEGRITDVIPPQAI
NEFTVLVNTIYFKGLWKSFKSPENTRKELYKADGESCSVLMQESKFRYRRVAESTQVLELPFKGDDITMVLILPKLEKTLAKVEQELTPDMLQE
WLDELTELTVVHMPRFRIEDSFVKEQLQDMGLELFSPEKSRLPGIVAEGRSDLYVSDAFHKAFLEVNEEGSEAAASTVIAGRSLRVTFKANRPFL
VLIREVALNTIIFMGRVANPCVD

>d1e05i_e.1.1.1 (I:) Antithrombin {Human (Homo sapiens)}

SPVDIRTAKPRDIPMNPMCIYRSPEKKATEDEGSEQKIPATNRRWELSKANSRFATTFYQHLADSKNDNDNIFLSPSISTAFAMTKLGACNDTLQ
QLMEVKFDTISEKTSQDHFFFAKLNCRLYRKANKSSKLVSANRLFGDKSITFNETYQDISEVVGAKLQPLDFKGNAEQSRAAINKWSNKTEGRITD
VIPSEAINELTVLVLVNTIYFKGLWKSFKSPENTRKELYKADGESCSASMMYQEGKFRYRRVAEGTQVLELPFKGDDITMVLILPKPEKSLAKVEKELTP
EVLQEWLDELEEMMLVHMPRFRIEDGFSLKEQLQDMGLVLDLFSPESKSLPGIVAEGRDDLYVSDAFHKAFLEVNEEGSEAAASTAVVIAGRSLNPN
RVTFKANRPFLVIREVPLNTIIFMGRVANPCV

>d1a7ca_e.1.1.1 (A:) Plasminogen activator inhibitor-1 {Human (Homo sapiens)}

HHPPSYVAHLASDFGVRVQQVAQASKDRNVVFSPYVASVLAQLQLTTGETQQQIAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTD
AIFVQRDLKLVQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKHTKGMISNLLKGAVDQLTRLVNVNLYFNGQWKTPFPDSSTHRRLFHKS
DGSTSVPMMMAQTNKFNYTEFTPDGHYYDILEPYHGDTLSMFIAAPYKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLE
NLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVIEVNESGTVESSSTAVIVSARMAPEEIIMDRPFLVVRHNPTGTVLFMGQVMEP

>d1by7a_e.1.1.1 (A:) Plasminogen activator inhibitor-2 {Human (Homo sapiens)}

EDLCVANTLFALNLFKHLAKASPTQNLFLSPWSISSTMAMVYMGSRGSTDQMAKVLFQNEVGAAADKIHSFRSLSAINASTGNYLLESVNKLFG
EKASFREYYIRLCQKYYSEPVQADFLECAEEARKKINSWVKTQTKGKIPNLLPEGSDGDTRMVLVNAVYFKGKWKTPFEKKLNGLPFRVNSAQR
TPVQMMYLREKLNIGYIEDLKAQILELPYAGDVSFMFLLPDEIADVSTGLELLESEITYDKLNKWTSDKMAEDEVVEVYIPQFKLEEHYELRSILRSMG
MEDAFNKGRANFSGMSERNDLFLSEVFHQAMVDVNEEGTEAAAGTGGVMTGRTGHGGPQFADHPFLIMHKITNCILFFGRFSSP

>g1jjo.1 e.1.1.1 (A.;C.;E;) Neuroserpin {Mouse (Mus musculus)}

TITEWSVNMYNHRLRTGEDENILFSPLSIALAMGMMELGAXENQYVMKLANSLFVQNGFHVNNEEFLQMLKMYFNAEVNHVDFSQNAVANSINKW
KVENYTNSLLKDLVSPEDFDGVTNLALINAVYFKGNWKSQFRPENTRTFSFTKDDSEEVQIPMMYQQGEFYGEFSDGSNEAGGIQVLEIPYEG
DEISMMLALSQRQEVPLATEPLLKAQLIEWANSVKKQKVEVYLPRTVEQEIDLKDLKALGVTEIFIKDANLTAMSDKKELFLSKAVHKSCIEVNEEGS
AAAAASGMIAISXPQVIVDHPFLYLIRNRKSGIIFMGRVMNPHH

>d1sek_e.1.1.1 (-) Serpin K {Tobacco hawkmoth (Manduca sexta)}

GETDLQKILRESNDQFTAQMFSSEVVKANPGQNVLASFVLPPLGQLALASVGESHDELLRALALPNDNVTKDVFADLNRGVRAVKGVDLKMASKI
YVAKGLELNDFAAVSRDVGSEVQNVDFVKSVEAGAAGAINWVVEDQTNRIRKNLVDPPDALDETRSVLVAIFKGWSWDKFNKERTMDRDFHVS
KDKTIKVPTMIGKKDVRYADPELDAKMIEMSYEGDQASMIIILPNQVDGITALEQKLKDPKALSRAEERLYNTEVEIYLPKFKIETTDLKEVLSNMNI
KKLFTPAGARLENLLKTKESLYVDAAIQKAFIEVNEEGAEAAAANAFKITTYSFHFVPKVEINKPFFSLKYNRNSMFSGVCVQP

>d1k9oi_e.1.1.1 (I:) Alaserpin (serpin 1) {Tobacco hornworm (Manduca sexta)}

GETDLQKILRESNDQFTAQMFSSEVVKANPGQNVLASFVLPPLGQLALASVGESHDELLRALALPNDNVTKDVFADLNRGVRAVKGVDLKMASKI
YVAKGLELNDFAAVSRDVGSEVQNVDFVKSVEAGAAGAINWVVEDQTNRIRKNLVDPPDALDETRSVLVAIFKGWSWDKFNKERTMDRDFHVS
KDKTIKVPTMIGKKDVRYADPELDAKMIEMSYEGDQASMIIILPNQVDGITALEQKLKDPKALSRAEERLYNTEVEIYLPKFKIETTDLKEVLSNMNI
KKLFTPAGARLENLLKTKESLTVDAAIQKAFIEVNEEGAEAAAANAFGIVPKSLILYPEVHIDRPFYFELKIDGIPMFNGKVIEP

>g1f0c.1 e.1.1.1 (A.;B;) Viral serpin crmA (cytokine response modifier protein) {Cowpox virus}

MDIFREIASSMKGGENVFISPPSISSVLTILYYGANGSTAEGQLSKYVEKEADKNKDDISFKSMNKVYGRYSAFKDSFLRKIGDNFQTVDFDCRTVDAIN
KCVDFTEGKINPLLDEPLSPDTCLLAISAVYFKAKWLMPEKEFTSDYPFYVSPTEMVDSMMSMYGEAFNHASVKEFGNFSIIELPYVGDTSMVVI

LPDNIDGLESIEQNLTDTNFKKWCDSDAMFIDVHIPFKVTGSYNLVDALVKLGLTEVGSTGDYSNCNSDVSVDAMIHKTYIDVNEEYTEAAAA
TCALVADCACTVTNEFCADHPFIYVIRHVDGKILFVGRYCSPTTN
>d1imva_e.1.1.1 (A:) Rgiment epithelium-derived factor, PEDF {Human (Homo sapiens)}
TGALVEEEDPFFKVPVNKLAAAVSNFGYDLYRVRSSMSPTTNVLSPSVALTALSALSGADERTEIIRALYYDLISSPDIHGTYKELLDVTAPQKNLK
SASRIVFEKKLRLKRSSFVAPLEKSYGTRPRVLGNPRLDLQEINNWVQAQMKGKLRSTKEIPDEISILLGVAFKGQWVTKFDSRKTSLEDFYLDER
TVRVPMMSDPKAVLRYGLDSLCKIAQLPLTGSMSIIFFLPLKVTQNLTLIEESLTSEFIHDIDRELKTVQAVLTVPLKLSYEGEVTKSLQEMKLQLSD
SPDFSKITGKPIKLTQVEHRAGFEWNEDGAGTPSPGLQPAHLTFPLDYHNLNQPFIFVLRDFTGALLFIGKILDPRGP
>d1ecra_e.2.1.1 (A:) Replication terminator protein (Tus) {Escherichia coli}
DLVDRLLNTFRQMEQELAIFAHHLEQHKLLVARVFSLPEVKKEDEHNPLNRIEVKQHGLNDAQLSLRHFRHLFIQQQSENRSSKAAVRLPGVLCYQV
DNLSQAALVSHIQHINKLKTTFEHIVTVESELPTAACRFEWVHRHLPGLITLNAYRTLTVLHDPAATRFGWANKHIIKNLHRDEVLAQLEKSLKSPRSVAP
WTREEWQRKLEREYQDIAALPQNAKLKIKRPVKVQPIARVWYKGDQKQVHACPTPLIALINRDNGAGVPGELLNYDADNVQHRYKPQAQPL
RLIIPRLHLYVAD
>d1es5a_e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., K15}
KPTIAAVGGYAMNNGTGTTLYTKAADTRRSTGTTKIMTAKVVLAQSNLNLDAKVTIQKAYSODYVVANNASQAHILVGDKVTVRQLYGLMLPSGCD
AAAYALADKYGSGSTRAARVKSFIGMNTAATNLGHNTFDSDFGIGNGANYSTPRDLTIASSAMKNSTFRVVKTAKTAKTVKTGSIRTMDTW
KNTNGLSSYSGAIGVKTGAGPEAKYCLVFAATRGKTVIGTVLASTSIPARESDATKIMNYGFAL
>d1hvba_e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., R61}
DLPADDDTGLQAVLHTALSQGAPGAMVRVDDNGTIHQLSEGIVADATGRAITTDTRFRVGSVTKFSAVVLLQLVDEGKLDLDASVNTYLPGLPDD
RITVRQVMSHRSGLYDYTNMDFAQTVPGFESVRNKVFSYQDLITLSKHGVTNAPGAAYSNTNFVAVGMLIEKLTGHSVATEYQNRIFTPLNLDT
FVYHPDTVPIGTHANGYLTPEAGGALV DSTEQTVSWAQSAGAVISSTDQLDTFFSALMSGQLMSAAQLAQMQQWTTVNSTQGYGLGLRRRDL
CGISVYGHGTQVQGYTYAFASKDGKRSVTALANTSNNVNLNTMARTLESAFCGKP
>d1ci9a_e.3.1.1 (A:) Esterase EstB {Burkholderia gladioli}
AASLAARLDVFQALRERRLVGAVAIVARHGEILYRRAQGLADREAGRPMREDTLFRLASVTKPIVALVRLVARGELALDAPVTRWLPEFRPRLA
DGSEPLVTIHLLHTSGLGYWLLEGAGSVYDRLGISDGIDLRFDLDENLRRLASAPLSFAPGSGWQYSLALDVLAGVERATGQPLAAVADALVAQ
PLGMRDCGFVSAEPPERFAPVYHDGQPEPVMRDGIEVPLPEGHGAAVRFAPSrvFEPGAYPSGGAGMYGSADDVRLALEAIRANPGFLPETLADA
ARRDQAGVGAETRGPGWGFGYLSA VLDPAAGTPQHAGTLQWGGVYGHWSFVDRALGLSVLLNTAYEGMSGPLTIALRDAVYA
>d1bt1_e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TEM-1}
HPETLVKVDAEDQLGARVGYIELDLSGKILESFRPEERFPMNSTFKVLLCGAVLSRIDAGQEQLGRRIHYSQNDLVEYSPVTEKHTDGMTVRELCS
AAITMSDNTAANLLTIGGPKELTAFLHNMGDHVTRLDRWEPELNEAIPNDERDTMPVAMATTRKLLTGEELTLASRQQLIDWMEADKVAGPL
LRSALPAGWIFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTGSQATMDERNRQIAEIGASLIKHW
>d1bza_e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TOHO-1}
SVQQQLEAKEKSSGGRLGVALINTADNSQILYRADERFAMCSTSJKVMAAAAVLKQSES DKHLLNQRVEIKKSDLVNYNPIAEKHVNGTMTLAELGAA
ALQYSDNTAMNKLI AHLGGPDKVTA FARS LGDETFR LDRTAP TLNTAIPGDPRD TTP LAMA QTLKNL TGK ALA ETQRAQ LVT WLKG NT GSASIRA
GLPKSWVVGDKGSGDY GTTNDIAVIW PENHAPL VLVTYFTQPEQKAERRD ILAAA AKIV
>d1g56a_e.3.1.1 (A:) beta-Lactamase, class A {Klebsiella pneumoniae, SHV-1}
SPQPLEQIKLSESQLSGRVGMIEMDLASGRTLTAWRADERFPMNSTFKVVLCAVLRDAGDEQLERKIHYRQQDLDYSPVSEKHLADGMTVG
ELCAA ITMSDNAA NLLATVGGPAGLTAFLRQIGDNVTRLDWETELNEALPGDARDTTTPASMAATLRKLLTSQRLSARSQRQLQWMVDDRV
AGPLIRSVPAGWIFIADKTGAGERGARGIVALLGPNNKAERIVVYIYLRTDPASMAERNQQIAGIGAALIEHWQR
>d1g6aa_e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PSE-4 carbenicillinase}
SKFQQVEQDVKAIEVLSARIGVSVLDTQN GYEWDYNGNQRFLTSTFKTIACAKLLYDAEQGKVNPNSTVEIKKADLVYSPVIEKQVGQAITLDDA
CFATMTTSDNTAANII SAVGGPKGVDFLRQIGDKETRLDRIEPDLNEGKLGLDRD TTPKAIASTLNKFLFGSALSEM NQKKLESWMVNNQVTGN
LLRSVLPAGWNIADKSGAGGF GARSITAVVWSEHQAPIIVSIYLAQTQASMEERND AIVKIGH SIFDVYTS
>d1alq_e.3.1.1 (-) beta-Lactamase, class A {Staphylococcus aureus}
SEPIVLFITNKDNKSDKPNDKLISETAKSVMKEFAAGSKNAAKELNDLEKKYNAHIGVYALDTKSGKEVKFN SDKRFAYASTSKAINSAILLEQV PYNKL

NKKVHINKDDIVAYSPILEYVGKDITLKALIEASMTYSDNTANNKIIKEIGGIKKVKQLKELGDKVTNPVRYEIELNYYSPSKKDTSTPAAFGKTLNKLI
ANGKLSKENKKFLDLMLNNKSGDTLIKDGVPKDVKADKSGQAITYASRNDVAFVYPK

>d1ghpa_ e.3.1.1 (A:) beta-Lactamase, class A {Staphylococcus aureus}

KELNDLEKKYNAHIGVYALDTKGKEVKFNSDKRFAYASTKAINSAILLEQPVYNLNKKVHINKDDIVAYSPILEYVGKDITLKALIEASMTYSDNTA
NNKIIKEIGGIKKVKQLKELGDKVTNPVRYDIELQYYSPSKKDTSTPAAFGKTLNKLIAKGKLSKENKKFLDLMLNNKSGDTLIKDGVPKDVKADK
SGQAITYASRNDVAFVYPKGQSEPIVLVIFTNKNKSDKPNDKLISETAKSVMKEF

>d4blma_ e.3.1.1 (A:) beta-Lactamase, class A {Bacillus licheniformis}

DDFAKLEEQFDAKLGIFALDTGTNRTVAYRPDERFAFASTIKALTGVLLQQKSIEDLNQRITYTRDDLNVNYNPITEKHVDGMLKELADASLRYSDNA
AQNLILKQIGGPESLKKELRKIGDEVTNPERFEPELNEVNPGTQDTSTARALVTSRALFALEDKLPSEKRELLIDWMKRNTGDALIRAGVPDGWEVA
DKTGAASYGTRNDIAIIWPPKGDPVVAVLSSRDKKDAKYDDKLIAEATKVMKALN

>d1buea_ e.3.1.1 (A:) beta-Lactamase, class A {Enterobacter cloaceae, NMC-A carbapenemase}

NTKGIDEIKNLETDFNGRIGVYALDTGSGKSFSYRANERFPLCSSFKGLAAVLKGSQDNRLNQNIVNYNTRSLEFHSPITTKYKDNGMSLGDMAA
AALQYSDNGATNIILERYIGGPEGMTKFMRSIGDEDFRLDRWEELNATAIPGDERDTSTPAAVAKSLKTLALGNILSEHEKETYQTWLKGNTTGAARIR
ASVPSDWVVGDKTGSCGAYGTANDYAVVWPKNRAPLISVYTTKNEKEAKHEDKVIAEASRIAIDNLK

>d1bsg_ e.3.1.1 (-) beta-Lactamase, class A {Streptomyces albus G}

SDAERRLAGLERASGARLGVYAYDTGSGRTVARYRADELFPMCSVFKTLSSAAVLRDLDRGEFLSRRILYTQDDVEQADGAPETGKPQNLANGMTV
EELCEVSITASDNCAANLMLRELGGPAAVTRFVRSLGDRVTRLRWEPELNSAEPGRVTDTSPRAITRTYGRVLGDAALNPRDRLLTSWLLANTTS
GDRFRAGLPPDDWTLDKTGAGRYGTNNDAGVTWPPGRAPIVLTVLAKTEQDAARRDGLVADAARVLAETLG

>d1mfoa_ e.3.1.1 (A:) beta-Lactamase, class A {Mycobacterium fortuitum}

APIDDQLAELERRDNVLIGLYAANLQSRRITHRPDEMFMACSTFKGYVAARVLQMAEHGEISLDNRVFVDADALVPNSPVTEARAGAEMTLAELC
QAALQRSDNTAANLLLTIIGGAAVTAFARSVGDERTRLDRWEVELNSAIPGDPRTSTPAALAVGYRAILAGDALSPPQRGLLEDWMRANQTSSM
RAGLPEGWTTADKTGSGDYGSTNDAGIAFGPDGQRLLVMMTRSQAHDPKAENLRPLIGELTALVPLSLL

>d1e25a_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PER-1}

SPLLKEQIESIVGKKATVGAVWGPDDLEPLLINPFEKFPMQSVFKLHLAMILVLHQVDQGKLDLNQTVIVNRAKVLQNTWAPIKAYQGDEFSPV
QQLLQYSVSHSDNVACDLLFELVGGPAALHDYIQSMGIKETAVVANEAMHADDQVQYQNWTSMKGAAEILKKFEQKQLSETSQALLWKWMV
ETTGPERLKGLLPAGTVVAHKTGTTSQIKAGKTAATNDLGIILLPDRPPLAVFKDSAESSRTNEAIIAQVAQTAYQFELKKLSAL

>d1dy6a_ e.3.1.1 (A:) beta-Lactamase, class A {Serratia marcescens, Sme-1}

NKSDAAKQIKKLEEDFDGRIGVFAIDTGSNTFGYRSDERFPLCSSFKGLAAVLERVQQKKLDINQKVYESRDLLEYHSPITTKYKGSGMTLGDM
ASAALQYSDNGATNIIMERFLGGPEGMTKFMRSIGDNFRLDRWELELNTAIPGDKRTSTPKAVANSLNKLALGNVLNAKVKAIYQNWLKGNTTG
DARIRASVPADWVVGDKTGSCGAYGTANDYAVIWPKNRAPLIVSIYTRKSKDDKHSKDTIAEASRIAID

>d1fr1a_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Citrobacter freundii}

AAKTEQQIADIVNRTITPLMQEQAIIPGMAVAVIYQGKPHYYFTWGKADIANRNPVTQQLFELGSVSFTFNGVLGGDAIARGEIKLSDPTQYWPELT
GKQWQGISLLHLATYTAGGLPLQVPDDVTDKAALLRFYQNWPQWAPGAKRLYANSSIGLFGALAVKPSGMSYEAMS KRVLHPLKLAHTWITVP
QSEQKDYAWGYREGKPVHVSPGQLDAEAYGVKSSVIDMTRWVQANMDASQVQEKTQLQQGIELAQSRYWRIGDMYQGLGWEMLNWPVKADSI
ISGSDSKVALAALPAVEVNPPAPAVKASWVHKTGSTGGFGSYVAFVPEKNLGIVMLANKSYPNPVRVEAAWRILEKLQ

>d1ga0a_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Enterobacter cloacee, P99, cephalosporinase}

PVSEKQLAEVVANTVTPLMKAQSVPGMAVAVIYQGKPHYYFTFGKADIAANKPVTPTQTLFELGSISKTFGVLGDAIARGEISLDDPVTRYWPQLTG
KQWQGIRMLLATYTAGGLPLQVPDEVTDNASLLRFYQNWPQWPGTTRLYANASIGLFGALAVKPSGMPYEQAMTRVLKPLKLDHTWINVP
KAAEEAHYAWGYRDGKAVRAVRVSPGMILDAQAYGVKTNVQDMANWVMANMAPENVADASLKGQIALAQSRYWRIGSMYQGLGWEMLNWP
VEANTVVEGSDSKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIEPKQIGIVMLANTSYPNPVRVEAAWRIEKLQ

>d1i5qa_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Escherichia coli, cephalosporinase}

APQQINDIVHRTITPLIEQQKIPGMAVAVIYQGKPHYYFTWGYADIACKQPVTQQTLFELGSVSFTFVGVLGGDAIARGEIKLSDPTT KYWPELTAKQW
NGITLLHLATYTAGGLPLQVPDEVKSSDLLRFYQNWPQWAPGQTQRLYASSIGLFGALAVKPSGMSFEQAMQTRVFQPLKLNHTWINVPPAEEKN
YAWGYREGKAVHVSPGALDAEAYGVKSTIEDMARWVQSNLKPPLDINEKTLQQGIQLAQSRYWQTGDMYQGLGWEMLDWPVNPDSDIINGSDNKI

ALAARPVKAITPPTPAVRASWVHKTGATGGFGSYVAFIPEKELGIVMLANKNYPNPARVDAAWQILNALQ

>d1k55a_e.3.1.1 (A:) Class D beta-lactamase {Pseudomonas aeruginosa, OXA-10}

SITENTSWNKEFSAEAVNGVFVLCKSSKCATNDLARASKEYLPASTFKIPNAIIGLETGVKNEHQVFKWDGKPRAMQWERDLTRGAIQVSAVP
VFQQIAREVGEVRMQKYLKKFSYGNQNISGGIDKFVLEGQLRISAVNQVEFLESLYLNKLSASKENQLIVKEALVTEAAPEYLVHSKTGFSGVGTESNP
GVAWWVGWVEKETEVYFFAFNMDIDESKLPLRKSIPTKIMESEGIIG

>d1k25a4 e.3.1.1 (A:264-631) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain {Streptococcus pneumoniae}

TLSSPLQSFMETQMADFLEVKKGKYMATTLSAKTGEILATTQRPTFNADTKEGITEDFVWRDILYQSNSYPEGSAMKVMTLASSIDNNTPSGEYFNS
SELKIADATTRDWDVNNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKFVGPTRFLTDEYAGQLPADNIVSIAQSSFGQQGISVT
QTQMLRAFTAIAANDGVMLEPKFISAIYDTNNQSVRSQKEIVGNPVSKEAASSTRNHMILVGTDPYGTMYNHTGKPIITVPGQNVAVKSGTAQIA
DEKNGGYLVGSTNYIFSATMNPAPENPDFILYVTVQQPEHYSQIQLGEFATPILERASAMKESLNQSPAQNLDKVT

>d1qmea4 e.3.1.1 (A:264-620) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain {Streptococcus pneumoniae}

TISSPLQSFMETQMADFQEVKKGKYMATTLSAKTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNSYPEGSTMKVMMMLAAIDNNTPGGEVF
NSSELKIADATTRDWDVNNEGLTTGGMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLKRKFVGPTRFLTDEYAGQLPADNIVSIAQSSFGQQGI
SVTQTQMIRFTAIAANDGVMLEPKFISAIYDPNDQTARKSQQKEIVGNPVSKAASLRTNMVLVGTDPYGTMYNHTGKPTVTPGQNVALKSGT
AQIADEKNNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSQIQLGEFANPILERASAMKDSLNL

>d1hd8a2 e.3.1.1 (A:3-262) Penicillin-binding protein 5, N-terminal domain {Escherichia coli}

LNIKTMIPGVPQIDAESYILIDYNSGKVLAEQNADVRRDPASLTKMMTSYVIGQAMKAGFKETDLVTIGNDAWATGNPVFKGSSLMFLKPGMQVP
VSQSLIRDINLQSGNDACVAMADFAAGSQDAFVGLMNSYVNALGLKNTFHQTQVHGLDADGQYSSARDMALIGQALIRDVPNEYSIYKEEFTFNGIR
QLNRNGLLWDNSLNVDGIKTGHTDKAGYNLVASATEGQMRLISAVMGGRTFKGREAESKKLTWGFRF

>d1ei5a3 e.3.1.1 (A:3-335) D-aminopeptidase, N-terminal domain {Ochrobactrum anthropi}

KFDTSALEAFVRHIPQNYKGPGGVAVVKGDEVVLQHAWGFADLRTTPMTLDTRMPICSFSKQFTCAVLLDAVGEPELDDALEAYLDKFEDERPA
VRDLCNNQSLR DYWALSVLCGADPEGVFLPAQASLRLKTTHFEPGSHSYCNGNFRILADLIEAHTGRTLV DILSERIFAPAGMKRAELISDTALF
DECTGYEGDTVRGFLPATNRIQWMGDAGICASLNDMIAWEQFIDATRDESGLYRRLSGPQTFKDGVAAPYGFGLNLHETGGKRLTGHGGALRG
WRCQRWHCADERLTIAMFNFEGGASEVAFKLMNIALGVSSS

>d1lbea_e.4.1.1 (A:) ADP ribosyl cyclase {Sea hare (Aplysia californica)}

IVPTRELENVFGRCKDYIETRYLDILPVRSDCSALWKDFFKAFSKNPQCDLGSYKDFTSAQQQLPKNKVFMWSGVYDEAHDYANTGRKYITLE
DTLPGYMLNSLVWCGQRANPGFNEKVCPDFKTCPVQARESFWMGASSSYAHSAEGETYMDGSNPKVPAYRPDSFFGKYELPNLTNKVTRVKVI
VLHLRGEKIEKCGAGSLLDLEKLVAKAHFAFDCVENPRAVLFLCSNDNPNARECRL

>d4blca_e.5.1.1 (A:) Catalase I {Cow (Bos taurus)}

NRDPASDQMHWKEQRAAQKPDVLTTGGGNPVGDKLNSLTVGPRGPLLVQDVFTDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITRYSKA
KVFEHIGKRTPIAVRFSTVAGESGADTVRDPRGFAVKFYTEDGNWDLVGNNTPIFFIRDALLFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLH
QVSFLFSDRGIPDGHRHMGDYGSHTFKLVNADGEAVYCKFHYKTDQGIKNLSVEDAARLAHEDPDYGLRDLFNIAITGNYPSWTLYIQVMTFSEAEI
FPFPNPFDLTKVWPHGDYPLIPVGKLVLNRPVNYFAEVEQLAFDPSNMPPGIEPSPDKMLQGRLFAYPDTHRHLGPNYLQIPVNCPYRARVANYQ
RDGPMCMMDNQGGAPNYYPNFSAPEHQPSALEHRTFSGDVQRFNSANDDNTQVRTFYLKVLNEEQRKRLCENIAGHLKDAQLFIQKKAVK
NFSDVHPEYGSRIQALLDKYNE

>d1dgfa_e.5.1.1 (A:) Catalase I {Human (Homo sapiens)}

RDPASDQMHWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVFTDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAK
VFEHIGKRTPIAVRFSTVAGESGADTVRDPRGFAVKFYTEDGNWDLVGNNTPIFFIRDPLFSPSIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQ
VSFLFSDRGIPDGHRHMGDYGSHTFKLVNANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGRDLFNIAITGKPSWTFYIQVMTFNAETF
PFNPFDLTKVWPHKDYPLIPVGKLVLNRPVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHLGPNYLHIPVNCPYRARVANYQ
DGPMCMMDNQGGAPNYYPNFSAPEHQPSALEHSIQYSGEVRFTNANDDNTQVRTFYLKVLNEEQRKRLCENIAGHLKDAQLFIQKKAVKNF
TEVHPDYGSHIQALLDKYNE

>d1a4ea_e.5.1.1 (A:) Catalase I {Baker's yeast (Saccharomyces cerevisiae)}

DVREDRVVTNSTGNPINEPFVTQRIGEHGPLLQDYNLIDS LAHFNRNIPQRNPHAHGSGAFGYFEVTDDITDICGSAMFSKIGKRTKCLTRFSTVG

GDKGSADTVRDPNGFATKFYTEEGNLDWVNNTPVFFIRDPSKFPHIHTQKRNPQTNLRADMFWDLTTENQVAIHQVMILFSDRGTPANYR
SMHGYSGHTYKWSNKNGDWHYVQVHIKTDQGIKNLTIEEATKIAGSNPDYCQQDLFEAIQNGNYPSTVYIQTMTERDAKKLPFSVFDLTKVWP
QQQFPLRRVGKIVLNENPLNFFAQVEQAFAFPSTVYQEASADPVLQARLFSYADAHRYRLGPNFHQIPVNCPYASKFFNPAIRDGPVNNGNFG
SEPTYLANDKSYTIQQDRPIQQHQEVWNGPAIPYHWATSPGDVDFVQARNLYRVLGKPGQQKNLAYNIGHVEGACPOIQQRVYDMFARVDK
GLSEAIKKVAE

>d1e93a_e.5.1.1 (A:) Catalase I {Proteus mirabilis}

KKLTTAAGAPVVDNNNVITAGPRGPMLLQDVWFLAKLAHDREVIPERRMHAKGSGAFGTFTVTHDITKYTRAKIFSEVGKKTEMFARFSTVAGER
GAADAERDIRGFALKFYTEEGNWDMVGNNTPVFYLRDPLKFPLDNHIVKRDPRTNMRNMAYKWDFSHLPESLHQQLTIDMSDRGLPLSYRFVHGF
GSHTYSFINKDNERFWVKFHFRCCQQGIKNLMDDEAEALVGKDRESSQRDLFEAIKRGDYPRWKLQIQIMPEKEASTVPYNPFDLTKVWPHADYPL
MDVGYFELNRNPNPDNYSDVEQAAFPANIVPGISFSPDKMLQGRLFSYGDAHYRLGVNHQIPVNAPKCPFHNYHRDGAMRVDGNNSGNGITYE
PNSSGGVFQEQQPDFKEPLSIEGAADHWNHREDEDYFSQPRALYESELLSDEHQRMFARIAGELSQASKETQQRQIDLFTKVHPEYAGVEKAIVLE

>d1hbza_e.5.1.1 (A:) Catalase I {Micrococcus lysodeikticus}

TTPHATGSTRQNGAPAVSDRQSLTVGSEGPIVLHDTHLLETHQHFNRNMNIPERRPHAKGSGAFGEFEVTEDVSKYTKALVFQPGTKTETLLRFSTVAG
ELGSPDTWRDVRGFALRFYTEEGNYDLVGNNTPIFFLRDPMKFTFIRSQKRLPDGLRDATAQMWDFTNNPESAHQVTYLMGPRGLPRTWRE
MNGYGSHTYLWVNAQGEKHVVKYHFISQQGVHNLSNDEATKIAGENADFHRQDLFESIAKGKDHPKWDLYIQAIPYEEGKTYRFNPFDLTKTISQKD
YPRIKVGTTLNRNPKNHFAQIESAAPSNTVPGIGLSPDRMLLGRAFAYHDAQLYRVAHVNLQPVNPVPNPKNAVHNAYFEGQMWYDHTGDRSTY
VPNSNGDSWSDETGPVDDGWEADGTLREAQALRADDDFGQAGTLVREVFSQERDDFVETVAGALKGVQARDVQARAFEWKNVDATIGQRI
EDEVKRHEGDGIPGVAGGEARI

>d1cf9a2 e.5.1.1 (A:27-597) Catalase II {Escherichia coli, HPII}

DSLAPEDGSHRPAAEPTPPGAQPTAPGSLKAPDTRNEKLNLEDVRKGSENYALTTNQGVRIADDQNSLRAGSRGPTLLEDIFLREKITHFDHERIPE
IVHARGSAAHGYFQPYKSLSDITKADFLSDPNKITPVFVRFSTCQGGAGSADTVRDIRGFATKFYTEEGIFDLVGNNTPIFFIQDAHKFPDFVHAVKPEP
HWAIPOQGQSAHDTFWDYVSLQPETLHNVMWAMSDRGIPRSYRTMEGFGIHTFRLINAEGKATVFRHWKPLAGKASLVWDEAQKLTGRDPDFH
RRELWEAIEAGDFPEYELGFLQIPEEDEFKFDLDPKLIPEELVPVQRVGKMLNRNPDNFAENEQAAFHPGHIVPGLDFTNDPLQGRLFSYT
DTQISRLGGPNFHEIPNRTCPYHNFQRDGMHRMGIDTNPANYEPNSINDNWPRETPPGPKRGGFESYQERVEGNKVRERSPSFGEYYSHPRLF
WLSQTPFEQRHIVDGFSFELSKVVRPYIRERVVDQLAHIDLTLAQAVAKNLGIETDDQLNITPPDVNGLKKDPSLSSYAIQDGD

>d1buca2 e.6.1.1 (A:1-232) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}

MDFNLTDIQQDFLKAHDGEKKLAPTVTERDHKGYDKELELLSLGITGAYFEEKYGGSGDDGGDVLSYILAVEELAKYDAGVAITLSATVSLCANPI
WQFGTEAQKEKFLVPLVEGTKLGAFLTEPNAGTDASGQQTIATKNDGTYTLNGSKIFITNGGAADIYIVFAMTDKSKGNHGITAFILEDGTGPGFT
GKKEDKMGMIHTSQTMELVFQDVKVAENMLGEE

>d1jqia2 e.6.1.1 (A:4-234) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus)}

YVQSVELPETHQMLRQTCRDFAEKELVPIAAQLDKEHLFPTSQVKKMGEGLLAMDVPEELSGAGLDYLAYSIAEEISRGCASTGVIMSVNNSLYLG
ILKFGSSQQKQQWITPFTNGDKIGCFALSEPGNGSDAGAASTTAREEGDSWVLNGTKAWITNSWEASATVVFASTDRSRQNKGISAFLVPMPTPGL
TLGKKEDKLGIRASSTANLIFEDCRIPKENLLGEPG

>d3mdda2 e.6.1.1 (A:11-241) Medium chain acyl-CoA dehydrogenase {Pig (Sus scrofa)}

GFSFELTEQQKEFQATARKFAREEIIIPVAAEYDRTGEYPVPLLKRAWELGLMNTHIPESFGGLGLGIIDSCLITEELAYGCTGVQTAIEANTLGQVPLIIGG
NYQQQQKKYLGRMTEEPLMCAYCTEPGAGSDVAGIKTKAEKKGDEYIINGQKMWITNGGKANWYFLARSDDPDKAPASKAFTGFIVEADTPGVQ
IGRKELNMGQRCSDTRGIVFEDVRVPKENVLTGE

>d1egda2 e.6.1.1 (A:10-241) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens)}

LGFSFETEQQKEFQATARKFAREEIIIPVAAEYDRTGEYPVPLIRRAWELGLMNTHIPENCGGLGLGFDACLISEELAYGCTGVQTAIEGNSLGQMPIII
AGNDQQKKYLGRTMEEPLMCAYCTEPGAGSDVAGIKTKAEKKGDEYIINGQKMWITNGGKANWYFLARSDDPDKAPASKAFTGFIVEADTPG
IQIGRKELNMGQRCSDTRGIVFEDVKVPKENVLTGE

>d1ivha2 e.6.1.1 (A:6-241) Isovaleryl-coa dehydrogenase {Human (Homo sapiens)}

VDDAINGLSEEQRQLRQTMKFLQEH LAPKAQEIDRSNEFKNLREFWKQLGNLGLVLTAPVQYGGSGLGYLEHVLVMEISRASGA VGLSYGAHS
NLCINQLVRNGNEAQKEKYLPLKISGEYIGALAMSEPAGSDVVSMLKAEEKGNHYI LNGNKFWITNGPDADVLIVYAKTDLAAVPASRGITA FIVE

KGMPGFSTSKLDKLGMRGSNTCELIFEDCKIPAANILGHEN

>d1frpa_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Pig (*Sus scrofa*)}

NIVTLTRFVMEQGRKARGTGEQTQLLNSLCTAVKAISTAVRKAGIAHYGIAGATNVTGDQVKKLDVLSNDLVINVLKSSFATCBLVTEEDKNAIIVEPE
KRGKYVVCFDPLDGSSNIDCLVSIGTIFGIYRKNSTDEPSEKDALQPGRNLVAAGYALYGSATMLVLAMVNGVNCMILDPAIGEFILVDRNVKIKKKGSI
YSINEGYAKEFDPAITEYIQRKKFPPDNSAPYGARYVGSMVADVHRTLVYGGIFMYPANKSPKGKLRLLYECNPMAVYMEKAGGLATTGKEAVLDIV
PTDIHQRAPIILGSPEDVTELLEIYQKHA

>d1ftaa_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Human (*Homo sapiens*)}

DVVTLTRFVMEEGRKARGTGEQTQLLNSLCTAVKAISAVRKAGIAHYGIAGSTNVTGDQVKKLDVLSNDLVNMNLKSSFATCBLVSEEDKHAIIVEPE
EKRGKYVVCFDPLDGSSNIDCLVSIGTIFGIYRKKSTDEPSEKDALQPGRNLVAAGYALYGSATMLVLAMDCGVNCMILDPAIGEFILVDKVKIKKKG
KIYSLNEAYAKDFDPAVTEYIQRKKFPPDNSAPYGARYVGSMVADVHRTLVYGGIFLYPANKSPNGKLRLLYECNPMAVYMEKAGGMATTGKEAVL
DVIPTDIHQRAPIILGSPDDVLEFLKVYEKHS

>d1bk4a_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Rabbit (*Oryctolagus cuniculus*)}

FDTDISTMTRFVMEEGRKAGGTGEQTQLLNSLCTAVKAISTAVRKAGIAHYGIAGSTNVTGDQVKKLDVLSNDLVNMNLKSSFATCBLVSEEDKNAI
IVEPEKRGKYVVCFDPLDGSSNIDCLVSIGTIFGIYRKKSTDEPSTKDALQPGRNLVAAGYALYGSATMLVLAGGSGVNSFMLDPAIGEFILVDKNVKIKK
KGNIYSLNEGYAKDFDPAVTEYIQRKKFPPDNSSPYGARYVGSMVADVHRTLVYGGIFLYPANKSPDGKLRLLYECNPMAFIMEKAGGMATTGKEAI
LDIVPTDIHQRAPVILGSPDDVQEFLIEYKKHAVK

>d1spia_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Spinach (*Spinacia oleracea*)}

AATQTKARTRSKYEIETLTGWLLKQPMAGVIDAELTIVLSSISMACKQIASLVQRAGISNLTIQGAVNIQGEDQKKLDVISNEVFSNCLRSGRTGIIASEEEDVPVAV
EEDVPVAVEESYSGNYIVVFDPLDGSSNIDAATVTSIFGIYSPNDECIVDSHDDESQLSAEEQRCVVNVQCQPGDNLLAAGYCMYSSVIFVLTIGKG
VYAFALDPMYGEFLTSEKIQPKAGKISFNNEGNYKMWPDKLKYMDDLKEPGESQPKYSSRYIGSLVGFHRTLLYGGIYGYPRDAIKSKNGKLRLLY
ECAPMSFIVEQAGGKGSDGHQRILDIQPTIEHQRPVLYIGSVEEVEKLEYLA

>d1dcua_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Garden pea (*Pisum sativum*)}

KRSGYEIITLTSWLLQQEQKGIDAEITIVLSSISMACKQIASLVQRANISNLGTQGAVNQGEDQKKLDVISNEVFSNCLRSGRTGIIASEEEDVPVAV
EESYSGNYIVVFDPLDGSSNLDAAVSTGSIFGIYSPNDECILPQDFGDDSDNTLGTEEQRCIVNVQCQPGDNLLAAGYCMYSSVIFVLTIGKG
VYAFALDPMYGEFLTSEKIQPKAGKISFNNEGNYKMWPDKLKYMDDLKEPGESQPKYSSRYIGSLVGFHRTLLYGGIYGYPRDAIKSKNGKLRLLY
ECAPMSFIVEQAGGKGSDGHQRVLDIOPTEIHQRPVLYIGSVEEVEKLEYLA

>d2hhma_e.7.1.1 (A:) Inositol monophosphatase {Human (*Homo sapiens*)}

WQECMDYAVTLARQAGEVVCEAIKNEMNVMLKSSPVDLVTADQKVEKMLISSIKEKYPHSFIGEESVAAGEKSILTDPWIIDPIDGTTNFVHRF
PFVAVSIGFAVNKKIEFGVVSCVEGKMYTARKKGKGAFNGQKLQVSQQEDITKSLVTELGSSRTPETVRMVLSNMEKFCIPVHGIRSVGTAANM
CLVATGGADAYYEMGIHCDWVAGAGIIVTEAGGVLMVTGGPFDLMSRRVIAANNRILAERIAKEIQVPLQRDDE

>d1g0ha_e.7.1.1 (A:) Archaeal inositol monophosphatase/fructose-1,6-bisphosphatase {Archaeon *Methanococcus jannaschii*, MJ0109}

MKWDEIGKNIAKEIEKELPYFGRKDKSYVVGTPSGDETEIFDKISEDIALKYLKSLNVNIVSEELGVIDNSSEWTVIDPIDGSNFINGIPFFACFGVF
KNNEPYGYGLTYEFLTKSFYEAYGKGAYLNGRKIKVKDFNPNNIVISYPSKKIDLEKLRNKVKRVRIFGAFGLEMCYVAKGTLDAVFDVRPKVRAVDIAS
SYIICKEAGALITDENGDELKFDLNATDRLNIIVANSKEMLDIILDL

>d1inp_e.7.1.1 (-) Inositol polyphosphate 1-phosphatase {Cow (*Bos taurus*), brain}

MSDILQELLRVSEKAANIAACRQQETLFQLLIEEKKEGEKKNKKFAVDFKTLADVLQEVIKENMENKFPGLKKIFGEESNELTNDLGEKIIMRLGPTE
EETVALLSKVLGNKLASEALAKVHVQDVFFSDPALDSVEINIPQDILGIWVDPIDSTYQYIKGSADITPNQGIFPSGLQCVTVLIGVYDIQTGVPLMGV
INQPVFSQDLHTRRWKGQCYWGLSYLGTNIHSLLPPVSTRNSEAQSGTQNPSSEGSCRFSVVISTSEKETIKGALKSHVCGERIFRAAGAGYKSLCVI
LGLADIYIFSEDFTFKWDSCAAHAILRAMGGGMVLDKECLERNPDTGLDLPQLVYHVGNEAGVDQWANKGLIAYRSEKQLETFLSRLLQHLAP
VATHT

>d1ka1a_e.7.1.1 (A:) 3';5'-adenosine bisphosphatase, PAP phosphatase {Baker's yeast (*Saccharomyces cerevisiae*)}

ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTICKNDNSPVTGTDYAAQTIINAISNFPDDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKK
DDFLFTNDQFPLKSLEDVRQIIDFGNYEGGRKGFWCLDPIDGPKGFLRGEQFVCLALIVDGVVQLGCIGCPNLVLSYGAQDLKGHESFGYIFRAVR

GLGAFYSPSSDAESWTIKHVRHLKDTKDMITLEGVKEGHSSHDEQTAIKNKLNIKSLHLDSSQAKYCLLALGLADVYLRPILSYQEKIWDHAAGNVIVHEAGGIHTDAMEDVPLDFGNVRTLATKVIASSGPRELHDLVSTSCDVIQSR

>d1jp4a_e.7.1.1 (A:) PIPase {Rat (*Rattus norvegicus*)}

HNVLMRLVASAYIAQKAGTIVRCVIAEGDLGIVQKTSATDLQTAKDRMVQMSICSSLRKFPKLTIIGEEDLPPGEVDQELIEDGQSEEILKQPCPSQYSAIKEEDLVVVWVDPVDGTKEYTEGLLDNVTVLIGIAYEGKAIAGIINQPYYNYQAGPDAVLGRTIWGVGLGAFGFLKEAPAGKHIITTRSHSNKLVTDCAAMNPNDNVLVGGAGNKIIQLIEGKASAYVFASPGCKWDTCAPEVILHAVGGKLDIHGNPLQYDKEVKHMNSAGVLAALRNYEYASRVEVKSA

ESVKSALIP

>d1kfsa2 e.8.1.1 (A:519-928) DNA polymerase I (Klenow fragment) {Escherichia coli}

HKGPLNVFENIEMPLVPVLSRIERNVGKIDPKVLHNHSEELTRLAELKAHEIAGEEFNLSSTKQLQTLFEKQGKPLKTPGGAPSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYDKLPLMINPKTGRVHTSYHQAVTATGRLSSTDPNLQNIPVRNEEGRRIHQAFIAPEPDYVIVSADYSQIELRIMAHLSRDKGLTAAFGKDHRATAAEVFGPLPLETVTSEQRRSAKAINFGILYGMMSAFLARQLNIPRKEAQKYMDFYERPGVLEYMERTRAQAKEQGYVETLDGRRLYLPDIKSSNGARRAAERAIAINAPMQGTAADIIRAMIAVDAWLQAEQPRVRMIMQVHDELVFEVHKDDVDAVAKQIHQLMENCTRLDVP

LLVEVGSGENWDQAH

>d1qtma2 e.8.1.1 (A:423-831) DNA polymerase I (Klenow fragment) {Thermus aquaticus}

EEERLLWLYREVERPLSAVLAHMEATGVRLDVAYLRLSLEVAAEIARLEAEVFRLAGHPFNLSRDQLERVLFDELGLPAIGKTEKTGKRSTSAAVLEARLEAHPIVEKILQYRELTKLKSTYDPLPDLIHPRTGRLHTRFNQTATATGRLSSDPNLQNIPVRPLGQRIRRAFIAEEGWLLVALDYSQIELRVLAHSGDENLIRVFQEGRDIHTETASWMFGVPREAVDPLMRRAAKTINFVLYGMMSAHLRSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLLEGRGGYVETLFGRRRYVPDLEARVKSREAAERMAFNMPVQGTAADLMKLAMVKLPRLEEMGARMLLQVHDELVLEAPKERAEEVARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAK

>d1xwl_2 e.8.1.1 (469-876) DNA polymerase I (Klenow fragment) {Bacillus stearothermophilus, newly identified strain as yet unnamed}

EQDRLLVELEQPLSSILAEMEFAGVKVDTKRLEQMGKELAEQLGTVECRIYELAGQEFNINSPKQLGVILFEKQLPVLKKTKGYSTSADVLEKLAPYHEIVENILHYRQLGKLQSTYIEGLLKVVPRDTKKVHTIFNOALTQTGRLSSTEPNLQNIPRLEGRKIRQAFVPSEDWLIFAADYSQIELRVLAHIAEDDNLMEAFRRLDDIHTKTAMDIFQVSEDEVTPNMRRQAKAVNFGIVYGISDYGLAQNLNISRKEAAEIFIERYFESFPGVKRYMENIVQEAKQKGYVTTLLRRRYLPDITSRNFNVRSAFAERMAMNTPIQGSAADIKKAMIDLNRALKEERLQAHLLQVHDELILEAPKEEMERLCRLVPEVMEQAVTLRVPLKVDHYGSTWYDAK

>d1t7pa2 e.8.1.1 (A:211-704) T7 phage DNA polymerase {Bacteriophage T7}

LEADIEHRAAWLLAKQERNGFPFDTKAIEELYVELAARRSELLRKLTETFGSWYQPKGGTEMFCHPRTGKPLPKYPRIKTPKVGGIFKKPKNKAQREGREPCELDTREYVAGAPYTPVEHVVNPSSRDHIQKKLQEAGWVPTKYTDKGAPVVDEVLEGVRVDDPEKQAAIDLKEYLMIQKRIGQSAEGDKAWLRYVAEDGKIHGSVNPNGAVTGRATHAFPNLAQIPGVRSPYGEQCRAAFGAEHHLGDITGKPWVQAGIDASGLELRLCAHFMARFDNGEYAHEILNGDIHTKNQIAELPTRDNAKTFIYGFYAGDEKIGQIVGAGKERGKELKKFLENTPAIAALRESIQQLVESSQWVAGEQQVKWKRRIWIKGLDRKVHVRSPHAALNTLQSAGALICKLWIKEEMLVEKGLKHGWDGDFAYMAWVHDEIQVGCRTTEIAQVVIETAQEMRWVGHDHNFRCLLDTEGKMGPNWAICH

>d1ih7a2 e.8.1.1 (A:376-903) T4-like DNA polymerase {Bacteriophage RB69}

QNKPQGRSHPVQPYGAFVKEPIPNRYKYVMSFDLTSYPSIIRQVNISPETIAGTFKVAPLHDYINAVAERPSDVYSCSPNGMMYYKDRGVVPTEITKVFNQRKEHKGYMLAAQRNGEIIKEAHNPNLSDVDEPLDVDYRFDSEDEIKEKIKKLSAKSLNEMLFRAQRTEAGMTAQINRKLLINSLYGALGNVWFRRYYDLRNATAITFGQMALQWIERKVNELYNEVCGETEAEFVLYGDTDSIYVSADKIIDKVGESKFRDTNHWVDFLDKFARERMEPAIDRGFREMCYMNKNQHLMFMDREIAGPPLGSKGIGGFWTGKKRYALNVWDMEGTRYAEPKLKIMGLETQSSTPKAVQKALKECIRRMLQGEESLQEYFKEFEKEFRQLNYISIASVSSANNIAKYDVGFFPGPKCPFHIGRILTYNRAIKGNIDAPQVVEGEKVVVLPLREGNPFGDKCIAWPSGTEITDLIKDDVLHWMDYTVLLEKTFIKPLEGFTSAAKLDYEKKASLFDMFDF

>d1tgoa2 e.8.1.1 (A:348-773) T4-like DNA polymerase {Archaeon *Thermococcus gorgonarius*}

STGNLVEWFLLRKAYERNELAPNPKPDERELARRRESYAGGYVKEPERGLWENIVYLDFRSLPSIITHNVSPDTLNREGCEEYDVPQVGHFKCKDFP_GFIPSLLGDLLEERQVKKKMKATIDPIEKLLDYRQRAIKLANSFYGGYAKARWYCKEAEVTAWGRQYIETIREIEEKFGFKVLYADTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLELEYGFYKRGFFVTKKYAVIDEEDKITRGLIEVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEK

LSKYEVPPPEKLVIEQITRDLKDYKATGPHVAVAKRLAARGIKIRPGTVISYIVLKGSGRIGDRAIPFDEFDPAKHYDAEYYIENQVLPAPERILRAFGYRK
EDLRYQKTRQVGLGAWLKPCT

>d1qhta2 e.8.1.1 (A:348-750) T4-like DNA polymerase {Archaeon Thermococcus sp., 9on-7}

STGNLVEWFLRKAYKRNEAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIITHNVSPDTLNREGCKEYDVAPEVGHKFCKDFP
GFIPSLLGDLLEERQKIKRKMKTVDPLEKKLDYRQRAIKLANSFYGGYAKARWYCKECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHA
TIPGADAETVKKKAKEFLKYINPKLPGLELEYEGFYVRGFFVTKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQARVLEALKHGDVEAVRIVKEVTE
KLSKYEVPPPEKLVIEHQITRDLRDYKATGPHVAVAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPADEFDPTKHYDAEYYIENQVLPAPERILKAFGY

>d1d5aa2 e.8.1.1 (A:348-756) T4-like DNA polymerase {Archaeon Desulfurococcus tok}

STGNLVEWFLRKAYERNDVAPNKPDERELARRTESYAGGYVKEPEKGLWENIVYLDYKSLYPSIITHNVSPDTLNREGCREYDVAPQVGHRFCKDFP
GFIPSLLGDLLEERQKVKKMKATVDPIERKLLDYRQRAIKLANSYYGYYANARWYCRECAESVTAWGRQYIETTMREIEEKFGFKVLYADTDGFFA
TIPGADAETVKNKAKEFLNYINPRPLGLELEYEGFYRGFFVTKKYAVIDEEDKITTRGLEIVRRDWSEIAKETQARVLEALKHGDVEAVRIVKEVTE
KLSRHEVPPPEKLVIEAGPHVAAAATVISYIVLKGPGRVGDRAIPFDEFDPACKHYDAEYYIENQVLPAPERILRAFGYRKEDLR

>d1gcxa2 e.8.1.1 (A:348-758) T4-like DNA polymerase {Archaeon Pyrococcus kodakaraensis}

STGNLVEWFLRKAYERNELAPNKPDEKELARRQSYESGGYVKEPERGLWENIVYLDYKSLYPSIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFP
GFIPSLLGDLLEERQKIKKMKATDPIERKLLDYRQRAIKLANSYYGYYARARWYCKECAESVTAWGRYITMTIKEEEKYGFVYISDTDGFFATIP
GADAETVKKKAMEFLKYINAKLPGALELEYEGFYKRGFFVTKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQARVLEALLKDGDVEKAVRIVKEVTE
LSKYEVPPPEKLVIEHQITRDLKDYKATGPHVAVAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPFDEFDPACKHYDAEYYIENQVLPAPERILRAFGYR
KEDLRYQ

>d1jx4a_e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus, DNA polymerase IV}

MIVLFVDFDYFAQVEEVLPNSLKGKPVVVCFSGRFEDSGAVATANYEARLKGKAGIPIIVEAKKILPNAVYLPMRKEVYQQVSSRIMNLLREYSEKI
EIASIDEAYLDISDKVRDYREAYNLGLEIKNKILEKEKEKITVTVGISKNVFAKIAADMAKPNGIKVIDEEVKRLIRELDIADVPGIGNITAEKKKLGINKLV
DTLSIEFDKLKGGMIGEAKAKYLISLARDEYNEPIRTRVRKSIGRIVTMKRNSRNLEEKPYLFRAIEESYYKLDKRIKPKAIIHVVAVTEDLDIVSRGRTFPHGIS
KETAYSESVKLLQKILEEDERKIRRIGVRFSKFI

>d1im4a_e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}

HHHHHIVIFVDFDYFFAQVEEVLPNPQYKGKPLVVCVYSGRTKTSGAVATANYEARLKGKAGMPIIKAMQIAPSAYVPMRKPYEAFSNRIMNLLNK
HADKIEVASIDEAYLDVTNKVEGNFENGIELARKIKQEILEKEKEKITVTVGAPNKILAKIIADSKPNGLGIVRPTEVQDFLNELDIDEIPGIGSVLARRLNE
LGIQKLRD

>d1k1sa_e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}

MIVIFVDFDYFFAQVEEVLPNPQYKGKPLVVSVYSGRTKTSGAVATANYEARLKGKAGMPIIKAMQIAPSAYVPMRKPYEAFSNRIMNLLNKHADKI
EVASIDEAYLDVTNKVEGNFENGIELARKIKQEILEKEKEKITVTVGAPNKILAKIIADSKPNGLGIVRPTEVQDFLNELDIDEIPGIGSVLARRLNEGIQK
LRDILSKNYNELEKITGAKAKALYLLKLAQNKYSEPVENKSKIPHGRYLTLPYNTRDVKVLPLYLKAINAEAYNKVNNGIPMRITVIAIMEDLDILSKGKKFH
GISIDNAYKVAEDLLRELLVRDKRRNVRRIGVKLDNIIIN

>d1jiha_e.8.1.5 (A:) DNA polymerase eta {Baker's yeast (Saccharomyces cerevisiae)}

MSKFTWKELIQLGSPSKAYESSLACIAHIDMNAFFAQVEQMRCGLSKEDPVCVQWNSIIAVSYAARKYGISRMDTIQEALKCSNLIPIHTAVFKGE
DFWQYHDGCGSWVQDPAKQISVEDHKVSEPYRRESRKALKIFKSACDLVERASIDEVFSDLGRICFNMLMDNEYELTGDLLKDALSNIREAFIGG
NYDINSHLPLIPEKIKSLKFEGDFVNPEGRLDITWDVVDVILALGSQVCKGIRDHSIKDILGTTSCGLSSTKVNCKLASNYKKPDAQTIVKNDCLLDFDCG
KFEITSFWTLGGVLGKELIDVLDLPHENSIKHIRETPDNAGQLKEFLDAVKQSDYDRSTSNDPLKTADLAELKFLKLSRGYGLPLSSRPVVKSMMS
NKNLRGKSCNSIVDCISLEVFCALTSRIQDLEQEYNNKIVIPRTVSISLTKSYEVYRKSGPVAYKGINFQSHELLKVGIFVTLDIKGKNKSYYPLTKLS
MTITNFII

>d1mml_e.8.1.2 (-) MMLV reverse transcriptase {Moloney murine leukemia virus}

TWLSDFPQAWAETGGMGLAVRQAPLIPLKATSTPVSIKQYPMQSLEARLGKPHIQRLLDQGILVPCQSPWNTPLPVKKPGTNDRPVQDLREVNK
RVEDIHPTVPNPYNLLSGLPPSHQWYTVDLKDAFFCLRLHTSQPLFAFEWRDPEMIGISGQLTWTRLPQGFNSPTLFDEALHRDLADFRIQHPDL
ILLQYVDDLLAATSELCQQGTRALLQTLGNLGYRASAKKAQICQKQVKYLGYLLK

>d1c9ra2 e.8.1.2 (A:1-429) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PISPIETVPVKLAPGMGDKVKQWPLTAEIAALVAICTAMEAEGKISKIGPENPYNTPVFAIKKAAAAAAALVDFRELNKRTQDFWEVQLGIPH
GLKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSIANATPGIRYQYNVLPGWKGSPAIFQSSMTKILEPFKKQNPDIVIYQYIDDLYVGSDEIGQHA
TKIAELRQHLLAWGLTPDKKHAAEPFLWMGYELHPDAWTVAPAALAAAASAAVNIDIQKLGVKLNWASQIYPGIAVRALSAAAAGTKAAEAAA
ATAAAALALAAREALAAPVHGVVYDPSKDLIAEIQAQGQQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPFKL
PIQKETWETWWTEYWQATWIPEWEFVNTPPLVWLWYQL

>d1c9rb1 e.8.1.2 (B:) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PISPIETVPVKLAPGMGDKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKDSTKWRKLVDRELNKRTQDFWEALGIPH
LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPGWKGSPAIFQSSMTKILEPFKAQNPDIVIYQYIDDLYVGSDEIGQHRT
KIEELRQHLLRWGLTPDKKHKEPPFLWMGYELHPDKWAAAAAAAAATVNIDIQKLGVKLNWASQIYPGIAAAALSAALAGTKALTAAAPL
TAAAALELAANRAAAAAAAAGVYDPSKDLIAEIQKQGQQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPFKL
IQKETWETWWTEYWQATWIPEWEFVNTPPLVALWYQL

>d1har__ e.8.1.2 (-) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PISPIETVPVKLPGMDGPKVAQWPLTAKIAALVAICTEMEKEGKISKIGPENPYNTPVFAIKKDSTKWAKLVDRELNKRTQDFWEVQLGIPH
LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPGWKGSPAIFQSSMTKILAPFKAANPDIVIYQYMDDLYVGSDEIGQH
RTKIEELRQHLLRWGLTT

>d1vrt2 e.8.1.2 (A:4-429) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PIETVPVKLPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKDSTKWRKLVDRELNKRTQDFWEVQLGIPH
PLKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLPGWKGSPAIFQSSMTKILEPFRKQNPDIVIYQYMDLYVGSDEIGQH
RTKIEELRQHLLRWGLTPDKKHKEPPFLWMGYELHPDKWTVQPIVLPKEDSNTVNDIQKLGVKLNWASQIYPGIKVRQLCKLLRGTKALTEV
ELELAENREILKEPVHGVVYDPSKDLIAEIQKQGQQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKITTESIVIWGKTPFKL
PIQKETWETWWTEYWQATWIPEWEFVNTPPLVWLWYQL

>d1ceza_ e.8.1.3 (A:) T7 RNA polymerase {Bacteriophage T7}

IAKNDFSDIELAAIPFNTLADHYGERLAREQLALEHESYEMGEARFRKMFERQLKAGEVADNAAAKPLITLLPKMIARINDWFEEVAKRGKRPTAF
QFLQEIKPEAVAYITKTLACLTSDNTTVQAVASAIGRAIEDEARFGRIRDLEAKHFKNVVEQLNKRVGHVYKKAFMQVVEADMLSKGLGGEAW
SSWHKEDSIHVGVRCIEMIESTGMVSLHRQNAGVVQGDSETIELAPEYAEAIATRAGALAGISPMFQPCVPPKPWTGITGGGYWANGRRPLALV
RTHSKKALMRYEDVYMPVEVYKAINIAQNTAWKINKVLAVANVITKWKHCPVEDIPAIREELPMKPEDIDMNPEALTAWKRAAAAVYRKDKARKS
RRISLEFMLEQANKFANHKAIWFPYNMDWRGRVYAVSMFNPQGNDMTKGLTLAKGKPIGKEYYWLKIHGANCAGVDKVPFPERIKFIEENHEN
IMACAKSPLENTWWAEQDSDFCFLAFCEYAGVQHHGLSYNCLSLPLAFDGSCSGIQHFSAMLRDEVGGRAVNLLPSETVQDIYGVAKKVNEILQAD
AINGTDNEVVTVDENTGEISEKVKLGTKALAGQWLAGVTRSVTCSRVMVTLAYGSKEFGFRQQVLEDTIOPAIDSGKGLMFTQPNQAAGYMAKLI
WESVSVTVVAVEAMNWLSKAALKLAAEVKDKKTGEILRKRCAVHWVTPDGFVWQYEYKPKIQTRLNLMFLGQFRLQPTINTNKDSEIDAHKQES
GIAPNFVHSQDGSHLRKTVVWAHEKYGIESFALIHDMSGTIPADAANLFKAVRETMVDTYESCDVLADFYDQFADQLHESQLDKMPALPAKGNLNR
DILESDFAA

>d1rdr__ e.8.1.4 (-) Viral RNA-dependent RNA-polymerase {Poliovirus type 1, strain Mahoney}

VGYPIINAPSJKLLEPSAFHVYFEGVKEPAVLKNDPRLKTFEEAIFSKYVGKITEVDEYMKEAVDHAGQLMSLDINTEQMCL
EAMYGTGLEALDLSTSAGYPYVAMGKKRDLNKQTRDTKEMQKLLDTYGINLPLTVKDELRSKTKVEQGKSRLIEASSLND
SVAMRMAGFNLYAAFHKNPVGITSAVGCDPDLFWSKPVLMEEKLFADFYTGYDASLSPAWFEALKMVLEKIGFGDRDVYD
YDYLNHSHHLYKNKTYCVKGGMPSGCSGTSIFNSMII
NLLIIRLLLKTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGGLT
MPADKSATFETVTVENVFLKRFRADEKYPFLIHPVMPMKEIHESIRWT
KDPRNTQDHVRSCLLAWHN
GEEENKFLAKIRSVPIGRALLPEYSTLYRRWLDSF

>d1c2pa_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Hepatitis C virus}

HHSYTWGALITPCAAEESKLPINALNSNLLRHNNM
VYATT
RSAGLQQKVFDRQLQV
LDDHYRDVLKEM
KAKASTVKAKL
LSVEEACKLTPPHSAK
SKFGYGA
KDV
RNLS
SKAV
NHI
HSV
W
K
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GVPPRLVWRHRARSVRARLLSQGGRAATCGKYLNFNWAVKTKLKLTPIPAASQLDLSGWVFAGYSGGDIYHS

>d1khva_e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Rabbit hemorrhagic disease virus}

FCGEPIDYRGITAHLVGAPEPRPPVSGTRYAKVPGVPDEYKTGYRPANLGRSDPSDKSLMNIAVKNLQVYQQEPKLDKVDEFIERAAADVLGYLRFLT
KGERQANLNFKAAFNTLDSLSTCGPVPGKKIDHVKGMDQVLAKHLYKCWSVANSKGALHHIYACGLKDELRLDKVKEGKKRLLWGC DVGA
VCAAAVFHNICYKLKMVARFGPIAVGVDMTSRDVDVIINNLTKASDFLCLDYSKWDMSPCVVRAIDILACCEQTELTKSVVTLKSHPM TIDA
MIVQTKRLPGLSGMPFTSINSICHWLLWSAAVYKSCAEIGLHCSNL YEDAPFYTYGDDGVYAMTPMMVSLLPAIIENLRDYGLSPTAADKTEFIDVC
LNKISFLKRTFELTDIGWVSKLDKSSILRQLEWSKTTSRHMVIEETYDLAKEERVQLEELQVAAAAGQEFFNFVCREL RQQAYTQFSVSYDAARK
ILADRKR

>d1hhsa_e.8.1.6 (A:) dsRNA phage RNA-dependent RNA-polymerase {Bacteriophage PHI-6}

PRRAPAFPLSDIKAQMILFANNIKAQQASKRSFKEGAIETYEGLSVDPRLFSKNELSRYLTDHF PANVDEYGRVYGNVRTNFFGMRHNGFPMIP
ATWPLASNLKKRADADLA DGPVSE RDNL FRAAVRLMFS DLP VP LKRG S STCIPYFSNDMGT KIE AERA LEKAEEAGN LMLQGKFDDAYQLHQ
MG GAY VVYRAQSTD AITLDPKTGK FVSKDRM VADFEYAVTGGEQGSLFA ASK DAS RLKE QYGI DVPDGFFCERRT AMGGPF ALNAPI MAVAQP
VRNKIY SKYAYTFHHTRLNKEEKVKEW SLCV ATD VS DHD TF WPGW RL DIC DELL NMG YAPWWV KLFET SLKLPV YVGAP APEQ GH TL LGDPSNP
DLEV GLSSGQGATDLMGTLLMSITYLV MQLDHTAPH LNSRIKDMPSACRF L DS YWQGHEEIRQISK SDDA MLGWT KGR ALVGGHRLF EMLKEGV
NPSPYMKISYE HGG AFLG DILYDSR REPSA IFVGN INSM LNQFSPE YGVQ SGV RDR SKR PFP GLA W ASM KDT YGAC PIY SDV LEA IERCWW
NAFGESYRAYREDMLKRTDLELSRYVASM ARQAGLA ELTPID LEVLADPNKLQYKWT EAD VSANIHEV LMHG VSV EKTERFLR SVMP R

>d1i50a_e.29.1.1 (A:) RBP1 {Baker's yeast (Saccharomyces cerevisiae)}

VGQQYSSAPLRTVKEVQFGLFSPEEVRAISVAKIRPETMDETQTRAKIGLNDPLRGSI DRN LKC QT CQEGMNECPGHFGHIDLAKPVFH GFI AKI
KKVCECVCMHCGKLLLDEHNE LMRQALAIKDSKKRFAAIWTLCKTMVCETDVPSE DDPTQLV SRGGCG NTQPTIRKDGLKL VGSW KKDRATGDA
DEPEL RVL STEE ILNIFKHISVKDFTSLGF NEVFSR PEW MILT CLPV PPPV RPS ISFN ESQR GE DDLT FKLA DILK ANS LET LEH NGAP HAAIE EAES LLQ
FH VATYMDNDIAGQPQALQKSGRPVKSIRARLGKEGRIRGNLMGKRVDFSARTVISGDPNLELDQVGVPKSIAKTLTYPEVVT PYNIDRLT QLVRNG
PNEHPGAKYVIRD SGDRIDL RYSK RAGD IQLQY GWKVERHIMDNDPVL FN RQPSLHKMSMMA HRV KVIP YSTFR NLN SVP NADFDGDEMNL
HVPQSEETRAELSQLCAVPLQIVSPQSNKPCM GIVQDTLCGIRKLT RD TFIELD DQVLN MLYWVPDWGVIPTAI KPKPLW SGKQI LSV AIPNGIHL
QRFDEGTTLSPKDN GM LIIDGQJIFGVV EKKT VGSSN GGLI HVV T RKG P QVCA KLF GN IQK VV NF WLL HNG FSTG IDT I ADG PTM REIT TIA EA
KKK VLD VT KEAQ ANL TA KHM TL RES FED NV VR FL NEARD KAG RL AEVN LKDL NN VQ MV MAGSK GS FINIA QMS ACVG QQS VEG KRIA FG FV
DRTLPHFSKDDYSPESKG FVENS YL RG LTP QEFF FHAM GGREG LIDT AVKTA ETG YIQ RRL VKA LE DIMV H YDNT TRN S LGN V I QF YG EDG MDA AH
EK QSL DTIGGSDAA FEK RYR VD LNTD HTL DP S LLES GSE I GL DLK LQV L DEE YK QL V KDR KFL REV FV DGE ANW PL PV N IRRI QN A QQT FH ID HTK P
SDLT KDI VLG V KDL QEN L L VLR G KNE II QNA QR DAV TL FC C LRS RL A T R R V LQ EY RLT KQ AF DW V L S NIE A QFL RS V VHP GEM VGV LA QSIG EPAT
QMTLNTFHAGVASKV TSGV PR LKE I NVAK NM KTP S LTV LEP GHA ADQ EQ A K L R S AIE HTT L K S V TIA E IYY DPD PR S T V IPE DE E IQL HF S LD
EEAEQSFDQQSPWLLRLELDRAAMNDKDL TMGQVGERIKQTFKNDL FV I W SED N D E K I I R C R V R P K S L D A E T E A E E D H M L K I E N T M L E N I T L R G
VENIERVVMMKYDRKVPSPTGEYVKEPEWVLET DG VNL SEV M TV PGID P T R Y T N S FID IM E VLG IE A GRA ALY KEV NVN IAS DGS YV NY RH M ALL V
DVMTTQGGLTSVTRHGFNRSNTGALMRC SFEET VEIL FEAGA SAE LDCRG VSEN VIL QM API GTG A FD VM I D E S L

>d1i6vc_e.29.1.1 (C:) RNA-polymerase beta {Thermus aquaticus}

KIKRFGRI REVIPLPPLTEI QVES YKK ALQAD VPPE KRENV GIQAA FKET P IEG DKG KGG LVDFLEY RIGD PPF SQDC E KDL TYQAP LYAR LQI HK
DTG LIKE DEVFLG HPLM TEDGS F IING ADR VIV S QI HR SP GVY F TD PPAR P GRYIASI I PLK RGP WID LEVE ASGV VTM KV NK RKFPLV L R VLG YD
QET LV REL SAY GDLV QGLL D EAVL MRP EAM VRL FT L RGP D PPK K D KALAY LFG LAD P K RY D L G E A G R Y K A E E K L G V G L S G R T L V R F E D G E F K D E
VFLPTL RY LFALT AGV PG H E V D D I D H L G N R I R T V G E L M A D Q F R V G L A R L A R G V R E R M V M G S P D L T P A K L V N S R P L E A L R E F F S R Q L S Q F K D E T
NPLSS LR H K R R I S A L G P G G L T R E A G F D V R D V H R T H Y G R I C P V E T P E G A N G L I T S L A A Y A R V D A L G F I R T P Y R R V K N G V V T E E V V Y M T A S E E D R Y T I A Q
A N T P L E G D R I A T D R V V A R R G E P V I V A P E E V F M D V S P K Q V F S L N T N L I P F L E H D D A N R A L M G S N M Q T Q A V P L I R A Q A P V V M T G L E E R V V R D S L A A
L Y A E E D G E V V K V D G T R I A V R Y E D G R L V H P L R R Y A R S N Q G T A F D Q R P R V R V G Q R V K K G D L L A D G P A S E E G F L A L G Q N V L V A I M P F D G Y N F E D A I V I S E
E L L K R D F Y T S I H I E R Y E I E A R D T K L G P E R I T R D I P H L S E A L R D L D E E G I V R I G A E V K P G D I L V G R T S F K G E Q E P S P E E R L L S I F G E K A R D V K D T S L R V P P G E
G G I V V G R L R R G D P G V E L K P G V R E V V R V F V A Q K R K L Q V G D K L A N R H G N K G V V A K I L P V E D M P H L P D G T P V D V I L N P L G V P S R M N I L G Q I L E T H L G L
A G Y F L G Q R Y I S P V F D G A T E P E I K E L L A E A F N L Y F G K R Q G E G F G V D K R E K V L A R A E K L G L V S P G K S P E E Q L K E L F D L G K V V L Y D G R T G E P F E G P I V V G Q
M F I M K L Y H M V E D K M H A R S T G P Y S L I T Q Q P L G G K A Q F G G Q R F G E M E V W A L E A Y G A A H T L Q E M L T I K S D D I E G R N A A Y Q A I K G E D V P E P S V P E S F R V

LVKELQALALDVQLDEKDNPVDVFEGL

>d1i50b_e.29.1.2 (B:) RBP2 {Baker's yeast (*Saccharomyces cerevisiae*)}

FEDESAPITAEDSWAVISAFFREKGGLVSQQLDSFNQFVDTLQDIICESTLILEQLAQHTTESDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARNLNLYSSGLFDVKKRTYEIDVPGRELKYELIAEESEDSESGKVFIGRLPIMLSKNCYLSEATESDLYKLKECPFDMMGGYFIINGSEKVLIAQERSAGNIVQVFKAAPSPISHVAEIRSALEKGSRFLSTLQVKLYGREGSSARTIKATLPYIKQDIPIVIFRALGIIPDGEILEHICYDVNDWQMELKPCVEDGFVHQDRETALDFIGRRGTALGIKEKRIQYAKDILQKEFLPHITQLEGFESRKAFFLGYMINRLLLALDRKDQDDRDHFGKKRLLAGPLAQLFKTLFKKLTKDIFRYMQRTVEEAHDFNMKLAINAKTITSGLKYLATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRNTNPIGRDGKLAKPRQLHNTHWLVCAPETPEGQACGLVKNLSLMSCISVGTDPMPIITFLSEWGMEMPLEDYVPHQSPDATRVFVNGVWHGVHRNPARLMETLRTLRRKGDIINPEVSMIRDIREKELKIFTAGRVRVYRPLFIVEDDESLGHKELKVRKGHIAKLMATEYQDIEGGFEDVEEYTWSLLNEGLVEYIDAEEEESILIAMQPEDLEPAEANEENDLDVDPAKRIRVSHATTFTHEIHPMSMILGVAASIIPFDPDHNQSPrNTYQSAMGKQAMGVFLTNYNVRMDTMANILYPQKPLGTTAMEYLFRELPGAGQNAIVAIACYSGYNQEDSMIMNQSSIDRGLFRSLFFRSYMDQEKKYGMISITETFEKPQRTNLRMKHGTYDKLDDGLIAPGVRVSGEDVIIGKTPISPDEELGQRTAYHSKRDASTPLRSTENGIVDQVLVTTNQDGLKFVVKVRRTKIPQIGDKFASRHGQKGITGITYRREDMPFTAEGIVPDLIINPHAIPSRMTVAHLIECLLSKVAALSGNEGDAASPFTDITVEGISKLLREHGQYQSRGFEMVYNGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARRGPMQVLTRQPVEGRSRDGGGLRGEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMTVIAKLNHNQFECKGCDNKIDIQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF

>d1i6vd_e.29.1.2 (D:) RNA-polymerase beta-prime {Thermus aquaticus}

KEVRKVRIALASPEKIRWSYGEVEKPETINYRTLKPERDGLFDERIFGPICKYKRQRFEAKVCERCAVEVTRSIYRRYMAHIELATPAAHWFVKDVPSKIATLDSLATELEQVLYFNKYIVLDPKAAVLDAVPVEKRQLLTDXXXXXXXXXXXXXXXXXXXXXXXXXXIDARMGAEAIQELLKELDLEKLERELLEEMKHPSRARRAKARKLEVRAFLDSGNRPEWMILEAVPVLPPLDRPMVQVDGGRFATSDLNDYRRLINRNNRLKKLAQGAPEIIIRNEKRLMQLQEAVDAVIDNGRRGSPVTNGPGERPLRS LTDILSGKQGRFRQNLLGKRVVDYSGRSVIVVGPQLKLHQCGLPKRMALFKPFLKKMEEKAFAPNVKAARRMLERQRDIKDEVWDALEEVIHGVVLLNRAPTLHRLGIQAFQPVLVEGQSIQLHPLVCEAFNADFDGDQMAHVPLSSFAQAEARIQMLSAHNLLSPASGEPLAKPSRDIILGLYYITQVRKEKKGAGMAFATPEEALAAYERGEVALNAPIVAGRETSVGRKFVANPDEALLAVAHGLLDLQDTVTRYLGRRLETSPGRILFARIVGEAVGDEKVAQELIQMDVPQEKNLKDLYQAFLRLGMEKTARLLDALKYYGFTLTTSGITIGIDDAVIPEEKQRYLEEAADRKLQRQIEQAYEMGFLDRERYDQVIQLWTETTEKVTQAVFNNFEENYPNPLYVMAQSGARGNPQQIRQLCGMRGLMQKPSGETFEVPVRSSFREGTVLEYFISHGARKGGADTALRTADSGYLTTRKLVDVAHEIVVREADCGTTNYISVPLFQMDEVTRTLRLRKRSDIESGLYGRVAREVEALGRRLEEGRYLSLEDVHFLIKAAEAGEVREVVPVSLTCQTRYGVCQKCYGDLMSMARPVSIGEAVGVVAEISIGEPGTQLTMRTFHGGVAVGTDITQGLPRVIELFEARRPKAKAVISEIDGVVRIEEGEDRLSVFVESEGFSKEYLPKDARLLVKDGDYVEAGQPLTRGAIDPHQLEAKGPEAVERYLVDEIQKVYRAQGVKLHDHKHIEIVVRQMLKYEVTDGDSRLLEGQVLEKWDVEALNERLIAEGKVPVAWKPLLGMVTKSALSTKSWLSAASFQNTTHVLTAAIAGKKDELIGLKENVILGRIPAGTGSDFVRTQVVDQRTLKAIE

>d1bpva2_e.9.1.1 (A:92-335) DNA polymerase beta, catalytic (31 kD) fragment {Human (*Homo sapiens*)}

DTSSSINFTRVSGIGPSAARKFVDEGIKTLEDLRKNEDKLNNHHQRIGLKYFGDFEKIRIPREEMILOMQDIVLNEVKKVDSEYIATVCGSFRRGAESSGDMDVLLTHPSFTSESTKQPKLHQVVEQLQKVHFITDTLSKGETKFMGVQLPSKNDEKEYPHRRRIDIRLIPKDQYYCGVLYFTGSDIFNKNMRAHALEKGFTINEYTIPLGVTGVAGEPLPVDSKIDFYIQWKYREPKDRSE

>d1jn3a_e.9.1.1 (A:) DNA polymerase beta, catalytic (31 kD) fragment {Rat (*Rattus norvegicus*)}

DDTSSSINFTRVTGIGPSAARKLVDEGIKTLEDLRKNEDKLNNHHQRIGLKYFEDFEKIRIPREEMILOMQDIVLNEVKKLDPEYIATVCGSFRRGAESSGDMDVLLHPNFTSESSKQPKLHRVVEQLQKVRFITDTLSKGETKFMGVQLPSSENDENEYPHRRRIDIRLIPKDQYYCGVLYFTGSDIFNKNLRAHALEKGFTINEYTIPLGVTGVAGEPLPVDSSEQDIFDYIQWKYREPKDRSE

>d1jmsa2_e.9.1.1 (A:243-510) Terminal deoxynucleotidyl transferase {Mouse (*Mus musculus*)}

DERYKSFKLFTSVFGVGLKTAEKWFRMGFRTLSKIQSDKSLRFTQMOKAGFLYYEDLSCVNRPEAEAVSMLVKEAVVTFPLDALVTMTGGFRRGKMTGHDVDFLITSPEATEDEEQQLLHVKVDFWKQQGLLYCDILESTFEKFKQPSRKVDALDHFQKCFILKLDHGRVHSEKGQQEGKGWKAIRDLVMCPYDRRAFALLGWTGSRQFERDLRRYATHERKMMLDNHALYDRTKRVFLEAESEEI AHLGLDYIEPWERNA

>d1jaja_e.9.1.1 (A:) DNA polymerase X {African swine fever virus}

MLTLIQGKKIVNHLRSRLAFYNGQLIKILSKNIVAVGSLRREEKMLNDV DLLIIVPEKKLLKHVLPNIRIKGLSFSVKCGERKCVLFIEWEKKYQLDLFTALAAEKPYAIFHFTGPVSYLIRIRAALKKKNYKLNQYGLFKNQTLVPLKITTEKEKELIGFTYRIPKKRL

>d1fa0a2 e.9.1.2 (A:3-351) Poly(A) polymerase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

SQKVFGITGPVSTVGATAAENKLNSLICELKKEGSFETEQETANRVQLKILQELAQRFVYEVSKKNMSDGMARDAGGKIFTGSYRLGVHGPSS
DIDTLVVVPKHVTREDFFTVDSSLRERKELDEIAPVPDFAVPIIKFKSGISIDLICARLDQPQVPLSNTLSKNNLLDEKDRLALNGTRVTDEILELPVK
PNVFRIALRAIKLWAQRRAVYANIFGPGGVAWAMILVARICQLYPNACSAVLNRFFIILSEWNWPQPVILKPIEDGPLQVRVWNPKIYAQDRSHRM
PVITPAYPSMCATHNITESTKKVILQEFTVRGVQITNDIFSNKKSWANLFKE

>d1f5aa2 e.9.1.2 (A:20-364) Poly(A) polymerase, catalytic domain {Cow (Bos taurus)}

YGITSPISLAAPKETDCLLTQKLVETLKPFGVFEEEEELQRRILGKLNLLKEWIREISESKNLPQSVIENVGGKIFTGSYRLGVHTKGADIDALCVAPR
HVDRSDFFTFSYDKLKLQEEVKDLRAVEEAFPVVIKLCFDGIEIDILFARLALQTIPELDLRRDDSLKNLDIRCIRSLNGCRVTDEILHLVPNIDNFRRTLRA
IKLWAKRHNIYSNILGFLGGVSWAMLVARTCQLYPNAIASTLVHKKFLVFSKWEWPNPVLLQPEECNLNPVWDPRVNPSDRYHLMPIITPAYPQQ
NSTYNVSVSTRMVMVEEFKQGLAITDEILLSKAESWSKLFEA

>d1knya_ e.9.1.3 (A:) Kanamycin nucleotidyltransferase (KNTase) {Staphylococcus aureus}

MNGPIIMTREERMKIVHEIKERILDKYGDDVKAIGVYGGSLRQTDGPYSDIEMMCVMSTEEAEFSHEWTGEWKVEVNFYSEEILLDYASQVESDW
PLTHGQFFSILPIYDSGGYLEKVYQTAKSVEAQTFHDIAICALIVEELFEYAGKWRNIRVQGPTTFLPSLTQVQAMAGAMIIGLHHRICYTTSAVLTEAV
KQSDLPSGYDHLCQFVMSGQLSDSEKLLSLENFWNGIQEWTERHGYIVDVSKRIPF

>d1k8ta_ e.9.1.4 (A:) Adenyllycyclase toxin (the edema factor) {Bacillus anthracis}

DRIDVLKGKALKASGLVPEHADAFKKIARELNNTYILFRPVNKLATNLKSGVATKGLNVHGKSSDWGPVAGYIPFDQDLSKKHGQQLAVEKGNNLENK
KSITEHEGEIGKIPKLKDHLRIEELKENGIIKGKKEIDNGKKYLLSNNQVYEFRISDENNEVQYKTKEGKITVLGEKFNWRNIEVMAKNVEGVLKPLT
ADYDLFALAPSLEIKKQIPQKEWDKVVNTPSLEKQKGVTNLLIKYIERKPDSTKGTLNWNQKQMLDRNNEAVKYTGTDVNVHGTEQDN
PEKDNEIFIINPEGEFILTKNWEMTGRFIEKNITGKDLYYYFRNSYNIAPGNKAYIEWTDPITKAKINTIPTSAEFIKNLSSIRRSSNVGVYKDSGDKDEFA
KKESVKKIAGYLSYYNSANHIFSQEKKRISIFRGIQAYNEIENVLKSQIAPEYKNYFQLKERITNQVQLLTHQKSNIEFKLLYKQLNFTENETDNFEV
FQKIIDF

>d1cy9a_ e.10.1.1 (A:) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}

FVPEEFWEVDASTTPSGEALALQVTHQNDKPFRPVNKEQTQAAVSLEKARYSVLEREKPTTSKPGAPFITSTLQQAATRLGFGVKTMMAQ
RLYEAGYITYMRTDSTNLSQDAVNMRGYISDNFGKKYLPESPNQYASKENSQEAHEAIRPSDVNVMAESLKDMEADAQKLYQLIWRQFVACQMT
PAKYDSTTLTVGAGDFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKGDALTLVELTPAQHFTK
>d1ecl_ e.10.1.1 (-) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}

GKALVIVESPAKAKTINKYLGSDYVVKSSVGHIRDLSGSAAKKSADSTSTKAKPKKPDERGALVNRMGVDPWHNWEAHYEVLPGKEKVSELKQ
LAEKADHIYLATDLDREGEAIAWHLREVIGDDARYSRVVFNEITKNAIRQAFNKGELNIDRVNAQQARFMDRVGYMVSPLLWKKIARGLSAG
RVQSVAVRLVVEREREIKAFVPEEFWEVDASTTPSGEALALQVTHQNDKPFRPVNKEQTQAAVSLEKARYSVLEREKPTTSKPGAPFITSTLQQA
ASTRLGFGVKTMMAQRLYEAGYITYMRTDSTNLSQDAVNMRGYISDNFGKKYLPESPNQYASKGSQEAHEAIRPSDVNVMAESLKDMEAD
AQKLYQLIWRQFVACQMTPAKYDSTTLTVGAGDFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKGDALTLVELTPAQHFTKPPARFSEASLVK
ELEKRGIGRPSTYASIISTIQDRGYVRVENRRFYAEKMGEIVTDRLEENFRELMDFTAQMENSLDQVANHEAEWKAVIDHFFSDTQQQLDKAEKD
PEEGGMRPN

>d1i7da_ e.10.1.1 (A:) DNA topoisomerase III {Escherichia coli}

MRLFIAEKPSLARAIADVLPKPHRKGDGFIECGNGQVVTWCIGHLEQAQPDAYDSRYARWNLADLPIVPEKWQLQPRPSVTQLNVIKRFLHEASE
IVHAGDPDREGQLLVDEVLDYQLAPEKRQQVQRCLINDLNPQVAVERAIDRLRSNSEFVPLCVSALARARADWLYGINMTRAYTILGRNAGYQGVLS
VGRVQTPVGLVRRDEEINFVAKDFFEVKAHVTPADERFTAIWQPSACEPYQDEEGRLLHRPLAEHVNRISGQPAIVTSYNDKRESESAPLPFSL
SALQIEAAKRGFLSAQNVLIDCQKLYETHKLITFPDRSDCRLPEEHFAGRHMNAISVHAPDLPQPVVDPDIRNRCWDDKKVDAHHAIPTARSSAI
NLTEANEAKVYNNLIARQYLMQFCDAVFRKCIELDIAKGKFVAKARFLAEAGWRTLLGSKERDEENDGTPLPVVAKGDELLCEKGEVVERQTQPPRH
TDATLLSAMTGIARFVQDKDLKKRATDGLTEATRAGIELLFKRGFLKKGRYIHSTDAGKALHSLPEMATRPMTAHWESVLTQISEKQCQYQDF
MQPLVGTLYQLIDQAKRTPVRQFRGIVAP

>d1gkub3 e.10.1.1 (B:499-1054) Topoisomerase "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

QEFDLIKPALFIVESPTKARQISRFFGKPSVKLDGAVVYIPEMQKYVLMVTASIGHVVLDITNRGFHGVNVGRFVPPVYASIKCRDCGYQFTEDRES
CPKCGSENVDSRSRRIEALRKLAHDAEVIVGTDPTEGEKIAWDLKNLLSGCGAVKRAEFHEVTRRAILEALESLRDVDENLVKAQVVRRIEDRWIG

FVLSQKLWERFNNRNLSAGRAQTLVLGWIIDRFQESRERRKIAIVRDFDLVLEHDEEEFDLTIKLVEEREELRTPLPPYTETMLSDANRILKFSVKQTM
QIAQELFENGLITYHRTDSTRSDVGQRIAKEYLGDDFVGREWGESGAHECIRPTRPLRDDVQRЛИQEGVLVVEGLRWEHFALYDLIFRRFMASQCR
PKFKVVKKYSIEFDGKTAEEERIVRAEGRAYELYRAVVVKNELEPGTFRVKAEVSKVLPFTQSEIIQMMKRGIGRPSTYATIVDRLFMRNYVVEK
YGRMIPTKLGIDVFRFLVRRYAKFVSEDRTDLESRMDAIERGELDYKALEDMYAEIKSID

>d1bjt__ e.11.1.1 (-) DNA topoisomerase II, C-terminal fragment (residues 410-1202) {Baker's yeast (*Saccharomyces cerevisiae*)}
RKSRTNYPKLEDANKAGTKEGYKCTLVTEGDSALSLAVAGLAVGRDYYGCYPLRGKMLNVREASADQILKNAEIQAIIKIMGLQHRKKYEDTKSLR
YGHLMIMTDQDHGSHKGLIINFLFSSFLGLLDIQGFLLEFITPIIKVSITKPTKNTIAFYNMMPDYEKWEEESHKFTWKQKYYKGLGTSLAQEVR
NLDRHLKIFHSLQGNDKDYLDAFSKKKADDRKEWLRLQYEPGTVLDPYLKEIPISDFINKELILFSADNIRSIPNVLGFKPGQRKVLYGCFKKNLKSEL
KVAQLAPYVSECTAYHHGEQSLAQTIIGLAQNFGSNNIYLLPNGAFGTRATGGKAAAARYIYTELNKLTRKIFHPPADDPLYKYIQEDEKTVEPEWYL
PILPMILVNGAEGIGTGWSTYIPFNPLEIIKNIRHLMNDEELEMHQMPWFRGWGTGIEIEPLRYRMYGRIEQIDNVLEITELPARTWTSTIKEYLLL
LSGNDKIKPWIKDMEEQHDDNIKFIITLSPPEMAKTRKIGFYERFKLISPLMNMVAFDPHGKIKKYNNSVNEILSEFYYVRLEYYQKRKDHMSERLQW
EVEKYSFQVKFKMIIKELTVTNKPRNAIIQLENLGFPRFNKEGKPYYGPNDNDEIAEQINDVKATSDEEDEESSHEDTENVINGPEELYGTYEYLLGM
RIWSLTKERYQKLLKQKQEKETELENLLKSAKDIWNTDLKAFEVGYQEFQLQRDAEARG

>d1ab4__ e.11.1.1 (-) DNA Gyrase A {Escherichia coli}

VGRALPDVRDGKPVHRRVLYAMNVLGNDWNKAYKKARSARVVGDVIGKYHPHGDSAVYDTIVRMAQPFSLRYMLVDGQGNFGSIDGDSAAAMRY
TEIRLAKIAHELMADLEKETVDFVDNYDGTEKIPDMPTKIPNLLVNGSSGIAVMATNIPPHNLTEVINGCLAYIDDEDISIEGLMEHIPGPDFPTAAII
NGRRGIEEAYRTGRGKVIYRARAEEVETIIVHEIPYQVNKARLIEKIAELVKEKRVEGISALRDESNDGMRIVIEGEVVLNNLYSQTLQVSFGINMV
LHHGQPKIMNLKIIIAFVHRREVVTRRTIFELRKARDRAHILEALAVALANIDPIIELRHAPEAATLVNPWQLGNVAAMLEDAARPEWLEP
EFGVRDGLYLYLTERQQAQAILDLRLQKLTGLEHEKLLDEYKELLDQIAELLRLGSADRMEVIREEELVREQFGDKRRTET

>d1d3ya__ e.12.1.1 (A;) DNA topoisomerase IV, alpha subunit {Archaeon *Methanococcus jannaschii*}

QAKIFAQTTKMLEFAKQLLETDDFSTLREAYYVSKNWGEARFDDQQASNNVIEDLEAALGVLRHGLFPEEDGSSVVGPKLIIETPEGELVVDC
GTGAYNIPNDVTKLNLETADFLAIETSGMFARLNAERFWDKHNCILVSLKGVPARATRRFIKLHEEHDLPVLFVFTDGDGYLNIYRTLKV
GSGKAI
HLADKLSIPAARLIGVTPQDIIDYDLPTHPLKEQDIKRIKDGKLNDDFVRSFPEWQKALKQMLDMGVRAEQQSLAKYGLKVVNTYLPEKIKDESTWL
P

>d1dd9a__ e.13.1.1 (A;) DNA primase DnaG catalytic core {Escherichia coli}

TLYQLMDGLNTFYQQSLQQPVATSARQYLEKRLSHEVIARFAIGFAPPWDNVLKRGFPNNPENRQSLIDAGMLVTDQGRSYDRFRERVMFPIRD
KRGVRIGFGGRVLGNDTPKYLNSPETDIFHKGRQLYGLYEAAQDNAEPNRLLVVEGYMDVVALAQYGINYAVASLGTTADHIQLLFRATNNVICCY
DGDRAGRDAAWRALETALETPYMTDGRQLRFMFLPDGEDPDTLVRKEGKEAFEARMEQAMPLSAFLNSLMPQVDLSTPDGRARLSTLALPLISQVP
GETLRIYLRLQELGNKLGLDDSQL

>d1ee8a__ e.14.1.1 (A;) DNA repair protein MutM (Fpg) {Thermus thermophilus}

PELPEVETRRRLRPLVLGQTLRQVVHRDPARYRNTALAEGRRILEVDRRGKFLLFALEGGVELVAHGMTGGFLEPTPHTRAALVLEGRTLYFHDPR
RFGRLFGVRRGDXREIPLLRLGPEPLSEAFAPGFFRGLKESARPLKALLDQRLAAGVGNIYADEALFRARLSPFRPARLSEEARRLYRALREV
AELA
VELGGSTLSDQSYRQDPGLPGFQTRHAVYGREGLPCACGRPVERRVAGRGTHFCPTCQGEGP

>d1i3ja__ e.30.1.1 (A;) DNA-binding domain of intron endonuclease I-TevI {Bacteriophage T4}

KFKCGVRIQTSAYCSKCRNRSGENNSFFNHKSDITSKKISEKMKGKKPSNIKKISCDGVIFDCAADAARHFKISSGLTYRVKSDKWNWFYIN

>d1a31a2 e.15.1.1 (A;215-430) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment {Human (*Homo sapiens*)}

IKWKFLEHKGPVFAPPYEPPLPVNFYDGKVMKLPKAEEVATFFAKMLDHEYTTKEIFRKNNFKDWKEMTNEEKNIITNLSCDFTQMSQYFKA
QTEARKQMSKEEKLKIKEENEKLLKEYGFCIMDNHKERIANFKIEPPGLFRGRGNHPKMGMLKRRIMPEDIICNSKDAKVPSSPPGHKWKEVRHDN
KVTWLVSWTENIQGSIKYIMLN

>d1ois__ e.15.1.1 (-) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment {Baker's yeast (*Saccharomyces cerevisiae*)}
DTIKWVTLKHNGVIFPPPYQPLPSHIKLYDGKPVDLPPQAEEVAGFFAALLESDHAKNPVFQKNFFNDFLQLKESGGPLNGIEIKEFSRCDFTKMFD
YFQLQKEQKKQLTSQEKKQIRLEREKFEEDYKFCELDGRREQVGNFKVEPPDLFRGRGAHPKTGKLKRRVNPDIVLNLSKDAPVPPAEGHKWGEIR
HDNTVQWLAMWRENIFNSFKYVRLAA

>d1g71a_e.16.1.1 (A:) DNA primase {Archaeon Pyrococcus furiosus}

MLMREVTKEERSEFYSKEWSAKKIPKFIVDTLESREFGFDHNGEGPSDRKNQYSDIRDLEDYIRATSPYAVYSSVAFYENPREMEGWRGAEVFIDA
KDLPLKRCNHEPGTVCPICLEDAKELAKDTLILREELGFENIHVVYSGRYHIRLDEWALQLDSKSRRILAFISASEIENVEEFRFLLEKRGWFVLKH
GYPRVFRLRLGYFILRVNVPHLLSIGIRRNIKKILDHKEEIYEGFVRKAILASFPEGVGIESMAKLALSTRFSKAYFDGRVTVDIKRILRPSTLHSKVGLIA
TYVGTKEERVMKFNPFHRAVPKRKVEVREAYKLWRESL

>d1jeya_e.31.1.1 (A:) Ku70 subunit {Human (Homo sapiens)}

GRDSLIFLVASKAMFESQSEDELTPFDMSIQCISQVYISKIISDRDLLAVFYGTEKDKNVSNFKNIYVLQELDNPAGAKRILELDQFKGQQGKRFQ
DMMGHGSDYSLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDASKRARTKAGDLRTGIFLDMHLKKPGGFISLYRDIISIAEDED
LRVHFEESSLKEDLLRKVRAKERKRALSRKLKLKNKDIVISVGINYLNQKALKPPIKLYRETNEPVKTTRTFNTSTGLLPSDTKRSQIYGSRQIILEKE
ETEELKRFDDPGMLMGFKPLVLLKKHHYLRLPSLFVYPEESLVIGSSTLSALLIKCLEKEVAALCRYTPRNIPPFVALVPQEEELDDQKIQVTPPGFQL
VFLPFADDKRKMPTEKIMATPEQVGKMKAIKEVLRFTYRSDSFENPVLQQHFRNLEALALDLMEPHQAVDLTPKVEAMNKRLGSLVDEFKELVYP
PDY

>d1jeyb_e.31.1.2 (B:) Ku80 subunit {Human (Homo sapiens)}

NKAAVVLCMDVGFTMSNSIPGIESPFEQAKKVTMFVQRQVFAENKDEIALVFGTDGTNPLSGGDQYQNITVHRHMLPDFDLLEDIESKIQPGS
QQADFLDALIVSMSDVIQHETIGKKFKEKRHIEIFTDLSSRFSKSQLDIIHSLKCDISLQFFLPFSLKGEDGSGDGRDPFRGGHGPSPFLKGITEQQKEG
LEIVKVMVMSLEGEDGLDEIYFSESLRKLCVFKKIERHSIHWCRLTIGSNSLIRIAYKSILQERVKKTWTVVDAKTLKEDIQKETVYCLNDDDETEVL
KEDIIQGFRYGSIVPFSKVDDEEQMKYKSEGKCFSVLGFCSSQVQRRFFMGNGNQVLKVAARDDEAAVALSSLIHALDDLMVAIVRYAYDKRANP
QVGVAFPHIKHNYECLVYVQLPFMEDLRQYMFSSLKNSKKYAPTEAQLNAVDALIDSMSLAKKDEKTDTLEDFPTTKIPNPRFQRLFQCLLHRALHP
REPLPIQHQHIWNMLNPPAEVTTKSQIPLSKIKTLFPLIEAKK

>d1daaa_e.17.1.1 (A:) D-amino acid aminotransferase {Bacillus sp., strain YM-1}

GYTLWNDQIVKDEEVKIDKEDRGYQFGDGVEVVKVYNGEMFTVNEHIDRLYASAEKIRITIPYTKDFHQLLHELVEKNEINTGHIYFQVTRGTSPR
AHQFPENTVKVPIGYTKENPRPLENLEKGVKATFVEDIRWLRCDIKSLNLLGAVLAKQEAHEKGCYEALHRNNNTVTEGSSSNVFGIKDGILYTHPANN
MILKGITRDVVIACANEINMPVKEIPFTTHEALKMDELFTTSEITPVIEIDGKLIRDGKVGEWTRKLQKQFETKIP

>d1i1ka_e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Escherichia coli}

KADYIWFNGEMVRWEDAOKVHVMshalHYGTSVFEgIRCYDShKGpvvfrREHMQLHDSAKIYRFPVSQSIDELEMACRDVIRKNNLTSAYIRPL
IFVGDVGMGVNPPAGYSTDVIIFPWGAYLGAEALEQGIDAMVSSWNRAAPNTIPTAAKAGGNYLSLLVGSEARRHGYQEGIALDVNGYISEGA
GENLFEVKDGVLFPTPFTSSALPGITRDAIIKLAKELGIEVREQVLSRESLYLADEVMSGTAEEITPVRSDGIQVGEGRCPVTKRIQQAFFGLFTGET
EDKGWGLDQVNQ

>d1ekfa_e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Human (Homo sapiens), mitochondrial}

ASSSFKAADLQLEMTQPKHKKPGPGEPLVFGKFTDHMLMVEWNDKGWGPRIQPQFQNLTLHPASSSLHYSLQLFEGMKAFKGKDQQVRLFRP
WLNMDRMLRSAMRLCLPSFDKLELLECIRRLIEVDKDWVPDAAGTSLYVRPVLIGNEPSLGVSQPRRALFVILCPVAGFPGSVTPVSLADPAFIR
AWVGGVGNYKLGNGYGPVTVLQQEALKRGCEQVLWLYGPDHQLTEVGMNIFVYWTHEGVLELVTPLNGVILPGVVRQSLLDMAQTWGEFR
VVERTITMKQLLRALEEGRVREVFGSGTACQVCPVHRIILYKDRNLHPTMENGPELIRFQKELKEIYQGIRAHWMFPV

>d1et0a_e.17.1.1 (A:) Aminodeoxychorismate lyase {Escherichia coli}

MFLINGHKQESLAVSDRATQFGDGCFTTARVIDGKVSSLAHIQRLQDACQRLMISCDFWPQLEQEMKTLAAEQQNGVLKVVISRGSGGRGYSTLN
SGPATRILSVTAYPAHYDRLRNEGITALSPVRLGRNPHLAGIKHLNRLEQVLIRSHLEQTNADEALVLDSEGWVTECCAANLFWRKGNGVYTPRLDQ
AGVNGIMRQFCIRLLAQSSYQLVEVQASLEESLQADEMVICNALMPVMPCACGDVSFSATLYEYLAPLCE

>d2frvb_e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit {Desulfovibrio gigas}

NKIVVDPITRIEGLHLIEVEVEGGKIKNAWSMSTLFRGLEMILKGRDPRAQHFTQRACGVCTVHALASVRAVDNCVGVKIPENATLMRNLTMG
QYMHDHLVHFYHLHALDWNVANALNADPAKAARLANDLSPKTTESLKAVQAKVKALVESGQLGIFTNAYFLGGHPAYVLPAEVLDIATAHYLEA
LRVQVKAARAMAIFGAKNPHTQFTVVGCTNYDSLRPERIAEFRKLYKEVREFIEQVYITDLLAVAGFYKNWAGIGKTSNFTCGEFPTDEYDLSRYT
PQGVIWGNDSLKVDDFNPDLIIEEEHVKYSWYEGAGAHHPYKGVTKPWTTEFHGEDRYSWMKAPRYKGEAEFVGPLASVLVAYAKKHEPTVKAVDL
VLKTLGVGPEALFSTLGRTAARGIQCLTAAQEVEVWLDKLEANVKAGKDDLYTDWQYPTESQGVGFVNAPRGMLSHWIVQRGGKIENFQLVVPST
WNLGPRCAEGKLSAVEQALIGTPADIOPKRPVEILRTVHSYDPCIACGVH

>d1h2rl_e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio vulgaris}

SSYSGPIVVDPVTRIEGHLRIEVEENGKVKNAYSSSTLFRGLEIILKGRDPRDAQHFTQRTGVCTYTHALASTRCVDNAVGHIPKNATYIRNLVLGA
QYLHDHVHFYHLHALDFDVTAALKADPAKAQVASSISPRKTTAIDLKAVQDKLKTFTVETGQLGPFTNAYFLGGHPAYLDPETNLIATAHYLEALRL
QVKAARAMAVFGAKNPHTQFTVGGVTCYDALTPQRIAEEFAWKETKAFVDEVYIPDLLVAAAYKDWTQYGGTDNFITFGEFPKDEYDLNSRFF
KPGVVFKRDFKNIKPFDMQIEEHVRHSWYEGAEARHPWKQTQPKYTDLHGDDRSWMKAPRYMGEPMETGPLAQVLIASQGHPKVKAVT
DAVLAKLGVGPEALFSTLGRTAARGIETAVIAEYVGMLQEYKDNIAKGDNVICAPWEMPQAEGVGFVNAPRGGLSHWIRIEDGKIGNFQLVVPST
WTLGPRCDKNVSPVEASLIGTPVADAKRPVEILRTVHSFDPCIACGVH

>d1frf1_e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio fructosovorans}

TPQSTFTGPIVVDPITRIEGLRIMVEENGKVDAWSSSQLFRGLEIILKGRDPRDAQHFTQRCGVCTYHALASSRCVDDAVKVSIPANARMMR
NLVMASQYLHDHVLHFYHLHALDWVDTAALKADPNKAALKASIDTARTGNSEKALKAVQDKLKFVESGQLGIFTNAYFLGGHKAYYLPPENVLI
ATAHYLEALHMQMVKAAASAMAILGGKNPHTQFTVGGCSNYQGLTKDPLANYLALSKEVCQFVNCEYIPDLLAVAGFYKDWWGGGTSNYLAFGEFA
TDDSSPEKHLSQFPGVITGRDLGVNDVLGAIYEDVKYSWYAPGGDGKHPYDGVTDPKTYKLDDKDHYSWMKAPRYKGKAMEVGPLARTFI
AYAKGQPDFKKVDMVLGKLSVPATALHSTLGRTAARGIETAVCANMEKWIKEADSGAKDNTLCAKWEMPEESKGVGLADAPRGSLSHWIRIK
GKKIDNFQLVVPSTWNLGPGRPQGDKSPVEEALIGTPIADPKRPVEILRTVHAFDPCIACGVH

>d1cc1l_e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfomicrobium baculum}

VKISIDPLTRVEGHLKIEVEVKDGKVVDAKCSGGMFGRGFEQILGRDRDPRDSSQIVQRICGVCPТАCTASVMAQDDAFGVKVTNGRITRNLIFGANY
LQSHILHFYHLAALDYVKGPDVSPFVPRYANADLLDIRKDGAKADATNTYGLNQYLKALEIRRICHEMVAMFGGRMPHVQGMVVGATEIPTADK
VAEYARFKEVQKVFIEEYPLIYTLGSVYTDLFETGIGWKNVIAFGVFPEDDYKTFLLKPGVYIDGKDEFDSKLVKEYVGHSSFDHSAPGLHYSVG
ETNPNDKPGAYSFVKAPRYKDKPCEVGPLARMWVQNPESPVGQKLLKELYGIEAKKFRDLGDKAFSIMGHRVLRAEETWLTAAVEKWLKQVQP
GAETYVKSEIPDAEAGTGTEAPRGALLHYLKIKDKKNIENYQIVSATLWNANPRDDMGQRGPIEEALIGVPVPDIKNPVNVGRLVRSYDPXLGCAVH

>d1e3db_e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit {Desulfovibrio desulfuricans}

TPRSNYTGPIVVDPITRIEGLRIVVEVEGGVIKEARSCATLFRGIETILKGRDPRDAQHFTQRTGVCTYTHALASTCLEDAINKPIPANATYIRNLVLG
NQFMHDHVLHFYHLHALDFDVTSALLADPAKAALKLANSISPRKATTEFAAVQAKLTFVASGQLGPFTNAYFLGGHEGYMDPEANLVCTAHYL
QALRAQVEAKGMAVFGAKNPHTQFTVAGGVTCEYALPERIKQFRELYVKARAFIEEVYIPDLLVASYKDWGKIGGTNNFMAFGEFPAPGGERD
LNSRWYKPGVIYDRKVGSVQPFDPSKIEEVRHSWYEGKARAPFEGETNPHTFMGDTDQYSWNKAPRYDGHAVETGPLAQMLVAYGHNHKTIK
PTIDAVLGKLNGLPEALFSTLGRTAARGIQLTVIAQQMENWLNEYENNIVKDKQIVVEDYAVPTSARGVGFADSRGGLSHWMTIEDGKIDNFQLVVP
TTWNLGPRDDKGVPSEAAALVGTPVADPKRPVEILRTIHSFDPCIACSTH

>d2frva_e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio gigas}

KKRPSVVLHNAECTGCSESVLRTVDPYDELILDVISMDYHETLMAGAGHAVEEALHEAIKGDFVCIEGGIPMGDGYYWGKVGGRNMYDICAЕ
VAPKAKAVIAIGTCATGGVQAQKPNPTGTVGVNEALGKLGVKAINIAGCPPNPMNFVGTVHLLTKGMPELDKQGRPVMFGETVHDNCPRLKHF
FEAGEFATSFGSPEAKKGYCLYELGCKGPDTYNNCPKQLFNQVNWPVQAGHPCIACSEPNFWDLYSPFYSA

>d1h2rs_e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfovibrio vulgaris}

LMGPRRPSVVLHNAECTGCSESVLRAFEPYIDTLILDTLSYHETIMAAGDAAEALEQAVNSPHGFIAVVEGGIPTAANGIYGKVNHTMLDIC
SRLPKAQAQVIAIGTCATGGVQAQKPNPTGAKGVNDALKLGVKAINIAGCPPNPMNFVGTVHLLTKGMPELDKQGRPVMFGETVHDNCPRLKHF
HFDAGEFAPSFESEEARKGWCLYELGCKGPVTMNNCPKIKFNQTNWVVDAGHPCIGCSEPDFWDAMTPFYQN

>d1frfs_e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfovibrio fructosovorans}

KHRPSVVLHNAECTGCTEAAIRTIKPYIDALILDTSYDQETIMAAAGDAAEALEQAVNSPHGFIAVVEGGIPTAANGIYGKVNHTMLDIC
AAAAKAKGIIIGTCSPYGGVQKAKPNPSQAKGVSEALGVTINIPGCCPPNPINFVGAVVHVLTGKIPDLDENGPRPKLYGELVHDNCPRLPHFEASEFA
PSFDSEEAKKGFCLYELGCKGPVTYNNCPKVLNFNQVNWPVQAGHPCIGCSEPDFWDATMTPFYEQG

>d1cc1s_e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfomicrobium baculum}

KKAPVIWVQQGCTGCSVSLLNAVHPRIKEILLDVISLEFHPTVMASEGEMALAHMYEIAEKFNGNFFLLVEGAIP TAKEGRYCIVGETLDAKHHHE
VTMMELIRDLPKSLATVAVGTCASYGGPAAEGNVTSKSRDFFADEKIEKLLVNPGCPHPDWMVGLTVAASHVLPTEHPLPELDDDRP
LLFFGDNIHENCPYLDKYDNSEFAETFKPGCKAELGCKGPSTYADCAKRRWNNGINWCVENAVCIGCVEPDFPDGKSPFYVAE

>d1e3da_e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio desulfuricans}

SRPSVVLHAACTGCSEALLRTYQPFIDLILDTISLDYHETIMAAAGEAAEAEALQAAVNGPDGFICLVEGA IPTGMDNKYGYIAGHTMYDICKNIPK
AKAVVSIGTCACYGGIQAAPNPTAAKGINDCYADLGVKAINVPGCPPNPLNMVGTLVAFLKGQKIELDEVGRPMFFGQSVDLCERRKHFDAGE
FAPSFNSEEARKGWCLYDVGCKGPETYNNCPKVLFNETNWPAAGHPCIGCSEPNFWDDMTPFYQN

>d1dg4a_e.20.1.1 (A:) DnaK {Escherichia coli}

LSLGIETMGGVMTTLIAKNTTIPKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKS LGQFNLDGINPAPRGMPQIEVTFIDADGILHVSACKNS
GKEQKITIKASSGL

>d1dkza_e.20.1.1 (A:) DnaK {Escherichia coli}

VLLLDVTPLSLGIETMGGVMTTLIAKNTTIPKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKS LGQFNLDGINPAPRGMPQIEVTFIDADGILHV
SAKDKNSGKEQKITIKASSGLNEDEIQKMRDAEANAEADRKEELVQTRNQGDHLLHSTRKQVEEAGDKLPADDKTAIESALTALETALKGEDKAAIE
AKMQELAQVSQKLMEIAQ

>d2bpr_e.20.1.1 (-) DnaK {Escherichia coli}

SIEGRVKDVLLDVTPSLGIETMGGVMTTLIAKNTTIPKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKS LGQFNLDGINPAPRGMPQIEVTFDI
DADGILHVSACKNSGKEQKITIKASSGLNEDEIQKMRDAEANAEADRKEELVQTRNQGDHLLHSTRKQVEEA

>d1ckra_e.20.1.1 (A:) DnaK {Rat (Rattus norvegicus)}

SENVQDLLLLDVTPLSLGIETAGGVMTVLIKRNNTTIPKQTQFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKFELTGIPPA PRGVQPQIEVTFIDAN
GILNVSADVDKSTGKENKITNDKGRSLKEDIERMVQEAEKYKAEDEKQRDKVSSKNSLE

>d1dqs_a_e.22.1.1 (A:) Dehydroquinate synthase, DHQS {Aspergillus nidulans}

PTKISILGRESIADFGLWRNYVAKDLISDCSSTTVLVTDTNIGSIYTPSFEAEFRKRAAEITPSPRLLIYNRPPGEVSKSRQT KADIEDWMLSQNPPCGR
DTVIALGGVIGDLTGFVASTYMRGVRYVQVPTTLLAMDSSIGGKTAIDTPLGKNLIGAIWQPTKIYIDLEFLETLPVREFINGMAEVKTAISEEE
FTALEENAETILKAVRREVTGPEHFRFEGTEELKARILASARHKAYVVSADEREGGLRNLLNWGHSGIGHAIEAILTPQILHGECVAIGMVKEAELARHLGI
LKGVA VSRIVKCLAAYGLPTSLKDARIRKLTAGKHCSV DQLMFN MALDKNDGPKKIVLLSAIGTPYETRASV VANEDIRVVL

>d1jq5a_e.22.1.2 (A:) Glycerol dehydrogenase {Bacillus stearothermophilus}

AAERVFISP A KVQGK NVITKIAN YLEG IGNKTVVIADEIVWKIAGHTIVNELKKG NIAAEVVFSGEASRNEVERIANIARKAEA AIVG VGGGKTLD
AKAVADEL DAYIVIVPTA STADAPT SALS VIY SDDGV FESYRFYKKNP DVLVDTKIIAN APPR LLAS GIADALATW VEAR SVIKSGGKT MAGG PI TIAA
AIAEKCEQTLFKYKGK LAYESV KAKV VTPA LEAV VEA NTLLS GLGF ESGG LAAA HAIH NGFTALE GEIHH LHGEK VAF GTLV QLAEE HSQQ E IERYI ELY
LCLDP VTLED I KLKD ASRED I LVKA AATAE GETI HNA FNV TADD VADA IF AAD QYAK YKEK

>d1kq3a_e.22.1.2 (A:) Glycerol dehydrogenase {Thermotoga maritima, TM0423}

HMITTTIFPGRYVQGAGA INILEE ELSRFGERAFV VIDD FVDK NVLGEN FF SFTK VRVN KQIF GGECS DEEIER LSGL VEEET DVVGIGGGKTL DTAK
AVAYKLKP VVIVPTA STDAPCS ALSVIY TPNG EFKY LFLPRN PDV VLV DTEIVAKA PARFLV AGMG DALATW FEAESCKQY APNMTGRLGSM TAY
ALAR CYETLLEYGV LAKRS VEEKS VTPA LEKIVEA NTLLS GLGF ESGG LAAA HAIH NGFTALE GEIHH LHGEK VAF GTLV QLAEE HSQQ E IERYI ELY
VGLPTT LAEIG LDGV SDE DLMK VAEKAC DKNETI HNEP QPVTS KDV FF ALKA ADRY GRMR KNL

>d1lci_e.23.1.1 (-) Luciferase {Firefly (Photinus pyralis)}

AKNIKKGPAPFYP LEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVNITYAEYFEMSVRLAEAMKRYGLNTNHRI VV CSEN SLQFFMPV LGAL FIGVA
VAPANDIYNERELL NSMN ISQPTV VFVSKK GLQK ILNVQ KKLPII QKII MDSK TDYQ GFQS MYT FVTSHL PPGFNEYDFV PESFDRDKTIALIM NSSGS
TGLPKGVALPHRTACVRFSHARDPIFGNQIIPDTA ILSV VP FHGF GMFT TLGYL ICGR FRV VL MYR FEE ELF RLSL QDYK IQS ALLV PTL FSFFAK STL IDK
YDLSNLHEIASGGPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPGAVGKVVPFFEA KVVD LDTG KTLGVN QRGE LCV RGPM IMSGY
VNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDR LKSLIKYKG YQVAPAELESILLQHPNIFDAGVAGLPDD DAGELPA AVVLEHG KTM TEKEIV
DYVASQVTTAKKL RGGVVVF DEV PKGL TGKLD KIRE LIKAKK

>d1amua_e.23.1.1 (A:) Phenylalanine activating domain of gramicidin synthetase 1 {Bacillus brevis}

GTHEEEQYLFAVNNTKA EYPRDKTIHQLFEEQVSKRPNVVAICENEQLT YHELN V KANQLARIFIEKGIGKDTL VGIMMEKSIDLFIGI AVL KAGGAY
VPI DIEYPKERI QYI LDDSQARMLL TQKHLV LHIHN IQFNGQ VEI FEEDT KIRE GTNLH VPSKSTD LAYVI TSGT GNPK GTM LEHK G ISNL KVFFENSL
NVTEKDRIGQFASISFDASV WEMF MALLT GAS LYI ILDTI NDFV KF EQYI NQKE ITV TLP PTYV VHLD PERI LS I QT LITAG SATPS SLV NKW KEK VTYI N
AYGPTETICATTW VATK ETI GHSP VPIG APIQ NTQI YIVDEN LQLK SVGEAGE L CIGG E GLARG YWKRPEL TSQKF VDN PFV PG EKLY KTGD QAR WLS
DGNIEYLGRIDNQVKIRGHR VELE EESILL KHMYI SETAVS VHKDHQ E QPYLCAYF VSEK HIPL EQLR QFS SEEL PTY MIPSYFIQLDKMPLTSNGKIDR

KQLPEPDLT

>d1ad2__ e.24.1.1 (-) Ribosomal protein L1 {Thermus thermophilus}

KRYRALLEKVDPNKIYTIDEAAHLVKELETAKFDETVEHAKLGDPRRSRSDQNVRGTVSLPHGLGKQVRVLIAKGEKIKEAEAGADYVGEEIIQKIL
DGWMDFDAVVATPDVMGAvgSKLGRILGPRGLLPNPKAGTVGFNIIGEIREIKAGRIEFRNDKTGAIHAPVGKACFPPEKLADNIRAFIRALEAHKP
GAKGTFRLRSVYVTMMGSPVRINPHS

>d1cjsa_e.24.1.1 (A:) Ribosomal protein L1 {Archaeon Methanococcus jannaschii}

MDREALLQAVKEARELAKPRNFTQSFEIATLKEIDMRKPENRIKTEVVLPHGRGKEAKIAVIGTGDLAKQAELGLTVRKEEIEELGKNKRKLRKIAKA
HDFIAQADLMPLIGRYMGVILGPRGKMPKPVPANANIKPLVERLKTVVINTRDKPYFQVLVGNEKMTDEQIVDNIEAVLVVAKKYEKGLYHIKDA
YVKLTMGPAVKVKK

>d1dwua_e.24.1.1 (A:) Ribosomal protein L1 {Archaeon Methanococcus thermolithotrophicus}

MDRENILKAVKEARSLAKPRNFTQSLSLILKELDLSRPENRLKEQVVLPGNGRKEPKIAVIAKGDLAAQAEEMGLTVRQDELELGKNKKMAKKIA
NEHDFFIAQADMMPLIGVGTLPVLGPRGKMPQPVPANANLTLVERLKTVVINTRDKPLFHVVLVGNNEKMSDEELAENIEAILNTSRKYEKGLYHV
KSAYTKLTMGPPAQIEK

>d1dn1a_e.25.1.1 (A:) Neuronal Sec1, NSec1 {Rat (Rattus norvegicus)}

IGLKAVVGEKIMHDVKKVKKGEWKVLLDQLSMRMLSSCKMIDIMTEGIVDINKREPLPSLEAVYLITPSEKVHSLISDFKDPTAKYRAA
HVFFTDSCPDAFLNELVSKRAAKVIKLTIEINIAFLPYESQVYSLSDASFQSFYSPHKAQMKNPILERLAEQIATLCATLKEYPAVRYRGEYKDALLAQ
LIQDKLDAYKADDPTMGEGPDKARSQQLLDRGFDPSSPVHLHETFQAMSYDLPPIENDVYKYETSGIGEARVKEVLLDEDLWIALRHKHIAEVSQE
VTRSLKDFSSSKRMNTGEKTTMRDLSQMLKKMPQYQKELSKYSTHLHAEDCMKHYQGTVDKLCRVEQDLAMGTDAEGERIKDPMRAIVPILLDA
NVSTYDKIRIILLYIFLNGITEENLNKLIQHAQIPPEDSEITNMAHLGVPIVTDSTLRRSKPERKERISEQTQLSRWTPIIKDIMEDTIEDKLDTHYPYI
STRSSASFSTTAVSARYGHWHKNKAPGEYRSGPRLIIFLGGVSLNEMRCAYEVQTANGKWEVLIGSTHILTPQKLDTLKKLNKTDEEI

>d1epua_e.25.1.1 (A:) Neuronal Sec1, NSec1 {Longfin inshore squid (Loligo pealei)}

ALKTAVHEKIMNDVVLAVKKNAEWKVLIVDQLSMRMSVSACKMHEIMSEGITLVEDINRRREPLPLEAVYLITPTEESVKCLMADFQNPDNPQYR
GAHIFFTEACPEELFKELCKSTTARFIKTLKEINIAFLPYESQIFSLSPDTFQVYNNPSRAQGGIPNKERCAEQIATLCATLGEYPSVRYRSDFDENASFAQ
LVQQKLDAYRADDPTMGEGPQKDRSQLLDRGFDPISPLLHELTFOAMAYDLPPIENDVYKYVNTGGNEVPEKEVLDEKDDLWVEMRHQHIAVV
SQNVTKKLQFADEKRMGTAADKAGIKDLSQMLKKMPQYQKELSKYSTHLHAEDCMKQYQQHVDKLCKVEQDLAMGTADGEKIRDHMRNIV
PILLDQKISAYDKIRIILLYIHKGGESENLAQVQAHIPAEEKWIINDMQNLGVPIQDGRRRKIPQPYHTHRKERQADHTYQMSRWTPYMKDIM
EAAVEDKLDRHYPFLNGGGPRPSCQQPVSVRYGHWHKDKGQASYKSGPRLIIFVGGISYSEMRSAYEVQTAKNNWEVILGSTHILTPEGLLRDLR
KISNP

>d1e2ua_e.26.1.1 (A:) Hybrid cluster protein (prismane protein) {Desulfovibrio vulgaris}

MFCFQCQETAKNTGCTVKGMCGKPEETANLQDLLIFVLRGIAIYGEKELKELGQPDERSNDDFVQLGLFATITNANWDDARFEAMISEGLARRDKLRN
AFLAVYKAKNGKDFSEPLPEAATWTGDESTAFAEKAKSVGILATEINEDVRSRRELLIIGLGVAAAYAEHAAVLGRKTEIDFMLEALASTTKDLSVDEM
ALVMKAGGMAVTMALLDEANTTYGNPEITQVNIGVGKNGPILISGHDLKDMAELLKQTEGTGVDVYTHGEMLPANYPAFKKYPHFVGNYGG
WWQQNPEFESFNGPILLTTNCLVPLKKENTYLDRLYTTGVVGYEGAKHIADRPGAGAKDFSALIAQAKKCPPVETGSIVGGFAHHQVLALADKVV
EAVKSGAIKRFVVMMAGCDGRQKRSYYTEVAENLPKDTVILTAGCAKYRYNKLNLGDIGGIPRVLADGCNDSYSLAVIALKEVFGLDDINDLPSV
DIAWYEQKAVAVLALLFLGVKGIRLGPFLPAFLSPNVAKLVENFNKPIGTVQDDIAAMMAGK

>d1jjya_e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase {Carboxydothermus hydrogenoformans}

QNLKSTDRAVQQMLDKAKREGIQTVWDRYEAMKPQCGFGETGLCCRHCLQGPCRINPFGDEPKVGICGATAEVIVARGLDRSIAAGAAGHSGHAK
HLAHTLKKAVQGKAASYMIKDRKLHSIAKRLGIPTEGQKDEDIALEVAKAALADFHEKDTPLVWTTVLPPSRVKVLSAHLGIPAGIDHEIAEIMHRT
SMGCDADAQNLLGGRLCSLADLAGCYMGTDLADILFGTPAPVVTESNLGVLKADAVNVAVGHNPVLSDLIVSVSKEMENEARAAGATGINVVG
CCTGNEVLMRHGIPACTHSVSQEMAMITGALDAMILDYQCIQPSVATIAECTGTTVITMEMSKITGATHVNFAEEAENAKQILRAIDTFKRRKG
KPVEIPNIKTVVAGFSTEAIINALSKLNANDPLKPLIDNVVNGNIRGVCLFAGCNNVKVHQDQNFTTIARKLLKQNVLVATGCGAGALMRHGFM
PANVDELCGDGLKAVLTAIGEANGLGGPLPPVLHMGSVDNSRSVALAANRLGVDMDRLPVVASAAQAMHEKAVAIGTWAVTIGLPTHIGVF
PPITGSLPVTVQILTSSVKDITGGYFIVELDPQVAADKLLAINERRAGLGLPR

>d1jqka_e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase {Rhodospirillum rubrum}

ETAWHRYEKQQPQCGFSGAGLCRCLKGPCRIDPFGEQPKYGVCGADRDТИARHLVRMIAAGTAHSEHGRHIALAMQHISQGELHDYSIRDEA
KLYIAIKTLGVATEGRGLLAIVGDLAAITLGFQNQDYDKPCAWLAASLTPRRVKRLGDLPLPHNIDASVAQTMSRTHVGCDADPTNLILGGLRVA
MADLDGSMLATELSDALFGTPQPVVSAANLGVMKRGAVNIAVNGHNPMLSDIICDVAADLRDEAIAAGAAEGINIIGCCTGHEVMMRHGVPLAT
NYLSQELPILTGALEAMVVVDVQCIMPSLPRIAECFHTQIITDKHNKISGATHVPFDEHKAVETAKTIIRMAIAAFGRDPNRVAIPAFKQKSIVGSAEA
VVAALAKVNADDPLKLPLDNVNVNGNIQGVLFVGNCNTKVQQDSAYVDLAKSLAKRNVLVLATGCAAGAFAKAGLMTSEATTQYAGEGLKGVLSAI
GTAAGLGGPLPLVMHMGSVDNSRAVALATALANKGVDSLSDPLVASAPECMSEKALAIQSWAVTIGLPTHVGSPPPVIGSQIVTKLTETAKDLVG
GYFIVDTDPKSAGDKLYAAIQERRAGL

>d1h5wa_e.27.1.1 (A:) Upper collar protein gp10 (connector protein) {Bacteriophage PHI29}

RQKRNRFIHYLNLYQLFEEWENLPPTINPSFLEKSIHQFGYVGFYKDPVISYIACNGALSGQRDVYNQATVRAASPVYQKEFKLYNYRDMKE
EDMGVVIIYNNDMAFPPTTLEFAELAEALKIEISVNQNAQKTPVLIRANDNNQLSLKQVYNQYEGNAPVIFAHEALDSDSIEVFKTDAPYVVDKLN
AOKNAVWNEMMTFLGKNNANLEKKERMVTDEVSSNDEOJESSGTFLKSREEFACEKINELYGLNVKVKFRYDI

>d1io1a_e.32.1.1 (A:) F41 fragment of flagellin {Salmonella typhimurium}

NIGKLTQASRNANDGISIAQQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLSIQAEITQLNEIDRVSQQTQFNGVKVLAQDNTLTIQVGANDG
ETIDIDLKQINSQTLGLDTLNVQQKYKVSDTAATVTGYADTTIALDNSTFKASATGLGGTDQKIDGDLKFDDTTGKYAKVTVTGGTGKDGYEVSDK
TNGEVTLAGGATPLTGGPATATEDVKNVQVANADLTEAKAALTAAGVTGTASVVKMSYTDNNNGKTIDGLGLAVKGDDYYSATQNKGDSISINTTK
YTADDGTSKTALNKGADGKTEVVSIGGKTYAASKAEGHNFKAQPDLEAAATTENPLQKIDAALAQVDTLRSLAAVQNRFNSAITNLGNTVN
NLTSAR

>d1htya_ e.33.1.1 (A:) Golgi alpha-mannosidase II {Fruit fly (*Drosophila melanogaster*)}

CQDVVQDVNVQMLYDGRMSFKDIDGGVWKQGWNIKYDPLKYNAAHHKLKVFFVPHSHNDPGWIQTFFEEYYQHDTKHILSNALRHLDNP
MKFIWAEISYFARFYHDLGENKKLQMKSIVKNGQLEFVTGGWVMPDEANSHWRNVLLQLTEGQTWLQFMNVTPTASWAIDPFGHSPTMPYIL
QKSGFKNMLIQRTHYSVKELAQQRQLEFLWRQIWDNKGDALTHTHMMPFYSDIPHTCGPDPKVCQDFKRMGSGLSCPWKVPPRTISDQN
VAARSDLVQDWKKKAELYRTNVLLPLGDDFRFKQNTEDVQRVNYERLFEHINSQAHFNVQAQFGTLQEYFDAVHQAERAGQAEPFTLSGDF
TYADRSNDYWSGYYTSRPYHKRMDRVLMHVRAAEMLSAWHSWDGMARIEERLEQARRELSLFQHHGDITGTAKTHVVVDYEQRMQEALKAC
QMVMQQSVYRLTKPSIYSPDFSFSYFTLDDSRWPMSGVEDSRTIILEDILPSKHVMHNTLPHWREQLVDFYSSPVSVTLANNPVEAQVSP
VWSWHHDLTKTIHQPQGSTTKYRIIFKARVPPMGLATYVLTISDKPEHTSYASNLRLKNPDSLQGQYPEDVKFGDPREISLRVGNGPTLAFSEQGLL
KSIQLTQDSHPVPHFKFLKGVRSHGDRSGAYLFLPNGPASPVELGQPVVLTKGKLESSSVSGLPSVWHQTIMRGGAPEIRNLVDIGSLDNTIEVMR
LETHIDSGDIFYTDLNGLQFIKRRRLDKLPLQANYYPIPSGMFIEDANTRLLTGQPLGGSSLASGELEIMQDRLLASDDERGLGQGVLDNKPVLIYR
LVLEKVNNCVRPSKLHPAGYLTSAAHKASQSLLDPLDKFIFAENEWIGAQGQFGGDHPSAREDLDSVMRRLTKSSAKTQRVGYVLHRTNLMQCGT
PFEHTOKLDVCHLLPNVARCERTTLEFLONLEHLDGMVAPEVCPMETAAYVSSHS

>d1knza_e.34.1.1 (A:) NSP3 homodimer {Simian 11 rotavirus}

TQQMAVSISSFEAAVVAATSALENMGIEYDYQDIYSRKVNKFDFMDSGVKNNPIGKAITDQALNNKFGSAIRNRNWLA DTSRPAKLDDEVN
KLRLMMILSSKGIDQKMRVLNACFSVKRIPGKSSSIKCTKLMRDKLERGEVEVDDSFVDEKM

>g1jmu.1 e.35.1.1 (A;;B;) Membrane penetration protein mu1 {Reovirus}

TINVTGDGVFKPSAETSTAVPSLSPGMLNXPQGPVWIAIGDETSVTPGALRRMTSKDIPETAIINTDNGAVPSESALVPYNEPLVVTHAE
ANFTKAEMALEFNREFLDKLRVLVSVPKYSQDLTYVDCYVGVSARQALNNFQKQPVITPTRQTMYVDSIQAALKALEKWEIDLRAVATQLPTNVPIG
EVSCPMQSIVKLDDQLPDDSLIRRYPKEAAVALAKRNQGIQWMDVSEGTVMNEAVNAVASALAPSASAPPLEEKSKLTEQAMDLVTAEEPEIIA
SLVPVPAPVFAIPPKPADYNVRTKIDEATWLRMIPKTMGTLFQIQVTDNTGTNWHFNLRGGRVNVLDQIAPMRFLDLGGKSYKETSWDPNGK
KVGFIVFQSKIPFELWTAASQIGQATVVNVQLYAEDSSFTAQSIIATTSLAYNEPEQLNKTDPEMNYYLLATFIDSAAITPTNMTPQDVWDALLTMS
PLSAGEVTVKGAVVSEVVPaeligSYtPESLNAsLPNDAARCMIDRASKIAEAIKIDDDAGPDEYSPNSVPIQGQLAISQLETGYGVRIFNPKGILSKIAS
RAMOAFIGDPSTIIQAAVLSDKNNWIALAOGVKTSRTKLSAGVKTAVSKLSSSIONWTOGFLDKVSTHFPAP

>d2btva_e.28.1.1 (A:) BTV inner layer core protein vp3 {Bluetongue virus, strain 1}

VDFTVPDVQQLDDIKALAAEQVYKIVKVPSTSFRHVTQSRDRVLRVDTYYEEMSQVGDVITEDEPEKFYSTIIKKVRFIRGKGSFILHDIPARDHGM
EVAEPEVLGVFKNVLPVLTAEHRAMIQNALDGSIENGNVATRDVDFIGACSEPIYRINYRLQGYIEAVQLQELRNSIGWLERLGQRKRITYSQEVLT
DERRQDMIWVLAOLQPVNPOVVWDVPRSSIANLIMNIATCLPTGEYIAPNPRISITLTQRTTTGPFAILTGSTPAQQLNDVRKIYIALLMFPGQIILDL

KIDPGERMDPAVRMVAGVVGHLFTAGGRFTNLTNQNMARQLDIALNDYLLYMYNTRVQVNYGPTGEPLDFQIGRNQYDCNVFRADFATGTGYNG
WATIDVEYRDPAPYVHAQRYIRYCGIDSRELINPTTYGIGMTYHCYNEMRLMLVAAGKDSEAAYFRSMLPFHMVRFARINQIINEDLHSVFSLPDDM
FNALLPDLIAGAHQNADPVVLDWSWISLWFAFNRSFEPTHRNELEMIAPILESVYASELSVMKVDMRHLSLMQRFFPDVLIQARPSHFWKAVLNS
PEAVKAVMNLSHSHNFNIRDMMRWVLLPSLQPSLKLVLEEEAWAAANDFEDMLMTDQVYMHARDMLPEPRLDIERFRQEGFYTNMILEAPPEID
RVVQYTYEIRLQANMGQFRAALRRIMDDDWVRFGGLVRTVRVKFFDARPPDILQGLPFSYDTNEKGGLSYATIKYATETTIFYLIYNVEFSNTPD
SLVLINPTYTMTKVFINKRIVERVRVGQILAVLNRRFVAKGKMRIMDTQSLKMGTKLAAPTV

>d1cola_f.1.1.1 (A:) Colicin A {Escherichia coli}

AKDERELLEKTSELIAGMGDKIGEHLGDKYKAIKDIADNIKNFQGKTIRSFDAMASLNKITANPAMKINKADR DALVNAWKHVDAQDMANKLG
NLSKAFKVADVVMKVEKvreksiegyetgnwgplmleveswvlsgiassvalgifsatlgayalslgvpaivagi gillaavvgaliddkfadalnnei
IR

>d1a87_f.1.1.1 (-) Colicin N {Escherichia coli}

SAKVGEGITIPDNSKPGRYISSNPEYSLLAKLIDAESIKGTEVYTFRKGQYVKTVPDSNIDKMRVDYVNWKGPYNNKLVKRFVSQFLFRKEEK
NEKEALLKASELVS GMGDKLGEYLGVKYKNVAKEVANDIKNFHGRNIRSYNEAMASLNKVLANPKMKVNKS DKDAIVNAWKQVNAKDMANKIGN
LGKAFKVADLAIKVEKIREKSIEGYNTGNWGPLLVEVESWIIGGVVAGVAISLFGAVLSFLPISGLAVTALGVIGIMTISYLSFIDANRVSNIINNISVIR

>d1cii_1 f.1.1.1 (451-624) Colicin Ia {Escherichia coli}

DAINFTTEFLKSVEKYGAKAEQ LAREMAGQAKGKIRNVEEALKTYEKYRADINKKINA DRAAIAAALESVKLSDISSNLNRFSRGLGYAGKFTSLAD
WITEFGKAVRTENWRPLFKTETIIAGNAATALVALVFSILTGSALGIIGYGLLMAVTGALIDESLVEKANKFW

>d1f0la3 f.1.2.1 (A:201-380) Diphtheria toxin, middle domain {Corynebacterium diphtheriae}

CINLDWDVIRDKT KTKIESLKEHGPIKNKMSESPNKTVSEEKAKQYLEEFHQTALEHPESELKTVGTGTPVFA GANYAAWAVNVAQVIDSETADNLE
KTTAALSILPGIGSVMGIA DGAVHHNTEEVAQSIALSSLMVAQAIPLV GELVDIGFAAYNFV ESIINLFQVVHNSYNRPAY

>d1dlc_3 f.1.3.1 (61-289) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}

TTKDVIQKGISVVG DLLGVVGFPGGALSFYQSFLNTIWPSED PWKA FM EQV EALMDQKIA DYAKN KALAELO QGLQNN VEDYV SALSSWQKNPV
SSRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEVFLTTYAQAANTHFLLKDAQIYGE EWGYEKEDIAEFYKRQLKLTQEYTDHCVKWYNVGLDK
LRGSSYESWVN FN RYRREM TLVLD LIALFPLPYDVR

>d1ji6a3 f.1.3.1 (A:64-290) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis, CRY3bb1}

DAVGTGISVVGQILGVVGP FAG ALTSFYQSFLNTIWP SADP WKA FMA QV E V L IDKKIEEYAKS KALAELO QGLQNN FEDYV NAL NSW KKPLS LRS
KRSQDRIRELFSQAESHFRNSMPSFAVSKFEVFLPTYQA ANTHLLL KDAQVFGEEWGSSEDVA EFYHRQLKLTQ QT DHC VN W NV GLN GLR
GSTYDAWVKF NFR RREM TLVLD LIVLFPFYDIR

>d1ciy_3 f.1.3.1 (33-255) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis, CRYIA (A)}

YTPIDISLTLQFLLSEFVPGAGFVLGLVDIWI GFGPSQWDAFLVQIEQLINQRIEFARNQAISRLEG LSNLYQIYAESFREWEADPTNPALREEMRIQF
NDMNSALT TAIPLLAVQNYQVPLLSVYVQAANLHSVLRDVSFGQRWFDAATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPD SRDWVRY
NQFRRELTLVLDIVALFSNYSRYY

>d1i5pa3 f.1.3.1 (A:1-263) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

MNNV LNSG RTTICDAYNVVAHD PFSFEHKSLDTIQKEW MEW KRTDH SLYVAPV VGTVSSFLKKVGSLIGKRIL SELV GII F P SG STN LM QDIL RE TE
QFLNQRLNTDTLARVNAELIGLQANIREFNQQV DNPLNTQNPVPLSITSSVNTMQQLFLNRLPQFQI QGYQ LLLLPLFAQAANM HLSFIRDVILNA
DEWGISAATLRTYRD YL RN YTRD YS NCINTYQTA FRGLNTRLHD MLE FRT YMFLN VFEY VSI WSLFK

>d1g5ma_f.1.4.1 (A:) Bcl-2 {Human (Homo sapiens)}

HAGR TYDNREIV MKYI HYL KLSQ RG YEW D AG DD VEEN R TEA PEG TE SEV V H LA LR QAG D DF S R R YRG D FA EM SS QL H LTP FT AR GR F AT V V E E L F R
DG V NW GRIV AFF E FGG V MC V ES V N RE M SP L V D N I AL W M T E Y L NR H L HT WI QD NG G W D AF V E LY GPS MR

>d1bxla_f.1.4.1 (A:) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSMAMS QSN REL VVDF LSYKLSQ KG YWS QF SD VEE NR TEA PEG TE SE AV K Q AL RE AG D E F E L R Y R RA F S D L T S Q L H I T P G T A Y Q S F E Q V V N E L F R D
GV NW GRIV AFF S FGG AL C V S D K E M Q V L V S R I A A W M A T Y L N D H L E P W I Q E N G G W D T F V E LY G N N A A A E S R K G Q E R L E H H H H H

>d1xl_f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSMAMS QSN REL VVDF LSYKLSQ KG YWS QF SD VEE NR TEA PEG TE SE M P S A I N G N P S W H L A D S P A V N G A T G H S S L D A R E V I P M A A V K Q A L

REAGDEFELRYRRAFSDLTSQHLITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSGGALCVESVDKEMQVLVSRIAAMATYLNDHLEPWIQENG
GWDTFVELYGNAAAESRKQERLEHHHHHH

>d1maz_ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSQSNNRELVDFLSYKLSQKGYSWSQFDVEENRTEAPEGESEMTPSAINGNPSPWHLADSPAUNGATGHSSLDAREVIPMAAVKQALREAGD
EFELRYRRAFSDLTSQHLITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSGGALCVESVDKEMQVLVSRIAAMATYLNDHLEPWIQENG
VELYG

>d2bida_ f.1.4.1 (A:) Proapoptotic molecule Bid {Human (Homo sapiens)}

GSMDCEVNNGSSLDECITNLLVFGFLQSCSDNSFRRELDALGHELPVAPQWEGYDELQTDGNRSSHSRLGRIEADSESQEDIIRNIARHLAQVGDS
MDRSIPPGLVNLALQLRNTSRSEEDRNRLATALEQLLQAYPRDMEKEKTMVLALLAKKVASHTPSLLRDVFHTTVNFINQNLRTYVRSLARNG
MD

>d1ddba_ f.1.4.1 (A:) Proapoptotic molecule Bid {Mouse (Mus musculus)}

MDSEVSNGSGLGAKHITDLLVFGFLQSSGCTRQELEVLRGELPVQAYWEADLEDELQTDGSQASRSFNQGRIEPDSESQEEIIHNIA
RHQAQGDEM
DHNIQPTLVRQLAAQFMNGSLSEEDKRNCALAKALDEVKTA
PRDMENDKAMLI
MTMLLA
KKVASHAPSLLRDVFHTTVNFINQNLFSYVRNLVRN
EMD

>d1f16a_ f.1.4.1 (A:) Proapoptotic molecule Bax {Human (Homo sapiens)}

MDGSQEPRGGGPTSSEQIMKTGALLQGFQDRAGRMMGEAPELADPVPQDASTKKSECLKRIGDELDNSNMELQRMIAAVD
TDSPREVFFR
AADMFSDGNFNWGRVVALFYFASKVLKALCTKVPELIRTIMGWT
LDFLERLLGWIQDQGGWDGLLSYFGPTWQTVTIFVAGVLT
ASLTI
KKM
G

>d1ikpa3 f.1.5.1 (A:252-394) Exotoxin A, middle domain {Pseudomonas aeruginosa}

EGGSLAALT
AHQACHLPE
LFTTRHRQPRGA
EQLEQCGYPV
QRLVALY
AARLSWNQDV
QVIRNALASPG
SGGD
LGEAIRE
QPEQARL
ALT
AAA
ESE
RFVRQGTGN
DEAGAANAD
VSLTCP
VAAGECAG
PADSGD
ALLERNY

>d1c3wa_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIW
LALGTALM
GLGTL
YFLVK
GMGV
SDPDA
KKFYAIT
LVP
AFT
MYLS
MLLG
YGLT
MV
PF
GGE
QNPI
WARY
ADWL
FTPL
LLDL
ALLVD
ADQGT
ILALVG
GADG
IMIGT
GLVG
ALT
KV
SYRF
VWW
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ISTA
AMLY
IILY
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LFFG
FSMR
PEV
ASTF
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SAY
PV
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LIG
SEGAG
IV
PLNI
ETL
LFM
VLD
VSA
KVG
FG
L
L
RS
RA
IFG

>d1c8sa_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIW
LALGTALM
GLGTL
YFLVK
GMGV
SDPDA
KKFYAIT
LVP
AFT
MYLS
MLLG
YGLT
MV
PF
GGE
QNPI
WARY
ADWL
FTPL
LLLN
LALLVD
ADQGT
ILALVG
GADG
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>d1e12a_ f.2.1.1 (A:) Halorhodopsin {Halobacterium salinarum}

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QESATTQKAKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIMFTPAFFAKTSAVYNPIYIMMNQFRNCMVTLCCGKNPLGDDEAST
TVSKTETSQVAPA

>d1dxrh2 f.2.1.2 (H:1-36) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

MYHGALAQHLDIAQLVWVYAQWLVIWTVVLLYLRRED

>d1dxrl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

ALLSFERKYVRGGTLIGGDLDFWVGPFVGFVGSAIFFILGVSLIGYAASQGPTWDPFAISINPPDLKYGLGAAPLLEGGFWQAITVCALGAFISW
MLREVEISRKLGIGWHVPLAFCVPIMFCVLQVFRLPILLGSWGHAFPYGILSHLDVNNFGYQYLNWFYNPNGHMSVSFLVNAMALGLHGGIILS
VANPGDGDVKTAEHENQYFRDVVGYSIGALSIHRLGLFLASNIFTGAGFTIASGPFWTRGWPEWWGWWLDIPFWS
>d1dxrm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

ADYQTIYTQIQARGPHITVSGEWGDNDRVGKPFYSWLGKIGDAQIGPIYLGASGIAAAFGSTAILILFNMAAEVHDPLQFRQFFWGLYPPKAQ
YGMGIPPLHDGGWWLMAGLFMTLSGSWWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVPFGIWP HIDWLAFSIRYGNFY
YCPWHGFSIGFAYCGGLFAAHGATILAVARFGGDREIEQITDRGTAVERAALFWRWWTIGFNATIESVHRWGFFSLVMVMSASVGILLTGTVDN
WYLWCVKHGAAPDYPAYLPATPDPASLPGAKP

>d1qovh2 f.2.1.2 (H:11-35) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

DLASLAIYSFWIFLAGLIYLYLQTN

>d1qovl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

ALLSFERKYRVPGGTLVGGNLDFWVGPFYVGFFGATFFAALGIILIAWSAVLQGTWNPQLISVYPALLEYGLGGAPLAKGGLWQIITCATGAFVS
WALREVEICRKLIGIGYHPPFAFAFAILAYLTVLFRPVMMGAWGYAFPYGIWTHLDWVNSNTGYTYGNFHYNPAHMIAISFFTNALALALHGALVSA
ANPEKGKEMRTPDHEDTFRDLVGYSIGTLGIHRLGLLLSLSAVFFSALCMIITGTIWFDQWVWDWWQWWVLPWWANIPGGING

>d1qovm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

AEYQNIFSQVQRGPADLGMTEDVNLANRSGVGPSTLLGWFNAQLGPIYLGSLGVLSLFSGLMWFFTIGIWFYWQAGWNPAVFLRDLEFSLEP
PAPEYGLSFAAPLKEGGLWLIASFMMFVAWSSWGRTYLRAQALGMKHTAWAFLSAIWLWMVLGFIRPILMGWSSEAVPYGIFSHLDWTNNFS
LVHGNLFYNPFHGLSIAFLYGSALLFAMHGATILAVSRFGGERELEQIADRGTAERAALFWRWWTMGFNWTMEGIHRWAIWMAVLVLTGGIGILL
SGTVVDNWYVVGQNHG

>d2rcrh2 f.2.1.2 (H:1-35) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

MVGTAFGNFDLASLAIYSFWIFLAGLIYLYLQTN

>d1eysh2 f.2.1.2 (H:7-43) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

HYIDAAQITIWAFLWFFGLIIYLRRDKREGYPLDS

>d1eysl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

AMLSFEKKYVRGGTLIGGDLDFWVGPFYVGFFGVGFCFTLLGVLLIVWGATIGPTGPTSDLQTYNLWRISIAPPDSYGLRMAPTEGGLWQIITI
CAAGAFISWALREVEICRKLIGIFHVPFAFSFAIGAYLVLVFRPLLMGAWGHGFPYGILSHLDWVNVGYQFLHFHNPAHMLAISFFTNCALSM
HGSLILSVTPNQQRGEVKTSEHENFFRDIVGYSIGALAIHRLGLFLALSAAFWASCVCILISGPFWTRGWPEWWNWWLELPLW

>d1eysm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

PEYQNIQTVQVRAPAYPGVPLPKGNLPRIGRPISFYWLKGKIGDAQIGPIYLGTLTLSIFFGLVAISIIGFNMLASVHWDVFQFLKHFFWLGLEPPPPQY
GLRIPPLSEGGWWLIAGLFLTLSILLWWVRTYKRAEALGMSQHLSWAFAAAIFFYLVLFIRPVMMGSWAKAVPFGIFPHLDWTAFSIRYGNLYNN
PFHMLSIAFLYGSALLFAMHGATILSVSRFGGDREIDQIADRGTAEEGAALFWRWWTMGFNATMESIHRWAWWCAVLTVITAGIGILLSGTVVDNWY
LWAVKHGMAPAYPEVVTAVNPYET

>d1ocra1 f.2.1.3 (A:) Cytochrome c oxidase {Cow (Bos taurus)}

MFINRWLFSTNHKDIGTLYLLGAWAGMVGTLALSLLIRAEGLQPGTLLGDDQIYNNVVTAAHFMVIMFFMVPIMIGFGNWLVPLMIGAPDMAF
PRMNNMSFWLPPSFLLLASSMVEAGAGTGWTVPPLAGNLAHAGASVDLTIFSLHLAGVSSILGAINFTTIINMKPPAMSQYQTPLFWVSVMIT
AVLLLSPVLAAGITMLLDRNLNTFFDPAGGGDPILYQHLFWFFGHPEVYILILPGFGMISHIVTYSGKKEPFGYMGMVWAMMSIGFLGFIWVA
HHMFTVGMVDVDRAYFTSATMIIAIPGKVFSWLATLHGGNIKWSAMMWALGFIFLFTVGGLTGIVLANSSLIVLHDTYVVVAFHYVLSMGA
VFAIMGGFVHWFPLFSGYTLNDTWAKIHFAIMFVGVNMTFFPQHFLGLSGMPRRYSDYPDAYTMWNTISSMGSFISLTAVMLMVFIIWEAFASKR
EVLTVDLTTNLEWLNCGPPYHTFEEPTYVNLK

>d1ocrb2 f.2.1.3 (B:1-90) Cytochrome c oxidase {Cow (Bos taurus)}

MAYPMQLGFQDATSPIMEELLHFHDHTLMIVFLISSLVYIISLMLTTKLHTSTMDAQEVETIWTILPAIIILIALPSLRILYMMDEI

>d1ocrc1 f.2.1.3 (C:) Cytochrome c oxidase {Cow (Bos taurus)}

MTHQTHAYHMVNPSWPPLTALSALLMTSGLTMWFFNSMTLLMIGLTTNMLTMYQWWRDVIRESTFQGHHTPAVKGLRYGMILFISEVLFF
TGFFWAFYHSSLAPTELGGCWPPGTIHPLNPLEVPLNTSVLASGVSVTAHHSLMEGDRKHMLQALFITITLGVYFTLLQASEYYEAPFTISDGVV
GSTFFVATGFHGLHVIGSTFLIVCFRQLKFHFTSNHHFGFEAGAWYWHFVDVWLFLYVSIYWWGS

>d1ocrd1 f.2.1.3 (D:) Cytochrome c oxidase {Cow (Bos taurus)}

SVVKSEDYALPSYVDRDYLPDVAVKKNLSASQKALKKEKEKASWSSLIDEKVELYRLKFESFAEMNRSTNEWKTVVGAAMFFIGFTALLIWEKHY
VYGPIPHTEEEWAKQTKRMLDMKVAPIQGFSAKWYDKNEWKK

>d1ocrg1 f.2.1.3 (G:) Cytochrome c oxidase {Cow (Bos taurus)}

ASAAKGDHGGTGARTWRFLTFGLALPSVALCTNSWLHSGHRERPAFIPYHHLRIRTKPFSWGDGNHTFFHNPRVNPLPTGYEK

>d1ocri1 f.2.1.3 (I:) Cytochrome c oxidase {Cow (Bos taurus)}

STALAKPQMQRGLLARRLRFHIVGAFMVSLGFATFYKFAVAEKRKKAYADFYRNYDSMKDFEEMRKAGIFQSAK

>d1ocrj1 f.2.1.3 (J:) Cytochrome c oxidase {Cow (Bos taurus)}

FENRVAEKQKLFQEDNGLPVHLGGATDNILYRVTMTCGGTLYCLGWASFPHK

>d1ocrk1 f.2.1.3 (K:) Cytochrome c oxidase {Cow (Bos taurus)}

APDFHDKYGNALASGATFCVAVWVYMATQIGIEWNPSPVGRVTPKEWR

>d1ocrl1 f.2.1.3 (L:) Cytochrome c oxidase {Cow (Bos taurus)}

SHYEEGPKNIPFSVENKWRLAMMTLFFSGSGFAAPFFIVRHQLKK

>d1crm1 f.2.1.3 (M:) Cytochrome c oxidase {Cow (Bos taurus)}

ITAKPAKTPSPKEQAIGLSVTFLSFLPAGWVLYHLDNYKK

>d1ar1a1 f.2.1.3 (A:) Cytochrome c oxidase {Paracoccus denitrificans}

GFFTRWFNSTNHKDIGILYLTAGIVGLISVCFTVYMRMELQHPGVQYMCLEGARLIADASAECTPNIGHLNVMITYHGVLMMFFVIPALFGGF
GNYFMPLHIGAPDMAFPRLNNLSWYMYVCVVALGVASLLAPGGNDQMGSVGWWVLYPPLSTTEAGYSMDLAIFAVHVGASSILGAINIITFLN
MRAPGMTLFVPLFAWSVIFTAWLILLSPVLAGAITMLLMDRNFGTQFFDPAGGGDPVLYQHILWFFGHPEVYIIIPGFGIISHVISTFAKKPIFGYLP
MVLAMAAIGILGFVVAHHMYTAGMSLTQQAYFMLATMTIAVPTGIKVFSWIATMWGGSIEFKTPMLWAFGLFLFTVGGVTGVVLSQAPLDRV
YHDTYYVVAHFHYVMSLAGAVFGIFAGVYYWIGKMSGRQYPEWAGQLHFWMMFIGSNLIFFPQHFLRQGMRRYIDYPVEFAYWNNISSIGAYIS
FASFLFFIGIVYTLFAGKRVNVNPVNEHAFTLEWTLPSPPPEHTFET

>d1ar1b2 f.2.1.3 (B:1-107) Cytochrome c oxidase {Paracoccus denitrificans}

QDVLGDLPIGKPVNGGMNFQPASSPLAHDQQWLDHFVLYIITAVTIVCLLLICIVRFNRRANPVPARFTHNTPIEVIWTLVPLVILVAIGAFSLPILFR
SQEMP

>d1qlec1 f.2.1.3 (C:) Cytochrome c oxidase {Paracoccus denitrificans}

AHVKNHDYQILPPSIWPFFGAIGAFVMLTGAIAWMKGITFFGLPVEGPWMFLIGLVGVLYMFGWWADVNEGETGEHTPVVRIGLQYGFILFIM
SEVMFFVAWFWAFIKNALYPMGPDSPIKDGVWPPEGIVTFDPWHLPLINTLILLSGVAVTHAHFVLEGDRKTTINGLIVAVILGVCFTGLQAYEY
SHAAFGLADTVYAGAFYMATGFHGAHVIIGTIFLVCLIRLLKGQMTQKQHVGFEAAAWYWHFVDVWLFLVVIYIWGR

>d1qled1 f.2.1.3 (D:) Cytochrome c oxidase {Paracoccus denitrificans}

TDHKHGEMDIRHQQTAFGFIKGATWVSILSIAVLVFLALANS

>d1ehka1 f.2.1.3 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AYPEKKATLYFLVLGLALIVGSLFGPFQALNYGNVDAYPLLKRLLPFVQSYYQGLTLHGVLNIAIVFTQLFAQAIMVYLARELNMRPNMGLMWLSW
WMAFIGLVAALPPLANETAVLYTFYPPPLKGHWAFYLGASVFVLSVSIYIVLDLWRRWKAANPGKVTPLVTVMAVFWLMWFLASLGLVLEAVL
FLLPWSFGLVEGVDPVLARTFWWTGHPIVYFWLLPAYAIYTILPKQAGGKLVSDPMARLAFLFLLSTPGFHHQFADPGIDPTWKMIHSVLTFLV
AVPSLMTAFTVAASLEFAGRRLRGGRGLFGWIRALPWNDNPAPVAPVLGLLGIPGGAGGIVNASFTLDYVHNTAWVPGFHHLQVASLVTAMGSL
YWLLPNLTGKPISDAQRRLGLAVVWLWFLGMMIMAVGLHWAGLLNPRRAYIAQVPDAYPHAAVPMVFNLAGIVLLVALLFIYGLFSVLLSRERK
PELAEAPLPFAEVISGPEDRRVLAMDRIGFWFAVAAILVVLAYGPTLVQLFGHLPVPGWRLW

>d1ehkb2 f.2.1.3 (B:3-40) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

DEHKAHKAILAYEKWLAFSLAMLFVFIALIAYTLATH

>d1ehkc1 f.2.1.3 (C:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

EEKPKGALAVILVLTILVFWLGVYAVFFARG

>d1ffa1 f.2.1.3 (A:) Ubiquinol oxidase {Escherichia coli}

VDHKRLGIMYIIVIAIVMLLRGFADAIMMRSQQALASAGEAGFLPPHYDQIFTAHGVIMIFFVAMPFVIGLMNLVVPLQIGARDVAPFLNNSFWFTVVGVILNVNVLGVGEFAQTGWLAYPPLSGIEYSPGVGVWDYWIWSLQLSGIGTTLTGINFFVTILKMRAPGTMFKMPVFTWASLCANVLIASFPILT
VTVALLTLDRLGTHFFTNDMGGNMMMYINLIWAWGHPEVYILIPVFGFSEIAATFSRKRLFGYTSLVWATVCITVLSFIVWLHFFTMGAGANV
NAFFGTTMIIAIPGVKIFNWLFMTMYQGRIVFHSAWLWTGFVTSVGGMTGVLLAVPGADFVLHNSLFLIAHFHNVIIGGVFGCFAGMTYWWPKA
KAFGFKLNETWGKRAFWIIGFFVAFMPLYALGFMGMTRRLSQIDPQFHTMLMIAASGAVLIALGILCLVIQMYVSIRDRDQNRLTGDPWGG
RTLEWATSSPPPFYNF

>d1fftb2 f.2.1.3 (B:27-117) Ubiquinol oxidase {Escherichia coli}

SALLDPKGQIGLEQRSLILTAFLGLMLIVVIPAILMAVGFAWKYRASNKDAKYSPNWHSNKVEAVVWTVPIIIIFLAVLTWKTTHALEPS

>d1fftc1 f.2.1.3 (C:) Ubiquinol oxidase {Escherichia coli}

HDAGGTIFGFWIYLMSDLICLISLFTAYAVLNGTAGGPTGKDIFELPFVLVETFLFFSITYGMAAIAMYKNNKSQVISWLALTWLFAGFIGMEIYE
FHHILVNGMGPDRSGFLSAFFALVGTHGLHVTSGLIWMAVLMVQIARRGLTSTNRTRIMCLSLFWHFLDVWICVFTVVYLMGA

>d1c0va_ f.2.1.4 (A:) Subunit C {Escherichia coli}

MENLNMDLLYMAAAVMGMLAAIGAAIGILGGKFLEGAARQPDLIPLLRTQFFIVMGLVDAIPMIAVGLGLYVMFAVA

>d1c17m_ f.2.1.4 (M:) Subunit A {Escherichia coli}

HGKSKLIAPLALTIFVWVFLMNLMDDLPILFATYAEHVGLPALRVVPSADVNTLSMALGVFILIFYSIKMKIGGGFTKELTLQPFNHWA
FIPVNLLIEGVSSLKPVSLGLRLFGNMYAGELIFILIAGLLPWWSQWILNPWAIFHILITLQAFIFMVLTIVLS

>d1h6ia_ f.2.1.5 (A:) Aquaporin-1 {Human (Homo sapiens)}

LFWRRAVVAEFLATTLFVFIISIGSALGFKYPVGNNQTAVQDNVKVSLAFGLSIATLAQSVGHISGAHLNPATLGLLSCQISIFRALMYIIACVGAIVATA
ILSGITSSLTGNSLGRNDLADGVNSGQGLGIEIIGTLQLVLCVLATTDRRRDLGGSAPLAIGLVALGHLLAIDYTGCINPARSGSAVTHNFSNHWIF
WVGPFIGGALAVLIYDFILAP

>d1fx8a_ f.2.1.5 (A:) Glycerol uptake facilitator protein GlpF {Escherichia coli}

TLKGQCIAEFLGTGLLIFFVGCVAAALKVAGASFGQWEISVIWGLVAMAIYLTAGVSGAHLNPATIALWLFACFDKRKVIPFIVSQVAGAFCAAALV
YGLYYNLFDFEQTHHIVRGSVESVDLAGTFSTYPNPHINFVQAFAVEMVITAILMLGILALTDDGNGVPRGPLAPLLIGLIAVIGASMGPLTGFMNPA
ARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGPIVGAIVGAFAYRKLIGRHL

>d1kpka_ f.2.1.13 (A:) Clc chloride channel {Escherichia coli}

QAARLRRRQLRQLLERDKTPLAIFMAAVVGTIVGLAAVAFDKGVAWLQNQRMGALVHTADNYPLLLTVAFLCSAVLAMFGYFLVRKYAPEAGGSG
IPEIEGALEDQRPVWRWVRLVPVKFFGGLTLGGGMVLREGPTVQIGGNIGRMVLDIFRLKGDEARHTLLATGAAAGLAAPLAGILFIIEMMR
PQFRYTLISIKAVFIGVIMSTIMYRIFNHEVALIDVGKLDAPLNTLWLYLILGIIFGPIFNKWVLMQDLLHRVHGGNITKWVLMGGAIGGLCGLL
GFVAPATSGGGFNLIPIATAGNFSMGMLVFIVARVITLLCFSGGAPGGIFAPMLALGTVLGTAFGMVAELFPQYHLEAGTFAIAGMGALMAASV
RPLTGIVLLEM TDNYQLILPMIITGLGATLLAQFTGGKPLYSAILARTLAKQEAEQL

>d1kpla_ f.2.1.13 (A:) Clc chloride channel {Salmonella typhimurium}

TPLAIFMAAVVGTLTGLGVAFEKAWSVWQNMRIGALVQVADHAFLWPLAFILSALLAMVGYFLVRKFAPEAGGSGIPEIEGALEELRPVWW
LPVKFIGGMLGTGAGMVLGREGPTVQIGGNIGRMVLDVFRMRSLEARHTLLATGAAAGLSAAFNAPLAGILFIIEMRPQFRYNLISIKAVFTGVIM
SSIVFRIFNGEAPIIEVGKLDAPVNTLWLYLILGIIFGVVGPVFSNLVLTQDMFQRFHGGEIKKWVLMGGAIGGLCGILGLIEPAAGGGFN
LIPIAAA
GNFSVGLLFIFITRVVTTLCFSGGAPGGIFAPMLALGTLGTAFGMAAAVLFQYHLEAGTFAIAGMGALMAASV
RPLTGIVLLEM TDNYQLILPMIITCLGATLLAQFLGGKPLYSTILARTLAKQDAEQ

>d1f6ga_ f.2.1.11 (A:) Potassium channel protein {Streptomyces lividans}

MPPMLSGLLARLVKLLLGRHGSALHWAAAAGAATVLLVILLAGSYLAVLAERGAPGAQLITYPAALWW
SVEATTVGYGDLYPVTLWGRCVAVV
VAGITSGLVTAALATWFVGREQERRGHFVRHSEKAAEAYTRTTRALHERFDRLERMLDDNRR

>d1jq2a_f.2.1.11 (A:) Potassium channel protein {Streptomyces lividans}
LWGRCVAVVMVAGITSFGLVTAALATWFVGREQ

>d1k4cc_f.2.1.11 (C:) Potassium channel protein {Streptomyces lividans}
SALHWRAAGAATVLLVILLAGSYLAVLAERGAPGAQLITYPRALWWVSETATTVGYGDLYPVTLWGRCAVVMVAGITSFGLVTAALATWFVGREQERRGH

>d1g4yb_f.2.1.11 (B:) Small conductance potassium channel {Rat (Rattus norvegicus)}
DTQLTKRVKNAANVLRETWLIVKNTKLVKIDHAKVRKHQRKFQAIHQRLRSVKMEQRKLNDQANTLVDLAKTQLEHHHHH

>d1kkda_f.2.1.11 (A:) Small conductance potassium channel {Rat (Rattus norvegicus)}
RKLELTKAEKHVHNFMMDTQLTKRVKNAANVLRETWLIVKNTKLVKIDHAKVRKHQRKFQAIHQRLRSVKMEQRKLNDQANTLVDLAKTQ

>d1msla_f.2.1.11 (A:) Gated mechanosensitive channel {Mycobacterium tuberculosis}
ARGNIVDLAVAVVIGTAFTALVTKFTDSIITPLINRIGVNAQSDVGILRIGIGGGQTIDLNVLLSAAINFFLIAFAVYFLVLPYNTLRKKGEVEQPQGDTQVV
LLTEIR

>d1be3c1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
MTNIRKSHPLMKIVNNAFIDLAPSNISSWWNFGSLLGICLILQILTGLFLAMHYTSDDTTAFSSVTHICRDVNNGWIIRYMHANGASMFFICLYMHV
GRGLYYGSYTFLETWNIGVILLTVMATAFMGYVLPWGQMSFWGATVITNLSSAIPYIGTNLVEWIWGGFSVDKATLTRFFAHFILPFIIMAIAMVHL
LFLHETGSNNPTGISSDVKDIPFHPPYTIKDILGALLLALMLLVLFAPDLLGDPDNTPANPLNTPPHIKPEWYFLFAYAILRSIPNKLGGVLALAFSILILA
LIPLLHTSKQRSMMFRPLSQCLFWALADLLTWIGGQPVEHPYITIGQLASVLYFLLILVLMPTAGTIENKLLKW

>d1be3e2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
SHTDIKVPDFSDYRRPEVLDSTKSSKESSEARKGFSYLTATTVGVAYAAKNVVSQFVSSMSASADVL

>d1be3f1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
AVSASSRWLEGIRKWYNAAGFNKLGLMRDDTIHENDDVKEAIRRLPENLYDDRVFRIKRALDLSMRQQILPKEQWTKYEEDKSYLEPYLKEVIRERKK
EREWEWAKK

>d1be3g1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
GRQFGHLTRVRHVITYSLSPFEQRAPHYFSKGIPNVLRRTRACILRVAPPVAFYLVYTWTQEFEEKSKRKNPAAYENDR

>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)}
GRQFGHLTRVRHVITYSLSPFEQRAPHYFSKGIPNVLRRTRACILRVAPPVAFYLVYTWTQEFEEKSK

>d1qcrh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
TTVREQCEQLEKCVKARERLELCERVSSRSQTEEDCTEELDFLHARDHCVAHKFLNSL

>d1qcrk1 f.2.1.8 (K:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}
MLTRFLGPYRQLARNWVPTAQLWGAVGAVGLVSATDSRLILDWV

>d1bccc1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
APNRKSHPLLKMINNSLIDLPAPSNISSWWNFGSLLAVCLMTQILTGLLLAMHYTADTSFASVAHTCRNVQYGWLIRNLHANGASFFFICILHIGR
GLYYGSYLYKETWNTGVILLTMATAFVGYVLPWGQMSFWGATVITNLSSAIPYIGHTLVEWAAGGFSVDNPTLTRFFALHFLLPFAIAGITIIHLTFLH
ESGSNNPLGISSDSDKIPFHPPYSFKDILGLTMLTPFLTALFSPNLLGDPENFTPANPLVTPPHIKPEWYFLFAYAILRSIPNKLGGVLALAASVLIFLIPF
LHKSKQRTMTFRPLSQLFWLLVANLLITWIGSQPVEHPFIIQGMASLSYFTILLFPTIGTLENKMLNY

>d1bccd3 f.2.1.8 (D:196-241) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
PEHDHRKRMGLKMLLMMGLLVPLVYYMKRHKWSVLSRKLAYRPPK

>d1bcce2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
SHTDIKVPNFSDYRRPPDDYSTKSSRESDPSRKGF SYLTAVTTLGVAYAAKNVVTQFVSSMSASADVL

>d1bccf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}
SRWLEGIRKWYNAAGFNKYGLMRDDTIYENDDVKEAIRRLPENLYDDRMFRIKRALDLSMRQQILPKEQWTKYEEDVPYLEPYLKEVIRERKERE
WDK

>d1bccg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

RQFGHLTRVRHLITYSLPFEQRPFPHFSKGVPNVWRRLRACILRVAPPFLAFYLTYWTGTQEFEKSKRKNPAAYVN

>d1bcch1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

LDVPLTTVREQCEQLEKCVKARERLELCDEVSSRSQTEEDCTEELDFLHARDHCVAHKLFNSLK

>d1bccj1 f.2.1.8 (J:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

TLTARLYSLLFRRSTFALTIVVGALLFERAFDQGADAIYEHINEGKLWKHIKHYENK

>d1ezvc1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

MAFRKSNVYLSLVNSIIDSPQPSSINYWWNMGSLLGLCLVIQIVTGIFMAMHYSSNIELAFSSVEHIMRDVHNGYILRYLHANGASFFFVMFMH
MAKGLYYGSYRSRPTVLWNVGIIFTLTIAFLGYCCVYQGMWSHGATVITNLFSAIIPFGVNDIVSWLWGGFSVSNPQTQRFALHYLVPFIAMVI
MHLMALHIHGSSNPLGITGNLDIPMHSYFIFKDLVTFLMLILALFVFYSPNTLGHDNYIPGNPLVTPASIVPEWYLLPFYAILRSIPDKLLGVITMFA
AIVLVLVLPFTDRSVVRGNTFKVLSKFFFFIFVNFVLLGQIGACHVEPVYLMGQIATFYFAYFLIIVPVISTIENVLFYIGRVNK

>d1ezvd2 f.2.1.8 (D:261-306) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

PEHDERKRLGLKTIVLSSYLLSIWVKKFKWAGIKTRKFVNPPK

>d1ezve2 f.2.1.8 (E:31-86) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

KSTYRTPNFDVLKENNDAKGRSYAYFMVGAMGLSSAGAKSTVETFISSMTATA

>d1ezvf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

QSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRRLPEDESYARAYRIIRAHQTELTHHLLPRNEWIKAQEDVPYLL
PYILEAAAKEDELDNIEVSK

>d1ezvg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

GPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGIFHNAVFNSRFRKSQFLYVLPAGIYWYWWKNGNEYNEFLYSKAGREELERVNV

>d1ezvh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

VTDQLEDLREHFKNTEEGKALVHHYECAERVKIQQQQPGYADLEHKEDCVEFFHLQHYLDTATAPRLFDKLK

>d1ezvi1 f.2.1.8 (I:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

SSLYKTFFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWVDVKARIAA

>d1fumc_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {Escherichia coli}

TTKRKPVVRPMSTWWKKLPFYRFYMLREGTAVPAVVFSIELIFGLFALKNGPEAWAGFVDFLQNPVIVIINLITLAALLHTKWELAPKAANIIVK
DEKMGPEPIIKSLWAVTVVATIVILFVALY

>d1fumd_ f.2.1.9 (D:) Fumarate reductase respiratory complex transmembrane subunits {Escherichia coli}

INPNPKRSDEPVFWGLGAGGMWSAIIAPVMILLVGILLPLGLFPGDALSYERVLAFQSFIGRVFLFLMIVLPLWCGLHRMHHAMHDLKIHVPAKG
WVFYGLAAILTVTLLIGVV

>d1qlac_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {Wolinella succinogenes}

MNTNESILESYGVTPERKKSRMPAKLDWWQSATGLFLGLMIGHMFVSTILLGDNVMLWVTKKFELDFIFEGGKPIVVSFLAAFVFAVIAHFLA
MRKFPINYRQYLTFKTHKDLMRHGDTTLWWIQAQMGTGFAMFFLGSVHLYIMMTQPQTIGPVSSFRMVSEWMWPLYLVLFAVELHGSVGLYRLAV
KWGWFDFGETPDKTRANLKLKTLMSAFLIVLGLLTFGAYVKKGLEQTDPNIDYKYFDYKRTH

>d1jb0a_ f.2.1.12 (A:) Photosystem I {Synechococcus elongatus}

RVVVDNDPVPTSFEKWAQPGHFDRTLARGPQTTWIWNLHALAHDFDTHTSDLEDISRKIFSAGHGLAVVFIWLSGMYFHGAKFNSNYEAWLADP
TGIKPSAQVWPIVGQGILNGDVGGGFHQIQTSGFLQLWRASGITNEFQLYCTAIGGLVMAGLMLFAGWFHYHKRAPKLEWFQNVESMLNHHL
AGLLGLGLSLAWAGHQIHSVLPINKLDAVGAAKDIPLPHEFILNPSLMAELYPKWDWGFFSGVLPFFTNWAAYSDLTFNGGLNPVTGGLWLSDTAH
HHLAIAVLIIAGHMYRTNWGIGHSLKEILEAHGPFTGAGHKGLYEVLTTSWHAQLAINLAMMGSLSIIVAQHMYAMPPYPYLATDYPTQLSLFTHH
MWIGGFLVVGAAAHGAIFMVRDYDPAMNQNNVLDRLVRHRDAIISHLNWVCIFLGFHSFGLYVHNNDTMRAFGRPQDMFSDTGIQLQPVFAQW
VQNLHTLAPGGTAPNAAATASVAFGGVVAVGGVAMMPIVLTADFMVHHIHAFTIHTVTLILLKGVLFARSSRLIPDKANLGFRFPCDGPGRG
TCQVSGWDHVFLGLFWMYNCISVVFHFSWKMQSDVWGTVPADGTVSHITGGNFAQSAITINGWLRDFLWAQASQVIGSYGSALSAYGLLFLGA
HFIWAFLSMLFLSGRGRGYWQELIESIVWAHNLKVAPAIQPRALSIIQGRAVGVAHYLLGGIATTWAFFLARIISVG

>d1jb0b_ f.2.1.12 (B:) Photosystem I {Synechococcus elongatus}

ATKFPKFSQDLAQDPTRRIWYAIAMAHDFESHDGMTEENLYQKIFASHFGHLAIIFLWVSGSLFHVAWQGNFEQWWQDPVNTRPIAHAIWDPQF
GKAADVDAFTQAGASNPVDIAYSGVYHWWYTIGMRTNGDLYQGAIFLLIASLALFAGWLHLQPKFRPSLSWFKNAESRLNHHLAGLFGVSSLAWA
GHЛИHVAIPESRGQHVGDNLFSTMPHPAGLAPFFTGNWGVYAQNPDTASHVFGTAQGAGTAILTFLGGFPQTESLWLTDMAHHHLAIAVLFIV
AGHMYRTQFGIGHSIKEMMDAKDFFGTKVEGPFNMPHQGIETYNNSLHFQLGWHLACLGVITSVAQHMYSLPPYAFIAQDHHTMAALYTHHQ
YIAGFLMVGAFAHGAIFLVRDYDPAQNKGNVLDRLVQHKЕAIISHLSVSLFLGFHTLGLYHNDVVVAFGTPEKQILIEPVFAQFIQAHGKLGYGFD
TLLSNPDSIASTAWPNYGNVWLPGLDAINSGTNSLFTIGPGDFLVHHAIALGLHTTLILVKGALDARGSKLMPDKDFYAFPCDGPGRGGTCDI
SAWDASFYLAMFWMLNTIGWVTFYWHKHLGVWEGNVAQFNESTYLMGWLRYLWLNSSQLINGYNPFGTNNLSVWAWMFLFGHLVVAT
GFMFLISWRGYWQELEITLVWAHERTPLANLVRWKDKPVALSIVQARLVLGAHFSVGYIILTYAAFLIASTAALK
>d1jb0f_f.2.1.12 (F:) Photosystem I {*Synechococcus elongatus*}
DVAGLVPCKDSPAFKRAAA AVNTTADPASGQKRFERYSQALCGEDGLPHLVVDGRSLRAGDFLIPSVLFLYIAGWIGWVGRAYLIAVRNSGEANEK
EIIDVPLAIKCMLTGFAWPLAALKELASGELTAKDNEITVSPR
>d1jb0i_f.2.1.12 (I:) Photosystem I {*Synechococcus elongatus*}
MMGSYAASFLPWIFIPVCWLMPVVMMGLFLYIEGEA
>d1jb0j_f.2.1.12 (J:) Photosystem I {*Synechococcus elongatus*}
MKHFLTYLSTAPVLAIIWMTITAGILIEFNRFYPDLLFHPL
>d1jb0k_f.2.1.12 (K:) Photosystem I {*Synechococcus elongatus*}
ILCNLFAIALGRYAIQSRGKGPGLPIALPALFEGFGLPELLATTSFGHLLAAGVVSGL
>d1jb0l_f.2.1.12 (L:) Photosystem I {*Synechococcus elongatus*}
LVKPYNGDPFVGHLSTPISDGLVKTFIGNLPAYRQGLSPILRGLEVGMAGHYFLIGPWVKLGPLRSDVANLGGISIALILVATACLAAYGLVSFQKG
GSSSDPLKTSEGWSQFTAGFFVGAMGSAFVAFFLENFLVVVDGIMTGLFN
>d1jb0m_f.2.1.12 (M:) Photosystem I {*Synechococcus elongatus*}
MALTDTQVYVALVIAALLPAVLAFLRSTELYK
>d1jb0x_f.2.1.12 (X:) Photosystem I {*Synechococcus elongatus*}
PTYAFRTFWAVLLLAINFLVAAYYFAAAA
>d1eula_f.2.1.10 (A:) Calcium ATPase {Rabbit (*Oryctolagus cuniculus*)}
MEAAHSKSTECLAYFGVSETTGLTPDQVKRHLEYGHNELPAEEGKSLWELVIEQFEDLLVRILLAACISFVLAWFEEGEETITAFVEPFVILLIANAI
VGWQERNAENAIEALKEYEP EMGKVYRADRKSVQRICKARDIVPGDIVEAVGDKVPADIRILSIKSTLVDQSILTGESVSVIKHTEPVPDPRAVNQ
DKKNMLFSGTNIAAGKALGIVATTGVSTEIGKIRDQMAATEQDKTPLQQKLDEFGEQLSKVISLICVAVWLINIGHFNPDVHGGSWIRGAIYYFKIAVA
LAVAIIPEGLPAVITCLALGTRRMAKKNAIVRSLPSVETLGCTSVICSDKTGTLTNQMSVCKMFIDKVDGDFCSLNFSITGSTYAPEGEVLKNDKPI
RSGQFDGLVELATICALCNDSSLDFNETKGVYEKGVEATETATLTLVEKMNVFNTEVRNLSKVERANACNSVIRQLMKKEFTLEFSRDRKSMSVYCSPA
KSSRAAVGNKMFVKGAPEGVIDRCNYVRGTTRVPMTPVKEKILSVIKEWTGRDTLCLALATRDPKREEMVLDDSSRFMEYETDLTFVGVV
GMLDPPRKEVMGSIQLCRDAGIRVIMITGDNKGTAIAICRRIGIFGENEEVADRAYTGREFDDPLAEQREACRRACC FARVEPSHKSIVEYLQSYDEI
TAMTGDGVNDAPALKAEIGIAMGSGTAVAKTASEMVLADDNFSTIVA AVEEGRAIYNNMKQFIRYLISSNVGEVVCIFLTAALGLPEALIPVQLLWV
NLVTDGLPATLGFNPPDLDIMDRPPRSPKEPLISGWLFYRMAIGGYVGAATVGAIAWWFMYAEDGPGVTVHQLHFMQCTEDPHFEGLDCEI
FEAPEPMTMALSVLVTIEMCNALNSLSENQSLMRMPPWNIWLLGSICLSMSLHFILYVDPLPMIFKLKALDLTQWLMVLKISLPVIGLDEILKFIAR
NYLEG
>d1kzua_f.3.1.1 (A:) Light-harvesting complex subunits {Purple bacterium (*Rhodopseudomonas acidophila*)}
MNQGKIWTVVNPAIGIPALLGSVTIAILVHLAILSHTTWFPAYWQGGV
>d1kzub_f.3.1.1 (B:) Light-harvesting complex subunits {Purple bacterium (*Rhodopseudomonas acidophila*)}
ATLTAEQSEELHKYVIDGTRVFLGLALVHFLAFSATPWLH
>d1lgha_f.3.1.1 (A:) Light-harvesting complex subunits {*Rhodospirillum molischianum*}
SNPKDDYKIWLVINPSTWLPVIWVATVVAIAVHAAVLAAPGFNWIALGAAKSAAK
>d1lghb_f.3.1.1 (B:) Light-harvesting complex subunits {*Rhodospirillum molischianum*}
RSLSGLTEEEAIAVHDQFKTTFSAFIILAIAVAVHLVWVWKPWF

>d1jo5a_f.3.1.1 (A:) Light-harvesting complex subunits {Rhodobacter sphaeroides}
ADKSDLGTYGLTDEQAQELHSVYMSGLWLFSAVAIVAHAVIWRPWF

>d1ijda_f.3.1.1 (A:) Light-harvesting complex subunits {Rhodopseudomonas acidophila}
MNQGKIWTVVPPAFGLPLMLGAVAITALLVHAALVHTTWYAAFLQ

>d1ijdb_f.3.1.1 (B:) Light-harvesting complex subunits {Rhodopseudomonas acidophila}
AEVLTSEQAEELHKVIDGTRVFLVIAIAHFLAFTLTPW

>d1g90a_f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}
APKDNTWYTGAKGFSQYHDTGFINNNGPTHENQLGAGAFGGYQVNPYVGFMGYDFLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIY
TRLGGMVFRADTKSNVYGNHDTGVSPVFAGGVEAYTPEIATRLEYQFTNNIGDAHTIGTRPDNGMMSLGVSYRGQQGEAA

>d1qjpa_f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}
APKDNTWYTGAKGFSQYHDTGLINNNGPTHENQLGAGAFGGYQVNPYVGFMGYDWLGRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIY
YTRLGGMVWRADTYSNVYGNHDTGVSPVFAGGVEAYTPEIATRLEYQWTNNIGDAHTIGTRPDNGMMSLGVSYRG

>d1qj8a_f.4.1.1 (A:) Outer membrane protein X (OMPX) {Escherichia coli}
ATSTVTGGYAQSDAQGQMNKMGGFNLKYRYEEDNSPLGVISFTYTEKSRTASSGDYNKNQYYGITAGPAYRINDWASIYGVVGVGKFQTTEYP
TYKNDTSYDGFSGYAGLQFNPMENVALDFSYEQSRIRSVDVGTIAGVGYRF

>d1i78a_f.4.4.1 (A:) Outer membrane protease OMPT {Escherichia coli}
STETLSFTPDNINADISLGLSGKTKERVYLAEGGRKVSQLWKFNNAAIKGAINWDLMPQISIGAAGWTLGSRRGNMVDQDWMDSSNPGT
WTDEARHPDTQLNYANEFDLNKIGWLLNEPNYRLGLMAGYQESRYSFTARGGSYISSEEGFRDDIGSFPNGERAIGYKQRFKMPYIGLTGSYRYEDF
ELGGTFKYSGWVESSDNDEHYDPKGRITYRSVKDQNYYSAVNAGYYVTPNAKVVVEGAWNRVTNKKNTSLYDHNNNTSDYSKNGAGIENYN
FITTAGLKTYF

>g1qd6.1 f.4.2.1 (A;C:) Outer membrane phospholipase A (OMPLA) {Escherichia coli}
AVRGSIIANMLQEXFTLYPYDNTYLIYTQTSIDLNEKIAISYDWAENARKDEVKFLQLSLAFPLWRGILGPNVLGASYTQKSWWQLNSEESSPFRET
YEPQLFLGFATDYRFAGWTLRDVEMGYNHDSNRSRSDPTSRSWNRLYTRLMAENGNWLVVKPWYVGNTDDNPDTKYMYYQLKIGYHLGDA
VLSAKGQYWNWTGYGGAELGLSYPITKHVRLYTQVSGYGESLIDYNFNQTRVGVGVMNDLF

>d1hxxa_f.4.3.1 (A:) Porin {Escherichia coli, different sequences}
AEIYNKDGKNDVLYKGAVGLHYFSKGNGENSYGGNGDMTYARLGFKGETQINSDLTGYGQWEYNFQGNSEGADAQTGNKTRLAFAGLKYADVG
SFDYGRNYGVFDALGYTDMLPEFGGDATYSDFFVGRGGVATYRNSNFFGLVDGLNFAVQYLGKNERDTARRSNGDGVGGSISYEYEGFGIVGA
YGAADRTNLQEAQPLGNKGKAEQWATGLKYDANNIYLANYGETRNPATNKFTNTSGFANKTQDVLLVAQYQDFGLRPSIAYTKSKAKDVEGIG
DVDLVNYFEVGATYYFNKNMSTYVDIINQIDSNDNKLGVGSDDTVAVGIVYQF

>d1pho_f.4.3.1 (-) Porin {Escherichia coli, different sequences}
AEIYNKDGKNDVLYKGKAMHYMSDNASKDGDQSYIRGFKGETQINDQLTGYGRWEAEFAGNKAESDTAQKTRLAFAGLKYKDLGSFDYGRNL
GALYDVEAWTDMFPEFGGDSSAQTDNFMTKRASGLATYRNTDFFVGDGLNLTQYQGKNENRDVKKQNGDGFGLTSYDFGGSDFAISGAYTN
DRTNEQNLQSRGTGKRAEAWATGLKYDANNIYLATFYSETRKMTPITGGFANKTQNFEAVAQYQDFGLRPSLGYVLSKGKDIEGIGDEDLVNYIDVG
ATYYFNKNMSAFVDYKINQLSDNDKLNINNDDIVAVGMTRYQF

>d2por_f.4.3.1 (-) Porin {Rhodobacter capsulatus}
EVKLSGDARMGVMYNGDDWNFSSRSRVLFTMSGTTDSGLEFGASFKAHESVGAETGEDGTVFLSGAFGKIEMGDALGASEALFGDLYEVGYTDLD
DRGGNDIPYLTDERLTAEDNPVLLYTSAGAFSVAASMSDGKVGETSEDDAQEMAAYTGFNYTVGLGYEKIDSPDTALMADMEQLEAAIAK
FGATNVKAYYADGELDRDFARAVFDLTPAAAATAVDHKAYGLSVDFSTGATTGGYVQLDIDTIDDVTYGLGASYDLGGGASIVGGIADNDLPS
DMVADLGVKFKF

>d3prn_f.4.3.1 (-) Porin {Rhodopseudomonas blastica, strain DSM2131}
MISLNGYGRGLQYVEDRGVGLEDISSRLRINIVGTTEDQGVTFGAKLRMQWDDGDAFAGTAGNAAQFWTSYNGVTVSGNVDTAFDSVAL
YDSEMGYEWSSFGDAQSSFFAYNSKYDASGALDNYNGIAVTYSISGVNLILSYVDPDQTVDSLVEEFGIAADWSNDMISLAAAYTTDAGGIVDND
IAFVGAAYKFNDAGTVGLNWYDNLSTAGDQVTLYGNYAFGATTVRAYVSDIDRAGADTAYGIGADYQFAEGVKVSGSVQSGFANETVADVGVRDF
F

>d1osma_f.4.3.1 (A:) Porin {Klebsiella pneumoniae}

AEIYNKDGNKLDLYGKIDGLHYFSDDKDVGDQTYMRLGVKGETQINDQLTGYGQWEYNVQANNTESSSDQAWTRLAFAGLKFGDAGSFYGRNYGVVYDVTSTVLPEFGGDTYGSNDLFLQSRANGATYRNSDFGLNLFALQYQKGNGSVSGEGATNNRGALKQNGDGFTSVTYDIFGIGSAGFAYANSKRTDDQNQLLGEGDHAETYTGGLKYDANNIYLATQYTQTYNATRAGSLGFANKAQNFVEAAQYQDFGLRPSVAYLQSKGKDNGYGDQDILKYVVDVGATYYFNKNMSTYDVKINLLDNFTRSAGISTDDVVALGLVYQF

>d1e54a_f.4.3.1 (A:) Porin {Comamonas acidovorans}

ESSVTLFGIVDTNVAYVNKDAAGDSRYGLGTSGASTSRLGLRGTEDLGGGLKAGFWLEGEIFGDDGNASGFNFKRRSTVLSGNFGEVRLGRDLVPTSQKLTSYDLFSATGIPFMGFRNWAAGQQGADDNGIRANNLISYTPNFGGFNAFGFYAFDEKQTIGTADSVGRYIGGYVAYDNGPLSASLGLAQKKTAVGGLATDRDEITLGASYNFGVAKLSSLLQQTKFKRDIGGDIKTNSYMIGASAPVGGVGEVKLQYALYDQKAIDSKAHQITLGYVHNLSKRTALYGNLAFLKNKDASTLGLQAKGVYAGGVQAGESQTGVQVGIRHAF

>d1af6a_f.4.3.2 (A:) Maltoporin (also LamB protein) {Escherichia coli}

VDFHGYARSGIGWTGSGGEQQCFQTTGAQSKEYRLGNECETYAELKLQEVWKEGDKSFYFDTNVAYSVAQQNDWEATDPAFREANVQGKNLIEWLPGSTIWAGKRFYQRHDVHMIDFYWDISPGAGLENIDVFGKLSLAATRSSEAGGSSSFASNNIYDVTNETANDVFDVRLAQMEINPGGTLELVDYGRANLRDNYRLVDGASKDGWLFTAETHQSVLKGFNKVVQYATDSMTSQGKGLSQSGVAFDNEKFAYNINNNGHMLRILDHGAISMGDNWDMMYVGMYQDINWDNDNGTKWWTVGIRPMYKWTPISTMVEMIGYDNVESQRTGKNNQYKITLAQQWQAGDSIWSRPAIRVFATYAKWDEKWGYDVTGNADNNNANFGKAVPADFNGGSFGRGDSDEWTFGAQMEIWW

>d2mpa_f.4.3.2 (A:) Maltoporin (also LamB protein) {Salmonella typhimurium}

VDFHGYARSGIGWTGSGGEQQCFQATGAQSKEYRLGNECETYAELKLQEVWKEGDKSFYFDTNVAYSVNQQNDWESTDPAFREANVQGKNLIEWLPGSTIWAGKRFYQRHDVHMIDFYWDISPGAGLENIDLGFGLKLSAATRSTEAGGSYTFSSQNIYDEVKDTANDVFDVRLAGLQTNPDGVLELDYGRANTTDGYKLADGASKDGWMFTAETHQSMLKGYNKFVVQYATDAMTTQGKQARGSDGSSSFTEKINYANKVINNNNMWRILDHGAISLGDKWDLMYVGMYQNIWDNNNLGTEWWTVGVRPMYKWTPISTMVLEVGYDNVKSQQTGDRNNQYKITLAQQWQAGDSIWSRPAIRFATYAKWDEKEWKGYIKDGNISRYAAATNSGISTNSRGDSDEWTFGAQMEIWW

>d1a0tp_f.4.3.2 (P:) Sucrose-specific porin {Enterobacterium (Salmonella typhimurium)}

SGFEFHGYARSGVMNDGASTKSGAYITPAGEGETGGAIIGRLGNQADTYVEMNLEHKQTLNGATTRFKVMVADGQTSYNDWTASTSDLNVRQAFVELGNLPTFAGPKGKSTLWAGKRFDRDNFDIHVIDSDVVFLAGTGGGIYDVKWNDGLRSNFSLYGRNFGDIDDSNSVQNYILTMNHFAGPLQMMVSGLRAKDNDERKDSNGNLAKGDAANTGVHALLGLHNDSYGLRGSSKTALLYGHGLGAEVKIGGSDGALRPGADTWRIASYGTPLESENWSVAPAMILAQRSKDRYADGDSYQWATFNLRLIQAINQNFALEYEGSYQYMDLKPEGYNDRQAVNGSFYKLTFAPTFKVGSIGDFFSRPEIRFTSWMDWSKKLNYYASDDALGSDGFNSGGGEWSFGVQMETWF

>d1by5a_f.4.3.3 (A:) Ferric hydroxamate uptake receptor FhuA {Escherichia coli}

QESAWGPAATIAARQSATGTKTDPPIQKVPQSISSVTAEEMALHQPKSVEALKSYTPGVSGBTGASNTYDHLIIRGFAAEQGSQNNYLNGLKLQGNFYNDAVIDPYMLERAIEIRGPVSVLYGKSSPGGLNNMVKRPTTEPLKEVQFKAGTDSLFQTFDFSDSLDDGVSYRLGLARSANAQQKGSEEQRYAIAPAFTWRPDDKTNFTFLSYFQNENPETGYYGWLPKEGTVEPLPNGKRLPTDFNEGAKNNTYSRNEKMGYFSDFHEFNDTFTVRQLRFAENKTSQNSVYGYGVCSDPANAYSQCAALAPADKGHLARKYVVDEKLQNFSDTQLQSKFATGDDHTLLGVDFMRMRNDINAWFGYDDSVPLLNLYNPVNTDFDNAKDPANSGPYRILNKQKQTGVYVQDQAQWDKVLTGGRYDWADQESLNRVAGTTDKRDKQFTWRGGVNYLFDNGVTPYFYSSESFPSSQVGKDGNIIFAPSKGKQYEVGVKYVPEDRPIVVTGAVYNLTNNLMADPEGSFFSVEGGEIRARGVEIEAKRPLSASNVVGSYTYDAEYTTDTTYKGNTPAQVPHMASLWADYTFDGLPSGLTGTGGRYTGSSYGDPAFSKVGSYTVDALVRYDLARVGMAHSNVALHVNNLFDREYVASCFCNTYGCFWGAERQVVAATATFRF

>d1fepa_f.4.3.3 (A:) Ferric enterobactin receptor FepA {Escherichia coli}

DDTIVTAAEQNLQAPGVSTITADEIRKNPVARDVSKIIRTMPGVNLGNSTGQRGNRQDIRGMGPENTLILDGKPVSSRNSVRQGWRGERDTRGDTSWPPPEMIERIEVLRGPAARAYGNGAAGGVVNIITKKGSEWHGSWDAYFNAPEHKEEGATKRTNFSLTGPLGDEFSFRLYGNLDKTQADAWDINQGHQSARAGTYATLPAREGVINKDINGVVRWDFAVLQSLLEAGYSRQGNLYAGDTQNTNSDSYTRSKEYDETNRLYRQNYALTWNNGWDNGVTTSNWVQYEHTRNSRIPEGLAGGTGKFNEKATQDFVIDLDDVMLHSEVNLPIDFLVNQTLTGEWNQQRMKDLSNTQALTGTNTGGAIDGVSTDSPYSKAEIFSLFAENNMLDSTIVTPGLRFDHHSIVGNNWSPALNISQGLGDDFTLKMGIARAYKAPSLYQTNPNYILYSGQGCYASAGGCYLQGNDDLKAETSINKEIGLEFKRDGWLAGVTWFRNDYRNKIEAGYVAVGQNAVGTLYQWDNVPKAVVELEGSLNPVSETVMWNT

NITYMLKSENKTTGDRLSIPIEYTLNSTLWQAREDLSMQTTFTWYGQQPKKYNYKGQPAVGPETKEISPYSIVGLSATWDVTKNVSLTGGVDNLFD
KRLWRAGNAQTTGDLAGANYIAGAGAYTYNEPGRTWYMSVNTHF

>d1ek9a_f.5.1.1 (A:) Integral outer membrane protein TolC, efflux pump component {Escherichia coli}

ENLMQVYQQARLSNPELRKSAADRDAAFEKINEARSPLLPQLGLGADYTYSNGYRDANGINSNATASLQLTQSIFDMSKWRALTQEKAAQIQDVT
YQTDQQTLILNTATAYFNVLNAIDVLSYTQAQKEAIYRQLDQTTQRNFNGLVAITDVQNARAQYDTVLANELTARNNLNAVEQLRQITGNYYPELAA
LNVENFKTDKPQPVNALLKEAEKRNLSSLQARLSQDLAREQIRQAQDGHLPTLDLASTGISDTSYSGSKTRGAAGTQYDDSNMGQNKVGLSFLPIY
QGGMVNSQVKQAAQYNFVGASEQLESAHRSVVQTVRSSFNNINASISSINAYKQAVVSAQSSLDAMEAGYSGVTRTIVDVLDAATTLYNAKQELANA
RYNYLINQLNIKSALGTLNEQDLLALNNALSKPVSTNPE

>d7ahla_f.6.1.1 (A:) Alpha-hemolysin {Staphylococcus aureus}

ADSDINIKTGTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFIDDKNHNKLLVIRTKGTIAGQYRVYSEEGANKSGLAWSAFKVQLQLPDNEVAQI
SDYYPRNSIDTKEYMSTLTGYFNGNVTGDDTGKIGGLIGANVSIGHTLKVQPDFKITLESPTDKKVGVWKVIFNNMVQNQNWGPYDRDSWNPVYGN
QLFMKTRNGSMKAADNLFDPNKASSLSSGFSPDFAT/ITMDRKASKQTNIIDVIYERVRDDYQLHWSTTNWKGNTNTDKWTDRSSERYKIDWEK
EEMTN

>d1pvl_f.6.1.1 (-) Leucocidin K component LukF-PV {Staphylococcus aureus}

AQHITPVSEKKVDDKITLYKTTATSDSDKLISQILTTFNFIKDKSYDKDTLILKAAGNIYSGYTKPNPKDTISSQFYWGSKYNISINSDNSDVSNNVVDYAPK
NQNEEFQVQQTVGYSYGGDINISNGLSGGGNGSKSFETINYKQESYRTSLDKRTNFKKIGWDVEAHKIMNNNGWGPYGRDSHPTYGNEMFLGSR
QSNLNAGQNFFLEYHKMPVLSRGNFNPEFIGVLSRKQNAAKSKITVTYQREMDRYTNFWNQLHWIGNNYKDENRATHTSIYEVDWENHTVKLID
TQSKEKNPMS

>d3lkfa_f.6.1.1 (A:) Leukocidin F (HlgB) {Staphylococcus aureus}

EGKITPVSVKKVDDKVTLKYKTTATADSDKFKISQILTTFNFIKDKSYDKDTLVLKATGNINSGFVKPNPNDYDFSKLYWGAKYNSISSQSNDSVNVVDY
PKNQNEEFQVQNTLGYTFGGDISNGLSGGLNGNTAFSETINYKQESYRTTLSRNTNYKNVGWGVEAHKIMNNNGWGPYGRDSHPTYGNELFLA
GRQSSAYAGQNFIAQHQMPPLRSRNPNPEFLSVLSHRQDGAKKSITVTYQREMDLYQIRWNGFYWAGANYKNFKRTFKSTYEIDWENHKVLL
DTKETENNKK

>d1prea2_f.8.1.1 (A:85-470) (Pro)aerolysin, pore-forming lobe {Aeromonas hydrophila}

IPTLSALDIPDGDEVQWRLVHDSANFIKPTSYLAHYLGAWVGGNHSQYVGEDMDVTRDGDGWVIRGNNDGGCDGYRCGDKTAIKVSNFAYN
LDPDSFKHGDVTQSDRQLVKTVVGAWVNDSDTPQSGYDVTLYDTATNWSKNTYGLSEKVTTKNFKWPVGETELSIEIAANQSWSAQNGGST
TTSLSQSVRPTVPARSKIPVKIELYKADISYPYEFKADVSYDLTSGFLRWGGNAWYTHPDNRPNWNHTFVIGPYKDKASSIRYQWDKRYIPGEVKW
WDWNWTIQQNLSTMQNNLARLVRPVRAGITGDFSAESQFAGNIEGAPVPLAADSKVRRARSVDGAGQGLRLEIPLDAQELSGLGFNNVSLVT
PAANQ

>d1pfo_f.9.1.1 (-) Perfringolysin {Clostridium perfringens}

DITDKNQSIDSGISSLSYNRNEVLASNGDKIESFPKEGKAGNKFIVVERQKRSLLTSPVDISIIDSVNDRTPGALQLADKALVENRPTILMVKRKPINI
NIDLPGLGKGENSIKVDDPTYKGKVSGAIDELVSKWNEKYSSTHTLPARTQYSESMSVYSKSQQISSALNVNAKVLLENGLGVDFNAVANNEKKVMILAYKQIF
YTVSADLPKNPSDLFDDSVTFNDLKQKGVSNEAAPLMSNVAYGRTIYVKLETTSSSKDVQAAFKALIKNTDIKSQQYKDIYENSSFTAVVLGGDAQ
EHNKVVTKDFDEIRKVIKDNATFSTKNPAPYISYTSVFLKDNNSVAAVHNKTDYIETTSTEYSGKGINLDHSGAYVAQFEAWDEVSYDKEGNEVLTHKT
WDGNYQDKTAHYSTVIPLEANARNIRIKAECTGLAWEWWRDVISEYDVPLTNNINVSIWGTLYPGSSITYN

>d1svb_2_f.10.1.1 (1-302) Envelope glycoprotein, central and dimerisation domains {Tick-borne encephalitis virus}

SRCTHLENRDFVTGTQGTRTVLLELGGCVITAEGKPSMDVWLDAIYQENPAKTREYCLHAKLSDTKVAARCPTMGPATLAEEHQGGTVCKRDQ
SDRGWGNHCGLFGKGKGSIVACVKAACEAKKKATGHVYDANKIVTVKVEPHTGDYVAANETHSGRKKTASFTTSEKTIITMGEYGDVSSLCRVASGVD
LAQTVILELDKTVHLPTAWQVHRDWFDNLALPWKHEGAQNWNNAERLVEFGAPHAVKMDVYNLGDQTGVLLKALAGPVVAHEGTKYHLKSG
HVTCEVGLEKLKMKG

>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}

DGRPLAAAGIVVTGDKAVNIYTSSQTGSIIKLLXQITSPALTQLTIQALYNLAGGNMDYLLTKLGVGNQLSSLISSGLITGNPILYDSQTQLLGIVQVTLPS
VGNLNNMRATYLELTSVSTTKGFASALVPVVTQVGSVIEELDTSYCIETDLDLYCTRIVTFPMSPGIYSCLSGNTSACMYSKTEGALTPYMTLKGSVIA

NCKMTTCR CADPPGIISQNYGEAVSLIDRQSCNILSLDGITRLSGEF DATYQKNISIQDSQ
>d1acc__ f.11.1.1 (-) Anthrax protective antigen {Anthrax bacillus (Bacillus anthracis)}
SSSQGLLGYYSQDLSNFQAPMVVTSSSTGDLIPSSELENIPSENQYFQS A IWSGFIKVKK SDEYT FATSADNHVTM W VDDQE VINKASNSNKIRLEKG
RLYQIKI QYQREN PTEKGLDFKLW TDSQN KKEVISSDN LQLPELKQKSNSRK RSTSAGPTV PDRNDGIPDS LEVE GYTV DVKNKRTFLSPW ISNI
HEKKGLTKYKSSPEKW STASDPYSDFEK VGRIDKNVSPEARHPLVAAYPIVHVDMENII LSKNEDQSTQNTDSETRTIS KNTTSRTH TSEVHGNAEV
HASFFDIGGSVSAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLPTTSLVGKNQTLATIKAENQLSQLAPN
NYYP SKNL APIALNAQDDFSSTPITM NYNQFLELEKTQKQLR DTDQVYGNIA TYNFENG RVRV DTGS NWSEVLPQI QETTARIIFNGKD LNVERRIA
VNPSDPLETTKPDMLKEALKIAFGFNEPNGNLQYQGKDITEFDNF DQQT SQNIKNQLAELNATN IYTVLDKIKLNAKM NIIRD KRFHYDRNNIAV
GADESVVKEAHRE VINSSTEGLLNIDKDIRKILSGYI VEIEDTEGLKEVINDRYDMLNISSLRQDGKTFIDFKKYNDKLPL YISNP NYKVNVYAVT KENTII
NPSENGDTSTNGIKKILFSKKGYEIG
>g1cph.1 g.1.1.1 (B;A:) Insulin {Cow (Bos taurus)}
FVNQHLCGSHLVEALYLVCGERGFFYTPKAXGIVEQCCASVCSLYQLEN YCN
>g1pid.1 g.1.1.1 (B;A:) Insulin {Cow (Bos taurus)}
FVNQHLCGSHLVEALYLVCGERGFFXGIVEQCCASVCSLYQLEN YCN
>d1fea_g.1.1.1 (A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSHLVEALYLVCGERGFFYTPKTRRPGDVKRGIVEQCCTSICSLYQLEN YCN
>g1a7f.1 g.1.1.1 (B;A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSHLVEALYLVCGERGGFYTPKXGIVEQCCTSICSLYQLEN YCN
>g1g7a.1 g.1.1.1 (B;A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSHLVEALYLVCGERGFFYTPKTXGIVEQCCTSICSLYQLEN YCN
>g1hui.1 g.1.1.1 (B;A:) Insulin {Human (Homo sapiens)}
EVNQHLCGSELVEALELVCGERGFFYEPKXGIVEQCCTSICSLYQLEN YCN
>g1qj0.1 g.1.1.1 (B;A:) Insulin {Human (Homo sapiens)}
VNQYLCGSHLVEALYLVCGERGFFYTPKXGIVEQCCTSICSLYQLEN YCN
>g1sjt.1 g.1.1.1 (B;A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSDLVEALYLVCGERGFFYTDKXGIVEQCCTSICSLYQLEN YCN
>g1vks.1 g.1.1.1 (B;A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSDLVEALYLVCGERGFFYTKPTXGIVEQCCTSICSLYQLEN YCN
>d1zeia_g.1.1.1 (A:) Insulin {Pig (Sus scrofa)}
FVNQHLCGSHLVEALYLVCGERGFFYTDKAAGGIVEQCCTSICSLYQLEN YCN
>g1dei.1 g.1.1.1 (B;A:) Insulin {Pig (Sus scrofa)}
FVNQHLCGSHLVEALYLVCGERGFXGIVEQCCTSICSLYQLEN YCN
>g1sdb.1 g.1.1.1 (B;A:) Insulin {Pig (Sus scrofa)}
NQHLCGSHLVEALYLVCGERGFFYTDKXGIVEQCCTSICSLYQLEN YCN
>g6rlx.1 g.1.1.1 (B;A:) Relaxin {Human (Homo sapiens)}
SWMEEVIKLCGRELVRAQIAICGMSTWXELY SALANKCCHVGCTKRS LARFC
>d1b9ga_g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}
GPETLCGAELVDALQFVCGDRGFYFNKPGIVDECCFRSCDLRRLEM YCAPLPAKSA
>d1igl__ g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}
AYRPSETLCGGELVDTLQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLALLETYCATPAKSE
>d1imxa_g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}
ETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEM YCAPL
>d2gf1__ g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}
GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRRAPQTGIVDECCFRSCDLRRLEM YCAPLPAKSA

>d3lria_g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}

MFPAMPLSSLFVNGPRTLCGAELVDALQFVCGDRGFYFNKPTGYGSSRRACQTGIVDECCFRCDLRLEMYCAPLPAKSA

>g1bom.1 g.1.1.1 (B;A;) Bombyxin-II {Silkworm (Bombyx mori)}

EQPQAVHTYCGRHLARTLADLCWEAGVDXGIVDECLLRPCSVDLLSYC

>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)}

ASATWGAAYPACENNCRKKYDLCIRCQGKWAGKRGKCAAHCIIQKNNNCKGKCKKE

>d1wgt3 g.3.1.1 (A:87-129) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}

IKCGSQAGGKLCPPNLCCSQWGYCGLGSEFCGEGCQNGACSTD

>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)}

ERCGEQGSNMECPNNLCCSQYGYCGMGGDYCGKGCCQNGACWTSKRCGSQAGG

>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)}

IKCGSQSGGKLCPPNLCCSQWGFCGLGSEFCGGGCQSGACSTD

>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}

ERCGSQGGGATCPGLRCCSIWGWC GDSEPYCGRTCENKCWSGERS

>d1ehda2 g.3.1.1 (A:46-89) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

DHRCGAAVGNP PCGQDRCCSVHGWC GGGNDYCSGGKCQYRCSS

>d1en2a1 g.3.1.1 (A:1-45) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

ERCGSQGGGGTCPALWCCSIWGWC GDSEPYCGRTCENKCWSGERS

>d1en2a2 g.3.1.1 (A:46-86) Isolectin VI {Stinging nettle (Urtica dioica), UDA}

DHRCGAAVGNP PCGQDRCCSVHGWC GGGNDYCSGGKCQYRC

>d1hev__ g.3.1.1 (-) Hevein {Hevea brasiliensis}

EQCGRQAGGKLCPPNLCCSQWGWC GDSEPYCGRTCENKCWSGERS

>d1mmc__ g.3.1.2 (-) Antimicrobial peptide 2, AC-AMP2 {Tassel (Amaranthus caudatus)}

VGECVRGRCPGMCCSQFGYCGKGPKYCG

>d1f2si_g.3.2.1 (I:) Trypsin inhibitor {Bitter gourd (Momordica charantia), linn. Cucurbitaceae, seed}

RICPRIWMECKRDSDCMaecicVMGHG

>d1mcti_g.3.2.1 (I:) Trypsin inhibitor {Bitter gourd (Momordica charantia), linn. Cucurbitaceae, seed}

RICPRIWMECTRDSDCMAK CICVAGHCG

>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}

SGSDGGVCPKILKKR RDSDCPGACICRGNGYCG

>d2btci_g.3.2.1 (I:) Trypsin inhibitor {Vegetable marrow (Cucurbita pepo)}

RVC PKILMECKKDSDCLAEC CICLEHGYCG

>d2let__ g.3.2.1 (-) Trypsin inhibitor {Jumping cucumber (Ecballium elaterium)}

GCP RLLMRCKQDSDCLAGCVCGPNGFCG

>d4cpai_g.3.2.1 (I:) Carboxypeptidase A inhibitor {Potato}
ZHADPICNKPKTHDDSGAWFCQACWNSARTCGPYV

>d1clvi_g.3.2.1 (I:) alpha-amylase inhibitor (AAI) {Prince's feather (Amaranthus hypochondriacus)}
CIPKWNRCGPMDGVPCCEPYTCTSDYYGNCS

>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}
CGESCVWIPCISAALGCSCKNVKCYRNGIP

>d1c4ea_g.3.4.1 (A:) Gurmarin, a sweet taste-suppressing polypeptide {Gymnema sylvestre}
EQCVKKDELCPYYLDCCPLECKKVNWWDHKCIG

>d1dkca_g.3.4.2 (A:) Antifungal peptide PAFP-S {Pokeweed (Phytolacca americana)}
AGCIKNGGRCNASAGPPYCCSYCFQIAGQSYGVCKNR

>d1hyka_g.3.5.1 (A:) Agouti-related protein {Synthetic, based on Homo sapiens sequence}
CVRLHESCLGQQVPCCDCATCYCRFFNAFCYCRKLGTMNPCSRT

>d1omc_g.3.6.1 (-) Conotoxin {Sea snail (Conus geographus), G IVa}
CKSPGSSCPTSYNCCRSCNPYTKRCY

>d1ag7_g.3.6.1 (-) Conotoxin {Synthetic, based on Conus geographus, GS}
ACSGRGSRCPPQQCMGLRCGRGNPQKCIGAHEDV

>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}
CKGKGAKCSR禄MYDCCTGSCRSRGKC

>d1mvj_g.3.6.1 (-) Conotoxin {Conus striatus, S VIb}
CKLKQGQSCRKTSYDCCSGSGCRSGKC

>d1fyga_g.3.6.1 (A:) Conotoxin {Conus striatus, SO3}
CKAAGKPCSR禄IAYNCCTGSCRSRGKC

>d1kcp_g.3.6.1 (-) Conotoxin {Conus purpurascens, kappa-pVIIa}
CRIPNQKCFQHLDDCCSRKCNRNFNCV

>d1eyoa_g.3.6.1 (A:) Conotoxin {Conus tulipa, T VIIa}
SCSGRDSRCPPVCCMGLMCMSRGKCVSIYGE

>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)}
EDNCIAEDYGKCTWGGTKCCRGRPCRCMSIGTNCECTPRLIMEGLSFA

>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)}
CIAEDYGKCTWGGTKCCRGRPCRCMSIGTNCECTP

>d1eit_g.3.6.2 (-) mu-Agatoxin-I {Funnel web spider (Agelenopsis aperta)}
ECVPENGHCRDWYDECCEGYCSCRQPPKICRNNN

>d1kqha_g.3.6.2 (A:) ACTX-HI:OB4219 {Funnel-web spider (Hadronyche infensa)}

KCLAEAADCSPWSGDSCCKPYLCSCIFFYPCSCRPKGW

>d1axh__g.3.6.2 (-) Atracotoxin-hvl (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}

SPTCIPSGQPCPYENCCSQSCTFKENENGNTVKRCD

>d1hvwa_g.3.6.2 (A:) Atracotoxin-hvl (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}

CIPSGQPCPYENCCSQSCTGGRCD

>d1vtx__g.3.6.2 (-) Atracotoxin-hvl (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}

CAKKRNWCGBTEDCCCPMKCVYAWYNEQGSCQSTISALWKKC

>d1dl0a_g.3.6.2 (A:) J-atracotoxin-hv1c {Australian funnel-web spider (Hadronyche versuta)}

ACTGADRPCAACCPCPGTSCAKAESNGVSYCRKDEP

>d1g9pa_g.3.6.2 (A:) Atracotoxin-hv2a {Funnel-web spider (Hadronyche versuta)}

LLACLFNGNRCSSNRDCELTpvCKRGSCVSSGPGLVGGILGGIL

>d1qdp__g.3.6.2 (-) Robustoxin {Funnel-web spider (Atrax robustus)}

CAKKRNWCGBTEDCCCPMKCIYAWYNQQGSCQTTITGLFKKC

>d1qk6a_g.3.6.2 (A:) Huwentoxin-I {Chinese bird spider (Selenocosmia huwena)}

ACKGVFDATPGKNECCPNRVCSDKHKWCKWKL

>d1i25a_g.3.6.2 (A:) Huwentoxin-II {Chinese bird spider (Selenocosmia huwena)}

LFECSFSCEIEKEGDKPCKKKCKGGWKCKFNMCVVK

>d1qk7a_g.3.6.2 (A:) Lectin SHL-I {Chinese bird spider (Selenocosmia huwena)}

GCLGDKCDYNNNGCCSYVCSRTWKWCVLAGPW

>d1d1ha_g.3.6.2 (A:) Hanatoxin 1 {Tarantula (Grammostola spatulata)}

ECRYLFGGCKTTSDCCKHLGCKFRDKYCAWDFTS

>d1emxa_g.3.6.2 (A:) Heteropdatoxin 2, hptx2 {Spider (Heteropodidae venatoria)}

DDCGKLFGCCTDNADCCEGYVCRWLWCKLDW

>d1c6wa_g.3.6.2 (A:) Maurocalcin {Scorpio maurus}

GDCLPHLKLCENKDCCSKKCKRRGTNIEKRCR

>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}

KEGYLVNKSTGCKYGCCKLGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC

>d2sn3__g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing, variant 3}

KEGYLVKKSDGCKYGCCKLGENEGCDTECKAKNQGGSYGYCYAFACWCEGLPESTPTYPLPNKSC

>d1b3ca_g.3.7.1 (A:) Scorpion toxin {Centruroides sculpturatus ewing, beta}

KDGYLVEKTGCKKTCYKLGENDFCNRECKWKHIGGSYGYCYGFCYCEGLPDSTQTWPLPNKTC

>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}

KKDGYVPDSGNCKYECLKDDYCLNDLCLERKADKGYCYWGKVSCYCYGLPDNSPTKSGKCNPA

>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}

KEGYLVDKNTGCKYECCLKLDNDYCLRECKQQYGKGAGGGYCYAFACWCTHLYEQAIWPLPNKSC

>d1bcg__g.3.7.1 (-) Scorpion toxin {Scorpion (Buthotus judaicus), BJXTR-IT}

MKKNGYPLDRNGKTTECSGVNAIAPHYCNCSECTKVYYAESGYCCWGACYCFGLEDDKPIGPMKDITKKYCDVQI

>d1snb__ g.3.7.1 (-) Scorpion toxin {Scorpion (Buthus martensi), toxin m8}
GRDAYIADSENCTYFCGSNPYCNDVCTENGAKSGYCQWAGRYGNACYCIDLPASERIKEGGRCG
>d1dja_g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus martensi), toxin m1}
VRDAYIAKPHNCVYECARNEYCNDLCTKNGAKSGYCQWVGKYGNGCWCIELPDNVPIRPGKCH
>d1sn4a_g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus martensi), toxin m4}
VRDAYIAKPENCVYHCAGNEGCKLCTDNGAESGYCQWGGRYGNACWCICLPPDVPIRPGKCH
>d1dq7a_g.3.7.1 (A:) Scorpion toxin {Indian red scorpion (Buthus tamulus), neurotoxin}
GEDGYIADGDNCTYICTFNNYCHALCTDKKGDSGACDWVVPYGVVCWCEDLPTVPIRGSGKCR
>d1b7da_g.3.7.1 (A:) Scorpion toxin {Scorpion (Tityus serrulatus)}
KEGYLMDHEGCKLSCFIRPSGYCGRECGIKKGSSGYCAWPACYGLPNWVKVWDATNK
>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, LQIII}
VRDAYIAKNYNCVYECFRDSYCNDLCTKNGASSGYCQWAGKYGNACWCYALPDNVPIRPGKCH
>d1lqi__ g.3.7.1 (-) alpha toxin {Scorpion (Leiurus quinquestriatus hebraeus)}
MVRDAYIAKNYNCVYECFRDAYCNELCTKNGASSGYCQWAGKYGNACWCYALPDNVPIRPGKCR
>d1bmr__ g.3.7.1 (-) LQH III alpha-like toxin, LQH {Hebraei scorpion (Leiurus quinquestriatus hebraeus)}
VRDGYIAQPENCVYHCFPGSSGCDTLCKEKGGSGHCGFKVGHGLACWCNALPDNVGIVEGEKCHS
>d1big__ g.3.7.2 (-) Bmtx1 {Buthus martensi}
EFTDVKTGSKQCPVCKQMFHKPKNGKCMNGKRCYS
>d1bkt__ g.3.7.2 (-) Bmktx {Buthus martensi}
VGINVKCKHSQCLPKCKDAGMRFKGKINGKCDCTPK
>d2bmt__ g.3.7.2 (-) Bmtx2 {Buthus martensi}
EFTNVSCSASSQCWPVCKLFGTYRGKCMNSKRCYS
>d1du9a_g.3.7.2 (A:) Bmp02 neurotoxin {Chinese scorpion (Buthus martensi)}
VGCEECPMHCKGKNAKPTCDDGVCNCV
>d1hp2a_g.3.7.2 (A:) alpha-KTX, K+-channel blocker {Brazilian scorpion (Tityus serrulatus), Tstx-k alpha}
VFINAKCRGSPECLPKCKEAIKGKAAGKCMNGKCKCYP
>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 noxious hoffmann)}
TIINVKCTSPKQCSKPCKELYGSSAGAKCMNGKCKCYNN
>d1txm__ g.3.7.2 (-) Maurotoxin {Scorpion (Scorpio maurus)}
VSCTGSKDCYAPCRKQTGCPNAKCINKSCKCYGC
>d1cmr__ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
CTTSKECWVCQRLHNTSKGWCDHRCICES
>d2crd__ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
EFTNVSCTTSKECWVCQRLHNTSRGKCMNKKCRCYS
>d1scy__ g.3.7.2 (-) Scyllatoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
AFCNLRCMQLSCRSLGLGKIGDKCECVKH
>d1agt__ g.3.7.2 (-) Agitoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
GVPINVSTGSPQCIPCKDAGMRFKGKCMNRKCHCTPK

>d1chl__ g.3.7.2 (-) Chlorotoxin {Scorpion (Leiurus quinquestriatus), venom}
MCMPCFTTDHQMARKCDDCCGGKGRGKCYGPQCLCR

>d1c55a_g.3.7.2 (A:) Butantoxin {Brazilian scorpion (Tityus serrulatus)}
WCSTCLDLACGASRECYDPCFKAFGRAHGKCMNNKRCY

>d1tsk__ g.3.7.2 (-) Toxin ts kappa {Scorpion (Tityus serrulatus)}
VVIGQRCYRSPDCYSACKLVGKATGKCTNGRCDC

>d1sis__ g.3.7.2 (-) Toxin I5a {Scorpion (Buthus eupeus)}
MCMPCFTTDPNMAKKCRDCCGGNGKCFGPQCLCNR

>d1phn__ g.3.7.2 (-) Toxin analog {Scorpion (Androctonus mauretanicus mauretanicus)}
TCVNLRRQLSRLGKICGVKCECVKH

>d1acw__ g.3.7.2 (-) Toxin analog P01 {Scorpion (Androctonus mauretanicus mauretanicus)}
VSCECDPEHCSTQKAQAKCDNDKCVCEPI

>d1sco__ g.3.7.2 (-) OSK1 TOXIN {Central asian scorpion (Orthochirus scrobiculosus)}
GVIINVKCKISRQCLEPKKAGMRFGKCMNGKCHCTPK

>d2ktx__ g.3.7.2 (-) Kalitoxin (KTX) {Scorpion (Androctonus mauretanicus mauretanicus)}
GVEINVKGSPQCLKPCKDAGMRFGKCMNRKCHCTPK

>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}
TISCTNEKQCYPHCKKETGYPNAKCMNRKCKCFG

>d1qky__ g.3.7.2 (A:) PI7 {Scorpion (Pandinus imperator)}
DEAIRCTGTDCYIPCRYITGCFNSRCINKSCKCYGCT

>d1fjna__ g.3.7.3 (A:) Defensin MGD-1 {Mediterranean mussel (Mytilus galloprovincialis)}
GFGCPNNYQCHRHKCSIPGRGCGGYCGGWHLRCTCYRCG

>d1i2ua__ g.3.7.4 (A:) Heliomicin {Tobacco budworm (Heliothis virescens)}
DKLIGSCVVGAVNYTSDCNGECKRRGYKGGHCGSFANVCWCET

>d1myn__ g.3.7.4 (-) Drosomycin {Fruit fly (Drosophila melanogaster)}
DCLSGRYKGPCAVWDNETCRRVCKEEGRSSGHCSPLKCWCEGC

>d1ica__ g.3.7.4 (-) Defensin A {Flesh fly (Phormia terraenovae), larva}
ATCDLLSGTGINHSACAAHCLLRGNRGYCNGKGVCVRN

>d1gpt__ g.3.7.5 (-) gamma-Thionin {Barley (Hordeum vulgare)}
RICRRRSAGFKGPCVSNKNCQAQVQCQQEGWGGGNCDGPLRRCKCMRRC

>d1gps__ g.3.7.5 (-) gamma-Thionin {Wheat (Triticum turgidum)}
KICRRRSAGFKGPCMSNKNCQAQVQCQQEGWGGGNCDGPFRRKCIRO

>d1ayj__ g.3.7.5 (-) Antifungal protein 1 (RS-AFP1) {Radish (Raphanus sativus)}
EKLCEPSTGWSGVCGNNNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC

>d1bk8__ g.3.7.5 (-) Antimicrobial protein 1 (AH-AMP1) {Horse chestnut (Aesculus hippocastanum)}
LCNERPSQTWSGNCGNTAHCDKQCQDWKEASHGACHKRENHWKCFCTQNC

>d1jkza__ g.3.7.5 (A:) Defensin 1 (PSD1) {Pea (Pisum sativum)}
KTCEHLADTYRGVCFTNASCDDHCKNKAHLISGTCHNWKCFCTQNC

>d1brz__ g.3.7.5 (-) Brazzein {J'oublier (Pentadiplandra brazzeana)}
EDKCKKVYENYPVSKQLANQCNYDCKLDKHARSGEFCYDEKRNLQCIDYCEY

>d2cbh__ g.3.8.1 (-) Cellulohydrolase 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)}

ALAEQSCGVYTERCAQGLRCLPRQDEEKPLHALLHGRGVCLNEKS

>d1igra3 g.3.9.1 (A:150-299) Cys-rich domain of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

DLCPGTMEEKPMCEKTTINNEYNYRCWTTNRCQKMCPCSTCGKRACTENNECCHPECLGCSAPDNDTACVACRHYYYAGVCVPACPPNTYRFEG

WRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFIRNGSQSMYCIPCEGPCP

>d1lpba1 g.3.10.1 (A:6-44) (Pro)colipase {Pig (Sus scrofa)}

GIIINLDEGEELCLNSAQCKSNCCQHDTILSLRCALKAR

>d1lpba2 g.3.10.1 (A:45-90) (Pro)colipase {Pig (Sus scrofa)}

ENSECSAFTLYGVYYKPCERGLTCEGDKSLVGSITNTNFGICHNV

>d1pco_1 g.3.10.1 (1-44) (Pro)colipase {Pig (Sus scrofa)}

VPDPRGIIINLDEGEELCLNSAQCKSNCCQHDTILSLRCALKAR

>d1imt_1 g.3.10.1 (1-36) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}

AVITGACERDLQCGKGTCACAVSLWIKSVRVCTPVGT

>d1imt_2 g.3.10.1 (37-80) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}

SGEDCHPASHKIPFSQCRMHHHTCPACPNLACVQTSPKKFKCLSK

>d1edmb_g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}

VDGDQCESNPCLNGGSKDDINSYECWCPCFGFEGKNCEL

>d1rfnb_g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}

MTCNIKNGRCEQFKNSADNKVVCSCTEGYRLAENQKSCPAVPFPCGRVSQSQTSK

>d1pfxl1 g.3.11.1 (L:47-86) Factor IX (IXa) {Pig (Sus scrofa)}

DGDQCEPNPCLNGGLCKXDINSYECWCQVGFEKGNCLEDA

>d1pfxl2 g.3.11.1 (L:87-146) Factor IX (IXa) {Pig (Sus scrofa)}

TCNIKNGRCKQFCKTGADSKVLCSCTTGYRLAPDQKSCPKPAVPFPCGRVSVSHSPTTLR

>d1danl1 g.3.11.1 (L:49-86) Coagulation factor VIIa {Human (Homo sapiens)}

QCASSPCQNGGSKDQLQSYICFCLPAFEGRNCETHKD

>d1danl2 g.3.11.1 (L:87-142) Coagulation factor VIIa {Human (Homo sapiens)}

DQLICVNENGCEQYCSHTGTKRSCRCHEGYSLLADGVSVTVEYPCGKIPILE

>d1dval1 g.3.11.1 (L:42-86) Coagulation factor VIIa {Human (Homo sapiens)}

ISYSDGDQCASSPCQNGGSKDQLQSYICFCLPAFEGRNCETHKD

>d1f7ea_g.3.11.1 (A:) Coagulation factor VIIa {Human (Homo sapiens)}

SDGDQCASSPCQNGGSKDQLQSYICFCLPAFEGRNCETHKDGS

>d1g1sa2 g.3.11.1 (A:119-158) E-selectin, EGF-domain {Human (Homo sapiens)}

TASCQDMSCSKQGECLETIGNYTCSCYPGFYGPCEYVRD

>d1g1ta2 g.3.11.1 (A:119-157) E-selectin, EGF-domain {Human (Homo sapiens)}

TAACNTSCSGHGECEVTINNYTCKCDPGFSGLKCEQIV

>d1fjsl_g.3.11.1 (L:) Factor X, N-terminal module {Human (Homo sapiens)}

KLCSDLNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGPYPCGKQTLE

>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

>d1kig_g.3.11.1 (L:) Factor X, N-terminal module {Cow (Bos taurus)}

CSLDNGGCDQFCREERSEVRCSAHGYVLGDDSKSCVSTERFPCGKFTQGR

>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)}
VNPCCYYPCQHQGICVRGFLDRYQCDCTRTGYSGPNCTIPE
>d1cvua2 g.3.11.1 (A:33-73) Prostaglandin H2 synthase-1, EGF-like module {Mouse (Mus musculus)}
ANPCCSNPCQNRGECKMSTGFDQYKCDCTRTGFYGENCTTPE
>d1a3p__ g.3.11.1 (-) Epidermal growth factor, EGF {Mouse (Mus musculus)}
PGXPSSYDGYCLNGGVXMHIESLDSYTCNCVIGYSGDRCQTRDLRWELR
>d3egf__ g.3.11.1 (-) Epidermal growth factor, EGF {Mouse (Mus musculus)}
NSYPGCPSSYDGYCLNGGVCMHIESLDSYTCNCVIGYSGDRCQTRDLRWELR
>d1jl9a_g.3.11.1 (A:) Epidermal growth factor, EGF {Human (Homo sapiens)}
CPLSHDGYCLHDGVCAMYIEALDKYACNCVVGYIGERCQYRDL
>d3tgf__ g.3.11.1 (-) Transforming growth factor alpha {Human (Homo sapiens)}
VVSHFNCDPDSHTQFCFHGTCRFLVQEDKPACVCHSGYVGARCEADLLA
>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)}
QVPSNCDCLNNGGTCVSNKYFSNIHWNCNPKKFGQQHCEIDKSKT
>d1hae__ g.3.11.1 (-) Heregulin-alpha, EGF-like domain {Human (Homo sapiens)}
SHLVKCAEKEKTFCVNGGECEFMVKDSLNSPNSRYLCKCQPGFTGARCTENVMKVNQNQEKAEELY
>d1adx__ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
QMFCNQTACPADCDPNTQASCECP EGYILDDGFICTDIDE
>d1dx5i1 g.3.11.1 (I:345-387) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
VEPVDPFCFRANCEYQCQLDQTSYLCVCAEGFAPIPHEPHRCQ
>d1dx5i2 g.3.11.1 (I:388-422) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
MFCNQTACPADCDPNTQASCECP EGYILDDGFICT
>d1dx5i3 g.3.11.1 (I:423-462) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
DIDECENGFCSGVCHNLPGT FECICGPDSALAGQIGTDC
>d1zaq__ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
EPVDPFCFRANCEYQCQLNQTSYLCVCAEGFAPIPHEPHRCQMF
>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)}
CSEPRCFNNGGTCQQALYFSDFVCQCPEGFAGKSCEIDTRAT
>d1hz8a1 g.3.11.1 (A:1-41) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}
GTNECLDNNGGCSHVNDLKIGYECLCPDFQLVAQRRCED
>d1hz8a2 g.3.11.1 (A:42-82) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}
IDECQDPDTCSQLCVNLEGGYKCQCCEEGFQLDPHTKACKAV
>d1ijqa2 g.3.11.1 (A:643-692) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}

VNWCERTTLSNGGCQYLCLPAPQINPHSPKFTCACPDGMILLARDMRSCLT
>d1jv2b4 g.3.11.6 (B:532-562) Integrin beta EGF-like domains {Human (Homo sapiens)}
KGEMCSGHGQCSCGDCLCDSDWTGYCNCTT
>d1jv2b5 g.3.11.6 (B:563-605) Integrin beta EGF-like domains {Human (Homo sapiens)}
RTDTCMSSNLLCSGRGKCECGSCVCIQPGSYGDTCEKCPCTP
>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)}
CPCPGGSSCAIVPKTKEVVVCTHCPTGTAGKRCELDDGYFGDPLGSNGPVRLCRP
>d1klo_2 g.3.11.2 (66-121) Laminin gamma1 chain {Mouse (Mus musculus)}
CQCNDNIDPNAVGNCRNLGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKA
>d1klo_3 g.3.11.2 (122-172) Laminin gamma1 chain {Mouse (Mus musculus)}
CACNPYGTVQQQSSCNPVTGQCQLPHSGRDCGTCDPGYNNLQSGQGCER
>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}
NISQHQCVKKQCPQNSGCFRHLDERECKLLNYKQEGDKCVENP
>d1ceja2 g.3.11.4 (A:46-96) Merozoite surface protein 1 (MSP-1) {Plasmodium falciparum}
NPTCNENNNGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSN
>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)}
TACSECVCPRLXEEYKCYCXDLISPNDVK
>d1pi2__ g.3.13.1 (-) Bowman-Birk inhibitor, BBI {Soybean (Glycine max), PI-II}
YSKPCCDLCMCTRSMPQCSCEDRINSCHSDCKSCMCTRSQPGQCRCLDTNDFCYKPKCSR
>d1d6ri_g.3.13.1 (I:) Bowman-Birk inhibitor, BBI {Soybean (Glycine max)}
KPCCDQCACTKSNPPQRCSDMRLNSCHSACKSCICALSYPAQCFCVDITDFCYEPCKPSEDDKEN
>d2bbi__ g.3.13.1 (-) Bowman-Birk inhibitor, BBI {Soybean (Glycine max)}
DDESSKPCCDQCACTKSNPPQRCSDMRLNSCHSACKSCICALSYPAQCFCVDITDFCYEPCKPSEDDKEN
>d1pbia_g.3.13.1 (A:) Bowman-Birk inhibitor, BBI {Winter pea (Pisum sativum)}
KSACCDTCLTKSNPPTCRCVDVGETCHSACLSCICAYSNPPKCQCFDTQKFCYKQCHNSELEEVIKN
>d1df9c_g.3.13.1 (C:) Bowman-Birk inhibitor, BBI {Mung bean (Vigna radiata)}
SHDEPSSEPCCDSCDCTKSIPPQCHCANIRLNSCHSACKSCICTRSMPGKCRCLDDFCYKPCESMDKD
>d1c2aa1 g.3.13.1 (A:4-64) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}
KRPWKCCDEAVCTRSIPPICTCMDEVFECPKTCKSCGPSMGDPSSRRICQDQYVGDPGPICR
>d1c2aa2 g.3.13.1 (A:65-123) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}
PWECCDKAICTRSPNPPTCRVDEVKKCAPTCKTCLPSRSRPSRRVCIDSYFGPVPPRCT
>d1tabi_g.3.13.1 (I:) Bowman-Birk inhibitor, BBI {Adzuki bean (Phaseolus angularis)}

SESKPCCDQCSCTKSMPPKCRCSDIRLNSCHSACKSCACTYSIPAKCFCTDINDFCYEPC
>d1flei_g.3.14.1 (I:) Elafin, elastase-specific inhibitor {Human (Homo sapiens)}
TKPGSCPIIIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
>d2rel_g.3.14.1 (-) Elafin, elastase-specific inhibitor {Human (Homo sapiens)}
AQEPVKGPVSTKPGSCPIIIRCAMLNPPNRCLKDTDCPGIKKCCEGSCGMACFVPQ
>d1bx7_g.3.15.1 (-) Hirustasin {Medicinal leech (Hirudo medicinalis)}
GNTCGGETCSAAQVCLKGKVCNEVHCRIRCKYGLKKDENGEYPCSCAKA
>d1ejab_g.3.15.1 (B:) Bdellastasin {Medicinal leech (Hirudo medicinalis)}
TTPCGPVTCSGAQMCEVDKVCSDLHCKVKEHGFKKDDNGCEYACICADAPQ
>d1skz_1 g.3.15.1 (7-58) Factor Xa inhibitor antistatin {Mexican leech (Haementeria officinalis)}
GCEEAGCPEGSACNIITDRCTSGVRCRVHCPHGFQRSRYGCEFCKRLEPM
>d1skz_2 g.3.15.1 (59-110) Factor Xa inhibitor antistatin {Mexican leech (Haementeria officinalis)}
KATCDISECPEGMMCSRLTNKCDCKIDINCRKTCPNGLKRDKLGCEYCECRP
>d1hic_g.3.15.2 (-) Hirudin {Leech (Hirudo medicinalis)}
VVYTDCTESGQNLCLEGSNVCGQGNKICLGSDEKNQCVTGEGTPKPQSHNDGFEEIPEEYLQ
>d1hrti_g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}
VVYTDCTESGQNLCLEGSNVCGQGNKICLGSDEKNQCVTGEGTPKPQSHNDGFEEIPEEYLQ
>d4htci_g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}
ITYTDCTESGQNLCLEGSNVCGGNKICLGSNGKGNQCVTGEGTPKPQSHNDGFEEIPEEYLQ
>d1dec_g.3.15.2 (-) Decorsin {North american leech (Macrobdella decora)}
APRLPQCQGDDQEKLCKNDECPPGQCRFPRGDADPYCE
>d1e0fi_g.3.15.2 (I:) Haemadin {Indian leech (Haemadipsa sylvestris)}
IRFGMGKVPCPDGEVGYCDCGEKICLYGQSCNDGQCGDPKPSSEEEFEIDEEEK
>d1qgma_g.3.16.1 (A:) N-terminal domain of granulin-1 {Carp (Cyprinus carpio)}
VIHCDAATICPDGTTCSLPYGVWYCSPFS
>d1g26a_g.3.16.1 (A:) N-terminal domain of granulin-1 {Human (Homo sapiens)}
VVHCDMEVICPDGYTCRRLPSGAWGCCPFTQ
>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)}
YQQVPMCDAGEQCAVRKGARIGKLCDPRGTSCNSFLLKCL
>d1gl1i_g.4.1.1 (I:) Protease inhibitor PMP-C {Migratory locust (Locusta migratoria)}
ISCEPGKTFDKCNTCRCGADGKSACTLKACPN
>d1gl0i_g.4.1.1 (I:) Protease inhibitor PMP-D2V {Migratory locust (Locusta migratoria)}
KCTPGQVKQQDCNTCTPTGVWGCTLMGCQP
>d1kgma_g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}
EVTCEPGTTFDKCNTCRCGSDGKSACTLKACPQ
>d1kioa_g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}
EVTCEPGTTFDKCNTCRCGSDGKSACTRMACPQ
>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}
KKDKVKKKGGPGSECAEWAWGPCTPSSKDCGVGFREGTCGAQTQRIRCRVPCNWKKEFG
>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}
DDGLCYEGTNCGKVGKYCCSPIGKYCVYDSKAICNKNT
>d3ebx__ g.7.1.1 (-) Erabutoxin B (also neurotoxin B) {Sea snake (Laticauda semifasciata)}
RICFNHQSQQPTTKCSPGESSCYHKQWSDFRGTIIERGCGCPTVKPGIKLSCCEVCNN
>d1tgxa__ g.7.1.1 (A:) gamma-Cardiotoxin {Snake (Naja nigricollis)}
LKCNLIPPFWKTCPKGKNLCYKMTMRAAPMVVKRGCIDVCPKSSLIKYMCCNTDKCN
>d1fas__ g.7.1.1 (-) Fasciculin {Green mamba (Dendroaspis angusticeps)}
TMCYSHTTTSRAILNCGENSCYRKSRHPPKMVLGRGCGCPGDDYLEVKCCTSPDKCNY
>d1qm7a__ g.7.1.1 (A:) Fasciculin {Green mamba (Dendroaspis angusticeps)}
TMCYSHTTTSRAILNCGETCYKKSRRHPPKMVLGRGCGCPTVAPGIKLNCCNTDKCNY
>d1tnr__ g.7.1.1 (-) Neurotoxin I {Snake (Naja naja oxiana)}
ITCYKTPITSETCAPGQNLCYTKTWCDAWCGSRGKIELGCAATCPTVESYQDIKCCSTDNCNPHPKQKRP
>d1cdta__ g.7.1.1 (A:) Cardiotoxin V4II (Toxin III) {Naja mossambica mossambica}
LKCNLIPPIAKTCPEGKNLCKMMIASKKMVPVKRGCIINVCPKNSALVKYVCCSTDRCN
>d1kxia__ g.7.1.1 (A:) Cardiotoxin V {Taiwan cobra (Naja naja atra)}
LKCHNTQLPFIYKTCPEGKNLCKFATLKKPLKFPVKRGCADNCPKNSALLKYVCCSTDRCN
>d2ctx__ g.7.1.1 (-) alpha-Cobratoxin {Cobra (Naja naja siamensis)}
IRCFITPDITSKDCPNGHVCTKTCDAFCISRGKRVDLGCAATCPTVKTGVDIQCCSTDNCNPFPTRKRP
>d1si__ g.7.1.1 (-) Long neurotoxin 1 (component LSIII) {Sea snake (Laticauda semifasciata)}
RECYLNPHDTQTCPMSGQEICYVKSWCNAWCSSRGKVLEFGCAATCPVNTGTEIKCCSADKCNTYP
>d1tfs__ g.7.1.1 (-) FS2 toxin {Black mamba (Dendroaspis polylepis polylepis)}
RICYSHKASLPRATKTCVENTCYKMFIRTHREYISERGCCTAMWPYQTECCKGDRCKN
>d1hc9a__ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), Alpha-bungarotoxin}
IVCHTTATSPISAVTCPPGENLCYRKMWCDFCSSRGKVVELGCAATCPSSKKPYEEVTCCSTDCKCNPHPKQRPG
>d2abxa__ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), Alpha-bungarotoxin}
IVCHTTATIPSSAVTCPPGENLCYRKMWCDAFCSSRGKVVELGCAATCPSSKKPYEEVTCCSTDCKCNHPPKRQPG
>d1kbaa__ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), kappa-bungarotoxin}
RTCLISPSSTPQTCPNGQDICFLKAQCDKFCISRGPIEQGCVATCPQFRSNYRSLLCCTTDNCNH
>d1f94a__ g.7.1.1 (A:) Bucandin {Malayan krait (Bungarus candidus)}
MECYRCGVSGCHLKICSAETFCYKWLNIKISNERWLGAKTCTEIDTWNVYNKCCNTNLNCNT
>d2cdx__ g.7.1.1 (-) Cardiotoxin CTXI {Taiwan cobra (Naja naja atra)}
LKCNLIPPIASKTCPAGKNLCKMFMMSDLTIPVKRGCIDVCPKNSLLVKYVCCSTDRCN
>d1chvs__ g.7.1.1 (S:) Cardiotoxin II {Taiwan cobra (Naja naja atra)}
LKCNLVPLFYKTCAGKNLCKMFMSNVKPMVKRGCIDVCPKSSLVKYVCCSTDRCN
>d1cb9a__ g.7.1.1 (A:) Cardiotoxin II {Central asian cobra (Naja naja oxiana)}
LKCKKLVPLFSKTCPAGKNLCKMFMVAPHPVKRGCIDVCPKSSLVKYVCCSTDRCN
>d1i02a__ g.7.1.1 (A:) Cardiotoxin III {Taiwan cobra (Naja naja atra)}
LKCNLVPLFYKTCAGKNLCKMFMVATPKVPVKRGCIDVCPKSSLVKYVCCSTDRCN
>d1kbs__ g.7.1.1 (-) Cardiotoxin IV {Taiwan cobra (Naja naja atra)}
RKCNKLVPLFYKTCAGKNLCKMFMSNLTVPKRGCIDVCPKNSALVKYVCCSTDRCN
>d1cod__ g.7.1.1 (-) Cobrotoxin II (ct2) {Taiwan cobra (Naja naja atra)}
LECHNQQSSQPTTTGCSGGETCYKKRWRDHRGYRTERGCGCPSVKNGIEINCCTTDRCNN
>d1g6ma__ g.7.1.1 (A:) Cobrotoxin II (ct2) {Monocled cobra (Naja kaouthia)}

LECHNQQSSQPTTGCSSGENNCYKKEWRDNRGYRTERGCGPSVKKGIGINCCTDRCNN
>d1nea__ g.7.1.1 (-) alpha-Toxin {Snake (*Naja nigricollis*)}
LECHNQQSSQPPTTKTCGETNCYKKVWRDHRTIIERGCGCPTVKPGIKLNCCTDKCNN
>d1ntx__ g.7.1.1 (-) alpha-Toxin {Black mamba (*Dendroaspis polylepis polylepis*)}
RICYNHQSTTRATTKSCEENSCYKKYWRDHRTIIERGCGCPKVKGPGVGIHCCQSDKCNY
>d1nor__ g.7.1.1 (-) Neurotoxin II (Nt2) {Central asian cobra (*Naja naja oxiana*)}
LECHNQQSSQPPTTKTCGETNCYKKWWSDHRTIIERGCGCPKVKGPGVNLNCRTDRCNN
>d1txb__ g.7.1.1 (-) Toxin B (long neurotoxin) {King cobra (*Ophiophagus hannah*)}
TKCYVTPDATSQTCPDGQDICYTWTCDGFSSRGKRIDLGAATCPVKPGVDIKCSTDNCNPFTWKRH
>d1jgka_g.7.1.1 (A:) Candoxin {Malayan krait (*Bungarus candidus*)}
MKCKICNFDTCRAGELKVCASGEKYCFKESWREARGTRIERGCAATCPKGSVYGLYVLCCCTDDCN
>d1drs__ g.7.1.2 (-) Dendroaspin {Dendroaspis jamesoni kaimosae}
RICYNHLGTPPPTETCQEDSCYKNIWTFDNIIRRGCGCFTPGRDMPGPYCCESDKCNL
>d1erh__ g.7.1.3 (-) CD59 {Human (*Homo sapiens*)}
LQCYNCPNPTADCKTAVNCSSDFDACLITKAGLQVYNKCKWFHNCNDVTTRLRENLYCCKDLCN
>d1btea_g.7.1.3 (A:) Type II activin receptor {Mouse (*Mus musculus*)}
ETQECLFFNANWERDRTNQTGVEPCYGDKDCKRRHCFATWKNISGSIEVKQGCWLDDINCYDRTDCIEKKDSPEVYFCCCEGNMCNEKFSYFPEME
>d1es7b_g.7.1.3 (B:) BMP receptor Ia ectodomain {Human (*Homo sapiens*)}
TLPFLKCYCSGHCPDDAINNTCTNGHCFAIIEEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRRTIECCRNLNCNQYLQPTLPP
>d1ktzb_g.7.1.3 (B:) TGF-beta type II receptor extracellular domain {Human (*Homo sapiens*)}
PQLCKFCDFVRSTCDNQKSCMSNCITSICEKPQEVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAAASPCKIMKEKKPGETFFMCSSDECND
NIIIFSEYY
>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*)}
RPDFCLEPYTGPCLRRIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>d1faki_g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (*Bos taurus*)}
APDFCLEPYDGPCCRALKRLRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTC
>d1g6xa_g.8.1.1 (A:) Pancreatic trypsin inhibitor, BPTI {Cow (*Bos taurus*)}
RPDFCLEPYAGACRARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>d3bthi_g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (*Bos taurus*)}
DFCLEPYTGPCHARIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>d5pti_g.8.1.1 (-) Pancreatic trypsin inhibitor, BPTI {Cow (*Bos taurus*)}
RPDFCLEPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTCGGA
>d1ktha_g.8.1.1 (A:) Collagen type VI (domain C5 from alpha 3 chain) {Human (*Homo sapiens*)}
ETDICKLPKDEGTCRDFILKWYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCAPV
>d1adz_g.8.1.1 (-) Tissue factor pathway inhibitor {Human (*Homo sapiens*)}
DYKDDDDKLKPDCFCLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEECKNICEDGPNGF
>d1irha_g.8.1.1 (A:) Tissue factor pathway inhibitor {Human (*Homo sapiens*)}
EFHGPSWCLTPADRGCRANEFRYYNSVIGKCRPFKYSGCGGNENNFTSKQECLRACKKG
>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)}
SCQLGYSAGPCMGMTSRYFYNGTSMACETFQYGGCMNGNNFTEKECLQTCRT

>d1bik_2 g.8.1.1 (79-134) Bikunin from inter-alpha-inhibitor complex {Human (Homo sapiens)}
VAACNLPIVRGCRCAFIQLWAFDAVKGKCVLPYGGCGNGNKFYSEKECREYCGV

>d1dtx__ g.8.1.1 (-) alpha-Dendrotoxin {Green mamba (Dendroaspis angusticeps)}
EPRRKLCILHRNPGRCYDKIPAFYYNQKKQCERFDWSGCGGNSNRFKTIEECRRTCIG

>d1bunb_ g.8.1.1 (B:) beta2-bungarotoxin, neurotoxin chain {Many-banded krait (elapid) (Bungarus multicinctus)}
RKRPDPDKPPDTKICQTVVRAFYKPSAKRCVQFRYGGCNGNGNHFSDHLCRCECLEYR

>d1shp__ g.8.1.1 (-) Trypsin inhibitor {Sea anemone (Stichodactyla helianthus)}
SICSEPKVGRCKGYFPRFYFDSETGKCTPFIYGGCGGNNGNNFETLHQCRACRA

>d1dtk__ g.8.1.1 (-) Dendrotoxin K {Black mamba (Dendroaspis polylepis polylepis)}
AAKYCKLPLIRGPCKRKIPSFYYKWAKQCLPDFDYGCGGNANRFKTIEECRRTCVG

>d1den__ g.8.1.1 (-) Dendrotoxin I {African elapid snake (Dendroaspis polylepis polylepis)}
QPLRKLCILHRNPGRCYQKIPAFYYNQKKQCEGFTWSGCGGNSNRFKTIEECRRTCIRK

>d1bf0__ g.8.1.1 (-) Calcyclidine (cac) {Green mamba (Dendroaspis angusticeps)}
WQPPWYCKEPVRIGSCKQFSSFYFKWTAKKCLPFLSGCGGNANRFQTIGECRKKCLGK

>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)}
HSSEMHSCLGDPPTSCAEGTDIYYDSDSKTCKVLAASCPSGENTFESEVECQVACGAPIEG

>d1d0da_ g.8.1.2 (A:) Anticoagulant protein, factor Xa inhibitor {Soft tick (Ornithodoros moubata)}
YNRLCIKPRDWIDECDSNEGGERAYFRNGKGCGDSFWICPEDHTGADYYSSYRDCFNACI

>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}
PVTCLKSGAICHCPVFCPRRYKQIGTCGLPGTKCCKKP

>d1fd3a_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}
GIGDPVTCLKSGAICHCPVFCPRRYKQIGTCGLPGTKCCKKP

>d1e4ta_ g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD5}
NSKRACYREGGECLQRICIGLFHKIGTCNCFRFKCCKFQ

>d1e4ra_ g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD6}
NEPVSCIRNGGICQYRCIGLRHKGTCGSPFKCCK

>d1bnb__ g.9.1.1 (-) Beta-defensin, BD {Cow (Bos taurus), BD12}
APLSCGRNNGGVCIPRCVPVMRQIGTCGRPVKCRSW

>d1ewsa_ g.9.1.1 (A:) Alpha-defensin rk-1 {Rabbit (Oryctolagus cuniculus)}
MPCSCCKYCDPWEVIDGSCGLFNSKYICCREK

>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}
IMFFEMQACWSHSGVCRDKSERNCKPMMAWTYCENRNQKCCEY

>d2bds__ g.9.1.1 (-) BDs-I defensin {Sea anemone (Anemonia sulcata)}
AAPCFCSGKPGRGDLWILRGTCPGGYGYTSNCYKWPNIICCYPH

>d1sh1__ g.9.1.1 (-) Sea anemone neurotoxin-1 {Sea anemone (Stichodactyla helianthus)}

AACKCDDEGPDIRTAPLTGTVDLGSCNAGWEKCASYTIIADCCRKKK

>d1atx__ g.9.1.1 (-) Sea anemone toxin IA {Sea anemone (Anemonia sulcata)}

GAACLKSDGPNTRGNMSGTIWVFGCPGWNCEGRAIIGYCKQ

>d1ahl__ g.9.1.1 (-) Anthopleurin-A {Giant green sea anemone (Anthopleura xanthogrammica)}

GVSLCLSDGPSVRGNTLSGLWLYPSGCPGWHNCKAHGPTIGWCCKQ

>d1apf__ g.9.1.1 (-) Anthopleurin-B {Giant green sea anemone (Anthopleura xanthogrammica)}

GVPCLCDSDGPRPRGNTLSGILWFYPSGCPGWHNCKAHGPNIGWCCKK

>d1bhta1 g.10.1.1 (A:35-126) Hepatocyte growth factor {Human (Homo sapiens)}

RRNTIHEFKKSAKTTLIKIDPALKIKTKVNTADQCANRCTRNKGLPFTCAFKVFDKARKQCLWFPMNSMSGVKKEFGHEFDLYENKDYIR

>d1gmnb1 g.10.1.1 (B:42-125) Hepatocyte growth factor {Human (Homo sapiens)}

FFKSAKTTLIKIDPALKIKTKVNTADQCACRTRNKGLPFTCAFKVFDKARKQCLWFPMNSMSGVKKEFGHEFDLYENKDYI

>d1i8na__ g.10.1.2 (A:) Anti-platelet protein {Leech (Haementeria officinalis)}

ETITAGNEDCWSKRPWKLPDNLLTKEFTSVDECRCMCEESAVEPSCYILQINTETNECYRNNEGDTWSSLQYDQPNVVQWHLHACS

>d1ans__ g.11.1.1 (-) Neurotoxin III (ATX III) {Sea anemone (Anemonia sulcata)}

RSCCPCYWGCPWGQNCYPEGCSGPKV

>d1ajj__ g.12.1.1 (-) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

PCSAFHFHLSGEIHSSWRCDDGGPDCKDKSDEENCA

>d1cr8a__ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

PGGCHTDEFQCRDGICPLRWRCGDGTDCMDSSDEKSCEGV

>d1d2la__ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

GSPPQCQPGEFACANSRCIQCERWKCDGNDCLDNSDEAPALCHQH

>d1f5ya1 g.12.1.1 (A:1-44) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

GSAVGDRCRERNEFQCQDGK CISYKWVCDGSAECQDGSDSQETC

>d1f5ya2 g.12.1.1 (A:45-85) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

LSVTCKSGDFSCGGGRVNRCIPQFWRCDGQVDCDNGSDEQGC

>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)}

GHSHCSSTQFKCNCSRICEHWTCGDNDGCDYSDETHANCTNQ

>d1ldl__ g.12.1.1 (-) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

AVGDRCRERNEFQCQDGK CISYKWVCDGSAECQDGSDSQETCLSVT

>d1k7ba__ g.12.1.1 (A:) soluble Tva ectodomain, sTva47 {Quail (Coturnix coturnix)}

SCPPGQFRCEPPIGAHGECYPQDWLCGDGHPCDDGRDEWGCG

>d1ejga__ g.13.1.1 (A:) Crambin {Abyssinian cabbage (Crambe abyssinica)}

TTCCPSIVARSNFNVCRLPGTPEALCATYTGCIIPGATCPG DYAN

>d1bhp__ g.13.1.1 (-) beta-Purothionin {Wheat (Triticum aestivum)}

KSCCKSTLGRNCYNLRCRARGAQKLCANCRCKLTSGLSCP KDFPK

>d2plh__ g.13.1.1 (-) alpha-1-Purothionin {Wheat (Triticum aestivum)}

KSCCRSTLGRNCYNLRCRARGAQKLCAGVCRKISSGLSCP KGF PK

>d1ed0a__ g.13.1.1 (A:) Viscotoxin a3 {European mistletoe (Viscum album)}

KSCCPNTTGRNIYNACRLTGAPRPTCAKLSGCKIISG STCP SDY PK

>d1i5ka__ g.14.1.1 (A:) Plasminogen kringle {Human (Homo sapiens)}

ECMHGSGENYDGKISKTMSGLEQAWDSQSPHAHGYIPS KFPNKNLKKNYC RNPD RLPWCFTDPNKRWEYCDIPRC

>d1krn__ g.14.1.1 (-) Plasminogen kringle {Human (Homo sapiens)}

DCYHGDGQSYRGTSTTGGKKCQSWSSMTPHRHQTPENYPNAGLTNYCRNPADKGWCFTTDPSVRWEYCNLKCC

>d1pmla_g.14.1.1 (A:) Plasminogen kringle {Human (Homo sapiens)}

SDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVTAQNPSAQALGLGKHNYCRNPDGDAKPWCHVLKNRRLTWEYCDVPSCST

>d1ceaa_g.14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}

ECKTGNGKNYRGTMSKNGITCQKWSSTSPhRPRFSPATHPSEGLEENYCRNPDNDPQGPWCYTTDPEKRYDYCDILEC

>d5hpg_a_g.14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}

DCMFGNGKGYRGKRVTTGTPCQDWAAQEPHRHSIFTPETNPRAGLEKNYCRNPDGDVGGWCYTTNPRKLYDYCDVPQCAAP

>d2pf1_1 g.14.1.1 (66-156) Prothrombin kringle domain {Cow (Bos taurus)}

CAEGVGMNYRGNVSVRTSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSIITGPWCYTTSPTRLREECSPVCVGQDRVTVEIPR

>d2pf2_1 g.14.1.1 (66-146) Prothrombin kringle domain {Cow (Bos taurus)}

CAEGVGMNYRGNVSVRTSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSIITGPWCYTTSPTRLREECSPVCVGQ

>d1a0ha1_g.14.1.1 (A:164-270) Meizothrombin kringle domain {Cow (Bos taurus)}

SPLLETCPDGRGREYRGRЛАVTHGSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVADQPGDFEYCDLNCEEPVDGLGD
RLGEDPPDAAIEG

>d2hppp_g.14.1.1 (P:) Meizothrombin kringle domain {Cow (Bos taurus)}

CVPDRGREYRGRЛАVTSGSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVADQPGDFEYCNLYC

>d2hpqp_g.14.1.1 (P:) Meizothrombin kringle domain {Human (Homo sapiens)}

CVPDRGQQYQGRLAVTTHGLPCAWasAQAKALSKHQDFNSAVQLVENFCRNPDGDEEGVWCYVAGKPGDFGYCDLNYC

>d1kdu__g.14.1.1 (-) Urokinase-type plasminogen activator kringle domain {Human (Homo sapiens)}

TCYEGNGHFYRGKASTDTMGRPCLPWNSSATVLQQTYHAHRSDALQLGLGKHNYCRNPDNRRPWCYVQVGLKPLVQECMVHDCAD

>d3kiv__g.14.1.1 (-) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-10/M66 variant}

QCYHGNGQSYRGTSTTVGRTCSWSSMTPHRHQTPENYPNDGLTMNYCRNPADTGPWCFTTDPSIRWEYCNLTRC

>d1i71a_g.14.1.1 (A:) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-7 variant}

DCYHGDGQSYRGSFSTTVGRTCSWSSMTPHWHQRTTEYYPNGGLTRNYCRNPDAEIRPWCYTMDDPSVRWEYCNLTQCPVME

>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)}

AVTQTYGGNSNGEPCVLPFTYNGRTFYSCCTTEGRQDGHLWCSTSNEYEQDQKYSFCTDHT

>d1e88a2_g.14.1.2 (A:102-160) Fibronectin {Human (Homo sapiens)}

VLVQTRGGNSNGALCHFPFLNGKEYNSCTDTGRSDGFLWCSTTYNFEKDGKYGFCPMA

>d1ck7a3_g.14.1.2 (A:217-277) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

EGQVVVRVKYGNADGEYCKFPFLNGKEYNSCTDTGRSDGFLWCSTTYNFEKDGKYGFCPHE

>d1ck7a4_g.14.1.2 (A:278-335) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

ALFTMGGNAEGQPCFKPFRFQGTSYDSCTTEGRTDGYRWCGTTEDYDRDKKYGFCPET

>d1ck7a5_g.14.1.2 (A:336-393) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

AMSTVGGNSEAPCVFPFTFLGNKYESCTSAGRSDGKMWCAATTANYDDDRKGFCPDQ

>d1j7ma_g.14.1.2 (A:) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

SWMSTVGGNSGGAPCVFPFTFLGNKYESCTSAGRSDGKMWCAATTANYDDDRKGFCPDQG

>d1ks0a_g.14.1.2 (A:) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

RIPVKYGNADGEYCKFPFLNGKEYNSCTDTGRSDGFLWCSTTYNFEKDGKYGFCPHEA

>d1sgpi_g.15.1.1 (I:) Ovomucoid III domain {Turkey (Meleagris gallopavo)}

VDCSEYPKPACTAEYRPLCGSDNKTYGNKCNFCNAVVESNGTTLHFGKC
>d3ovo__ g.15.1.1 (-) Ovomucoid III domain {Japanese quail (*Coturnix coturnix japonica*)}
LAAVSVDCSEYPKACPKDGYRPVCVGSDNKTYSNKCNFCNAVVESNGTTLHFGKC
>d2ovo__ g.15.1.1 (-) Ovomucoid III domain {Silver pheasant (*Lophura nycthemera*)}
LAAVSVDCSEYPKACTMEYRPLCGSDNKTYGNKCNFCNAVVESNGTTLHFGKC
>d1hpt__ g.15.1.1 (-) Secretory trypsin inhibitor {Human (*Homo sapiens*)}
DSLGREAKCYNELNGCTYEYRPVCAGTDGDTYPNECVLCFENRKRTQTSILIQKSGPC
>d1tgsi__ g.15.1.1 (I:) Secretory trypsin inhibitor {Pig (*Sus scrofa*)}
TSPQREATCTSEVSGCPKIYNPVCAGTDGITYSNECVLCSENKKRQTPVLIQKSGPC
>d1tbrr1 g.15.1.1 (R:1-51) Rhodniin {Bug (*Rhodnius prolixus*)}
EGGEPCACPHALHRVCAGSDGETYSNPCTLNCAFKNGKPELVKVDGPCEPD
>d1tbrr2 g.15.1.1 (R:52-103) Rhodniin {Bug (*Rhodnius prolixus*)}
EDEDVCQCEDGDEYKPVCGSDDITYDNNCRLECASISSPGVELKHEGPCRT
>d1nuba3 g.15.1.1 (A:78-135) Domain of BM-40/SPARC/osteonectin {Human (*Homo sapiens*)}
CQDPTSCPAPIGEFEVKCSNDNKTDFSSCHFFATKCTLEGTKGHKLHLDYIGPCKYI
>d2bus__ g.15.1.1 (-) Seminal plasma inhibitor Ila {Cow (*Bos taurus*)}
EGAQVDCAEFKDPKVYCTRESNPHCGSNGETYGNKCAFCKAVMKSGGKINLKHRGKC
>d1pce__ g.15.1.1 (-) PEC-60 peptide {Pig (*Sus scrofa*)}
EKQVFSRMPICEHMTESPDCSRIYDPVCAGTDGVTESECKLCLARIENKQDIQIVKDGE
>d1an1i__ g.15.1.1 (I:) Leech derived tryptase inhibitor (LDTI-C) {Medicinal leech (*Hirudo medicinalis*)}
KVCACPKILKPVCGSDGRTYANSCIARNGVSIKSEGSCP
>d1ldtl__ g.15.1.1 (L:) Leech derived tryptase inhibitor (LDTI-C) {Medicinal leech (*Hirudo medicinalis*)}
KKVCACPKILKPVCGSDGRTYANSCIARNGVSIKSEGSCPTGILN
>d4sgbi__ g.15.1.2 (I:) Plant chymotrypsin inhibitor {Potato tuber (*Solanum tuberosum*)}
PICTNCCAGYKGNCYNSANGAFICEGQSDPKPKACPLNCDPHIAYSKCPR
>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*)}
EKPAACRCRSRQDPKNRVNCGFPGITSDQCFDSQVPGVPWFCKPLPAQ
>d2pspa2 g.16.1.1 (A:54-106) Pancreatic spasmolytic polypeptide {Pig (*Sus scrofa*)}
ESEECVMQVSARKNCGYPGISPEDCAARNCCFSDTIPEVPWCFFPMMSVEDCHY
>d1hi7a__ g.16.1.1 (A:) PNR-2/PS2, TFF1 {Human (*Homo sapiens*)}
EAQETETCTVAPRERQNCGFPGVTPSQCANKGCCFDDTVRGVPWCFYPNTIDVPPEEECEF
>d1e9ta__ g.16.1.1 (A:) Intestinal trefoil factor {Human (*Homo sapiens*)}
EEYVGLSANQCAVPAKDRVDCGYPHVTPKECNNRGCCFDSRIPGVWCFKPLQEAECTF
>d1pdga__ g.17.1.1 (A:) Platelet-derived growth factor BB {Human (*Homo sapiens*)}
EPAMIAECKTRTEVFEISRLIDRTNANFLVWPPCVEVQRCSGCCNNRNVQCRPTQVQLRPVQVRKIEIVRKPIFKKATVLEDHLACKCETVAA
>d1fltv__ g.17.1.1 (V:) Vascular endothelial growth factor, VEGF {Human (*Homo sapiens*)}

EVVKFMDVYQRSYCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTEESNITMQIMRIKPHQGQHIGEMSFLQHNKCECRPK
>d1fvva_g.17.1.1 (A:) Placenta growth factor-1, PLGF-1 {Human (Homo sapiens)}
SSEVEVVPFQEVTGRSYCRALERLVDVVSEYPSEVEHMFPSCVSLLRCTGCCDENLHCVPVETANVTMQLLKIRSGDRPSYVELTSQHVRCECRP
LR
>d1ktza_g.17.1.2 (A:) TGF-beta3 {Human (Homo sapiens)}
ENCCVRPLYIDFRQDLGWKVWHEPKGYYANFCSGPCPYLSADTTHSTVLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSC
CS
>d1tgj_g.17.1.2 (-) TGF-beta3 {Human (Homo sapiens)}
ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKVWHEPKGYYANFCSGPCPYLSADTTHSTVLGLYNTLNPEASAPCCVPQDLEPLTILYYVGRTPKVE
QLSNMVVKSC
>d2tgi_g.17.1.2 (-) TGF-beta2 {Human (Homo sapiens)}
ALDAAYCFRNVQDNCLRPLYIDFRQDLGWKWIHEPKGYHANFCAGACPYLWSSDTQHSRVLSLYNTINPEASAPCCVSQDLEPLTILYYIGKTPKIE
QLSNMVVKSC
>d1klaa_g.17.1.2 (A:) TGF-beta1 {Human (Homo sapiens)}
ALDTNYCFSSTEKNCCVRQLYIDFRQDLGWKWIHEPKGYHANFCAGACPYLWSSDTQHSRVLSLYNTINPEASAPCCVPQALEPLPIVYYVGRKPK
VEQLSNMIVRSCKCS
>d1bmp_g.17.1.2 (-) Bone morphogenetic protein-7 (BMP-7) {Human (Homo sapiens)}
QACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIQTLVHFINPETVPKPCCAPTQLNAISVLYFDDSSNVILKKYRNMV
RACGCH
>d1es7a_g.17.1.2 (A:) Bone morphogenetic protein-2 (BMP-2) {Human (Homo sapiens)}
KSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECFPPLADHLNSTNHAIVQTLVNSVNSKIPKACCVPTELSAISMLYLDENEKVLKNYQDM
VVEGCGCR
>d1agqa_g.17.1.2 (A:) Glial cell-derived neurotrophic factor, GDNF {Rat (Rattus norvegicus)}
NRGCVLTAIHLNTDLGLGYETKEELIFRYCSGSCAAETMYDKILKNLRSRRLTSDKVGQACCRPVAFDDDSFLDDSLVYHILRKHSAKRCGCI
>d1bnda_g.17.1.3 (A:) Brain-derived neurotrophic factor/neurotrophin 3 heterodimer, BDNF/NT3 {Human (Homo sapiens)}
GQLSVCDSEWVTAADKTAVDMGGTVTLEKPVSKGQLKQFYETKCNPMGYTKEGCRGIDKRHWNSQCRTSQSYVRALTMDSKKRIGWRF
IRIDTSCVCTLTIK
>d1bndb_g.17.1.3 (B:) Brain-derived neurotrophic factor/neurotrophin 3 heterodimer, BDNF/NT3 {Human (Homo sapiens)}
RGEVSVCDSSELWVTDKSSAIDIRGHQVTVLGEIKTNQSPVKQFYETRCKEARPVKNGCRGIDDKHWNSQCKTSQTYVRALTSENNKLGVWRWIRI
DTSCVCALSRK
>d1b8mb_g.17.1.3 (B:) Neurotrophin 4 {Human (Homo sapiens)}
GELAVCDAVSGWVTDRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRRHVSECKAKQSYVRALTADAQ
GRVGWRWIRIDTACVCTLSSRTGRA
>d1hcfa_g.17.1.3 (A:) Neurotrophin 4 {Human (Homo sapiens)}
GVSETAPASRRGELAVCDAVSGWVTDRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVDRRHVSECKAKQ
SYVRALTADAQGRVGWRWIRIDTACVCTLSSRT
>d1bet_g.17.1.3 (-) beta-Nerve growth factor {Mouse (Mus musculus)}
GEFSVCDSVSVVGDKTATDIKGKEVTVAEVNIINNSVFRQYFFETKCRASNPVESGCRGIDSKHWNNSYCTTHTFVKALTTDEKQAAWRFIRIDTA
CVCVLSRK
>d1wwwv_g.17.1.3 (V:) beta-Nerve growth factor {Human (Homo sapiens)}
SSHPIFHRGEFSVCDSVSVVGDKTATDIKGKEVMVLGEVNINNSVFKQYFFETKCRDPNPVDSGCRGIDSKHWNNSYCTTHTFVKALTMDGKQA
AWRFIRIDTACVCVLSRK
>d1hcna_g.17.1.4 (A:) Glycoprotein hormones alpha chain (Gonadotropin A, Follitropin alpha) {Human (Homo sapiens)}
QDCPECTLQENPFFSQPGAPILCMGCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVENHTACHCSTCY

>d1hcnb_g.17.1.4 (B:) Gonadotropin B chain {Human (Homo sapiens)}

KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVNYRDVRFESIRLPGCPRGVNPVSYAVALSCQCALCRSTTDC
GGPKDHPLCD

>d1f7b_g.17.1.4 (B:) Follicle stimulating hormone, follitropin, beta chain {Human (Homo sapiens)}

CELTNITIAKEECRFCISINTAWCAGCYTRDLVYKDPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTYPVATQCHCGKCSDSTDCTVRGLGPSY
CSFGEM

>d1jpya_g.17.1.6 (A:) Interleukin 17F, IL-17F {Human (Homo sapiens)}

HTFFQKPESCPPVPGGSMKLDIGIINENQRVMSMRNIESRSTSPWNYTVWDPNRYPSEVVQAQCRLGCINAQGKEDISMNSVPIQQETLVRRK
HQGCSVSFQLEKVLVTVGCTCVTPV

>d1aoca_g.17.1.5 (A:) Coagulogen {Japanese horseshoe crab (Tachypleus tridentatus)}

ADTNAPICLCDEPGVGLRTQIVTTEIKDKIEKAVEAVAQESGVSGRGSFSIFSHHPVFRECGKYECRTVREPEHSRCYNFPFTHKSECPVSTRDCEPVFG
YTVAGEFRVIVQAPRAGFRQCVWQHKCRFGSNSCGYNGRCTQQRSVRLVTYNLEKDGFLCESFRCCGCP CRSF

>d1hcc_g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}

EGLCKSPPEISHGVVAHMSDSYQYGEEVTYKCFEGFGIDGPAlAKCLGEKWSHPPSCI

>d1hfi_g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}

EKIPCSQPPQIEHGTINSSRSSQESYAHGTLKSYTCEGGFRISEENETTCYMGKWSSPPQCE

>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}

RRCPSPRDIDNGQLDIGGVDFGSSITYCNSGYHLIGESKSYCELGSTGSMVWNPEAPICES

>d1g40a3_g.18.1.1 (A:127-184) Complement control protein {Vaccinia virus}

VKCQSPPSISNGRHNGYEDFYTDGSVVTYSNCNSGSLIGNSGVLCSSGEWSDPPTCQI

>d1g40a4_g.18.1.1 (A:185-243) Complement control protein {Vaccinia virus}

VKCPHPTISNGYLSGFKRSYSYNDNVDFKCKYGYKLSGSSSTCSPGNTWKPELPKCV

>d1ckla1_g.18.1.1 (A:1-62) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}

CEEPPTFEAMELIGKPKPYYEIGERVVDYKCKKGYFYIPPLATHITCDRNHTWLPSDDACYR

>d1ckla2_g.18.1.1 (A:63-126) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}

ETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCELGSVAIWSGKPPICEKV

>d1c1za5_g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}

SCKLPVKKATVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFKEHSSLAFWKTDA SDVKPC

>d1quba1_g.18.1.1 (A:1-62) beta2-glycoprotein I {Human (Homo sapiens)}

GRTCPKPDLPFSTVPLKTFYEPGEEITYSCKPGYVSRGGMRKFICPLTGLWPINTLKCTP

>d1quba2_g.18.1.1 (A:63-120) beta2-glycoprotein I {Human (Homo sapiens)}

RVCVFAGILENGAVRYTTFEYPNTISFSCNTGFYLN GADS A KCTEEGKWSPELPCAP

>d1quba3_g.18.1.1 (A:121-183) beta2-glycoprotein I {Human (Homo sapiens)}

IICPPPSIPTATLRVYKPSAGNNNSLYRDTAVFECLPQHAMFGNDITCTTHGNWTKLPECRE

>d1quba4_g.18.1.1 (A:184-243) beta2-glycoprotein I {Human (Homo sapiens)}

VKCPFPSPRDPNGFVNYPAKPTLYYKDKATFGCHDGYSLDGPEEIECTKLG NWSAMPSCKA

>d1quba5_g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}

SCKVPVKKATVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFKEHTDASDVKPC

>d1ghqb1_g.18.1.1 (B:1-66) Complement receptor 2, cr2 {Human (Homo sapiens)}

AISCGSPPPILNGRISYYSTPIAVGT VIRYSCSGTFR LIGEKSLLCITKDKV DGTWDK PAPKCEYF

>d1ghqb2_g.18.1.1 (B:67-129) Complement receptor 2, cr2 {Human (Homo sapiens)}

NKYSSCPEPIVPGGYKIRGSTPYRHGDSVTFA CKTNFSMNGNKS VWCQANNMWGPTRLPTCVS

>d1elva2 g.18.1.1 (A:342-409) Complement C1S protease domain {Human (Homo sapiens)}
LDCGIPESIENGKVEDPESTLFGSVIRYCEEPYYMENGGGEYHCAGNGSWVNEVLGPELPKCPV
>d1bgk__ g.19.1.1 (-) Sea anemone toxin k {Sea anemone (Bunodosoma granulifera), BGK}
VCRDWFKETACRHAKSLGNCRTSQKYRANCATC
>d1c2ua_g.19.1.1 (A:) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}
RSXIDTIPKSRCTAFQCKHSKYRLSFCRKTGTX
>d1roo__ g.19.1.1 (-) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}
RSCIDTIPKSRCTAFQCKHSMKYRLSFCRKTGTC
>d2ech__ g.20.1.1 (-) Echistatin {Echis carinatus}
ECESGPCCRNCFLKEGTICKRARGDDMDDYCNGKTCDCPRNPKGPAT
>d1fvl__ g.20.1.1 (-) Flavordin {Snake (Trimeresurus flavoviridis)}
GEECDCGSNSPCCDAATCKLRPGAQCGADGLCCDQCRCFKKKRTICRIARGDFPDDRCTGLSNDCPRWNDL
>d1kst__ g.20.1.1 (-) Kistrin {Agkistrodon rhodostoma}
GKECDCSSPENPCCDAAATCKLRPGAQCGEGLCSEQCKFSRAGKICRIPRGDMPDDRCTGQSADCPRYH
>d1mdal__ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}
VDPRAKWQPQDNDIQACDYWRHCSIAGNICDCSAGSLTCPGTLVASGSWVGSCYNPPDPNKYITAYRDCCGYNVSGRCACLNTEGELPVYNKD
ANDIIWCFGGEDGMTYHCSISPVSGA
>d2bbkl__ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}
TDPRAKWVPQDNDIQACDYWRHCSIDGNICDCSGGSLTNCPGTLATASWVASCYNPTDGQSYLIAYRDCCGYNVSGRCPLNTEGELPVYRPEF
ANDIIWCFGGAEDDAMTYHCTISPIVGKAS
>d1atb__ g.22.1.1 (-) Ascaris trypsin inhibitor, ATI {Pig roundworm (Ascaris Lumbricoides), variant suum}
EAEKCTKPNEQWTKCGGCEGTCQAQKIVPCTRECKPPRCEIASAGFVRDAQGNCIKFEDCPK
>d1eaic__ g.22.1.1 (C:) Ascaris elastase inhibitor {Pig roundworm (Ascaris suum)}
GQESCPNEVWTECTGCDEMKGPDENTPCPLMCRRPSCESPGRGMRRNDGKCIKIPASQCP
>d1coua__ g.22.1.1 (A:) Anticoagulant protein {Dog hookworm (Ancylostoma caninum)}
KATMQCGENEKYDSCGSKECDKKCKYDGVVEEDDEEPNVPCLVRCVHQDCVCEEGFYRNKDDKCVSAEDCELDNMDFIYPGTRNP
>d1ccva__ g.22.1.1 (A:) Chymotrypsin inhibitor AMCI {Honeybee (Apis mellifera)}
EECPNEVFTCGSACAPTCAPKTRICTMQCRIGCQCQEGFLRNGEGACVLPENC
>d1hx2a__ g.22.1.2 (A:) BSTI {Fire-bellied toad (Bombina bombina)}
NFVCPGQQTFCASSCPKTCTRNLVLCDDKKCNQRCGCISGTVLKSQDSSECVHPSKC
>d1apj__ g.23.1.1 (-) Fibrillin {Human (Homo sapiens)}
SAQDLRMSYAKFEGGKCSSPKSRNHSKQECCALKGEGWGDPELCPTPDEAFRQICPYGSGIIVGPDDSA
>d1exta1 g.24.1.1 (A:13-71) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}
SVCVPQGYIHPQNNSCCTKCHKGTYLYNDCPGPGQDTCRECESGSFTASENHLRHCL
>d1exta2 g.24.1.1 (A:72-115) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}
SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYSSENLFQCF
>d1exta3 g.24.1.1 (A:116-172) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}
NCSLCLNGTVHLSCQEKKQNTVCTCHAGFFLRENNECVSCSNCKSLECKLCLPQIEN
>d1ncfa3 g.24.1.1 (A:116-150) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}
NCSLCLNGTVHLSCQEKKQNTVCTCHAGFFLRENNECVSCSN
>d1ncfb3 g.24.1.1 (B:116-155) Tumor necrosis factor (TNF) receptor {Human (Homo sapiens)}
NCSLCLNGTVHLSCQEKKQNTVCTCHAGFFLRENNECVSCSN
>d1d0gr1 g.24.1.1 (R:21-61) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
SSPSEGGLCPGHHISEDGRDCISCKYGQDYSTHWNDLLFCL

>d1d0gr3 g.24.1.1 (R:102-128) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
KCRTGCPGMVKVGDCTPWSDIECVHK

>d1d4va1 g.24.1.1 (A:69-114) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
PQQKRSPSEGLCPPGHIISEDGRDCISCKYQDYSTHWNDLLFCL

>d1d4va2 g.24.1.1 (A:115-154) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
RCTRCDSGEVELSPCTTRNTVCQCCEEGTFREEDSPEMCR

>d1d4va3 g.24.1.1 (A:155-185) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
KCRTGCPGMVKVGDCTPWSDIECVHKESGD

>d1du3a3 g.24.1.1 (A:102-123) Death receptor-5 (dr5) fragment {Human (Homo sapiens)}
KCRTGCPGMVKVGDCTPWSDI

>d1jmab1 g.24.1.1 (B:4-59) Cellular receptor HveA {Human (Homo sapiens)}
CKEDEYPVGSECCPKCSPGYRVKEACGEITGTVCCEPCPPGTYIAHLNGLSKCLQCQ

>d1jmab2 g.24.1.1 (B:60-105) Cellular receptor HveA {Human (Homo sapiens)}
MCDPAMGLRASRNCSRTEAVCGCSPGHFCIVQDGDHCAACRAYAT

>d1vgh__ g.25.1.1 (-) Heparin-binding domain from vascular endothelial growth factor {Human (Homo sapiens)}
ARQENPCGCSERRKHLFVQDPQTCKCSCCKNTDSRKARQLELNERTCRCDKPRR

>d1afp__ g.26.1.1 (-) Antifungal protein (AGAFP) {Mold (Aspergillus giganteus)}
ATYNGKYKKDNICKYKAQSGKTAICKCYVKKPRDGAKCEFDSYKGKCYC

>d1e88a3 g.27.1.1 (A:1-41) Fibronectin {Human (Homo sapiens)}
YGHCVTDGGVVSVGMQWLKTQGNKQMLCTLGNGVSCQET

>d1fbr_1 g.27.1.1 (1-46) Fibronectin {Human (Homo sapiens)}
AEKCFDHAAGTSYVGETWEKPYQGWMMDCTCLGEGSGRITCSR

>d1fbr_2 g.27.1.1 (47-93) Fibronectin {Human (Homo sapiens)}
NRCNDQDRTSYRIGDTWSKKDNRGNLLQCCTGNGRGEWKERHTS

>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)}
EAEEETCFDKYTGNTRYVGDTYERPKDSMIWDCTCIGAGRGRISCTIANR

>d1tpg_2 g.27.1.1 (1-50) Tissue-type plasminogen activator, t-PA {Human (Homo sapiens)}
SYQVICRDEKTQMIYQQHSWLRPVLSNRVEYCWNCNSGRAQCHSPVPKS

>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}
MGNQQCNWYGTLYPLCVTTNGWGVEDQRSCIARSTCAAQPAPFGIVGSG

>d1e8qa_g.55.1.1 (A:) Cellulose docking domain, dockering {Piromyces equi}
ASCWAQSQGYNCCNNPSSTKVEYTDASGQWGVQNGQWCGIDYSYQQ

>d1tdb_g.30.1.1 (B:) Carboxypeptidase inhibitor {Medicinal leech (Hirudo medicinalis)}
DESFLCYQPDQVCCFCRGAAPLSEGECPNPHPTAPWCREGAVEWVYPCNTGQCRTTCIPYV

>d1hdla_g.57.1.1 (A:) Serine proteinase inhibitor lekti, domain one {Human (Homo sapiens)}
KNEDQEMCHEFQAFMKNGKLFCPQDKFFQSLDGIMFINKCATCKMILEKEAKSQ

>d1dqca_g.31.1.1 (A:) Tachycitin {Horseshoe crab (Tachypleus tridentatus)}

YLAFCRGRYSPCLDDGPNVNLYSCCSFYNCHKCLARLENCPKGLHYNAYLKVCWDPSKAGCTSVNKECHLWKT

>d1ha8a_g.58.1.1 (A:) Pheromone ER-23 {Euploites raikovi}

GECEQCFSDGGDCTTCFNNGTGPCANLAGYPAGCSNSDCTAFLSQCYGGC

>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)}

ANKGFLEEVRKGNLREECLEEPSREEAFELESLSATDAFWAKYTACESARNPREKLNECLEGN

>d1cfi__ g.32.1.1 (-) Coagulation factor IX (IXa) {Human (Homo sapiens)}

YNSGKLEEFVQGNLERECKEEMEKSFEEAREVFENTERTEFWKQYVD

>d1pxl3 g.32.1.1 (L:1-46) Coagulation factor IX (IXa) {Pig (Sus scrofa)}

YNSGKLEEFVRGNLERECIEEKCSFEEAREVFENTEKTNFVKQYV

>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)}

MDVVDSLLVNGSNITPPCELGLENELFCQLDQPRPSKEWQPAQVILL

>d1vpu__ g.34.1.1 (-) HIV-1 VPU cytoplasmic domain {Human immunodeficiency virus type 1}

LQIDRLRIDRITERAEDSGNESEGDQEELSALVERGH LAPWDVDDL

>d1isua__ g.35.1.1 (A:) HIPIP (high potential iron protein) {Rhodococcus tenuis}

GTNAAMRKAFNYQDTAKNGKKCSGCAQFVPGASPTAAGGCKVIPGDNQIAPGGYCDAFIVKK

>d1b0ya__ g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochromatium vinosum, (formerly Chromatium vinosum)}

SAPANAVAADNATAIALKYNQDATKSERVAARPGPLPPEEQHCANCQFMQADAAGATDEWKGCQLFPGKLINVNGWCASWTLKAG

>d1js2a__ g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochromatium vinosum, (formerly Chromatium vinosum)}

MEFMSAPANAVAADDATAIALKYNQDATKSERVAARPGPLPPEEQHCANCQFMQADAAGATDEWKGCQLFPGKLINVNGWSASWTLKAG

>d3hipa__ g.35.1.1 (A:) HIPIP (high potential iron protein) {Chromatium purpuratum}

VPANAVTESDPAVALKYHRDAASSERVAARPGPLPPEEQHCENCQFMNPDSAAADWKGCLFPGKLINLSGWCAWSWTLRAG

>d2hipa__ g.35.1.1 (A:) HIPIP (high potential iron protein) {Ectothiorhodospira halophila}

EPRAEDGHAHDYVNEAADASGHPRYQEGQLCENCAFWFGEAVQDGWGRCTHPDFDEVLVKAEGWCSVYAPAS

>d1hpi__ g.35.1.1 (-) HIPIP (high potential iron protein) {Ectothiorhodospira vacuolata}

MERLSEDDPAAQALEYRHADSSVQHPAYEEGQTCLNCLLYTDASAQDWGPCSVFPGKLVSANGWCTAWVAR

>d1eyta__ g.35.1.1 (A:) HIPIP (high potential iron protein) {Thermochromatium tepidum}

AAPANAVTADDPTAIALKYNQDATKSERVAARPGPLPPEEQHCANCQFMQANVGEDWKGCLFPGKLINVNGWCASWTLKAG

>d1dj7a__ g.36.1.1 (A:) Ferredoxin thioredoxin reductase (FTR), catalytic beta chain {Synechocystis sp.}

NNKTLAAMKNFAEQYAKRTDTYFCSDLVTAVVIEGLARHKEELGSPLCPCRHEDKEAEVKNTFWNCPCVPMRERKECHMLFLTPNDNFAGDA

QDIPMETLEEVKAS

>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)}

QKPFQCRICMRNFSRSRSHLTTHIRTHTG

>d1a1ia3 g.37.1.1 (A:160-187) ZIF268 {Mouse (Mus musculus)}

EKPFA CDICGRKFARSDERKRHTKIHLR

>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)}
LMVKCPAQDCNEEVSLKYNHHVSSHKESK
>d2drpa1 g.37.1.1 (A:103-139) Tramtrack protein (two zinc-finger peptide) {Drosophila melanogaster}
FTKEGEHTYRCKVCSRVTYTHISNFCRHYVTSHKRNVK
>d2drpa2 g.37.1.1 (A:140-165) Tramtrack protein (two zinc-finger peptide) {Drosophila melanogaster}
VYPCPFCFKEFTRKDNNMTAHVKIIHK
>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}
YKCGLCERSFVEKSALSRRHQRVHKN
>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)}
TLPRGSIDKVVKEMPDKTFECLFPGCTKTFKRRYNIRSHIQTHLEDR
>d1zfd__ g.37.1.1 (-) SWI5 zinc-finger domains {Baker's yeast (Saccharomyces cerevisiae)}
DRPYSCDHPGCDKAFAVRNHDLIRHKKSHQEKA
>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)}
KEFVCHWGGCSRELRFKAQYMLVVHMRRHTGE
>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)}
KPYVCKLPGCTKRYTDPSLRKHVKTVHG
>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)}
PYHCTYCNFSFKTKGNLTGHMKSKAHSKK
>d4znf__ g.37.1.1 (-) Enhancer binding protein {Human (Homo sapiens)}
RPYHCSYCNFSFKTKGNLTGHMKSKAHSKK
>d1sp1__ g.37.1.1 (-) Transcription factor sp1 {Human (Homo sapiens)}
KKFACPECPKRFMRSDHLSKHKITHQNKK
>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)}
MSDDKPFLCTAPCGQQRFTNEDHLAVHKHKHEMLTKFG
>d1ubdc1 g.37.1.1 (C:295-322) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}
TIACPHKGCTKMF RDNSAMRKHLHTHGP
>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)}
RPYVCPFDGCNKFAQSTNLKSHILTHA
>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}
KPFPCKEEGCEKGFTSLHHLTRHSLHTGE
>d1tf3a3 g.37.1.1 (A:71-101) Transcription factor IIIA, TFIIIA {Xenopus laevis}
KNFTCDSDGCDLRFTTKANMKHHFNRFHNK
>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}
GYPCKKDDSCSFVGKTWTLYLKVAECH
>d1yuja_ g.37.1.1 (A:) GAGA factor {Drosophila melanogaster}
PKAKRAKHPPGTEKPRSRSQSEQPATCPICYAVIRQSRNLRRLELRHFAKPGV
>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)}
MKLLSSIEQACDICRLLKKSKEKPKCAKCLKNNWECRYSPK
>d1d66a1 g.38.1.1 (A:8-48) Gal4 {Baker's yeast (Saccharomyces cerevisiae)}
EQACDICRLLKKSKEKPKCAKCLKNNWECRYSPK
>d1pyia1 g.38.1.1 (A:30-71) PPR1 {Baker's yeast (Saccharomyces cerevisiae)}
SRTACKRCRLLKKCDQEFPSCRKCAKLEVPCVSIDPATGKD
>d1zmc1 g.38.1.1 (C:31-66) PUT3 {Baker's yeast (Saccharomyces cerevisiae)}
SVACLSCRKRHIKCPGGNPQCQCVTSNAICEYLEPS
>d1hwtc1 g.38.1.1 (C:59-97) Hap1 (Cyp1) {Baker's yeast (Saccharomyces cerevisiae)}
RIPLSCTICRKRKVKCDCDKLPHCQQCTKTGVAHLCHYME
>d2hapc1 g.38.1.1 (C:55-97) Hap1 (Cyp1) {Baker's yeast (Saccharomyces cerevisiae)}
RKRNRIPLRCTICRKRVKCDCDKLPHCQQCTKTGVAHLCHYME
>d1cld__ g.38.1.1 (-) CD2-Lac9 {Milk yeast (Kluyveromyces lactis)}

QACDACRKKWKCSKTVPTCTNCLKYNLDCVYS

>d2alca_g.38.1.1 (A:) Ethanol regulon transcriptional activator ALCR DNA-binding domain {Aspergillus nidulans and Emericella nidulans}

GSMADTRRRQNHSMDPCRKGKRCDAPENRNEANENGWVSCSNCKRWNKDCTFWLSSQRSKNNS

>d3gata_g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}

KRAGTVCNCQTSTTLWRRSPMGDPVCNACGLYYKLHQVNRPLTMRKDGIQTRNRKVSSKGKRR

>d7gata_g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}

MKNGEQNGPTTCTNCFTQTPVWRRNPEGQPLCNACGLFLKLHGVRPLSLKTDVIKKRNRSANS

>d1gnf_g.39.1.1 (-) Erythroid transcription factor GATA-1 {Mouse (Mus musculus)}

GSEARECVNCGATATPLWRRDRTHYLNCAGLYHKMNGQNRLIR

>d1dszb_g.39.1.2 (B:) Retinoid X receptor (RXR-alpha) DNA-binding domain {Human (Homo sapiens)}

GSFTKHICAICGDRSSGKHYGVYCEGCKGFFKRTVRKDLYTCRDNKDCLIDKRQRNRQCQYCRYQKCLAMGMKREAVQEERQR

>d2nlla_g.39.1.2 (A:) Retinoid X receptor (RXR-alpha) DNA-binding domain {Human (Homo sapiens)}

CAICGDRSSGKHYGVYCEGCKGFFKRTVRKDLYTCRDNKDCLIDKRQRNRQCQYCRYQKCLAMGM

>d2nllb_g.39.1.2 (B:) Thyroid hormone receptor (TR-beta) DNA-binding domain {Human (Homo sapiens)}

DELCVVCGDKATGYHYRCITCEGCKGFFRTIQKNLHPSYSCKYEGKCIDVKVTRNQCQECRFKKCIVGMATDLVLDISKRLAKRKLIENREKRRRE

ELEK

>d1cita_g.39.1.2 (A:) Orphan nuclear receptor NGFI-B {Rat (Rattus norvegicus)}

GRCAVCGDNASCQHYGVRTCEGCKGFFKRTVQKSAYICLANKDCPVDKRRRNRCQFCRFQKCLAVGMVKEVVRTDSLKGRRGRLPSKP

>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)}

MKPARPCLVCSDEASGCHYGVLTGSKVFFKRAVEGQHNYLCAGRNDIIDKIRRKNCPACRYRKCLQAGMNLEARKTKK

>d1lata_g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain {Rat (Rattus norvegicus)}

RPLCVCSDEASGCHYGVLTCEGCKAFFKRAVEGQHNYLCKYEGKCIIDKIRRKNCPACRYRKCLQAGMNLE

>d2gda_g.39.1.2 (-) Glucocorticoid receptor DNA-binding domain {Rat (Rattus norvegicus)}

LCLVCSCDEASGCHYGVLTGSKVFFKRAVEGQHNYLCAGRNDIIDKIRRKNCPACRYRKCLQAGMNLEAR

>d1dsza_g.39.1.2 (A:) Retinoic acid receptor DNA-binding domain {Human (Homo sapiens)}

PCFVCQDKSSGYHYGVSAEGCKGFFRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLOQCFEVGMSKESVRND

>d1hra_g.39.1.2 (-) Retinoic acid receptor DNA-binding domain {Human (Homo sapiens)}

PPRVYKPCFVCQDKSSGYHYGVSAEGCKGFFRSIQKNMVIYTCHRDKNCVINKVTRNRCQYCRLOQCFEVGMSKESVRN

>d1a6ya_g.39.1.2 (A:) Orphan nuclear receptor reverb {Human (Homo sapiens)}

LLCKVCGDVASGFHYGVHACEGCKGFFRSIQQQNIQYKRCLKNENCSIVRINRNRCQQCRFKCLSVGMSRDAVRFGR

>d1b8ta1_g.39.1.3 (A:1-35) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

MPNWGGKKCGVCQKAVYFAEEVQCEGSSFHKSCF

>d1b8ta2_g.39.1.3 (A:36-100) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

LCMVCKKNLDSTTVAHGDEIYCKSCYGKKYGPKGKGKGMAGTLSTDKGESLGIKYEEGQSHRP

>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)}

RCAKGKSLESTTLADKGDEIYCKGYAKNFGPKGFGFGQGAGALIHSQ

>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}

NKCGACGRTVYHAEVQCDGRSFHRCCF
>d1a7i_2 g.39.1.3 (36-67) Cysteine-rich (intestinal) protein, CRP, CRIP {Japanese quail (*Coturnix coturnix japonica*), CRP2}
LCMVRKNLDSTTVAIHDAEVYCKSCYGKKY
>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}
FRCAKGKSLESTTLTEKEGEIYCKGCYAKN
>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*)}
KCEKCGKTLTSGGHAEGKPYCNHPCYSAMFGPKGFRGGAESHTFK
>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*)}
MNPNCARCGKIVYPTEKVNLCKFWHKACF
>d1d4ua2 g.39.1.5 (A:1-36) DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain {Human (Homo sapiens)}
MEFDYVCEECGKEFMDSYLMDHFDLPTCDCRDAD
>d1xpa_2 g.39.1.5 (98-133) DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain {Human (Homo sapiens)}
MEFDYVCEECGKEFMDSYLMNHFDLPTCDNCRDAD
>d1jj2t_g.39.1.6 (T:) Ribosomal protein L24e {Archaeon *Haloarcula marismortui*}
RECDYCGTDIEPGTGTMFVHKDGATTHFCSSKCENNADLGREARNLEWTD TAR
>d1fjgn_g.39.1.7 (N:) Ribosomal protein S14 {Thermus thermophilus}
ARKALIEKAKRTPKFVKRAYTRCVRCGRARSVYRFFGLCIRICLRELAHKQLPGVRKASW
>d1aaaf__ g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
MQRGNFRNQRKIIKCFNCGKEGHIAKNCRAPRKRCGCKGKEGHQMKDCTERQAN
>d1eska__ g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
NVKCFNCGKEGHTARNCRAPRKKGCKGKEGHQMKDCTERQ
>d1f6ua__ g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
MQKGNFRNQRKTVKCFNCGKEGHIAKNCRAPRKKGCKGKEGHQMKDCTERQAN
>d1nc8__ g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 2}
AQQRKVIRCWNCGKEGHSARQCRAPIRRQG
>d1cl4a__ g.40.1.1 (A:) Nucleocapsid protein from mason-pfizer monkey virus (MPMV) {Mason-pfizer monkey virus}
VPGLCPRCKRGKHANECKSKTDNQGNPIPPH
>d1a6bb__ g.40.1.1 (B:) Zinc finger protein ncp10 {Moloney murine leukemia virus}
GERRRSQLRDQCAYCKEKGHWAKDCPKKPRGPRGPRPQT
>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}
PPGLCPRCKKGYHWKSECKSKFDKDGNPPLP
>d1f4la3 g.41.1.1 (A:141-175) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}
VKGTCPKCKSPDQYGDNCEVCAGATSPTELIEPKS
>d1mea__ g.41.1.1 (-) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}

GSDFVKGTCPKCKSPDQYGDNCEVCGA
>d1zin_2 g.41.2.1 (126-160) Microbial and mitochondrial ADK, insert "zinc finger" domain {Bacillus stearothermophilus}
GRRICRNCATYHLIFHPPAKPGVCDKCGGELYQR
>d1e4ya2 g.41.2.1 (A:122-156) Microbial and mitochondrial ADK, insert "zinc finger" domain {Escherichia coli}
GRRVHAPSGRVYHVFKNPPKVEGKDDVTGEELTTR
>d2ak3a2 g.41.2.1 (A:125-161) Microbial and mitochondrial ADK, insert "zinc finger" domain {Cow (Bos taurus), mitochondrial isozyme-3}
ARWIHPGSGRVYNIEFNPPKTMGIDDLTGEPLVQRED
>d1ak2_2 g.41.2.1 (147-176) Microbial and mitochondrial ADK, insert "zinc finger" domain {Cow (Bos taurus), mitochondrial isozyme-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)}
GRRLLDPVTGKIYHLKYSPPNEEIASRLTQR
>d1tfi__ g.41.3.1 (-) Transcriptional factor SII, C-terminal domain {Human (Homo sapiens)}
KTGGTQTDLFTCGKCKKNCTYTQVQTRSADEPMTFVVCNECGNRWKFC
>d1pft__ g.41.3.1 (-) Transcription initiation factor TFIIB, N-terminal domain {Archaeon Pyrococcus furiosus}
MVNKQKVC PACESAEI LYD PERGEIVCAKCGYVIEENIIDMGPEWRAFDA
>d1dl6a_ g.41.3.1 (A:) Transcription initiation factor TFIIB, N-terminal domain {Human (Homo sapiens)}
ASTSRLDALPRVTCPNHPDAILVEDYRAGDMICPECGLVVGDRVIDVGSEWRFSNDK
>d1d0qa_ g.41.3.2 (A:) Zinc-binding domain of DNA primase {Bacillus stearothermophilus}
GHRIPEETIEAIRRGVDIVDVIGEYVQLKRQGRNYFGLCPFHGEKTPSFVSPEKQIFHCFGCGAGGNAFTFLMDIEGIPFVEAAKRLAAKAGVDSLVE
ELD
>d1yua_1 g.41.3.3 (1-65) Prokaryotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}
MNGEVAPPKEDPVPLPELPCEKSDAYFVLRDGAAGVFLAANTFPSRETRAPLVEELYRFRDRLP
>d1yua_2 g.41.3.3 (66-122) Prokaryotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}
EKLRYLADAPQQDPEGNKTMRFSRKTQQYVSSEKDKGATGWSAFYVDGKWEGKK
>d1qf8a_ g.41.4.1 (A:) Casein kinase II beta subunit {Human (Homo sapiens)}
VSWISWFCLRGNEFFCEVDEDYIQDKFNLTLNEQVPHYRQALDMILDLEPDEELEDNPNSQSDLIEQAAEMLYGLIHARYILTRGIAQMЛЕKYQQ
GDFGYCPRVCYCENQPMILPIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHTDGAYFGTGFPHMLFMVHPEYRPKRP
>d1rb9__ g.41.5.1 (-) Rubredoxin {Desulfovibrio vulgaris}
MKKYVCTVCGYEYDPAEGDPDNGVKPGTAFEDVPADWVCPVCGAPKSEFEAA
>d2rdva_ g.41.5.1 (A:) Rubredoxin {Desulfovibrio vulgaris}
MKKYVCTVCGYEYDPAEGDPDNGVKPGTAFEDVPADWVCPVCGAPKSEFEPA
>d1rdg__ g.41.5.1 (-) Rubredoxin {Desulfovibrio gigas}
MDIYVCTVCGYEYDPAKGDPDSGIKPGTKFEDLPDDWACPVCVGASKDAFEKQ
>d6rxn__ g.41.5.1 (-) Rubredoxin {Desulfovibrio desulfuricans, strain 27774}
MQKYVCNVCGYEYDPAEHDNVPFDQLPDDWCCPVCVGVSQDFSPA
>d1iro__ g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}
MKKYTCTVCGYIYNPEDGDPDNGVNPGTDFKDIPDDWVCPLCGVGKQDFEEVE
>d5rxn__ g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}
MKKYTCTVCGYIYDPEDGDPDDGVNPGBTDFKDIPDDWVCPLCGVGKQDFEEVE

>d1brfa_g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}
AKWVCKICGYIYDEDAGDPDNGISPGTKFEELPDDWVCPIGAPKSEFEKLED

>d1qcva_g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}
AKWVLKITGYIYDEDAGDPDNGISPGTKFEELPDDWVAPITGAPKSEFEKLED

>d1dx8a_g.41.5.1 (A:) Rubredoxin {Guillardia theta}
MEIDEGKYEACGYIYEPEKGDKFAGIPPGTPFDLSDSFMCACRSPKNQFKSIKKVIAGFAENQKYG

>d1h7va_g.41.5.1 (A:) Rubredoxin {Guillardia theta}
MEIDEGKYEACGYIYEPEKGDKFAGIPPGTPFDLSDSFMCACRSPKNQFKSIKKVI

>d1dvba2_g.41.5.1 (A:148-191) Rubrerythrin, C-terminal domain {Desulfovibrio vulgaris}
FLREQATKWRCRNCGYVHEGTGAPELCPACAHPKAHFELLGINW

>d1dxga_g.41.5.2 (A:) Desulforedoxin {Desulfovibrio gigas}
ANEVDVYKCELCGQVVVKLEGGGTLVCCGEDMVQK

>d1dfx_2 g.41.5.2 (1-36) Desulfoferodoxin N-terminal domain {Desulfovibrio desulfuricans}
PKHLEVYKCTHCGNIVEVLHGGGAELVCCGEPMKHM

>d1ocrf_g.41.5.3 (F:) Cytochrome c oxidase Subunit F {Cow (Bos taurus)}
ASGGGVPTDEEQATGLEREVMLAARKGQDPYNILAPKATSGTKEDPNLVPSITNKRIVGCCEEDNSTVIWFWLHKGEAQRCPSGTHYKLVPHQLA
H

>d1gh9a_g.41.6.1 (A:) Hypothetical protein MTH1184 {Archaeon Methanobacterium thermoautotrophicum}
MYIIFRCDCRALYSREGAKTRKCVCGRTNVKDRRIFFGRADDFFEEASELVRKLQEEKYGSCHFTNPSKRE

>d1d09b2_g.41.7.1 (B:101-153) Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain {Escherichia coli}
ERIDNVLCVCPNSNCISHAEPVSSSFAVRKRANDIALKCKYCEKEFSHNVVLAN

>d2atcb2_g.41.7.1 (B:101-152) Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain {Escherichia coli}
ERNIDNVLCVCPNSNCISHAEPVSSSFAVRKRANDIALKCKYCEKEFSHNVVLAN

>d1ffkw_g.41.8.1 (W:) Ribosomal protein L37ae {Archaeon Haloarcula marismortui}
PTGRFGPRYGLKIRVRVDVEIKHKKYKCPVCGFPKLRASTSIWCGHCGYKIAGGAYTPETVAGKAVMKA

>d1jj2y_g.41.8.1 (Y:) Ribosomal protein L37ae {Archaeon Haloarcula marismortui}
RTGRFGPRYGLKIRVRVADVEIKHKKHKCPVCGFKLKRAFTGIWMCGHCGYKIAGGCYQPETVAGKAVMKA

>d1jj2z_g.41.8.2 (Z:) Ribosomal protein L37e {Archaeon Haloarcula marismortui}
TGAGTPSQGKNTTHTKCRRCGEKSYHTKKVCSSCFGKSAKRRDYEWQSKAGE

>d1jj22_g.41.8.3 (2:) Ribosomal protein L44e {Archaeon Haloarcula marismortui}
MQMPRRFNTYCPHCNEHQEHIVEKVRSGRQTGMWIDQRERNSIGNDGKFSKVPGGDKPTKTDLKRCGECGKAHLREGWRAGRLEFQE

>d1qyp_g.41.9.1 (-) RBP9 subunit of RNA polymerase II {Archaeon Thermococcus celer}
GSHMEQDLKTLPTTKITCPKCGNDTAYWWEMQTRAGDEPSTIFYKCTKGHTWRSYE

>d1i50i1_g.41.9.1 (I:1-49) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}
MTTFRFRDCNNMLYPREDKENRLLFECRTCSYVEAGSPLVYRHELI

>d1i50i2_g.41.9.1 (I:50-122) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}
TNIGETAGVVQDIGSDPTLPRSDRECPKCHSRENVFQSQQRKDTSMLFFVCLSCSHIFTSDQKNKRTQFS

>d1i50l_g.41.9.2 (L:) RBP12 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}
ATLKYICAECSSKLSLSRTDAVRCKDCGHRILLKARTKRLVQFEAR

>d1fea_g.42.1.1 (A:) Ribosomal protein L36 {Thermus thermophilus}
MKVRASVKRICDKCKVIRRHGRVYVICENPKHKQRQG

>d1fre_g.43.1.1 (-) Nuclear factor XNF7 {African clawed frog (Xenopus laevis)}

EKCSEHDERLKLKLYCKDDGTLSCVICRDSLKHASHNFLPI

>d1fbva4_g.44.1.1 (A:356-434) CBL {Human (Homo sapiens)}

TPQDHIKVTQEYELYCEMGSTFQLCKICAENDKDVIEPCGHLMTSCLTSWQESEGQGCPFCRCEIKGTEPIVVDPF
>d1rmd_2 g.44.1.1 (1-86) V(D)J recombination activating protein 1 (RAG1), dimerization domain {Mouse (Mus musculus)}
NCSKIHLSKLLAVDFPAHFVKISICQCIEHILADPVETSKHLFCRICILRCLKVMGSYCPSCRYPCPTDLESPVKSFLNILNS
>d1chc__ g.44.1.1 (-) Immediate early protein, IEEHV {Equine herpes virus type 1}
MATVAERCPILEDPSNSMALPCLHAFCYVCITRWIRQNPTCPLCKVPVESVVHTIESDFGDQLI
>d1bor__ g.44.1.1 (-) Acute promyelocytic leukaemia proto-oncoprotein PML {Human (Homo sapiens)}
EEEFQFLRCQQCQAEAKCPKLLPCLHTLCSGCLEASGMQCPICQAPWPLGADTPAL
>d1g25a__ g.44.1.1 (A:) TFIID Mat1 subunit {Human (Homo sapiens)}
MDDQGCPCKTTKYRNPSLKLMLNVNCGHTLCESCVDLLFVRGAGNCPECGTPLRKSFRVQLFED
>d1e4ua__ g.44.1.1 (A:) Not-4 N-terminal RING finger domain {Human (Homo sapiens)}
MSRSPDAKEDPVECPCLMEPLEIDDINFFPCTCGYQICRCWHRIRTDENGLCPACRKPYPEDPAVYKPLSQEELQRI
>d1jm7a__ g.44.1.1 (A:) brca1 RING domain {Human (Homo sapiens)}
MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLKNDITKRSLQESTRFSQLVEELLKIICAFQLDTGLEYA
N
>d1jm7b__ g.44.1.1 (B:) bard1 RING domain {Human (Homo sapiens)}
MEPDGRGAWAHSRAALDRLEKLLRCSRCTNLREPVCCLGCEHIFCSNCVSDCIGTGCPVCYTPAWIQDLKINRQLDSMIQLCSKLRNLLHDNE LSD
>d1dcqa2 g.45.1.1 (A:247-368) Pyk2-associated protein beta ARF-GAP domain {Mouse (Mus musculus)}
LTKEIISEVQRMTGNDVCCDGAPDPTWLSTNLGILTIECSGIHRELGVHYSRMQSITLDVLGTSELLLAKNIGNAGFNEIMECCCLPSEDPKPNPGS
DMIARKDYITAKYMERRYARKKH
>d1mhu__ g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}
KSCCSCCPVGCAKCAQGCICKGASDKCSCCA
>d2mhu__ g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}
MDPNCSAAAGDSCTCAGSCKCKECKCTSCK
>d2mrb__ g.46.1.1 (-) Metallothionein {Rabbit (Oryctolagus cuniculus)}
MDPNCSAAAGDSCTCANSTCKACKCTSCK
>d1mrt__ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
KSCCSCCPVGCAKCSQGCICKEASDKCSCCA
>d2mrt__ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
MDPNCSCATDGSCSCAGSCKCKQCKCTSCKKSCCCPVGCAKCSQGCICKEASDKCSCCA
>d4mt2__ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
MDPNCSATDGSCSCAGSCKCKQCKCTSCK
>d1dfa__ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
KSCCSCCPVGCSKAQGCVCKGAADKCTCCA
>d1dfta__ g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
MDPNCSCTGGSCTTSSCACKNCKCTSCK
>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}
PGPCCNDKVCVQEGGCKAGCQCTSCRC
>d1fmya__ g.46.1.1 (A:) Metallothionein {Baker's yeast (Saccharomyces cerevisiae)}
QNEGHECQCQCGSCKNNNEQCQKSCSCPTEGCNSDDKPCPGN
>d1qjka__ g.46.1.1 (A:) Metallothionein {Purple sea urchin (Strongylocentrotus purpuratus)}

PDVKCVCTEGKECACFGQDCCVTGECCKDGTCCG
>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}
TLVKCACEPCLCNVDPASKAIDRNGLYYCSEACADGHTGGSKGCGBTGCNCHG
>d1co4a_g.47.1.1 (A:) Zinc domain conserved in yeast copper-regulated transcription factors {Synthetic}
MVVINGVKYACDSCIKSHKAAQCEHNDRPLKILKPRGRPPPT
>d1adn__g.48.1.1 (-) Ada DNA repair protein, N-terminal domain (N-Ada 10) {Escherichia coli}
MKKATCLTDDQRWQSVLARDPNADGEFVFAVRTTGIFCRPSCRARHALRENVSFYANASEALAGFRPKRCQPDKANPRQHRLDKITHACR
>d1ptq__g.49.1.1 (-) Protein kinase C-delta (PKCdelta) {Mouse (*Mus musculus*)}
HRFKVYNYSPTFCDHCGSLLWGLVKQGLKCEDCGMNVHHKCREKVANLC
>d1faq__g.49.1.1 (-) RAF-1 {Human (*Homo sapiens*)}
LTTHNFARKTFLKLAFCDICQKFLLNGFRCQTCGYKFHEHCSTKVPTMCVDW
>d1tbo__g.49.1.1 (-) Protein kinase c-gamma {Rat (*Rattus rattus*)}
QTDDPRNKHFKRFLHSYSSPTFCDHCGSLLYGLVHQGMKSCCEMNVRHRCVRSPSLCGVDHTERR
>d1kbea__g.49.1.1 (A:) Kinase suppressor of Ras, Ksr {Mouse (*Mus musculus*)}
GSVTHRFSKSWLSQVCNCQKSMIFGVKCKHCRLKCHNKCTKEAPACR
>d1e53a_g.49.1.2 (A:) TFIH p44 subunit cysteine-rich domain {Human (*Homo sapiens*)}
LDAFQEIPLEYNGERFCYGCQGELKDQHVYVCAVCQNVFCVDCDFVHDSLHCCPGI
>d1vfy_a_g.50.1.1 (A:) vps27p protein {Baker's yeast (*Saccharomyces cerevisiae*)}
DWIDSDACMICSKKFSLLNRKHHCRSCGGVFCQEHSNSIPLPDGIYEPVRVCDSCFEDYEFIGTD
>d1joca1_g.50.1.1 (A:1348-1411) Eea1 {Human (*Homo sapiens*)}
KWAEDNEVQNCMACGKGFSVTVRHHCRQCGNIIFCAECSAKNALTPSSKKPVRCACFNDLQG
>d1dvpa2_g.50.1.1 (A:149-220) Hrs {Fruit fly (*Drosophila melanogaster*)}
MFTADTAPNWADGRVCHRKRVEFTFTNRKHHCRNCQVFQCGQCTAKQCPLPKYIEKEVRVCDGCFAALQRG
>d1zbdb_g.50.1.1 (B:) Effector domain of rabphilin-3a {Rat (*Rattus norvegicus*)}
EELTDEEKEIIIRVIARAEMETMEQERIGRLVDRLETMRKNVAGDGVNRCILCGEQLGMLGSASVVCEDCKKNVTKCGVETSNNRHPVWLCKI
CLEQREVWKRSGAFFKGFPKQVLPQPM
>d1f62a_g.50.1.2 (A:) Williams-Beuren syndrome transcription factor, WSTF {Human (*Homo sapiens*)}
ARCKVCRKKGEDDKLILCDECNKAFLFCLRPALYEVPDGEWQCPACQPAT
>d1fp0a1_g.50.1.2 (A:19-88) Nuclear corepressor KAP-1 (TIF-1beta) {Human (*Homo sapiens*)}
GTLDDSATICRVCQKPGDLMCNQCEFCFHLDCHLPALQDVPGEEWCSCLCHVLPDLKEEDVDLQACKLN
>d1adt_2_g.51.1.1 (266-385) First Zn-domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}
TGCALWLHRCAEIEGELKCLHGSIMKEHVIEMDVTSENGQRALKEQSSKAKIVKNRWGRNVVQISNTDARCCVHDAACPANQFSGKSCGMFFS
EGAKAQVAFKQIKAFMQALYPNAQT
>d1adt_3_g.51.1.1 (386-529) Second Zn-domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}
GHGHLLMPRLCECNSKPGHAPFLGRQLPKLTPFALSNAEDLDADLISDKSVLASVHHPALIVFQCCNPVYRNSRAQGGGNPDFKISAPDLLNALVM
VRSLLSENFTELPRMVVPQFKWSTKHQYRNVS LPVAHSDARQNPFD
>d1qbha_g.52.1.1 (A:) 2MIHB/C-IAP-1 {Human (*Homo sapiens*)}
GSHMQTHAARMRTFMYWPSSVPVQPEQLASAGFYVGRNDDVKCFCCDGGLRCWESGDDPWVEHAKWPRCEFLIRMKGQEFVDEIQGRYP
HLLEQLLSTS
>d1f9xa_g.52.1.1 (A:) BIR domains of XIAP {Human (*Homo sapiens*)}
MSDAVSSDRNFPNSTLPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPGCKYLLEQ
KGQEYINNIHLTHSLEECLVRTT

>d1g73c_g.52.1.1 (C:) BIR domains of XIAP {Human (Homo sapiens)}

LPRNPSMADYEARIIFTFGTWIYSVNKEQLARAGFYALGEGDKVCFHC GG LTDWKPSED PWEQHAKWYPGCKYLL EQKGQEYINNIHL

>d1g73d_g.52.1.1 (D:) BIR domains of XIAP {Human (Homo sapiens)}

LPRNPSMADYEARIIFTFGTWIYSVNKEQLARAGFYALGEGDKVCFHC GG LTDWKPSED PWEQHAKWYPGCKYLL EQKGQEYINNIHLHSLEEC

LVRTTE

>d1i3oe_g.52.1.1 (E:) BIR domains of XIAP {Human (Homo sapiens)}

FALDRPSETHADYLLRTGQVV DISDTIYPRNPAMYSEEARLKS FQNWP DYAHLP RELASAGLYYT GIGDQV QCFACGGKLKNWEPGDRAWSEHRR

HFPNCFFVLGRNLNI

>d1jd5a_g.52.1.1 (A:) BIR2 domain of DIAP1 {Fruit fly (Drosophila melanogaster)}

GNYFPQYPEYAIETARLRTFEAWPRNLKQKPHQLA EAGFFYTGVGDRVRCFSCGGGLMDWNDNDEPWEQHALWLSQCRFVKLMKGQLYIDTVAA

KPVLAEEKEES

>d1e31a_g.52.1.1 (A:) Anti-apoptotic protein survivin {Human (Homo sapiens)}

TLPPAWQPFLKDHRISTFKNWP FLEGCACTPERMAAGFIHCPTENEPDLAQ CFFCFKELEG WEPDDPIEEHKHHSSGCAFLSVKKQFEELTLGEFL

KLDRERAKNKIAKETNNKKEFEETAKKV RRAIEQLAA

>d1f81a_g.53.1.1 (A:) CREB-binding transcriptional adaptor protein CBP {Mouse (Mus musculus)}

SPQESRRLSIQRCIQSLVHACQCRNANC LPSCQKM KRVVQHTKGCKRK TNGGCPVCKQLIALCCYHAKHCQENKCPVPFCLNIHK

>d1hc7a3 g.56.1.1 (A:404-477) C-terminal domain of ProRS {Thermus thermophilus}

TRKVDTYEAFKEAVQEGFALAFHCGDKACERLIQEETTATTRCVPFEAEPEEGFCVR CGRPSAYGKRVVFAKAY

>d1exka_g.54.1.1 (A:) Cysteine-rich domain of the chaperone protein DnaJ. {Escherichia coli}

GVTKEIRIPTLEEC DVCHGSGAKPGTQPQTCPTCHGSGQVQMRQGF AVQQTCPHCQGRGTLIKDPCNKCHGHGRVERS