

Online Supporting Information S1.

The benchmark dataset S1 includes 7,329 proteins

from 1070 super-families and 1824 families (see Ref. 12).

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

SLFEQLGGQAAVQAVTAQFYANIQADATVATFFNGIDMPNQTNKAAFLCAALGGPNAWTGRNLKEVHANM
GVSNAQFTTIGHLRSALTGAGVAAALVEQTVAVAETVRGDVVTV

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

SLFAKLGGREAVEAAVDKFYNKIVADPTVSTYFSNTDMKVQRSKQFAFLAYALGGASEWKGKDMRTAHKDLVP
HLSDVHFQAVARHLSDTLTELGVPPEDITDAMAVVASTRTEVLNMPQQ

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

GLLSRLRKREPISIYDKIGGHEAIEVVVEDFYVRVLADDQLSAFFSGTNMSRLKGKQVEFFAAALGGPEPYTGAP
MKQVHQGRGITMHHSFLVAGHLADALTAAGVPSETITEILGVIAPLADVTS

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

VDAAVAKVCGSEAIKANLRRSWGVLSADIEATGLMLMSNLFTPDTKTYFTRLGDVQKGKANSKLRGHAITLT
YALNNFVDSLDDPSRLKCVVEKFVNHNIRKISGDAFGAIVEPMKETLKARMGNYYSDDVAGAWAALGVVQ
AAL

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

KVAELANAVVSNAQKDLLRMSWGVLSVDMEGTGMLMANLFKTSPSAKGKFARLGDSAGKDNSKLRGHS
ITLMYALQNFVDALDDVERLKCVVEKFVNHNIRQISADEFGEIVGPLRQTLKARMGNYFDEDVTAAWASLVAV
VQASL

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

SVYDAAAQLTADVKKDLRDSWKVIGSDKKNGVALMTTFADNQETIGYFKRLGNVSQGMANDKLRGHSITL
MYALQNFIDQLDPDDLCVVEKFVNHNTRKISAAEFGKINGPIKKVLASKNFGDKYANAWAKLVAVVQAAL

>d1b0b_a.1.1.2 (-) Hemoglobin I {Clam (Lucina pectinata)}

SLSAAQKDNVKSSWAKASAAGTAGPEFFMALFDAHDDVFAKSGLFSAAKGTVKNTPEMAAQASFKGL
VSNWVDNLDNAGALEGQCKTFAANHKARGISAGQLEAAFKVLAGFMKSYGGDEGAWTAVAGALMGMI
DM

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

TLTKHEQDILLKELGPHVDTPAHVETGLGAYHALFTAHPQYISHFSRLEGHTIENVMQSEGIKHYARTLTEAIVH
MLKEISNDAEVKKIAAQYKGKDHTSRKVTKDEFMSGEPIFTKYFQNLVKDAEGKAAVEKFLKHVFPMMAAEI

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

GLSAAQRQVVASTWKDIAGSDNGAGVGKECFKFLSAHHDMAAVFGFSGASDPGVADLGAKVLAQIGVAVS
HLGDEGKMVAEMKAVGVRHKGYGNKHKA耶FEPLGASLLSAMEHRIGGKMAAAKDAWAAAYADISGALIS
GLQS

>d2hbg_a.1.1.2 (-) Glycera globin {Marine bloodworm (Glycera dibranchiata)}

GLSAAQRQVIAATWKDIAGADNGAGVGKKCLIKFLSAHPQMAAVFGFSGASDPGVAAALGAKVLAQIGVAVSH
LGDEGKMVAQMKAvgvrhkgygnkhika耶FEPLGASLLSAMEHRIGGKMAAAKDAWAAAYADISGALIS
GLQS

>d1a6m_a.1.1.2 (-) Myoglobin {Sperm whale (Physeter catodon)}

VLSEGEWQLVLHVWAKVEADVAGHGQDILIRLFKSHPETLEKFDRFKHLKTEAEMKASEDLKKHGVTVL
ILKKKGHHEAEKPLAQSHATKHKIPIKYLEFISEAIIHVLHSRHPGDFGADAQGAMNKALELFRKDIAKYKELGY

>d1mba_a.1.1.2 (-) Myoglobin {Sea hare (Aplysia limacina)}

SLSAEADLAGKSWAPVFANKNANGLDFLVALFEKFPDSANFFADFKGSVADI
KASPKL RDVSSRIFT RLNEFV
NNAANAGKMSAMLSQFAKEHVGFGVGSAQFENVRSMFPGFVASVAAPPAGADA
AWTKLFGLIIDALKAGA

>d1mbs__ a.1.1.2 (-) Myoglobin {Common seal (*Phoca vitulina*)}
GLSDGEWHLVNVWGKVETDLAGHGQEVLIRLFKSHPETLEKFDKFHLKSEDDMRRSEDLRKHGNTVLTALG
GILKKKGHHEAELKPLAQSHATKHKIPIKYLEFISEAIIHVLHSKHPAEGADAQAAMKKALELFRNDIAAKYKELG
FHG

>d1mwca_ a.1.1.2 (A:) Myoglobin {Pig (*Sus scrofa*)}
GLSDGEWQLVNVWGKVEADVAGHGQEVLIRLFKGHPETLEKFDKFHLKSEDEMKAESDLKKHGNTVLTALG
GILKKKGHHEAELTPLAQSHATKHKIPVKYLEFISEAIIQVLQSKHPGDFGADAQGAMSKAELFRNDMAAKYKE
LGFQG

>d1dwta_ a.1.1.2 (A:) Myoglobin {Horse (*Equus caballus*)}
GLSDGEWQQVLNVWGKVEADIAGHGQEVLIRLFKGHPETLEKFDKFHLKTEAEMKAESDLKKHGTVVLTALG
GILKKKGHHEAELKPLAQSHATKHKIPVKYLEFISDAIIHVLHSKHPGDFGADAQGAMTKALELFRNDIAAKYKE
GFQ

>d2mm1__ a.1.1.2 (-) Myoglobin {Human (*Homo sapiens*)}
GLSDGEWQLVNVWGKVEADIPGHGQEVLIRLFKGHPETLEKFDKFHLKSEDEMKAESDLKKHGATVLTALG
GILKKKGHHEAEIKPLAQSHATKHKIPVKYLEFISEAIIQVLQSKHPGDFGADAQGAMNKALELFRKDMASNYKE
LGFQG

>d1emy__ a.1.1.2 (-) Myoglobin {Asian elephant (*Elephas maximus*)}
GLSDGEWELVLKTWKVVEADIPGHGETVFVRLFTGHPETLEKFDKFHLKTEGEMKAESDLKKQGVTVLTALG
GILKKKGHHEAEIQPLAQSHATKHKIPVKYLEFISDAIIHVLQSKHPAEGADAQGAMKALELFRNDIAAKYKELG
FQG

>d1lht__ a.1.1.2 (-) Myoglobin {Loggerhead sea turtle (*Caretta caretta*)}
GLSDDEWNHVLGIWAKVEPDLSAHGQEVIIRLFQLHPETQERFAFKNLTTIDALKSSEEVKKHGTTVLTALGRIL
KQKNNHEQELKPLAESHTKHKIPVKYLEFICEIIVKIAEKHPSDFGADSQAAMKKALELFRNDMASKYKEFGF
QG

>d1myt__ a.1.1.2 (-) Myoglobin {Yellowfin tuna (*Thunnus albacares*)}
ADFDAVLKCWGPVEADYTTMGGVLVTRLFKEHPETQKLFPKFAGIAQADIAGNAISAHGATVLKKLGELLKAK
GSHAAILKPLANSHTKHKIPINNFKLISEVLVKVMHEKAGLDAGGQTALRNVMGIIIADLEANYKELGFSG

>d1eco__ a.1.1.2 (-) Erythrocytochrome c {Midge (*Chironomus thummi thummi*), fraction III}
LSADQISTVQASFSDKVKGDGPVGILYAVFKADPSIMAKFTQFAGKDLESIKGTAPFETHANRIVGFFSKIIGELPNIEA
DVNTFVASHKPRGVTHDQLNNFRAGFVSYMKAHTDFAGAEAAWGATLDTFFGMIFSJM

>d2gdm__ a.1.1.2 (-) Leghemoglobin {Yellow lupin (*Lupinus luteus*)}
GALTESQAALVKSSWEEFNANIPKHTHRFFILVLEIAPAACKDLFSFLKGTEVPQNNPELQAHAGKVFKLVYEAAI
QLEVTGVVVTDATLKNLGSVHSVSKGVADAHFVVKEAILKTIKEVVGAKWSEELNSAWTIAYDELAIVIKKEMD
DAA

>d1fsla_ a.1.1.2 (A:) Leghemoglobin {Soybean (*Glycine max*), isoform A}
VAFTEKQDALVSSSEAFKANIPQYSVVFYTSILEKAPAAKDLFSFLANGVDPTNPKLTGHAEKLFAVLVRSAGQLK
ASGTVVADAALGSVHAQKAVTDPQFVVVKEALLKTIKAAGDKWSDELSRAWEVAYDEAAAIKKA

>d1d8ua_ a.1.1.2 (A:) Non-symbiotic plant hemoglobin {Rice (*Oryza sativa*)}
ALVEDNNAVAVSFSEEQEALVLKSWAILKKDSANIALRFFLKIFEVAPSASQMFSFLRNSDVPLEKNPKLKTHAMS
VFVMTCEAAAQLRKAGKVTVRDTTLKRLGATHLKYGVGDAHFEVVKFALLDTIKEEVPAADMWSPAMKSAWSE
AYDHLVAAIKQEMKPAE

>d1i3da_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (*Homo sapiens*)}
GHFTEEDKATITS娄GVNVEDAGGETLGRLVVYPWTQRFFDSFGNLSSASAIGGNPKVKAHGKKVLTSLG
AIKHLDDLKGTFQLSELHCDKLHVDPENFKLLGNVLTVLAIHFGKEFTPEVQASWQKMVTAVASALSSRYH

>d1irda_a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (*Homo sapiens*)}
VLSPADKTNVKAAWGKVGGAHAGEYGAEALERMFLSPTTKTYFPHFDLHGSAQVKGHGKKVADALNAVAH
VDDMPNALSALSDLHAHKLRVPVNFKLLSHCLLTAAHLPAEFTPAVHASLDKFLASVSTVLTSKYR
>d1jeba_a.1.1.2 (A:) Hemoglobin, alpha-chain {Human (*Homo sapiens*), zeta isoform}
SLTKTERIIVSMWAKISTQADTIGTETLERLFLSHPQTCKTYFPHFDLHPGSAQLRAHGSKVVAVGDAVKSIDDI
GGALSKLSELHAYILRVDPVNFKLLSHCLLTAAARFPADFTAEAHAAWDKFLSVSSVLTKEYR
>d1ibeaa.1.1.2 (A:) Hemoglobin, alpha-chain {Horse (*Equus caballus*)}
VLSAADKTNVKAAWSKVGGHAGEFGAEALERMFGLFPPTTKTYFPHFDLHGSAQVKAHGKKVGDALTLAVGH
LDDLPGALSDLSNLHAHKLRVPVNFKLLSHCLLSTLAHVLPNDFTPAPVHASLDKFLSSVSTVLTSKYR
>d1hdса_a.1.1.2 (A:) Hemoglobin, alpha-chain {Deer (*Odocoileus virginianus*)}
VLSAANKSNVKAAWGKVGGNAPAYGAQALQRMFLSFPTTKTYFPHFDLHGSAQQKAHGQKVANALTKAQG
HLNDLPGTLSNLNLHAHKLRVPVNFKLLSHSLLVTASHLPTNFTPAPVHANLNKFLANDSTVLTSKYR
>d1g08a_a.1.1.2 (A:) Hemoglobin, alpha-chain {Cow (*Bos taurus*)}
VLSAADKGNVKAAWGKVGHHAAEYGAEALERMFGLFPPTTKTYFPHFDLHGSAQVKGHGAKVAAALTКАVEH
LDDLPGALSELSDLHAHKLRVPVNFKLLSHSLLVTASHLPSDFTPAPVHASLDKFLANVSTVLTSKYR
>d1qpwa_a.1.1.2 (A:) Hemoglobin, alpha-chain {Pig (*Sus scrofa*)}
VLSAADKANVKAAWGKVGQQAGAHGAEALERMFGLFPPTTKTYFPHFDLHGSDQVKAHGQKVADALTKAV
GHLDLPGALSDLHAHKLRVPVNFKLLSHCLLTAAHHPPDDFNPSVHASLDKFLANVSTVLTSKYR
>d1fhja_a.1.1.2 (A:) Hemoglobin, alpha-chain {Maned wolf (*Chrysocyon brachyurus*)}
VLSPADKTNIKSTWDKIGGHAGDYGGAEALDRTFQSFTTCKTYFPHFDLSPGSAQVKAHGKKVADALTTAVAHLD
DLPGALSALSDLHAYKLRLVPVNFKLLSHCLLTACCHPTEFTPAPVHASLDKFFTAVSTVLTSKYR
>d1hbra_a.1.1.2 (A:) Hemoglobin, alpha-chain {Chicken (*Gallus gallus*)}
MLTAEDKKLIQQAWekaashqeeFGAEALTRMFTTYPQTCKTYFPHFDLSPGSDQVRGHGKKVLGALGNAVKN
VDNLSQAMAELSNLHAYNLRVPVNFKLLSQCIQVVLAVHMGKDYTPEVHAADFDFLSAVSAVLAEKYR
>d1a4fa_a.1.1.2 (A:) Hemoglobin, alpha-chain {Bar-headed goose (*Anser indicus*)}
VLSAADKTNVKGVFSKISGHAAEYGAETLERMFTAYPQTCKTYFPHFDLQHGSAQIKAHGKKVVAALVEAVNHID
DIAGALSKLSDLHAQKLRLVPVNFKFLGHCFLVVVAIHPSALTAEVHASLDKFLCAVGTVLAKYR
>d1outa_a.1.1.2 (A:) Hemoglobin, alpha-chain {Trout (*Oncorhynchus mykiss*)}
SLTAKDKSVVKAFWGKISGKADVVGAEARLGRMLTAYPQTCKTYFSHWADLSPGSPVKKHGGIIMGAIGKAVGL
MDDLVGGMSALSDLHAFKLRVPNGNFKILSHNILVTLAIHPSDFTPEVHIAVDKFLEAVSAALADKYR
>d1cg5a_a.1.1.2 (A:) Hemoglobin, alpha-chain {Cartilaginous fish acae (*Dasyatis akajei*)}
VLSSQNKKAAEELGNLIKANAEGADALARLFELHPQTCKTYFSKFGFEACNEQVKKHGKRVMNALADATHH
LDNLHLHLEDLARKHGENLLVDPHNFLFADCIVTAVNLQAFTPVTHCAVDKFLELVAYELSSCYR
>d1t1na_a.1.1.2 (A:) Hemoglobin, alpha-chain {Fish (*Trematomus newnesi*)}
SLSDKDKAAVRALWSKIGKSSDAIGNDALSRMIVVYPQTCKYFSHWPDVTPGSPNIKAHGKKVMGGIALAVSKI
DDLKTGLMELSEQHAYKLRLVDPNSFKILNHCIILVVISTMFPKEFTPEAHVSLDKFLSGVALALAERYR
>d1spga_a.1.1.2 (A:) Hemoglobin, alpha-chain {Teleost fish (*Leiostomus xanthurus*)}
SLSATDKARVKALWDKIEGKSAELGAEALGRMLVSFPQTCKYFSEWQGDLGPQTPQRNHGAVIMAAGKAVK
SIDNLVGGSQLSELHAFKLRLVPANFKILAHHNIIIVISMYFPGDFTPEVHLSVDKFLACLALALSEKYR
>d1gcva_a.1.1.2 (A:) Hemoglobin, alpha-chain {Houndshark (*Mustelus griseus*)}
AFTACEKQTIGKIAQVLAKSPEAYGAECLARLFVTHPGSKSYFEYKDYSAGAKVQVHGGKVIRAVVKAEEHVD
DLHSHLETLALTHGKKLLVDPQNFPMLSECIIVTLATHLTFSPDTCAVDKLLSAICQELSSRYR
>d1irdb_a.1.1.2 (B:) Hemoglobin, beta-chain {Human (*Homo sapiens*)}
VHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAMGNPKVKAHGKKVLGAFS

DGLAHLNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVLAHHFGKEFTPVQAAYQKVAGVANALAHKYH

>d1a9we_a.1.1.2 (E:) Hemoglobin, beta-chain {Human (*Homo sapiens*), embryonic gower II} VHFTAEKAAVTSLWSKMNVVEAGGEALGRLLVYPWTQRFFDSFGNLSSPSAILGNPKVKAHGKKVLTSFGD AIKNMDNLKPAFAKLSELHCDKLHVDPENFKLLGNVMVIILATHFGKEFTPVEQAAWQKLVSABAIALAHKY

>d1ibeb_a.1.1.2 (B:) Hemoglobin, beta-chain {Horse (*Equus caballus*)} VQLSGEEKAAVLALWDKVNEEVGGEALGRLLVYPWTQRFFDSFGDLSNPGAVMGNPKVKAHGKKVLHSF GEGVHHLDNLKGTFAALSELHCDKLHVDPENFRLLGNVLVVVLARHFGKDFTPELQASYQKVAGVANALAHKYH

>d1hdsb_a.1.1.2 (B:) Hemoglobin, beta-chain {Deer (*Odocoileus virginianus*)} MLTAEEKAAVTGFWGKVDVVGQAQALGRLLVYPWTQRFFQHFGNLSSAGAVMNNPKVKAHGKRVLDAT TQGLKHLDLKGTFAALSELHCDKLHVDPENFKLLGNVLVVVLARNFGKEFTPVLQADFQKVAGVANALAHKYH

>d1g08b_a.1.1.2 (B:) Hemoglobin, beta-chain {Cow (*Bos taurus*)} MLTAEEKAAVTAFWGKVKVDEVGGEALGRLLVYPWTQRFFESFGDLSTADAVMNNPKVKAHGKKVLDSFSN GMKHLDLKGTFAALSELHCDKLHVDPENFKLLGNVLVVVLARNFGKEFTPVLQADFQKVAGVANALAHRYH

>d1qpwb_a.1.1.2 (B:) Hemoglobin, beta-chain {Pig (*Sus scrofa*)} VHLSAEEKEAVLGLWGKVNDEVGGEALGRLLVYPWTQRFFESFGDLSNADAVMGNPKVKAHGKKVLQSFS DGLKHLDNLKGTFAKLSELHCDQLHVDPENFRLLGNVIVVVLARRLGHDNPDVQAAFQKVAGVANALAHKYH

>d1fhjb_a.1.1.2 (B:) Hemoglobin, beta-chain {Maned wolf (*Chrysocyon brachyurus*)} VHLTAEKSLVSGLWGKVNDEVGGEALGRLLVYPWTQRFFDSFGDLSTDAVMSNAKVKAHGKKVLNSFSD GLKNLDNLKGTFAKLSELHCDKLHVDPENFKLLGNVLCVLAHHFGKEFTPQVQAAYQKVAGVANALAHKYH

>d1jebb_a.1.1.2 (B:) Hemoglobin, beta-chain {Mouse (*Mus musculus*)} VHLTDAEKAAVSGLWGKVNNAEVGGEALGRLLVYPWTQRFFDSFGDLSSASAIMGNNAKVKAHGKKVITAFN DGLNHLDLSKGTFAFLSELHCDKLHVDPENFRLLGNMIVIVLGHHLGKDFTPAAQAAFQKVAGVAAALAH

>d1hbrb_a.1.1.2 (B:) Hemoglobin, beta-chain {Chicken (*Gallus gallus*)} VHWTAEEKQLITGLWGKVNVAECGAEARLLIVYPWTQRFFASFGNLSSPTAILGNPMVRAGKKVLTSFGD AVKNLDNIKNTFSQLSELHCDKLHVDPENFRLLGDILIIVLAAHFSKDFTPECQAAWQKLVRVVAHALARK

>d1a4fb_a.1.1.2 (B:) Hemoglobin, beta-chain {Bar-headed goose (*Anser indicus*)} VHWSAEKQLITGLWGKVNADCGAEALARLLIVYPWTQRFFSSFGNLSSPTAILGNPMVRAGKKVLTSFGD AVKNLDNIKNTFAQLSELHCDKLHVDPENFRLLGDILIIVLAAHFAKEFTPDCQAAWQKLVRVVAHALARKYH

>d1outb_a.1.1.2 (B:) Hemoglobin, beta-chain {Trout (*Oncorhynchus mykiss*)} VEWTDAEKSTISAWGKVNIDEIGPLALARVLIVYPWTQRYFGSGNVSTPAAIMGNPKVAAHGVCGALDK AVKNMGNILATYKSLSETHANKLFVDPDNFRVLADVLTVIAAKFGASFTPEIQATWQKFMKVVAAMGSRYF

>d1pbxb_a.1.1.2 (B:) Hemoglobin, beta-chain {Antarctic fish (*Pagothenia bernacchii*)} VEWTDKERSIISDFSHMDYDDIGPKALSRCCLIVYPWTQRHFSGFGNLYNAEAIIGNANVAAHGIKVLHGLDRGV KNMDNIAATYADLSTLHSEKLHVDPDNFKLLSDCITIVLAAKMGHAFTAETQGAFQKFLAVVVSALGKQYH

>d1cg5b_a.1.1.2 (B:) Hemoglobin, beta-chain {Cartilaginous fish akaei (*Dasyatis akajei*)} VKLSEDQEHYIKGVWKDVDHKQITAKALERVFVVPWTTRFLFSKLQGLFSANDIGVQQHADKVQRALGEAIDD LKKVEINFQNLSGKHQEIGVDTQNFKLLGQTFMVELALHYKKTFRPKEHAAAYKFFRLVAEALSSNYH

>d1t1nb_a.1.1.2 (B:) Hemoglobin, beta-chain {Fish (*Trematomus newnesi*)}

VEWTDKERSIISDISSHMDYDDIGPKALSRLVVPWTQRYFSGFGNLYNAEGIMSNANVAAHGIKVLHGLDRG
MKNMDNIADAYDLSTLHSEKLHVDPDNFKLLSDCITIVLAAMGHAFTAETQGAFQKFLAAVSALGKQYH
>d1spgb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Teleost fish (*Leiostomus xanthurus*)}
VDWTDAERAIAKALWGKIDVGEIGPQALSRLLIVYPWTQRHFKGFGNISTNAAILGNNAKVAEHGKTVMGGLDR
AVQNMDNIKNVYKQLSIKHSEKIHVDPDNFRLLGEIITMCVGAKFGPSAFTPEIHEAWQKFLAVVVSALGRQYH
>d1gcvb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Houndshark (*Mustelus griseus*)}
VHWTQEERDEISKTQGTDMKTVVTQALDRMFVYPWTNRFYQKRTDFRSSIHAGIVGALQDAVKHMDDV
KTLFKDLSKKHADDLHVDPGSFHLLDCIIVELAYLRKDCFTPCHIPGIWDKFFEVVIDAIISKQYH
>d1ch4a_ a.1.1.2 (A:) Chimeric hemoglobin beta-alpha {Synthetic, based on *Homo sapiens*
sequence}
VHLTPEEKSAVTALWGKVNDEVGGEALGRLLVVYPWTQRFFESFGDLSTPPAVMGNPKVKAHGKKVLGAFS
DGLAHDNLKGTFATLSELHCDKLRVDPVNFKLLSHCLLVTAAHLPAEFTPAPHASLDKVLASVSTVLTSKYR
>d1it2a_ a.1.1.2 (A:) Hagfish hemoglobin {Inshore hagfish (*Eptatretus burgeri*)}
PIIDQGPLPTLDGDKKAINKIWPKIYKEYEQYSLNILLRFLKCFPQAQASFKFKLTTADELKKSADVWHAEI
KVNEIINSMDNQEEIIKSLKDSLQHKTVFKVDSIWFKELSSIFVSTIDGGAEEFKLFSIICILLRSAY
>d2lh_b_ a.1.1.2 (-) Lamprey globin {Sea lamprey (*Petromyzon marinus*)}
PIVDTGSVAPLSAAEKTIRSAWAPVYSTYETSGVDILVKFFTSTPAAQEFFPKFKGLTTADELKKSADVWHAEI
INAVIDAVASMDTEKMSMKLRNLSGKHAKSFQVDPEYFKVLAADIATVAAGDAGFEKLMMSMICILLRSAY
>d1ash_ a.1.1.2 (-) Ascaris hemoglobin, domain 1 {Pig roundworm (*Ascaris suum*)}
ANKTRELCMKSLEHAKVDTNEARQDGIDLYKHMFENYPLRKYFKSREEYTAEDVQNDPFFAKQGQKILLACH
VLCATYDDRETFNAYTRELLDRHARDHVHMPPEVWTDFWKLFEYLGKKTTLDEPTKQAWHEIGREFAKEINK
>d1itha_ a.1.1.2 (A:) Hemoglobin {Innkeeper worm (*Urechis caupo*)}
GLTAAQIKAIQDHWFNLNIKGCLQAAADSIFFKYLTAYPEGLAFFHKFSSVPLYGLRSNPAYKAQTLTVINYLDKVVD
ALGGNAGALMKAKVPSHDAMGITPKHFGQLLKLVGGVFQEEFSADPTTVAAWGDAAGVLVAAMK
>d1hl_b_ a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (*Caudina (Molpadia) arenicola*)}
GGTLAIQAGQDLTLAQKKIVRKTHQLMRNKTSVTDVFIRIFADPSAQNKFPQMAGMSASQLRSSRQM
AHAIRVSSIMSEYVEELSDILPELLATLARTHDLNKVGADHYNLFAKVLMEALQAEGLGDFNEKTRDAWAKAFS
VVQAVLLVKHG
>d1hlm_ a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (*Caudina (Molpadia) arenicola*)}
GATQSFSVGDLTPAEKDLIRSTWDQLMTHRTGFVADVIFIRIFHNDPTAQRKFPQMAGLSPAELRTSRQMHA
HAIRVSALMTTYIDEMDTEVPELLATLTRTHDKNHVGKKNYDLFGKVLMEAIAKAEVGFTKQVHDAWAKTF
AIVQGVЛИTKHAS
>d1vhba_ a.1.1.2 (A:) Bacterial dimeric hemoglobin {Vitreoscilla stercoraria}
LDQQTINIИKATVPVLKEHGVTTTFYKNLFAKHPEVRPLFDMDGRQESLEQPKALAMTVAAAQNIENLPAILPA
VKKIAVKHCQAGVAAHYPIVGQELLGAIKEVLGDAATDDILDAWGKAYGVIADVFIQVEADLYAQAV
>d1cqxa1_ a.1.1.2 (A:1-150) Flavohemoglobin, N-terminal domain {Alcaligenes eutrophus}
MLTQKTKDIVKATAPVLAHGYDIICKFYQRMFEAHPKLNVFNMAHQEQGQQQQALARAVYAYAENIEDPN
SLMAVLKNIANKHASLGVKPEQYPIVGEHLLAAIKEVLGNAATDDIISAWAQAYGNLADVLGMMESELYERSAE
QPGG
>d1ew6a_ a.1.1.2 (A:) Dehaloperoxidase {Marine worm (*Amphitrite ornata*)}
GFKQDIATRGDLRTYAQDIFLAFLNKYPDERRYFKNYVGKSDQELKSMAKFGDHTEKVFNLMMEVADRATDC
VPLASDANTLVQMKQHSSLTTGNFEKLFVALVEYMRASGQSFDSQSWDRFGKNLVSALSSAGMK
>d1phna_ a.1.1.3 (A:) Phycocyanin {Red alga (*Cyanidium caldarium*)}

MKTPITEAIAAADNQGRFLSNTTELQAVNGRYQRAAASLEAARS LTSNAERLINGAAQAVYSKFPYTSQMPGPQ
YASSAVGKAKCARDIGYYLRMVTYCLVGGTGPMD EYLIAGLEEINRTFDLSPSWYVEALNYIKANHGLSGQAA
NEANTYIDYAINALS

>d1phnb_a.1.1.3 (B:) Phycocyanin {Red alga (*Cyanidium caldarium*)}

MLDAFAKVVAQADARGEFLSNTQLDALKMVSEGNKRLDVNRITSNASAIVTNAARALFSEQPQLIQPGGNA
YTNRMAACLRDMEIILRYVSYAIAGDSSILDDRCLNGLRETYQALGVPGASAVGIEKMKDSAIAIANDPSGIT
TGDCSALMAEVGTYFDRAATAVQ

>d1f99a_a.1.1.3 (A:) Phycocyanin {Red alga (*Polysiphonia urceolata*)}

MKTPLTEAIAAADSQGRFLSNTQVVNGRYNRATSLEAAKALTANADR LISA NGGAANAVYSKFPYTTQMPGP NY
SSTAIGKAKCARDIGYYLRMVTYCLVGGTGPMD DYLVAGLEEINRTFELSPSWYEALKYIKNNHGLSGDVANE
ANTYIDYAINTLS

>d1f99b_a.1.1.3 (B:) Phycocyanin {Red alga (*Polysiphonia urceolata*)}

MLDAFAKVVAQADARGEFLSNTQIDALLAIVSEGNKRLDVVNKITNNASAIVTNAARALFAEQPQLISP GGNAY
TSRRMAACLRDMEIVLRYVSYAMIAGDASVLDDRCLNGLRETYQALGTPGASVAVAIQKMKA ALALALVNDTTG
TPAGDCASLVAE IATYFDRAAAA A

>d1cpca_a.1.1.3 (A:) Phycocyanin {Cyanobacterium (*Fremyella diplosiphon*)}

MKTPLTEAVAAADS QGRFLSSTEIQTAFGRFRQASASLAAKALTEKASSLASGAANAVYSKFPYTTSQNGPNFA
STQTGKDKCVRDIGYYLRMVTYCLVGGTGPLDDYLIGGIAEINRTFDLSPSWYVEALKYIKANHGLSGDPAVEA
NSYIDYAINALS

>d1cpcb_a.1.1.3 (B:) Phycocyanin {Cyanobacterium (*Fremyella diplosiphon*)}

MLDAFAKVVSQADARGEYLSGSQIDALSALVADGNKRMDVNRITGNSSTIVANAARSLFAEQPQLIAPGGNA
YTSRRMAACLRDMEIILRYVTYAI FAGDASVLDDRCLNGLKETYLA LGTPGSSVAVGVQKMKA ALAIAGDTNG
ITRGDCASLMAEVASYFDKAASAVA

>d1i7ya_a.1.1.3 (A:) Phycocyanin {*Synechococcus vulgaris*}

MKTPITEAIAAADTQGRFLSNTELQAVDGRFKRAVASMEAARALTNNAQSLIDGAAQAVYQKFPYTTMQGS
QYASTPEGKAKCARDIGYYLRMITYCLVAGGTGPMD EYLIAGLSEINSTFDLSPSWYEALKYIKANHGLTGQAAV
EANAYIDYAINALS

>d1i7yb_a.1.1.3 (B:) Phycocyanin {*Synechococcus vulgaris*}

MLDAFAKVVAQADARGEFLTNAQFDALSNLVKEGNKRLDAVN RITSNASTIVANAARALFAEQPQLIQPGGNA
YTNRMAACLRDMEIILRYVTYAILAGDSSVLDDRCLNGLRETYQALGTPGSSVAVAIQKMKA ALAIANDPNGI
TPGDCSALMSEIAGYFDRAAAA A

>d1gh0a_a.1.1.3 (A:) Phycocyanin {*Spirulina platensis*}

MKTPLTEAVSVAD SQGRFLSSTEI QVAFGRFRQAKAGLEAAKALTSKADSLISGAAQAVYNKFPYTTQM QGP NY
AADQRGKDKCARDIGYYLRMVTYCLIAGGTGPMD EYLIAGIDEINRTFELSPSWYEALKYIKANHGLSGDAAVE
ANSYLDYAINALS

>d1gh0b_a.1.1.3 (B:) Phycocyanin {*Spirulina platensis*}

MFDAFTKVV SQADTRGEMLSTAQIDALSQMVAESNKRLDVNRITSNASTIVSNAARSLFAEQPQLIAPGGNA
YTSRRMAACLRDMEIILRYVTYAVFAGDASVLEDRCLNGLRETYLA LGTPGSSVAVGVGKMKEA ALAI VNDPAGI
TPGDCSALASEIAGYFDRAAAA AVS

>d1alla_a.1.1.3 (A:) Allophycocyanin {*Spirulina platensis*}

SIVTKSIVNADA EARYLSPGELDRIKSFTSGERRVRIAETMTGARERIIKQAGDQLFGKRPDV VSPGGNAYGAD
MTATCLRDLDYYLR LITYGIVAGDVTPIEEIGVVGVR EMYKSLGTPIEAIAEGV RAMKSVATSL SGADAAEAGSYF
DYLIGAMS

>d1allb_a.1.1.3 (B:) Allophycocyanin {*Spirulina platensis*}

MQDAITSVINSSDVQGKYLDASAIQKLKAYFATGELRVRAATTISANAANIVKEAVAKSLLSDVTRPGGNMYTT
RRYAAACIRLDYYLRYATYAMLAGPSILDERVLNGLKETYNSLGVPIGATVQAIQAMKEVTAGLVGGAGKEM
GIYFDYICSGLS

>d1b33a_a.1.1.3 (A:) Allophycocyanin {Cyanobacterium (*Mastigocladus laminosus*)}
SIVTKSIVNADAEARYLSPGEELDRIKSFVSSGEKRLRIAQILTDNRERIVKQAGDQLFQKRPDVSPGGNAYGQE

MTATCLRDLDYYLRLITYGIVAGDVTPIEEIGIVGVREMYKSLGTPIDAVAAGVSAMKNVASSILSAEDAAEAGAY
FDYVAGALA

>d1b33b_a.1.1.3 (B:) Allophycocyanin {Cyanobacterium (*Mastigocladus laminosus*)}

MQDAITAVINSSDVQGKYLDATALEKLKSFYFSTGELRVRAATTIAANAAAIVKEAVAKSLLSDITRPGGNMYTR
RYAACIRLDYYLRYATYAMLAGPSILDERVLNGLKETYNSLGPISATVQAIQAMKEVTASLVGPDAGKEMGV
YFDYICSGLS

>d1liaa_a.1.1.3 (A:) Phycoerythrin {Red alga (*Polysiphonia urceolata*)}
MKSVITTTISAADAAGRYPSTSVDLQSVQGNIQRRAARLEAAEKLGSNHEAVVKEAGDACFSKYGYKNPGEAG

ENQEKINKCYRDIDHYMRLINYTLVGGTGPLDEWGIAGAREVYRTLNLPSAAYIAAFVFTRDRLCIPRDMSAQ
AGVEFTALDYLINSLS

>d1liab_a.1.1.3 (B:) Phycoerythrin {Red alga (*Polysiphonia urceolata*)}
MLDAFSRVVVNSDSKAAYVGGSDLQALKTFINDGNKRLDAVNYIVSNSSCIVSDAISGMICENPGLITPGGNCYT

NRRMAACLRDGEIILRYVSYALLAGDASVLEDRCNLGLKETYIALGVPNSTRAVSIMKAAAVCFISNTASQRKV
EVIEGDCSALASEVASYCDRVVAAVS

>d1b8da_a.1.1.3 (A:) Phycoerythrin {Red alga (*Griffithsia monilis*)}
MKSVITTTISAADAAGRFPSSDLESIQGNIQRRAARLEAAQKLSGNHEAVVKEAGDACFAKSYLKNAEAGD

SPEKINKCYRDIDHYMRLINYSLVGGTGPVDEWGIAGSREVYRALNLPGSAYIAAFTFRDRLCIPRDMSQA
GVEFTSALDYVINSLC

>d1b8db_a.1.1.3 (B:) Phycoerythrin {Red alga (*Griffithsia monilis*)}
MLDAFSRVVVTSDAKAAYVGGSDLQSLKFINDGNKRLDAVNYIVSNASCIVSDAISGMICENPGLIAPGGNCY

TNRRMAACLRDGEIILRYVSYALLAGDSSVLEDRCNLGLKETYIALGVPASSRAVSIMKATATAFITNTASGRKV
EVAAGDCQALQAEASYFDKVGSSID

>d1eyxa_a.1.1.3 (A:) Phycoerythrin {Red algae (*Gracilaria chilensis*)}
MKSVITTVISAADSAGRFPSSDLESVQGNIQRASARLEAAEKLASNHEAVVKEAGDACFGKYGYLNPNPEAGE

NQEKINKCYRDIDHYMRLVNYSLVGGTGPLDEWGIAGAREVYRTLNLPTSAYIAAFTRDRLCIPRDMSQA
GVEYSTALDYIINSLC

>d1eyxb_a.1.1.3 (B:) Phycoerythrin {Red algae (*Gracilaria chilensis*)}
MLDAFSRVISNADAKAAYVGGSDLQALRTFISDGNKRLDAVNYIVSNSSCIVSDAISGMICENPGLITPGGNCYT

NRRMAACLRDGEIILRYISYALLAGDSSVLEDRCNLGLKETYIALGVPNSTRAVSIMKAAVGAFISNTASQRKG
EVIEGDCSALAAEIASYCDRISAACS

>d1qgwc_a.1.1.3 (C:) Phycoerythrin {Cryptophite (*Rhodomonas* sp.), cs24}
DAFSRVVTNADSKAAYVGGADLQALKFISEGNKRLDSVNSIVSNASCIVSDAISGMICENPSLISPGNCYTNR

RMAACLRDGEIILRYVSYALLSGDASVLEDRCNLGLKETYSSLGVPANSNARAVSIMKACAVAFVNNTASQKKLS
TPQGDGCSGLASEVGGYFDKVTAIS

>d1fumb1_a.1.2.1 (B:106-243) Fumarate reductase iron-sulfur protein, C-terminal domain
{*Escherichia coli*}

MTHFIESLEAIKPYIIGNSRTADQGTNIQTPAQMAKYHQFSGCINCGLCYAACPQFGLNPEFIGPAAITLAHRYNE
DSRDHGKKERMAQLNSQNGVWSCTFVGYCSECPKHDVDPAAAIQQGKVESSKDFLIATLKPR

>d1qlab1_a.1.2.1 (B:107-239) Fumarate reductase iron-sulfur protein, C-terminal domain

{Wolinella succinogenes}

TGNWFNGMSQRVESWIHAQKEHDISKLEERIEPEVAQEVFELDRICIEGCCIAACGTKIMREDVGAAGLNRV
VRFMIDPHDERTDEDYYELGDDGVFGCMTLACHDVC PKNLPLQSKIAYLRRK MVSN

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

APVLSKDVADIESILANPRTQSHAALHSTLA KKLDKKHWKRNPDKNCFHCEKLENNFDDIKHTTLGERGALRE
AMRCLKCADAPCQKSCPTHLDIKSFTISNKNYYGAAKMIFSDNPLGLTCGMVCPTSDLCVGGCNLYATEEGSI

NIGGLQQFASEVFKA MNIPQIRNPCLPSQE KMP

>d1grj_1 a.2.1.1 (2-79) GreA transcript cleavage protein, N-terminal domain {Escherichia coli}
QAIPMTLRGAEKLREELDFLKS VRRPEII AIAEAREHDLKENAEYHAAREQQGFCEGRIK DIEAKLSNAQVIDV
TK

>d1jj2u_ a.2.2.1 (U:) Ribosomal protein L29 (L29p) {Archaeon Haloarcula
marismortui}

TVLHVQEIRD MTPAEREAELDDLKTELLNARAVQAAGGAPENPGR IELRKAIARIKTIQGEEGD

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

MDYFTLFG LPARYQLDTQALSLRFQDLQRQYHPDKFASGSQAEQLAAVQQSATINQAWQTLRHPLMRAEYLLS
LHG

>d1hdj_ a.2.3.1 (-) HSP40 {Human (Homo sapiens)}

MGKDYYQTGLARGASDEEIKRAYRRQALRYHPDKNKEPGAE EKFKEIAEAYDVLS DPKREIFDRYGE EGLKGS
GC

>d1xbi_ a.2.3.1 (-) DnaJ chaperone, N-terminal (J) domain {Escherichia coli}

AKQDYYEILGVSKTAEEREIRKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEAYEVLTDSQKRAAYDQYGHAAFE
Q

>d1faf a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Murine polyomavirus}

MDRVLSRADKERLLELLKLPRQLWGDFGRM QQAYKQSQLLLHPDGSHALMQELNSLWGT FKTEVYNLRM
NLGGTG FQ

>d1gh6a_ a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Simian virus 40, Sv40}

SHMREESLQLMDLLGLERSAWGNIPLMRKAYLKKCKEFHPDKGGDEEKM KKMNTLYKKMEDGVKYAHQPDF
GGFWDATEIPTYGTDEWEQWWNAFNEENLFCSEEMPSSDDEAT

>d1du2a_ a.2.4.1 (A:) Theta subunit of DNA polymerase III {Escherichia coli}

MLKNLAKLDQTEM DKVNVDLAAAGVAFKERYNMPVIAEAVEREQPEHLRSWFRERLIAHRLASVNL SRPYEP
KLK

>d1fxkc_ a.2.5.1 (C:) Prefoldin alpha subunit {Archaeon Methanobacterium
thermoautotrophicum}

AALAEIVAQLNIYQS QVELIQQQMEAVRATISELEILEKTL SDI QGKDGSETLPVGAGSF IKAE LKDTSEVIM SVG
AGVAIKKNFEDAMESI KSQKNELESTLQKMG ENLRAITDIMMKLSPQAEELLA AVA

>d1fxka_ a.2.5.1 (A:) Prefoldin beta subunit {Archaeon Methanobacterium
thermoautotrophicum}

QNVQHQLAQFQQLQQQAQ AISVQKQT VEMQ INETQKALEELSRA ADDAEV YKSSGNIL R VAKDELTEELQEK
LET LQLREKTIERQE ERVMKKLQEMQVN I QEAMK

>d1cxzb_ a.2.6.1 (B:) Effector domain of the protein kinase pkn/prk1 {Human (Homo sapiens)}

WSLLEQLGLAGADLA APGVQQQ LE RERL RREIRK ELKL KEGAEN LR RATT DLGRSLGP VELL RGSS RRL DLLH
QQLQEL HAHV

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

MVDLKRLRQEPEVFHRAIREKGVALDLEALLALDREVQELKKRLQEVQTERNQVAKRVPKAPPEEKEALIARGK
ALGEEAKRLEEALREKEARLEALLQVPLPPWPGAP

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

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

EKSMMNLQTAKIDAKKEQLADARRDLKSAKADAKVMKDAKTKVVESKKAVQRLEELMKLEVQATDREENK

>d1e52a_ a.2.9.1 (A:) C-terminal, UvrC-binding domain of UvrB {Escherichia coli}
LEPDNVPMMDMSPKALQQKIHELEGMMIQHAQNLEFEEAAQIRDQLHQLRELFAIAS

>d1qoja_ a.2.9.1 (A:) C-terminal, UvrC-binding domain of UvrB {Escherichia coli}
SPKALQQKIHELEGMMMQHAQNLEFEEAAQIRDQLHQLRELFAIAS

>d1aqt_1 a.2.10.1 (87-136) Epsilon subunit of F1F0-ATP synthase C-terminal domain {Escherichia coli}

QDLDEARAMEAKRKAEEHISSHGVDVYAQASAEELAKAIQLRVIELTKK

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

DMLDLGAAKANLEKAQSELLGAADEATRAEIQIRIEANEALVKAL

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

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

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

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

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

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

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

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

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

fumigatus}

QQYTLPPLPYPYDALQPYISQQIMELHHKKHQTYVNGLNAALEAQKAAEATDVPKLVSQQAIKFNGGGHI
NHSLFWKNLAP

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

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

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

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

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

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

PEFLEDPSVLTKDKLKSELVANNVTLPAGEQRKDVVYVQLYLQHLTARNRPLPAGT

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

RQEDKDDLDVTELTNEDLLDQLVKYGVNPGPIVGTRKLYEKLLKLREQGTESRSS

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

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

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

TVKLSFLQHICKLTGLSRSGRKDELLRRIVDSPIYP

>d1a62_1 a.140.3.1 (1-47) Rho termination factor, N-terminal domain {Escherichia coli}

MNLTELKNTPVSELITLGENMGLENLARMRKQDIIFAILKQHAKSGE

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

IHPNFVGDKSKEFSRLGKEEMMAEMLQRGFEYNESDTKTQLIASFKQLRKSLK

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

VDAEAVVQQKCISCHGDLTGASAPAIDKAGANYSEEILDIIQNGQGGMPGGIAKGAEAEAVAALWAEKK

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

EADLALGKAVFDGNCAACHAGGGNNVIPDHTLQKAAIEQFLDGGFNIEAVYQIENGKGAMPAWDGRLEDE
IAGVAAYVYDQAAGNKW

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

ADGAALYKSCVGCHGADGSQAMGVGHAVKGQKADEFKKLGYADGSYGGEEKAVMTNLKRYSDDEEMK
AMADYMSKL

>d2dvh_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Desulfovibrio desulfuricans}

ADGAALYKSCIGCHGADGSKAAMGSAKPVKGQGAEELYKKMKGYADGSYGERKAMMTNAVKKASDEELKA
LADYMSKL

>d1cyi_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Chlamydomonas reinhardtii}

ADLALGAQVFNGNCAACHMGGRNSVMPEKTLKAALEQYLDGGFKVESIIYQVENGKGAMPAWADRLSEEE
IQAVAЕYVFKQATDAAWK

>d1c6s_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Cyanobacterium (Synechococcus elongatus)}

ADLANGAKVFSGNCAACHMGGGNVVMANKTLKKEALEQFGMYSEDAAIYQVQHGKNAMPAFAGRLTDEQI
QDVAAYVLDQAAKGWAG

>d1f1fa_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Arthrosphaera maxima}

DVAAGASVFSANCAACHMGGRNIVANKTLSKSDLAKYLKGFDAAAQVQVTNGKNAMPGFNGLSPL
QIEDVAAYVVDQAEKGW

>d1c6ra_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Green alga (Scenedesmus obliquus)}

ADLALGKQTFEANCAACHAGGNNSVIPDHTLRKAAMEQFLQGGFNLEAITYQVENGKGAMPAWSGTLDDE
IAAVAAYVYDQASGDKW

>d1gdva_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Red alga (Porphyra yezoensis)}

ADLDNGEKVFSANCAACHAGGNNAIMPDKTLKDVLEANSMTIDAITYQVQNGKNAMPAFGGRLVDDEDIE
DAANYVLSQSEKGW

>d1c52_ a.3.1.1 (-) Cytochrome c552 {Thermus thermophilus}

QADGAKIYAQCAGCHQQNGQGIPGAFPLAGHVAEILAKEGGREYLILVLLYGLQQQIEVKGMKYNGVMSSFA
QLKDEEIAAVLNHIATAWGDAKKVKGFKPFTAEEVKKLRACKLTPQQVLAERKKLGLK

>d1cnoa_ a.3.1.1 (A:) Cytochrome c552 {Pseudomonas nautica}

AGDIEAGKAKAAVCAACHGQNGISQVPIYPNLAGQKEQYLVAALKAYKAGQRQGGQAPVMQGQATALSDAD
IANLAAYYASNPAAA

>d1ql3a_ a.3.1.1 (A:) Cytochrome c552 {Paracoccus denitrificans}

ADPAAGEKVFHKCKACHKLDGNDGVPHLNQVGRTVAGVDFNYSDPMAHGGDWTPPEALQEFLTPKA
VVKGTKMAFAGLPKIEDRANLIAYLEGQQ

>d1ayg_ a.3.1.1 (-) Cytochrome c552 {Hydrogenobacter thermophilus}

NEQLAKQKGCMACHDLKAKKVGPAYADVAKKYAGRKDADYLAGKIKGGSGVWGSVPMPQNVTDAEAK
QLAQWILSIK

>d1a56_ a.3.1.1 (-) Cytochrome c552 {Nitrosomonas europaea}

DADLAKKNNCIACHQVETKVVGPAKLDIAAKYADKDDAATYLAGKIKGGSSGVWGQIPMPPNVNSDADAKA
LADWILTLK

>d1e29a_ a.3.1.1 (A:) Photosystem II associated cytochrome c549 {Synechocystis sp., pcc 6803}

VELTESTRTIPLDEAGGTTLTARQFTNGQKIFVDTCTQCHLQGKTNTNNVSLGLADLAGAEPRRDNVLALVEF
LKNPKSYDGEDDYSELHPNISRDPDIYPEMRNYTEDDIFDVAGYTLIAPKLDERWGGTIYF

>d1f1ca_ a.3.1.1 (A:) Photosystem II associated cytochrome c549 {Arthrosphaera maxima}

LTEELRTFPINAQGDTAVSLKEIKKGQQVFNAACAOCHALGVTRTNPDVNLSPEALALATPPRDNIAALVDYIK
NPTTYDGFVEISELHPSLKSSDIFPKMRNISEDDLYNVAGYILLQPKVRGEQWG

>d1ycc_ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}

TEFKAGSAKKGATLFKTRCLQCHTVEKGGPHKVGPNLHGIFGRHSGQAEGYSYTDANIKKNVLWDENNMSSEYL
TNPKKYIPGTKMAFGLKEKDRNDLITYLKKACE

>d1yeb_ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}

TEFKAGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTDANINKVWDEDMSMSEYL
TNPKKYIPGTKMAFGLKEKDRNDLITYLKKACE

>d1yc_ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}

AKESTGFPGSAKKGATLFKTRCQQCHTIEEGGPNKVGPNLHGIFGRHSGQVKGYSYTDAIINKVWDEDMSM
SEYLTNPKKYIPGTKMAFAGLKKEKDRNDLITYMTKAAK

>d1wejf_ a.3.1.1 (F:) Mitochondrial cytochrome c {Horse (Equus caballus)}

GDVEKGKKIFVQKCAQCHTVEKGGKHKTGPNLHGLFGRKTGQAPGFTYTDANKNGITWKEETLMEYLENPK
KYIPGTKMIFAGIKKKTEREDLIAYLKKATNE

>d1ccr_ a.3.1.1 (-) Mitochondrial cytochrome c {Rice embryos (Oryza sativa)}

ASFSEAPPGNPKAGEKIFKTKCAQCHTVDKGAGHKQGPNLNGLFGRQSGTTPGYSYSTADKNMAVIWEENTLY
DYLLNPKKYIPGTKMVFPGLKKPQERADLISYLKEATS

>d5cytr_ a.3.1.1 (R:) Mitochondrial cytochrome c {Tuna (Thunnus alalunga and Thunnus thynnus)}

GDVAKGKKTFVQKCAQCHTVEENGGKHKVGPNLWGLFGRKTGQAEGRSYTDANKSGIVWNNDLMEYLEN
PKKYIPGTKMIFAGIKKKGERQDLVAYLKSATS

>d1qn2a_ a.3.1.1 (A:) Cytochrome ch {Methylobacterium extorquens}

EGDAAAGEKAFAPCKACHNFEKNGVGPTLKGVVGAKEGEGADGYAFSDALKSGLTWDQADLKQWLADPKK
KVPGTKMVFPGISDPKKVDDIIAYLKT

>d3c2c_ a.3.1.1 (-) Cytochrome c2 {Rhodospirillum rubrum}

EGDAAAGEKVSKKCLACHTFDQGGANKVGPNLFGVFENTAAHKDNYAYSESYTEMKAKGLTWTEANLAAYVK
NPKAFLVLEKSGDPKAKSKMTFKLTDDEIENVIAYLKT

>d1c2ra_ a.3.1.1 (A:) Cytochrome c2 {Rhodobacter capsulatus}

GDAAKGEKEFNKCKTCHSIIAPDGTEIVKGAKTGPNIYGVVGRTAGTYPEFKYKDSIVALGASGFAWTEEDIATYV
KDPGAFLKEKLDDKKAKTGMAFKLAKGGEDVAAYLASVVK

>d1cxc_ a.3.1.1 (-) Cytochrome c2 {Rhodobacter sphaeroides}

QEGDPEAGAKAFNQCQTCHIVDDSGTTIAGRRNAKTPNLYGVVGRTAGTQADFKGYGEGMKEAGAKGLAW
DEEHFVQYVQDPTKFLKEYTGDAAKGKMTFKLKEADAHNIWAYLQQVAVRP

>d1co6a_ a.3.1.1 (A:) Cytochrome c2 {Rhodopseudomonas viridis}

QDAASGEQVFQCLVCHSIGPGAKNKVGPNLNGLFGRHSGTIEGFAYSDANKNSGITWTEEVFREYIRDPKAKI
PGTKMIFAGVKDEQKVSQDIIAYIKQFNADGSKK

>d1i8oa_ a.3.1.1 (A:) Cytochrome c2 {Rhodopseudomonas palustris}

EDAKAGEAVFKQCMTCRADCNMVGPALAGVVGRKAGTAAGFTYSPLNHNSGEAGLVWTADNIVPYLADPN
AFLKKFLTEKGKADQAVGVTKMTFKLANEQQRKDVVAYLATLK

>d1hrao_ a.3.1.1 (A:) Cytochrome c2 {Rhodopila globiformis}

SAPPGDPVEGKHLFTICITCTDIKGANKVGPSLYGVVGRHSGIEPGYNSEANIKGIVWTPDVLKYIEHPQK
IVPGTGMGYPGQPPDPQKRADIAYLETLK

>d155c__ a.3.1.1 (-) Cytochrome c2 {Paracoccus denitrificans}
NEGDAAKGEKEFNKCKACHMIQAPDGTDIKGGKTGPNLYGVVGRKIASEEGFKYGEGILEVAEKNPDLTWTEA
NLIEYVTDPKPVLVKMTDDKGAKTKMTFKMGKNQADVVAFLAQDDPDAXXXXXXXXXXXXX
>d1cot__ a.3.1.1 (-) Cytochrome c2 {Paracoccus denitrificans}
DGDAAKGEKEFNKCKACHMIQAPDGTDIIGGGKTGPNLYGVVGRKIASEEGFKYGEGILEVAEKNPDLTWTEAD
LIEYVTDPKPVLVKMTDDKGAKTKMTFKMGKNQADVVAFLAQNSPDA
>d1jvla_a.3.1.1 (A:) Cytochrome c2 {Rhodospirillum centenum}
GDPAKGEAVFKKCMACHRVGPDAKNLVGPALTVIDRQAGTAPGFNSAINHAAGEAGLHWTPENIIAYLPDP
NAFLRKFLADAGHAEQAKGSTKMVFKLPEQERKDVVAYLKQFSP
>d1cc5__ a.3.1.1 (-) Cytochrome c5 {Azotobacter vinelandii}
GGGARSGDDVVAKYCNACHGTGLLNAPVGDSAAWKTRADAKGGLDGLLAQSLSGLNAMPPKGTCADCSD
DELKAAIGKMSGL
>d1kx2a_a.3.1.1 (A:) Mono-heme c-type cytochrome ScyA {Shewanella putrefaciens}
ADLQDAEAIYNKACTVCHSMGVAGAPKSHNTADWEPRLAGVDNLVKSVKTGLNAMPPGMCTDCTDEDY
KAAIEFMSKAK
>d1cch__ a.3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}
QDGEALFKSKPCAACHSVDTKMGVPALKEVAAKNAGVEGAADTLALHIKNGSQGVWGPPIPMPNNPVTEEEA
KILAEWWVLSK
>d1cor__ a.3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}
EDGEALFKSKPCAACHSIDAKLVGPFAKEVAAKYAGQDGAAADLLAGHIKNGSQGVWGPPIPMPNNPVTEEEAKI
LAEWILSQK
>d1dvva_a.3.1.1 (A:) Cytochrome c551 {Pseudomonas aeruginosa}
EDPEVLAKNKGCMACHAIDTKMVGPAYKDVAAKYAGQAGAEAYLAQRIKNGSQGVWGPPIPMPNNAVSDDE
AQTLAKWILSQK
>d451c__ a.3.1.1 (-) Cytochrome c551 {Pseudomonas aeruginosa}
EDPEVLFKNKGCVACHAIDTKMVGPAYKDVAAKFAGQAGAEELAQRIKNGSQGVWGPPIPMPNNAVSDDEA
QTLAKWVLSQK
>d2mtac_a.3.1.1 (C:) Cytochrome c551 {Paracoccus denitrificans}
APQFFNIIDGSPLNFDDAMEEGRDTEAVKHLETGENVYNEDPEILPEAEELYAGMCSCGHGHYAEKGKIGPGLN
DAYWTYPNETDVGLFSTLYGGATGQMGPWMGSRTLDEMRLRTMAWVRHLYTGDPKDASWLTDEQKAGFTP
FQP
>d1gks__ a.3.1.1 (-) Cytochrome c551 {Ectothiorhodospira halophila}
DGESIYINGTAPTCSSCHDRGVAGAPELNAPEDWADRPSSVDELVESTLAGKGAMPAYDGRADREDLVKAIEY
MLSTL
>d05c1__ a.3.1.1 (-) Cytochrome c555 {Chlorobium thiosulfatophilum}
YDAAAGKATYDASCAMCHKTGMMGAPKVGDKAAWAPHIAKGGMNVMVANSIKGYKGTKGMPAKGGNPK
LTDAQVGNAVAYMVGQSK
>d1dw0a_a.3.1.1 (A:) SHP, an oxygen binding cytochrome c {Rhodobacter sphaeroides}
GDTSPAQLIAGYEAAAGAPADAERGRALFLSTQTGGKPDTPSCTTCHGADVTRAGQTRGKEIAPLAPSATPDR
FTDSARVEKWLGRNCNSVIGRDCTPGEKADLLAWLAAQ
>d1e8ea_a.3.1.1 (A:) Cytochrome c" {Methylophilus methylotrophus, strain w3a1}
DVTNAEKLVKYTNIAHSANPMYEAPSITDGKIFFNRKFKTPSGKEAACASCHTNNPANVGKNIVTGKEIPPLAP
RVNTKRFTDIDKVEDEFTHCNDILGADCSPSEKANFIAYLLTETKPTK
>d1diqc__ a.3.1.1 (C:) p-Cresol methylhydroxylase, cytochrome c subunit

{Pseudomonas putida}

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

LAQQDVAAPGAPEGVSALSDAQYNEANKIYFERCAGCHGVLKGATGKALTPDLTRDLGFDYLQSFITYGSPAG
MPNWGTSGELSAEQVDLMANYLLDPAPP

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

APEGVSALSDAQYNEANKIYFERCAGCHGVLKGATGKALTPDLTRDLGFDYLQSFITYGSPAGMPNWGTSGEL
SAEQVDLMANYLLDPAA

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

HKTRTDNRYEPSLDNLQAQQDVAAPGAPEGVSALSDAQYNEANKIYFERCAGCHGVLKGATGKALTPDLTRDL
GFDYLQSFITYGSPAGMPNWGTSGELSAEQVDLMANYLLDPAA

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

VRTNGAPDMSEEFNEAKQIYFQRCAGCHGVLKGATGKPLPDITQQRGQQYLEALITYGTPLGMPNWGS
GELSKEQITLMAKYIQHTPPQPP

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

AAEQYQGAASAVDPAHVVRTNGAPDMSEEFNEAKQIYFQRCAGCHGVLKGATGKPLPDITQQRGQQYLE
ALITYGTPLGMPNWGSSEGELSKEQITLMAKYIQHTPPQPP

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

YEPSLDNLQAQQDVAAPGAPEGVTALSDAQYNEANKIYFERCAGCHGVLKGATGKALTPDLTRDLGFDYLQSFIT
YASPAGMPNWGTSGELSAEQVDLMANYLLDPAPP

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

DPAAALEDHKTRTDNRYEPSLDNLQAQQDVAAPGAPEGVTALSDAQYNEANKIYFERCAGCHGVLKGATGKAL
TPDLTRDLGFDYLQSFITYASPAGMPNWGTSGELSAEQVDLMANYLLDPAPP

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

TGQLLQGVKYDPAKVEAGTMLYVANCVFCHGVPVGDRGGNIPNLGYMDASYIENLPNFVKGPAMVRGMPD
FTGKLSGDDVESLKAIFIQGTADAIRP

>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)}

SDLELHPPSYPWSHRGPLSSLSDHTSIRRGFQVYKQVCSSCHSMMDYVAYRHLVGVCYTEDEAKALAEEVEVQDGP
NEDGEMFMRRPGKLSDYFPKPYPNPEAARAANNGALPPDLSYIVRARHGGEDYVFSLLTGYCEPPTGVSVREGLY
FNPYFPGQAIQMAPPIYNDVLEFDDGTPATMSQVAKDVCTFLRWAAE

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

MTAAEHGLHAPAYAWSHNGPFETFDHASIRRGYQVYREVCAACHSLDRVWRTLGVGSHTNEEVRNMAEEF
EYDDEPDEQGNPKKRPGKLSDYIPGPYPNEQAARAANQGALPPDLSLIVKARHGGCDYIFSLLTGYPDEPPAGV
ALPPGSNYNPYFPGGSIAMARVLFFDMVEYEDGTPATTSQLMAKVDTTFLNWCAE

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

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

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

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

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

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

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

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

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

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

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

EQGPSLLQNKCMBGCHIPEGNDTYSRISHQRKTPEGWLMSIARMQVMHGLQISDDDRRTLVKYLADKQGLAPS
ETDGVRVYAMERR

>d1jmx2 a.3.1.7 (A:86-162) Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
{*Pseudomonas putida*}

LNTVEQFDTQLSETGRCHSGARVALQRRPAKEWEHLVNFHLGQWPSLEYQAQARDRWLPIALQQVVPDL
AKRYPL

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

RPRTAFSSEQLARLKREFNENRYLTERRRQQQLSSELGLNEAQIKIWFQNKRKAI

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

RTAFSSEQLARLKREFNENRYLTERRRQQQLSSELGLNEAQIKIWFKNKRKAKIKKS

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

ISPQARAFLEEVFRRKQSLNSKEKEEVAKKCGITPLQVRVWFINKRMRS

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

KKEKSPKGKSSISPQARAFLEQVFRRKQSLNSKEKEEVAKKCGITPLQVRVWFINKRMRSK

>d1akhb_ a.4.1.1 (B:) mat alpha2 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}

TKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTLSRIQIKNWVSNRRRKEKTITIAPELADLLSGE
PL

>d1aplc_ a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}

YRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTLSRIQIKNWVSNRRRKEKT

>d1mnmc_ a.4.1.1 (C:) mat alpha2 Homeodomain {Baker's yeast (Saccharomyces cerevisiae)}

GLVFNVVTQDMINKSTKPYRGHRFTKENVRILESWFAKNIENPYLDTKGLENLMKNTLSRIQIKNWVSNRRRKEKT

>d1lfb_ a.4.1.1 (-) Transcription factor LFB1 {Rat (*Rattus rattus*)}

RFKWPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGSNLVTEVRVYNWFANRRKEE
AFRHK

>d2lfb_ a.4.1.1 (-) Transcription factor LFB1 {Rat (*Rattus rattus*)}

MARIDPTKKGRNRNRFKWPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGSNLVTEV
RVYNWFANRRKEEAFRHKLAMDTYKLN

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

KRTSIETNIRVALEKSFMENQKPTSEITLIAEQLNMEKEVIRVWFSNRRQKEKRIN

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

RKKRTSIETNIRVALEKSFLENQKPTSEEITMIADQLNMEKEVIRVWFSNRRQKEKRIN

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

KRRTTISIAAKDALERHFGEHSKPSSQEIMRMAEELNLEKEVVRVWFNCNRQREKRVK

>d1ftt_ a.4.1.1 (-) Thyroid transcription factor 1 homeodomain {Rat (*Rattus norvegicus*)}

MRRKRRVLFSQAQVYELERRFKQQKYLSAPEREHLASMIHLPTQVKIWFQNHRYKMKRQAKDKAQQ

>d1hdp_ a.4.1.1 (-) Oct-2 POU Homeodomain {Human (*Homo sapiens*)}

RRKKRTSIETNVRALEKSFLANQKPTSEEILLIAEQLHMEKEVIRVWFNCNRQKEKRINPCS

>d1ocp_ a.4.1.1 (-) Oct-3 POU Homeodomain {Mouse (*Mus musculus*)}

METLVQARKRKRTSIENRVRWSLETMFLKCPKPSLQQITHIANQLGLEKDVVRVFCNRRQKGKRSS
>d1b72a_a.4.1.1 (A:) Homeobox protein hox-b1 {Human (Homo sapiens)}
ARTFDWMVKRNPPAKTAKVSEPLGSPSGLRTNFTTRQLTEKEFHFNKYLSRARVEIAATLELNETQVKIWF
QNRRMKQKKRERE
>d1b72b_a.4.1.1 (B:) pbx1 {Human (Homo sapiens)}
RKRRNFNKQATEILNEYFYSHLSNPYPSEEAKELAKKCGITVSQVSNWFGNKRIRYKKNIGKFQEEANIYAA
>d1du6a_a.4.1.1 (A:) pbx1 {Mouse (Mus musculus)}
SSGHIEGRHMNKQATEILNEYFYSHLSNPYPSEEAKELAKKCGITVSQVSNWFGNKRIRYKKN
>d1bw5_a.4.1.1 (-) Insulin gene enhancer protein isl-1 {Rat (Rattus norvegicus)}
MKTTRVRTVLNEKQLHTLRTCYAANPRPDALMKEQLVEMTGLSPRVIRVWFQNKRCDDKRSIMMK
>d1ig7a_a.4.1.1 (A:) Msx-1 homeodomain {Mouse (Mus musculus)}
RKPRTPFTTAQLLALERKFRQKQYLSIAERAESLAFSSSLTETQVKIWFQNRRAKAKRL
>d1ahdp_a.4.1.1 (P:) Antennapedia Homeodomain {Drosophila melanogaster}
MRKRGRQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRRMKWKKENTKGEPG
>d1san_a.4.1.1 (-) Antennapedia Homeodomain {Drosophila melanogaster}
MTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRRMKWKKENTKGEPG
>d9anta_a.4.1.1 (A:) Antennapedia Homeodomain {Drosophila melanogaster}
RQTYTRYQTLELEKEFHFNRYLTRRRRIEIAHALSLTERQIKIWFQNRRMKWKKEN
>d1b8ia_a.4.1.1 (A:) Ultrabithorax (ubx) homeodomain {Drosophila melanogaster}
FYPWMAIAGTNGLRRGRQTYTRYQTLELEKEFHTNHYLTRRRRIEHALSLTERQIKIWFQNRRMKLKKEI
>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)}
MDSKTRQTYTRYQTLELEKEFHFNRYITRRRIDIANALSLSERQIKIWFQNRRMKSKDRTLDSSPEH
>d1nk3p_a.4.1.1 (P:) VND/NK-2 protein {Fruit fly (Drosophila melanogaster)}
KKRKRRLFTKAQTYELEERRFRQQRYLSAPEREHLASLIRLPTQVKIWFQNHRYKTKRAQNE
>d1vnd_a.4.1.1 (-) VND/NK-2 protein {Fruit fly (Drosophila melanogaster)}
ASDGLPNKKRKRRVLFTAQTYELEERRFRQQRYLSAPEREHLASLIRLPTQVKIWFQNHRYKTKRAQNEKGYEG
HP
>d1fjla_a.4.1.1 (A:) Paired protein {Fruit fly (Drosophila melanogaster)}
KQRRSRTTFASQLDELERAFERTQYPDIYTREELAQRTNLTEARIQVWFQNRRARLRKQHTSVS
>d1fjlba.4.1.1 (B:) Paired protein {Fruit fly (Drosophila melanogaster)}
QRRSRTTFASQLDELERAFERTQYPDIYTREELAQRTNLTEARIQVWFQNRRARLRK
>d1hcra_a.4.1.2 (A:) HIN recombinase (DNA-binding domain) {Synthetic}
GRPRAINKHEQEIQISRLLEKGHPRQQLAIIFGIGVSTLYRYFPASSIKKRMN
>d1ijwc_a.4.1.2 (C:) HIN recombinase (DNA-binding domain) {Synthetic}
GRPRAINKHEQEIQISRLLEKGHPRQQLAIIFGIGVSTLYRYFPASSI
>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}
PRGSALSDTERAQLDMVKLLNVSLHEMSRKISRSRHCIRVYLKDPVSYGTS
>d2ezl_a.4.1.2 (-) Ibeta subdomain of the mu end DNA-binding domain of phage mu transposase

{Bacteriophage mu}

MIARPTLEAHDYDREALWSKWDNASDSQRRLAEKWLPAVQADEMLNQGISTKTAFATVAGHYQVSASTLRD
KYYQVQKFAKPDWAAALVDGRGASRRN

>d2ezh__ a.4.1.2 (-) Transposase {Bacteriophage mu}

SEFDDEDAWQFLIADYLPEKPAFRKCYERLEAAREHGWSIPSRTAFRRIQLDEAMVVACREG

>d2ezi__ a.4.1.2 (-) Transposase {Bacteriophage mu}

MNVHKSEFDEDAWQFLIADYLPEKPAFRKCYERLEAAREHGWSIPSRTAFRRIQLDEAMVVACREG
EHA
LM

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

GKTRWTREEDEKLKKLVEQNGTDDWKVIANYLPNRTDVQCQHRWQKVLPN

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

ELIKGPWTKEEDQRVILVKYGPKRWSVIAKHLKGRIGKQCRERWHNHNLNPEVK

>d1idz__ a.4.1.3 (-) c-Myb, DNA-binding domain {Mouse (Mus musculus)}

MEVKKTSWTEEDRILYQAHKRLGNRWAEIAKLLPGRTDNAIKNHWNSTMRRKV

>d1a5j_1 a.4.1.3 (1-55) b-Myb DNA binding domain {Chicken (Gallus gallus)}

GIPDLVKGPWTKEEDQKVIELVKYGTQWTЛИAKHLKGRIGKQCRERWHNHLPN

>d1a5j_2 a.4.1.3 (56-110) b-Myb DNA binding domain {Chicken (Gallus gallus)}

EVKKSSWTEEDRIIFEAKVLGNRWAEIAKLLPGRTDNAVKNHWNSTIKRKVDT

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

NPELNKGPWTKEEDQRVIEHVQKYGPKRWSDIAKHLKGRIGKQCRERWHNHNLNPEVK

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

KTSWTEEDRIIYQAHKRLGNRWAEIAKLLPGRTDNAVKNHWNSTMRR

>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)}

RKRQAWLWEEDKNLRSRVRKYGEGNWSKILLHYKFNNRTSVMLKDRWRTMKKL

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

GVNQLGGVFVNNGRPLPDVVRQRIVELAHQGVRPCDISRQLRVSHGCVSKILGRYYETGSIKPG

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

VIGGSKPKVATPKVVEKIAEYKRQNPTMFAWEIRDRLAERVCDNDTVPSVSSINRIIRTK

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

SHSGVNQLGGVFVNNGRPLPDSTRQRIVELAHSGARPCDISRILQVSNGCVSKILGRYYATGSIRPRAI

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

GGSKPRVATPEVVKIAQYKQECPSIFAWEIRDRLSEGVCCTNDNIPSVSSINRVLNLASEKQQ

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

QGRVNQLGGVFINGRPLPNNIRLKIVEMAADGIRPCVISRQLRVSHGCVSKILNRYQETGSIRPGVIGGSKPRIAT

PEIENRIEEYKRSSPGMFSWEIREKLIREGVCDRSTAPSVAISRLV

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

KASFTDEEDEFILDVVRKNPTRRTHTLYDEISHYVPNHTGNSIRHRFRVYLSKRLEYVYEVDFGKLVRDDDGNL
IKTKVLPPSI

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

KRKFSADEDYTLAIAVKKQFYRDLFQIDPDTGRSLITDEDPTAIARRNMTMDPNHVGSEPNFAAYRTQSRRG
PIAREFFKHFAEEHAAHTENAWRDRFRKFLLAYGIDDYISYYAEKAQNREPEPMKNLTNPKRPGVPTPGNYNS
S
>d1bw6a_ a.4.1.7 (A:) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASE
>d1hlva1 a.4.1.7 (A:1-66) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}
MGPKRRQLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVASTCR
>d1hlva2 a.4.1.7 (A:67-131) DNA-binding domain of centromere binding protein B (CENP-B) {Human (Homo sapiens)}
TKTNKLSPYDKLEGLIAWFQQIRAAGLPVKGIILKEKALRIAELGMDDFTASNGWLDRFRRRS
>d1g2ha_ a.4.1.10 (A:) Transcriptional regulator TyrR, C-terminal domain {Haemophilus influenzae}
SAVISLDEFENKTLDIIGFYEAQVLKLFYAEYPSTRKLAQRLGVSHATAIANKLKQYGIGK
>d1bl0a1 a.4.1.8 (A:9-62) MarA {Escherichia coli}
DAITIHSILDWIEDNLESPLSLEKVSERSGYSKWHLQRMFKETGHSLGQYIRS
>d1bl0a2 a.4.1.8 (A:63-124) MarA {Escherichia coli}
RKMTEIAQKLKESNEPILYLAERYGFESQQTLTRFKNYFDVPPHKYRMTNMQGESRFLHPL
>d1d5ya1 a.4.1.8 (A:3-56) Rob transcription factor, N-terminal domain {Escherichia coli}
QAGIIIRDLLIWLEGHLDQPLSLDNVAAKAGYSKWHLQRMFKDVTGHAIGAYIRA
>d1d5ya2 a.4.1.8 (A:57-121) Rob transcription factor, N-terminal domain {Escherichia coli}
RRLSKSAVALRLTARPILDIALQYRFDSQQFTRAFKKQFAQTPALYRRSPEWSAFGIRPPLRLG
>d1a6i_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}
SRLDKSKVINSALLELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAVEILARHHDYS
>d2tct_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}
ARLNRESVIDAALELLNETGIDLTTTRKLAQKLGIEQPTLYWHVKNKRALLDALAVEILARHHDYS
>d1jt6a1 a.4.1.9 (A:2-72) Multidrug binding protein QacR {Staphylococcus aureus}
NLKDKILGVAKEFIKNGYNATTGEIVKLSESSKGNLYYHFKTKENLFLEILNIEESKWQEYWKEQIKA
>d1sfe_1 a.4.2.1 (93-176) Ada DNA repair protein {Escherichia coli}
GTAFQQQVWQALRTIPCGETVSYQQLANAIGKPKAVRAVASACAANKLAIVIPCHRVRGDGSLSGYRWGVSK
RKAQLLRREAEN
>d1qnta1 a.4.2.1 (A:92-176) O6-alkylguanine-DNA alkyltransferase {Human (Homo sapiens)}
ESFTRQVLWKLLKVVKFGEVISYQQLAALAGNPKAARAVGGAMRGNPVPILIPCHRVCSSGAVGNYSGLAV
KEWLLAHEGHRL
>d1mgta1 a.4.2.1 (A:89-169) O6-alkylguanine-DNA alkyltransferase {Archaeon Pyrococcus kodakaraensis}
VTPFEKKVYEWLTKNVKRGSVITYGDLAKALNTSPRAVGGAMKRNPYPIVVPCHRVAHDGIGYYSSGIEEKFL
LEIEGV
>d1c20a_ a.4.3.1 (A:) DNA-binding domain from the dead ringer protein {Fruit fly (Drosophila melanogaster)}
GWSFEEQFKQVRQLYEINDDPKRKEFLDDLFSFMQKRGTPINRLPIMAKSVLDLYELYNLVIARGGLVDVINKKL
WQEIIKGLHLPSITSAAFLRTQYMKYLYPYCECEKKNLSTPAELQAAIDGNR
>d1ig6a_ a.4.3.2 (A:) MRF-2 DNA-binding domain {Human (Homo sapiens)}

RADEQAFLVALYKYMKERKPIERIPYLGFQINLWTMFQAAQKLGGYETITARRQWKHIYDELGGNPGSTSAA
TCTRRHYERLILPYERFIKGEEDKPLPIKPRK

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

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

>d1aoy__ a.4.5.3 (-) Arginine repressor (ArgR), N-terminal DNA-binding domain
{Escherichia coli}

MRSSAKQEELVKAFKALLKEEKFSSQGEIVAALQEQQFDNINQSFKSRMLTKFGAVRTRNAKMEMVYCLPAEL
GVPTT

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

GQRHIKIREIIMSNDIETQDELVDRRLREAGFNVTQATVSRSRDIKEMQLVKVPMANGRYKYSLPSDQRFNPLQKLKR
R

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

KGQRHIKIREIITSNEIETQDELVDMLKQDGKVTKVATVSRDIKELHLVKVPTNNGSYKYSLPADQRFNPLSKLKR

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

DVTGRIAQTLLNLAKQPDAMTHPDGMQIKITRQEIGQIVGCSRETVGRIILKMLEDQNLISAHGKTIVVYGT

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

DIKQRIAGFFIDHANTTGRQTQGGVIVSVDFTEEEIANLIGSSRQTTSTALNSLIKEGYISRQGRGHYTIPNLVRLK
AAA

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

IDERDKIILEKLDARTPFTEIAKKLGISETAVRKRVKAEEKGIIEGYTIKINPKKLG

>d1smta_ a.4.5.5 (A:) SmtB repressor {Cyanobacteria (Synechococcus), pcc7942}

ELQAIAPEVAQSLAEFFAVLADPNRLRLSLLARSELCVGDLAQAIQVSESAVSHQLRSLRNRLVSYRKQGRHVY
YQLQDHHVIVALYQNALDHLQEC

>d1jgsa_ a.4.5.28 (A:) Multiple antibiotic resistance repressor, MarR {Escherichia coli}

LFNEIIPLGRLIHMVNQKKDRLLNEYLSPLDITAAQFKVLCSIRCAACITPVELKKVLSVDLALTRMLDRLVCKGW
VERLPNPNDKRGVLVKKLTGGAAICEQCHQLVGQDLHQELTKNLTADDEVATLEYLLKKVLP

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

MSKINDINDLVNATFQVKFFRDTKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPYYLTKALQKLKDLKLLS
KKRSLQDERTVIVYVTDTQKANIQKLISELEEYIKN

>d1fzpb_ a.4.5.28 (B:) Pleiotropic regulator of virulence genes, SarA {Staphylococcus aureus}

AITKINDCFELLSMVTYADKLKSLIKKEFSISFEFAVLTYISENKEKEYYLKDIINHLNYKQPQVVKAVKILSQEDYFD
KKRNEHDERTVLILVNAQQRKKIESLLSRVNKRIT

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

AQSPAGFAEEYIIESIWNNRFPPGTILPAERELSELIGVTRTTLREVLQRLARDGWLTIQHGKPTKVNNFWETS

>d1bm9a_ a.4.5.7 (A:) Replication terminator protein (RTP) {Bacillus subtilis}

EEKRSSTGFLVKQRAFLKLYMITMTEQERLYGLKLEVRSEFKEIGFKPNHTEVYRSLHELLDDGILKQIKVKKEGA

KLQEVVLYQFKDYAAKLYKKQLKVELDRCKKIEKALSDNF
>d1b9ma1 a.4.5.8 (A:-1-126) N-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}
HMQAEILLTLKLQQKLFADPRTISLLKHIALSGSISQGAKDAGISYKSAWDAINEMNQLSEHILVERATGGKG
GAVLTRYGQRQLIQYDLLAQIQQKAFCVDLSDDDALPLNSLLAISRFSLQTS
>d1bjaa_a.4.5.9 (A:) Transcription factor MotA, activation domain {Bacteriophage T4}
SKVTYIJKASNDVLNEKTATILITIAKKDFITAAEVREVHPDLGNNAVNSNIGVLIKGLVEKSGDGLIITGEAQDIIS
AATLYAQENAPELLK
>d1repc1 a.4.5.10 (C:15-143) RepE54 {Escherichia coli, mini-F plasmid}
SPRIVQSNDLTEAAYSLRDQKRMLYLFVDQIRKSDGTLQEHDGICEIHVAKYAEIFGLTSAEASKDIRQALKSFAG
KEVVFYRPEEDAGDEKGYESFPWFIKPAHSPSRGLYSVHINPYLIPFFIGLQ
>d1repc2 a.4.5.10 (C:144-246) RepE54 {Escherichia coli, mini-F plasmid}
NRFTQFRLSETKEITNPYAMRLYESLCQYRKPDGSGIVSLKIDWIIERYQLPQSYQRMPDFRRFLQVCVNEINSR
TPMRLSYIEKKKGRQTTHIVFSFRDIT
>d1hqca1 a.4.5.11 (A:243-318) Holliday junction helicase RuvB {Thermus thermophilus}
LGLEKRDREILEVLILRGFGGPVGLATLATALEDPGTLEEVHEPYLIRQGLLKRTPRGRVPTELAYRHLGYPPPV
>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}
ISEEVLIGLPLHEKLFLAIVRSLKISHTPYITFGDAEESYKIVCEEYGERPRVHSQQLWSYLNDLREKGIVTRQNKR
EGVRGRRTTLISIGTEPLDTLEAVITKLIKEELR
>d1foka3 a.4.5.12 (A:287-386) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
VPKRVVYWEMLATNLTDKEYVRTRRALILELIKAGSLKIEQIQDNLKLGFDVIETIENDIKGLINTGIFIEIKGRFYQ
LKDHLQVIPNRGVTKQLV
>d2foka1 a.4.5.12 (A:5-143) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
IRTFGWVQNPDKFENLKRVVQVFDRNSKVHNEVKNIKIPTLVKESKIQKELVAIMNQHDLIYTKEVGTGTSIRS
EAPCDAIQATIADQGNKKGYIDNWSSDGFLRWAHALGFIEYINKSDSFVITDVGLAGSKSAD
>d2foka2 a.4.5.12 (A:144-286) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
GSAIEKEILIEAISSYPPAIRLTLLEDGQHLTKFDLGKNLGFSGESGFTSLPEGILLDTANAMPDKGEIRNNWEG
SSDKYARMIGGWLDKLGVLQKGKKEFIPTLGKPDNKEFISHAFKITGEGLKVLRRAKGSTKFR
>d2foka3 a.4.5.12 (A:287-386) Restriction endonuclease FokI, N-terminal (recognition) domain {Flavobacterium okeanokoites}
VPKRVVYWEMLATNLTDKEYVRTRRALILELIKAGSLKIEQIQDNLKLGFDVIETIENDIKGLINTGIFIEIKGRFYQ
LKDHLQVIPNRGKPDLV
>d1f1za1 a.4.5.27 (A:169-267) TnsA endonuclease, C-terminal domain {Escherichia coli}
NPVVKENIEWLYSVKTEEVSAELLAQLSPLAHILQEKGDENIINVCKQVDIAYDLELGKTLSEIRALTANGFIKFNIY
KSFRANKCADLCISQVNMEE
>d1fp1d1 a.4.5.29 (D:19-128) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}
QTEDSACLSAMVLTTLVYPAVLNAAIDLNLFEIIAKATPPGAFMSPSEIASKL PASTQHSDLPNRLDRMLRLLAS
YSVLTSTTRTIEDGGAERVYGLSMVGKYLPDES

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

RKPSEIFKAQALLYKHIYAFIDSMSLKAVEMNIPNIIQNHGKPISLNLVSILQPSSKIGNVRRLMRYLAHNGFF
EIITKEEESYALTVASELLVRGSD

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

SHPTYSEMAIAIRAEKSRRGGSSRQSIQKYIKSHYKVGHNAQLQKLSIRRLAAGVLQTKGTGASGSFRLAK

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

MAGPSVTELITKAVSASKERKGSLAALKALAAGGYDVEKNNRSRIKGLKSLVSKGTLVQTKGTGASGSFRLSK

>d1e17a_a.4.5.14 (A:) Afx (Foxo4) {Human (Homo sapiens)}

SRRNAWGNQSYAELISQAIESAPEKRILTALQIYEWVMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKVHN
EATGKSSWWMLNPEGG

>d1d5va_a.4.5.14 (A:) Adipocyte-transcription factor FREAC-11 (s12, fkh-14) {Human (Homo sapiens)}

MLVKPPYSYIALITMAIQNAPEKKITLNGIYQFIMDRFPFYRENKQGWQNSIRHNLSNECFVKVPRDDKKPGK
GSYWTLDPDSYNMFENGSL

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

VKPPYSYIALITMAILQSPQKKLTLGICEFISNRFPYYREKFPAWQNSIRHNLSNDCFVKIPREPGNPGKGNYW
TLDPQSEDMDNGSFLRRRK

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

YIALITMAIRDSAGGRRTLAEINEYLMGKFPFFRGSYTGWRNSVRHNLSNDCFVKVLRDPSRPWGKDNYWML
NP

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

RARADKQHVLDMLFSAFEKHQYYNLKDLVDITKQPVVYLKEILKEIGVQNVKGHKNTWELKPEYRHQ

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

GPLGSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKKTGLSEQTVNVLAQILKRLNPERKMINDKMHFSLKE

>d1dpua_a.4.5.16 (A:) C-terminal domain of RPA32 {Human (Homo sapiens)}

ANGLTVAQNQVNLNIKACPRPEGLNFQDLKNQLKHMSVSSIKQAVDFLSNEGHYISTVDDDFKSTD

>d1fsha_a.4.5.31 (A:) Segment polarity protein Dishevelled-1 {Mouse (Mus musculus)}

EAPLTVKSDMSAIVRVMQLPDSGLEIRDRLWLKITIANAVIGADVVDWLTHVEGFKERREARKYASSMLKHG
FLRHTVNKITFSEQCYYVFGD

>d1cf7a_a.4.5.17 (A:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}

SRHEKSLGLLTTKFVSLLQEAKDGVLSDLKLAADTLAVRQKRRYDITNVLEGIGLIEKKSKNSIQWK

>d1cf7b_a.4.5.17 (B:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}

GKGLRHFSMKVCEVKQRKGTTSYNEADELVSEFTNSNNHLAADSAYDQKNIRRKYDALNVLMAMNIISKEK
KEIKWIGLP

>d1d8ja_a.4.5.18 (A:) The central core domain of TFIIE beta {Human (Homo sapiens)}

ALSGSSGYKFGVLAKIVNYMKTRHQRGDTPLTLDEILDETQHLDIGLQKQWLMTEALVNNPKIEVIDGKYAF
KPKYNVR

>d1qbja_a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1 {Human (Homo sapiens)}

SIYQDQEQRILKFLEELGEGKATTAHDSLGLGTPKKEINRVLYSLAKKGKLQKEAGTPPLWKIA

>d1qgpa_a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1 {Human (Homo sapiens)}

LSSHFQELSIYQDQEQRILKFLEELGEGKATTAHDSLGLGTPKKEINRVLYSLAKKGKLQKEAGTPPLWKIAVSD

>d1j75a_a.4.5.19 (A:) Dlm-1 {Mouse (Mus musculus)}

NLEQKILQVLSDDGGPVKIGQLVKKCQVPKKTLNQVLYRLKKEDRVSSPEPATWSIG
>d1dp7p_a.4.5.20 (P:) MHC class II transcription factor RFX1 {Human (Homo sapiens)}
TVQWLLDNYETAEGVSLPRSTLYNHYLLHSSEQKLEPVNAASFGKLIRSVFMGLTRRLGTRGNSKYHYYGLRIKA
>d1flia_a.4.5.21 (A:) Fli-1 {Human (Homo sapiens)}
PGSGQIQLWQFLLELLSDSANASCITWEGTNFGEFKMTDPDEVARRWGERKSCKPNMNYDKLSRALRYYDKNI
MTKVHGKRYAYKFDFHGIAQALQPHP
>d1k78b_a.4.5.21 (B:) ETS-1 transcription factor, residues 331-440 {Mouse (Mus musculus)}
IQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNPKMNYEKLSRGLRYYDKNIIHKTAGK
RYVYRFVCDLQSLLGYTPEELHAMLDVK
>d2stta_a.4.5.21 (A:) ETS-1 transcription factor, residues 331-440 {Human (Homo sapiens)}
VIPAAALAGYTGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNPKMNYEKLSRG
LRYYDKNIIHKTAGKRYVYRFV
>d1puee_a.4.5.21 (E:) Transcription factor PU.1, residues 171-259 {Mouse (Mus musculus)}
KIRLYQFLDLLRSGDMKDSIWVVDKDKGTFQFSSKHKEALAHRWGIQKGNNRKMTYEKMARALRNYGKTGE
VKKVKKKLTYQFSGEV
>d1awca_a.4.5.21 (A:) GA binding protein (GABP) alpha {Mouse (Mus musculus)}
IQLWQFLLELLTDKDARDCISWVGDEGEFKLNQPELVAQKGQRKNKPTMNYEKLSRALRYYDGDMICKVQ
GKRFVYKFVCDLKTIGSAAELNRLVIECEQKKLARM
>d1bc8c_a.4.5.21 (C:) Serum responce factor accessory protein 1a, SAP-1 {Human (Homo sapiens)}
MDSAITLWQFLLQLLQKPQNKHMICWTSNDGQFKLQAEEVARLGIRKNKPNMNYDKLSRALRYYVKNII
KKVNGQKFVYKFVSYPEILNM
>d1hbwg_a.4.5.21 (G:) Serum responce factor accessory protein 1a, SAP-1 {Human (Homo sapiens)}
DSAITLEWQFLLQLLQKPQNKHMICWTSNDGQFKLQAEEVARLGIRKNKPNMNYDKLSRALRYYVKNIIKK
VNGQKFVYKFVSYPEILNMDPMVTGRIEGDCESLNFEVSSSKDVENGKDKPPQPGAKTSSRNDYIHSGLYS
SFTLNSLN
>d1duxc_a.4.5.21 (C:) Elk-1 {Human (Homo sapiens)}
VTLWQFLLQLLREQNGNGHIISWTSRDGGEFKLVDAEEVARLGIRKNKTNMNYDKLSRALRYYDKNIIRKVS
GQKFVYKFVSYPE
>d1hks_a.4.5.22 (-) Heat-shock transcription factor {Drosophila melanogaster}
GSGVPAFLAKLWRLVDDADTNRLICWTKGQSFVIQNQAQFAKEPLNKHNNMASFIRQLNMYGFHKITSI
DNGGLRFDRDEIEFSHPFFKRNSPFLLDQIKRK
>d1fbqa_a.4.5.22 (A:) Heat-shock transcription factor {Milk yeast (Kluyveromyces lactis)}
PAFVNKLWSMVNDKSNEKFIHWSTSGESIVVPNRRERFVQEVLKKYFKHSNFVRQLNMYGWHKVQDVKS
GSMLSNNDSRWEFENERH
>d2hts_a.4.5.22 (-) Heat-shock transcription factor {Milk yeast (Kluyveromyces lactis)}
ARPAFVNKLWSMVNDKSNEKFIHWSTSGESIVVPNRRERFVQEVLPKYFKHSNFVRQLNMYGWHKVQDV
KSGSNDSRWEFENERHA
>d1if1a_a.4.5.23 (A:) Interferon regulatory factor 1 (IRF-1) {Mouse (Mus musculus)}
RMRPWLEMQINSNQIPGLIWINKEEMIFQIPWKHAAKHGWDINKDACLFRSWAIHTGRYKAGEKEPDPKTW
KANFRCAMNSLPDIEEVKDQSRNKGSSAVRVYRM
>d2irfg_a.4.5.23 (G:) Interferon regulatory factor-2, IRF-2 {Mouse (Mus musculus)}
RMRMRPWLEEQINSNTIPGLKWLNEKKIFQIPWMHAARHGWDVEKDAPLFRNWAIHTGKHQPGIDKPD
KTWKANFRCAMNSLPDIEEVKDRSIKKGNNAFRVYRMLP

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

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

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

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

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

>d1tns_ a.4.5.26 (-) mu transposase, DNA-binding domain {Bacteriophage mu}
MELWVSPKELANLPGLPKTSAGVIYVAKKQGWQNTRAGVKGGKAIEYNANSLPVEAKAALLRQGEIETSLG
YFE

>d1opc_ a.4.6.1 (-) OmpR {Escherichia coli}
VIAFGKFKLNLGTREMFRDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNLLARGREYSAMERSIDVQISRLRR
MVEEDPAHPRYIQTWGLGYVFVPD

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

>d1qqia_ a.4.6.1 (A:) PhoB {Escherichia coli}
MAVEEVIEMQGLSLDPTSHRVMAGEEPELMPTEFKLLHFFMTHPERVYSREQLLNHVWGTNVYVEDRTVD
VHIRRLRKALEPGGHDRMVQTVRGTGYRFSTRF

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

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

>d1fc3a_ a.4.6.3 (A:) SpoOA {Bacillus stearothermophilus}
NKPKNLDASITSIIHEIGVPAHKGYLYLREAIAMVYHDIELLGSITKVLYPDIAKKYNTTASRVERAIRHAIEVAWSR
GNLESISSLFGYTVSVSKAKPTNSEFIAMVADKLRLRHKA

>d1fox_ a.4.7.1 (-) Ribosomal protein L11, C-terminal domain {Bacillus stearothermophilus}
MTFITKTPPAVLLKKAAGIESGSGEPNRNKVATIKRDKVREIAELKMPDLNAASIEAAMRMIEGTARSMGIVVE
D

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

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

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

PSRKAKVKATLGEFDLRDYRNVEVLKRLFSETGKILPRTTGLSGKEQRILAKTIKRARILGLLPTEKLVRK
>d1g1xc_a.4.8.1 (C:) Ribosomal protein S18 {Thermus thermophilus}
DLRDYRNVEVLKRLFSETGKILPRTTGLSGKEQRILAKTIKRARILGLLPFT
>d1i94r_a.4.8.1 (R:) Ribosomal protein S18 {Thermus thermophilus}
KPKKEAQRRPSRKAKVKATLGEFDLRDYRNVEVLKRLFSETGKILPRTTGLSGKEQRILAKTIKRARILGLLPTEK
LVRK
>d1e3ha1 a.4.9.1 (A:263-345) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 3 {Streptomyces antibioticus}
YQDDVLEALSAAVRPELSAAITAGKQDREAELDRVKALAAEKLPEFEGREKEISAAYRALTKSLVRERVIAEKKRI
DGRGV
>d1k6ya1 a.4.10.1 (A:1-46) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 1}
FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLK
>d1wjba_a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 1}
FLDGIDKAQEEHEKYHSNWRAMASDFNLPPVVAKEIVASCDKCQLKGEAMHGQVD
>d1e0ea_a.4.10.1 (A:) N-terminal Zn binding domain of HIV integrase {Human immunodeficiency virus type 2}
FLEKIEPAQEEHEKYHSNVKELSHKFGIPNLVARQIVNSCAQCQQK
>d1ef4a_a.4.11.1 (A:) RNA polymerase subunit RPB10 {Archaeon Methanobacterium thermoautotrophicum}
MIPVRCLSCGKPVSAFYNEYQRRVADGEDPKDVLDLGLKRYCCRRMLISHVETW
>d1i50j_a.4.11.1 (J:) RNA polymerase subunit RPB10 {Baker's yeast (Saccharomyces cerevisiae)}
MIVPVRCFSCGKVVGDKWESYLNLQEDELDEGTALSRLGLKRYCCRRMILTHVDLIEKFRLRNP
>d1cuk_1 a.5.1.1 (156-203) DNA helicase RuvA subunit, C-terminal domain {Escherichia coli}
TDDAEQEAVRLVALGYKPQEASRMVSKIARPDasSETLIREALRAAL
>d1bvsal a.5.1.1 (A:148-203) DNA helicase RuvA subunit, C-terminal domain {Mycobacterium leprae}
NAVRGSVVEALVGLGFAAKQAAEATDQVLGELGKDGAVALSSALRAALSLGKTR
>d1f4ia_a.5.2.1 (A:) C-terminal UBA domain of the hhr23a DNA repair protein {Human (Homo sapiens)}
QEKEAIERLKALGFEESLVIQAYFACEKNENLAANFLLSQNFDD
>d1efub3 a.5.2.2 (B:1-54) Elongation factor Ts (EF-Ts), N-terminal domain {Escherichia coli}
AEITASLVKELERTGAGMMDCKKALTEANGDIELAIENMRKSGAIKAACKAGN
>d1aipc1 a.5.2.2 (C:2-53) Elongation factor Ts (EF-Ts), N-terminal domain {Thermus thermophilus}
SQMELIKKLREATGAGMMDVKRALEDAGWDEEKAVQLLERGAMKAACKADR
>d1go5a_a.5.2.3 (A:) FG-binding, C-terminal domain of TAP {Human (Homo sapiens)}
PAPTPSSSPVPTLSPEQQEMLQAFSTQSGMNLEWSQKCLQDNNWDYTRSAQAFTHLKAKGEIPEVAFMK
>d1aua_1 a.5.3.1 (4-96) N-terminal domain of phosphatidylinositol transfer protein sec14p {Baker's yeast (Saccharomyces cerevisiae)}
QQEKEFLESYPQNCPDPDALPGTPGNLDSAQEKAELRKLEDAGFIERLDDSTLLRFLRARKFDVQLAKEMFEN
CEKWRKDYGTDILQDFH
>d1enwa_a.5.4.1 (A:) Elongation factor TFIIS domain 2 {Baker's yeast (Saccharomyces cerevisiae)}
GSHMPRNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESHEPPQSILHTAKAIESEMNKVNNDTNEAAYKARY

RIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
>d1fjgm_a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}
ARIAGVEIPRNKRVDALTYIYGIGKARAKEALEKTGINPATRVKDLTEAEVVRLEYVENTWKLEGELRAEVAANI
KRLMDIGCYRGLRHRRGLPVRGQRTRTNARTRKGPRKTVAGKKKAPRK
>d1i94m_a.5.5.1 (M:) Ribosomal protein S13 {Thermus thermophilus}
ARIAGVEIPRNKRVDALTYIYGIGKARAKEALEKTGINPATRVKDLTEAEVVRLEYVENTWKLEGELRAEVAANI
KRLMDIGCYRGLRHRR
>d1eija_a.5.6.1 (A:) Hypothetical protein MTH1615 {Archaeon Methanobacterium
thermoautotrophicum}
MRQQLEMQKKQIMMQILTPEARSRLANLRTRPDFVEQIELQLIQLAQMGGRVKRSKITDEQLKELLKRVAGKK
>d1jjcb1 a.6.1.1 (B:1-38,B:152-190) Domains B1 and B5 of PheRS-beta, PheT {Thermus
thermophilus (Thermus aquaticus)}
MRVPFSLWLKAYVPELESPEVLEERLAGLFETDRIERVXEEVVLLEVTPNRPDALGLLGLARDLHALGYALVEPE
AA
>d1jjcb2 a.6.1.1 (B:400-474) Domains B1 and B5 of PheRS-beta, PheT {Thermus thermophilus
(Thermus aquaticus)}
PPEAIPFRPEYANRLLGTSYPEAEQIAILKRLGCRVEGEGPTYRTPPSHRLDLRLEEDLVEEVARIQGYETIPL
>d1d4ua1 a.6.1.2 (A:37-111) DNA repair factor XPA DNA- and RPA-binding domain, C-terminal
subdomain {Human (Homo sapiens)}
DKHKLITKTEAKQEYLLKDCDLEKREPPLKFIVKKNPPHSQWGDMKLYLKQIVKRSLEVWGSQEALEAKEVR
Q
>d1exja1 a.6.1.3 (A:3-120) Transcription activator BmrR {Bacillus subtilis}
ESYYSIGEVSKLANVSIKALRYYDKIDLFPAYVDPDTSYRYYTDSQLIHLDLIKSLKYIGTPLEEMKKAQDLEMEELF
AFYTEQERQIREKLDLFSALEQTISLVKKRMKRQMEYPA
>d1jbga_a.6.1.3 (A:) Multidrug transporter activator MtaN {Bacillus subtilis}
KYQVKQVAISGVSVIRTLHHYDNIEELLNPSALTDAGYRLYSDADLERLQQILFFKEIGFRLDEIKEMLDHPNFDRKA
ALQSQKEILMKKKQRMDEMIQTIDRTLLS
>d2spca_a.7.1.1 (A:) Spectrin {Fruit fly (Drosophila sp.)}
QNLDLQLYMRDCELAESWMSAREAFLNADDANAGGNVEALIKKHEDFDKAINGHEQKIAALQTVADQLIAQ
NHYASNLVDEKRKQVLERWRHLKEGLIEKRSRLGD
>d1aj3_a.7.1.1 (-) Spectrin {Chicken (Gallus gallus)}
HQFFRDMDDDESWIKEKKLLVSSEDYGRDLTGVQNLRKHKRLEAELAAHEPAIQGVLDTGKKLSDDNTIGKEEI
QRQLAQFVDHWKELKQLAAARGQ
>d1cuna1_a.7.1.1 (A:7-115) Spectrin {Chicken (Gallus gallus)}
MVHQFFRDMDDDESWIKEKKLLVSSEDYGRDLTGVQNLRKHKRLEAELAAHEPAIQSVLDTGKKLSDDNTIGK
EEIQQRQLAQFVDHWKELKQLAAARGQRLLEESLEYQ
>d1cuna2_a.7.1.1 (A:116-219) Spectrin {Chicken (Gallus gallus)}
QFVANVEEEEAWINEKMTLVASEDYGDTLAAIQGLLKHEAFETDFTVHKDRVNDVCANGEDLIKNNHHVE
NITAKMKGLKGKVSDLEKAAAQRKAKLDENSA
>d1hcia1_a.7.1.1 (A:272-396) alpha-actinin {Human (Homo sapiens)}
SSAVNQENERLMEEYERLASLEWIRRTIPWLENRTPEKTMQMAMQKKLEDFRDYRRKHKPPKVQEKCQLEIN
FNTLQTQLRISNRPAFMSEGKVMVDIAGAWQRLEQAEGYEEWLNEIRRL
>d1hcia4_a.7.1.1 (A:633-746) alpha-actinin {Human (Homo sapiens)}
HANERLRRQFAAQANAIGPWIQNKMEEIARSSIQITGALEDQMINQLKQYEHNIIINYKNNIDKLEGDHQLIQEA

LVDNKHTNYTMEHIRVGWELLTTIARTINEVETQILRD
>d1quua1 a.7.1.1 (A:1-124) alpha-actinin {Human (Homo sapiens)}
GSSNEIRRRLERLEHAAKFRQKASTHETWAYGKEQILLQKDYESASLTVRALLRKHEAFESDLAAHQDRVEQIAA
IAQELNELDYHDAVNNDRCQKICDQWDRGTLTQKRREALERMEKLL
>d1quua2 a.7.1.1 (A:125-248) alpha-actinin {Human (Homo sapiens)}
ETIDQLHLEFAKRAAPFNNWMEGAMEDLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSIMAIQNEVEKV
IQSYNIRISSNPYSTVTMDELRTKWDKVQLVPIRDQLQEELARQHAN
>d1e2aa_ a.7.2.1 (A:) Enzyme Ila from lactose specific PTS, Ila-lac {Lactococcus lactis}
MNREEMTLLGFEIVAYAGDARSKLLEALKAAENGDFAKADSLVVEAGSCIAEAHSSQTGMLAREASGEELPYSV
TMMHGQDHLMTTILLKDVIIHHIELYKR
>d1chua1 a.7.3.1 (A:423-533) L-aspartate oxidase {Escherichia coli}
DESRVENPDERVVIQHNWHELRLFMWDYVGIVRTTKRLERALRRITMLQQEIDEYYAHFRVSNNLLELRNLVQ
VAELIVRCAMMRKESRGLHFTLDYPELLTHSGPSILSP
>d1fuma1 a.7.3.1 (A:443-575) Fumarate reductase flavoprotein subunit {Escherichia coli}
DGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKLAELQERFKVRITDTSSVFNTDLLYIELGHGLNVAE
CMAHSAMARKESRGAHQRLLDEGCTERDDVNFLKHTLAFRDADGTRLEYSDVKITTLPP
>d1qlaa1 a.7.3.1 (A:458-655) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}
KGTEDVFKIKNRMKDVMDDNVGIFRDGPHLEKSVKELEELYKKSKNVGKIKNKLHANPELEEAYRVPMMLKVA
LCVAKGALDRTESRGAHNREDYPKRDDINWLNRTLASWPNEQLPTLEYEALDVNEMEIAPRYRGYAKGNY
IENPLSVKRQFEIDKIQSELEAGKDRHAIQEALMPYELPAKYKARNERLGD
>d1jnra1 a.7.3.1 (A:503-643) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}
TADDVNPEYILPWQGLVRLQKIMDEYAAGIATIYKTNEKMLQRALELLAFLKEDLEKLAARDLHELMRAWELVH
RVWTAEAHVRHMLFRKETRWPGYYYRTDYPELNDEEWKCFVCSKYDAEKDEWTFEKVPYVQVIEWSF
>d1fewa_ a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}
SLSSEALMRRAVSLVTDSTSTFLSQTTYALIEAITEYTKAVYTLTSLYRQYTSLLGKMNSEEEDEVWQVIIGARAEM
TSKHQEYLKLETTWMTAVGLSEMAAEAAYQTGADQASITARNHIQLVKLQVEEVHQLSRKAETKLAEAQIEELK
QKTQEEGEERAEESEQEAYLRED
>d1g73a_ a.7.4.1 (A:) Smac/diablo {Human (Homo sapiens)}
AVPIAQKSEPHSLSSEALMRRAVSLVTDSTSTDLSQTTYALIEAITEYTKAVYTLTSLYRQYTSLLGKMNSEEEDEV
WQVIIGARAEMTSKHQEYLKLETTWMTAVGLSEMAAEAAYQTGADQASITARNHIQLVKLQVEEVHQLSRKA
ETKLAEAQ
>d1hx1b_ a.7.7.1 (B:) BAG-family molecular chaperon regulator-1, BAG1 {Human (Homo sapiens)}
GNSPQEEVELKKLKHELEKSVKIAQDQLEELNKELTGIIQQGFLPKDLQAEALCKLDRRVKATIEQFMKILEEIDTLIP
ENFKDSRLKRKGVLKKVQAFLAECDTVEQNQCQE
>d1i6za_ a.7.7.1 (A:) BAG-family molecular chaperon regulator-1, BAG1 {Mouse (Mus musculus)}
GSPEFMLIGEKSNPEEEVELKKLKDEVSAEKIANHLQELNKELSGIQQQGFLAKELQAEALCKLDRKVKATIEQFM
KILEEIDTMVLPEQFKDSRLKRKNLVKKVQVFLAECDTVEQYICQETERLQSTNLALAE
>d1qsda_ a.7.5.1 (A:) beta-Tubulin binding post-chaperonin cofactor Rbl2p {Baker's yeast (Saccharomyces cerevisiae)}
TQLDIKVKALKRLTKEEGYYQQELKDQEAHVAKLKEDKSVDPYDLKKQEEVLDKTKRLLPTLYEKIREFKEDLEQFL
KTYQGTEDVSDARSAITSAQELLDS
>d1fjgt_ a.7.6.1 (T:) Ribosomal protein S20 {Thermus thermophilus}
RNLSALKRHRQLSKRRLRNKAKKSAIKTLSKKAVQLAQEGKAEEALKIMRKAESLIDKAAGSTLHKNAARRKS

RLMRKVRQLLEAAGAPLIGGGGLSA
>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}
AQHDEAQQNAFYQVLNMPNLNADQRNGFIQSLKDDPSQSANVLGEAQKLNDSQAPK
>d1fc2c_ a.8.1.1 (C:) Immunoglobulin-binding protein A modules {Staphylococcus aureus}
FNKEQQNAFYEILHLPNLNEEQRNGFIQSLKDDPSQSANLLAEA
>d2spza_ a.8.1.1 (A:) Immunoglobulin-binding protein A modules {Staphylococcus aureus}
VDNKFNKEQQNAFYEILHLPNLNEEQRNAFIQSLKDDPSQSANLLAEAKKLNDQAPK
>d1gab_ a.8.1.2 (-) PAB {Peptostreptococcus magnus}
TIDQWLLKNAKEDAIKELKKAGITSDFYFNAINKAKTVVEVNALKNEILKAHA
>d1gjta_ a.8.1.2 (A:) IgG binding protein G {Streptococcus sp., group G}
MKAIFVINAQHDEAVDANSIAEKVLANRELDKYGVSDYYKNLINNAKTVEGVKALIDEILAALP
>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}
YASLEEQNNDALSPAIRLLAEHNLDASAIAKGTGVGGRLTREDVEKHLAKA
>d1bbi_ a.9.1.1 (-) E3-binding domain of dihydrolipoamide succinyltransferase {Escherichia coli}
LSPAIRLLAEHNLDASAIAKGTGVGGRLTREDVEKHL
>d2erl_ a.10.1.1 (-) ER-1 {Euplotes raikovi}
DACEQAAIQCVESACESLCTEGEDRTGCYMYIYSNCPPYV
>d1erd_ a.10.1.1 (-) ER-2 {Euplotes raikovi}
DPMTCEQAMASCEHTMCGYCQGPLYMTCIGITTDPECGLP
>d1erp_ a.10.1.1 (-) ER-10 {Euplotes raikovi}
DLCEQSALQCNEQGCHNFCSPEDKPGCLGMVWNPELCP
>d1ery_ a.10.1.1 (-) ER-11 {Euplotes raikovi}
DECANAAAQCSITLCNLYCGPLIEICELTVMQNCEPPFS
>d1hd6a_ a.10.1.1 (A:) ER-22 {Euplotes raikovi}
DICDIAIAQCSLTLCQDCENTPICELAVKGSCPPPWS
>d1aca_ a.11.1.1 (-) Acyl-CoA binding protein {Cow (Bos taurus)}
SQAEDKAAEEVKHLKTPADEEMLFIYSHYKQATVGDINTERPGMLDFKGAKWDWNLKGTSKEDAMKA
YIDKVEELKKKYGI
>d1hbka_ a.11.1.1 (A:) Acyl-CoA binding protein {Plasmodium falciparum}
HMAQQVFEEECVSFINGLPRTINNLPNELKLDLYKYYKQSTIGNCNIKEPSAHKYIDRKYEEAWKSVENLNRED

AQKKRYVDIVSEIFPYWQD
>d1ef1a1 a.11.2.1 (A:88-198) Moesin {Human (Homo sapiens)}
DVSEELIQDITQRLFLQVKEGILNDDIYCPPETAVLLASYAVQSKYGDFNKEVHKSGYLAGDKLLPQRVLEQHKL
NKDQWEERIQVWHEEHRGMLREDAVLEYLKIAQDL
>d1gc7a1 a.11.2.1 (A:88-198) Radixin {Mouse (Mus musculus)}
DVSEELIQEITQRLFLQVKEAILNDEIYCPPETAVLLASYAVQAKYGDYNKEIKPGYLANDRLLPQRVLEQHKL
KEQWEERIQNWHEEHRGMLREDSMMEYLKIAQDL
>d1gg3a1 a.11.2.1 (A:82-187) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
PDPAQLTEDITRYYLCLQLRQDIVAGRLPCSFATLALLGSYTIQSELG DYDPELHGVDYVSDFKLAPNQTKELEEKV
MELHKSYSRSMTPAQADLEFLENACKLSMY
>d1h4ra1 a.11.2.1 (A:104-214) Merlin {Human (Homo sapiens)}
NAEEELVQEITQHLEFLQVKKQILDEKIYCPPEASVLLASYAVQAKYGDYDPSVHKRGFLAQEELLPKRVINLYQM
TPEMWEERITAWYAEHRGRARDEAEMEYLKIAQDL
>d1kdx_a.12.1.1 (A:) Kix domain of CBP (creb binding protein) {Mouse (Mus musculus)}
GVRKGWHEHVTQDLRSHLVHKLVQAIFPTPDPAALKDRRMENLVAYAKKVEGDMYESANSRDEYYHLLAEKIV
KIQKELEE
>d1lre_ a.13.1.1 (-) alpha-2-Macroglobulin receptor associated protein (RAP) domain 1
{Human (Homo sapiens)}
GEEFRMEKLNQLWEKAQRLHLPPVRLAELHADLKIQERDELA WKKLKDGLDEDGEKEARLIRNLNVILAKYGL
DGKKDAR
>d1qqva_ a.14.1.1 (A:) Thermostable subdomain from chicken villin headpiece {Chicken (Gallus gallus)}
PTKLETPLDVNTAAEDLPRGVDP SRKENHLSDEFKAVFGMTRSAFANLPLWKQQNLKEKGLF
>d1vii_ a.14.1.1 (-) Thermostable subdomain from chicken villin headpiece {Chicken (Gallus gallus)}
MLSDEDFAVFGMTRSAFANLPLWKQQNLKEKGLF
>d1tbaa_ a.15.1.1 (A:) TAF(II)230 TBP-binding fragment {Fruit fly (Drosophila melanogaster)}
EGSIGNGLDTGILFGNIDSEGRLLQDDDGEGRRGGTGFDAELRENIGSLSKLGLDSMLLEVIDLKEA
>d1ail_ a.16.1.1 (-) N-terminal, RNA-binding domain of nonstructural protein NS1 {Influenza A virus}
MDSNTVSSFQVDCFLWHVRKQVV DQELGDAPFLDRLRRDQKSLRGRGSTLGLNIEATHVGKQIVEKILK
>d1a32_ a.16.1.2 (-) Ribosomal protein S15 {Bacillus stearothermophilus}
LTQERKREIIEQFKVHENDTGSTEVQVALTLRINRLSEHLKVHKDHHSRRGLLMVGQRRLLRYLQRED
PERYRMLIEKLGI
>d1dk1a_ a.16.1.2 (A:) Ribosomal protein S15 {Thermus thermophilus}
PITKEEKQKVMQEFA RFPGDTGSTEVQVALTLRINRLSEHLKVHKDHHSRRGLLMVGQRRLLRYLQRED
PERYRMLIEKLGI
>d1g1xb_ a.16.1.2 (B:) Ribosomal protein S15 {Thermus thermophilus}
PITKEEKQKVIQEFA RFPGDTGSTEVQVALTLRINRLSEHLKVHKDHHSRRGLLMVGQRRLLRYLQREDPE
RYREIVEKLGLRG
>d1d2da_ a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS) second repeated element
{Chinese hamster (Cricetulus griseus)}
MVYDKIAAQGEVVRKLKAEKAPKAKVTEAVECLLSLKA EYKEKTGKEYVPGLEHHH

>d1fyja_a.16.1.3 (A:) Multifunctional Glu-Pro-tRNA synthase (EPRS) second repeated element {Human (Homo sapiens)}

DSLVLYNRVAVQGDVVRELAKKAKPKEDVDAAVKQLLSLKALEYKEKTGQEYKPGNPP

>d2hp8_a.17.1.1 (-) p8-MTCP1 {Human (Homo sapiens)}

MPQKDPCQKQACEIQKCLQANSYMEKCQAVIQELRKCCAQYPKGRSVVCSGFEKEEEENLTKSASK

>d1ijxa_a.141.1.1 (A:) Secreted Frizzled-related protein 3 (SFRP-3;fzb) {Mouse (Mus musculus)}

AACEPVRIPLCKSLPWEMLTKMPNHLHHSTQANAILAMEQFEGLLTHCSPDLLLLCAMYAPICTIDFQHEPIK
PCKSVCERARQGCEPILIKYRHSWPESLACDELPVYDRGVCISPEAIVTAD

>d1ijya_a.141.1.1 (A:) Frizzled 8 (FZ8) {Mouse (Mus musculus)}

ELACQEITVPLCKIGYEYTYMPNQFNHTQDEAGLEVHQFWPLVEIQCSPDLKFFLCMSMYTPICLEDYKKPLPP
CRSVCERAKAGCAPLMRQYGFAWPDRMRCDRLPEQGNPDTCMDYER

>d2end_a.18.1.1 (-) T4 endonuclease V {Bacteriophage T4 (Escherichia coli)}

TRINLTLSSELADQHLMAEYRELPRVFGAVRKHVANGKVRDFKISPTFILGAGHVTFFYDKLEFLRKQIELIAEC
LKRGFNIKDTTVQDISDIPQEFRGDYIPHEASIAISQARLDEKIAQRPTWYKYYGKAIYA

>d2lisa_a.19.1.1 (A:) Lysin {Red abalone (Haliotis rufescens)}

HYVEPKFLNKAFFEVALKVQIIAGFDRLGLVKWLRVHGRTLSTVQKKALYFVNRRYMQTHWANYMLWINKKIDAL
GRTPVVGDYTRLGAEIGRRIDMAYFYDFLKDKNMIPKYLPMEEINRMRPADVPVKYM

>d3lyna_a.19.1.1 (A:) Lysin {Green abalone (Haliotis fulgens)}

INKAYEVTMKIQIISGFDRQLTAWLRVHGRRLTNQKKTTLFFVNRRYMQTHWQNYMLWVKRKIKALGRPAAV
GDYTRLGAEIGRRVDMVFFYNFLSGRKIMPYSAYMAKLNALRPADVPVK

>d1gaka_a.19.1.1 (A:) SP18 {Abalone (Haliotis fulgens)}

FDDVVVSRQEQQSYVQRGMVNFLDEEMHKLVKRFRDMRWNLPGFVFLLKKVNRRMMRYCMDYARYSKKI
LQLKHPVNKKTLTKMGRFVGGRNYGVIRELYADVFRDVQGFRGPKMTAACMRKYSSKDPGTFPCKNE

>d1lbu_1 a.20.1.1 (1-83) Zn2+ DD-carboxypeptidase, N-terminal domain {Streptomyces albus G}

DGCYTWSGTLSEGSSGEAVRQLQIRVAGYPGTGAQLAIDGQFGPATKAAVQRFQSAYGLAADGIAGPATFNKIY
QLQDDDCTP

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

PSPIIKFPGDVAPKTDKELAVQYLNTFYGCPKESCNLFVLKDTLKKMQKFFGLPQTGDLDQNTIETMRKPRCGN
PDV

>d1slm_1 a.20.1.2 (16-80) Stromelysin-1 (MMP-3) {Human (Homo sapiens), fibroblast}

LVQKYLENNYDLKKDKVQFVRRKDSGPVVKKIREMQKFLGLEVTGKLDSDTLEVMRKPRCGVPDV

>d1aab_a.21.1.1 (-) HMG1, domains A and B {Rat (Rattus norvegicus)}

GKGDPKKPRGKMSYYAFFVQTSREEHKKKHPDASVNFSKKSERWKTMSAKEKGKFEDMAKADKARYER
EMKTYIPPKGE

>d1ckta_a.21.1.1 (A:) HMG1, domains A and B {Rat (Rattus norvegicus)}

KPRGKMSYYAFFVQTCREEHKKKHPDASVNFSKKSERWKTMSAKEKGKFEDMAKADKARYEREMKTY

>d1hme_a.21.1.1 (-) HMG1, domains A and B {Rat (Rattus norvegicus)}

FKDPNAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKDIAAY
RAK

>d1hsm_a.21.1.1 (-) HMG1, domains A and B {Hamster (Cricetus griseus)}

NAPKRPPSAFFLFCSEYRPKIKGEHPGLSIGDVAKKLGEMWNNTAADDKQPYEKKAALKKEKYEKDIAAYRAKG
KPDA

>d1qrva_a.21.1.1 (A:) HMG-D {Drosophila melanogaster}

SDKPKRPLSAYMLWLNSARESIKRENPGIKVTEVAKRGHELWRAMKDKSEWEAKAAKDDYDRAVKEFEAN
G

>d1cg7a_ a.21.1.1 (A:) NHP6a {Baker's yeast (*Saccharomyces cerevisiae*)}
MVTPREPKRTRKKKDNPAPKRALSAYMFFANENRDIRSENPDITFGQVGKKLGEWKALTPEEKQPYEAK
AQADKKRYESEKELYNATLA

>d1hrza_ a.21.1.1 (A:) SRY {Human (*Homo sapiens*)}
DRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQAMHREKYPN
YKYR

>d1j46a_ a.21.1.1 (A:) SRY {Human (*Homo sapiens*)}
MQDRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFFQEAQKLQAMHREKY
PNKYRPRRKAKMLPK

>d1i11a_ a.21.1.1 (A:) Sox-5 {Mouse (*Mus musculus*)}
PHIKRPMPNAFMWAKDERRKILQAFPDMHNSNISKILGSRWKAMTNLEKQPYYEEQARLSKQHLEKYPDY

>d2lefa_ a.21.1.1 (A:) Lymphoid enhancer-binding factor, LEF1 {Mouse (*Mus musculus*)}
MHIKKPLNAFMLYMKEMRANVVAESTLKESAAINQILGRRWHALSREEQAKYYELARKERQLHMQLYPGWSA
RDNYGKKKKRKREK

>d1k99a_ a.21.1.1 (A:) Upstream binding factor, the first HMG box {Human (*Homo sapiens*)}
MKKLKKHPDFPKPLTPYFRFFMEKRAKYAKLHPEMSNLDLTKILSKKYKELPEKKMKYIQDFQREKQEERNL
ARFREDHPDLIQNAKK

>d1eqza_ a.22.1.1 (A:) Histone H2A {Chicken (*Gallus gallus*), erythrocytes}
SGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLRKGNYAERVGAGAPVYAAVLEYLAEILELAGNAARDNK
KTRIIPRHLQLAIRNDEELNKLLGKVTAQGGVLVPNIQAVLLPKTDSHKA

>d1hioa_ a.22.1.1 (A:) Histone H2A {Chicken (*Gallus gallus*), erythrocytes}
KSRSRAGLQFPVGRVHRLRKGNYAERVGAGAPVYAAVLEYLAEILELAGNAARDNKTRIIPRHLQLAIRND
EELNKLLGKVTAQGGVLP

>d1hq3a_ a.22.1.1 (A:) Histone H2A {Chicken (*Gallus gallus*), erythrocytes}
KAKSRSSRAGLQFPVGRVHRLRKGNYAERVGAGAPVYAAVLEYLAEILELAGNAARDNKTRIIPRHLQLAIR
NDEELNKLLGKVTAQGGVLVPNIQAVLLPK

>d1aoic_ a.22.1.1 (C:) Histone H2A {African clawed frog (*Xenopus laevis*)}
GKQGGKTRAKAKTRSSRAGLQFPVGRVHRLRKGNYAERVGAGAPVYAAVLEYLAEILELAGNAARDNKTR
IIIPRHLQLAVRNDEELNKLLGKVTAQGGVLVPNIQSVLLPK

>d1f66c_ a.22.1.1 (C:) Histone H2A {Human (*Homo sapiens*), variant H2A.Z}
AVRSRSQRAGLQFPVGRIRHLKSRTSHGRVGATAAVYSAILEYLAEVLELAGNASKDLKVKRITPRHLQLAIR
GDEELDSLIKATIAGGGVIPHIHKSLI

>d1id3c_ a.22.1.1 (C:) Histone H2A {Baker's yeast (*Saccharomyces cerevisiae*), H2A.1}
QSRSAKAGLTGKTRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAEILELAGNAARDNKTRIIPRHLQLAIRND
DELNKLLGNTIAQGGVLVPNIHQNLKPSSAKAT

>d1eqzb_ a.22.1.1 (B:) Histone H2B {Chicken (*Gallus gallus*), erythrocytes}
VTKTQKKGDKKRKKSRSYISIYVYKVLQVHPDTGISSKAMGIMNSFVNDIFERIAGEASRLAHYNKRSTITSREI
QTAVRLLLPGELAKHAVSEGTKAVTKYTSSK

>d1hiob_ a.22.1.1 (B:) Histone H2B {Chicken (*Gallus gallus*), erythrocytes}
SYSIYVYKVLQVHPDTGISSKAMGIMNSFVNDIFERIAGLASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAV
EGTKAVTKHTSSK

>d1hq3b_ a.22.1.1 (B:) Histone H2B {Chicken (*Gallus gallus*), erythrocytes}

RKESYSIYVYKVLQVHPDTGISSKAMGIMNSFNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLPHELAKH
AVSEGTKAVTKYTSS

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

KKRRKTRKESYAIYVYKVLQVHPDTGISSKAMSIMNSFNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLP
GELAKHAVSEGTAKVTKYTSAK

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

RKETYSSYIYKVLQTHPDTGISQKMSILNSFNDIFERIATEASKLAAYNKKSTISAREIQTAVRLILPHELAKH
SEGTRAVTKYSSST

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

APATGGVKPKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFE
DTNLCAIHAKRVTIMPKDIQLARRIRGERA

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

PRKQLATKAARKSAPATGGVKPKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMA
LQEASEAYLVGLFEDTNLCALIHAKRVTIMPKDIQLARRIRGERA

>d1hq3c_a.22.1.1 (C:) Histone H3 {Chicken (*Gallus gallus*), erythrocytes}

YRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCALIHAKRV
TIMPKDIQLARRIRGERA

>d1id3a_a.22.1.1 (A:) Histone H3 {Baker's yeast (*Saccharomyces cerevisiae*)}

PHRYKPGTVALREIRRFQKSTELLIRKLPFQRLVREIAQDFKTDLRFQSSAIGALQESVEAYLVSLFEDTNLAIIHAK
RTVIQKKEIKLARRRLRGER

>d1eqzh_a.22.1.1 (H:) Histone H4 {Chicken (*Gallus gallus*), erythrocytes}

KGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVTYTEHAKRKTVA
MDVVYALKRQGRRTLTYGFGG

>d1hq3d_a.22.1.1 (D:) Histone H4 {Chicken (*Gallus gallus*), erythrocytes}

KVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVTYTEHAKRKTVTAMDVVYALKRQGR
TLYGFGG

>d1id3b_a.22.1.1 (B:) Histone H4 {Baker's yeast (*Saccharomyces cerevisiae*)}

DNIQGITKPAIRRLARRGGVKRISGLIYEEVRAVLKSLESVIRDSVTYTEHAKRKTVTSDLVVYALKRQGRRTL
YFGFG

>d1b67a_a.22.1.2 (A:) Archaeal histone {Archaeon *Methanothermus fervidus*, histone A}

GELPIAPIGRIIKNAGAERSDDARIALAKVLEEMGEEIASEAVKLAKHAGRKTIAEDIELARKMFK

>d1a7w_a.22.1.2 (-) Archaeal histone {Archaeon *Methanothermus fervidus*, histone B}

MELPIAPIGRIIKDAGAERSDDARITLAKILEEMGRDIASEAIKLARHAGRKTIAEDIELAVRRFK

>d1f1ea_a.22.1.2 (A:) Archaeal histone {Archaeon *Methanopyrus kandleri*}

ELPKAAIERIFRQGIGERRLSQDAKDTIYDFVPTMAEYVANAACKVLDASGKKTLMEEHLKALADVLMEVGVED
YDGEGLFRATVRRILKLAGIERASSDAVDLYNKLICRATEELGEKAAEYADEDGRKTQGEDVEKAITYSMPKG
EL

>d1tafa_a.22.1.3 (A:) TAF(II)42 {Fruit fly (*Drosophila melanogaster*)}

PKDAQVIMSILKEVNQYEPRVVNQLLEFTFRYVTSILDDAKVYANHARKKTIDLDDVRLATEVTLD

>d1tafb_a.22.1.3 (B:) TAF(II)62 {Fruit fly (*Drosophila melanogaster*)}

MLYGSSISAESMKVIAESIGVGSLSDAACELAEDVSIKLKRIVQDAAKFMNHAKRQKLSVRDIDMSLK

>d1bh9a_a.22.1.3 (A:) TAF(II)18 {Human (*Homo sapiens*)}

LFSKELRCMMYGFQDDQNPyTESVDILEDVIEFITEMTHKAMSI

>d1bh9b_a.22.1.3 (B:) TAF(II)28 {Human (*Homo sapiens*)}

FSEEQLNRYEMYRRSAFPKAAIKRLIQSITGTSVSQNVVIAMSGISKVFVGEVVEEALDVCEKWGEMPLQPKH
MREAVRRLKSKGQIP

>d1jfia_a.22.1.3 (A:) Negative cofactor 2, NC2, alpha chain {Human (Homo sapiens)}
ARFPPARIKKIMQTDEEIGKAAAAPVIISRALELFLESLLKKACQVTQSRNAKTMTTSHLKQCIE

>d1fib_a.22.1.3 (B:) Negative cofactor 2, NC2, beta chain {Human (Homo sapiens)}
DDLTIPIRAAINKMIKETLPNVRVANDARELVNCCTEFIHLISSEANEICNKSEKKTISPEHVIQALESLGFGSYISEV
KEVLQECKTVALKRKASSRLENLGIPEEEELLRQQQELFAKARQQQAELAQQEWLQ

>d1fpoa2_a.23.1.1 (A:77-171) HSC20 (HSCB), C-terminal oligomerisation domain {Escherichia coli}
FDLASEQHTVRDTAFLMEQLELREELDEIEQAKDEARLESFIKRVKKMFTRHQLMVEQLDNETWDAAADTCR
KLRLFLDKLRSSAEQLEEKLLDF

>d1eexg_a.23.2.1 (G:) Diol dehydratase, gamma subunit {Klebsiella oxytoca}
SARVSDYPLANKHPEWVKTATNKTLDFTLENVLSNKVTAQDMRITPETRLQASIAKDAGRDRRLAMNFERAA
ELTAVPDDRILEIYNALRPYRSTKELLAIADDLESRYQAKICAAFVREAATLYVERKKLGDD

>d1mtyg_a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit {Methylococcus capsulatus}
LGIHSNDTRDAVVNKIAHVNTLEKAAEMILKQFRMDHTTPFRNSYELDNDYLWIEAKLEEKVAVLKARAFNEVD
FRHKTAFGEDAKSVLDGTVAKMNAAKDKWEAEKIHIGFRQAYKPPIMPVNFLRTDAALGTVLMEIRNTDYGTPLEGL
DTPLEELRKQRGVRVVH

>d1mhyg_a.23.3.1 (G:) Methane monooxygenase hydrolase, gamma subunit {Methylosinus trichosporium}
AKREPIHDNSIRTEWEAKIAKLTSDQATKFIQDFRLAYTSPFRKSYDIDVDYQYIERKIEEKSLVLTKEKPVADLIT
KATTGEDAAAVERTWIAKIKAAKSKEYEAEAIHIEFRQLYKPPVLPVNVLRTDAALGTVLMEIRNTDYGTPLEGL
RKERGVKVLHLQ

>d1om2a_a.23.4.1 (A:) Mitochondrial import receptor subunit Tom20 {Rat (Rattus norvegicus)}
RAGLSKLPDLKDAEAVQKFFLEIQLGEELLAQGDYEKGVDHLTNAIAVCQQPQQLQVLQQTLPPPVFQMMLT
KLPTISQRIVSAQSLGEDDVE

>d1jw2a_a.23.5.1 (A:) Hemolysin expression modulating protein HHA {Escherichia coli}
MSEKPLTKTDYLMRLRRCQTIDTLERVIEKNKYELSDNELAVFYSAADHRLAELTMNKLYDKIPSSVWKFIR

>d1nfn_a.24.1.1 (-) Apolipoprotein E3 {Human (Homo sapiens)}
GQRWELALGRFWDYLWRVQTLSEQVQEELLSSQVTQELRALMDETMKELKAYKSELEEQLTPVAEETRARLSK
ELQAAQARLGADMEDVCGRIVQYRG EVQAMLGQSTEELRVRLASHLRKLKRLRDADDLQKRLAVYQA

>d2asr_a.24.2.1 (-) Aspartate receptor, ligand-binding domain {Escherichia coli}
KSFVVSNQLREQQGELTSTWDLMLQTRINLSRSAVRMMMDSSNQQSNAKVELDSARKTLAQAATHYKKFKS
MAPLPEMVATSRNIDEKYKNYYTALTELIDYLDYNGT GAYFAQPTQGMQNAMGERFAQYALSSEKLYRDI

>d1vlta_a.24.2.1 (A:) Aspartate receptor, ligand-binding domain {Salmonella typhimurium}
GFVISNELRQQQSELTSTWDLMLQTRINLSRSAARMMMMDASNQSSAKTDLLQNAKTTLAQAAAHYANFKN
MTPLPAMA EASANVDEKYQRYQAALAEIQLDNGNMDAYFAQPTQGMQNALGEALGNYARVSENLYRQTF

>d2liga_a.24.2.1 (A:) Aspartate receptor, ligand-binding domain {Salmonella typhimurium}
MGGLLFSSLQHCQQGFVISNELRQQQSELTSTWDLMLQTRINLSRSAARMMMMDASNQSSAKTDLLQNAKT
TLAQAAAHYANFKNMTPLPAMA EASANVDEKYQRYQAALAEIQLDNGNMDAYFAQPTQGMQNALGEAL
GNYARVSENLYRQTFD

>d256ba_a.24.3.1 (A:) Cytochrome b562 {Escherichia coli}
ADLEDNMETLNDNLKVIEKADNAAAQVKDALTKMRAAALDAQKATPPKLEDKSPDSPEMKDFRHGFDILVGQI
DDALKLANEGKVKEAQAAAQLKTTRNAYHQKYR

>d2ccya_a.24.3.2 (A:) Cytochrome c' {Rhodospirillum molischianum}
QSKPEDLLKLRQGLMQTLKSQWVPIAGFAAGKADLPADAQRAENMAMVAKLAPIGWAKTEALPGETKP
EAEGSKSAEFLLEGWKALATESTKLAAAAGPDALKAQAAATGKVCKACHEEFKQD

>d1bbha_a.24.3.2 (A:) Cytochrome c' {Chromatium vinosum}
AGLSPEEQIETRQAGYEFMGWNMGKIKANLEGEYNAQVEAAANVIAIANSGMGALYGPGETDKNVGDVK
RVKPEFFQNMDVGKIAREFGAANTLAEVAATGEAEAVKTAFGDVGAACKSCHEKYRAK

>d1e85a_a.24.3.2 (A:) Cytochrome c' {Alcaligenes sp.}
EFAKPEDAVKYRQSALTMASHFGRMTPVVKGQAPYDAAQIKANVEVLKTSALPWAAFGPGTEGGDARPEI
WSDAASFQKQQAFQDNIVKLSAADAGDLDKLRAAFGVDVGASCKACHDAYRK

>d1jafa_a.24.3.2 (A:) Cytochrome c' {Rhodococcus gelatinosus}
QFQKPGDAIEYRQSAFTLIANHFGRAVAAAMAQGKAPFDAKVAENIALVSTLSKPLTAFGPGTDKGHGTEAKPA
VWSDAAGFKAAADKFAAAVIDKDAAGKTGDFQAQIKAAVGETGGACKGCHDKFKE

>d1cpq_a.24.3.2 (-) Cytochrome c' {Rhodobacter capsulatus}
ADTKEVLEAREAYFKSLGGSMKAMTGVAKAFDAEAAKVEAAKLEKILATDVAPLFPAGTSSTDLPQTEAKAAI
WANMDDFGAKGKAMHEAGGAVIAAANAGDGAAGFAALQQLGGTCKACHDDYREED

>d1a7va_a.24.3.2 (A:) Cytochrome c' {Rhodopseudomonas palustris}
QTDVIAQRKAILKQMGEATKPIAAMLKGEAKFDQAVVQKSLAAIADDSSKKLPAFPADSKTGGDTAALPKIWED
KAKFDDLFAKLAAATAAQGTIKDEASLKANIGGVLGNCKSCHDDFRAKKS

>d2hmza_a.24.4.1 (A:) Hemerythrin {Sipunculid worm (Themiste dyscrita)}
GFPIPDPYCWDPSFRFTYSIIDDEHKTLFNGILLSQADNADHLNELRRCTGHFLNEQQLMQASQYAGYAEHK
KAHDDFIHKLDTWGDVTYAKNWLVNHIKTIDFKYRGKI

>d1hrb_a.24.4.1 (-) Hemerythrin {Phascolopsis gouldii}
GFPIPDPYVWDPSFRFTYSIIDDEHKTLFNGIFHLAIDDNNADNLGELRRCTGHFLNQEVLMEASQYQFYDEHKK
EHDDFINALDNWKGDVKWAKAWLVNHIKTIDFKYKGKI

>d1i4ya_a.24.4.1 (A:) Hemerythrin {Phascolopsis gouldii}
GFPIPDPYVWDPSFRFTYSIIDDEHKTLFNGIFHLAIDDNNADNLGELRRCTGHFLNEQVLMQASQYQFYDEHK
KEHETFIHALDNWKGDVKWAKSWLVNHIKTIDFKYKGKI

>d2mhr_a.24.4.1 (-) Myohemerythin {Sipunculan worm (Themiste zostericola)}
GWEIPEPYVWDESFRVFYEQLDEEHKKIFKGIFDCIRDNSAPNLATLVKVTTNHFTHEEAMMDAAKYSEVPHK
KMHKDFLEKIGGLSAPVDAKNVDYCKEWLVNHIKTIDFKYKGKL

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

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

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

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

SYNITNSNQYQYFAAVWAEP TPMLNQCVSALSQS YQTQAGRDTVRQQFANLLSTIVAPNQRFPDTGFRVYVN
SAVIKPLYEALMKSFDRNRIETEEESRPSASEVANATQRVDDATVAIRSQIQLLLNELSNGHGMNRAEFEAILP
WTTAPAT
>d3fapb_ a.24.7.1 (B:) FKBP12-rapamycin-binding domain of FKBP-rapamycin-
associated protein (FRAP) {Human (Homo sapiens)}
VAILWHEMWHEGLEEASRLYFGERNVKGMFEVLEPLHAMMERGPQLKETSFNQAYGRDLMEAQEWC
RKYMKGSGNVKDLTQAQWDLYYHVFR
>g1avo.1 a.24.8.1 (A:,B:) Proteasome activator reg(alpha) {Human (Homo sapiens)}
LRVQPEAQAKVDFVREDLCTKTENLLGSYFPKKISELDAFLKEPALNEANLSNLKAPLDIXAVNCNEKIVV
LLQRLKPEIKDVIEQLNLVTTWLQLQIPRIEDGNNFGVAVQEKFELMTSLHTKLEGFTQISKYFSERGD
AVTKAAKQPHVGDYRQLVHELDEAEYRDIRLMVMEIRNAYAVLYDIILKNFEKLKKPRG
>d1dova_ a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}
ESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCSSVKRGNMVRAARALLSAVTRLLILAD
MADVYKLLVQLVVEDGILKLRNAGNEQDLGIQYKALKPEVDKLNIMA
AKRQQELKDVGNDQMAAARGILQKNVPILY
TASQACLQH
PVAAYKANRDLIYKQLQQAVTG
ISNAAQAT
>d1dowa_ a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}
KAHVLAASVEQATENFLEKGDKIAKESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDPCSSVKRG
NMVRAARALLSAVTRLLILAD
MADVYKLLVQLVVEDGILKLRNAGNEQDLGIQYKALKPEVDKLNIMA
AKRQQELKDVG
NDQMAAARGILQKNVPILY
TASQACLQH
PVAAYKANRDLIYKQLQQAVTG
ISNAAQAT
>d1h6ga1 a.24.9.1 (A:377-507) alpha-catenin {Human (Homo sapiens)}
DLRRQLRKAVMDHVSDSLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACS
ISNNEGVKL
MSASQLEALCPQVIN
AALALA
AAKPKQSKL
AQENMDLFKEQWEKQ
VRLTDA
DDITS
>d1h6ga2 a.24.9.1 (A:508-631) alpha-catenin {Human (Homo sapiens)}
IDDFLAVSENHILEDVNKC
VIALQEKD
VGD
LRTAGAIRGRA
ARV
I
H
V
V
T
SEMDNY
EPGVY
TEK
V
LEAT
KLL
SNT
VM
PRF
TEQ
V
EA
A
V
E
A
L
S
S
D
P
A
Q
P
M
D
E
N
E
F
I
D
A
S
R
L
V
Y
D
G
I
R
D
I
R
K
A
V
L
M
>d1h6gb1 a.24.9.1 (B:392-507) alpha-catenin {Human (Homo sapiens)}
DSFLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANLACS
ISNNEGVKL
RMSASQLEALCPQVIN
A
A
L
A
A
K
P
Q
S
K
L
A
Q
E
N
M
D
L
F
K
E
Q
W
E
K
Q
V
R
V
L
T
D
A
V
D
D
ITS
>d1qkra_ a.24.9.1 (A:) Vinculin {Chicken (Gallus gallus)}
KDEEFPEQKAGEAINQP
M
M
M
A
R
Q
L
H
D
E
A
R
K
W
S
S
K
G
N
D
I
I
A
A
K
R
M
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K
R
A
L
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Q
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AKD
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K
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A
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Q
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V
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N
A
Q
N
L
M
Q
S
V
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R
E
A
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K
I
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D
A
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T
L
R
W
V
R
>d1k04a_ a.24.14.1 (A:) FAT domain of focal adhesion kinase {Human (Homo sapiens)}
EISPPPTANLDRSNDKVY
E
N
V
T
G
L
V
K
A
V
I
E
M
S
S
K
I
Q
P
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>d1k40a_ a.24.14.1 (A:) FAT domain of focal adhesion kinase {Mouse (Mus musculus)}
NDKVY
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>d2a0b_ a.24.10.1 (-) Aerobic respiration control sensor protein, ArcB {Escherichia coli}
SKSEALLDIPMLEQY
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RIELSKYYNTNL

>d1i5na_a.24.10.3 (A:) Chemotaxis protein CheA P1 domain {Salmonella typhimurium}
DISDFYQTFFDEADELLADMEQHLLDLVPESPDAEQLNAIFRAAHSIKGGAGTGFITLQETTHLMENLLDEARR
GEMQLNTDIINLFLETKDIMQEQLDAYKNSEEPDAASFEYICNALRQLALEAK
>d1he1a_a.24.11.1 (A:) ExoS toxin {Pseudomonas aeruginosa}
ASSAVVFKQMVLQQALPMTLKGLDKASELATLTPEGLAREHSRLASGDALRSLSTALAGIRAGSQVEESRIQAG
RLLERSIGGIALQQWGTGGAASQLVLDASPELRREITDQLHQVMSEALLRQAVESEVS
>d1g4us1_a.24.11.1 (S:167-296) SptP tyrosine phosphatase {Salmonella typhimurium}
SKQPLLDIALKGLKRTLPQLEQMDGNSLRENFQEMASGNGPLRSLMTNLQNLNKIPEAKQLNDYVTTLTNIQV
GVARFSQWGTGGEVERWVDKASTHELTQAVKKIHVIAKELKNVTAELEKIEAGAPM
>d1hy5a_a.24.11.1 (A:) YopE {Yersinia pestis}
TSFSDSIKQLAAETLPKYMQQQLNSLDAEMILQKNHDQFATGSGPLRGSITQCQGLMQFCGGELOQAEASAILNTP
VCGIPFSQWGTIGGAASAYVASGVDLTQAANEIKGLAQQMOKLLSLM
>d1f1ma_a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}
PNLTEISKKITESNAVVLAVKEVETLLSIDEALAKAIGKKIKSDVSLDNEADHNGSLMSGAYLISTLITKKISAIKDSGE
LKAIEIKAACKCSEEFTAKLGKGEHTDLGKEGVTDNAKKAILKTNNDKTKGADELEKLKFESVKNLSKAAKEMLTNS
VKELTSP
>d1g5za_a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}
PNLTEISKKITESNAVVLAVKEVETLLSIDEALAKAIGKKIGNNGLEANQSKNTSLLSGAYAISDLIAEKLNVLKNEE
LKEKIDTAKQCSTEFNKLKSEHAVLGLDNLTDDNAQRAILKKHANKDKGAAELEKLKAVENLSKAAQDTLKNA
VKELTSPIVA
>d1ggqa_a.24.12.1 (A:) Outer surface protein C (OspC) {Lyme disease spirochete (Borrelia burgdorferi), different strains?}
GPNLTEISKKITDSNAVLLAVKEVEALLSSIDEIAAKAIGKKIHQNNGLDENNHNHSLLAGAYAISTLIKQKLDGLK
NEGLKEKIDAACKCSETFTNKLKEKHTDLGKEGVTDADAKEAILKTNGTKGAELGKLFESVEVLSKAAKEML
ANSVKELTS
>d1jpna1_a.24.13.1 (A:1-88) Signal sequence recognition protein Ffh {Thermus aquaticus}
MFQQLSARLQEAIGRLGRGRITEEDLKATLREIRRALMDADVNLLEVARDFVERVREEALGKQVLESLTPAEVILA
TVYEALKEALGG
>d1j8mf1_a.24.13.1 (F:3-86) Signal sequence recognition protein Ffh {Archaeon Acidianus ambivalens}
LLDNLRLTVRKFLTGSYYDKAVEDFIKELKQLISADVNVKLVSLTNKIKERLKNEKPPTYIERREWFIKIVYDELS
NLFGG
>d1fts_1_a.24.13.1 (201-284) Signal recognition particle receptor, FtsY {Escherichia coli}
RSLLTKENLGSGFISLFRGKKIDDLFEELEEQLLIADVGVETTRKIITNLTEGASRKQLRDAEALYGLLKEEMGEIL
AKVDE
>d1jr8a_a.24.15.1 (A:) Thiol oxidase Erv2p {Baker's yeast (Saccharomyces cerevisiae)}
DDKVKEVGRASWKYFHTLLARFPDEPTPEEREKLHTFIGLYAELYPCGECSYHFVKLIEKYPVQTSSRTAAAMW
GCHIHNKVNEYLKKDIYDCATILEDYDCGC
>d1h99a1_a.142.1.1 (A:54-168) Transcriptional antiterminator LicT {Bacillus subtilis}
GAMEKFKTLLYDIPICMEVSEEISYAKLQLGKKLNDSIYVSLTDHINFQIQRNQKGLDIKNALLWETKRLYKDEFQI

GKEALVMVKNKTGVSLPEDEAGFIALHIVNAELNEE

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

MPNIINITKVMEEILSIVKYHFKIEFNEESLHYRFVTDLKFFAQRLFNGTHMESEDDFLLDLVKEKYHRAYECTKK
IQTYIEREYEHKLTSDELLYLTIERVVK

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

MKSLKGSRTEKNILTAFAGESQARNRYFGGQAKKDGFBQISDIFAETADQEREHAKRLFKFLEGGDLEIVAAF
PAGIIADTHANLIASAAGEHHHEYTEMPSFARIAREEGYEEIARVFASIAVAEEFHFKRFLDFARNIKEGRV

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

MKGDTKVINYLNKLLGNELVAINQYFLHARMFKNWGLKRLNDVEYHESIDEMKHADRYIERILFLEGLPNLQDL
GKLNIGEDVEEMLRSIDLAELEDGAKNLREAIGYADSVHDYVSRDMMIEILRDEEGHIDWLETLDLIQKMGLQ
NYLQAQIREEG

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

MKGDAKVIENFLNAALRSELTAISQYWVHFRLQEDWGLAKMAKSREESIEEMGHADKIIARILFLEGHPNLQKL
DPLRIGEGPRETLECDLAGEHDALKLYREARDYCAEVGDIVSKIFESLITDEEGHVDLFLETQISLYDRLGPQGFAL
LNAAPMDAA

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

LKPEMIEKLNEQMNLLEYSSLLYQQMSAWCSYHTFEGAAAFLRRHAQEEMTHMQQLFDYLTDTGNLPRINTVE
SPFAEYSSLDEFQETYKHEQLITQKINELAHAAMTNQDYPTFNFLQWYVSEQHEEEKLFKSIIDKLSLAGKSGEG
LYFIDKELSTLD

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

MLSKEVVKLLNEQINKEMYAANLYLSMSSWCYENSLSGAGAFLFAHASEESDHAKKLITYLNETDSHVELQEVK
QPEQNFKSLLDVFEKTYEHEQFITKSINTLVEHMLTHKDYSTFNFLQWYVSEQHEEEALFRGIVDKIKLIGEHGNG
LYLADQYIKNIALSR

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

SKATNLLYTRNDVSDSEKKATVELNRQVIQFIDLSLITKQAHWNMRGANFIAVHEMLDGRTALIDHLDTMAE
RAVQLGGVALGTTQVINSTPLKSYPPLDIHNVQDHLKELADRYAIVANDVRKAIGEAKDDDTADILTAASRDLDK
FLWFIECNIE

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

VDTKEFLNHQVANLNVFTVKIHQIHWMRGHNFTLHEKMDDLYSEFGEQMDEVAERLLAIGGSPFSTLKEFL
ENASVEEAPYTKPKTMDQLMEDLVGTLELRDEYKQGIELTDKEGDDVTNDMLIAFKASIDKHIWMFKAFLGK
APLE

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

TSQVRQNYHQDSEAAIRQINLELYASYVYLSMSYYFDRDDVALKNFAKYFLHQSHEREHAEKLMLQNLQRG
GRIFLQDIQKPDCCDWESGLNAMECALHLEKNVNQSLLEHKLATDKNDPHLCDFIETHYLNEQVKAIKEGDH
VTNLRKMGAPESGLAEYLFKDHTLG

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

SQIRQNYSTEVEAAVNRLVNLYLRASYTYLSGFYFDRDDVALEGVCHFFRELAEEKREGAERLLKMQNQRGGR
ALFQDQLQKPSQDEWGTPDAMKAAIVLEKSLNQALLDLHALGSAQADPHLCDFLESHFLDEEVKLIKMGDHL
TNIQRLVGSQAGLGEYLFERLT

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

TSQIRQNYSTEVEAAVNRLVNLLRASYTYLSGFFFDRDDVALEGVGHFFRELAEEKREGAERLLEFQNDRGGR
ALFQDVQKPSQDEWGKTQEAMEAALAMEKLNQALLDLHALGSARADPHLCDFLESHYLDKEVKLIKMG
HTNLRRVAGPQPAQTGAPQGSLGEYLFERLT

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

DSQVRQNFHRDCEAAINRMVN MELYASYTYLSMAFYFDRDDIALHNVAKFFKEQSHEEREHAEKLMDQNK
RGGRIVLQDVQKPERDEWGNTLEAMQAALQLEKTVNQALLDLKVGSDKVDPHLCDFLETEYPEEQVKSIKQL
GDYITNLKRLGLPQNGMGEYLFDKHTMGE

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

VSQVRQNYHSDCEAAVNRMLNLEYASYTYSSMYAFFDRDDVALHNVAEFFKEHSHEEREHAEKFMKYQNKR
GGRVVLQDIKKPERDEWGNTLEAMQAALQLEKTVNQALLDLHKLATDKVDPHLCDFLESEYLEEQVKDIKRIG
DFITNLKRLGLPENGGMGEYLFDKHSV

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

SQVRQNFHQDCEAGLNRTVNLKFHSSYVYLSMASYFNRRDVALSNFAKFRERSEEKEHAEKLIEYQNQRGG
RVFLQSVEKPERDDWANGLEALQTALKLQKSVNQALLDLHAVAADKSDPHMTDFLESPYLSESvetiklgdhi
TSLKKLWSSHPGMAEYLFNKHTLG

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

ERRRG LTDPEMAAVILKALPEAPLDGNNKMGYFVTPRWKRLTEYEALT VYAQPNA DWIAGGLDWGDWTQKF
HGGRPSWGNETTELRTVDWFKH RDPLRRWHAPYVKDKAEEWRYTDRFQ LGYSADGQIRAMNPTWRDEFI
NRYWGAFLFNEYGLFNAHSQGAREALSDVTRVSLAFWGFDKIDIAQM IQLERGFLAKIVPGFDESTAVPKAEW
TNGEVYKSARLA VEG LWQE VFDWNE SA FS VHA VY DAL FG QF VR RE FF QRLA PRFGDN LTPFF INQA QT YF QIA
KQGVQDLYNCLGDDPEFSDYNRTVMRNWTGK WLEPTIAALRDFMGLFAKLPAGTTDKEEITASLYRVVDDWI
EDYASRIDFKADR DQIVKA VLAGLK

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

AANRAPTSVNAQE VHRWLQSFNWDFKNNRTKYATKYKMANETKEQFKLIAKEYARMEAVKDERQFGSLQVA
LTRLNAGVRVHPKWNETMKVVS NFLEVGEYNAIAATGMLWDSAQAAE QKNGYLAQVLDEIRHTHQCAVNY
YFAKNGQDPAGHNDARRTRTIGPLWKG MKRVFSDGFISGDAVECSNLQLVGEACFTNPLIVAVTEWAAANG
DEITPTVFLSIETDELRH MANGYQTVVI ANDPASAKYLTDLNNAFWTQQKYFTPVLGMLFEYGS KFKVEPW
VKTWDRWVYEDWGGIWIGRLGKYGVESPRSLKDQDAYWAHHDLYLLAYALWPTGFFRLALPDQEE MEWF
EANYPGWYDHYGKIYEEWRARGCEDPSSGFIPLMWFIENNHPYIDRVSQVFCPSLAGASTLRVHEYNGEM
HTFSDQWGERMWLAEPERYECQNI FEQYEGRELSE VIAELHGLRS DGKTLIAQPHVRGDKLWTLDI KRLNCV
FKNPVKAF

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

KRG LTD PER AIIAA VP DH ALDT QR KYHYFIQPRWKPLSEYEQLSCYAQPNPDW IAGGLDWGDWTQKF HGG
RPSWGNESTELRTTDWYRHRDPARRWH PYVKDKSEEARYTQRFLAAYSSEGSIRTIDPYWRDEILNKYFGALL
YSEYGLFNAHSSV GRDCLSDTIRQ TAVFA ALDKV DNAQMIQMERL FIAKLV PGFDASTDVPKKIWT TDPI YSGA
RATVQEIWQGVQDWNEILWAGH A VYDATFGQFARRE FFQRLATVYGD TL PFFT AQSQTYF QTTRGAIDDLFV
YCLANDSEFGA HNRFLNAWTEHYLASSVAALKDFV GLYAKVEK VAGAT DSAGVSEAL QRVFGDWKIDYADKI
GFRVDVDQKVDAVL AGY

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

NRAPVGVEPQE VHKWLQSFNWDFKENRTKYPTKYHMANETKEQFKVIAKEYARMEA AKDERQFGTLLDGLT
RLGAGNKVHPRWGETMKVISNFLEVGEYNAIAASAMLWDSATAAEQKNGYLAQVLDEIRHTHQCAF INHYY
KHYHDPAGHNDARRTRAIGPLWKG MKRVFADGFISGDAVECSNLQLVGEACFTNPLIVAVTEWASANGDEIT
PTVFLS VETDELRH MANGYQTVVI ANDPASAKFLNTDLNNAFWTQQKYFTPVLGMLFEYGS KFKVEPWVKT
WNRWVSEDWGGIWIGRLGKYGVESPRSLRDAKRDAYWAHHDLALAAYAMWPLGFARLALPDEEDQAWFE

ANYPGWADHYGKIFNEWKKLGYEDPKSGFIPYQWLLANGHDVYIDRVSQVPFIPSLAKGTGSLRVHEFNGKKH
SLTDDWGERQWLIEPERYECHNVFEQYEGRELSEVIAEGHGVRSDGKTLIAQPHTRGDNLWTLEDIKRAGCVF
PDPLAKF

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

AYTTSQTKNDQLKEPMFFGQPVNARYDQQKYDIFEKLIEKQLSFFWRPEEVDSRDRIDYQALPEHEKHIFIS
NLKYQTLLDSIQGRSPNVALLPLISIPELETWVETWAFSETIHSRSYTHIIRNIVNDPSVFDDIVTNEQIQKRAEGI
SSYYDELIEMTSYWHLLGEHTVNGKTVSLRELKKLYLCMSVNALEAIRFYVSFACSFABAERELMEGNAK
IIRLIARDEALHTGTQHMLNLLRGADDPEMAEIAEECKQECYDLFVQAAQQEKDWADYLFRDGSMIGLNKDI
LCQYVEYITNIRMQAVGLDPFQTRSNSNPIPWINTWLV

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

ISAINWNKIQDDKDLEVWNRLTSNFLPEKVPNSNDIPAWQTLAAEQQLTIRVFTGLTLLTIQNIAGAPSLM
ADAITPHEEAVLNSISFMEAVHARSYSSIFSTLCQTKEVDAAYAWESENPPQLQRKAQIIAHYVSDEPLKKIASVF
LESFLFYSGFWLPMYFSSRGKLTNTADLIRLIIRDEAVHGGYIGYKYQIALQKLSAIEREELKLFALDLLMELYDNEIR
YTEALYAETGWVNDVKAFLCYNANKALMINLGYEALFPPEMADVNPAILAALSP

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

SNEYDEYIANHTDPVKAINWNVIPDEKDKLEVWDRITGNFWLPEKIPVSNDIQSWNKMTPEQLATMRVFTGL
TLLDTIQGTVGAISLLPDAETMHEEAVYTNIAMESVHAKSYSNIFMTLASTPQINEAFRWSEENENLQRKAKII
MSYYNGDDPLKKKAVASTLLESFLYSGFVLPMLSSRAKLTNTADIIRLIIRDESvhGYYIGYKYQQGVKKLSEAEQ
EEYKAYTFDLMYDLYENEIEYTEDIYDDLGWTEDVKRFLRYNANKALNNLGYESGLFPTDETkvspailssls

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

NPSVEDEPLLRENPRRFVVFPPIEHDIWQMYKKAESFWTAEEVDSLKDQHWEALKPDERHFISHVLAFFAAS
DGIVNENLVERFSQEVTQTEARCFYGFQIAMENIHSEMSLLIDTYIKDPKEREYLFNAIETMPCVKKKADWALR
WIGDKEATYGERVVAFAAVEGIGFFSGSFASIFWLKKRGLMPGLTSNELISRDEGLHCDFACLMFKHLVHKPAEQ
RVREIITNAVRIEQEFLTEALPVKLGMNCTLMQYIEFVADRLMLELGFNKIFRVENPFDME

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

LNKELETLREENRVKSDLMLKEKLSKDAENHKAYLKSHQVHRHKLKEMEKEEPLLNEDKERTVLFPIKYHEIWQAY
KRAEASFWTAAEIDLSDKDIHDWNNRMNENERFFISRVLAFFAASDGIVNENLVENFSTEVQIPEAKSFYGFQIMI
ENISETSYLLIDTYIKDPKESEFLFNAIHTIPEIGEKAEWALRWIQQDADALFGERLVAFASIEGVFFSGSFASIFWLK
KRGMMPGLTSNELICRDEGLHTDFACLLFAHLKNKPDAIVEKIVTEAVEIEQRYFLDALPVALLGMNADLMN
QYVEFVADRLLVAFGNKKYYKVENPFDME

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

FQKERHDMKEAEKDEILLMENSRRFVMFPIKYHEIWAAYKKVEASFWTAAEIELAKDTEDFQKLTDQKTYIGN
LLALSISSDNLVNYLIENFSAQLQNPEGKSFYGFQIMMENIYSEVYSMMVDAFFKDPKNIPLFKEIANLPEVKHK
AAFIERWISNDDSLYAERLVAFAAKEGIFQAGNYASMFWLTDKIMPGLAMANRNICRDRGAYTDFSCLLFAHL
RTKPNPKIIEKIITEAVEIEKEYYSNSLPVEKFGMDLKSIIHTYIEFVADGLLQGFGNEKYY

>d1afra_a.25.1.2 (A:) delta 9-stearoyl-acyl carrier protein desaturase {Castor bean (Ricinus communis)}

MPPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKVEKCWQPQDFLPDPASDGFDEQVRELRERAKEIP
DDYFVVLVGDMITEEALPTYQTMNLTLDGVRDET GASPTSWAIWTRA WTAEENRHGDLLNKYLYLSGRVDMR
QIEKTIQYLIGSGMDPRTENSPLYGFIYTSFQERATFISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIV
EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDHFSAVAQRLGVYTA KDYADILEFLVGRWKVDKL
TGLSAEGQKAQDYYCRLPPIRRLEERAQGRAKEAPTMPFSWIFDRQVKL

>d1rhga_a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF) {Human (Homo sapiens)}

LPQSFLLKCLEQVRKIQGDGAALQEKLATYKLCHPEELVLLGHSLGPWAPLSSCPSQLQLAGCLSSQLHSGLFLY

QGLLQALEGISPELGPTLDLQLDVADFATTIWQQMEELGMAPALQPTQGAMPAFASAFQRRAGGVLVASHL
QSFLEVSYRVLRLA

>d1bgc_ a.26.1.1 (-) Granulocyte-colony stimulating factor (G-CSF) {Cow (Bos taurus)}

SLPQSFLLKCLEQVRKIQADGAELQERLCAAHKLCHPEELMLLRHSLGIPQAPLSSCSSQLRGCLNQLHGGI
FLYQGLLQALAGISPELAPTLDTLQLDVTDFATNIWLQMEDLGAAPAVQPTQGAMPTFTSAFQRRAGGVLVAS
QLHRFLELAYRGLRYLA

>d1bgea_ a.26.1.1 (A:) Granulocyte-colony stimulating factor (G-CSF) {Dog (Canis familiaris)}

PLPQSFLLKCLEQMRKVQADGTALQETLCATHQLCHPEELVLLGHALGIPQPPPLSSCSSQLQMGCLRQLHSG
LFLYQGLLQALAGISPELAPTLDTLQLDFTTDFAINIWQQMEDLGMAPAVPPTQGTMFTAFAFQRRAGGVLA
SNLQSFLELAYRALRHFAK

>d1alu_ a.26.1.1 (-) Interleukin-6 {Human (Homo sapiens)}

LTSSERIDKQIRYILDGISALRKETCNKSNCESSEKAEALAEENNLPKMAEKDGCFQSGFNEETCLVKIITGLLEFEV
YLEYLQNRFESSEEQARAVQMSTKVLIQFLQKKAKNLDAITTPDPTTNASLLTKLQAQNQWLQDMTTHLILRSF
KEFLQSSLRALRQM

>d1i1rb_ a.26.1.1 (B:) Interleukin-6 {Human herpesvirus 8, Kaposi's sarcoma herpes-virus}

EFEKDILLQRLNWMLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINTDHCGLIGFNETSCLKLADGFFEFE
VLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPPKFDRGLLGRLQGLKYWVRHFASFYVLSAM
EKFAGQAVRVLDsip

>d1a7m_ a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (Mus musculus)}

SPLPITPVNATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEPPNNLDKLCGPNVTDFFPHAN
GTEKAKLVELYRMVAYLSASLTNITRDQKVNLPSAVSLHSKLNATIDVMRGLLSNVLCRLCNKYRVGHVDVPPV
DHSDKEVFQKKKLGQCLLGYKQVISVVVQAF

>d1lki_ a.26.1.1 (-) Leukemia inhibitory factor (LIF) {Mouse (Mus musculus)}

NATCAIRHPCHGNLMNQIKNQLAQLNGSANALFISYYTAQGEPPNNVEKLCAPNMDFPSFHGNGETKLV
ELYRMVAYLSASLTNITRDQKVNLPTAVSLQVKLNATIDVMRGLLSNVLCRLCNKYRVGHVDVPPV
FQRKKLGQCLLGYKQVISVVVQAF

>d1emra_ a.26.1.1 (A:) Leukemia inhibitory factor (LIF) {Human (Homo sapiens)}

LMNQIRSQLAQLNGSANALFILYYTAQGEPPNNLEKLCGPNVTDFFPHANGTEKAKLVELYRIVVYLGTSLGNI
TRDQKILNPSALSLHSKLNATADILRGLLSNVLCRLCSKYHVGHDVTVGPDTSGKDVFQKKKLGQCLLGYKQVI
SVLAQAF

>d1a22a_ a.26.1.1 (A:) Growth hormone, somatotropin {Human (Homo sapiens)}

FPTIPLSRLFDNAMLRAHRLHQLAQDFTYQEFEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLLELR
SLLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEERIQTLMGRLEGQIFKQTYSKFDTDALLKNYGLLYCF
RKMDKVETFLRIVQCRSVEGSCGF

>d1axia_ a.26.1.1 (A:) Growth hormone, somatotropin {Human (Homo sapiens)}

TIPLSRLFDNAMLRAHRLHQLAQDFTYQEFEAYIPKEQKYSFLQNPQTSLCFSESIPTPSNREETQQKSNLLELRISL
LLIQSWLEPVQFLRSVFANSLVYGASDSNVYDLLKDLEERIQTLMGRLEDGSPRTGQAFKQTYAKFDANSHND
LLKNYGLLYCFRDRMTYVATYLRIVQCRSVEGSCGF

>d1hgu_ a.26.1.1 (-) Growth hormone, somatotropin {Human (Homo sapiens)}

PTIPLSRLFQNAMLRAHRLHQLAQDFTYQEFEAYIPKEQKYSFLQAPQASLCFSESIPTPSNREQAQQKSNLQLLRI
SLLIQSWLEPVGFLRSVFANSLVYGASDSNVYDLLKDLEEGIQTLMGRLEDGSPRTGQAFKQTYAKFDANSHND
DALLKNYGLLYCFRKDMDKVETFLRIVQCRSVEGSCGF

>d1huw_ a.26.1.1 (-) Growth hormone, somatotropin {Human (Homo sapiens)}

FPTIPLSRLADNAWRADRLNQLAQDFTYQEFEAYIPKEQIHSFWWNPQTSLCPSESIPTPSNKEETQQKSNLLELL

RISLLIQSWEPEVQFLRSVFANSLVYGASDSNVYDLLKDLLEGIQTLGRLEALLKNYGLYCFNKDMSKVSTYLR
TVQCRSVEGSCGF

>d1f6fa_a.26.1.1 (A:) Placental lactogen {Sheep (Ovis aries)}

AQHPPYCRNQPGKCQIPLQLFDRATTVANYNSLAGEMVNRFDEQYGQGINSESKVINCHTSSITTPNSKAEAINTEDKILFKLVISLLHSWDEPLHHAVTELANSKGTPALLTKAQEIKEAKVLVDGVEVIQKRIHPGEKNEPYPVWSEQSSLTSQDENVRRVAFYRLFHCLHRDSSKIYTIRLIKCRLTSC

>d1cnt1_a.26.1.1 (1:) Ciliary neurotrophic factor (CNTF) {Human (Homo sapiens)}

PHRRDLCRSIWLARKIRSDLTALTESYVKHQGLNKNINLDSADGMPVASTDQWSELTEAERLQENLQAYRTFH
VLLARLLEDQQVHFPTEGDFHQAIHTLLQVAAFAYQIEELMILLEYKIPRNEADGMPINVGDGGLFEKKLWGL
KVLQELSQWTVRSIHDLRFISSHQTGIP

>d1ax8_a.26.1.1 (-) Leptin (obesity protein) {Human (Homo sapiens)}

IQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTLDFIFPGLHPILTSLKMDQTLAVYQQILTSMPSRNVIQISNDL
ENLRDLLHVLAFSKSCHLPEASGLETLDSLGGVLEASGYSTEVALSRLQGSLQDMLWQLDLSPGC

>d1evsa_a.26.1.1 (A:) Oncostatin M {Human (Homo sapiens)}

GSCSKEYRVLLGQLKQTDLMQDTSRLLDPYIRIQGLDVPKLREHCRERPGAFPSEETRGLGRRGFLQTLNATL
GCVLHRLADLEQRLPKAQDLERSGLNIEDLEKLQMARPNILGLRNNIYCMAQLLDNSDTAEPTKAGRGAQPP
TPTPASDAFQRKLEGCRFLHGYHRFMHSGRVSFSKW

>d1f45b_a.26.1.1 (B:) Heterodimeric interleukin-12 alpha chain {Human (Homo sapiens)}

QNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITDKTSTVEACLPLELTKNESCLNSRETTSFITNGSCLASRKTSF
MMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMALVIDELMQALNFNSETVPQKSSLEEPDFYK
TKIKLCILLHAFRIRAVTIDRVMSYLNAS

>d1eera_a.26.1.2 (A:) Erythropoietin {Human (Homo sapiens)}

APPRLICDSRVLERYLLEAKEAKITTGCAEHCSLNEKITVPDTKVNFYAWKRMEVGQQAVEVWQGLALLSEAV
LRGQALLVKSSQPWEPLQLHVDKAVSGLRSLLRALGAQKEAISNSDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR

>d2gmfa_a.26.1.2 (A:) Granulocyte-macrophage colony-stimulating factor (GM-CSF) {Human (Homo sapiens)}

RSPSPSTQPWEHVNAIQEARLLNLSRDTAAEMNETVEVISSEMFDLQEPTCLQTRLELYKQGLRGSLTKKGPLT
MMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFDCWEP

>d1hzia_a.26.1.2 (A:) Interleukin-4 (IL-4) {Human (Homo sapiens)}

HKCDITLQAIKTLNSLTEQKTLCTELTVTDIFAASKNTTEKFRCATVLRQFYSHHEKDTRCLGATAQQFHRHK
QLIRFLKRLDRNLWGLAGLNSCPVKLEANQSTLENFLERLKTIMREKYSKCSS

>d1hula_a.26.1.2 (A:) Interleukin-5 {Human (Homo sapiens)}

IPTSALVKETLALLSTHRTLLIANETLRIPVPHKNHQLCTEIFQGIGTLESQTVQGGTVERLFKNLSLIKYYIDGQK
KKCGEERRRNQFLDYLQEFLGVMNTEWI

>d1hmca_a.26.1.2 (A:) Macrophage colony-stimulating factor (M-CSF) {Human (Homo sapiens)}

SEYCSHMGSGHLQLQLRIDSQMETSCQITFEFVDQEQLKDPVCYLKKAFLLVQDIMEDETMFRDNTPNAIAIVQLQELSLRKSCFTKDYEEDKACVRTFYETPLQLLEKVKNVFNETKNLLDKDWNIIFSKNCNNSAECSSQGH

>d1etea_a.26.1.2 (A:) Flt3 ligand {Human (Homo sapiens)}

TQDCSFQHSPISSDFAVKIRELSDYLLQDYPVTVASNLQDDELCGGLWRLVLAQRWMERLKVAGSKMQGLLE
RVNTEIHVTKCAFQPPPCLRFTQTNISRLLQETSEQLVALKPWITRQNFSRCLELQCQP

>d1scfa_a.26.1.2 (A:) Stem cell factor, SCF {Human (Homo sapiens)}

NVKDVTKLVANLPKDYMITLEKVVPGMDVPSHCWISEMVVQLSDSLTLLDKFSNISEGLSNYSIIDKLVNIVDDL
VECVKENSSKDLKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVVASETSDCVVS

>d1scfc_a.26.1.2 (C:) Stem cell factor, SCF {Human (Homo sapiens)}

NVKDVTKLVANLPKDYMITLKVVPGMDVLPSHCWISEMVVQLSDSLTDLLDKFSNISEGLSNYSIIDKLVNIVDDL
VECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFNRSIDAF

>d3inkc_a.26.1.2 (C:) Interleukin-2 (IL-2) {Human (Homo sapiens)}

STKKTQLQLEHLLLQLQMILNGINNYKNPKLTRMLTFYMPKKATELKHLQCLEELKPLEEVNLNAQSKNFHLR
PRDLISNINVIVLELGSETTFMCEYADETATIVEFLNRWITFAQSIISTLT

>d1jli_a.26.1.2 (-) Interleukin-3 (IL-3) {Human (Homo sapiens)}

ANCSIMIDEIHHLRPPNPLDPNNLNSEDMILMERNLRTPNLLAFVRAVKHLENASAIESILKNLLPCPLATA
APTRHPIHKDGDWNEFRRKLTYLKTLENAQAQQ

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

GGPVPPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESLINSGCSAIKTOQMLSGFCPHKV
SAGQFSSLHVVRDTKIEVAQFVKDLLLHLKKLFREGRFN

>d2ilk_a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory factor, CSIF) {Human (Homo sapiens)}

TQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQLDNLLKESLLEDFKGYLGQCQALSEMIQFYLEEVMP
QAENQDPDIKAHVNSLGENLKTLLRLRRCHRFPCENKSKEAVEQVKNAFNKLQEKGYKAMSEFDIFINYIEAY
MTMKIRN

>d1vfk_a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory factor, CSIF) {Epstein-Barr virus}

CDNFPQMLRDLRDAFSRVKTFFQTKDEVDNLLKESLLEDFKGYLGQCQALSEMIQFYLEEVMPQAENQDPEAK
DHVNSLGENLKTLLRLRRCHRFPCENKSKEAVEQIKNAFNKLQEKGYKAMSEFDIFINYIEAYMTIK

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

MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIYEMLQNIIFRQDS
SSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLHLKRYYGRILHYLKAKEYSHCAWTIVRVEI
LRNFYFINRLTGYLRN

>d1rmi_a.26.1.3 (-) Interferon-beta {Mouse (Mus musculus)}

INYKQLQLQERTNIRKCQELLEQLNGKINLYRADFKIPMEMTEKMQKSYTAFAIQEMLQNVFLVFRNNFSSTG
WNETIVVRLDELHQQTVFLKTVLEEKQEERLTWEMSSTALHLKSYWVQRYLKLMKYNSYAWMVVRAEIFR
NFLIIIRRLLTRNFQ

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

THSLGSRRTLMLLAQMRRISLFSCLKDRHDFGPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKDSSAAWDET
LLDKFYTELYQQLNDLEACVIQGVGVTEPLMNEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEIMRSFSLST
NLQE

>d1b5l_a.26.1.3 (-) Interferon-tau {Sheep (Ovis aries)}

CYLSRKLMILDARENKLDRMNRLSPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLYEMLQQSFNLFYTEH
SSAAWDTTLEQLCTGLQQQLDHLTCRGQVMGEEDSELGNMDPIVTKKYFQGIYDYLQEKGYSDCAWEIV
RVEMMRALTVSTTLQKRLTK

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

QGQFFREIENLKEYFNASSPDVAKGGPLFSEILKNWKDESDKKIIQSQIVSFYFKLFENLKDQNQVIQRSMDIICKQD
MFQKFLNGSSEKLEDFKKLIQIPVDDLQIQRKAINELIKVMNDLS

>d1fyha1_a.26.1.3 (A:0-124) Interferon-gamma {Human (Homo sapiens)}

MQDPYVKEAENLKKYFNAGHSVDADNGTLFLGILKNWKEESDRKIMSQIVSFYFKLFKNFKDDQSIQKSVETI
KEDMNVKFFNSNKKRDDFEKLTNSVTDLNVQRKAIDELIQVMAELGANV

>d1fyha2_a.26.1.3 (A:201-324) Interferon-gamma {Human (Homo sapiens)}

SGEFVKEAENLKKYFNAGHSVDADNGTLFLGILKNWKEESDRKIMSQIVSFYFKLFKNFKDDQSIQKSVETIKE

DMNVKFFNSNKKRDDFEKLTNYSVTDLNVQRKAIHELIQVMAELSPAA
>d2rig_ a.26.1.3 (-) Interferon-gamma {Rabbit (*Oryctolagus cuniculus*)}
QDTLTRETEHLKAYLKANTSDVANGGPLFLNLIRNWKESDNKIIQSQIVSFYFKLFDNLKDHEVIKKSMESIKEDI
FVKFFNSNLTKMDDFQNLTTRISVDDRLVQRKAVSELSNVLF
>d1a8h_1 a.27.1.1 (349-500) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}
LADDLGNLVQRTRAMILFRFAEGRIPEPVAGEELAEGTGLAGRLRPLVRELKFHVALEEAMAYVKALNRYINEKKP
WELFKKEPEEARAVLYRVVEGLRIASILLTPAMPDKMAELRRALGLKEEVRLLEAERWGLAEPRPIPEAPVLFPK
K
>d1f4la1 a.27.1.1 (A:389-548) Methionyl-tRNA synthetase (MetRS) {Escherichia coli}
VVNLASRNAGFINKRFDGVLAELADPQLYKTFTDAEVIDGEAWESREFGKAVREIMALADLANRYVDEQAPW
VVAKQEGRDADLQAICSMGINLFRVLMTYLKPVLPLTERAEAFNTELWDGIQQPLLGHKVNPFKALYNRID
MRQVEALVEASKE
>d1ile_1 a.27.1.1 (642-821) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}
YFLTLWNVYSFFVTYANLDRPDLKNPPPKEPRPEMDRWLLARMQDLIQRVTEALEAYDPTTSARALRDFVVED
LSQWYVRRNRRRFWKNEDALDREAAYATLYEALVLVATLAAPFTPFLAEVLWQNLVRSRVLEAKESVHLADWPE
ADPALADEALVAQMRAVLKVVDLARAARAKSGV
>d1ffya1 a.27.1.1 (A:645-917) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}
YRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNQEVQNFINVELSNFY
DYGKDILYIEQRDSSHRRSMQTVLYQILVDMTKLLAPIVHTAEVWSHTPHVKEESVHLADMPKVVEVDQALL
DKWRTFMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNAEFLTSFDALHQLFIVSQVKVVDKDDQAT
AYEHGDIVIEHADGEKERCWNYSEDLGADELTHLCPRCQQVVKSLV
>d1qu3a1 a.27.1.1 (A:645-881) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}
YRKIRNTLRFMLGNINDFNPDTDSIPESELLEVDRYLLNRLREFTASTINNYENFDYLNQEVQNFINVELSNFY
DYGKDILYIEQRDSSHRRSMQTVLYQILVDMTKLLAPIVHTAEVWSHTPHVKEESVHLADMPKVVEVDQALL
DKWRTFMNLRDDVNRALETARNEKVIGKSLEAKVTIASNDKFNAEFLTSFDALHQLFIVSQVKVVDKDDQAT
AYEHGDIVIEHA
>d1gaxa1 a.27.1.1 (A:579-862) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}
ANKLYNAARFVLLSREGFQAKEDPTLADRMRSLRGVEEITALYEALDLAQAAREVYELVSEFCDWYLEA
AKPALKAGNAHTLRTLEEVLAFLKLLHPMPMPFLTSELYQALTGKEELALEAWPEPGGRDEEAERAFAEALKQAVT
AVRALKAEGLPPAQEVRYLEGETAPVEENLEVFRFLSRADLLPERPAKALVKAMPRVTARMPLEGLLDVEEW
RRRQEKRKELLALAERSQRKLASPGFREKAPKEVVEAEEARLKENLEQAERIREALSQLIG
>d1f7ua1 a.27.1.1 (A:484-607) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast (*Saccharomyces cerevisiae*)}
DTGPYLYQAHRSRLRSVERNAGITQEWINADFSLLKEPAAKLLIRLLGQYPDVLRNAIKTHEPTTVTYLFKLTHQ
VSSCYDVLWVAGQTEELATARLALYGAARQVLYNGMRLLLTPVERM
>d1iq0a1 a.27.1.1 (A:467-592) Arginyl-tRNA synthetase (ArgRS) {Thermus thermophilus}
GDTGPYVQYAHARAHSILRKAGEWGAPDLSQATPYERALALDLDFFEEAVLEAAEERTPHVLAQYLLDLAASW
NAYYNARENGQPATPVLTAP EGLRELRLSLVQLQRTLATGLDLLGIPAPEVM
>d1acp_ a.28.1.1 (-) Acyl carrier protein {Escherichia coli}
STIEERVKKIIGEQLGVKQEEVTNNASFVEDLGADSLDTVELVMALEEEFDTEIPDEEAEKITTQAAIDYINGHQ
A
>d1f80d_ a.28.1.1 (D:) Acyl carrier protein {Bacillus subtilis}

SADTLERVTKIIVDRLGVDEADVKEASFKEDLGADXLDVVELVMELEDEFDMEISDEDAEKIATVGDAVNYIQ
>d1af8__ a.28.1.1 (-) Actinorhodin polyketide synthase acyl carrier protein, ACT ACP {Streptomyces coelicolor, A3(2)}
MATLLTDDLRRALVECAGETDGTDLSGDFLDLRFEDIGYDSLALMETAARLESRYGVSIPDDVAGRVDTPRELL
DLINGALAEAA
>d1dnya_ a.28.1.2 (A:) Peptidyl carrier protein (PCP), thioester domain {Bacillus brevis}
YVAPTNVESKLAEIWERVLGVSGIGILDNFFQIGGHSLKAMAVAAQVHREYQVELPLKVLFAQPTIKALAAQYVA
T
>d1dv5a_ a.28.1.3 (A:) apo-D-alanyl carrier protein {Lactobacillus casei}
ADEAIKNGVLDILADLTGSDDVKKNLDNLNFETGLDSMGTQVLLLELQSQFGVDAPVSEFDRKEWDTPNKIIAK
VEQAQ
>d1unka_ a.28.2.1 (A:) ImmE7 protein (Im7) {Escherichia coli}
MELKNSISDYTEAEFVQLLKEIEKENVAATDDVLDVLLHEHFVITEHPDGTDLIYYPSDNRDDSPEGIVKEIKEWR
AANGKPGFKQG
>d1imy__ a.28.2.1 (-) ImmE8 (Im8) {Escherichia coli}
MELKNSISDYTEAEFLQLVTTICNADTSSEEELVKLVTHFEEMTEHPSGSDLIYYPKEGDDDPSGIVNTVKQWRAAN
GKSGFKQG
>d1emva_ a.28.2.1 (A:) ImmE9 protein (Im9) {Escherichia coli}
LKHSISDYTEAEFLQLVTTICNADTSSEEELVKLVTHFEEMTEHPSGSDLIYYPKEGDDDPSGIVNTVKQWRAAN
GKSGFKQG
>d2eiaa1 a.28.3.1 (A:148-222) EIAV capsid protein p26 {Equine infectious anemia virus}
PKAQNIROQGAKEPYPEFVDRLLSQIKSEGHQPQEISKFLTDTLTIQNANEECRNAMRHLRPEDTLEEKMYACRDIG
>d1qrjb1 a.28.3.1 (B:131-214) HTLV-I capsid protein {Human T-cell leukemia virus type 1}
PSWASILQGLEEPYHAFVERLNIALDNGLPEGTPKDPIRLSAYSANKECQKLLQARGHTNSPLGDMRLACQT
WTPKDKTKVL
>d1a8o__ a.28.3.1 (-) HIV capsid protein, dimerisation domain {Human immunodeficiency virus type 1}
MDIRQGPKEPFRDYVDRFYKTLRAEQASQEVKNWMTETLLVQ NANPDCKTILKALGPGATLEEMMTACQG
>d1d1da1 a.28.3.1 (A:151-230) RSV capsid protein {Rous sarcoma virus}
GPWADITQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRAAPSTLTPGEIIKYVLDRQK
IAP
>d1eoqa_ a.28.3.1 (A:) RSV capsid protein {Rous sarcoma virus}
MDIMQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIQQLIRTA PSLTPGEIIKYVLDRQKTAP
>d1e6ia_ a.29.2.1 (A:) GCN5 {Baker's yeast (Saccharomyces cerevisiae)}
RGPHDAAIQNLTELQNHAAA WPFLQPVNKEEVPDYYDFIKEPM DLSTMEIKLESNKYQKMEDFIYDARLFVN
NCRM YNGENTSYKYANRLEKFFNNKVKEIPEYSHLID
>d1f68a_ a.29.2.1 (A:) GCN5 {Human (Homo sapiens)}
GDQLYTTLNLLAQIKSHPSAWPFM EPVKKSEAPDYYEVIRFPIDLKTMTERLRSRYYTRKL FVADLQRVIANCR
EYNPPDSEYCRCASALEKFFYFKLKEG
>d1b91a_ a.29.2.1 (A:) P300/CAF histone acetyltransferase bromodomain {Human (Homo sapiens)}
GSHMSKEPRDPDQLYSTLKSILQQVKSHQSAWPMEPVKRTEAPGYYEVIRSPMDLKTMSERLKNRYYVSKLF
MADLQRVFTNCKEYNAP ESEYYKCANILEKFFF SKIKEAGLIDK
>d1eqfa1 a.29.2.1 (A:1359-1497) TAFII250 double bromodomain module {Human (Homo sapiens)}

GTTVHCDYLNRPHSIHRRRTDPMVTLSSILESIINDMRDLPNTYPFHTPVNAKVKDYYKIITRPMQLQTLREN
VRKRRLYPSREEFREHLELIVKNSATYNGPKHSLTQISQSMLDLCKEKLKEKEDKLARLEKAINP
>d1eqfa2 a.29.2.1 (A:1498-1625) TAFII250 double bromodomain module {Human (Homo sapiens)}
LLDDDDQVAFSFILDNIVTQKMMAVPDSWPFFHPVNKKFVPDYYKVIVNPMDLETIRKNISKHYQSRESFLD
DVNLILANSVKYNGPESQYTKTAQEIVNVCYQTLTEYDEHLTQLEKDICTAKEAA
>d1gm5a1 a.29.4.1 (A:7-105) RecG, N-terminal domain {Thermotoga maritima}
FTSSLFLWGEALPTLLEFLNEVEKMLKNQVNTRRIHQQLKEELDDPLLENKDEEKLQAFLDYVKEIPNLPEARKR
YRIQKSLEMIKLRSWFLIDYLE
>d1gkza1 a.29.5.1 (A:38-185) Branched-chain alpha-ketoacid dehydrogenase kinase
(BCK) {Rat (Rattus norvegicus)}
VRLPTMMLYSGRSQDGSHLLKSGRYLQQELPVRIAHRIGFRSLPFIIGCNPTILHVHELYIRAFQKLTDFPPIKD
QADEAQYCQLVRQLLDDHKDVVTLLAEGLRESRKHIEDEKLVRYFLDKTLTSRLGIRMLATHHLALHEDKP
>d1jm6a1 a.29.5.1 (A:1003-1169) Pyruvate dehydrogenase kinase {Rat (Rattus norvegicus),
isozyme 2}
ASLAGAPKYIEHFSKFSPSPLSMKQFLDFGSSNACEKTSFTLRQELPVRLANIMKEINLLPDRVLSPTSVQLVQS
WYVQSLLDIMEFLDKDPEDHRTLSQFTDALVTIRNRHNDVVPTMAQGVLEYKDTYGDDPVSQNQNIQYFLDRF
YLSRISIRMLINQHTLIFD
>d1buca1 a.29.3.1 (A:233-383) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}
GKGFKIAMMTLDGGRIGVAAQALGIAEAALADAVEYSKQRVQFGKPLCKFQSISFKLADMKMQIEARNLVYK
AACKKQEGKPFTVDAAIKRVASDVAMRVTTAEVQIFGGYGYSEEYPVARHMRDAKITQIYEGTNEVQLMVTG
GALLR
>d1jqia1 a.29.3.1 (A:235-387) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus)}
MGFKIAMQTLDMGRIGIASQALGIAQASLDCAVKYAENRHAFGAPLTKLQNIQFKLADMALAESARLLTWRA
AMLKDNNKPFTKESAMAKLAASEAATAISHQAIQILGGMGYVTEMPAERYYRDARITEIYEGTSEIQLRVIAGHL
LRSYR
>d3mdda1 a.29.3.1 (A:242-395) Medium chain acyl-CoA dehydrogenase {Pig (Sus scrofa)}
GAGFKIAMGTFDKTRPPVAAGAVGLAQRALDEATKYALERKTFGKLLAEHQGISFLADMAMKVELARLSYQR
AAWEIDSGRRNTYYASIKAAYADIANQLATDAVQVFGGNGFNTEYPVEKLMRDAKIYQIYEGTAQIQRIIIARE
HIGRYK
>d1egda1 a.29.3.1 (A:242-396) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens)}
GAGFKVAMGAFDKERPVVAAGAVGLAQRALDEATKYALERKTFGKLLVEHQAFQKIGHFQLMQGKADMYTRLMACRQYVV
QRAAWEVDSGRRNTYYASIKAFAAGDIANQLATDAVQILGGNGFNTEYPVEKLMRDAKIYQIYGGTSQIQRLIV
AREHIDKYKN
>d1ivha1 a.29.3.1 (A:242-392) Isovaleryl-CoA dehydrogenase {Human (Homo sapiens)}
KGVYVLMSGLDLERLVLAGGPLGLMQAVLDHTIPYLHVREAFGQKIGHFQLMQGKADMYTRLMACRQYVV
NVAKACDEGHCTAKDCAGVILYSAECATQVALDGIQCFGGNGYINDFPMGRFLRDAKLYEIGAGTSEVRLVIGR
AFNAD
>d1b6q_ a.30.1.1 (-) ROP protein {Escherichia coli}
MTKQEKTALNMARFIRSQTLLKEKLNEELDPDEQADICESLHDHADELYRSCLARF
>d1f4na_ a.30.1.1 (A:) ROP protein {Escherichia coli}
GTKQEKTILNMARFIRSQALTILEKANELDADEIADIAESIHDHADEIYRSALARFGDDG
>d1f4nb_ a.30.1.1 (B:) ROP protein {Escherichia coli}
EKTILNMARFIRSQALTILEKANELDADEIADIAESIHDHADEIYRSALAR
>d1gtoa_ a.30.1.1 (A:) ROP protein {Escherichia coli}

GTKQEKTALNMARFIRSQTLLTLEKLNEGADEQADICESLHDHADELYRSCLARFGDDGEN
>d1nkd_ a.30.1.1 (-) ROP protein {Escherichia coli}
MTKQEKTALNMARFIRSQTLLTLEKLNEADAQADICESLHDHADELYRSCLARFG
>d1joya_ a.30.2.1 (A:) EnvZ histidine kinase {Escherichia coli}
MAAGVKQLADDRTLLMAGVSHDLRPLTRIRLATEMMSEQDGYLAESINKDIEECNAIIEQFIDYLR
>d1b3qa1 a.30.2.1 (A:293-354) Histidine kinase CheA {Thermotoga maritima}
SQTVRV DIEKLDNLMDLMGELVIARSRILETLK KYNIKE LDESLHLSRITLDLQNVVMKIR
>d1r2aa_ a.31.1.1 (A:) Dimerization-anchoring domain of cAMP-dependent type II PK regulatory subunit {Mouse (Mus musculus)}
HMGHIQIPPGLTLLQGYTVEVLRQQPPDLVDFAVEYFTRLREARR
>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}
WSTIVKLTICPTLKSMAKKCEGSIATMIKKCDK
>d1b0na1 a.34.1.1 (A:74-108) SinR repressor (dimerisation domain)-SinI anti-repressor complex {Bacillus subtilis}
LDSEWEKLVRDAMTSVSKKQFREFLDYQKWRKSQ
>d1b0nb1 a.34.1.1 (B:) SinR repressor (dimerisation domain)-SinI anti-repressor complex {Bacillus subtilis}
FELDQEWEVLMVEAKEANISPEEIRKYLLN
>d1f93f_ a.34.1.1 (F:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}
LSQLQTELLAALLESGLSKEALIQALG
>d1g2ya_ a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}
MVSKLSQLQTEMLAALLESGLSKEALIQALG
>d1g2za_ a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}
MVSKLSQLQTELMAALLESGLSKEALIQALGE
>d1g39a_ a.34.1.1 (A:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}
MVSKLSQLQTELLAALLESGLSKEALIQ
>d1jb6b_ a.34.1.1 (B:) Dimerization cofactor of HNF-1 alpha {Mouse (Mus musculus)}
SKLSQLQTELMAALLESGLSKEALIQAL
>d1e3oc2 a.35.1.1 (C:1-75) Oct-1 {Human (Homo sapiens)}
EEPSDLEELEQFAKTFKQRRIKLGFTQGDVGLAMGKLYGNDFSQTTISRFEALNLSFKNMSKLKPILLEWLNDAE
>d1au7a2 a.35.1.1 (A:5-76) Pit-1 {Rat (Rattus norvegicus)}
GMRALEQFANEFKVRRIKLGFTQTNVGEALAAVHGSEFSQTTICRFENLQLSFKNACKLKAILSKWLEEAEQ
>d1llib_ a.35.1.2 (B:) lambda C1 repressor, DNA-binding domain {Bacteriophage lambda (Escherichia coli)}
STKKKPLTQEQLLEDARRLKAIYEKKKNELGLSQESLADKLMGQSGIGALFNGINALNAYNAALLAKILKVSVEEF
SPSIAREIYEMYEAWS

>d1lmb3_ a.35.1.2 (3:) lambda C1 repressor, DNA-binding domain {Bacteriophage lambda (Escherichia coli)}

PLTQEQLEDARRLKAIYEKKKNELGLSQESVADKMGMGQSGVGALFNGINALNAYNAALLAKILKVSVEEFSPSI
AREIYEMYEAVS

>d1r69_ a.35.1.2 (-) 434 C1 repressor, DNA-binding domain {Bacteriophage 434 (Escherichia coli)}

SISSRVKS KRIQLGLNQAELAQKVGT TQQSIEQLENGTKRPRFLPELASALGVSVDWLLNGT

>d2cro_ a.35.1.2 (-) cro 434 {Bacteriophage 434}

MQTL SERLKKRRIALKMTQTELATKAGVKQQS IQLIEAGVTKRPRFLFEIAMALNCDPVWLQYGT

>d1adr_ a.35.1.2 (-) P22 C2 repressor, DNA-binding domain {Salmonella bacteriophage P22}

MNTQLMGERIRARRKKL KIRQAALGK MVGVSNVAISQWERSETP NGENLL ALSKALQCSPD YLLKG DLS QTN
VAY

>d1copd_ a.35.1.2 (D:) cro lambda repressor {Bacteriophage lambda (Escherichia coli)}

MEQRITLKDYAMRGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEV KPFPSNKKTTA

>d1d1la_ a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda (Escherichia coli)}

MEQRITLKDYAMRGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEV KPWPSN

>d3orca_ a.35.1.2 (A:) cro lambda repressor {Bacteriophage lambda (Escherichia coli)}

EQRITLKDYAMRGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEV KDGEV KPFPSN

>d1ner_ a.35.1.2 (-) Ner {Bacteriophage mu}

CSNEKARDWHRADVIAGLKKRK L SLSRSQFGYAPTT LANALERHWP KGEQII ANALETKPEV I WPSRYQAGE

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

MIGQRIKQYRKEKG YSL SELAEKAGVAKSYLSSIERNLQTNPSIQFLEK VSAVL DVSVHT LLDEKHET

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

MIQSQINRNIRLDLADA ILLSKAKK DLSFAEIADGTGLAEAFVTA ALLGQQ ALPADAARLVGA KLDL DEDSILLQ
MIPLRG CIDD

>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}

TIKDVAK RANVSTTVSHVINKTRFVAEETRNAVWAAIKELHYSPSAVARSMKVNH

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

KPVTL YDVAEYAGV SYQT VSRVV NQASHVSAKTREK VEAAMAELNYIPN RV AQQLAGKQ

>d1lcca_ a.35.1.5 (A:) Lac repressor (LacR), N-terminal domain {Escherichia coli}

MKPVTLYDVAEYAGV SYQT VSRVV NQASHVSAKTREK VEAAMAELNYIPNR

>d1uxc_ a.35.1.5 (-) Fructose repressor (FruR), N-terminal domain {Escherichia coli}

MKLDEIARLAGV SR TT ASY VING KAKQYR VSDKT VEKVM AVVREH NYHPN
AAGLRLQ

>d1uxd_ a.35.1.5 (-) Fructose repressor (FruR), N-terminal domain {Escherichia coli}

MKLDEIARLAGV SR TT ASY VING KAKQYR VSDKT VEKVM AVVREH NYHPN
AAGLRLQ

>d1dula_ a.36.1.1 (A:) Signal sequence binding protein Ffh {Escherichia coli}

FDLND FLEQ KV LVRM EAIINS MTM KERAK P EII KGS R KRIA AGSGM QVQ DVN RLL KQF DDM QRMM KK
M

>d1hq1a_ a.36.1.1 (A:) Signal sequence binding protein Ffh {Escherichia coli}

GFDLND FLEQ L RQM K NMGG M ASLM GKL PG MGQ IPDN VKS QM DD KVL VRM EAIINS MTM KERAK P EII KGS
R KRIA AGSGM QVQ DVN RLL KQF DDM QRMM KK
M

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

ELSLED FLKQM QNL KRL GP FSEIL GLL PG VPQ GLK VDEKA IKR LEAI VL SMT PEER K DP RIL NG SRR KRI AKG SGTS

VQEVRFIKAFEEEMKALMKSLEK
>d1qb2a_a.36.1.1 (A:) SRP54M {Human (Homo sapiens)}
QFTLRDMYEQFQNIMKMGPSQILGMIPGFTDFMSKGNEQESMARLKKLMTIMDSMNDQELDSTDGAKV
FSKQPGRIQRVARGSGVSTRDVQELLQYTKFAQMVK
>d1sknp_a.37.1.1 (P:) Binding domain of Skn-1 {Caenorhabditis elegans}
GRQSKDEQLASDNELPVSAFQISEMSLSELQQVLKNESLSEYQRQLIRKIRRRGKNKVAARTCRQRRTDRHDKM
>d1hloa_a.38.1.1 (A:) Max protein {Human (Homo sapiens)}
NDDIEVESDADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRKRNHTHQQDI
DDLKRQN
>d1an2a_a.38.1.1 (A:) Max protein {Mouse (Mus musculus)}
ADKRAHHNALERKRRDHIKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRKRNHTHQQDIDDLKRQNAL
LEQQVRALEKARS
>d1mdya_a.38.1.1 (A:) Myod B/H LH domain {Mouse (Mus musculus)}
MELKRKTTNADRRKAATMRERRRLSKVNEAFETLKRSTSSNPNQRLPKVEILRNAIRYIEGLQALLRD
>d1an4a_a.38.1.1 (A:) Usf B/H LH domain {Human (Homo sapiens)}
MDEKRRAQHNEVERRRDKINNWIVQLSKIIPDSSMESTKSGQSKGGILSKASDYIQELRQSNHR
>d1a0aa_a.38.1.1 (A:) Pho4 B/H LH domain {Baker's yeast (Saccharomyces cerevisiae)}
MKRESHKHAEQARRNRALVALHELASLIPAEWKQQNVSAAPSKATTVEAACRYIRHLQQNGST
>d1am9a_a.38.1.1 (A:) SREBP-1a {Human (Homo sapiens)}
QSRGEKRTAHNAIEKRYRSSINDKIELKDLVVGTEAKLNKSAVLRAKAI DYIRFLQHSNQKLQENLSIRTAVHKSKS
LK
>d1bod_a.39.1.1 (-) Calbindin D9K {Cow (Bos taurus)}
MKSPEELKGIFEKYDKEGDGQLSKEELKLLQTEFPSLLKGMS TLDEFELDKNGDGEVSFEFQVLVKKISQ
>d1ig5a_a.39.1.1 (A:) Calbindin D9K {Cow (Bos taurus)}
KSPEELKGIFEKYAAKEGDPNQLSKEELKLLQTEFPSLLKGPTSLDEFELDKNGDGEVSFEFQVLVKKISQ
>d1cb1_a.39.1.1 (-) Calbindin D9K {Pig (Sus scrofa)}
SAQKSPAELKSIFEKYAAKEGDPNQLSKEELKQLIQAEPSSLKGPTLDDLFQELDKNGDGEVSFEFQVLVKKIS
Q
>d1a03a_a.39.1.2 (A:) Calcyclin (S100) {Rabbit (Oryctolagus cuniculus)}
MASPLDQAIGLLIGIFHKYSGKEGDKHTLSKELKELQELTIGSKLQDAEIVKLMDDLRNKDQEVDNFQEYITFL
GALAMIYNEALKG
>d1k2ha_a.39.1.2 (A:) Calcyclin (S100) {Rat (Rattus norvegicus), s100a1}
GSELETAMETLINVFHAHSGKEGDKYKLSKKELKDLLQTELSSFLDVQKDADAVDKIMKELDENGDGEVDFQEF
VVLVAALTVCNNFFWENS
>d1qlka_a.39.1.2 (A:) Calcyclin (S100) {Rat (Rattus norvegicus), s100b}
MSELEKAMVALIDVFHQYSGREGDKHKLKSELKELINNELSHFLEEIKEQEVDKVMETLDEDGDGECDFQEF
MAFVSMVTTACHEFFEHE
>d1mho_a.39.1.2 (-) Calcyclin (S100) {Cow (Bos taurus), s100b}
SELEKAVVALIDVFHQYSGREGDKHKLKSELKELINNELSHFLEEIKEQEVDKVMETLSDGDGECDFQEF
FVAMITTACHEFF
>d1a4pa_a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), P11 s100a10, calpactin}
PSQMEHAMETMMFTFKFAGDKGYLTKEPLRVLMEKEFPGLENQKDPLAVDKIMKLDQCRDGKVGQSF
FSLIAGLTIACNDYFVVHMKQ
>d1psra_a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), psoriasin s100a7}

SNTQAERSIIGMIDMFHKYTRRDKIDKPSLLTMMKENFPNLSACDKKGTNYLADVFEKKDKNEDKKIDFSEFL
SLLGDIATDYHKQSHGAAPCSGGSQ

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

PTETERCIESLIAIFQKHAGRDGNNTKISKTEFLIMNTELAAFTQNQKDPGVLDMMKKLDLSDGQLDFQEFLNLIGGLAIACHDSFIKSTQK

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

MLTELEKALNSIIDVYHKYSLIKGNFHAVYRDDLKKLLETECPQYIRKKGADVWFKELDINTDGAVNFQEFLILVIKMGVAAHKKSHEES

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

TKLEEHLEGIVNIFHQYSVRKGHFDTLSKGELKQLLTKEANTIKNIKDAVIDEIFQGLDANQDEQVDFQEFLISVAIALKAAYH

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

TCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKENKNEKVIEHIMEDLDTNADKQLSFEEFIMLMARL

>d1sra_a.39.1.3 (-) C-terminal (EC) domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}

PPCLDSELTEFPLRMRDWLKNVLVTLYERDEDNNLLTEKQKLRVKKIHENEKRLEAGDHPVELLARDFEKNYNM
YIFPVHWQFGQLDQHPIDGYLSHTELAPLRAPIPMEHCTTRFFETCDLDNDKYIALDEWAGCFGIKQKDIDKDLVI

>d1rro_a.39.1.4 (-) Oncomodulin {Rat (Rattus norvegicus)}

SITDILSAEDIAALQECQDPDTFEPQKFFQTSGLSKMSASQVKDIFRFIDNDQSGYLDGDELKYFLQKFQSDARELTESETKSLMDAADNDGDGKIGADEFQEMVHS

>d1cdp_a.39.1.4 (-) Parvalbumin {Carp (Cyprinus carpio)}

AFAGVLNDADIAAALEACKAADSFNHKAFFAKVGLTSKSADDVKKAFAIIDQDKSGFIEEDELKLFLQNFKADAR
ALTDGETKTFLKAGDSDGDGKIGVDEFTALVKA

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

AAKDLLKADDINKALDAVKAEGSFNHKKFFALVGLKAMSANDVKKVFKaidaDASGFIEEEELKFLQVLKSFAADGR
DLTDAETKAFLKAADKDGDKIGIDEFTLVHEA

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

SFAGLKADVAALAAACSAADSFNKHKEFFAKVGLASKSLDDVKKAFYVIDQDKSGFIEEDELKLFLQNFSPSARALTDAETKAFLADGDKDGGMIGVDEFAAMIKA

>d5pal_a.39.1.4 (-) Parvalbumin {Leopard shark (Triakis semifasciata)}

PMTKVLKADDINKAISAFKDPGTFDYKRFHLVGLKGKTDAQVKEVFEILDKDQSGFIEEEELKGVLKGSFAHGR
DLNDTETKALLAAGDSDHDGKIGADEFAKMVAQA

>d1a75a_a.39.1.4 (A:) Parvalbumin {Whiting (Merlangius merlangus)}

AGILADADCAAARKACEAADSFSYKAFFAKCGLSGKSADDIKAFFVIDQDKSGFIEEDELKLFLQVFKAGARALT
DAETKAFLKAGDSDGDGAIGVEEWVALVKA

>d1bu3_a.39.1.4 (-) Parvalbumin {Silver hake (Merluccius bilinearis)}

AFSGILADADVAALKACEAADSFSNYKAFFAKVGLTAKSADDIKAFFVIDQDKSGFIEEDELKLFLQVFSAGARA
LTDAETKAFLKAGDSDGDGAIGVDEWAALVKA

>d1g33a_a.39.1.4 (A:) Parvalbumin {Rat (Rattus rattus)}

MKSADDVKKVFHILDKDKSGFIEEDELGSILKGSSDARDLSAKETKTLMAAGDKDGDKIGVEEFSTLVAES

>d1rtp1_a.39.1.4 (1:) Parvalbumin {Rat (Rattus rattus)}

SMTDLLSAEDIKKAGAFTAADSDFDHKFFQMVGLKKKSADDVKKVFHILDKDKGFIIEDELGSILKGFSSDARD
LSAKETKTLMAAGDKDGKGIVVEEFLVAES

>d1avsa_a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}

QAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEELDAIIIEVDEDGSGTIDFEEFLV
MMVRQMK

>d1ctda_a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}

KSEELANAFRIFDKNADGYIDIEELGEILRATG

>d1dtla_a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}

YKAAVEQLTEEQKNEFKAAFDIFVLGAEDGSISTKELGKVMRMLGQNPTPEELQEMIDEVDEDGSGTVDDEF
VMMVRSMKDDSKGKSEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNNNDGRIDY
DEFLEFMKGV

>d1jc2a_a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus)}

EDAKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVIEEDEDLMKDSKDNNDGRIDFDEFLKMMEGVQ

>d1ncx_a.39.1.5 (-) Troponin C {Chicken (Gallus gallus)}

ASMTDQQAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEELDAIIIEVDEDGS
IDFEEFLVMMVRQMKEAKGKSEEELANCFRIFDKNADGFIDIEELGEILRATGEHVTEEDIEDLMKDSKDNND
GRIDFDEFLKMMEGVQ

>d1smg_a.39.1.5 (-) Troponin C {Chicken (Gallus gallus)}

ASMTDQQAEARAFLSEEMIAEFKAAFDMFDADGGGDISTKALGTVMRMLGQNPTKEELDAIIIEVDEDGS
IDFEEFLVMMVRQMKEADA

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

KSEELANAFRIFDKNADGYIDIEELGEILRATGXVTEEDEDLMKDSKDNNDGRIDFDEFLKMMEGVQ

>d1tn4_a.39.1.5 (-) Troponin C {Rabbit (Oryctolagus cuniculus)}

TDQQAEARSYLSEEMIAEFKAAFDMFDADGGGDISVKELGTVMRMLGQPTKEELDAIIIEVDEDGS
TIDFEEFLVMMVRQMKEAKGKSEEELAELFRIFDRNAADGYIDAELAEIFRASGEHVTDEEIESLMKDGDKNNNDGRID
FDEFLKMMEG

>d1fi5a_a.39.1.5 (A:) Troponin C {Chicken (Gallus gallus), cardiac isoform}

MVRCMKDDSKGKTEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNNNDGRIDYDEF
LEFMKGVE

>d1ap4_a.39.1.5 (-) Troponin C {Human (Homo sapiens), cardiac isoform}

MDDIYKAAVEQLTEEQKNEFKAAFDIFVLGAEDGCISTKELGKVMRMLGQNPTPEELQEMIDEVDEDGS
TVD FDEFLVMMVRCMKDDS

>d1ih0a_a.39.1.5 (A:) Troponin C {Human (Homo sapiens), cardiac isoform}

GKSEEELSDLFRMFDKNADGYIDLEELKIMLQATGETITEDDIEELMKDGDKNNNDGRIDYDEFLEFMKGVE

>d2scpa_a.39.1.5 (A:) Sarcoplasmic calcium-binding protein {Sandworm (Nereis diversicolor)}

SDLWVQKMKTYFNRIDFDKDGAIITMDFESMAERFAKESEMKAEHAKVLMDSLTVWDNFLTAVAGGKGID
ETTFINSMKEMVKNPEAKSVVEGPLPLFRAVDTNEDNNISRDEYGIFGMLGLDKTMAPASFDAIDTNNDG
SLEEFVIAGSDFFMNDGDSTNKVFWGPLV

>d2sas_a.39.1.5 (-) Sarcoplasmic calcium-binding protein {Amphioxus (Branchiostoma
lanceolatum)}

GLNDFQKQKIKFTFDFFLDMNHGDSIQDNDFEDMMTRYKEVNKGSLSDADYKSMQASLEDEWRDLKGRADI
NKDDVVSWEEYLAMWEKIATCKSVADLPAWCQNRIPLFKGMDVSGDGIVDLEEFQNYCKNFQLQCADVPA
VYNVITDGGKVTFDLNRYKELYRLLTSPAADAGNTLMGQKP

>d1c7va_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma lanceolatum)}

EEEILRAFKVFDANGDGVIDFDEFKFIMQKVGEPLTDAEVEEAMKEADEDGNGVIDIPEFMDLIKKS

>d1j7qa_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma lanceolatum)}

AAPKARALGPEEKDEC MKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEARGPKGDKNIGPEE WLTLCSKWVRQDD

>d1j7ra_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma lanceolatum)}

LGPEEKDEC MKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEARGPKGDKNIGPEE WLTLCSK WVRQ

>d1ej3a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Jellyfish (Aequorea aequorea), aequorin} LTSDFDNPRWIGRH KHMNF LDVNHNGKISLDEM VYKASDIVINNLGATPEQAKRHKDAVEAFFGGAGMKY GVETDW PAYIEGWKKLATDELEYAKNEPTLIRIWGDALFDIVDKDQNGAITLDEWKAYTKAAGIIQSSEDCEET FRVCDIDES GQLD VDEMTRQHLGFWYTMDPACEKLYGGAVP

>d1el4a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa (Obelia longissima), obelin}

SSKYAVKLKTD FDN PRWIKRHKHMFD LINGNGKITLDEIVSKASDDICAKLEATPEQT KRHQVC VEAFFRGCG MEYGKEIAFPQFLDGW KQLATSELKKWARNEPTLIREWGDAVFDIFDKDGS GTITLDEWKAYGKISG ISPSQED CEATFRH C DLDNSG DLD VDEMTRQHLGFWYTLDPEADGLYNGNP

>d1jf0a_ a.39.1.5 (A:) Calcium-regulated photoprotein {Hydrozoa (Obelia geniculata), obelin}

KYAVKLQ TD FDN PKWIKRHKFMFD YLDINGNGQITLDEIVSKASDDICKNLGATPAQTQRHQDC VEAFFRGCG EYGKETKF PEFLEGW KNL ANADLAKWARNEPTLIREWGDAVFDIFDKDGS GTITLDEWKAYGRISG ISPSEEDC EKTFQH C DLDNSG ELDVDEMTRQHLGFWYTLDPEADGLYNGNP

>d1jfja_ a.39.1.5 (A:) EHCABP {Entamoeba (Entamoeba histolytica)}

MAEALFKEIDVNGDGA VS YEEVKAFVSKKRAIKNEQLQLIFKSIDADGN GEIDQNEFAK FYGSIQGQDLSDDKI GLKVLYKLMVDGDGKLTKEEVTSFFKKHGIEKVAEQVMKADANGDGYITLEEFLEFSL

>d1cmg_ a.39.1.5 (-) Calmodulin {Cow (Bos taurus)}

MKDTDSEE IREA FRVFDKDG NGYISAAELRH VMTNLGEKLTDEEVDEMIREADIDGDGQV NYEEFVQMM TA K

>d1fw4a_ a.39.1.5 (A:) Calmodulin {Cow (Bos taurus)}

SEEEIREAFRVFDKDG NGYISAAELRH VMTNLGEKLTDEEVDEMIREADIDGDGQV NYEEFVQMM

>d1g4yr_ a.39.1.5 (R:) Calmodulin {Rat (Rattus rattus)}

ADQLTEEQIAEFKEAFSLFDKDG DTITKELGTVMRS LGQNPTEAE LQDMINEV DADG NGTIDFPEFLTMMA RKM KDTDSEE IREA FRVFDKDG NGYISAAELRH VMTNLGEKLTDEEVDEMIREADIDGDGQV NYEEFVQMM TA

>d1f70a_ a.39.1.5 (A:) Calmodulin {African frog (Xenopus laevis)}

ADQLTEEQIAEFKEAFSLFDKDG DTITKELGTVMRS LGQNPTEAE LQDMINEV DADG NGTIDFPEFLTMMA RKM

>d1exra_ a.39.1.5 (A:) Calmodulin {Ciliate (Paramecium tetraurelia)}

EQLTEEQIAEFKEAFALFDKDG DTITKELGTVMRS LGQNPTEAE LQDMINEV DADG NGTIDFPEFLS LMARK MKEQDSEEE LIAF KVFD RDG NGLISAAELRH VMTNLGEKLTDEEVDEMIREADIDGDGHINYEEFVRMMVS

>d1ggwa_ a.39.1.5 (A:) Cdc4p {Fission yeast (Schizosaccharomyces pombe)}

STDDSPYKQAFSLFDRHGTGRIPKTSIGDLLRACGQNPTLAEITEIESTLPAEVDMEQFLQLVNRPNFGFDMPGDP
EEFKGKFQVFDFDKDATGMIGVGELRYVLTSLGKEKLSNEEMDELLKGVPVKDGMVNHYHDFVQMILAN
>d1wdcb_ a.39.1.5 (B:) Myosin Essential Chain {Bay scallop (Aequipecten
irradians)}
LPQKQIQEMIKEAFSMIDVDRDGFVSKEDIKAISEQLGRAPDDKELTAMLKEAPGPLNFTMFLSIFSDKLSGTDSE
ETIRNAFAMFDEQETKKLNIEYIKDLLENMGDNFNKDEMRTFKEAPVEGGKFDYVKFTAMIKGSGE
>d1br1b_ a.39.1.5 (B:) Myosin Essential Chain {Chicken (Gallus gallus)}
FSEEQTAEFKEAFQLFDRTGDGKILYSQCGDVMRALGQNPTNAEVMKVLGNPKSDEMNKTLKFEQFLPMM
QTIAKNKDQGCFEDYVEGLRVFDKEGNNTVMGAEIRHVLVTLGEKMTEEEVEQLVAGHEDSNGCINYELVR
MVLSG
>d2mysb_ a.39.1.5 (B:) Myosin Essential Chain {Chicken (Gallus gallus)}
FDETEIEDFKEAFTVIDQNADGIIDKDDLRETFAAMGRLNVKNEELDAMIKEASGPINFTVFLTMFGEKLKGADP
EDVIMGAFKVLDPDGKGSIKKSFLEELLTTGGGRFTPEEIKNMWAAFPDVAGNVVDYKNICVITHGEDA
>d1wdcc_ a.39.1.5 (C:) Myosin Regulatory Chain {Bay scallop (Aequipecten
irradians)}
LSQDEIDDLKDVFELFDWDGRDGAVDAFKLGDVCRCLGINPRNEDVFAVGGTHKMGEKSLPFEELPAYEGL
MDCEQGTFADYMEAFKTFDREGQGFISGAELRHVLGERLSDEDVDEIILTDLQEDLEGNVKYEDFVKVVM
AGPY
>d2mysc_ a.39.1.5 (C:) Myosin Regulatory Chain {Chicken (Gallus gallus)}
AAADDFFKEAFLLFDRTGDAKITASQVGDIAARALGQNPTNAEINKLGNPSKEEMNAAAITFEEFLPMIQLQAAANN
KDQGTFEDFVEGLRVFDKEGNNTVMGAEIRHVLATLGEKMTEEEVEELMKGQEDSNGCINYEAFKVHIMSV
>d1auib_ a.39.1.5 (B:) Calcineurin regulatory subunit (B-chain) {Human (Homo sapiens)}
SYPLEMCSSHFDADEIKRLGKRFKKLDLNSGSLVEEFMSLPELQQNPLVQRVIDIFDTDGNGEVDFKEFIEGV
QFSVKGDKEQKLRFAFRIYDMDKDGYISNGELFQVLKMMVGNNLKTQLQQIVDKTIINADKGDGRISFEFF
CAVVGGLDIHKKMVVVDV
>d1rec_ a.39.1.5 (-) Recoverin {Cow (Bos taurus)}
LSKEILELQLNTKFTEELSSWYQSFLKECPGSRITRQEFTIYSKFFPEADPKAYAQHVFRSFANDSGTLDK
YVIALHMTSAGKTNQKLEWAFLYDVGNGTISKNEVLEIVTAIFKMICPEDTKLPEDENTPEKRAEKIWGFFG
KKDDDKLTEKEFIEGLANKEILRLIQFEPQKVKEKLK
>d1g8ia_ a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Human (Homo sapiens)}
SNSKLKPEVVEELTRKTYFTEKEVQQWYKGFIKDCPSGQLDAAGFQKIYKQFFPGDPTKFATFVFNVDENKDG
RIEFSEFIQALSCTSRTLDEKLRWAFKLYDLDNDGYITRNEMLDIVDAIYQMVGNTELPEEENTPEKRVDRIFA
MMDKNADGKLTQEFQEGSKADPSIVQALSLYDGLV
>d1fpwa_ a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Baker's yeast (Saccharomyces
cerevisiae)}
MGAKTSKLSKDDLTCLKQSTYFDRREIQQQWHKGFLRDCPSGQLAREDFVKIYKQFFPGSPEDFANHLFTVFDK
DNNGFIHFEEFITVLSTTSRGTLEEKLSWAFELYDLNHGDGYITFDEMLTIVASVYKMMGSMVTLNEDEATPEMR
VKKIFKLMKDKNEDGYITLDEFREGSKVDPSIIGALNLNYDGLI
>d1jbaa_ a.39.1.5 (A:) Guanylate cyclase activating protein 2, GCAP-2 {Cow (Bos taurus)}
GQQFSWEEAEENGAVGAADAAQLQEYWKKFLEECPSGTLFMHEFKRFFKVPDNEEATQYVEAMFRAFDTNG
DNTIDFLEYVAALNLVLRGTLLEHKLWTFKIYDKDRNGCIDRQELLDIVESIYKLKKACSVEVEAEQQGKLLTPEEV
VDRIFLLDENGDGQLSLNEFVEGARRDKWVMKMLQMDLNP
>d1bjfa_ a.39.1.5 (A:) Neurocalcin {Cow (Bos taurus)}
NSKLRPEVMQDLLESTDTEHEIQEWYKGFLRDCPSGHLSMEEFKKIYGNFFPYGDASKFAEHVFRTFDANGD

GTIDFREFIIALSVTSRGKLEQKLKWAFSMYDLDGNGYISKAEMLEIVQAIYKMWSSVMKMPEDESTPEKRTEKI
FRQMDTNRDGKLSLEEFIRGAKSDPSIVRLLQC
>d1dgu_a.39.1.5 (A:) Calcium- and integrin-binding protein, CIB {Human (Homo sapiens)}
SKELLAEYQDLTFLTKQEILLAHRRCCELLPQEQRSESSLRAQVPFEQILSPELKANPFKERICRVFSTSPAKDSL
FEDFLDLLSVFSDTATPDIKSHYAFRIFDFDDDGTLNREDSRLVNCLTGEGEDTRLSASEMKQLIDNILEESDIDRD
GTINLSEFQHVISRSPDFASSFKIVL
>d1qjta_a.39.1.6 (A:) Eps15 {Mouse (Mus musculus)}
LSLTQLSSGNPVYEKYYRQVEAGNTGRVLALDAAAFLKKSGLPDLILGKIWDLADTDKGKVLSKQEFFVALRLVA
CAQNGLEVSLSLAVPPPRFHD
>d1c07a_a.39.1.6 (A:) Eps15 {Human (Homo sapiens)}
TWVVSPAECAKYDEIFLKTDKMDGFVSGLEVREIFLKTGLPSTLLAHIWSLCDTKDCGKLSKDQFALAFHLISQK
LIKGIDPPPHVLTPEMIPPS
>d1f8ha_a.39.1.6 (A:) Eps15 {Human (Homo sapiens)}
PWAVKPEDKAKYDAIFDSLSPVNGFLSGDKVVPVLLNSKLPVDILGRVWELESIDHDGMLRDEFAVAMFLVYC
ALEKEPVPMSPALVPPSKR
>d1iq3a_a.39.1.6 (A:) Pob1 {Human (Homo sapiens)}
GSLQDNSSYPDEPWRITEEQREYYVNQFRSLQPDPSFISGSVAKNFTKSLSIPELSYIWELSDADCDGALTLP
EFCAAFHLIVARKNGYPLPEGLPPTLQPEFIVTD
>d1fi6a_a.39.1.6 (A:) Reps1 {Mouse (Mus musculus)}
WKITDEQRQYYVNQFKTIQPDLNGFIPGSAAKEFFTTSKPILELSHIWELSDFDKGALTDEFCAAFHLVARK
NGYDLPEKLPESLMPK
>d1hqva_a.39.1.8 (A:) Apoptosis-linked protein alg-2 {Mouse (Mus musculus)}
PGPGGGPGPAAGAALPDQSFLWNVFQRVDKDRSGVISDNELOQQALSNGTWTPFPVTVRSIISMFDRENKA
GVNFSEFTGVWKYITDWQNVFRTYDRDNGMIDKNELKQALSGFGYRLSDQFHDLIRKFDRQGRGQIAFDDF
IQGCIVLQRLTDIFRRYDTDQDGWIQVSYEQYLSMVF
>d1juoa_a.39.1.8 (A:) Sorcin {Human (Homo sapiens)}
FPGQTQDPLYGYFAAVAGQDGQIDAELQRCLTQSGIAGGYKPFNLETCLMVSMLDRDMSGTMGFNEFKEL
WAVLNGWRQHFISFDTDRSGTVDPQELQKALTTMGFRLSPQAVNSIAKRYSTNGKITFDDYIACCVKLRALTDS
FRRRTAQQGVVNFPYDDFIQCVMSV
>d1dxb1 a.39.1.7 (B:158-298) Phosphoinositide-specific phospholipase C,
isozyme D1 (PLC-D!) {Rat (Rattus norvegicus)}
NKMFNFKELKDFLKELENIQVDDGYARKIFRECDHSQTSLEDEEIEFYKMLTQRAEIDRAFEAAGSAETLSVERL
VTFLQHQREEEAGPALALSLIERYEPSETAKAQRQMTKDGFLMYLLSADGNAFLAHRRVYQDM
>d1qasa1 a.39.1.7 (A:205-298) Phosphoinositide-specific phospholipase C,
isozyme D1 (PLC-D!) {Rat (Rattus norvegicus)}
YKMLTQRAEIDRAFEAAGSAETLSVERLVTFLQHQREEEAGPALALSLIERYEPSETAKAQRQMTKDGFLMYL
LSADGNAFLAHRRVYQDM
>d1k94a_a.39.1.7 (A:) Grancalcin {Human (Homo sapiens)}
SVTYFSAVAGQDGEVDAEELQRCLTQSGINGTYSPFSLETCRIMIAMILDRDHTGKMGFNAFKELWAALNAWK
ENFMTVDQDGSGTVEHHLRQAIGLMGYRLSPQTLTTIVKRYSKNGRIFFDDYVACCVKLRALDFFRKRDHLQ
QGSANFIYDDFLQGTMAI
>d1kfus_a.39.1.7 (S:) Calpain small (regulatory) subunit (domain VI) {Human (Homo sapiens)}
THYSNIEANESEEVRQFRLFAQLAGDDMEVSATELMNILNKVVTRHPDLKTDGFGIDTCRSMVAVMDSDTTG
KLGEEFKYLWNNIKRWQAIYKQFDTDRSGTICSELPGAFEAAGFHNEHLYNMIIIRRYSDESGNMDFDNFISC

LVRLDAMFRAFKSLDKDGTGQIQVNIQEWLQLTMYS
>d1dvia_a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI) {Rat (Rattus norvegicus)}
EEERQFRKLFVQLAGDDMEVSATELMNILNKVVTRHPDLKTDFGIDTSRSMVAVMDSDTTGKLGFEFKYLW
NNIKKWQGIYKRFDTDRTSGTIGSNELPGAFEAAGFHNLQHIYSMIIRYSDETGNMDFDNFISCLVRLDAMFRA
FRSLDKNGTGQIQVNIQEWLQLTMYS
>d1alva_a.39.1.7 (A:) Calpain small (regulatory) subunit (domain VI) {Pig (Sus scrofa)}
EEVRQFRRFLAQLAGDDMEVSATELMNILNKVVTRHPDLKTDFGIDTCRSMVAVMDSDTTGKLGFEFKYL
WNNIKKWQAIYKQFDVDRSGTIGSSELPGAFEAAGFHNLNEHLYSMIIRYSDEGGNMDFDNFISCLVRLDAMF
RAFKSLDKDGTGQIQVNIQEWLQLTMYS
>d1kful1 a.39.1.7 (L:515-700) Calpain large subunit, C-terminal domain (domain IV) {Human (Homo sapiens)}
EIEANLEEFDISSEDDIDDGVRRRLAQLAGEDAEISAFELQTILRRVLAKRQDIKSDGFSIETCKIMVDMLDSDGS
GK LGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKMPCQLHQVIVARFADDQLIIDFDNFVRCL
VRLETLFKIFKQLDPENTGTIELDLISWLCSVL
>d1df0a1 a.39.1.7 (A:515-700) Calpain large subunit, C-terminal domain (domain IV) {Rat (Rattus norvegicus)}
EIEANIEIEANEEDIGDGFRRLAQLAGEDAEISAFELQTILRRVLAKREDI
KSDGFSIETCKIMVDMLDEDGS
GK LGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGFKLPCQLHQVIVARFADDELIIDFDNFVRCL
RLEILFKIFKQLDPENTGTIQLDLISWLSFSVL
>d1eg3a1 a.39.1.7 (A:85-209) Dystrophin {Human (Homo sapiens)}
HPKMTELYQSLADLNNVRFSA
RTAMKLRLQKALC
L DLLLSAACD
DALDQHNLKQNDQPM
DILQIINCLTTIYD
RLEQEHN
NLLVNP
PLC
VDM
CLNW
LLNV
YDTG
RTGR
IRV
LSFK
TGI
ISL
CKA
>d1eg3a2 a.39.1.7 (A:210-306) Dystrophin {Human (Homo sapiens)}
HLEDKYRYLFKQVASSTGFCDQRRLG
LLLHDSIQIPRQLGEV
ASFGGSNIEPS
VRSCFQ
FANNKPE
IEAALFLDW
MRLEP
QSMV
WLPV
LHRV
AAAET
>d2cba1 a.39.1.7 (A:178-263) Cbl {Human (Homo sapiens)}
TFRITKADA
AAEFWRKA
FGEK
TIVPW
KSFR
QALHEV
HPISS
GLEAM
ALKST
IDL
TCND
YISV
FEFD
IFTRL
FQP
WSS
LLRN
WNSL
AV
>d1h8ba_a.39.1.7 (A:) alpha-Actinin {Human (Homo sapiens)}
MADTD
TAEQVI
ASF
RIL
ASDK
KPY
ILA
EEL
RREL
PPD
QA
QYC
I
KRMP
AY
SGPG
VP
GAL
DY
AAF
SSA
LY
GES
DL
>d1c3za_a.39.2.1 (A:) Thp12-carrier protein {Yellow mealworm (Tenebrio molitor)}
ETPRE
KLQH
SDACK
AEGV
SEES
LNK
VRN
REE
VDD
PKL
KEHA
FCIL
KRA
GFID
ASGE
FQL
DH
IKTK
F
K
NSE
HPE
KV
DDL
VAK
CAV
KK
DTP
QH
SSAD
FF
KCV
HD
NRS
>d1dqe_a.39.2.1 (A:) Pheromone binding protein {Silkworm (Bombyx mori)}
SQEV
MKN
LSN
FGK
AL
DECK
KEM
TLD
AINED
DFY
NF
W
KE
GY
EI
KN
RET
G
CA
IM
CL
ST
KLN
M
LD
PEG
NL
HH
GN
AME
FA
KK
GA
DET
MA
QQ
L
DIV
HG
CE
K
ST
P
AND
DK
CI
WT
LG
VAT
CF
KAE
IH
KLN
WAP
SMD
DV
AV
GE
>d1iioa_a.39.4.1 (A:) Hypothetical protein MTH865 {Archaeon Methanobacterium thermoautotrophicum}
GSH
MKMG
VKED
IRG
QI
GAL
AGA
DFP
INS
SPE
ELMA
ALP
NGP
DT
CKSG
D
VEL
KAS
DAG
QVL
ADD
FP
K
SAE
E
VAD
TIV
NK
AGL
>d1cpo_1 a.39.3.1 (0-119) Cloroperoxidase {Fungus (Caldariomyces fumago)}
EEP
GSG
IGY
PYD
NNT
LPY
VAP
GPT
DSR
ACP
PAL
NAL
ANH
GYI
PHD
GRA
ISRE
TLQ
NAFL
NH
GIAN
S
V
IEL
ALTN
AFVV
CEY
VTG
SDCG
DSL
VNLT
LLA
E
PHAF
EHD
HS
FSR
KD
YK
QG
VA
>d1cpo_2 a.39.3.1 (120-298) Cloroperoxidase {Fungus (Caldariomyces fumago)}

NSNDFIDNRNFDAETFQTSLDVAGKTHFDYADMNEIRLQRESLSNELDFPGWFTESKPIQNVESGFIFALVSDF
NLPDNDENPLVRIDWWKYWFTNESFPYHLGWHPPSPAREIEFVTSASSAVLAASVTSTPSSLPSGAIGPGAEAV
PLSFASTMTPFLLATNAPYYAQDPTLGPND
>d1h67a_a.40.1.1 (A:) Calponin {Chicken (Gallus gallus)}
MPQTERQLRVWIEGATGRRIGDNFMDGLKDGVILCELINKLQPGSVQVNNDPVQNWHKLENIGNFLRAIKHY
GVKPHDIFEANDLFENTNHTQVQSTLIALASQAKTK
>d1bkra_a.40.1.1 (A:) beta-spectrin {Human (Homo sapiens)}
KSAKDALLWCQMKTAGYPNVNIHNFTTSWRDGMAFNALIHHRPDLIDFDKLKKSNAHYNLQNAFNLAEQ
HLGLTKLLDPEDISVDHPDEKSIITYVVYHYFSKM
>d1aoa_1 a.40.1.1 (121-251) N-terminal actin-crosslinking domain from fimbrin {Human (Homo sapiens)}
YSEEEKYAFVNWINKALENDPDCRHVIPMNPNTDDLFKAVGDIVLCKMINLSVPDTIDERAINKKLTPFIQE
NLNLALNSASAIGCHVNIGAEDLRAGKPHLVGLLWQIIKIGLFADIERSREAL
>d1aoa_2 a.40.1.1 (260-375) N-terminal actin-crosslinking domain from fimbrin {Human (Homo sapiens)}
TLEELMKLSPEELLRWANFHLENSGWQKINNSADIKDSKAYFHLLNQIAPKGQKEGEPRIDINMSGFNETDD
LKRAESMLQQADKLGCRQFVTPADVSGNPKLNLAFLVANLFN
>d1bhda_a.40.1.1 (A:) Utrophin {Human (Homo sapiens)}
LQQTNSEKILLSWVRQTRPYSQVNVLNFTTSWTGLAFNAVLRHKPDLFSWDKVVKMSPIERLEHAFSKAQ
TYLGIEKLLDPEDVAVLPDFKKSIIIMYLTSLEFV
>d1qaga1 a.40.1.1 (A:31-151) Utrophin {Human (Homo sapiens)}
DVQKKTFTKWINARFSKSGKPPINDMFTDLKDRKLLLEGTLGTSLPKERGSTRVHALNNVRVLQVLHQN
NVELVNIGGTDIVDGNHKLTGLLWSIILHWQVKDVMKDVMSDLQQTN
>d1dxxa1 a.40.1.1 (A:9-119) Dystrophin {Human (Homo sapiens)}
DSYEREDVQKKTFTKWVNAQFSKFGKQHIENLSDLQDGRRLLLEGTLGQKLPKEKGSTRVHALNNVNKALR
VLQNNNVDLVNIGSTDIVDGNHKLTGLIWIINLHWQ
>d1dxxa2 a.40.1.1 (A:120-246) Dystrophin {Human (Homo sapiens)}
VKNVMKNIMAGLQQTNSEKILLSWVRQSTRNYPQVNINFTTSWSDGLALNALIHSHRPDLFDWNSVVSQQ
SATQRLEHAFNIARYQLGIEKLLDPEDVDTTPDKKSILMYITSFLQVLPQQVSIE
>d1a26_1 a.41.1.1 (662-796) Domain of poly(ADP-ribose) polymerase {Chicken (Gallus gallus)}
KSKLAKPIQDLIKMIFDVESMKKAMVEFEIDLQKMPPLGKLSKRQIQSAYSILNEVQQAVSDGGSESQILDLSNRF
YTLIPHDGMKKPPLLSNLEYIQAKVQMLDNLLDIEVAYSLLRGGNEDGDKDPIDINYEK
>d1ycqa_a.42.1.1 (A:) MDM2 {African clawed frog (Xenopus laevis)}
EKLVQPTPLLSLLKSAGAQKETFTMKEVIYHLGQYIMTKRLYDEKQQHIVYCSNDPLGELFGVQEFSVKEPRLY
AMISRNLVSANV
>d1ycra_a.42.1.1 (A:) MDM2 {Human (Homo sapiens)}
ETLVRPKPLLLKLLKSVGAAQKDTYTMKEVLFLYLGQYIMTKRLYDEKQQHIVYCSNDLLGDLFGVPSFSVKEHRKIY
TMIYRNLLV
>d1b28a_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
MKGMSKMPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFKKEGRIGA
>d1baza_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
SKMPQVNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIGA
>d1babz_a.43.1.1 (B:) Arc repressor {Salmonella bacteriophage P22}
KMPQVNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFK

>d1bdta_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
MKGMSKMPQFNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIG
>d1myka_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
KMLQFNLRWPREVLDLVRKVAEENGRSVNSEIYQRVMESFKKEGRIG
>d1myla_a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}
KMPQFNLRWPREVLDLVRKVAEENGMSVNSIYQLVMESFKKEGR
>d1mylb_a.43.1.1 (B:) Arc repressor {Salmonella bacteriophage P22}
MPQFNLRWPREVLDLVRKVAEENGMSVNSIYQLVMESFK
>d1mnta_a.43.1.1 (A:) Mnt repressor {Salmonella bacteriophage P22}
ARDDPHFNFRMPMEVREKLKFRAEANGRSMNSELLQIVQDALSKPSPVTGYRNDALERLADEQSELV
>d2cpga_a.43.1.2 (A:) Transcriptional repressor CopG {Streptococcus agalactiae}
MKKRLTITLSESVLENLEKMAREMGLSKSAMISVALENYKKQQ
>d1irqa_a.43.1.2 (A:) Omega transcriptional repressor {Streptococcus pyogenes}
IMGDKTVRVRADLHHIIKIETAKNGGNVKEVMDQALEEYIRKYLPDKL
>d1cmba_a.43.1.2 (A:) Met repressor, MetR {Escherichia coli}
AEWSGEYISPYAEHGKKSEQVKITVSIPLKVLKILTDERTRRQVNRLHATNSELLCEAFLHAFTGQPLPDDADL
RKERSDEIPEAAKEIMREMGINPETWEY
>d1fvka1 a.44.1.1 (A:65-128) Disulphide-bond formation facilitator (DSBA), insertion domain {Escherichia coli}
GGDLGKDLTQAQAVAMALGVEDKVTVPFEGVQKTQTIRSASIDRVFINAGIKGEEYDAAWNS
>d1bed_1 a.44.1.1 (63-126) Disulphide-bond formation facilitator (DSBA), insertion domain {Vibrio cholerae}
GNMGQAMSKAYATMIALEVEDKMPVPMFNRIHTLRKPPKDEQELRQIFLDEGIDAALKFDAAYNG
>d1aqwa1 a.45.1.1 (A:77-209) Glutathione S-transferase {Human (Homo sapiens), class pi}
GLYGKDQQEAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDYVKALPGQLKPFETLLSQNQGGKTFIVGDQISF
ADYNLLDLLIHEVLAPGCLDAFPILLSAYVGRLSARPKLKAFLASPEYVNLPINGNGKQ
>d2gsra1 a.45.1.1 (A:77-207) Glutathione S-transferase {Pig (Sus scrofa), class pi}
YGKDQKEAALVDMVNDGVEDLRCKYATLIYTNYEAGKEKYVKELPEHLKPFETLLSQNQGGQAFVVGQSQISFAD
YNLLDLLRIHQVLNPSCDAFPILLSAYVARLSARPKIKAFLASPEHVNRPINGNGKQ
>d1glqa1 a.45.1.1 (A:79-209) Glutathione S-transferase {Mouse (Mus musculus), class pi}
YGKNQREAAQMMDMVNDGVEDLRGKYVTLYTNYENGKNDYVKALPGHLKPFETLLSQNQGGKAFIVGDQISF
ADYNLLDLLIHQVLAPGCLDNFPILLSAYVARLSARPKIKAFLSSPEHVNRPINGNGKQ
>d1gtua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Human (Homo sapiens), class mu}
LCGETEEEKIRDILENQTMDNHNMQLMICYNPEFEKLKPYLEELPEKLKLYSEFLGKRPWFAGNKITFVDFLVY
DVLDLHRIFEPEPKCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPRPVFSKMAVWGNK
>d1hn_a_1 a.45.1.1 (85-217) Glutathione S-transferase {Human (Homo sapiens), class mu}
LCGESEKEQIREDILENQFMDSRMQLAKLCYDPDFEKLKPYPEYLQALPEMLKLYSQFLGKQPWFGLDKITFVDFIA
YDVLERNQVFEPSCDAFPNLKDFISRFEGLEKISAYMKSSRFLPRPVFTKMAVFGNK
>d3gtub1 a.45.1.1 (B:85-224) Glutathione S-transferase {Human (Homo sapiens), class mu}
RKHNMCGETEEEKIRDILENQVMDFRQLIRLCYSSDHEKLKPQYLEELPGQLKQFSMFLGKFSWFAGEKLT
DFLTYDILDQNRIFPKCLDEFPLKAFMCRFEALEKIAAYLQSDQFCMPINNKMAQWGNKPVC
>d4gtua1 a.45.1.1 (A:85-217) Glutathione S-transferase {Human (Homo sapiens), class mu}
LCGETEEEKIRDILENQAMDVSNQLARVCYSPDFEKLKPYPEYLEELPTMMQHFSQFLGKRPWFVGDKITFVDFL
AYDVLDLHRIFEPEPNCLDAFPNLKDFISRFEGLEKISAYMKSSRFLPKPLYTRVAWGNK

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

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

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

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

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

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

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

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

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

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

>d2gsq_1 a.45.1.1 (76-202) Glutathione S-transferase {Squid (Ommastrephes sloani pacificus), class sigma}
LDGKTSLEYRVDEITETLQDIFNDVVKIKFAPEAAKEAVQQNYEKSCCKRLAPFLEGLLVSNGGDGFFVGNNSMT
LADLHCYVALEVPLKHTPELLKDCPKIVALKRVAECPKIAAYLKKRPVRDF

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

WFERLEAMKLNECVDHTPKLKLWMAAMKEDPTVSALLSEKDWWQGFLELYLQNSPEACDYGL
>d1fw1a1 a.45.1.1 (A:88-212) Glutathione S-transferase {Human (Homo sapiens), class zeta}
LLPQDPKKRASVRMISDLIAGGIQPLQLNLSVLKVQGEEMQLTWAQNAITCGFNALEQILQSTAGIYCVGDEVTM
ADLCVPQVANAERFKVDLTPYPTISSINKRLLVLEAFQVSHPCRQPDPT
>d1bg5_1 a.45.1.1 (81-254) Glutathione S-transferase {Schistosoma japonicum}
MLGGCPKERAESMLEGAVLDIYGVSRAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFM
LYDALDVVLYMDPMCLDAFPKLVCFKKRKIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLVPRGSYY
QEAKSSKIMESFKNMVPQQALVNSS
>d1duga1 a.45.1.1 (A:81-220) Glutathione S-transferase {Schistosoma japonicum}
LGGCPKERAESMLEGAVLDIYGVSRAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLY
DALDVVLYMDPMCLDAFPKLVCFKKRKIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDP
>d1gne_1 a.45.1.1 (80-232) Glutathione S-transferase {Schistosoma japonicum}
MLGGCPKERAESMLEGAVLDIYGVSRAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFM
LYDALDVVLYMDPMCLDAFPKLVCFKKRKIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLVPRGSME
LDKWA
>d1fhe_1 a.45.1.1 (81-214) Glutathione S-transferase {Fasciola hepatica}
LGTTPEERARISMIEGAAMDLRIGFGRVCYNPKFEEVKEEYVKELPKTLKMWSDFLGDRHYLTGSSVSHVDFML
YETLDSIRYLAPHCLDEFPKLKEFKSRIEALPKIKAYMESKRFIKWPLNGWAASFAGADA
>d2fhea1 a.45.1.1 (A:81-216) Glutathione S-transferase {Fasciola hepatica}
IGTTSEERARVSMIEGAAVDLRQGISRISYQPKFEQLKEGYLKDLPTTMKMWSDFLGKNPYLRGTSVSHVDFMV
YEALDAIRYLEPHCLDHFPNLQQFMSRIEALPSIKAYMESNRFIKWPLNGWHAQFGGGDAPP
>d1gnwa1 a.45.1.1 (A:86-211) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}
LQTDSKNISQYAIMAIGMQVEDHQFDPVASKLAFEQIFKSIYGLTDEAVVAEEAKLAKVLDVYEARLKEFKYLA
GETFTLTLHHIPAIQYLLGPTKKLFTERPRVNEWVAEITKRPASEKVQ
>d1axda1 a.45.1.1 (A:81-210) Glutathione S-transferase {Maize (Zea mays), type I}
ELLREGNLEEAAMVDVIEVEANQYTAALNPILFQVLISPMGLGGTTDKVVDENLEKKVLEVYEARLTCKYL
AGDFSLADLNHVSVTLCFLATPYASVLDAYPHVKAWWSGLMERPSVQKVAALM
>d1aw9_1 a.45.1.1 (83-217) Glutathione S-transferase {Maize (Zea mays), type III}
GTDLLPATASAALKLEVWLEVESHHFYPNASPLVFQLLVRPLLGGAPDAAVVDKHAEQLAKVLDVYE AHLARNKY
LAGDEFTLADANHASYL禄SKTPKAGLVAARPHVKAWWEAIVPARPAFKTVAAIPLPPP
>d1e6ba1 a.45.1.1 (A:88-220) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana), class zeta}
PLLPRDLHKRAVNYQAMSIVLSGIQPHQNLAVIRYIEEKINVEEKTAWVNNAITKGFTALEKLLNCAGKHATGD
EIYLADLFLAPQIHGAINRFQINMEPYPTLAKCYESNELPAFQNALPEKQPDAPSST
>d1a0fa1 a.45.1.1 (A:81-201) Glutathione S-transferase {Escherichia coli}
QLLAPVNSISRYKTIEWLNYYATELHKGFTPLFRPDTPEEYKPTVRAQLEKKLQYVNEALKDEHWICGQRFTIADA
YLFTVLRWAYAVKLNLEGLEHIAAFMQRMAERPEVQDALSAEGLK
>d1b8xa1 a.45.1.1 (A:81-260) Glutathione S-transferase {Escherichia coli}
LGGCPKERAESMLEGAVLDIYGVSRAYSKDFETLKVDFLSKLPEMLKMFEDRLCHKTYLNGDHVTHPDFMLY
DALDVVLYMDPMCLDAFPKLVCFKKRKIEAIPQIDKYLKSSKYIAWPLQGWQATFGGGDHPPKSDLVPRGSRRAS
VGSRMHYPGAFTYSPTPVTSIGIGMSAMGS
>d1pmt_1 a.45.1.1 (81-201) Glutathione S-transferase {Proteus mirabilis}
NLIAPPKALERHYQIEWLNFLASEVHKGYSPLFSSDTPESYLPVVKNKLKSFKVYINDVLSKQKCVCGDHFTVADA
YLFTLSQWAPHVALDLTDLQLDYLARIAQRPNVHSALVTEGLI

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

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

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

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

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

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

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

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

>d1bg1a1 a.47.1.1 (A:136-321) STAT3b {Mouse (Mus musculus)}
VVTEKQQMLEQHQLQDVRKRVQDLEQKMKVVENLQDDDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQL
EQMLTALDQMRRSIVSELAGL SAMEYVQKLTDEELADWKRQQIACIGGPPNCLDRLENWITS LAESQLQT
RQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAF

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

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

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

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

YQSLQQSYNQRKSLFPLK

>d2cbla2 a.48.1.1 (A:47-177) N-terminal domain of cbl (N-cbl) {Human (Homo sapiens)}
PPGTVDDKKMVEKCWKLMDKVVRLCQNPALKNSPPYILDLLPDTYQHLRTILSRYEGKMETLGENEYFRVFM
ENLMKKTKQTISLFKEGKERMYEENSQPRRNLTKLSLIFSHMLAELKGIFPSGLFQGD
>d1de4c1 a.48.2.1 (C:609-756) Transferrin receptor ectodomain, C-terminal domain {Human (Homo sapiens)}
LDYERYNSQLLSFVRDLNQYRADIKEMGLSLQWLYSARGDFFRATSRLTDFGNAEKTDVFVMKKLNDRVMRV
EYHFLSPYVSPKESPFRHVFWGSHTLPALLENLKLRKQNNGAFNETLFRNQLALATWTIQGAANALSGDVW
DI
>d1eo0a_ a.48.3.1 (A:) Transcription elongation factor TFIIS N-domain {Baker's yeast (Saccharomyces cerevisiae)}
MDSKEVLVHVKNLEKNKSNDAAVLEILHVLDKEFVPTEKLLRETKVGVENVNKFKSTNVEISKLVKKMISSWKDA
IN
>d1f6va_ a.49.1.1 (A:) C-terminal domain of B transposition protein {Bacteriophage mu}
GSRIAKRTAINKKADVKAIADAWQINGEKELELLQQIAQKPGALRILHSLRLAAMTAHGKGERVNEDYLRQ
AFRELDLDVDISTLLRN
>d1i6ve_ a.143.1.1 (E:) RNA polymerase omega subunit {Thermus aquaticus}
MAEPGIDKLFGMVDSKYRLTVVVAKRAQQLLRHRFKNTVLEPEERPKMRTLEGLYDDPNAVTWAMKELLTR
LFFGENLVPEDRLQKEMERLYPTEEE
>d1cfaa_ a.50.1.1 (A:) C5a anaphylotoxin {Human (Homo sapiens)}
MLQKKIEEIAAKYKHSVVKKCCYDGASVNNDETCEQRAARISLGPRCIKAFTECCVVASQLRANISHKDMC
>d1c5a_ a.50.1.1 (-) C5a anaphylotoxin {Pig (Sus scrofa domestica)}
MLQKKIEEEAAKYKYAMLKKCCYDGAYRNDDETCEERAARIKIGPKCVKAFCDCCYIANQVRAEQS
>d0c3a_ a.50.1.1 (-) C3a anaphylotoxin {Human (Homo sapiens)}
SVQLTEKRMNKVGKYPKELRKCCEDGMRQNPMRFSCQRRTRFISLGEACKVFLDCCNYITELRRQHARASHL
GLAR
>d1ocrh_ a.51.1.1 (H:) Cytochrome c oxidase subunit h {Cow (Bos taurus)}
KIKNYQTAPFDSDRFPNQNQTRNCWQNYLDFHRCEKAMTAKGDDVSVCWYRRVYKSLCPISWVSTWDDRRA
EGTFPGKI
>d1hyp_ a.52.1.1 (-) Soybean hydrophobic protein {Soybean (Glycine max)}
PSCPDLICLNILGGSLGTVDDCCALIGGLGDIEAIVCLCIQLRALGILNLNRNLQLILNSCGRSYPNSATCPRT
>d1bwoa_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Wheat (Triticum aestivum), L. seeds}
IDCGHVDSLVRPCLSYVQGGPGPSGQCCDGVKNLHNQARSQSDRQSACNCLKGIAARGIHNLNEDNARSIPPCK
GVNLPYTISLNIDCSRV
>d1be2_ a.52.1.1 (-) Plant non-specific lipid-transfer protein (ns-LTP) {Barley (Hordeum vulgare)}
LNCGQVDSKMKPCLTYVQGGPGPSGECCNGVRDLHNQAQSSGDRQTCNCNLKGIAARGIHNLNLNAASIPSK
CNVNVPYTISPDIDCSRY
>d1fk5a_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Maize (Zea mays)}
AISCGQVASAIAPCISYARGQGSGPSAGCCSGVRSLNNAARTTADRRAACNCLKNAAAGVSGLNAGNAASIPS
KCGVSIPYTISTSTDCSRVN
>d1rzl_ a.52.1.1 (-) Plant non-specific lipid-transfer protein (ns-LTP) {Rice (Oryza sativa)}
ITCGQVNSAVGPCLTYARGGAGPSAACCSGVRSLKAAASTTADRRTACNCLKNAARGIKGLNAGNAASIPSKCG
VSVPYTISASIDCSRVS

>d1hssa_a.52.1.2 (A:) 0.19 alpha-amylase inhibitor {Wheat (*Triticum aestivum*)}
MCYPGQAFQVPALPACRPLLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSMLDSMYKEHGAQEGQA
GTGAFPRCRREVVKLTAASITAVCRLPIVVDASGDGAYVCKDVAAYPDA

>d1tmqb_a.52.1.2 (B:) Trypsin/alpha-amylase inhibitor RBI {Ragi (*Elucine coracana gaertneri*), seeds}
SVGTSCIPGMAIPHNPPLDSRWWYVSTRTCVGPRLATQEMKARCCRQLEAIPAYCRCEAVRILMDGVVTSSGQ
HEGRLLQDLPGCPRQVQRAFAPKLVTEVECNLATIHGGPFCLSL

>d1bea_a.52.1.2 (-) Hageman factor/amylase inhibitor {Maize (*Zea mays*)}
SCVPGWAIPHNPPLPSRWWYVTSRTCGIGPRLPWPELKRRCCRELADIPAYCRCTALSILMDGAIPPGPDAQLEGR
LEDLPGCPREVQRGFAATLVTEAECLNATISGVAECPWILG

>g1pnb_1 a.52.1.3 (A;;B;) Napin BNlb {Rape (*Brassica napus*)}
QPQKCQREFQQEQHLRACQQWIRQQLAGSPFXQSGPQQGPWLREQCCNELYQEDQVCVCP TLKQAAKSVR
VQGQHGPFQSTRIYQIAKNLNPVCNMKQIGTCPFIAI

>d1a1ua_a.53.1.1 (A:) p53 tetramerization domain {Human (*Homo sapiens*)}
EYFTLQIRGRERFEKIREYNEALELKDAQ

>d1aie_a.53.1.1 (-) p53 tetramerization domain {Human (*Homo sapiens*)}
EYFTLQIRGRERFEMFRELNEALELKDAQAG

>d1hs5a_a.53.1.1 (A:) p53 tetramerization domain {Human (*Homo sapiens*)}
DGEYFTLQIRGRERFEQFRERNEALELKDAQAGK

>d1saia_a.53.1.1 (A:) p53 tetramerization domain {Human (*Homo sapiens*)}
KKKPLDGEYFTLQIRGRERFEMFRELNEALELKDAQAGKEPG

>d1k1fa_a.147.1.1 (A:) Bcr-Abl oncoprotein oligomerization domain {Human (*Homo sapiens*)}
MVDPVGFAEAWKAQFPDSEPPRMELRSVGDIQELEAKASIRRLEQEVNQERFRMIYLQTLLAKEK

>d1adt_1 a.54.1.1 (176-265) Domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}
PIVSAWEKGMEAARALMDKYHVDNDLKANFKLLPDQVEALAAVCKTWLNEEHRLQLTFTSNKTFVTMMGR
FLQAYLQSFAEVTYKHHEP

>d1ihfa_a.55.1.1 (A:) Integration host factor (IHF) {Escherichia coli}
ALTKAEMSEYLFDKLGLSKRDAKELVELFFEEIRRALENQEVKLSFGFNFDLRDKNQRPGRNPKTGEDIPIARR
VVTRPGQKLRSVENASPK

>d1ihfb_a.55.1.1 (B:) Integration host factor (IHF) {Escherichia coli}
MTKSELIERLATQQSHIPAKTVEDAVKEMLEHMASTLAQGERIEIRGFGSFSLHYRAPRTGRNPKTGDKVELEGK
YVPHFKPGKELDRANIYG

>d1hns_a.55.1.1 (-) DNA-binding domain of H1 protein, (H-NS) {Escherichia coli}
AQRPAKSYVDENGETKTWTGQGRTPAVIKKAMDEQGKSLDDFLIKQ

>d1huua_a.55.1.1 (A:) HU protein {Bacillus stearothermophilus}
MNKTELINAVAETSGLSKKDATKAVDAVFDSITEALRGDKVQLIGFGNFEVRERAARKGRNPQTGEEMEIPAS
KVPAFKPGKALKDAVK

>d1b8za_a.55.1.1 (A:) HU protein {Thermotoga maritima}
MNNKTELIDRVAKKAGAKKKDVKLILD TILETITEALAKGEKVQIVGFGSFEVRKAAARKGVNPQTRKPTIPERKVP
KFKPGKALKEKVK

>d1exe_a.55.1.1 (A:) Transcription factor 1, TF1 {Bacteriophage SPO1 (Bacillus subtilis)}
MNKTELIAIAQDTGLTQVSVKMLASFKEIITETVAKGDKVQLTGFNLKPVARQARKGFNPQTQEALIAPSVG
VSVKPGESLKAAEGLKYEDFAK

>d1dp3a_a.55.1.2 (A:) DNA-binding domain (fragment?) of the TraM protein {Escherichia coli}
AKVQAYVSDEIVYKINKIVERRRAEGAKSTDVFSSISTMLLEGLRVYEAQMER

>d1hlra1_a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2 {Desulfovibrio gigas}
QPENLHPLQKAWVLHGGACGFCSPGFIVSAKGLDTNADPSREDVRDWFQKHRNACRCTGYKPLVDAVM
AAAVINGKKPETDLEFKMPADGRIWGSKYPRPTAVAKVTGLT

>d1dgja1_a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2 {Desulfovibrio desulfuricans}
APDCLHPLQHAWIQQHGAAQCGFCTPGFIVSAKALLDENVAPSREDVRDWFQKHHNICRCTGYKPLVDAVM
AAAILRGEKTVEEISFKMPADGRIWGSSIPRPSAVAKVTGLA

>d1fo4a1_a.56.1.1 (A:93-165) Xanthine oxidase, domain 2 {Cow (Bos taurus)}
STKTRLHPVQERIAKSHGSQCGFCTPGIVMSMYTLLRNQPEPTVEEIEDAFQGNLCRCTGYRPILQGFRTFAK

>d1jroa1_a.56.1.1 (A:85-166) Xanthine dehydrogenase chain A, domain 2 {Rhodobacter capsulatus}
DGRLHPVQQAMIDHHGSQCGFCTPGFIVSMAAHDRDRKDYDDLLAGNLRCTGYAPIRRAEAAAGEPPA
DWLQADAATL

>d1qj2a1_a.56.1.1 (A:82-161) Carbon monoxide (CO) dehydrogenase iron-sulfur protein, C-domain {Pseudomonas carboxydovorans}
APDGTL SALQEGFRMMHGLQCGYCTPGMIMRSRLLQENPSSTEAEIRFGIGGNLCRCTGYQNIVKAIQYAAA
KINGVPF

>d1ffva1_a.56.1.1 (A:82-157) Carbon monoxide (CO) dehydrogenase iron-sulfur protein, C-domain {Hydrogenophaga pseudoflava}
NKGVLHAVQEGFYKEHGLQCGFCTPGMLMRAYRFLQENPNPTEAEIRMGMTGNLCRCTGYQNIVKAVQYAA
RKLQE

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

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

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

>d1af7_1_a.58.1.1 (11-91) Chemotaxis receptor methyltransferase CheR, N-terminal domain {Salmonella typhimurium}
SVLLQMTQRLALSDAHFRRICQLIYQRAGIVLADHKRDMVYNRLVRRRALGLDDFGRYLSMLEANQNSAEW
QAFINALTT

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

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

>d1bqv__a.60.1.1 (-) Ets-1 transcription factor pointed domain {Mouse (Mus musculus)}
MECADVPLTPSSKEMMSQALKATFSGFTKEQQRLGIPKDPRQWTETHVRDWVMWAVNEFSLKGVDQFQKFC
MSGAALCALGKECFLELAPDFVGDLWEHLEILQKEDVK

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

FSAVSVGDWLQAIKMDRYKDNFTAAGYTTLEAVVHMSQDDLARIGITAITHQNKLSSVQAMRTQMQQMH
G

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

PDYTSFNTVDEWLEAIKMGQYKESFANAGFTSFDVVSQMMMEDILRVGVTLAGHQKKILNSIQVMRAQM
NQIQS

>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)}

YHADPSLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRLQDLKGHDY

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

SLVSFLTGLGCPNCIEYFTSQGLQSIYHLQNLTIEDLGALKIPEQYRMTIWRLQDL

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

NKQERTLFKELIKTNVGPKLALAILSGMSAQQFVNAVEREEVGALVKLPGIGKKTAERLIVEMKDRFKGLHGDL
FTP

>d1bvs2 a.60.2.1 (A:64-134) DNA helicase RuvA subunit, middle domain {Mycobacterium leprae}

DAENRDLFLALLSVVGVPRLAMATLAVHDAALRQALADSDVASLDRVPGIGRRGAERIVLEADKVGPV

>d1dgsa1 a.60.2.2 (A:401-581) NAD+-dependent DNA ligase, domain 3 {Thermus filiformis}

RWPEACPECGHRLVKEGVHRCNPPLCPAKRFEAIRHYASRKAMDIEGLGEKLERLLEKGLVRDVADLYHLRKE
DLLGLERMGEKSAQNLLRQIEESKRGLERLLYALGLPGVGEVLARNLARRFGTMDRLLEASLEELIEVEVGELT
ARAILETLKDPAFRDLVRRRLKEAGVSMESK

>d1coo_a.60.3.1 (-) C-terminal domain of RNA polymerase alpha subunit {Escherichia coli}

FPDILLRPVDDLELTVRSANCLKAEAIHYIGDLVQRTEVELLKTPNLGKKSSTEIKDVLASRGSLGMRLENWPPAS
IADE

>d1doqa_a.60.3.1 (A:) C-terminal domain of RNA polymerase alpha subunit {Thermus thermophilus}

EQEEELDPLEELGLSTRVLHSLKEEGIESVRALLALNLKDLKNIPGIGERSLEEIKEALEKKGFTLKE

>d1b22a_a.60.4.1 (A:) DNA repair protein Rad51, N-terminal domain {Human (Homo sapiens)}

EEESFGPQPISRLEQCGINANDVKKLEEAGFHTVEAVAYAPKKELINKGISEAKADKILAAKLVPMG

>d1ci4a_a.60.5.1 (A:) Barrier-to-autointegration factor, BAF {Human (Homo sapiens)}

MTTSQKHDFVAEPMGEKPGVSLAGIGEVLGKLEERGFDKAYVVLGQFLVKKDEDLFREWLKDTCGANAK
QSRDCFGCLREWCD AFL

>d1bp2a1_a.60.6.1 (A:10-91) DNA polymerase beta, N-terminal (8 kD)-domain {Human (Homo sapiens)}

TLNGGITDMTELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKLPGVGTKIAEKIDEFLATGKLRKLE
KIRQD

>d1dk2a_a.60.6.1 (A:) DNA polymerase beta, N-terminal (8 kD)-domain {Rat (Rattus norvegicus)}

SKRKAPQETLNGGITDMVELANFEKNVSQAIHKYNAYRKAASVIAKYPHKIKSGAEAKLPGVGTKIAEKIDEFL
ATGKLRKLEK

>d1jmsa1_a.60.6.1 (A:148-242) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}

KKISQYACQRRTTNNYNQLFTDALDILAENDELRENEGSCLAFMRASSVLKSLPFPITSMDTEGIPCLGDKVKS
IIEGIIEDGESSEAKAVLN

>d1tfr_1_a.60.7.1 (183-305) T4 RNase H {Bacteriophage T4}

GSAEIDCMTKILKGDKKDNVASVKVRSDFWFTRVEGERTPSMKT SIVEAIANDREQAKVLLTESEYNRYKENLVL
IDFDYIPDNIASNIVNYNSYKLPPRGKIYSYFVKAGLSKLTNSINEF

>d1bgxt1 a.60.7.1 (T:174-289) 5' to 3' exonuclease domain of DNA polymerase Taq {Thermus aquaticus}
LRPDQWADYRALTGDESDNLPGVKIGEKTARKLLEWGSLEALLKNLDRLKPAIREKILAHMDDLKLSWDLAK
VRTDLPLEVDFAKRREPDRERLRAFLERLEFGSLLHEFGILLE

>d1xo1a1 a.60.7.1 (A:186-290) T5 5'-exonuclease {Bacteriophage T5}
VDDVEQFISLKAIMGDLGDNIRGVEGIGAKRGYNIIREFGNVLDIIDQLPLPGKQKYIQNLNASEELLFRNLILVDL
PTYCVDAIAAVGQDVLDKFTKDILEIAE

>d1a77_1 a.60.7.1 (209-316) Flap endonuclease-1 {Archaeon Methanococcus jannaschii}
ISLDDLIIDIAIFMGTDYNPGGVKGIGFKRAYELVRSGVAKDVLKKEVEYYDEIKRIFKEPKVTDNYSLSLKLKDKEGII
KFLVDENDFNYDRVKKHVDKLYNLIANKT

>d1b43a1 a.60.7.1 (A:220-339) Fen-1 nuclease {Archaeon Pyrococcus furiosus}
LTREKLIELAILVGTDYNPGGIKGIGLKKALEIVRHSKDKPLAKFQKQSDVDLYAIKEFFLNPPVTNDYNLVWRDPDE
EGILKFLCDEHDFSEERVKNGLERLKKAIKSGKQSTLESWFKR

>d1d8ba_ a.60.8.1 (A:) HRDC domain from RecQ helicase {Baker's yeast (Saccharomyces cerevisiae)}
ELNNLRLMTYERLRELSNLGNRMVPPVGNFMPDSILKKMAAILPMNDSAFLGTVEDKYRRRFKYFKATIADL
SKKRSSE

>d1go3f_ a.60.8.2 (F:) RNA polymerase II subunit RBP7 (RpoF) {Archaeon Methanococcus jannaschii}
MIGKKILGERYVTVSEAAEIMYNRAQIGELSYEQGCALDYLQKFAKLDKEEAKLVEELISLGIDEKTAVKIADILPE
DLDDLRAIYYKRELPEAAEILEIVRKYI

>d1f44a1 a.60.9.1 (A:20-129) Cre recombinase {Bacteriophage P1}
SDEVRKNLMDMFRDRQAFSEHTWKMLSVCRSWAAWCKLNNRKWFPAEPEDVRDYLQARGLAVKTIQ
QHLGQLNMLHRRSGLPRPSDSNAVSLVMRRIRKENVDAGE

>d1a0p_1 a.60.9.1 (3-100) Recombinase XerD {Escherichia coli}
QDLARIEQFLDALWLEKNLAENTLNAYRRDLSMMVEWLHHRGTLATAQSDDLQALLAERLEGGYKATSSARL
LSAVRRLFQYLYREKFREDDPSAHL

>d1floa1 a.60.9.1 (A:2-129) Flp recombinase {Baker's yeast (Saccharomyces cerevisiae)}
PQFDILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWMITHNGTAIKRATFMSNTIISNSLSFDIVNKSLQ
FKYKTQKATILEASLKKLIPAWEFTIIPYYGQKHQSDITDIVSSLQLQFES

>d1zyma1 a.60.10.1 (A:22-144) Enzyme I of the PEP:sugar phosphotransferase system HPr-binding (sub)domain {Escherichia coli}
DEIVIDRKKISADQVDQEVERTLSGRAKASAQLETIKTKAGETFGEKEAIFEGHIMLLEDEELEQEIIALIKDKHM
TADAAAHEVIEGQASALEELDDEYLKERAADVRDIGKRLRNILGL

>d1jyga_ a.60.11.1 (A:) Hypothetical protein YjbJ {Escherichia coli}
MNKDEAGGNWKQFKGVKEQWGKLTDMMTIIEGKRDQLVGKIQERYGYQKDQAEKEVVWDWETRNEYRW

>d1hiwa_ a.61.1.1 (A:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}
VLSGGELDKWEKIRLRPGKKQYKLKHIVWASRELERFAVNPGLETSEGCRQILGQLQPSLQTGSEELRSLYNTI
AVLYCVHQRIDVKDTKEALDKIEEEQNKSKKQAQQAAAD

>d1hiws_ a.61.1.1 (S:) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}

VLSGGELDKWEKIRLRPGGKKQYKLKHIVWASRELERFAVNPGLETSEGCRQILGQLQPSLQTGSEELRSLYNTI
AVLYCVHQRIDVKDTKEALDKIEEEQN

>d1tam_ a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}

MGARASVLSGGELDRWEKIRLRPGGKKQYKLKHIVWASRELERFAVNPGLETSEGCRQILGQLQPSLQTGSEE
LRSLYNTVATLYCVHQRIEKDTKEALDKIEEEQNKSKKAAQQAAA

>d2hmx_ a.61.1.1 (-) HIV-1 matrix protein (HIV-1 MA, HIVp17, p17, MA) {Human immunodeficiency virus type 1}

HMGARASVLSGGELDKWEKIRLRPGGKKQYKLKHIVWASRELERFAVNPGLETSEGCRQILGQLQPSLQTGSE
ELRSLYNTIAVLYCVHQRIDVKDTKEALDKIEEEQNKSKKAAQQAAADTGNNSQVSQNY

>d1ed1a_ a.61.1.1 (A:) SIV matrix antigen {Simian immunodeficiency virus}

SVLSGKKADELEKIRLRPGGKKYMLKHVVWAANELDRFGLAESLLENKEGCQKILSVIAPLVPTGSENLKSLYNT
VCVIWCIAEAKVHTEAKQIVQRHLVVETGTAETMP

>d1jvr_ a.61.1.2 (-) HTLV-II matrix protein {Human T-cell leukemia virus type 2}

HMGQIHGLSPTPIPKAPRGLSTHHWLNLQAAYRLQPGPSDFDFQQLRRFLKLALKTPIWLNPIDYSLLASLIPK
GYPGRVVEIINILVKNQVSPSAPAAPVPTPICPTTTPPPPPPSPEAHVPPPYVEPTTQC

>d1bax_ a.61.1.3 (-) Mason-pfizer monkey virus matrix protein {Simian mason-pfizer virus}

MGQEISQHERYVEQLKQALKTRGVKVYADLLKFFDFVKDTCWFPQEGTIDIKRWRRVGDCFQDYNTFGP
EKVPVTAFSYWNLIKELIDKKE

>d1a6s_ a.61.1.4 (-) GAG polyprotein M-domain {Rous sarcoma virus}

GEAVIKVISSACKTYCGKTSPSKKEIGAMLSLLQKEGLLMSPSDLYSPGSWDPTAALSQRAMILGKGELKTWGL
VLGALKAAREE

>d1heka_ a.61.1.5 (A:) EIAV matrix antigen {Equine infectious anemia virus, EIAV}

AMADIGSMGDPLTWSKALKKLEKVTVQGSQKLTTGNNCNWALSLVDFHDTNFVKEKDWWQLRDVIPLLEDVTQ
TLSGQEREAFERTWWAISAVKMGLQINNVVDGKASFQLLRAKYE

>d1qgta_ a.62.1.1 (A:) Hepatitis B viral capsid (hbcag) {Hepatitis B virus}

MDIDPYKEFGATVELLSFLPSDFPSVRDLDDTASALYREALESPEHCSPHHTALRQAILCWGELMTLATWVGNN
LEDPASRDLVNVNTNMGLKIRQLWFHISCLTFRETGLEYLVSFGVWIRTPPAYRPPNAPIST

>d1aep_ a.63.1.1 (-) Apolipophorin-III {African locust (Locusta migratoria)}

NIAEAQQLNHTIVNAAHELHETLGLPTPDEALNLLTEQANAFKTKIAEVTSKLQEAHKQGSVAEQLNAFAR
NLNNNSIHDAATSLNLQDQLNLSQSLTNVGHQWQDIATKTQASAQEAWAPVQSAQEEAKTKEAAANLQN
SIQSAVQK

>d1eq1a_ a.63.1.1 (A:) Apolipophorin-III {Manduca sexta}

DAPAGGNAFEEMEKAKEFQKTFSEQFNSLNSKNTQDFNKALDGSDSVLQQLSAFSSLQGAISDANGKAK
EALEQARQNVEKTAELRKAHPDVEKEANAFKDKLQAAVQTTVQESQKLAKEVASNMEETNKKLAPKIKQAYD
DFVKHAEEVQKKLHEAATKQ

>d1nkl_ a.64.1.1 (-) NK-lysin {Pig (Sus scrofa)}

GYFCESCRKIIQKLEDMVGPQPNEDTVQAASQVCDKLKILRGLCKIMRSFLRRISWDILTGKKPQAICVDIKIC
KE

>d1qdma1 a.64.1.2 (A:1S-104S) (Pro)phyepsin {Barley (Hordeum vulgare)}

VVSQECKTIVSQYQQILDLLAETQPKKICSQVGLCTFDGTRGVSAIGRSVVDEPVKSNGLRADPMCSACEM
AVVWMQNQLAQNKTDQLILDYVNQLCNRLP

>d1e68a_ a.64.2.1 (A:) Bacteriocin AS-48 {Enterococcus faecalis}

MAKEFGIPAAVAGTVLNVVEAGGWVTTIVSILTAGSGGLSLLAAAGRESIKAYLKKEIKKGKRAVIW

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

GSAVSPYPTFPSSDVAALHKAIMVKGVDEATIIDILTKRNNAAQRQQIKAAYLQETGPLDETLKKALTGHLEEVV
LALLKTPAQFDAELRAAMKGGLTDEDTLIELASRTNKEIRDINRVYREELKRDIAKDTSDTSGDFRNALLSLAK
GDRSEDFGVNEDLADSARALYEAGERRKTDVNFTILTTRSYPLRRVFQKYTKYSKHDNMKVLDLELKG
DIEKCLTAIVKCATSKPAFFAEKLHQAMKGVGTRHKALIRIMVSREIDMNDIKAFYQKMYGISLCQAILDETKGD
YEKILVALCGGN

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

TFNPSSDVAALHKAIMVKGVDEATIIDILTKRNNAAQRQQIKAAYLQETGPLDETLKKALTGHLEEVVLALLK

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

AMVSEFLKQAWFIDNEEQEYIKTVGSKGPGSAVSPYPTFPSSDVEALHKAITVKGVDEATIIIEILTKRNTNAQR
QQIKAAYLQEKGKPLDEALKALTGHLEEVALLKTPAQFDAELRAAMKGGLTDEDTLNEILASRTNREIREIN
RVYKEELKRDIAKDTSDTSGDYQKALLSLAKGDRSEDLAINDDLADTDARALYEAGERRKTDLNFTILTTRSY
PHLRRVFQKYSKYSKHDNMKVLDLELKGDENCLVVVKCATSKPMFFAEKLHQAMKGIGTRHKTLLRIMVSRS
EIDMNDIKACYQKLYGISLCQAILDETKGDYEKILVALCG

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

SASIWVGHRGTVRDYPDFSPSVAEAIQKAIRGIGTDEKMLISILTERSNAQRQLIVKEYQAAYGKELKDDLKGDL
SGHFEHLMVALVTPPAVFDAKQLKKSMKGAGTNEDALIEILTTSRQMKDISHQAYYTYYKSLGDDISSETSGD
FRKALLTLADGRRDESLKVDLAKQDAQILYKAGENRWGTDDEKFTEILCLRSFPQLKLTFDEYRNISQKDIVDSI
KGELSGHFEDLLAIVNCVRNTPAFLAERLHRALKGITDEFTLNRMVSRSEIDLDIRTEFKKHGYGSLYSAIKSD
TSGDYEITLLKICGGDD

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

ASGFNAAEDAQTLRKAMKGGLTDEDAIINVLRSTAQRQEIRTAYKTTIGRDLMDLKSLSGNFEQVILGMM
TPTVLYDVQELRKAMKGAGTDEGCLIEILASRTPEEIRRINQTYQLQYGRSLEDDIRSDTSFMQRVLVLSAGGR
DESNYLDALMRQDAQDLYEAGEKKWGTDEVKFLTVLCSRNRNHLLHVDEYKRIAQKDIEQSIKSETGSFED
ALLAIVKCMRNKSAYFAERLYKSMKGTDDETLIRVMVSRAEIDMLDIRANFKRLYGKSLYSFIKGDTSGDYRKV
LLILCGGGDD

>d1ala_a.65.1.1 (-) Annexin V {Chicken (Gallus gallus)}

KYTRGTVTAFSPFDARADAELRKAMKGGMGTDEETILKILTSRNNAAQRQEIASAFKTLFGRDLVDDLKSELTGKF
ETLMVSLMRPARIFDAHALKHAIKGAGTNEKVLTEILASRTPAEVQNIQVYMQEYANLEDKITGETSGHFQRL
LVVLLQANRDPDGRVEEALVEKDAQVLFRAGELKWGTDEETFITLGTRSVSHLRRVFDKYMISGFQIEETIDRE
TSGDLEKLLLAVVKCIRSPAYFAETLYYSMKGAGTDDDTLIRVMVSREIDLLDIRHEFRKNFAKSLYQMIQKDT
GDYRKALLLCGG

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

VLRGTVTDFPGFDGRADAELRKAMKGGLTDEESILLLTSRNSAQRQEISAAFKTLFGRDLVDDLKSELTGKF
LIVALMKPSRLYDAYELKHALKGAGTNEKVLTEIIASRTPEELRAIKQVYEEYGSLEDDVVGDTGYYQRMLVVL
LQANRDPDAGIDEAQVEQDAQALFQAGELKWGTDEEKFITIFGTRSVSHLRRVFDKYMISGFQIEETIDRETSG
NLEQLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVMVSREIDLFNIRKEFRKNFATSLSYMIKGDTSGDYK
KALLLLC

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

ALRGTVTDFSGFDGRADAELRKAMKGGLTDEDSILNLLTARSNAQRQQIAEEFKTLFGRDLVNDMKSELTGKF
EKLIVALMKPSRLYDAYELKHALKGAGTDEKVLTEIIASRTPEELRAIKQAYEEYGSNLEDDVVGDTGYYQRMLV
VLLQANRDPDTAIDDAQVELDAQALFQAGELKWGTDEEKFITIFGTRSVSHLRRVFDKYMISGFQIEETIDRETS
GNLENLLLAVVKSIRSIPAYLAETLYYAMKGAGTDDHTLIRVIVSRSEIDLFNIRKEFRKNFATSLSYMIKGDTSGDYK
KALLLLCGGEDD

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

YRGSI RDFP FNPS QDAETLYNAMKG FGS DKEAIINLITSRSNKQRQ EICQNYKSLYKDLIADLK YELTG KFERLI
VGLMR PPA YADAKEIKDAISGIGTDEKCLIEILASRTNEQIHQ LVAAYKDAYERDLEADITGDTSGHFRKMLVLLQ
GTREEDDV VSEDLVQQDVQDLYEAGELKWGTDEAQFIYILGNRSKQHLRLVDEYLKTTGKPIEASIRGELSGDF
EKMLAVVKCIRSTA EYFAERLFKAMKGLGTRDNTLIRIMVRSELDMLDIREIFRTKYEKSLYSMIKNDTSGEYKK
TLLKLCGGDDDAAGQFFPEAAQVAYQMWE LSAVAR

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

VELKGTVRPAGDFNP DADAKALRKAMKGLGTDEDTIIDIITHRSNAQRQQI RQTFKSHFGRDLMADLKSEL SGD
LARLILGLMMPPA HYDAKQLK KAMEGAGTDEKALIEILATR TNAEIQAIN KAYKEDYHKTLEDALSSDTGHFKRI
LISLATGNREEGGEDRERAREDAQVAEILEIADTTSGDKSSLETRFMMILCTRSYPDLRRVFQE FVKMTNYDVE
HTIKKEMSGDVRDV FVAIVQS VKNKPLFFADKLYKSMKGAGTEEKTLTRIMVRSEIDL NIRREFIEKYDKSLHQ
AIEGDTSGHFLKALLAICGG

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

VVQGTVKPHASFNSREDAETLRKAMKG IGTDEKSITHILATRSNAQRQQI KTDYTTLFGKHLEDELKSEL SGNYE
AAALALLRK PDEF LAEQLHAAMKGLGT DKNALIDILCTQSNAQI HAIAKA AFKLLYKED LEKEISETSGNFQRLLV S
MLQGGRKEDEPVNAAHAAEDAAAIYQAGEGQIGTDESRFNAVLATRSYPQLHQ IFHEYSKISNKT ILQAIENFS
GDIKNGLLAIVKS VENRFAYFAERLHHAMKGLGTS DKLIRILV SRSEIDL NIKETFQAM YGKSLYEFIADD CSGD
YKDLLLQITGH

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

HHHHMASLTVPAHVPS AEDCEQLRSAFKG WGTNEKLI SILA HRTAAQRKLIRQTYAETFGEDLLKELDRELTH
DFEKLV LVWTLDPSER DAHLAKEATKRWTKSNFVLVELACTRSPKELV LAREAYHARYKKSLEEDVAYHTTGDHR
KLLVPLVSSYRYGGEVDLRLAKAESKILHEKISDKAYSDDEVIRI LATRSKAQLNATLNHYKDEHGEDILKQLEDGD
EFVALLRATIKGLVY PEHYFVEVRD AINRRGTEEDHLTRVIATRAEV DLKIIADEYQK RD S I PLGRAIA KDT RDY
SMLL ALLGQE

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

GEKATKVQDIKNNLKEA IETIVAAMS NLVPPVELANPENQFRDVYILS VMNVPDFDPPEFYEHAKALWEDEGV
RACYERSNEYQLIDCAQYFLDKIDV IKQDDYVPSDQ DLLRCR

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

YSLEECLEFIAIYGNTLQ SILAIVRAMTTLNIQY GDSARQDDARKLMHMADTIEEGT MPKEMSDIIQRLWKDSG
IQACFD RASEYQLNDSAGYYLSDLERLVT PGYV PTEQ DVLS RVKT

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

YSEECKQYKAVVYSNTIQSIIIRAMGRLKIDFGDAAR ADDARQLFVLAGAAEEGF MTAELAGVIKRLWKDSG
VQACFNRSREYQLNDSAA YYLNDL DRIAQP NYIPTQ QDV LRTRV KT

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

SGFKH VS HVG WD PQNG FDVN NLD PDL RSL FSRAG ISEA QLT DAE TS KLIY DFIED QGG LEAV RQEM RRQ GGS
GGSQSSEG LVG ALMHVMQ KRS RAIH SSDE GEDQAG

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

TRAMKQVAGTMKLELAQYREVAFAQFGSDL DAATQQLLSRGVR LTE LLKQGQYSPMAIEEQVAVIYAGVRGY
LDKLEPSKITKFEN AFLSHVISQHQ ALLGKIR TDGKISEESDAKLKEIV TNFLAG FEA

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

MDPNIVGSEHYDVARGVQKILQDYKSLQDII AILGM DELSEEDKLT VSRARKIQRFLS QPFQVAEVFTGHLGKLV

PLKETIKGFQQILAGEYDHLPEQAFYMGPIEEAVAKADKLAЕ
>d1skyb1 a.69.1.1 (B:372-502) C-terminal domain of alpha and beta subunits of F1 ATP synthase
{Bacillus sp., strain ps3}
IKAMKKVAGTLRLDAAYRELEAFAAQFGSDLKATQANVARGARTVEVLQDLHQPIPVEKQVLIYALTRGFLD
DIPVEDVRRFEKEFYWLQDNGQHLLHEHIRTTKDPNEDDLNQAIEAFKKTFVVSQ
>d1skye1 a.69.1.1 (E:357-470) C-terminal domain of alpha and beta subunits of F1 ATP synthase
{Bacillus sp., strain ps3}
EIVGEEHYQVARKVQQTLERYKELQDIIAILGMDELSDEDKLVVHRARRIQFFLSQNFHVAEQFTGQPGSYVPVK
ETVRGFKEILEGKYDHLPEDRFRLVGRIEEEVVEKAKAMG
>d1fx0a1 a.69.1.1 (A:373-501) C-terminal domain of alpha and beta subunits of F1 ATP synthase
{Spinach (Spinacia oleracea), chloroplast}
IKAMKKVAGKLKLEAQFALEAFAAQFASDLKATQNQLARGQRLLKQPQSAPLTVEEQVMTIYTGTNGYL
DSLELDQVRKYLVELRTYVKTNPKEFQEIISSSTKTFTEEAALLKEAIQEQMERC
>d1fx0b1 a.69.1.1 (B:378-485) C-terminal domain of alpha and beta subunits of F1 ATP synthase
{Spinach (Spinacia oleracea), chloroplast}
RIVGEEHYEIAQRVKETLQRYKELQDIIAILGLDELSEEDRLTVARARKIERFLSQPFFVAEVFTGSPGVLAETIR
GFQLILSGEELDSLPEQAFYLVGNIDEATA
>d1fkma1 a.69.2.1 (A:249-442) Ypt/Rab-GAP domain of gyp1p {Baker's yeast (Saccharomyces cerevisiae)}
NSIIQRISKFDNILKDKTIINQQDLRQISWNGIPKIHRPVVWKLLIGYLPVNTRQEGFLQRKRKEYRDSLKHTFSD
QHSRDIPTWHQIEIDIPRTNPHIPLYQFKSVQNSLQRILYLAIRHPASGYVQGINDLVTFFETFLTEYLPPSQIDD
VEIKDPSTYMVDEQITDLEADTFWCLTKLLEQITDNYIH
>d1fkma2 a.69.2.1 (A:443-630) Ypt/Rab-GAP domain of gyp1p {Baker's yeast (Saccharomyces cerevisiae)}
GQPGILRQVKNLSQLVKRIDADLYNHFQNEHVEFIQFAFRWMNCLLMREFQMGTVIRMWDTYLSETSQEVT
SYSMSSNDIKPPVTPTEPRVASFVTPKDFQSPTTALSNMPNAVEDSGKMRQSSLNEFHVFVCAAFLIKWS
DQLMEMDFQETITFLQNPPTKDWWTETDIEMLLSEAFIWQSLYK
>d1k5ha1 a.69.3.1 (A:301-398) 1-deoxy-D-xylulose-5-phosphate reductoisomerase, C-terminal domain {Escherichia coli}
KLSALTFAAPDYDRYPCLKLAMEAFEQGQAATTALNAANEITVAAFLAQHQIRFTDIAALNLSVLEKMDMREPQC
VDDVLSVDANAREVARKEVMRLAS
>d1abv__ a.70.1.1 (-) N-terminal domain of the delta subunit of the F1FO-ATP synthase {Escherichia coli}
SEFITVARPYAKAAFDFAVEHQSVWRQDMLAFAAEVTKNEQMAELLSGALAPETLAESFIAVCGEQLDENGQ
NLIRVMAENGRLNALPDVLEQFIHLRAVSEAT
>d1g7da_ a.71.1.1 (A:) Endoplasmic reticulum protein ERP29, C-domain {Rat (Rattus norvegicus)}
PGCLPAYDALAGQFIEASSREARQAILKQGQDGLSGVKETDKWASQYLKIMGKILDQGEDFPASELARISKLIE
NKMSEGKKEELQRSLNILTAFRKKGAKEEL
>d1dvka_ a.72.1.1 (A:) Functional domain of the splicing factor Prp18 {Baker's yeast (Saccharomyces cerevisiae)}
MRIQEAIAQDKTISIIDPSQIGSTEGKPLLSMKCNLYIHEILSRWKASLEAYHPELFLDTKKALFPLLQLRRNQLA
PDLLISLATVLYHLQPKEINLAVQSYMKLSIGNVAWPIGVTSGVIGHARSAHSIQGGRNAANIMIDERTRLWITS
IKRLITFEEWYTSNH
>d1ak4c_ a.73.1.1 (C:) HIV-1 capsid protein {Human immunodeficiency virus type 1}

PIVQNLQQGMVHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLK
ETINEEAAEWDRLHPVHAGPIAPGQMREPRGSDIAGTTSTLQEIQIGWMTHNPPIPVGEIYKRWIILGLNKIVR
MY
>d1e6jp2 a.73.1.1 (P:11-147) HIV-1 capsid protein {Human immunodeficiency virus type 1}
VHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALSEGATPQDLNTMLNTVGGHQAAMQMLKETINEEAAEWDR
RVHPVHAGPIAPGQMREPRGSDIAGTTSTLQEIQIGWMTHNPPIPVGEIYKRWIILGLNKIVRMYSP
>d2eiaa2 a.73.1.1 (A:17-147) EIAV capsid protein p26 {Equine infectious anemia virus}
PRGYTTWVNTIQTNGLLNEASQNLFGILSVDCTSEEMNAFLDVPGQAGQKQILLDAIDKIADDWDNRHPLP
NAPLVAPPQGPIPMTARFIRGLGVPRERQMEPAFDQFRQTYRQWIIEAMSEGIKVMIGK
>d1g03a_a.73.1.1 (A:) HTLV-I capsid protein {Human T-cell leukemia virus type 1}
PVMHPHGAPPNHRPWQMQLQAIKQEVSQAAPGSPQFMQTIRLAVQQFDPTAKDLQDLLQYLCSSLVASLH
HQQLDSLISEAETRGITSYNPLAGPLRVQANNPQQQGLRREYQLWLAAFAALPGSAKDPSWA
>g1qrj.1 a.73.1.1 (A;B:16-130) HTLV-I capsid protein {Human T-cell leukemia virus type 1}
HHHHHSSGHIEGRHMXQMQLQAIKQEVSQAAPGSPQFMQTIRLAVQQFDPTAKDLQDLLQYLCSSLVASLH
HQQLDSLISEAETRGITGYNPLAGPLRVQANNPQQQGLRREYQLWLAAFAALPGSAKD
>d1d1da2 a.73.1.1 (A:11-150) RSV capsid protein {Rous sarcoma virus}
WTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVLGPAPYALWMDAWGVQLQTVIAA
ATRDPRHPANGQGRGERTNLDRLKGLADGMVGNPQGQAALLRPGELVAITASALQAFREVARLAEP
>d1em9a_a.73.1.1 (A:) RSV capsid protein {Rous sarcoma virus}
PVVIKTEGPAWTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVLGPAPYALWMDAWG
VQLQTVIAAATRDPHPANGQGRGERTNLNRLKGLADGMVGNPQGQAALLRPGELVAITASALQAFREVAR
A
>d1jsub2 a.74.1.1 (B:310-432) Cyclin A {Human (Homo sapiens)}
TVNQFLTQYFLHQQPANCKVESLAMFLGEELSIDIADPYLKYLPSVIAGAAFHLALYVTGQSWPESLIRKTGYTLE
SLKPCLMDLHQTYLKAPQHAQQSIREKYKNSKYHGVSLNPPETLNL
>d1vin_1 a.74.1.1 (181-308) Cyclin A {Cow (Bos taurus)}
DIHTYLREMEVKCKPKVGYMKKQPDITNSMRAILVDLVEVGEEYKLQNETLHLAVNYIDRFLSSMSVLRGKLQ
LVGTAAMILLASKFEEYPPEVAEFVYITDDTYTKKQVLRMEHLVLKVLAFDLAA
>d1vin_2 a.74.1.1 (309-432) Cyclin A {Cow (Bos taurus)}
PTINQFLTQYFLHQQPANCKVESLAMFLGEELSIDIADPYLKYLPSVIAAAAFHLALYVTGQSWPESLVQKTGYTL
ETLKPCLLDLHQTYLRAPQHAQQSIREKYKNSKYHGVSLNPPETLNL
>d1jkw_1 a.74.1.1 (11-161) Cyclin H (mcs2) {Human (Homo sapiens)}
WTFSEEQLARLRADANRKFRCKAVANGKVLNDPVFLEPHEEMTLCKYYEKRLLFCCSVFKPAMPRSVVGTAC
MYFKRFYLNNSVMEYHPRIIMLTCAFLACKVDEFNVSSPQFVGVLNRESPLGQEKAQELEYELLIQQLNFH
H
>d1jkw_2 a.74.1.1 (162-287) Cyclin H (mcs2) {Human (Homo sapiens)}
NPYRPFEGFLIDLKTRYPILENPPEILRKTADDFLNRIALTDAYLLYTPSQIALTAILSSASRAGITMESYLS
RTCLSQLLDIMKSMRNLVKKYEPPRSEEVAVLKQKLDRCHS
>d1bu2a1 a.74.1.1 (A:22-148) Viral cyclin {Herpes virus saimiri}
RVLNNLKLRELLPKFTSLWEIQTEVTVDNRTILLWMHLLCESFELDKSVFPLSVSILD
AACVLIGSKIRTVKPMVTISKLYLSCDCFTNLELINQEKDILEALKWDTE
>d1bu2a2 a.74.1.1 (A:149-250) Viral cyclin {Herpes virus saimiri}

AVLATDFIPLCNALKIPEDLWPQLYEAASTTICKALIQPNIALSPGLICAGGLTTIEDNTNCRPWTYCLEDLSSI
LNFSTNTVRTVKDQVSEAFSLYD

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

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

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

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

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

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

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

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

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

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

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

>d1jfza_a.149.1.1 (A:) RNase III endonuclease domain {Aquifex aeolicus}
GMKMLEQLEKKLGTFKDKSLLKALTHVSYKKEHYETLEFLGDALVNFFIVDLLQYSPNKREGFLSPLKAYLISE
EFFNLLAQKLELHKFIRIKRGKINETIIGDVFEALWAAYVIDSGRDANFTRELFYKLFKEDILSAIKEGR

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

YQVPVEVRPDRRVSLGLRWLVQYARLRNEKTMEERLANEIMDAANNTGAAVKKREDTHKMAEAN
>d1rss__ a.75.1.1 (-) Ribosomal protein S7 {Thermus thermophilus}
LQPDLVYGDVLVTAFINKIMRDGKKNLAARIFYDACKIIQEKTGQEPLKVFQAVENVKPRMEVRSRRVGGANY
QVPMEVSPRRQQSLALRWLVQAANQRPERRAAVRIAHELMDAAEGKGAVKKKEDVERMAEANRAYAHYR
W
>d1iqva_ a.75.1.1 (A:) Ribosomal protein S7 {Archaeon Pyrococcus horikoshii}
IKVMGRWSTEDVEVKDPSLKPYINLEPRLPHTGRHAKKHFGKANVHIVERLINKVMRSGGSHYKVAGHF
RREHRSLSKKVRAYEVVKEAFKIIEKRTGKNPIQVLVWAIENAAPREDTTSVMFGGIRYHVAVDISPLRLDVAL
RNIALGASAKCYRTKMSFAEALAEIILAANKDPKSYASKKLEIERIAESSR
>d1jr3a1 a.80.1.1 (A:243-368) gamma subunit {Escherichia coli}
TLDDDQALS LVEAMVEANGERVMALINEAAARGIEWEALLVEMGLLHRIAMVQLSPAALGNDMAAIELRMR
ELARTIPPTDIQLYYQTLLIGRKELPYAPDPRRMGVEMTLLRALAFHPRMPLPEP
>d1a5t_1 a.80.1.1 (208-330) delta prime subunit {Escherichia coli}
DNWQARETLCQALAYSVPSGDWYSLLAALNHEQAPARLHWLATLLMDALKRHHGAAQVTNVDVPGVVAELA
NHLSPSRQLQAILGDVCHIREQLMSVTGINRELLTDLLRIEHYLQPGVVL
>d1jr3d1 a.80.1.1 (D:212-338) delta subunit {Escherichia coli}
FTPFHWVDALLMGKSKRALHILQQLRLEGSEPVILLRTLQRELLLVNLKRQSAHTPLRALFDKHRVWQNRRG
MMGEALNRLSQTQLRQAVQLLRTETLKQDYGQSVAELEGLSLLLCHKPLAD
>d1iqa1 a.80.1.1 (A:233-327) Replication factor C {Archaeon Pyrococcus furiosus}
RARPEDIREMMMLALKGNFLKAREKLREILLKQGLSGEDVLVQMHKEVFNLPIEPPKKVLLADKIGEYNFRLVEG
ANEIIQLEALLAQFTLIGKK
>d1jr5a_ a.150.1.1 (A:) Anti-sigma factor Asia {Bacteriophage T4}
MNKNIDTVREIITVASILIKFSREDIVENRANFIAFLNEIGVTHEGRKLNQNSFRKIVSELTQEDKKTIDEFNEGFE
GVYRYLEMINTNK
>d1f5ta2 a.76.1.1 (A:1065-1121) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}
PTPGRTLATAVMRKHRLAERLLTDIIGLDINKVHDEADRWEHVMDEVERRLVKVL
>d1g3sa2 a.76.1.1 (A:65-140) Diphtheria toxin repressor (DtxR) {Corynebacterium diphtheriae}
PTPGRTLATAVMRKHRLAERLLTDIIGLDINKVHDEASRWEHVMDEVERRLVKVLKDVSRSFGNPIPGLDELGV
>d1fx7a2 a.76.1.1 (A:65-144) Iron-dependent regulator {Mycobacterium tuberculosis}
TEKGRALIAAVMRKHLAERLLVDVIGLPWEEVHAEACRWEHVMSEDVERRLVKVLNNPTTSPFGNPIPGLDE
LGVGPEP
>d1gpja1 a.151.1.1 (A:303-404) Glutamyl tRNA-reductase dimerization domain {Archaeon
Methanopyrus kandleri}
EIPKVEKLIIEELSTVEEELEKLKERRLVADVAKSLHEIKDRELERALRRLKTGDPENVLQDFAEAYTKRLINVLTSAI
MELPDEYRRAASRALRRASELNG
>d1ngr__ a.77.1.1 (-) p75 low affinity neurotrophin receptor {Rat (Rattus norvegicus)}
GNLYSSLPLTKREEVEKLLNGDTWRHLAGELGQPEHIDSFTHEACPVRALLASWGAQDSATLDALLAALRRIQR
ADIVESLCSE
>d1ddf__ a.77.1.1 (-) Fas {Human (Homo sapiens)}
METVAINLSDVDSLKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQLRNWHQLHGKKE
AYDTLIKDLKKANLCTLAEKIQTIILKDISDSENSNFRNEIQSLVLEHHHHHH
>d1a1w__ a.77.1.1 (-) FADD (Mort1) {Human (Homo sapiens)}

MDPFLVLLHSVSSSLSSELTELKYLCLGRVGKRKLERVQSGLDLFSMLLEQNDEPGHTELLRELLASLRRHDLLR
RVDDFE

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

GSHMGEEDLCAAFNVICDNVGKDWRRLARQLVKSDTKIDSIEDRYPRNLTERVRESLRIWKNTEKENATVAHLVGALRSCQMNVLADLVQEQQARDLQNRSGA

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

AAPPGEAYLQVAFDIVCDNVGRDWKRRELKVSEAKMDGIEEKYPRSLSERVRESLKWKNAEKKNASVAGLVKALRTCRNLVADLVEEAQES

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

MEARDKQVLRSRLRELGAEVIVEGLVLQYLYQEGILTENHIQEINAQTTGLRKTMLLDILPSRGPKAFDTFLDSQEFPWVREKLKKAREEAMTDLPAG

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

MDAKARNCLLQHREALEKDIKTSYIMDHMISDGFLTSEEEKVRNEPTQQQRAAMLIKAMILKKDNDSYVSFYNALLHEGYKDLAALLHDGIPV

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

SMDEADRRLLRRCRRLVLELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRRDQARQLIIDLETRGSQALPLFISCLEDTGQDMLASFRLTNRQAG

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

ADQLLRKRRIFIHSVGAGTINALLDCILLEDEVISQEDMNKVRDENDTVMDKARVLIDLVTGKGPKSCCKFIKHLCEEDPQLASKMGLH

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

LDNTMAIRLLPLPVRAQLCAHLDALDVWQQLATAVKLYPDQVEQISSQKQRGRSASNEFLNIWGGQYNHTVQTLFALKKLKLHNAMRLIKDYVSEDLHKYI

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

LSSKYSRNTELRRVEDNDIYRLAKILDENSCWRKLMIIIPKGMDVQACSGAGCLNFPAEIKGFKYTAQDVFQIDEAANRLPPDQSKSQMMIDEWKTSGKLNERPTVGVLQLLVQAELFSAADFVALDFLNESTPARPVDPGPGALISE

>d1hw1a2 a.78.1.1 (A:79-230) Fatty acid responsive transcription factor FadR, C-terminal domain {Escherichia coli}

GLNILETLARLDHESVPQLIDNLLSVRTNISTIFIRTAFRQHPDKAQEVLATANEVADHADAFALDYNIFRGLAFA
SGNPIYGLLNGMKGLYTRIGRHYPANPEARSALGFYHKLSALCSEGHDQVYETVRRYGHESGEIWHRMQKNL

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

GRHQARKRAVALLFEAEVRGISAAEVVDTRAALAEAKPDIARLHPYTAAVARGVSEHAAHIDLITAHLRGWTL
DRLPAVDRAILRVSVWELLHAADVPEPVVDEAVQLAKELSTDDSPGVNGVLGQVM

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

MKPAARRRARECAVQALYSWQLSQNDIADVEYQFLAEQDVKDVDVLYFRELLAGVATNTAYLDGLMKPYLSRL
LEELGQVEKAVLRIALYELSRSRDPYKVAINEAIELAKSFGAEDSHKFVNGVLDKAAPVIRPNKK

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

PPHSIEAEQSVLGGMLDNERWDDVAERVVADDFYTRPHRHIFTEMARLQESGSPIDLTAELESERQGQLDSV
GGFAYLAELSKNTPSAANISAYADIVRE

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

MKVPPHSIEAEQSVLGGMLDNERWDDVAERVVADDFYTRPHRHIFTEMARLQESGSPIDLTAELESERQGQLDSV
LDSVGGFAYLAELSKNTPSAANISAYADIVRERAVVREMIS

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

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

>d1crka1_a.83.1.1 (A:1-98) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), mitochondria}
TVHEKRKLFPPSADYPDLRKHNNCMAECLTPAIYAKL RDKLTPNGYSLDQCIQTGV DNP GHPFI KTVGMVAGDE
ESYEVFAEIFDPVIKARHNGYDPR

>d1qh4a1_a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Chicken (Gallus gallus), brain-type}
PFSNSHNLKMKYSV D EYPDLSV HNNHMAKV LTLDLYKKLRD RQTS SGFT LDDV I QTGV DNP GHPFI M TVGC
VAGDEE SYEVFKELFDPVIEDR HGGYKP

>d1qk1a1_a.83.1.1 (A:1-102) Creatine kinase, N-terminal domain {Human (Homo sapiens), mitochondria}
AASERRRLYPPSAEY PDLRKHNNCMA SHLTPAVYARLCDKTTPTGWTL DQCIQTGV DNP GHPFI KTVGMVAG
DEETYEVFADLFDPVI QERHNGYD PR TMKH

>d2crka1_a.83.1.1 (A:8-102) Creatine kinase, N-terminal domain {Rabbit (Oryctolagus cuniculus)}
NKYKLNYKSEEY PDL SKHNNHMAKV LPDLYKKLRD KETPSGFT LDDV I QTGV DNP GHPFI M TVGC VAGDEES
YTVFKDLFDPIIQDRHGGFKP

>d1g0wa1_a.83.1.1 (A:2-102) Creatine kinase, N-terminal domain {Cow (Bos taurus), retinal isoform}
PFSNSHNTLKLRFPAEDEF PDL SGHNNHMAKV LP ELYAELRAKSTPSGFT VDDV I QTGV DNP GHPYIM TVGC
AGDEE SYDVFKELFDP II EDRHGGYKP

>d1bg0_1_a.83.1.1 (2-95) Arginine kinase {Horseshoe crab (Limulus polyphemus)}
VDQATLDKLEAGF KKLQEASDCKSLLKKHLTKDVFDSIKNKKTGMGATLLDVIQSGVENL DSGVG IYAPDAESYR
TGPLFDPIIDDYHGGFKL

>d1al01_a.84.1.1 (1:) Scaffolding protein gpD of bacteriophage procapsid {Bacteriophage phi-X174}
EQSVRFQ TALASI KLIQASAVLDLT EDDFDL TSNKVWIATDRSRARRC VEACVYGTDFVG YPRFPAPV EFIAAVI
AYYVHPVN IQTAC LIMEGA EFTENI INGVERPV KAAELFAFTL RV RAGNTD VLDAE ENVR QKLRA

>d1ll1_1_a.85.1.1 (1-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus polyphemus)}
TLHDKQIRVCHLFEQLSSATVIGDGDKHKHS DR LKNVGK LQPG AIFSCFH PDH LEE ARHLYEV FWEAGDFNDFIEIAKEARTFVNE
GLFAFAAEVAVLHRDDCKGLYVP

>d1lla_1_a.85.1.1 (2-109) Hemocyanin, N-terminal domain {Horseshoe crab (Limulus polyphemus)}
LHD KQIRCHLFEQLSSATVIGDGDKHKHS DR LKNVGK LQPG AIFSCFH PDH LEE ARHLYEV FWEAGDFNDFIEIAKEARTFVNE
AKEARTFVN EGLFAFAAEVAVLHRDDCKGLYVP

>d1hc2_1_a.85.1.1 (5-135) Hemocyanin, N-terminal domain {Spiny lobster (Panulirus interruptus)}
TGNAQKQQDINHLLDKIYEPTKYPDLK DIAENFNPLGDT SIYNDHGAAVETLMKELNDHRLLEQRHWYSLFNT
RQRKEALMLFAVLNQCKEWYCFRSNAAYFRERMNEGEFVYALYVSIHSKLGDGIVLP

>d1lla_2_a.86.1.1 (110-379) Hemocyanin {Horseshoe crab (Limulus polyphemus)}
PVQEIPDKFIPSAAINEAFKKAHV RPEFDES PILVDVQDTGNILDPEYRLAYYREDVGINAHHWHWHLVYPST

WNPKYFGKKDRKGELFYMMHQQM CARYDCERLSNGMHRMLPFNNFDEPLAGYAPHLTHVASGKYSPRP
DGLKLRLDLDIEISEMVRMRERILDSIHLGYVISEDGSHKTLDELHGTDLGALVESSYESVNHEYGNLHNWGH
VTMARIHD PDRFHEPGVMSDTSTSLRDPIFYNWHRFIDNIFHEYKNTLK
>d1hc2_2 a.86.1.1 (136-398) Hemocyanin {Spiny lobster (*Panulirus interruptus*)}
PLYQITPHMFTNSEVIDKAYSAKMTQKPGTFNVSFTGKKNREQRVAYFGEDIGMNIHHVTWHMDFPFWWE
DSGYHLDRKGEFFWVHQLTARFDFERLSNWLDPVDELHWDRIRREGFAPLTSYKGGEFPVRPDNIHFEDV
DGAHVHDLEITESRIHEAIDHGYITSDGHTIDIRQPKGIELLGDIESSKYSSNVQYYGSLHNTAHVMLGRQGD
PHGKFNLPPGVMEHFETATRDPSFFRLHKYMDNIFKKHTDSF
>d1js8a1 a.86.1.1 (A:2503-2791) Functional unit from octopus hemocyanin {Giant octopus (*Octopus dofleini*)}
AIIRKNVNSLTPSDIKELRDAMAKVQADTSNDGYQKIASYHGIPLSCHYENG TAYACCQHGMVTFPNWHRLLT
QM EDALVAKGSHVGIPYWDWTTTFANLPVLVTEKD NSFHH AIDVANTDTRSPRAQLFDDPKGDKSFFY
RQIALALEQTDFCDFEIQFEIGHNAIH SWVGSSPYGMSTLHYTSYDPLFYLHHSNTD RIWSVWQALQKYRGLP
YNTANCEINKLVKPLKPFNLDTNPNAVTKAHSTGATSF DYHKLGYDYDNLFHGMTIPELEEHLKEI QH
>d1bt3a_ a.86.1.2 (A:) Catechol oxidase {Sweet potato (*Ipomoea batatas*)}
APIQAPEISKCVVPPADLPPGAVVDNCCPPVASNIVDYKLP AVTTMKVRPAAH TMDKDAIAKFAKAVELMKALP
ADDPRNFYQQALVHCAYCNGGYDQVNFPDQEIQVHNSWLFFFHRWYLYFYERILGKLIGDPSFGLFWNWD
NPGGMVLPDFLNDSTSSLYDSNRNQSHLPPVV DLGYNGADTDVTDQQR ITDNLALMYKQMVTNAGTAELF
LGKAYRAGDAPSPGAGSIETSPHIPIHRWVG DPRNTNNEDMGNFYSAGR DIAFYCHHSNVDRMWTI WQQLA
GKPRKR DYTSDWLNATFLYDENGQAVKVRIGDSDLNQKMGYKYAKTPLPW
>d1dbha1 a.87.1.1 (A:198-404) Son of sevenless-1 (sos-1) {Human (*Homo sapiens*)}
EQTYYDLVKAFMAEIRQYIRELNLI KVFREPFVSNSKLF S AND VEN IF S RIV DIHELSVKLLGHIEDTV EMTDEGSP
HPLVGSCFEDLAELA FDP YES YARDI LRG FHDRFLSQLSKPGAA LYQSIGEGFKEAVQYVLP RL LAPVYHCLH
YFELLKQLEEKSEDQEDKECLKQAIT ALLNVQSGMEKICSKSLAKRRLSESA
>d1by1a_ a.87.1.1 (A:) beta-pix {Human (*Homo sapiens*)}
MKGFDTTAINKSYYNVVLQNILETENEYSKELQTVLSTYLRPLQTSEK LSSANISYLMGNLEEICSFQQMLVQSLEE
CTKLPEAQQRVGGCFLNLMPQMKTLYLTYCANHPSAVNLTEHSEELGEFMETKGASSPGILVTTGLSKPFMR
LDKYPTLLKELERHMEDYHTDRQDIQKSMAAFKNLSAQ CQE VRKRKELELQILTEAIR
>d1f5xa_ a.87.1.1 (A:) RhoGEF Vav {Mouse (*Mus musculus*)}
MKGDEIYEDLMRLESVPTPPKMT EYDKRCCLREIQQTEEKYDTLGSIQQHFMKPLQRFLKPQDMETIFVNIE
ELFSVHTHFLKELKDALAGPGATTLYQVFIKYKERFLVYGRYCSQVESASKHLDQVATA RDVQMKLEEC SQ RAN
NGRFTLRDLMVPMQRVLKYHLLQELVKHTQDATEKENRLA LDAMRD LAQCVNEV KR
>d1foea1 a.87.1.1 (A:1034-1239) GEF of TIAM1 (T-Lymphoma invasion and metastasis inducing protein 1) {Mouse (*Mus musculus*)}
QLSDADKLRKVICELLETERTYVKDLNCLMERYLKPLQKETFLTQD ELDVLFGNLTEMVEFQVEFLKTLEDGVRLV
PDLEKLEKV DQFKKVLFSLGGSF LYADRFKLYSAFCASHTKVPKVLVAKTDTAFKAFLDAQNPRQQHSSTLESY
LIKPIQRVLKYPLLL RELFALTDAESEEHYHLDVAIKTMNKVASHINEMQKIHE
>d1boua_ a.88.1.1 (A:) LigA subunit of an aromatic-ring-opening dioxygenase LigAB {Sphingomonas paucimobilis, formerly Pseudomonas paucimobilis}
IDVHAYLA EFDDIPGTRVFTAQRARKGYNLNQFAMSLMKAENRERKADESAYLDEWNLTPAAV LARDYN
AMIDE GGNVYFLSKLFSTDGKS FQFAAGSMTGMTQEEYAQM MIDGGRSPAGVRSIKGGY
>d1hbna1 a.89.1.1 (A:270-549) Alpha chain {Archaeon Methanobacterium thermoautotrophicum}
RRARGENE PGGVPGYLA DICQSSRVNYEDPVRVSLDV VATGAM LYDQIWLGSY MSGVGFTQYATAAYTDNI
LDDFTYFGKEYVED KYGLCEAPNNMDTVLDVATEVTYGLEQYEEYPALLE DQFGGSQRAV VAAAGCSTAFA

TGNAQTGLSGWYLSMYLHKEQHSRLGFYGYDLQDQCGASNVFSIRGDEGLPLELRGPNPNYAMNVGHQGE
YAGISQAPHAARGDAFVNPLVKIAFADDNLVDFTNVRGEFAKGALREFEPAGERALITPA
>d1e6va1 a.89.1.1 (A:273-552) Alpha chain {Archaeon Methanopyrus kandleri}
RRARGENEPPGVPGVLADCVQTMRKYPDDPAKVALEVIAAGAMLYDQIWLGSYMSGVGFTQYATAVYPD
NILDDYVYYGLEYVEDKYGIAEAEPMSMDVVKDVATEVTLYGLEQYERYPAAMETHFGGSQRAAVCAAAGCSTA
FATGHAQAGLNGWYLSQLHKEGQGRLGFYGYALQDQCGAANSLRSDEGLPLELRGPNPNYAMNVGHLG
EYAGIVQAAHAARGDAFCVHPVIKVAFADENLVFDFTEPRAKEFAKGALREFEPAGERDLIVPA
>d1e6ya1 a.89.1.1 (A:1284-1569) Alpha chain {Archaeon Methanosaerina barkeri}
RRARGPNEPGGLSGFGHLSDIVQTSRVSEDPAKIALEVVGAGCMLYDQIWLGSYMSGVGFTQYATAAYTDDILD
NNNTYYDVDYINDKYNGAATVGKDNKVKALEVVKDIATESTLYGIETYEKPTALEDHFQGSQRATVAAAAGVA
CSLATGNANAGLSGWYLSMYLHKEAWGRLGFFGFDLQDQCGATNVLSYQGDGLPDELGPNPNYAMNV
GHQGGYAGIAQAAHSGRGRDAFTVNPLLKVCFADDLLPFNFAEPREFGRGAIREFVPAGERSLVIPA
>d1hbnnb1 a.89.1.1 (B:189-443) Beta chain {Archaeon Methanobacterium thermoautotrophicum}
GYALRNIMVNHVVAATLKNTLQAAALSTILEQTAMFEMGDAVGAFERMHLLGLAYQGMNADNLVFDLVKAN
GKEGTGVSIAVLVERALEDGVIKVEKELTDYKVGTDDLAMWNAYAAAGLMAATMVNQGAARAAQGVSSAT
LLYYNDLIEFETGLPSVDFGKVEGTAVGFSFFSHSIYGGGGPGIFNGNHIVTRHSKGFAIPCVAAAMALDAGTQM
FSPEATSGLIKEVFSQVDEFREPLKYVVEAAAEIKNEI
>d1e6vb1 a.89.1.1 (B:190-442) Beta chain {Archaeon Methanopyrus kandleri}
GYALRNIMVNHVVAATRKNTMQAVCLAATLQQTAMFEMGDAVGAFERMHLLGLAYQGLNADNMVYDIVKKH
GKEGTGTVVREVVERALEDGVIEVKEELPSFKVYKANDMDLWNAYAAAGLVAAMVNQGAARAAQGVSSAT
ILYYNDLLEYETGLPGVDFGGRAEGTAVGFSFFSHSIYGGGGPGIFHGNHIVTRHSKGFAIPCVAAAMALDAGTQ
MFSPEVTSKLIGDVFGEIDEFREPMKYITEAAAEAK
>d1e6yb1 a.89.1.1 (B:2186-2433) Beta chain {Archaeon Methanosaerina barkeri}
GFSLRNIMANHVAISNRNAMNASALSSIYEQSGIFEMGGAVGMFERHQLGLAYQGLNANNLLYDIVKENG
KDGTTGTVIESVVRRAIEAGIISVDKTAPSGYNFYKANDVPKWNAACAVGTLAATLVNCAGRAAQNVSSLLYF
NDILEKETGLPGCDYKGKVEGTAVGFSFFSHSIYGGGGPGVFNGNHVVTRHSRGFAIPCVCAAVALDAGTQMFSI
ESTSGLIGDVFVGAYPEFREPIKAVAGV
>d1bgf__ a.90.1.1 (-) Transcription factor STAT-4 N-domain {Mouse (Mus musculus)}
GGSQWNQVQQLEIKFLEQVDDQFYDDNFPMEIRHLLAQWIETQDWEVASNNETMATILLQNLLIQLDEQLGRV
SKEKNLLIHNLRIRKVLQGKFHGNPMHVAVVISNCLREERRILAAANMPI
>d1agre_ a.91.1.1 (E:) Regulator of G-protein signalling 4, RGS4 {Rat (Rattus norvegicus)}
VSQEEVKKWAESLENLINHECGLAAFKAFLKSEYSEENIDFWISCEEYKKIKSPSKLSPKAKKIYNEFISVQATKEVN
LDSCTREETSRNMLEPTITCFDEAQKKIFNLMEKDSYRRFLKSRFYLDLT
>d1fqia_ a.91.1.1 (A:) RGS9, RGS domain {Cow (Bos taurus)}
KLVDIPTKMRVERWAFNSELIRDPKGRQSFQHFLRKEFSGENLGFWEACEIDLKYGDQSKVKEKAEEIYKLFLAP
GARRWINIDGKTMIDTVKGLKHPHYVLDAAQTHIYMLMKKDSYARYLKSPIYKEMLAKAIEP
>d1cmza_ a.91.1.1 (A:) Galph interacting protein, GaIP {Human (Homo sapiens)}
PSPEEVQSWAQSFDKLMHSPAGRSPVRAFLRTYESEENMLFWLACEELKAEANQHVVDEKARLIYEDYVSILSP
KEVSLDSRVREGINKKMQEPAHTFDDAQLQIYTLMRDSDYPRFLSSPTYRALL
>d1dk8a_ a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}
GSASPTPPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRKLARAIYRKYL
LDNNGIVSRQTKPATKSFIKGCMKQLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLEYTRTGSESPKV
>d1emua_ a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}
PPYLKWAESLHSLLDDQDGISLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNEEKRKLARAIYRKYILDNNGI

VSQTKPATKSFIKG CIMKQLIDPAMFDQAQTEIQATMEENTYPSFLKSDIYLEYT
>d1iapa_a.91.1.1 (A:) p115RhoGEF {Human (Homo sapiens)}
SQFQSLEQVKRRPAHLMALLQHVALQFEPGPLLCCCLHADMLGSLGPKEAKKAFLDFYHSFLEKTAVLRVPPN
VAFELDRTRADLISEDVQRRFVQEVVQSQQAVGRQLEDFRSKRLMGMTPWEQELAQLEAWVGRDRASYE
RERHVAERLLMHLEEMQHTISTDEEKSAAVVNAIGLYMRHLGV
>d1htjf_a.91.1.1 (F:) Pdz-RhoGEF RGS-like domain {Human (Homo sapiens)}
ESDIIFQDLEKLKSRAHGLVFLRYIFSQADPSPLLFLCAEVYQQASP KDSRSLGKDIWNIFKNAPLRVKIPEML
QAEIDSRLRNSEDARGVLCEAQEAAMPEI QEIQIHDYRTKRTLGLGS LYGEN DLLLDGDPLRERQVAEQLAAL
GDILSAYAADRSAPMDFA LNTYMSHAGIRL
>d1a9xa1 a.92.1.1 (A:403-555) Carbamoyl phosphate synthetase, large subunit connection domain
{Escherichia coli}
EVGATGFDPKVSLDDPEALTKIRRELKDAGADRIWYIADAFRAGLSVDGVFNLTNI DRWFLVQIEELVRLEEKVAE
VGITGLNADFLRQLKRKG FADARLA KLAGVRE AEIRKLRDQYDLHPVYKRVDTCAA EFATDTAYM STYEECEA
NP
>d1b80a_a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete (Phanerochaete
chrysosporium)}
VIEKRATCSNGKTVGDASCCA WFDV LDDIQQNLFHGGQCGAEAHESIRLVHDSIAISPAMEAQGKF GGGGA
DGSIMIFDDIETAFHPNIGLDEVKLQKPFVQKHGVTPGDFIAFAGAVALSNCPGAPQM NFFTGRAPATQPAPD
GLVPEPFHTVDQIINRVNDAGEFDELELVWMLS AHSVA AVNDV DPTVQGLPF DSTPGIFDSQFFVETQLRGTA
PGSGGNQGEVESPLPGEIRI QSDHTIARD SRTACEWQSFVNNQSKLVDDFQFIFLALTQLGQDPNAMTDCSDV
IPQSKPIPGNLPFSFPAGKTIKDVEQACAETPFTLTLPGPETSVQRIPPPP
>d1llp_a.93.1.1 (-) Lignin peroxidase {White rot basidiomycete (Phanerochaete chrysosporium)}
ATCANGKTVGDASCCA WFDV LDDIQANMFHGGQCGAEAHESIRLVHDSIAISPAMEAKGKF GGGGADGS
MIFDTIETAFHPNIGLDEVVAMQKPFVQKHGVTPGDFIAFAGAVALSNCPGAPQM NFFTGRKPATQPAPDGLV
PEPFHTVDQIARVN DAGEFDELELVWMLS AHSVA AVNDV DPTVQGLPF DSTPGIFDSQFFVETQFRGTLFPG
GGNQGEVESGMAGEIRI QT DHTLARDSRTACEWQSFVGNQSKLVDDFQFIFLALTQLGQDPNAMTDCSDVIP
LSKPIPGNGPFSFPAGKSHSDIEQACAETPFSLVTLPGPATSVARIPPHKA
>d1qpaa_a.93.1.1 (A:) Lignin peroxidase {White rot basidiomycete (Phanerochaete
chrysosporium)}
VACPDGVHTASNAACC AWFPV LDDIQQNLFHGGQCGAEAH EALRMVFHDSIAISP KLSQGKF GGGGADGS
IITFSSIETTYHPNIGLDEVVAIQKPFIAKHGVTPGDFIAFAGAVGVSNCPGAPQM QFFLGRPEATQAAPDGLV
PFHTIDQVLARMLDAGGFDEIETVWL SAHSIAA ANDVDPTISGLPF DSTPGQF DSQFFVETQLRGTA
PGKGTGI QGTVMSPLKG EMRLQTDH LFARDSRTACEWQSFVNNQTKLQEDFQFIFTALSTLGHDMNAMIDCSEVIP
PVNFGPSFFFAGKTHADIEQACASTPFPTLITAPGPSASVARIPPPP
>d1aru_a.93.1.1 (-) Peroxidase {Arthromyces ramosus}
SVTCPGGQSTSNSQCCVWFV LDDLQTNFYQGSKCES PVRKILRIVFHDAIGFSPALTAAGQF GGGGADGSII
HSNIELA FPANGGLTD TIEALRAVG INHGVSFGDLIQFATAVGM SNCPGSPR LEFLTGRSNS
SSQPSPPSLIPGP
GTVTAILDRM GDAGFSPDEV DLLAAHSLASQEGLNSAIFRSPLDSTPGQF DSQFFVETQLRGTA
PGKGTGI SPFPGEFRMRSD ALLARDSRTACRWQSMTSSNEVMGQRYRAAMAKMSV
LGFD RNAL TDCSDV IPSAV
NNA APVIPGGLTVDDIEVSCPSEPFPEIATASGPLPSLAPAP
>d1jdra_a.93.1.1 (A:) Cytochrome c peroxidase, CCP {Baker's yeast (Saccharomyces cerevisiae)}
TTPLVHV ASVEKGRSYEDFQKVNAIALKLR EDEYDN YIGYGPVLVRLAWH
TS GTWDKHD NTGGSYGGTYRF
KKEFNDPSNAGLQNGFKFLEPIHK EFPWISSGDLFSLGGV
TAVQEMQGP KIPWRCGRV
DTPEDTTPDNGRLPD
ADKDADYVRTFFQRLNMNDREVVALMGAHTLGKTHLKNSGYEGPWT
ANNNVFDNSFYLNLLNEDWKLEK

DANNEQWDSKSGYMMMLPTDYSIQLDPKYLSIVKEYANDQDKFFKDFSKAFEKLLENGITFPKDAPSPFIFKTLEE
QGL

>d1mn2_ a.93.1.1 (-) Manganese peroxidase {Basidiomycetos fungus (Phanerochaete chrysosporium)}

AVCPDGTRVSHAACCAFPIPLAQDLQETIFQNECGQDAHEVIRLFHDIAISRSQGPKAGGGADGSMLLFPTE
PNFSANGIDDSVNLLIPFMQKHNTISAADLVQFAGAVALSNCPGAPRLEFLAGRPNKIAAVDGLIPEPQDSV
TKILQRFEDAGGTPFEVVSLLASHSVARANKVDQTIDAAPFDSTPFTDTQVFLEVLLKGVGFGPSANNTGEVA
SPLPLGSGSDTGEMLQSDFAAHDPRTACIWQGFVNEQAFMAASFRAAMSKLAVLGHNRNSLIDCSDVVPV
PKPATGQPAMFPASTGPQDLELSCP SERFPTLTTQPGASQSLIAHCPDGSMSCPGVQFNGPA

>d1apxa_ a.93.1.1 (A:) Ascorbate peroxidase {Pea (*Pisum sativum*)}

GKSYPTVSPDYQKAIEKAKRKLRFIAEKKCAPLILRLAWSAGTFDSKTKTGGPFGTIKHQAELAHGANGLDI
AVRLLEPIKEQFPIVSYADFYQLAGVVAEITGGPEVFHPGRKDPEPPPEGRLPDATKGSIDLRLVFGKAMGI
SDQDIVALSGGHTIGAAHKERSGFEGPWTSNPLIFDNSYFTELLTGEKDGLLQLPSDKALLTDSVFRPLVEKYAAD
EDVFFADYAE AHLKLSELGFAEA

>d7atja_ a.93.1.1 (A:) Plant peroxidase {Horseradish (*Armoracia rusticana*)}

QLPTFYDNSCPNSNIVRDTIVNELRSDPRIAASILRLHFHDCFVNGCDASILLDNTTSRTEKDAFGNANSARG
FPVIDRMKAAVESACPRTVSCADLLTIAAQQSVTLAGGPSWRVPLGRRDSLQAFDLANANLPAPFFTLPQLKD
SFRNVGLNRSSDLVALSGGHTFGKNQCRFIMDRLYNFSNTGLPDTLNNTYLQTLRGLCPLNGNLSALVDFDLRT
PTIFDNKYYVNLEEQKGLIQSDQELFSSPNATDTIPLVRSFANSTQTFFNAFVEAMDRMGNITPLGTQGQIRLN
CRVVN

>d1scha_ a.93.1.1 (A:) Plant peroxidase {Peanut (*Arachis hypogaea*)}

ELSSNFYATKCPNALSTIKSAVNSAVAKEARMGASLLRLHFHDCFVQGCDASVLLDDTSNFTGEKTAGPNANSIR
GFEVIDTIKSQVESLCPGVVSCADILAVAARDSVVALGGASWNVLLGRRDSTASLSSANSSDLPAPFFNLGLISA
FSNKGFTTKEVLTSGAHTIGQAQCTAFRTRIYNESNIDPTYAKSLQANCPSVGGDTNLSPFDVTPNKFNDNAYYI
NLRNKKGLLHSQQQLFNGVSTDQSQTAYNNAAFTNTDFGNAMIKMGNLSPLTGTSGQIRTNCRKTN

>d1fhfa_ a.93.1.1 (A:) Plant peroxidase {Soybean (*Glycine max*)}

QLPTFYRETCPNLPIVFGVIFDASFTDPRIGASLMRLHFHDCFVQGCDGSVLLNNTDIESEQDALPNINSIRG
LDVVNDIKTAVENSCPDTVSCADILAAEIASVLGGPGWPVPLGRRDSLANTRLANQNLPAFFNLTKAS
FAVQGLNTLDLVTSGGHTFGRARCSTFINRLYNFSNTGNPDPTLNNTYLEVLRARCPQNATGDNLTNLDLSTPD
QFDNRYYSNLLQLNGLLQSDQELFSTPGADTIPIVNSFSSNQNTFFNSRVSMIKMGNIGVLTGDEGEIRLQCNF
VNG

>d1bgp_ a.93.1.1 (-) Plant peroxidase {Barley (*Hordeum vulgare*), peroxidase 1}

AEPPVAPGLSFDFYWTCPRAESIVREFVQEAVRKDIGLAAGLLRLHFHDCFVQGCDASVLLDGSATGPGEQQ
APPNLTRPSAFKAVNDIRDRLERECRGAVVSCSDILALAARDSVVSGGPDYRVPLGRRDSRSFASTQDVLSDL
PGPSSNVQSLALLGRLGLDATDLVTISGGHTIGLAHCSSFEDRLFPRPDPTISPTFLSRLKRTCPAKGTDRTTVLD
VRTPNVFDNKYYIDLVNREGLFVSDQDLFTNAITRPIVERFAQSQQDFFEQFGVSIGKMGQMVRRTSDQGEVR
RNCSVNRPGPG

>d1qgja_ a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (*Arabidopsis thaliana*), peroxidase N}

QLSPDIYAKSCPVLVQIVRKQVAIALKAEIRMAASLIRLFHDCFVNGCDASLLDGADSEKLAIPNINSARGFEVI
DTIKAIVENACPGVVSCADILTAARDSVVLSGGPGWRVALGRKDGLVANQNSANNLSPFEPLDAIIAKFVA
NLNITDVVALSGAHTFGQAKCAVFSNRLFNFTGAGNPDATLETSLLNLQTCPLGGNSNITAPLDRSTTDFDN
NYFKNLLEGKGLLSSDQILFSSDLAVNTTKLVEAYSRSQSLFFRDFTCAMIRMGNIANGASGEVRTNCRVINN

>d1pa2a_ a.93.1.1 (A:) Plant peroxidase {Mouse-ear cress (*Arabidopsis thaliana*), peroxidase A2}

MQLNATFYSGTCPNASAIVRSTIQQALQSDTRIGASLIRLFHDCFVNGCDASILLLDTGSIQSEKNAGPNVNSA

RGFNVVDNIKTALENACPGVVSCSDVLALASEASVSLAGGPSWTLLGRRDSLTLAGANSSIPSPIESLSNITF
KFSAVGLNTNDLVALSGAHTFGRARCGVFNNRLFNFSGTGNPDPTLNSTLLSTLQQLCPQNGSASTITNLDLSTP
DAFDNNYFANLQSNDGLLQSDQELFSTTGSSTIAIVTSASNQTLFFQAFQSMINMGNISPLTGSNGEIRLDCK
KVNGS

>g1cxp.1 a.93.1.2 (A:,C:) Myeloperoxidase {Human (Homo sapiens)}

CPEQDKYRTITGMCNNRRSPTLGASNRAFVRWLPAEYEDGFSLPYGTGPKRNGFPVALARAVSNEIVRFPT
DQLTPDQERSLMFMQWQGQLLDHLDFTPEPAXNCETSCVQQPPCFPLKIPPNDPRIKNQADCIFFRSCPAC
PGSNITIRNQINALTSFVDASMVGSEEPLARNLRNMSNQLGLAVNQRFQDNGRALLPDFNLHDDPCLLNR
SARIPCFLAGDTRSSEMPELTSMHTLLREHNRLATELKSLNPRWDGERLYQEARKIVGAMVQIITYRDYLPLVLG
PTAMRKYLPTYRSYNDSDVPRIANVFTNAFRYHTLIQPFMFRLDNRYQPMEPNPRVPLSRVFFASWRVLEG
GIDPILRGLMATPAKLNQRQNQIAVDEIRERLFEQVMRIGLDLPAALNMQRSRDHGLPGYNAWRRFCGLPQPETV
GQLGTVRLNLKLARKLMEQYQGTPNNIDIWMGGVSEPLKRKGKRVGPLACIIGTQFRKLRGDRFWWENEGVF
SMQQRQALAQISLPRIICDNTGITTISKNNIFMSNSYPRDFVCNSTLPALNLASWREA

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

IWTWLRTTLPSPSIHFLLTHGRWLWDFVNATFIRDLMRLVLTVRSNLIPSPPTYNIAHDYISWESFSNVSYYT
RILPSVPRDCPTPMGKGKKQLPDAEFLSRRFLRRKFIPDPQGTNLMFAFFAQHFTHQFFKTSGKMGPGFTKA
LGHGVDLGHIYGDMLERQYQLRLFKDGKLKYQMLNGEVYPPSVEEAPVLMHYPRGIPPPSQMAVGQEFG
PGLMLYATIWLREHNRVC DLLKAEHPTWGDEQLFQTARLILGETIKIVIEYVQQLSGYFLQLKFDPELLFGAQF
QYRNRIAMEFNQLYHWPLMPDSFRVGPQDYSEQFLNNTSMLVDYGVEALDAFSRQPAGRIGGGRNIDHH
ILHVAVDVIESRVRLQPFNEYRKRGKMPYTSFQEITGEKEMAAELEELYGDIDALEFYPGLLLEKCHPNSIFGE
SMIEMGAPFSLKGLGNPICSPYWKASTFGGEVGFNLVKTATLKLVCLNTKTCPYVSFHV

>d1cvua1 a.93.1.2 (A:74-583) Prostaglandin H2 synthase {Mouse (Mus musculus)}

FLTRIKLLLKPTPNTVHYILTHFKGVWNIVNNIPFLRSIMKYVLTSSYLI DSPTYNHYGYKSWEAFSNLSYYTR
ALPPVADDCTPMGVKGKNEKLPDSKEVLEKVLRRREFIPDPQGSNMMFAFFAQHFTAQFFKTDHKRGPGFTR
GLHGVDLNHIYGETLDRQHKLRLFKDGKLKYQVIGGEVYPPTVKDTQVEMIYPPHIPENLQFAVGQEFG
GLMMYATIWLREHQRVCDILKQEHPEWGDEQLFQTSLKLIGETIKIVIEDYVQHLSGYHFKLKDPELLFNQQF
QYQNRIASEFNTLYHWPLLPDTFNIEDQEYSFKQFLYNNNSILLEHGLTQFVESFTRQIAGRVA
GGRNVPIAVQA
VAKASIDQSREMKYQSLNEYRKRFSLKPYTSFEELTGEKEMAAEKLAYSIDVMELYPA
LLVEKPRPDAIFGETM
VELGAPFSLKGLGNPICSPQYWKPSTFGGEVGFKIINTASIQLC
NNVKGCPFTSFNVQ

>d1jj2o_ a.94.1.1 (O:) Ribosomal protein L19 (L19e) {Archaeon Haloarcula marismortui}

TDLSAQKRLAADVLVGKNRVWFNPERQGDIADAITREDVRELVDEGAIQAKDKGNSRGRARERQKKRAKG
HQKGAGSRKGKAGARQNSKEDWESRIRAQRTKLRELDEGTLS
SSQYRDLYDKAGGGFDSVADLERYIDA

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

MSLLTEVETYVLSIIPSGPLKAEIAQRLEDVFAGKNTDLEVLM
EWLKTRPILSPLTKGILGFVFTLTVPSERGLQRR
FVQNALNGNGDPNNMDKAVKLYRK
LREITFHGAKEISL
SYSAGALASC
MGLIYNRMGA
VTTEAFGLVCATC
EQIADSQ

>d2abk__ a.96.1.1 (-) Endonuclease III {Escherichia coli}

MNKAKRLEILTRLRENNPHPTTELNFSSPFELLIAVLLSAQATDVS
VNKATAKLYPVANTPAAMLELG
VEGVKTYIK
TIGLYNSKAENIIKTCRILLEQHNGEV
PEDRAALEALPGVGRKTANV
VLNTAFGWPTIA
VDTHIFRVCNRTQF
AGP
KNVEQVEEKLLKV
VPAEFKVDCHHWL
LILHGRYTCI
ARKPRCGSCI
EDLCEYKE
KVDI

>d1mun__ a.96.1.2 (-) Catalytic domain of MutY {Escherichia coli}

MQASQFSAQVLDWYDKYGRK
LWPQIDKTPYKV
WLSEVMLQ
QTQVATV
IPYFERF
MARFPT
VTD
LANAPLD
EVLHLWTGLG
YYARARNL
HKAQQV
ATLHGG
KF
PET
FEEVA
ALPGV
GRSTA
GAIL
LSLGK
HF
PILNG
NVK
RVL

RCYAVSGWPGKKEVENKLWSLSEQVTPAVGVERFNQAMMDLGAMICTRS PKC SLCPL QNG CIAAANNSWA
LYPGKKPK

>d1keaa_ a.96.1.2 (A:) Thymine-DNA glycosylase {Archaeon Methanobacterium thermoformicicum}

DATNKKRKVFVSTILFWNTDRDFPWRHTRDPYVILITEILLRRTAGHVKKIYDKFFVKYKCFEDILKTPKSEIAK
DIKEIGLSNQRAEQLKELARVVINDYGGRVPRNRKAILDLPVGVGKYTCAAVMCLAFGKKAAMVDANFVRVINR
YFGGSYENLNYNHKALWELAETLPGGKCRDFNLGLMDFS AII CAPRKPCEKGMSKLC SYYEK

>d1mpga1 a.96.1.3 (A:100-282) 3-Methyladenine DNA glycosylase II (gene alkA or aidA) {Escherichia coli}

AARPGLRLPGCVDAFEQGVRAILGQLVSAMAALKTARVAQLYGERLDDPEYICPTPQRLAAADPQALKALG
MPLKRAEALIHLANAALEGTLPM TIPGDVEQAMKTLQTFPGIGRWTANYFALRGWQAKDVFLPDDYLIKQRFP
GMTPAQIRRYAERWKPWRSYALLHIWYTEGWQPDEA

>d1ko9a1 a.96.1.3 (A:136-323) 8-oxoguanine glycosylase {Human (Homo sapiens)}

DPIECLFSFICSSNNNIARITGMVERLCQA FGPRLIQLDDVTYHGFPSLQALAGPEVEAHLRKLGLGYRARYVSAS
ARAILEEQGGLAWLQLRESSYEEAHKALCILPGVGTVKADCICLMA LDKPQAVPVDVHMWHIAQRDYSWHP
TTSQAKGPSPQTNKELGNFFRSLWGPYAGWAQAVLFSADL

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

DLEKLRWMNGKYIREVLSLEEV AERVKPF LREAGLSWESEAYL RRAVELMRPRFD TLKEFPEKARYLFTEDYPVS
EKAQRKLEEGPLLKELYPRLRAQEEWTEA ALEALLRGFAAEKG VKGQVAQPLRAALTGSLETPGLFEILALLGKE
RALRRLERALA

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

RDGSTERINLDKIHRVLDWAAEGLHNVSISQVELRSHIQFYDGIKTS DIHETIKAADLISRDAPDYQYLAARLAI
FHLRK KAYGQFEP ALYDHVV KM VEMGKYDNH LLEDYTEE EFKQMDTFIDHDRDMTFSYAAVKQLEGKYLVQ
NRVTGEIYESAQFLYILVAACLF SNYPRETRLQYV KRFYDAVSTFKISLPTPIMSGVRTPTRQ

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

PVEEKAAIAQLRQFCQNGAGEYEQQRDFPAVEGT SRLSASLATGG LSPRQCLH RLLAEQPQALDGGAGSVWL
NELIWREFYRHLITYHPSLCKHRPFIATDRVQWQS NP AHLQAWQEGKTG YPIVDAAMRQLNSTGWMHNR
LRMITASFLVKDLLIDWREGERYFMSQLIDGDLAANNGWQWA ASTGTD AAPYFRIFNPTTQGEKFDHEGEFI
RQWLPELRDVPKGKVVHEPWKWAQKAGVTLDYQPQPIVEHKEARVQTLAAYEARK

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

LPLPEP GEEA ALA GLR AFLEAKL PRYAE ERD RL DGE GEGS RLSPYF ALGV LSPRL AWEAERRGGEGARKWVAELL
WRDFSYHLLYHF PWMAERPLDPRFQAF PWQEDEALFQ AWYEGKTG VPLD AAMRELHATGFLSNRARMNA
AQFAVKHLLL PWKR CEEA FRHLL DGDR AVNLQGWQ WAGGLGV DAAPYFRV FN PVLQ GERHD PEG RWL KR
WAPEYPSYAPKDPVV DLE EARR YLRLARD

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

PVEPGETAAIARLQEFC DRAIADYDPQRNF PAEGT SGLSPALKFGAIGIRQ AWQAA SAHAL RSDE ARNS IRV
WQQELAWREFYQHALYHFPSLADGPYRSLWQQFPWENREALFTA WTQ AQTG YPIVDAAMRQLTETGWMH
NRCRMIVASFLTKD LIIDWRRGEQFFM QHLV DGD LAAN NGGWQ WSASS GM DP KPLR IFNP ASQAKK FDATA
TYIKRWLPELRHVHPKDLISGEITPIERRGYPAPIVNHNLRQKQFKALYNQLKAAI

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

GAGHFVKMVHNGIEYGDMQLICEAYHLMKDVGLGHKEMAKAFEEWNKTELDSTLIEITASILKFQDADGKHL
LPKIRDAGQKGTGKWTIAALEYGPVTLIGEAVFARCLSSLKDERIQASKKLKGPNIPFEGDKKSFLEDIRKALY
ASKIISYAQGFMLLRQAATEFGWTLNYGGIALMWRGCIIRSVFLGKIKDAFDRNPGLQNLLDDFFKSAVENC
QDSWRRAISTGVQAGIPMPCTTALSFYDGYRHAMLPAQRLAQARDYFGAHTYELLAKPGQFIHTNWTGHGG

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

GAGSCVKMYHNSGEYAILQIWGEVFDILRAMGLNNDEVAAVLEDWKSKNFLKSYMIDISIAARAKDKDGSYL
TEHVMDRIGSKGTGLWSAQEALEIGVPAPSLNMAVVSQRFTMYKTERQANASNAPGITQSPGYTLKNKSPSG
PEIKQLYDSVCIAIISCYAQMFQCLREMDKVHNFGNLNPATIFRAGCILQGYLLKPMTEAFEKNPNIISNLMCAP
QTEIRAGLQNYRDMVALITSKLEVSIPLSASLNVTAMFTPTLKYGQLVSLQRDVGRHGYERVDKGRESFQ
WPELQ

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

LEQEYKSDIFGERGILLGAVHGIVECLFRRTESGMSEDLAYKNTVECITGVISKTISTKGMLALYNLSSEEGKKDFQ
AAYSASYYPSMDILYECYEDVASGSEIRS VVLAGRRFYKEGLPAFPMGKIDQTRMWKVGKVRSPAGDLGP
LYPFTAGVYVALMMAQIEILRKKGHSYSEIINESVIEAVDSLNP FMHARGV SFMVDNCSTTARLGSRKWAPRFD
YILSQQALVAVDNGAPINQDLISNFLSDPVHEAIGVCAQLRPSVDISVTADADFVRPELRQA

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

GFIVNRLVPYLMEAIRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIVDGWHEMDAENPLHQ
PSPSLNKVAENKFGKKTGEGFYKYK

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

GFIVNRLVPYLIEAVRLYERGDASKEDIDTAMKLGAGYPMGPFELLDYVGLDTTKFIVDGWHEMDSQNPLFQPS
PAMNKLV AENKFGKKTGEGFYKYK

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

ASEAEAVKLFANTYLALRVAYFNE LD TYAESRKLN SHMIIQGISYDDRIGMHYN NPSFGYGGYSLPKDTKQLLAN
YNNIPQT LIEAIVSSNNVRKSYI

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

NVLHTSLNVNAVMHPLPTLLNAARCESGTPFQYYLEGITPSVGLAEKVDAERIAIAKAFDLNVPSVCEWYKES
YGQSPATIYEAVQGNPAYRGIAGPINLNTRYFFEDVSTGLVPLSELGRAVNPTPLIDAVLDLISSLI DTD F RKE GRT
LEKLGLSGLTAAGIRSAVE

>d1evya1 a.100.1.6 (A:189-357) Glycerol-3-phosphate dehydrogenase {Trypanosome (*Leishmania mexicana*)}

DRSFVCWATTDTVGC EVA SVAKNVLAIGSGV ANGL GMGLNARA ALIM RGLLEIRD LTAA LG GDGS AVF GLAGL
GDLQLTCSSELSRNFTVGKKLGKLPIEEI QRTSKAVAEGV ATADPLMRLAKQLKVKMPLCHQIYEIVYKKKNPRD
ALADLLSCGLQDEGLPPLFK

>d1ks9a1 a.100.1.7 (A:168-291) Ketopantoate reductase PanE {Escherichia coli}

NIRAEWLWRKLAVNCVINPLTAIWCNPNGELRHHPQEIMQICEEVAAVIEREGHHTSAEDLRDYVMQVIDATAEN
ISSMLQDIRALRHTEIDYINGFLLRRARA HGI AVPENTRLFEMVKRKESE

>d1utg_ a.101.1.1 (-) Uteroglobin {Rabbit (*Oryctolagus cuniculus*)}
GICPRFAHVIENLLLTPSSYETSLKEFEPDDTMKDAGMQMKVLDLSPQTRENIMKLT
EIVKVSPLCM
>d1ccd_ a.101.1.1 (-) Clara cell 17kDa protein {Rat (*Rattus norvegicus*)}
SSDICPGFLQVLEALLGSESNYEAALKPFNPASDLQNAGTQLKRLVDTLPQETRINIVKL
TEKILTSPLCEQDLRV
>d1utra_ a.101.1.1 (A:) Clara cell 17kDa protein {Rat (*Rattus norvegicus*)}
ICPGFLQVLEALLGSESNYEAALKPFNPASDLQNAGTQLKRLVDTLPQETRINIVKL
TEKILTSPLC
>d1gai_ a.102.1.1 (-) Glucoamylase {Aspergillus awamori, variant x100}
ATLDSWLSNEATVARTAILNNIGADGAWSGADSGIVVASPSTDNPDYFTWTRDGLVI
KTLDVLFRNGDTDL
LSTIEHYISSQAIQGVSNPSGDLSSGGLGEPKFNVDETAYTGSWGRPQRDGPA
LATAMIGFGQWL
DNGYTS
AAEIVWPLVRNDLSYVAQYW
NQTGYDLWEEVNGSSFTIAVQH
RALVEGSAFATAVGSSCSWCDSQAPQILC
YLQSFWTGSYI
LANFDSSRS
GKDNTLLGSI
HTFDPEAGC
DDSTFQPCSP
RALANH
KEVVDS
FRSIY
TLNDGLSD
SEAVAVG
RYPEDSY
YNGNP
WF
LCT
AAA
EQLY
DALY
QWD
KQGS
LEITD
VSLDF
FKALY
SGA
ATGT
YSSS
TYSSI
VSAV
KTFADGF
VSIV
ETHA
ASNG
SLSEQ
FDK
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ARDL
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RRNS
VPP
SWGET
SASS
VPG
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IVATG
>d1ayx_ a.102.1.1 (-) Glucoamylase {Baker's yeast (*Saccharomyces cerevisiae*)}
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>d1cem_ a.102.1.2 (-) CelA cellulase {Clostridium thermocellum}
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>d1faea_ a.102.1.2 (A:) Processive endocellulase CelF (Cel48F) {Clostridium cellulolyticum}

ASSPANKVYQDRFESMYSKIKDPANGYFSEQGIPYHSIETLMVEAPDYGHVTTSEAMSYYMWLEAMHGRFSGDFTGFDKSWSVTQEYLIPTEKDQPNTSMSRYDANKPATYAPEFQDPSKYPSPLDTSQPVGRDPINSQLTSAYGTSMLYGMHWILDVDNWYGFARADGTSKPSYINTFQRGEQESTWETIPQPCWDEHKFGGQYGFLDLFTKDTGTPAKQFKYTNAPDADARAVQATYWADQWAKEQGKSVSTVGKATKMGDYLRYSSFDKYFRKIGQPSQAGTGYDAAHYLLSWYYAWGGGIDSTWSWIIGSSHNFYQNPFAAWVLSTDANFKPKSSNGASDWAKSLDRQLEFYQWLQSAEGAIAGGATNSWNGRYEAVPSGTSTFYGMGYVENPVYADPGSNTWFGMQVWSMQRVAELYKTGDARAKLLDKWAKWINGEIKFNADGTFQIPSTIDWEGQPDWNPTQGYGNANLHVKVNVYGTDLGCASSLANTLTYAAKSGDETSRQNAQKLLDAMWNNSDSKGISTVEQRGDXHRFLDQEVFVPAWTGKMPNGDVIKSGVKFDIRSKYKQDPWQTMVAAALQAGQVPTQRLHRFWAQSEFAVANGVYAILFPD

>d1fp3a_ a.102.1.3 (A:) N-acyl-D-glucosamine 2-epimerase {Pig (Sus scrofa)}

MEKERETLQAWKERVGQELDRVMAFWLEHSHDREHGGFFTCLGRDGRVYDDLKYVWLQGRQVWMYCRLYRKLERFHRPELDAAKAGGEFLRHARVAPPEKKCAFVLTRDGRPVKVQRSIFSECFTMAMNELWRVTAEARYQSEAVDMMDQIVHWVREDPSGLGRPQLPQAVASESMAPMMMLCLVEQLGEEDEELAGRYAQLGHWCARIHQHVQRDGQAVLENVSEDEGEELSGCLGRHQNPQGHALEAGWFLLRHSSRSGDAKLRAHVIDTFLLPFRSGWDADHGGLFYFQDADGLCPTQLEWAMKLWWPHSEAMIAFLMGYSESQDPALLRLFYQVAEYTFRQFRDPEYG

EWFGYLNREGKVALTIKGGPKGCFHVPRCLAMCEEMLSALLSRLA

>d1h54a1 a.102.1.4 (A:269-753) Lactobacillus maltose phosphorylase, central domain {Lactobacillus brevis}

DTQESLTAAMHQLSDKVAQSSYEDLLNAHTAIWAQRWEKSDVVIKGDDESQQGIRFNLFQLFSTYYGEDARLNI GPKGFTGEKYGGATYWDTEAFAFPVYLGITDPKVTRNLLMYRYKQLDGAYINAQEQLKGALFPMVTFDGIECHNEWEIFEEIHRNGDIAFAIINYTRYTGDDSYVLHEGAKVLTISRFWADRVHFSKRNNQYMIHGVTGADEYE NNVDNNWDTNMLAQWTLKYTLEILGKVDQDTAKQLDVSDEEKTWKQDIVDRMYLPYDKDLNIFVQHDGFLDKDIEPVSSIPADQRPINQNWSWDKILRSPYIKQGDVLQGIWDFIDDYTPEQKKANFDFYEPLTVHESSLSPAHS VLAADLHYEDKAVELYSRSTARLDDNYNNNDTDGLHITSMTGAWIAVVQGFAGMRVRDGQLHYAPFLPKWT SYTFRQVFRDRRLIEVSvhADGPHFKLLSGEPLTIDVAGAAAAAAA

>d1dl2a_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

GAGEMRDRIESMFLESWRDYSKHGWGYDVYGPIEHTSHNMPRGNQPLGWIIVDSVDTLMLMYSNSTLYKSE FEAEIQRSEHWINDVLDFDIDAEVNPFETTIRMLGGLLSAYHLSDVLEVGNKTVYLNKAIDLGDRLALAFLSTQTG IPYSSINLHSGQAVKNHADGGASSTAFTTLQMEFKLAYLTGNRTYWELVERVYEPLYKNNDLLTYDGLVPIYTFPDTGKFGASTIRFGSRGDSFYEYLLQYLLTHELYDLYRKSMEGMKHHLLAQSKPSSLWYIGEREQGLHGQLSPKMDHLVCFMGGLLASGSTEGLSIHEARRPFFSKSDWDLAKGITDTCYQMYKQSSGLAPEIVFNDGNIQK DGWWRSSVGDFVKPLDRHNLQRPETVESIMFMYHLSHDHKYREWGAIEATSFFENTCVDCNDPKLRRFTSL SDCITLPTKSNMESPWLAETLKLYILFLDEFDLTKVVFNTAEHPFPVLDEEILKSQSLTTGWSL

>d1hcua_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Trichoderma reesei}

KRGSPNPTRAAVKAAFQTSWNAYHHFAFPHDDLHPVSNSFDDERNGWGSSAIDGLDTAILMGDADIVNTIL QYVPQINFNTTAVANQGSSVFETNIRYLGLLSAYDLLRGPFSSLATNQTLVNSLLRQAQTLANGLKVAFTTPSGV PDPTVFFNPTVRRSGASSNNVAEIGSLVLEWTRLSDLTGNPQYAQLAQKGESYLLNPKGSPEAWPGLIGTFVSTS NGTFQDSSGSWSGLMDSFYEYLIKMYLYDPVAFAHYKDRWVLGADSTIGHLGSHPSTRKDLTFLSSYNGQSTSP NSGHLASFGGGNFI LGILLNEQKYIDFGIKLASSYFGTYQTASGIGPEGFAWVDSVTGAGGSPPSSQSGFYSSA GFWVTAPYYILRPETLESLYYAYRVTGDSKWQDLAWEALSAIEDACRAGSAYSSINDVTQANGGGASDDMESF

WFAEALKYAYLIFAEESDVQVQATGGNKFVFNTAEHPFSIRS

>d1krea_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Fungus (Penicillium citrinum)}

SNQAKADAVKEAFQHAWNGYMKYAFPHDELTPVSNGHADS RNGWGASAVDALSTAVIMGKADV VNAILEH
VADIDFSKTSDTVSLFETTIRYLAGMLSGYDLLQGPAKNLVNDNQLIDGLLDQRNLADVLKFAFDTPSGVPYNN
INITSHGNDGATTNGLA VTGTLVLEWTRLSDLTGDEEYAKLSQKAESYLLKPQPSSEPFPGVGSSININDGQFA
DSRV SWNGGDDSFYEYLIKMYVYDPKRFETYKDRWVLA AESTIKHLKSHPKSRPDLTFLSSYSNRNYDLSSQHLT
CFDGGSFLLGGTVLDRQDFIDFGLELV DGCEATYNSTLT KIGPDSWGWDPKKVPSDQKEFYEKAGFYISSGSYVL
RPEVIESFYYAHRVTGKEIYRDWWNAFVAINSTCRTDGF AA VSDVN KANGGSKYDNQESFLFAEV MKY SYL
AHSEDA AWQVQKGGKNTFVYNTAEHPISVAR

>d1fo3a_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Human (Homo sapiens)}
QGPVHLNYRQKG VIDVFLHAWKG YRKFAWGHDELKP VSR SFSEWFG LGLTIDALDTMWILGLRKEFEEARK
WVSKKLHFEKD VDVL FESTIRI LGG LLSAYHLSGD SFLRKAEDFGNRLMPA FRTPS KIPSYD VNIGTGV AHPPR
WTSDSTVAEVTSIQLEFREL SRLTGD KK FQE AVK V TQHI HGLSGKKD GLVPMFIN THSGLFTHLG VFTL GARAD
SYYEYLLK QWIQGGKQETQLLEDYVEAIEGVRTHLLRHSEPSKLT FVGELA HGRFSAKMDH LVCFLPGT LALGVY
HGLPASHMELA QELMETCYQM NRQ METGLSPEIV HF NLYPQ PGRR DVEVK PADRHN LRPETV ELSF YLYRVT
GDRKYQDWGWEILQSFSRFT RVPSGGYSSINNVQDPQKPEPRDKM ESFFLGETLK YLFLLFSDDPNLLSDAYV
FNTEAHPPLIWT

>d1qaza_ a.102.3.1 (A:) Alginate lyase A1-III {Sphingomonas sp., A1}

GSHPF DQAVVKDPT ASYDV KARRT FLQSGQL DRLKA ALPK EYDCT TEAT PNPQQ GEMVIP RRYLS GNH GP
VNPDYEPVV TL YRDF EKISAT LGN LYV ATG KPVY ATCLN MLD KWAKA DALL NYDPK SQSW YQVE WSAATAA FA
LSTMMAEPN VDTA QRER VV KWL NR VARHQ TSFP GGDT SCCNN HS YWRG QEA TIIGV ISK DDEL FRW GL GR Y
VQAMGL INEDGSF VHEMTRHE QSLHYQ NYAML PLTMIA ETASRQ GIDLYAYKENG RD IHSARKF VFAAV KNPD
LIK KYASEP QD TRAFK PGRG DLN WIEYQRAR FGFA DELG FMTV PI FDP RTG GSAT LLAY K P

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

GTAELIMK RVML DLKPLRNMDKVAEKNLNTLQPDGSWKDV PYKDDAMTNWLPNNHLLQLETIIQAYIEKDS
HYYGDDKVFDQISKAFKYWYDSDPKSRNWWHNEIATPQALGEM LILMRGYK KPLDEALVHKLTERMKRGEPE
KKTGANKTDIALHYFYR ALLTSDE ALLSF AVKELFYPVQFVHYEEGLQYD SYLQHGPQLQISSYGA VFITGV LKA
NYVRDTPYALSTEKLAIFSKYYRDSYLAIRGSYMDNFNVEGRGVSRPDILNKKA EKKRLLVAKMIDLKHTEEWAD
AIARTD STVAAGYK

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

KDTYT DRLL DWNG IIAGNQ YYDSKNDQMAKLNQ ELEG KVADSL SISSQADRIYLWEKFSNYKTSANLTATYRK
LEEMAKQV TNPSS RYYQDET VVTRV RDSMEWMHKH VYNSEK SIVGNWW DYEIGT PRAIN NTLSMKEYFSD
EEIKKYTDVIEKFV PDPEHFRKTTDNPFK ALGGN LVD MGRV KVIAGL LRKDDQ EISSTIR SIEQV FKLV DQGEGF Y
QDG SYIDHTN VAYT GAYGN VLID GLSQL LPV IQKT KNP IDK DM QMT MYHWID KSFAP LLV NGELMDMSRGRSI
SRANSEG HVA AVEV LRG I HRIADM SEGET KQRL QSLV KTIV QSDS YYDVF KNL TYK DISLMQ SLL DAGV ASVP
R

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

EDNFTKLLK WNDVTIGNVY DTNDSNMQKLNQKL DETNAK NIEAI KLD SNRTFLW KLD NLNNSAQLTATYR
RLED LAKQ ITN PHSTIYKNEKA IRV KESLA WLHQ NFY NVN KDI EG SANWW DF EIGV PRSIT GTLS MN NYFTD
AEIKTYTDPIEH FV PDAEYFRK TLV NP FK ALGGN LVDM GRV KI EG L RKD NTIIE KTS HSL KNL FT TAKA EGF YAD
GSYIDHTN VAYT GAYGN VLID GLT QLLP I QETDYK ISNQ ELD MVYK WIN QSF LPLIV KGEL MDMSRGRSISREAA
SSHAA AVEV LRGFL RL ANMSNEERN LDKSTIKTIITSNK FYN VFNNLKS YSDIANMN KLL NDSTV ATKP

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

SPSLWGDQFLSFSIDNQVAEKYAKEIEALKEQTRNMLLATGMKLADTLNLIDTIERLGISYHFEKEIDDILDQIYNQ
NSNCNDLCTSALQFRLRQHGFNISPEIFSKFQDENGKFKESLASDVLGLLNLYEASHVRTHADDILEDALAFSTIH
LESAAPHLKSPREQVTHALEQCLHKGVPRVETRFFISSIYDKEQS

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

APAYARTLDRAVEYLLSCQKDEGYWWGPLXISPVWDTGLAVLRAAGLPADHDLVKAGEWLDRQITVPGD
WAVKRPNLKPGGFAFQFDNVYPDVCCTAVVVWALNTLRPDERRRDAMTKGFRWIVGMQSSNGGWGA
YDVEDNTSDLNPNHFPSDFGEVTDPSEDTVAVLVECFGSGYDDAWKVIRRAVEYLKREQKPDGSWFGRWGV
NYLYGTGAVVSALKAVGIDTREPYIQKALDWVEQHQNPDGGWGECRSYEDPAYAGKGASTPSQTAWALMAL
IAGGRAESEAARRGVQYLVETQRPDGGWDEPYYTGTGFPDFYLGTYMRYHFPTLALGRYKQAER

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

LSNVTMEAAYVLLCHILDVRDRDRMEKIRYLLHEQREDGTWALYPGGPPDLTTIEAYVALKYIGMSRDEEP
QKALRFIQSQGGIESSRVFTRMWLALVGEYPWEKPMVPPEIMFLGKRMPNLIYEGSWARATVVALSIVMSR
QPVFPLPERARVPELYETDVPPRRGAKGGGGWIFDALDRALHYQKLSVHPFRRAAEIRALDWLLERQAGDG
SWGGIQPPWFYALIALKILDMTQHPAFIKGWEGLYGVELDYGGWMFQAS

>d1d8db_a.102.4.3 (B:) Protein farnesyltransferase, beta-subunit {Rat (*Rattus norvegicus*)}
PVWSEPLYSRPEHARERLQDDSVETVTSIEQAKVEEKIQEVFSSYKFNFHLPRLVLRKHFHYLKRGRLQLTDA
YECLDASRPWLICYWILHSLELLDEPIQPIVATDVCQFLELCQSPDGGFGGGPGQYPHLAPTYAAVNALCIIGTEEA
YNVINREKLLQYLSKQPDGSFLMHVGGEVDVRSAYCAASVASLTNIITPDLFEGTAEWIARCQNWEGGIGGV
PGMEAHHGYTFCGLAALVILKKERSLNLSLLQWVTSRQMRFEFGFQGRCKNLVDGCYSFWQAGLLPLLHRAL
HAQGDPALSMSSHWMFHQQALQEYILMCCQCPAGGLDKPGKSRDFYHTCYCLSGLSIAQHFGSGAMLHDVV
MGVPENVLQPTHPVYNIGPDKVIQATTFLQKPVPGF

>d1dceb_a.102.4.3 (B:) Rab geranylgeranyltransferase, beta subunit {Rat (*Rattus norvegicus*)}
TQQKDVTIKSDAPDTLLKEHADYIASYGSKKDDYEYCMSEYLRMSGVYWGLTVMDLMGQLHRMNKEEILVFI
KSCQHECGGSASIGHDPHLLTSAVQILTDSIHVINVDKVVAYVQLQKEDGSFAGDIWGEIDTRFSFCAVA
TLALLGKLDAINVEKAIEFVLCMNFDDGGFCRPGSESHAGQIYCCTGFLAITSQLHQVNSDLLGWWLCEQLP
SGGLNGRPEKLPDVCSWWVLASLKIIGRLHWIDREKLSFILACQDEETGGFADRGDMVDPFHTLFGIAGLS
LLGEEQIKPVSPVFCMPEEVLQRVNQPELVS

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

MLDAERLKHLIVTPSGAGEQNMIGMPTVIAVHYLDTEQWEKFGLEKRQGALELIKKGYTQQLAFRQPSSAF
AAFVKRAPSTWLTAYVVKVFSLAVNLIAIDSQVLCGAVKWLILEKQKPDGVFQEDAPVIHQEMIGGLRNNNEKD
MALTAFLVLSLQEAKDICEEQVNSLPGSITKAGDFLEANYMNLQRSYTVAIAGYALAMQGRLKGPLLNKFLTTAK
DKNRWEDPGKQLYNVEATSYALLALLQLKDFVPPVWRWLNEQRYYGGYGSTQATFMVFQALAQYQKDAP

>d1qqfa_a.102.4.4 (A:) C3D, a C3 fragment and ligand for complement receptor 2 {Rat (*Rattus norvegicus*)}

CGEQNMIGMPTVIAVHYLDTEQWEKFGLEKRQEALELIKKGYTQQLAFKQPISAYAANRNPSTWLTAYVS
RVFSLAANLIAIDSQVLCGAVKWLILEKQKPDGVFQEDGPVIHQEMIGGFRNTKEADVSITAFVLIALQEARDICE
GQVNNSLPGSINKAGEYLEASYLNLRPYTVAIAGYALALMNKLEPYLTFLNTAKDRNRWEEPGQQQLYNVEAT
SYALLALLLKDSDVPPVWRWLNDERYYGGYGSTQATFMVFQALAQYRADV

>d1csc_a.103.1.1 (-) Citrate synthase {Chicken (*Gallus gallus*)}

ASSTNLKDVLAAALIPKEQARIKTFRQQHGGTALGQITVDMSSYGGMRGMKGLVYETSVLDPDEGIRFRGFSIPEC
QKLLPKGGXGGEPLPEGFWLLVTGQIPTGAQVSWLSKEWAKRAALPSHVVTMLDNFTNLHPMSQLSAAIT
ALNSESNFARAYAEGILRTKYWEMVYESAMDLIAKLPVCAAKIYRNLYRAGSSIGAIDSKLDWSHNFTNMLGYT
DAQFTELMLRLYLTIHSDHEGGNVAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLGWLAQLQKAX
XXAGADASLRDYIWNTLNSGRVPGYGHAVLRKTDPRYTCQREFALKHLPGDPMFKLVAQLYKIVPNVLLEQG
AAANPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPCKSMSTDGLIAL

>d1csh_ a.103.1.1 (-) Citrate synthase {Chicken (Gallus gallus)}

STNLKDVLASLIPKEQARIKTFRQQHGNATVGQITVDMSSYGGMRGMKGLIYETSVLDPDEGIRFRGFSIPECQKL
LPKAGGGEPLPEGFWLLVTGQIPTPEQVSWLSKEWAKRAALPSHVVTMLDNFTNLHPMSQLSAITALNS
ESNFARAYAEGINRTKYWEFVYEDAMDLIAKLPVCAAKIYRNLYRAGSSIGAIDSKLDWSHNFTNMLGYTDPQF
TELMRLYLTIHSDHEGGNVAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLWLSQLQKDLGADAS
DEKL RDYIWNTLNSGRVPGYGHAVLRKTDPRYTCQREFALKHLPGDPMFKLVAQLYKIVPNVLLEQGKAKNP
WPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPCKSMSTDGLIAL

>d2cts_ a.103.1.1 (-) Citrate synthase {Pig (Sus scrofa)}

ASSTNLKDILADLIPKEQARIKTFRQQHGNATVGQITVDMSSYGGMRGMKGLVYETSVLDPDEGIRFRGFSIPEC
QKMLPKAKGGEPLPEGFWLLVTGQIPTEEQVSWLSKEWAKRAALPSHVVTMLDNFTNLHPMSQLSAAIT
ALNSESNFARAYAEGIHRKYWELEYEDCMDLIAKLPVCAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYT
AQFTELMLRLYLTIHSDHEGGNVAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLWLTQLQKEVKG
DVSDEKL RDYIWNTLNSGRVPGYGHAVLRKTDPRYTCQREFALKHLPGDPMFKLVAQLYKIVPNVLLEQGKAK
NPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALGFPLERPCKSMSTDGLIKLVDSK

>d1aj8a_ a.103.1.1 (A:) Citrate synthase {Archaeon Pyrococcus furiosus}

LAKGLEDVYIDQTNICYIDGKEGKLYRGYSVEELAELSTFEEVYLLWWGKLPSLSELENFKKELAKSRGLPKEVIE
IMEALPKNTHPMGALRTISYLGNIIDSGDIPVTPEEVYRIGISVTAKIPTIVANWYRIKNGLEYVPPKEKLSHAAN
FLYMLHGEEPPKEWEKAMDVALILYAEHEINASTLAVMTVGSTLSDYYSSAILAGIGALKGPIHGGAVEEAIKQFM
EIGSPEKVEEWFFKALQQKRKIMGAGHRVYKTYDPRARIFKKYASKLGDKKLFEIAERLERLVEEYLSKKGISINV
YWSGLVFYGMKIPIELYTTIFAMGRIAGWTAHLAEYVSHNRIIRPRLQYVGEIGKKYLIELRR

>d1a59_ a.103.1.1 (-) Citrate synthase {Antarctic bacterium DS2-3R}

EPTIHKGLAGVTADVTISKVNSDTNSLLYRGYPVQELAAKCSFEQVAYLLWNSELNDSELKAFVNFRSHRKLD
ENVKGAIIDLSTACHPMDVARTAVSVLGANHARAQDSSPEANLEKAMSLLATFPSVVAYDQRRRRGEELIEPRE
DLDYSANFLWMTFGEAAPEVVEAFNVSMLYAEHSFNASTFTARVITSTLADLHSAVTAIGALKGPLHGGAN
EAVMHTFEEIGIRKDESLEAATRSKAWMVDAHQKKVVMGFGRVYKNGDSRVPTMKSALDAMIKHYDRP
EMLGLYNGLEAAMEEKQIKPNLDYPAGPTYNLMGFDTEMFTPLFIAARITGWTAHIMEQVADNALIRPLSEY
NGPEQRQVP

>d1dz4a_ a.104.1.1 (A:) Cytochrome P450-CAM {Pseudomonas putida}

LAPLPPHVPEHLVFDMDYNPSNLSAGVQEAWAVLQESNVPDLWTRCNGGHWIATRGQLIREAYEDYRHFS
SECPFIPREAGEAYDFIPTSMDPPEQRQFRALANQVVGMPVVDKLENRIQELACSLIESLRPQGQCNCFTEDYAE
PFPIRIFMILLAGLPEEDIPHLYTDQMTRPDGSMTFAEAKEALYDYLIPIIEQRRQKPGTDAISIVANGQVNGRPI
TSDEAKRMCGLLLGGGLTVVNFLSFSMEFLAKSPEHRQELIQRPERIPAACEELLRRFSLVADGRILTSYEFHG
VQLKKGDQILLPQMLSQLDERENACPMHVDFSRQKVSHTFGHGSHLCLGQHLARREIIVTLKEWLTRIPDFSI
APGAQIQHKSGIVSGVQALPLVWDPATTKAV

>d1jpza_ a.104.1.1 (A:) Cytochrome P450 bm-3 {Bacillus megaterium}

TIKEMPQPKTFGEKLNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEACDESRFDKNLSQALK
FVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMVVDIAVQLVQKWERLNADEHIEVPEDMT
RLTDTIGLCGFNYRFNSFYRDQPHPFITSVRALEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKII

ADRKASGEQSDDLTHMLNGKDPETGEPLDDENIRYQIITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAAR
VLVDPVPSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMVLIPQLHRDKTIWGDD
VEEFRPERFENPSAIPQHAFKPFNGQRACIGQQFALHEATLVLGMMKLHFDFEDHTNYELDIKETTLKPEGF
VVKAKSKKIPLGGI

>d1jfba_a.104.1.1 (A:) Cytochrome P450-NOR, nitric reductase {Fungus (Fusarium oxysporum)}
APSFPFSRASGPEPPAEFAKL RATNPVSQVKLFDSLAWLVTKHKDVCVATSEKLSKVRTRQGFPELSASGKQA
AKAKPTFVDMDPPEHMHQRSMVEPTFTPEAVKNLQPYIQRTVDDLEQMICKQKGANGPVDLVKEFALPVPS
YIIYTLGVPFNDLEYLTQNAIRNTGSSTAREASAANQELLDYLAILVEQRLVEPKDDIISKLCTEQVKPGNIDKSD
AVQIAFLLLVAGNATMVNMIALGVATLAQHPDQLAQLKANPSLAPQFVEELCRYHTASALAIKRTAKEDVMIGD
KLVRANEGIIASNQSANRDEEVFENPDEFNMNRKWPPQDPLGFGFDHRCIAEHLAKAELTTVFSTLYQKFPLD
KVAVPLGKINYTPLN RDVGIVDLPVIF

>d1jipa_a.104.1.1 (A:) Cytochrome P450-ERYF {Saccaropolyspora erythraea}
TTVPDLESDFHWDWYRTYAEI RETAPVTPVRFLGQDAWLVTGYDEAKAALSDLRLSSDPKKYPGV EFPAYL
GFPEDVRNYFATNMGTSDPPTHTRLRKLVSQEFTVRRVEAMRPRVEQITAELLDEVGDGVV DIVDRFAHPLPI
KVICELLGVDEK YRGFRWSSEILVMDPERAEQRGQAAREVVNFILD LVERRTEPGD DLLS ALRVQDDDG
RLSADELTSIALVLLLAGFESSVSLIGITYLLLHPDQLALVRRDPSALPNAVEEILRYIAPPETTRFAAEEVEIGGV
AIPQYSTVLVANGAANRDPKQFPDPHRFDVTRDTRGHLSFGQGIHFCMGRPLAKLEG EVALRALFGRFPALSLG
IDADDVVWRRSLLRGIDHLPVR LDG

>d1cpt_a.104.1.1 (-) Cytochrome P450-TERP {Pseudomonas sp.}
MDARATIPEHIARTVILPQGYADDEVIYPAFKWL RDEQPLAMA HIEGYDPMIWIATKHADVMQIGKQPG LFSN
AEGSEI LYDQNNEAFMRSISGGCPHVIDS LTSMDPPTHTAYRGLTNWFQPASIRKLEENIRRIAQASVQRLLDF
DGECDFMTDCALYYPLHVVMTALGPEDDEPLMLKL TDQFFG VEAARRFHETIATFYDYFNGFTD RRSCP KD
DVM SLLANSKLDG NYIDD KYIN AYYVAI ATAGHD TSSSGGAI GLSRNPEQLA LAKSDP ALIPR LVDEA VRWT A
PVKSF MRTALADTEVRGQNIKRGDRIML SYP SANRDEEVFSNPDEF DITRF PNRH LGFGWGAHMCLGQHLAK
LEM KIFFEELLPKLKSV ELSGPP RL VATNFVGGPKNVPIRFTKA

>d1e9xa_a.104.1.1 (A:) Cytochrome p450 14 alpha-sterol demethylase (cyp51) {Mycobacterium tuberculosis}

MSAVALPRVSGGHDEHGHL EEFRTDPIGLMQRVRDEC GDVGTFQLAGKQV VLLSGSHANEFFF RAGDDLD
QAKAYPFMTP IFGEGVVFDASPERRKEM LHNAALRGEQMKGHAA TIEDQVRRMIADWGEAGEIDLLDFFAEL
TIYTSSACI GKFRDQLDGRFAKLYHELER GTDPLAYVDPYLP IESFRR DEAR NGLVALVADIMNGRIANPPTD
KS DRDML DV LIAVKAETGTPR FSADE ITGMFISM MFAGHHTSSGTASWTLIELMRH RDAYAAVIDE LDELYGDG
RSV SFHALR QIPQLEN VLKETL RLH PPLI ILM RVAKGE FEVQ GHRIHEG DLVAAS PAISN RIPE DF PDH FVP ARY
EQ PRQED LLNRW TWIPFGAGR HRCVGA AFAIM QIK AIFS VLLREYE FEM AQ PPES YRN DHS KMV VQLA QPAC
VRYRRRT

>d1io7a_a.104.1.1 (A:) CYP119 {Archaeon Sulfolobus solfataricus}
MYDWFSEMRKKDPVYYDGNIWQVFSYRTKEV LNNFSK FSSDLTGYHERLEDLRNGKIRFDI PTRYTMLTS DPP
LHDELRSMSADIFSPQKLQ TLTFIRETT RSLLSD IDPRE DDIVKKL AVPLPIIVISKI LGPIEDKEKF KEWSDLV AFR
LGKPG E IELG KK YLELIGYVKDHLNSGTEV SVR VVNSNL SDIE KLG YI ILLIAGNETT NLISNS VIDTRFNLWQR
IREEN LYLK AIEE ALRYSPP VMRTV RKT KERVK LGDQ TIEEG EYVRV WIASANRDEEV FHD GEK FIPDRNPNPHL
SFGSGIHLCLGAPLARLEARIAIEFSKRF RHI EILD TEK VPNEV LNGYKRLV RLKS

>d1dt6a_a.104.1.1 (A:) Mammalian cytochrome p450 2c5 {Rabbit (Oryctolagus cuniculus)}

PPGPTPFPIIGNILQIDAKDISKSLTKFSECYGPVFTVYLG MKPTV VLH GYEAVKEALV DLGEEFAGR GSVP ILEK VS
KGLGIAFSNAKTW KEMRRFSLMTL RFMGKRSIEDRIQEEAR CLVEELRKT NASPCDPTFILGCAPCNVCS VI

FHNRFDYKDEEFLKLMESLHENVELLGTPWLQVNNFPALLDYFPGIHKTLLKNADYIKNFIMEKVKEHQKLLDV
NNPRDFIDCFLIKMEQENNLEFTLESLVIASDLFGAGTETTSTTLRYSLLLLKHPEVAARVQEEIERVIGRHRSPC
MQDRSRMPYTDAVIHEIQRFIDLLPTNLPHAVTRDVRFRNYFIPKGTDIITSLSVLHDEKAFTPNEPKVFDPGHFLD
ESGNFKKSDYFMPFSAGKRCMVGEGLARMELFLFTSILQNFKLQLSVEPKDLDITAVVNGFVSVPSSYQLCFPI
HH

>d1etob_a.105.1.1 (B:) FIS protein {Escherichia coli}

MFEQRVNSDVTSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEV EQPLDMVMQYTL
GNQTRAALMMGINRGTLRKKKLYGMN

>d1etxa_a.105.1.1 (A:) FIS protein {Escherichia coli}

VLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEV EQPLDMVMQYTRGNATRAALM
MGINRGTLRKKKLYGMN

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

PLRDSVKQALKNYFAQLNGQDVNDLYELVLAEV EQALLDVMQYTRGNQTRAALMMGINRGTLRKKKLYG
MN

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

MDLPGELEFASTPDSPSHLPPDSWATLLAQWADRALS RSGHQNLSEA QPELERTLLTALRHTQGHKQEAARLL
GWGAATLTAKLKE LGME

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

MHTSELLKHIYDINLSYLLAQRLIVQDKASAMFRLGINEEMATT LAALTLPQMVKLAETNQLVCHFRFD SHQT
TQLTQDSRVDDLQQIHTGIMLST

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

TSELLKHIYDINLSYLLAQRLIVQDKASAMFRLGINEEMATT LAALTLPQMVKLAETNQLVCHFRFD SHQT
TQDS

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

SAAMAEQRHQEWLRFVDLLKNAYQNDLHLPLLNLMTPDEREALGTRVRIEELLRGEMS QRELKNELGAGIAT
ITRGNSNLKAAPVELRQWLEEVLLKSD

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

AQQSPYSAAMAEQRHEEWRFVDLLKNAYQNDLHLPLLNLMTPDEREALGTRVRIVEELLRGEMS QRELKNE
LGAGIATITRGNSNLKAAPVELRQWLEEVLLK

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

MTIDEIIIAIEKLTVSELAELVKKLEDKFGVTAAAPVAVA APVAGAAAGAAQEEKT

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

MTIDEIIIAIEKLTVSELAELVKKLEDKFGVT

>d1dd4d1_a.108.1.1 (D:) 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)}

YGNMTEDHVMHLLQNADPLKVPPLKGSPENLRHLKNTMETIDWKVFESWMHHWLLFEMSRHSLEQKPT
DAPPK

>d1aora1_a.110.1.1 (A:211-605) Aldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus
furiosus}

IADKQKFMLVREKVNLRLNDPVAGGGLPKYGTAVLVNIINENGLYPVKNFQTGVYPYAYEQSGEAMAAKYLVR
NKPCYACPIGCGRVNRLPTVGETEGPEYESVWALGANLGINDLASIIEANHMCDELGLDTISTGGTLATAMELYE
KGHIKDEELGDAPPFRWGNTTEVLHYIEKIAKREGFGDKLAEGSYRALSMTVKKLELPAYDPRGAEG
HGLGYATNNRGGCHIKNYMISPEILGYPYKMDPHDVSDDKIKMLILFQDLTALIDSAGLCFTTFGLGADDYRDL
LNAALGWDFTTEDYLKIGERIWAERLFNLKAGLDPARDTLPKRFLEEMPMEGPNGHTVRLKEMLPRYYKLR
GWTEDGKIPKEKLEELGIAEFY

>d1b25a1 a.110.1.1 (A:211-619) Formaldehyde ferredoxin oxidoreductase
{Archaeon Pyrococcus furiosus}

DKEELKKLSQEAYNEILNSPGPFWKRQGTMAAVEWCNTNYALPTRNFSRGYFEFARSIDGYTMEGMKVQQR
GCPYCNMPGCVVLDAGQESLDYENVALLGSNLIGKLNEVSVLNRIADEMGMDTISLGVSIAHVMEAVER
GILKEGPTFGDFKGAKQLALDIYRKGEGLNLAEGVKAMAEGKLTHDFAMIVVKGLEVSGYNCIYPMALAY
GTSAGAHHKEAWVIAWEIGTAPIEGEKAEKVEYKISYDPIKAQKVVELQRLRGGLFEMLTACRLPWVVGSLSD
YYPKLLKAITGVTYTWWDDLYKAADRVYSLIRAYWVREFNGKWDRKMDYPPKRWFTEGLKSGPHKGEHLDEKKY
DELLSEYYRIRGWDERGPKKETLKELDLDVPIELEKVTNLE

>d1d2ta_ a.111.1.1 (A:) Acid phosphatase {Escherichia blattae}

GNDTTTKPDLYLKNSEAINSALLPPPAVGSIABLNDQAMYEQGRLRNTERGKLAEDANLSSGGVANA
GAFGSPITEKDAPALHKLLTNMIEDAGDLATRSAKDHYMRIRPFAFYGVSTCNTTEQDKLSKNGSYPSGHTSIG
WATALVLAEPQRQNEILKRGYELGQSRSVICGYHWQSDVDAARVVGSAVVATLHTNPAFQQQLQKAKAEFA
QHQK

>d1qi9a_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Ascophyllum
nodosum}

TCSTSDDADDPTPPNERDDEAFASRVAAKRELEGTGTVQCINNGETDLAAFKHKSPLHDDLQVDADAFAAL
EDCILNGDLSICEDVPVGNSEGDPVGRIVNPTAAFAIDISGPAFSATTIPPVPLPSPELAAQLAEVYWMALARD
VPFMQYGTDDITVAAANLAGMEGFPNLDASIGSDGTVPLSQLFRATFGVETGPFISQLLNSFTIDSITVE
PKQETFAPDVNYMVDFDEWLNIQNGGPPAGPELLDDELRFVRNARDLARVTFTDNINTEAYRGALILLGLDAF
NRAGVNGPFIDRQAGFVNFGISHYFRIGAAELAQRSSWYQKQVHFRARPEALGGTLHLTIKGELNADF
SLLENAELLKRVAAINAQNPNEVTYLLPQAIQEGSPTHPSYPSGHATQNGAFATVLKALIGLDRGGDCYPDP
VYPDDDGLKLIDFRGSCLTFEGEINKLAVNVAFGRQMLGIHYRFDGIQGLLGETITVRTLHQELMTFAEESTF
RLFTGEVIKLFQDGFTIDGFKCPGLVYTGVENC

>d1qhba_ a.111.1.2 (A:) Haloperoxidase (bromoperoxidase) {Red algae (Corallina officinalis)}

GIPADNLQSRAKASFDTAAAELALARGAVPSFANGEELLYRNSETGDPFIGSFTKGLPHDDNGAIIDPDDFL
AFVRAINSGDEKEIAALTGPARDPETGLPIWRSDLANSLEVRGWENSSAGLTFLEGPDQAQSVMAPPAPVL
TSPELIAEMAELYLMALGRDIEFSEFDSPKNAAFIRSAIERLNGLEWFNTPAKLGDPPAEIRRGEVTGNLFRGI
LPGSEVGPYLSQFIIVGSKQIGSATVGNKTLVSPNADEFGEIAYGSITISQRVRIATPGRDFMTDLKVFLDVQD
AADFRGFESYEPGARLIRTIRDLATWVHFDSLYEAYLNACILLANGVPFDNLPFQQEDKLDNQDVFGSA
HVLSLVTEVATRALKAVRYQKFNIHRRRLPEATGGLISVNKNALKSESVFPEVDLVEEELSI-DDSASSNEKQNI
DGDVSPGKSLLPMAFAEGSPFHPSYGSYHVVAGACVTILKAFFDANFQIDQVFEVDTDEDKLVKSSFPGLT
VAGELNKLADNVAIGRNMGVHYFSDQFESLLGEQIAIGILEEQSLTYGENFFFNLPKFDGTTIQI

>d1vns_ a.111.1.3 (-) Chloroperoxidase {Curvularia inaequalis}

VTPIPLPKIDEPEEYNTNYILFWNHVGLELNRTHTVGGPLTPPLSARALGMLHLAIHDAYFSICPPTDFTTFLSP
DTENAAYRLPSPNGANDARQAVAGAALKMLSSLYMKPVEQPNPNGANISDNAYAQLGLVLDHSVLEAPGGV
DRESASFMFGEDVADVFFALLNDPRGASQEGYHPTPGRYKFDDEPTHVVLIPVDPNNPMPKMPFRQYHAP
FYGKTTKRFATQSEHFLADPPGLRSNADETAEYDDAVRVIAIMGGAQALNSTKRSRWQTAQGLYWAYDGSNLI
GTPPRFYNQIVRRIAVTYKKEEDLANSEVNNADFARLFALVDVACTDAGIFSWKEKWEFEWRPLSGVRDDGR

PDHGDPFWLTGAPATNTNDIFKPPFPAYPSGHATFGGAVFQMVRRYYNGRVTWKDDEPDNIAIDMMISE
ELNGVNRLRLRQPYDPTAPIEDQPGIVRTRIVRFDSAELMFENAIISRIFLGVHWRFDAAAARDILIPPTTKDVY

AVDNNGATVFQNVEDIRYTTREDEEGLFPIGGVPLGIEIADEFNNGLKPTPPEIQP

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

MEGEIDIAKRIEDGINQVQCSVAEYPEAITYLLEQYNRVEAEEARLSLITGFVDPNAEEDLAPTATHVGSELSQE
DLDDDEDEDEEDGDDDSADDNSIDPELAREKFAELRAQYVVTREDTIKAKGRSHATAQEEILKSEVFQFRLVP
KQFDYLVNSMRVMMDRVRTQERLIMKLCVEQCKMPKKNFITLFTGNETSDFWFNAIAMNKPWSEKLHDVS
EEVHRALQKLQQIEETGLTIEQVKDINRRMSIGEAKARRAKKEMVEANRLVISIAKKYTNRGLQFLDIQEGNI

GLMKAVDKFEYRRGYKFSTYATWWIRQAITRSIADQ

>d1ewqa1 a.113.1.1 (A:267-541) DNA repair protein MutS, domain III {Thermus aquaticus}

RGQDTLFSVLDETRAPGRRLLQSWLRHPLDRGPLEARLDRVEGFVREGALREGVRRLYRLADLERLATRREL
GRASP KDLGALRRSLQILPEL RALLGEEVGLPDSL SPLKEELEA ALVEDPPLKVSEGG LIREGYDP DLD ALRAAHREG
VAYFLELEERERERTGIPTLKVGYN AVFGYY LEVTRPVY YER VPKEYRPV QTLKDRQRY TLPEMKEKEREVYRLEALI
RRREEEVFLEV RERAKRQAE ALREA ARILA ELDV AALAEV A VRYG

>d1e3ma1 a.113.1.1 (A:270-566) DNA repair protein MutS, domain III {Escherichia coli}

DAATRRNLEITQNLAGGAENTLASVLDC T VTPMGSRMLKRWLHMPVRDTRVLLERQQTIGALQDFTAGLQPV
LRQVGDLERILARLALRTARP RDLARMRHA FQQLPELRAQLETVD SAPVQALREKMGEFA RDLLERA IIDTPP
VLVRDGGVIASGYNEELDEW RALADGATDYLERLE VRERERTGLDTLKVG FNA VHGY YQISRGQSH LAPIN YM
RRQTLKNAERYI IPELKEYEDKVLTSKGKALALEKQLYEELFDLLLPHLEALQQ SASALA ELDVLVNLAERAYTLN

>d1f5na1 a.114.1.1 (A:284-583) Interferon-induced guanylate-binding protein 1 (GBP1), C-terminal domain {Human (Homo sapiens)}

GGIQVNGPRLES LVLT YVNA ISSGD LPCMENAVLALA QIENSAAVQKAIAHYEQQM GQKVQL PTE SLQ ELL DLH
RD SERAIEV FIRSS FKDV DHLF QKELAAQ LEKKR DDF CKQN QEA SDR CS GLL QV IFSP LE EV KAGI YSK PG YY
RLF VQKLQDLKKYYE PRKG I QAA EIL QTY LKS KES MTD AIL QTD QTL KE KEI EVER VKAESA QASAK MLHEM
QRKNEQMMEQKERSYQ EHL KQL TE KMEND RVQ LLKE QERT LALKLQ EQLLKE GFQ KES RIM KNE IQDL QT
KM

>d1bvp11 a.115.1.1 (1:1-120,1:255-349) Bluetongue virus capsid protein vp7 (BTV-10 vp7) {Bluetongue virus}

MDTIAARALTVMRACATLQEARIVLEANVMEILGIA INRYN GLT RGV TMRPTSLAQR NEMFFMCLDMMLSA
AGINVGPISPDYTQHMATIGV LATPEI PFTTEA ANE IARV TGETSTWG XKT LNQ YPA LTAEI FN VY SFRDHTWHG
LRTAILNRTTLPNMLPPIFPPNDRDSILTLLSTLADV YT VLRPEFAIHGVNPMPG PLTRAIARAAYV

>d1qhda1 a.115.1.2 (A:1-148,A:333-397) vp6, the major capsid protein of group A rotavirus {Bovine rotavirus}

MDVLYSLSKTLD KARDKIVE GTL YSNVSDLI QQFNQMIITMNGNEF QTGGIGNLPIRNWN FDFG LLGTT LLN D
ANYVETARNTIDYFVDFVN C MDEM VRES QRNGI APQSDS LIKSGIKF KRINF DN SSEYI ENW NLQ NRQR
TXSVLADASETMLANVTSV RQYE AIPV GPV FPPGMN WTD LITN YSPS R EDN LQ RVFT VASIRSM LVK

>d1tx4a_a.116.1.1 (A:) p50 RhoGAP domain {Human (Homo sapiens)}

PLPNQQFGVSLQH LQEK NPEQ EPIPIV LRET VAYLQA HALT TEGIF RRSANT QV VREV Q QKYNM GLPVDFDQY
NALHLP AVILKTF RLPEPLT FDLY PHVV GFLN IDES QRVPATLQV LQ TLPEEN YQV RLFTA FLV QISA HSDQ NK
MTNTNL AVVFGPNLLWAKDAA ITLKAINPINTFTKFL LDHQGE LF

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

LPD LAEQFAPPDI APP LLIK LVEA IEKK GLE CST LY RTQSSN LAELR QL LDC TPS VDLEM IDVHV LAD AFK RY LL
LPN PVI PA AVY SEMI S LAPE VQS SEYI QLLKKL IRSPS I PHQ YWLTQ YLLK HFF KLS QT SS KNLL NARV LSE IFSP M
LFR FSA ASSD NTEN LIK VIEI LIST EW

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

AQLDSIGFSIIKKCIHAVETRGINEQGLYRIVGVNSRVQKLLSILMDPKTATETEICAWEIKTITSALKTYLRMLP
GPLMMYQFQRSFIKAALKLENQESRVSEIHSVLVHRLPEKNRQMLHLLMNHLAKVADNHKQNLMTVANLGVV
GPTLLRPQEETVAAIMDIKFQNIVIEILLENHEKIFNTVPE

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

MPEEEYSEFKELILQKELHVYALSHVCQDRTLLASILLRIFLHEKLESLLCTNDREISMEDEATTLFRA
T LAST LMEQYMKATATQFVHHALKDSILKIMESQSCELSPSKLEKNEDVNTNLTHLLNILSELVEKIFMASEILPP
TLRYYI GCLQKSVQHKWPTNTTMTRVVSGFVFLRLICPAIINPRMFNIISDSPSPIAARTLILVAKSVQNL
ANLVEFGAKE PYMEGVNPFIKSINKHRMIMFLDELGNVPelpDTTEHSRTDLSRDLAALHEICVAH
SDELRTLSNERGAQQHVLK KLLAITELLQQKQNQYT

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

ERLVELVTMMGDQGELPIAMALANVPCSQWDELARVLVTLFDSRHLLYQLLWNMFSKEVELADSMQTLFRG
NSLASKIMTFCFKVGYATYLQKLLDPLLRI
VITSSDWQHVSFEVDPTRLEPSLEENQRNLLQMTEKFHHAISSS
SEFPPQLRSVCHCLYQVVSQRFPQNSIGAVGSAMFLRFINPAIVSPYEAGILDKKPPP
IERGLKLMSKILQSIANH VLFTKEEHMRPFNDFVKS
NFDAARRFLDIASDCPTSDAVNHSLFISDG
NVLA
LHRLWNNQEKGIGQYLSSNR DHKAVGRRPF
DKMATLLAYLGPPE

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

RLPSADVYRFAEPDSEENIIFE
EGIPIIKAGTVIKLIERLTYHMYADPNFVRTFLTYRSFCKPQELLSLII
ERFEIPEPRF RKEYIQPVQLRVLNVCRHWVEHHFYDFERDAYLLQRMEEFIGTVRGKAMKKW
VESITKIIQRKKITFQSSP
TVE WHISRPGHIETFDLLTLP
IEARQLTLES
DLYRAVQPSELGVSVWT
KEDKEINSPNLLKMIRHTTNLT
LWFEKCIV ETENLEERVA
VVSRIEILQVF
QELNNFNGVLEV
VSAMNSSPV
YRLDHTFEQIP
SRQKKILE
EAH
LEDHYKKYLA KLRSINPPCVPFFGIYLT
NILKTEEGNPEV
LKRHG
KELINFSKRR
KVA
EITGEI
QQYQ
NQPYCLR
VESDI
KRFFENLN PMGNS
MEKEFTD
YLFNKS
LEIEPR
NP
KPL
PRF
PK
KSY
PL
KSPG
VRPSN

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

EDAGLVAEAEAVAAGWM
LDLCLSLCRAFRDGR
SED
FRR
TRNS
AEAI
HGLSS
LTACQL
RTIYICQ
FLTRIAAG
KTL DAQF
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d1h6pa_a.146.1.1 (A:) TRF2 {Human (Homo sapiens)}

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

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

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WPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRQAHQDTQRRTSMGGTQQQFVEGVRMEEIVEGCTGA
LHILARDVHNRIVIRGLNTIPLFVQLYSPENIQRVAAGVLCELAQDKEAAEAIAEAGATAPLTELLHSRNEGVTY
AAAVLFRMS

>d1iala_a.118.1.1 (A:) Importin alpha {Mouse (Mus musculus)}

DEQMLKRRNVSSFPDDATSPHQENRNNQGTNVWSVEDIVKGINSNNLESQLQATQAARKLLSREKQPPIDNII
RAGLIPKFVSLGKTDCSIQFESAWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHAHISEQAVWALGNIAGD
GSAFRDLVIKGHAIDPPLLALLAVPDLSTLACGYLRNLTWLSNLCRNKNPAPPLDAVEQILPTLVRLHHNDPEVL
ADSCWAISYLTDPNERIEMVVKKGVVPQLVKLLGATELPVTPALRAIGNIVTGTDEQTQKVIDAGALAVFPSLL
TNPKTNIQKEATWTMSNITAGRQDQIQQQVNVHGLVPFLVGVLSKADFKTQKEAAWAITNYTSGGTVEQIVYL
HCGIIPLMNLLSAKDTKIIQVILDAISNIFQAAEKLGETEKLSIMIECGGLDKIEALQRHENESVYKASLNLIKEYF

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

ELITILEKTVSPDRLEAAQKFLERADEVNLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLTSKDPDIKAQYQQ
RWLAIDANARREVKNYVLQTLGTETYRPSSASQCVAGIACAEIPVNQWPELIPQLVANVTNPNSTEHMKESTLE
AIGYICQDIDPEQLQDKSNEILTIIQGMRKEEPSNNVLAATNALLNSLEFTKANFDKESERHFIMQVVCEATQC
PDTRVRAALQNLVKIMSYYQYMETYMPALFAITIEAMKSDIDEVALQGIEFWNSVCDEEMDLAIEASEAAE
QGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDDDDWNPCAKAGVCLMLLATCCEDDIVPHVLPFIKEHIK
NPDWRYRDAAVMAFGCILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTGRICELLPEAAINDVY
APLLQCLIEG

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

MELITILEKTVSPDRLEAAQKFLERADEVNLPTFLVELSRVLANPGNSQVARVAAGLQIKNSLTSKDPDIKAQY
QQRWLAIDANARREVKNYVLHTLGTEYRPSSASQCVAGIACAEIPVNQWPELIPQLVANVTNPNSTEHMKES
TLEAIGYICQDIDPEQLQDKSNEILTIIQGMRKEEPSNNVLAATNALLNSLEFTKANFDKESERHFIMQVVCEA
TQCPDTRVRAALQNLVKIMSYYQYMETYMPALFAITIEAMKSDIDEVALQGIEFWNSVCDEEMDLAIEASE
AAEQGRPPEHTSKFYAKGALQYLVPILTQTLTKQDENDDDDWNPCAKAGVCLMLLATCCEDDIVPHVLPFIKE
HIKNPDWRYRDAAVMAFGCILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVRDTAAWTGRICELLPEAAINDV
YLAAPLLQCLIEGLSAEPVASNCWFSSLAEAAYEADVADDQEEPATYCLSSFELIVQKLLETTDRPDGHQNN
LRSSAYESLMEIVKNSAKDCYPAVQKTLVIMERLQQVLQMESHIQSTSRIQFNDLQSLLCATLQNVLRKVQH
QDALQISDVVMASLLRMFQSTAGSGGVQEDALMAVSTLVELGGEFLKYMЕAFKPFLGIGLKNYAEYQVCLAA
VGLVGDLCRALQSNIIIPFCDEVMQLLLNLGNENVHRSVKPQILSVFGDIALAIGGEFKYLEVVLNTLQQASQA
QVDKSDYDMVVDYLNELRESCLEAYTIVQGLKDQENVHPDVMLVQPRVEFILSFIDHIAGDEDHTDGVVACA
AGLIGDLCTAFGKDVLKLVEARPMIHELLTEGRRSKTNKAKTLARWATKELRKLKNQA

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

YEWPDP EQGLQQILQLLKE SPDTTIQRTVQQKLEQLNQYPDFNNYLIFVLTKLKSEDEPTRSLGLILKNNVKA
HFQNFPNGVTDFIKSECLNNIGDSSPLIRATVGI LITIASKGELQNWPDLPKLCSLLSEDYNTCEGAFGALQKI
CEDSAEILDSDVLDRPLNIMIPKFLQFFKHSSPKIRSHAVACVNQFIISRTQALMLHIDSFTENLFALAGDEEPEVR
KNVCRALVMLEVRMDRLLPHMHNIVEYMLQRTQDQDENVAEACEFWLTLAEQPICKDVLVRHLPKLIPVLV
NGMKYSDIDIILLKGDVEEDETIPDSEQDIRPRFHRSRVVAQQHDEDGIEEEDDDDEIDDDDTISDWNLRKCS
AAALDVLANVYRDELLPHILPLLKELLFHHEWVVKESGILVLAIAEGCMQGMIPYLPELIPHLIQCLSDKKALVRS
ITCWTL SRYAHWVSQPPDTYLKPLMTELLKRILDSNKRQEAACSAFATLEEACTELVPLYI LDVLFAFSKY
QHKNLLILYDAIGTLADSGVGHHLNKPEYIQMLMPPLIQKWNLKDEDKDLFPLLECLSSVATALQSGFLPYCEPV
YQRCVNLVQKTLAQAMLNNAQPDQYEAPDKDFMIVALDLLSGLAEGLGGNIEQLVARSNILTMYQCMQDK
MPEVRQSSFALLGDLTACFQHVVKPCIADFMPILGTNLNEFISVNNATWAIGEISIQMGIEMQPYIPMVLHQ
LVEIINRPNTPKTLLENTAITIGRLGYVCPQEVA PMLQQFIRPWCTSRLNIRDNEEKDSA FRGICTMISVNPSGV
QDFIFFCDAVASWINPKDDL RDMFCKILHGFKNQVGDENWRRFSDQFPLPLKERLA AFYGV

>d1ee4a_ a.118.1.1 (A:) Karyopherin alpha {Baker's yeast (Saccharomyces cerevisiae)}

QELPQMTCQLNSDDMQEQLSATVKFRQILSREHRPPIDVVIQAGVVPRLVEFMRENQPEMLQLEAAWALTNIA
ASGTSAQTKVVVDADAVPLFIQLLYTGSVEVKEQAIWALGNVAGDSTDYRDYVLQCNAMEPILGLFNSNKPSLIR
TATWTLSNLCRGKKPQPDWSVSQALPTLAKLIYSMDTETLVACWAISYLSDGPQEAIQAVIDVRIPKRLVEL
LSHESTLVQTPALRAVGNIVTGNDLQTQVVINAGVLPALRLLLSSPKENIKKEACWTISNITAGNTEQIQAVIDANL
IPPLVKLLEVAEDKTKEACWAISNASSGGLQRPDIIYLVSQGCIKPLCDLLEIADNRIIEVTLDALENILKMGEAD
KEARGLNINENADFIEKAGGMEKIFNCQQQNENDKIYEKAYKIIETYF

>d1b3ua_ a.118.1.2 (A:) Constant regulatory domain of protein phosphatase 2a, pr65alpha {Human (Homo sapiens)}

AAADGDDSLYPIAVLVIDLRNEDVQLRLNSIKKLSTIALALGVERTRSELLPFLTDITYDEDEVLLALAEQLGTFTLV
GGPEYVHCLLPPLESLATVEETVVRDKAVESLRAISHEHSPSDLEAHFVPLVKRLAGGDWFTSRSTSACGLFSVCYP
RVSSAVKAELRQYFRNLCSDDTPMVRRAASKLGEFAVKLELDNVKSEIIPMFSNLASDEQDSVRLLAVEACVNI
AQLLPQEDLEALVMPTLRQAAEDKSWRVRYMVADKFTELQKAVGPEITKTDLVPAFQNLMDCEAEVRAAAS
HKVKEFCENLSADCRENVIMSQILPCIKEVLDANQHVKSALASVIMGLSPILGKDNTIEHLLPLFLAQLKDECPE
VRLNIISNLDCVNEVIGIRQLSQSLPAIVELAEDAKWRVRLAIIEYMPPLLAGQLGVEFFDEKLNLCMAWLVDHV
YAIREAATSNLKKLVEKFGKEWAHATIIPKVLAMSGDPNYLHRMTTLCINVLSEVCQDITTKHMLPTVLRMA
GDPVANVRFNVAKSLQKIGPILEKLTQDQDVKYFAQEALTVSLA

>d1hu3a_ a.118.1.2 (A:) Eukaryotic initiation factor eIF4G {Human (Homo sapiens)}

SDPENIKTQELFRKVRSLNKLTPQMNFNLQMKQVSGLTVDEERLKGVIDLVEKAIDEPSFSVAYANMCRLVTL
KVPMAKPGNTVNFRKLLNRCQKEFEKDACKDDVFEKKQKELEAASAPEERTRLHDELEEAKDCKARRRSIGNIK
KFIGELFKLKLTEAIMHDCVVKLLKNHDEESLECLCRLTTIGKLDLFEKAKPRMDQYFNQMEKIVKERKTSSRI
RFMLQDVIDLRLCNWVS

>d1h6ka1 a.118.1.2 (A:27-290) CBP80, 80kDa nuclear cap-binding protein {Human (Homo sapiens)}

TEDHLESICKVGEKSACSLESNLEGLAGVLEADLPNYKSILRLLCTVARLLPEKLTIVTTLVGLLNARNYNFGGEF
VEAMIRQLKESLKANNYNEAVYLVRFLSDLVNCHVIAAPSMVAMFENFVSVTQEEQDVPQVRRDWYVY AFLSSL
PWVGKELYEKDAEMDRIFANTESYLRQRKTHVPMLQWTADKPHPQEYLDCLWAQIQKLKKDRWQERH
ILRPYLAFDSILCEALQHNLPFTPPPHTEDSVYPMPRVIFR

>d1h6ka2 a.118.1.2 (A:291-480) CBP80, 80kDa nuclear cap-binding protein {Human (Homo sapiens)}

MFDYTDDPEGPVMPGSHSVERFVIEENLHCIKSHWKERKTCAAQLVSYPGKNKIPNYHIVEVIFAELFQLPAPP
HIDVMYTTLLIELCKLQPGSLPQVLAQATEMLYMRDLTMNTTCVDRFINWFSSHLSNFQFRWSWEDWSDCLS
QDPESPCKPKFVREVLEKCMRLSYHQRILDIVPPTFSALCPSN

>d1h6ka3 a.118.1.2 (A:481-790) CBP80, 80kDa nuclear cap-binding protein {Human (Homo sapiens)}

PTCIYKGDESSNSLPGHSVALCLAVAFSKATNDEIFSILKDVNPNNQDDDDDEGFSFNPLKIEVFVQTLLHAA
KSFSHSFSALAKFHEFKTLAESDEGKLHVLVRMFEVWRNHPQMIAVLVDKMIRTQIVDCAAVANWIFSELSD
DFTRLFVWEILHSTIRKMNHVLKIQKELEEAKELARQHDGVLEEQIERLQEKVESAQSEQKNLFLVIFQRFIMI
LTEHLVRCETDGTSVLPWYKNCIERLQQIFLQHHQIIQQYMTLENLLFTAELDPHILAVFQQFCALQA

>d1hs6a1 a.118.1.7 (A:461-610) Leukotriene A4 hydrolase C-terminal domain {Human (Homo sapiens)}

DMTLTNACIALSQRWITAKEDDLNSFNATDLKDLSSHQLNEFLAQLQRAPLPLGHIKRMQEYVNFNAINNSEI
RFRWLRLCIQSKEWDAIPLALKMATEQGRMKFTRPLFKDLAAFDSHDKSHDQAVRTYQEHKASMHPVTAMLVGK

DLKVD

>d1b89a_a.118.1.3 (A:) Clathrin heavy chain proximal leg segment {Cow (Bos taurus)}
RLAELEEFINGPNNAHIIQVGDRCYDEKMYDAAKLLNNVSNGFLASTLVHLGEYQAAVGARKANSTRW
KEVCFACVDGKEFRLAQMCGLHIVVHADEEELINYYQDRGYFEELITMLEAALGLERAHMGMFTELAILYSKFK
PQKMREHLELFWSRVNIPKVLRRAEQAHLWAELVFLYDKYEEYDNAITMMNHPTDAWKEGQFKDIITKVANV
ELYYRAIQFYLEFKPLLNNDLLMVLSPRLDHTRAVNYFSVKQLPLVKPYLRSVQNHNNKSVNESLNNLFITEEDY
QALRTSIDAYDNFDNISLAQRLEKHELIEFRRIAAYLFKG

>d1bpoa1_a.118.1.4 (A:331-487) Clathrin heavy-chain linker domain {Rat (Rattus norvegicus)}
EENIIPYITNVLQNPPDLALRMAVRNNLAGAEELFARKFNALFAQGNYSEAAKVAANAPKGILRTPDTIRRFQSVP
AQPGQTSPOLLQYFGILLDQGQLNKYESLELCRPVLQQGRKQLLEKWLKEDKLECSELGDLVKSVDPTLALSVYL
ANVPNK

>d1c9la1_a.118.1.4 (A:331-359) Clathrin heavy-chain linker domain {Rat (Rattus norvegicus)}
EENIIPYITNVLQNPPDLALRMAVRNNLAG

>d1lrv_a.118.1.5 (-) Leucine-rich repeat variant {Azotobacter vinelandii}
TPIGDCRVCFSRMSLLTGRCTPGDACPESGRQIDRRNNPHLAVQYLADPFWERRAIAVRYSPVEALTPLI
RDSDEVVRAVAYRLPREQLSALMFDEDREVRTVADRLPLEQLEQMAADRDLVRAYVQRIPPGRFLRFMR
DEDRQVRKLVAKRLPEESLGLMTQDPEPEVRRIVASRLRGDDLLELLHDPDWTVRLAAVEHASLEALRELDEPD
PEVRLAIGRL

>d1e8xa1_a.118.1.6 (A:525-725) Phosphoinositide 3-kinase (PI3K) helical domain {Pig (Sus scrofa)}

HPIALPKHRPTPDPEGDRVRAEMPNQLRKQLEAIATDPLNPLTAEDKELLWHFRYESLKDPKAYPKLFSSVKWG
QQEIVAKTYQLLAKREVWDQSALDVGLTMQLLDCNFSDENVRAIAVQKLESLEDDDVLYHLLQLVQAVKFEPY
HDSALARFLLKRLRNKRIGHFLFWFLRSEIAQSRHYQQRFAVILEAYLRGCG

>d1ib2a_a.118.1.8 (A:) Pumilio 1 {Human (Homo sapiens)}
GRSRLLLEDFRNNRYPNLQLREIAGHIMEFSQDQHGSRFIQLKLERATPAERQLVNEILQAAYQLMVDVFGNYVI
QKFFEGSLEQKLALAERIRGHVLSALQMVGCRVIQKALEFIPSDDQQNEMVRELDGHVLKCVKDQNGNHVV
QKCIECVQPQLQFIIDAFKGQVFALSTHPYGRVIQRILEHCLPDQTLPILEELHQHTEQLVQDQYGNVVIQHVL
EHGRPEDKSKIVAEIRGNVLVLSQHKFASNVEKCVTHASRTERAVLIDEVCTMNDGPHSALYTMMKDQYANY
VVQKMICVAEPGQRKIVMHKIRPHIA

>d1ho8a_a.118.1.9 (A:) Regulatory subunit H of the V-type ATPase {Baker's yeast (Saccharomyces cerevisiae)}

GATKILMDSTHFNEIRSIIRSRSAWDALARSEELSEIDASTAKALESILVKKNIGDGLSSNNAHSGFKVNGKTLIP
LIHLLSTDNECKSVQNLIAELLSSDKYGDDTVKFFQEDPKQLEQLFDVSLKGDFQTVLISGFNVVSLVQNGL
HNVKLVEKLLKNNNLINILQNIQMDTCYVCIRLLQELAVIPEYRDVIWLHEKKFMPTLFKILQRATDSQLATRIVA
TNSNHLGIQLQYHSLLIWLLTFNPVFANELVQKYLSDFLDLLKLVKITIKEVSRSLCISIILQCCSTRVKQHKKVIKQL
LLLGNALPTVQSLSERKYSDEELRQDISNLKEILENEYQELTSFDEYVAELDSKLLCSPPHVNGFWSDNIDEFK
KDNYKIFRQLIELLQAKVRNGDVNAKQEKKIIIQVALNDITHVVELLPESIDVLDKTGGKADIMELLNHSDSRVKYE
ALKATQAIIGYTFK

>d1ycsb1_a.118.2.1 (B:327-456) 53BP2 {Human (Homo sapiens)}

PLALLDSSLEGFDLVQRIIYEVDDPSLPNDEGITALHNAVCAGHTEIVKFLVQFGVNVAADSDGWTPLHCAA
SCNNVQVCKFLVESGAAVFAMTYSDMQTAADKCEEMEEGYTQCSQFLYGVQEKG

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

DLGKKLLEAARAGQDDEVRILMANGAPFTTDWLGTSPHLAAQYGHFSTTEVLLRAGVSRDARTKVDRTPLH
MAASEGHANIVEVLLKHGADVNAKDMKMTALHWATEHNHQEVVELLIKYGADVHTQSKFCFKTAFDISIDNG

NEDLAEILQ

>d1bd8__ a.118.2.1 (-) Cell cycle inhibitor p19ink4D {Human (Homo sapiens)}

RAGDRLSGAAARGDVQEVRLLLHRELVHPDALNRFGKTALQVMMFGSTIALELLKQGASPNVQDTSGTSPV
HDAARTGFLDTLKVLVEHGADVNPVDGTGALPIHLAVQEHTAVVSFLAAESDLHRRDARGLPLEALQRGA
QDLVDILQGHM

>d1blxb_ a.118.2.1 (B:) Cell cycle inhibitor p19ink4D {Mouse (Mus musculus)}

VCVGDRLSGAAARGDVQEVRLLLHRELVHPDALNRFGKTALQVMMFSPAVALELLKQGASPNVQDASGTSP
VHDAARTGFLDTLKVLVEHGADVNALDSTGSLPIHLAIREGHSSVVSFLAPESDLHHRDASGLTPLEALARQRGAQ
NLMDILQGHMMIP

>d1ihba_ a.118.2.1 (A:) p18ink4C(ink6) {Human (Homo sapiens)}

WGNELASAARGDLEQLTSLLQNNNVNAQNGFGRTALQVMKLNPEIARRLLLRGANPDLKDRTGFAVIHD
AARAGFLDTLQLLEFQADVNIEDNEGNLPLHLAAKEGHLRVVEFLVKHTASNVGHRNHKGDTACDLARLYGR
NEVVSLMQANG

>d1a5e__ a.118.2.1 (-) Cell cycle inhibitor p16ink4A {Human (Homo sapiens)}

MEPAAGSSMEPSADWLATAAAGRVEEVALLEAGANPNAPNSYGRRPIQVMMMG SARVAELLLLHGAEPNCADPATLTP
CADPATLTPVHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDAEELGH RDVARYLRAAAGGTRGSNHA
RIDAAEGPSDIPD

>d1bi7b_ a.118.2.1 (B:) Cell cycle inhibitor p16ink4A {Human (Homo sapiens)}

EPSADWLATAAAGRVEEVALLEAGANPNAPNSYGRRPIQVMMMG SARVAELLLLHGAEPNCADPATLTP
VHDAAREGFLDTLVVLHRAGARLDVRDAWGRLPVDAEELGH RDVARYLRAA

>d1iknd_ a.118.2.1 (D:) I-kappa-B-alpha {Human (Homo sapiens)}

DGDSFLHLAIHEEKALTMEVIRQVKGDLAFLNFQNLLQQTPLHLAVITNQPEIAEALLGAGCDPELRDFRGNTP
LHLACEQGCLASVGVLQSCTPHLHSILKATNYNGHTCLHLASIHYGLGIVELLVSLGADVNAQEPCNGRTALHL
AVDLQNPDLVSLLKCGADVNRVTYQGYSPYQLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTE

>d1k1aa_ a.118.2.1 (A:) bcl-3 {Human (Homo sapiens)}

EDGDTPLHIAVVQGNLPAVHRLVNLQQGGRELDIYNNLRQTPLHLAVITLPSVVRLLTAGASPMALDRHGQ
TA AHLACEHRSPTCLRALLDSAAPGTLDEARNYDGLTALHVAVNTECQETVQLLERGADIDAVDIKSGRSPLIH
AVENNLSLMVQLLQHG ANVN A QMYS GSSA LHSAS GRGLLPLV RSGA DSSLKNCHNDPLMVARSRRV
IDILRG

>d1myo__ a.118.2.1 (-) Myotrophin {Rat (Rattus norvegicus)}

MCDKEFMWALKNGDLDEVKDYVAKGEDVNRTLEGGRKPLHYADCGQLEILEFLLKGADINAPDKHHITPLL
SAVYEGHVSCVKLLSKGADKTVKGPDLTALEATDNQAIKALLQ

>d1sw6a_ a.118.2.1 (A:) Swi6 ankyrin-repeat fragment {Baker's yeast (Saccharomyces cerevisiae)}

GPIITFTHDLTSDFLSSPLKIMKALPSPVVNDNEQKMKLEAFLQRLFPEIQEMPTSNNDRSNSEGGSNNQQ
QQHVSFDSSLQEVNDAFPNTQLNLNIPVDEHGNPLHWLTSIANLELVKHLVKG SNR LYGD NMGE SCLVK AV
KSVNNYDSGT FE AL LDY LY PCL ILED SMN RTI LH III ITSG MTG CSAA KYY DIL MG WIV KK QN RP IQ SG T NE KE
SKPNDKNGERKDSILENLDLKWI ANMLNAQDSNGDTCLNIAARLGNISIVDALLDYGADPFIA NKSGL RP VDF
GAG

>d1dcqa1 a.118.2.1 (A:369-522) Pyk2-associated protein beta {Mouse (Mus musculus)}

ADTAAKLHSLCEAVKTRDIFGLLQAYADGVDLTEKIPLANGHEPDETALHLAVRSVDR TSLHIVDFLVQNSGNLDK
QTGKGSTALHYCC LTDNAECLKLLRGKASIEIANESGETPLDIAKRLKHEHCEELLTQALSGRFNSHVHVEYEW
LL

>d1pbv__ a.118.3.1 (-) Exchange factor ARNO {Human (Homo sapiens)}

ANE GS KTLQR NR KMAM GRKK FNMDPK KG IQFL VENELLQ NTPEE IARFL YKGE GLNK TAIGDYL GERE ELN LA V

LHAFVDLHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFAQRYCLCNPVGVFQSTDTCYVLSFAVIMLNTSL
HNPNVRDKPGLERFAMNRGINEGGDLPEELLRNLYDSIRNEPFKIP

>d1bc9_a.118.3.1 (-) Cytohesin-1/b2-1 {Human (Homo sapiens)}

MKNMQRNKQVAMGRKKFNMDPKKGIQFLIENDLLKNTCEDIAQFLYKGEGLNKAIGDYLGERDEFNIQVLH
AFVELHEFTDLNLVQALRQFLWSFRLPGEAQKIDRMMEAFAQRYCQCNCNGVFQSTDTCYVLSFAIIMLNTSLH
NPNVKDKPTVERFIAMNRGINDGGDLPEELLRNLYESIKNEPFKIPPELEHHHHHH

>d1qsa1_a.118.5.1 (A:1-450) 70 KDa soluble lytic transglycosylase (SLT70), superhelical domain
{Escherichia coli}

DSLDEQRSRYAQIKQAWDNRQMDVVEQMMMPGLKDYPYPLYRQITDDLMNQPAVTNFVRANPTLPPA
RTLQSRFVNELARREDWRGLLAFSPEKPGTTEACNCYYYAKWNTQSEAWQGAKEWLWTGKSQPNACDKLF
SVWRASGKQDPLAYLERIRLAMKAGNTGLTVLAGQMPADYQTIASAIISLANNPNTVLTFFARTTGATDFTRQ
MAAAVAFASVARQDAENARLMIPLAQAQQLNEDQIQLRDIVAWRLMGNDVTDEQAKWRDDAIMRSQSTS
LIERRVRMALGTGDRRGLNTWLARLPMEAKEKDEWRYWQADLLERGREAFAKEILHQLMQQRGFYPMVA
AQRIGEEYELKIDKAPQNVDALTQGPEMARVRELMYWNLDNTARSEWANLVSKSKTEQAQLARYAFNNQ
WWDSLVSQATIAGKLWDHLEERFP

>d1d8da_a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Rat (Rattus norvegicus)}

FLSLDSPTYVLYRDRAEWADIDPVQPQNDGPSPVVQIYSEKFRDVYDYFRAVLQRDERSERAFKLTRDAIELNAA
NYTVWHFRRVLLRSLQKDLQEEMNYIIIAIEEQPKNYQVWHHRRVLVEWLKDPSQELEFIADILNQDAKNYHA
WQHRQWVIQEFLWDNELQYVDQLLKEDVRNNNSVWNQRHFVISNTTGYSDRAVLEREVQYTLEMIKLVPHN
ESAUNYLKGILQDRGLSRYPNLLNQLLDLQPSHSSPYLIAFLVDIYEDMLENQCDNKEDILNKALELCEILAKEKD
TIRKEYWRYIGRSLQSKHSRESDIPAV

>d1jcqa_a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Human (Homo sapiens)}

FVSLDSPSYVLYRDRAEWADIDPVQPQNDGPNPVVQIYSDKFRDVYDYFRAVLQRDERSERAFKLTRDAIELNAA
NYTVWHFRRVLLKSLQKDLHEEMNYITAIIEEQPKNYQVWHHRRVLVEWLKDPSQELEFIADILNQDAKNYHA
WQHRQWVIQEFLWDNELQYVDQLLKEDVRNNNSVWNQRHFVISNTTGYNDRAVLEREVQYTLEMIKLVPHN
ESAUNYLKGILQDRGLSKYPNLLNQLLDLQPSHSSPYLIAFLVDIYEDMLENQCDNKEDILNKALELCEILAKEKD
TIRKEYWRYIGRSLQSKH

>d1dcea1_a.118.6.1 (A:1-240,A:351-443) Rab geranylgeranyltransferase alpha-subunit, N-terminal
domain {Rat (Rattus norvegicus)}

MHGRLKVKTSEEQAEAKRLEREQKLKYQSATQAVFQKRQAGELDESVLELTSQILGANPDFATLWNCRREVLQ
HLETEKSPEESAALVKAELGFESCLRVNPKSYGTWHHRCWLLSRLPEPNWARELELCARFLEADERNFHCWDY
RRFVAQAAVAPAAELAFTDSLITRNFNSYSSWHYRSCLLGPLHPQPDSGPQGRLPENVLLKELELVQNAFFTDP
NDQSAWFYHRWLLGRAEXLFRCELSVEKSTVLQSELESCKELQELEPENKWCLTIILLMRALDPLLKEKTLQYFS
TLKAVDPMRAAYLDDLRSKFLENSVLKMEYADV

>d1qjba_a.118.7.1 (A:) zeta isoform {Human (Homo sapiens)}

MDKNELVQKAKLAEQAERYDDMAACMKSVTEQGAELSNEERNLLSVAYKVVGARRSSWRVVSSIEQKTEG
AEKKQQMAREYREKIETLRDICNDVLSLEKFLIPNASQAESKVFLKMKGDDYYRYLAEVAAGDDKKGIVDQSQ
QAYQEAFEISKKEMQPTHPIRLGLALNFSVFYYEILNSPEKACSLAKTAFDEAIAELDTLSEESYKDSTLIMQLLRDN
LTLWTSDT

>d1a17_a.118.8.1 (-) Protein phosphatase 5 {Human (Homo sapiens)}

PPADGALKRAEELKTQANDYFKAKDYENAIFYSQAIENPSNAYYGNRSLAYLRTECYGYALGDATRAIELDKY
IKGYYRRAASNMALGKFRAALRDYETVVVKVPHDKDAKMKYQECNKIVKQKAFERAIAGDEHKRSVVDSDLIES
MTIEDEYS

>d1elra_a.118.8.1 (A:) Hop {Human (Homo sapiens)}

GKQALKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMITYITNQAAVYFEKGDYNKCRELCEKAIEVGRENRED
YRQIAKAYARIGNSYFKEEKYKDAIFYNKSLAEHRTPDVLKKCQQAEKILKEQ

>d1elwa_a.118.8.1 (A:) Hop {Human (Homo sapiens)}

EQVNELEKGNKALSVGNIDDALQCYSEAIKLDPHNHVLYSNRSAAYAKKGDYQKAYEDGCKTVDLKPDWGKG
YSRKAAALEFLNRFFEAkRTYEEGLKHEANNPQLKEGLQNMEAR

>d1qqea_a.118.8.1 (A:) Vesicular transport protein sec17 {Baker's yeast (Saccharomyces cerevisiae)}

ISDPVELLKRAEKKGPSSGFMKLFGSDSYKFEEAADLCVQAATIYRLKELNLAGDSFLKAADYQKKAGNEDE
AGNTYVEAYKCFKSGGNSVNAVDSENQIIFTHRGQFRGANFKFELGEILENDLHDYAKAIDCYELAGEWYA
QDQSVALSNKCFIKCADLKALDGQYIEASDIYSKLICKSSMGNRLSQWSLKDYLKKGLCQLAATDAVAARTLQE
GQSEDPNFADSRESNFLKSLIDAVNEGDSLQSEHCKEFDNFMRDKWKITLNKIKESIQQQEDD

>d1hh8a_a.118.8.1 (A:) Neutrophil cytosolic factor 2 (NCF-2, p67-phox) {Human (Homo sapiens)}

SLVEAISLWNEGVLAAKDKDWKGALDAFSAVQDPHSRICFNIGCMYTILKNMTEAEKAFTRSINRDKHLAVAYF
QRGMILYYQTEKYDLAIKDLKEALIQLRGNQLIDYKILGLQFKLFACEVLYNIAFMYAKKEEWKKAEEQLALATSMK
SEPRHSKIDKAMCEVWKQKLYEPVVIPVGRFLRPNERQVAQL

>d1fcha_a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Human (Homo sapiens)}

SATYDKGYQFEEENPLRDHPQPFE EGLRLQEGDLPNAVLLFEAAVQQDPKHM EAWQYL GTTQAENEQELLAI
SALRRCLELKPDNQTALMALAVSFTNESLQRQACEILRDWLRYTPAYAHVTPAEEGAGGA GLGPSKRILGSLLSD
SLFLEVKEFLA A VRLDPTSIDPDVQCGLGVLFNLNGEYDKAVDCFTAALSVRPN DYLWNLGATLANGNQSEE
AVAAYRRALELQPGYIRSRYNL GISCI NLGAH REAVEHF LEAL NMQRKSRGPRGE GGAMSENIWSTLRLALSML
GQSDAYGAADARDLSTLLTMFGLPQ

>d1hxia_a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Trypanosoma brucei}

NNTDYPFEANNPYMYHENPMEEGLSMLKLANLAEALAFEAVCQKEPEREEAWRSLGLTQAENEKDGLAIIAL
NHARMLDPKDIAVHAALAVSHTNEHNANAALASRAWLL

>d1ihga1_a.118.8.1 (A:197-365) Cyclophilin 40 {Cow (Bos taurus)}

GSGDSHPDFPEDADVDLKDVKILLISEDLKNIGNTFKSQNWE MAIKKYTKVLRYVEGSRAAAEDADGAKLQ
PVALSCVLNIGACKLMSDWQGAVDSCLE ALIDPSNTKALYRRAQGWQGLKEYDQALADLKKAQEIAPEDKA
IQAELLKVQKQKIKAQKDKEKAAY

>d1iipa1_a.118.8.1 (A:197-298) Cyclophilin 40 {Cow (Bos taurus)}

GSGDSHPDFPEDADVDLKDVKILLISEDLKNIGNTFKSQNWE MAIKKYTKVLRYVEGSRAAAEDADGAKLQ
PVALSCVLNIGACKLMSDWQGAVDSCLE

>d1hz4a_a.118.8.2 (A:) Transcription factor MafT domain III {Escherichia coli}

EIKDIREDTMHAEFNALRAQVAINDGNPDEAERLAKLAEE LPPGFYSRIVATS VLGEVLHCKGELTRSLALMQ
QTEQM ARQHDVWHYALWSLIQQSEILFAQGFLQTA WETQEKA FQLINEQHLEQLPMHEFLVRIRAQLLWA
ARLDEAEASARSGIEVLSSYQPQQQLQCLAMIQLCSLARGDLDNARS QLNRL ENLLGNGKYHSDWIS NANKVR
VIYWMQMTGDKAAAANWLRHTAKPEFANNHFLQGQWRNIARAQILLGEFEP AEIVLEELNENARSLRLMSDLN
RNLLLLNQLYWQAGR KSDAQ RVLLDALK LANRTGFISHF VIEGEAMA QQLRQLIQLNLTPELEQHRAQRILREIN

>d1eyha_a.118.9.1 (A:) Epsin 1 {Rat (Rattus norvegicus)}

HN YSEAEIKVREATSNDPWGPSSLMSEIADLT NVVAFSEIMSMIWKRLNDHGKNWRHVYKAMTLMEYLIK
TGSERVSQQCKENMYAVQTLKDFQYVDRDGKDQGVNVREKAKQLVALLRDEDRLREERA HALKTKEKLAQTA

>d1inza_a.118.9.1 (A:) Epsin 1 {Human (Homo sapiens)}

GSSRMSTSSLRRQMKNIVHNYSEAEIKVREATSNDPWGPSSLMSEIADLT NVVAFSEIMSMIWKRLNDHGK

NWRHVYKAMTLMEYLIKTGSERVSQQCKENMYAVQTLKDFQYVDRDGKDQGVNVREKAKQLVALLRDEDRL
REER

>d1dvpal a.118.9.2 (A:1-145) Hrs {Fruit fly (Drosophila melanogaster)}

MFRSSFCNKLENATSHLRLEPDWPSILLICDEINQKDVTPKNAFAAIKKMNSPNPHSSCYSLVLESIVKNCGAP
VHEEVFTKENCEMFSSFESTPHENVRQMELVQTWAYAFRSSDKYQAIKDTMTILKAGHTFPELRE

>d1elka_a.118.9.2 (A:) Tom1 protein {Human (Homo sapiens)}

SDFLLGNPFSVPVGQRIEKATDGLSQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNKNFHEVMLALTVE
TCVKNCGHRFHVLVASQDFVESVLVRTILPKNNPPTIVHDKVNLIQSWADAFRSSPDLTVVTTIYEDLRRKGLEF
PM

>d1juqa_a.118.9.2 (A:) Gga3 {Human (Homo sapiens)}

ESLESWLNKATNPSNRQEDWEYIIGFCQINKELEGPQIAVRLLAHKIQSPQEWEALQALTVEACMKNCGRFF
HNEVGKFRFLNELIKVVSPKYLGDRVSEKVTKVIELLYSWTMALPEEAKIKDAYHMLKRQGIVQSDDPIPVDRTL
I

>d1hf8a_a.118.10.1 (A:) Clathrin assembly lymphoid myeloid leukaemia protein, Calm {Rat (Rattus norvegicus)}

GSAVSKTVCKATTHEIMGPKKKHLDYLIQCTNEMNVNIPQLADSLFERTTNSSWWVFKSLITTHLMVYGN
FIQYLASRNTLFNLSNFLDKSGLQGYDMSTFIRRYSYRQLNEKAWSYRQVAFDFTVKRGADGVMRTMNTEKLLK
TVPIIQNQMDALLDFNVNSNELTNGVINAAMFLLFKDAIRLFAAYNEGIINLEKYFDMKKNQCKEGLDIYKKFLT
RMTRISEFLKVAEQVGIDRGDIPDLSQAPSSLDALEQH

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

QGLAKSVCKATTEECIGPKKKHLDYLVHCANEPMVSIPHANLLIERSQNANVVYKSLITTHLMAYGN
MQYLASSNSTFLNLSFLDKGTQDGGMGVPGRMGYDMSPFIRRYAKYLNEKSLSYRAMAFDFCKVKRGKEE
GSLRSMNAEKLLKTLPVLAQQLDALLEFDQCSNDSNGVINMSFMLLFRDLIRLFACYN
HARDALDLYKKFLVVRMDRVGEFLKVAENVGIDKGIDPDLTAKPSSLDALEQH
LATL

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

TDLSTFLSFPSPEKLLRLGPKVSVLIVQQTDTSPEKVVSAFLKVASVFRDDASVKTAVLDAIDALMKKAFSCSSFN
SNTFLTRLLIHMGLLKSEDKIKAIPLSHGPLMVLNHVVQRQDYFPKALAPLLAFVTKPNGALETCFSFARHNLLQTL
YNI

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

ARFRKVDVDEYDENKFVDEDDGGDGQAGPDEGEVDSCRLQGNMTAALQAAALKNPPINTKSQAVKDRAGSIV
LKVLISFKANDIEKAVQSLDKNGVDLLMKYIYKGFESP
DNSSAVLHQWHEKALAAGGVGSIVRVLTARKTV

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

SHGSHETDEEFDARWTVYFNKP
DIDAWELRKGMNTLVGYDLVPEPKIIDAALRACRRLNDFASA
VAVRILEVVKDK
AGPHKEIYPYVIQELRPTLNELGISTPEELGLDKV

>d1f8na1 a.119.1.1 (A:150-839) Lipoxigenase, C-terminal domain {Soybean (Glycine max), isozyme L1}

VPSETPAPLVSYREEELKSLRGNGTGERKEYDRIYDYDVNDLGNPDKSEKLARPVLGGSSTFPYPRRGRTGRGP
TVTDPNTEKQGEVYVPRDENLGHLSKDALEIGTKLSQIVQPAFESA
FDLKSTPIEFHSFQDVHDLYEGGIKLPR
DVISTIPLVIKELYRTDGQHILKFPQPHVVQVSQSA
WTDEEFAREMIAGVN
PCVIRGLEEFPPKSNL
DPAIYGDQSSKITADSL
LDGYTMDEALGS
RRLFMLDYH
DIFMPYVRQIN
QLNSAKTYAT
RTILFREDGTL
KPV
AI
ELSLP
HSAGDLS
AAVSQ
VVLPA
KEGV
ESTIW
LLAKAY
VIV
NDSCYH
QLMSH
WLNT
HAAMEPF
VIATHR
HLSVL
HPIYKL
LTPHYRN
NMN
N
ALAR
QSL
INANG
IIETT
FLPSK
YSV
EMSSA
V
YKN
W
V
FTD
QAL
PAD
LIK
RGVA
IKDP
STPH
GVR
LLIED
PYAAD
GLEI
WAA
KTW
V
QEY
V
PLY
Y
AR
DD
DV
K
N
D
SEL
QH
WW
KEA
VEK
GHG
DLK
DKP
WW
PKL
QTL

DLVEVCLIIIWIASALHAAVNFGQYPYGGILIMNRPTASRRLPEKGTPEYEEMINNHEKAYLRTITSKLPLTLISL��
ILSTHASDEVYLGQRDNPHWTSDSKALQAFQKFGNKLKEIEEKLVRRNNDPSLQGNRLGPVQLPYTLLYSSEEG
LTFRGIPNSI

>d1ik3a1 a.119.1.1 (A:168-857) Lipoxigenase, C-terminal domain {Soybean (Glycine max), isoyme L3}

LPSETPAPLVKYREEELHNLRGDGTGERKEWERIYDYDVYNDLGDPDKGENHARPVLGGNDTFPYPRRGRTGR
KPTRKDPNSESRSNDVYLPDDEAFGHLSSDFLTYGLKSQNVLPQQSAFDLNFTPREFDSFDEVHGLYSGGIK
LPTDIISKISPLPVLEIFRTDGEQALKFPPPQVIQVSKSAWMTDEFAREMLAGVNPNLIRCLKDFPPRSKLDQSQV
YGDHTSQTKEHLEPNLEGTVDEAIQNKRFLLLDHDPIMPYLRRINATSTKAYATRILFLKNDGTLRPLAIELSL
PHPQGDQSGAFSQVFLPADEGVESIWLAKAYVVVNDSCYHQLVSHWLNTHAVVEPFIIATNRHLSVVHPIYK
LLHPHYRDTMNINGLARLSLVNDGGVIEQTFLWGRYSVEMSAVYKDWWFTDQALPADLIKRGMAIEDPSCP
HGIRLVIEDPYTVDGLEIWDIAKTVVHEYVFLYKSDDTLREDPELQACWKELEVGHGDKKNEPWWPKMQ
TREELVEACIIIWTASALHAAVNFGQYPYGGILNRPLTSRRFMPEKGSAEYELRKNPQKAYLKTITPKFQTLID
LSVIEILSRHASDEVYLGERDNPNTSDTRALEAFKRGNKLAQIENKLSERNNDEKLRNRCGPVQMPYTLPS
SKEGLTFRGIPNSI

>d1lox_1 a.119.1.2 (113-663) 15-Lipoxygenase {Rabbit (Oryctolagus cuniculus)}

TGCTTVGDPQGLFQKHREQELEERRKLYQWGSWKEGLILNVAGSKLTDLPVDERFLEDKKIDFEASLAWGLAEL
ALKNSLNLAPWKTDDFNRFWCGRSKLARRVRDWSQEDSLFGYQFLNGANPMLLRRSVQLPARLVFPGM
EELQAQLEKELKAGTLFEADFALLNIKANVILYCQQYLAAPLVMKLQPDGKLMPMVQIQLHLPKIGSSPPPLFLP
TDPPMVWLLAKCWVRSSDFQVHELNSSLRGHLMAEVFTVATMRCPLSIHPVFKLIVPHLRYTLEINVRARNG
LVSDFGIFDQIMSTGGGGHVQLQQAGAFLTYSFCPPDDLADRGLLGESSFYAQDALRLWEIISRYVQGIMG
LYYKTDEAVRDDLELQSWCREITEIGLQGAQKQGFPTSLQSVAQACHFVTMCIFTCTGQHSSIHLGQLDWFTW
VPNAPCTMRLPPPPTKDATLETVMATPNLKQSSLQMSIVWQLGRDQPIMVPLGQHQEEYFSGPEPRAVLEK
FREELAIMDKEIEVRNEKLDIPYEYLPSIVENSAI

>d1c1ka_ a.120.1.1 (A:) gene 59 helicase assembly protein {Bacteriophage T4}

MIKLRMPAGGERYIDGKSVYKLYLMIKQHMNGKYDVKYNWCMRVSDAAYQKRRDKYFFQKLSEKYKLKELALI
FISNLVANQDAWIGDISDADALVFYREYIGRLKQIKFKFEEDIRNIYYFSKKVEVS AFKEIFEYNPKVQSSYIFKLLQS
NIISFETFILDSFLNIIIDKHDEQTDNLVWNNSIKLKAYRKILNIDSQKAKNVFIETVKSCKY

>d2tct_2 a.121.1.1 (68-208) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}

LPAAGESWQSFLRNNA MSFR ALLRYRDGAKVHLGTRPDEKQYDVTETQLRFMTENGFSLRDGLYAISAVSHF
TLGAVLEQQEHTAALTDRPAAPDENLPPLLREALQIMDSDDGEQAF LHGLESLIRGFEVQLTALLQIV

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

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

VSWDSLPELLLGIFSCLCLPELLKVSGVCKRWYRLASD

>d1fqvb1 a.122.1.1 (B:85-160) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}

IPVWDQEFLKVDQGTLFELILA ANYLDIKGLLDVTCKTVANMIKGKTPPEIRKTFNIKNDFTEEE AQRKENQWC

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

WDSLPELLLGIFSCLCLPELLKVSGVCKRWYRLASDES

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

PVWDQEFLKVDQGTLFELILA ANYLDIKGLLDVTCKTVANMIKGKTPPEIRKTFN

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

KRTDDIPVWDQEFLKVDQGTLFELILAANYLDIKGLDVCKTVANMIKGKTPEEIRKTFNIKNDFT
>d1g5ya_a.123.1.1 (A:) Retinoid-X receptor (RXR-alpha) {Human (Homo sapiens)}
PVERILEAELAVEPKTETYVEANMGLNPSSPNDPVTCQAAQDKQLFTLVEWAKRIPHSELPLDDQVILLRAGWNELLIASFSHRSIAVKDGILLATGLHVHRNSAHSAGVGAIFDRVLTTELVKMRDMQMIDKTELGCLRAIVLFNPDSKGLSNPAEVEALREKVASYASLEAYCKHKYPEQPGRFACKLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEAP
>d1dkfb_a.123.1.1 (B:) Retinoic acid receptor alpha (RAR-alpha) {Human (Homo sapiens)}
PEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLIDLWDFKSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDTMTFSDGLTNRTQMHNAGFGPLTDLVFAFANQLPLEMDDAETGLLSAICLICGDRQDLEQPDRVDMQLQEPILLEALKVYVRKRRPSRPHMFPMKMLMKITDLRSISAKGAERVITLKMEIPGSMPLI
QEMILEN
>d1fcya_a.123.1.1 (A:) Retinoic acid receptor gamma (RAR-gamma) {Human (Homo sapiens)}
ASPQLEELITKVSKAHQETFPSLCQLGKYTTNNSSADHRVQLDLGLWDKFSELATKCIIKIVEFAKRLPGFTGLSIADQTLLKAACLDILMLRICTRYTPEQDTMTFSDGLTNRTQMHNAGFGPLTDLVFAFAGQLPLEMDDTETGLLSAICLICGDRMDLEEPEKVDKLQEPILLEALKRLYARRRPSQPYMFPRMLMKITDLRGISTKGAERAITLKMEIPGPM
PPLIREMLE
>d1a28a_a.123.1.1 (A:) Progesterone receptor {Human (Homo sapiens)}
QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSLLTSLNQLGERQLLSVVKWSKSLPGFRNLHIDDQITLIQYSWMSLMVFLGLWRSYKHVGQMLYFAPDYLNEQRMKESSFYSLCLTMWQIPQEFVKLQVSQEEFLCMKVLLLLNTIPL
EGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVSSSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVFPEMMSEVIAAQLPKILAGMVKPPLL
FH
>d3erda_a.123.1.1 (A:) Estrogen receptor alpha {Human (Homo sapiens)}
SLALSLTADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELVHMINWAKRVPGFVDLTLHDQVHL
LECAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKCVEGMVEIFDMLLATSSRFRMMNLQGEEFVCLKSII
LLNSGVYTFLSSTLKSLEEKDHIIHRVLDKITDTLIELMAKAGLTLQQQHQRLAQLLLILSHIRHMSNKGMELYSMKCKNVV
VPLYDLLLEMDAHRLH
>d1qkma_a.123.1.1 (A:) Estrogen receptor beta {Human (Homo sapiens)}
LDALSPEQLVLTLEAEPPHVLSRPSAPTEASMMMSLTKLADKELVHMISWAKKIPGFVELSLFDQVRLL
ESCWMEVLMGGMWMRSIDHPGKLI
FAPDLVLDREGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLN
SSMYPLVTATQDADSSRKLAHLLNAVTDALWVIAKSGISSQQSMRLANLLM
LLSHVRHASNKGMELLN
MKCKNVVPVYD
LLLEM
LNAHVL
>d1qkna_a.123.1.1 (A:) Estrogen receptor beta {Rat (Rattus norvegicus)}
TLSPEQLVLTLEAEPPNVLSRPSMPFTEASMMMSLTKLADKELVHMIGWAKKIPGFVELSLLDQVRLL
ESCWMEVLMVGLMWRSIDHPGKLI
FAPDLVLDREGKCVEGILEIFDMLLATTSRFRELKLQHKEYLCVKAMILLN
SSMYPLASANQEAESSRKLT
HLLNAVTDALWVIAKSGISSQQSVRLANLLM
LLSHVRHISNKGMELLS
MKCKNVVPVYD
LLLEM
LNA
>d1i37a_a.123.1.1 (A:) Androgen receptor {Rat (Rattus norvegicus)}
IFLNVLEAIEPGVVCAGHDNNQ
PDSFAALLSSLNELGERQLV
HVV
KWA
LP
GFRNL
HV
DDQ
MA
VI
QYS
WM
GLMVFAMGWR
SFTNV
NSRM
IYFAP
DLV
NEYR
MHKS
RMY
SQCV
RM
RHS
LQ
SEFG
WL
QITP
QEFL
CMK
ALL
FSIIP
VDGL
KNQ
KFF
DELR
MN
YIK
ELD
RI
IAC
KR
KN
PTCS
RR
FY
QLT
KLL
DSV
QPI
ARE
LHQ
FTFD
LLIK
SHMV
SF
DFPE
MMA
EI
ISV
QVP
KIL
SGK
VK
KPI
YF
>d1k7la_a.123.1.1 (A:) Peroxisome proliferator activated receptor alpha, PPAR-alpha {Human (Homo sapiens)}
DLKSLAKRIYEAYLKNFNMNKVKARVILSGKASNNPPFV
IHDMETLCMAEK
TLV
AKL
VANG
IQN
KEAV
RIFHCC
QCTS
VET
VTEL
TEFA
KAIP
GF
FAN
LD
NDQ
V
TLL
K
Y
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F

CDIMEPKFDAMKFNALELDDSDISLFVAAIICCGDRPGLLNVGHIEMQEGIVHVLRLHLQSNHPDDIFLPKLL
QKMADLRQLVTEHAQLVQIIKKTESDAALHPLLQEYRDMY
>d2prga_a.123.1.1 (A:) Peroxisome proliferator activated receptor gamma, PPAR-gamma {Human (Homo sapiens)}
ESADLRALAKHYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHITPLQEKSKEVAIRIFQ
GCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIYTMLASLMNKDGVLISEGQGFMTRFLKSLRK
PFGDFMEPKFEFAVKFNAALELDDSDLAIFIAVIILSGDRPGLLNVKPIEDIQDNLLQALELQLKLNHPESQLFAKLL
QKMTDLRQIVTEHVQLQVIKKTETDMSLHPLLQEYKDLY
>d2gwxa_a.123.1.1 (A:) Peroxisome proliferator-activated receptor delta, PPAR-DELTA {Human (Homo sapiens)}
LKAFSKHINYAYLKNFNMTKKKARSILTGKASHTAPFVIHDIETLWQAEGLVWKQLVNGLPPYKEISVHFYRCQ
CTTVETVRELTEFAKSIPSFSLLFLNDQVTLLKYGVHEAIFAMLASIVNKDGLLVANGSGFVTREFLRLRKPFSDIIE
PKFEFAVKFNAALELDDSDLAIFIAAIILCGDRPGLMNVPRVEAIQDTILRALEFHQLQANHPDAQQQLFPKLLQKMA
DLRQLVTEHAQMMPQRRIKKTETETSLHPLLQEYKDM
>d1ilga_a.123.1.1 (A:) Pregnane x receptor, PXR {Human (Homo sapiens)}
GLTEEQRMMIRELMDAQMKTFDTFSHFKNFRLPGVLSGGCELPELSQAPSREEAAKWSQVRKDLCSLKVSLQ
LRGEDGSVWNYKPPADSGGKEIFSLLPHMADMSTYMFKGIIISFAKVISYFRDLPIEDQISLLKGAAFELCQLRFNT
VFNAETGTWECGRSLSYCLEDTAGGFQQLLEPMILKFHYMLKKQLHEEEYVLMQAISLFPDRPGVLQHRVVD
QLQEQQFAITLKSYIECNRPQPAHRLFNLKIMAMILTELRSINAQHTQRLLRIQDIHPFATPLMQELFGI
>d1ie9a_a.123.1.1 (A:) Vitamin D nuclear receptor {Human (Homo sapiens)}
DSLRLPKLSEEQQRIIAILDAHHKTYDPTYSDFCQFRPPRVNDGGSVTLELSQLSMLPHLADLVSYSIQKVIGF
AKMIPGFRDLTSEDQIVLLKSSAIEVIMLRSNESFTMDDMSWTCGNQDYKYRVDVTKAGHSLELIEPLIKFQVG
LKKLNLHEEEHVLLMAICIVSPDRPGVQDAALIEAIQDRLSNTLQTYIRCRRHPPPGSHLLYAKMIQKLADLRSLNE
EHSKQYRCLSFQPECMSKLTPLLEVFG
>d1bsxa_a.123.1.1 (A:) Thyroid hormone receptor beta (TR-beta) {Human (Homo sapiens)}
KPEPTDEEWELIKTVTEAHVATNAQGSHWKQKRKFPEDIGQAPIVNAPEGGKVDLEAFSHFTKIITPAITRVVD
FAKKLPMFCELPCEDQIILLKGCCMEIMSLRAAVRYDPESETTLNGEMAVTRGQLKNGGLGVVSDAIFDLGMS
LSSFNLDDEVALQAVLLMSSDRPGLACVERIEKYQDSFLAFAEHYINYRKHHVTHFWPKLLMKVTDLRMIGA
CHASRFLHMKVECPTELFPPFLLEVFGD
>d1hg4a_a.123.1.1 (A:) Ultraspiracle protein, usp {Drosophila melanogaster}
FSIERIIAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVSALCQVNVNQQLFQMVEYARMMPHFAQVPLDDQ
VILLKAALIELIANVAWSIVSLDDGGAGGGGGGLHDGSFERRSPGLQPQLFLNQSFSYHRNSAIAGVSA
IFDRILSELSVKMKRLNLDRELSCLKAIILYNPDIRGIKSRAEIMCREKVYACLDEHCRLEHPGDDGRFAQLLRL
PALRSISLKCQDHFLFRITSDRPLEELFLEQLEAPPPP
>d1g2na_a.123.1.1 (A:) Ultraspiracle protein, usp {Heliothis virescens}
AAVQELSIERLLEMESLVADPSEEFQFLRVGPDSNVPPKFRAPVSSLQIGNKQIAALVVWARDIPHFSQLEMED
QILLIKGSWNELLFAIAWRSMELTEERDGVDTGNRTTSPPQLMCLMPGMLHRNSALQAGVGQIFDRVLS
ELSLKMRTLVDQAEYVALKAIILLNPDVKGLKNRQEVEVLRKMFCLDEYCRRSRSSEGRFAALLRLPALRSI
SLKSFEHLFFFHLVADTSIAGYIRDALRNHA
>d1ah7_a.124.1.1 (-) Bacterial phospholipase C {Bacillus cereus}
WSAEDKHKEGVNSHLWIVNRAIDIMSNTLVKQDRVAQLNEWRTELENGIYAADYENPYDNSTFASHFYDP
DNGKTYIPFAKQAKETGAKYFKLAGESYKNKDMQAFFYLGLSLHYLGDNQPMHAANFTNLSYPQGFHSKYE
NFVDTIKDNYKVTDGNGYWNVWKGTNPEEWIHGAAVVAQDYSIVNDNTKDWVFVKAavsQeyADKWRAE
VTPMTGKRLMDAQRTAGYIQLWFDTYGDR

>d1ca1_1 a.124.1.1 (1-249) Alpha-toxin, N-terminal domain {Clostridium perfringens}
WDGKIDGTGTHAMIVTQGVSIENDLSKNEPESVRKNLEILKENMHELQLGSTYPDYDKNAYDLYQDHFWDP
DTDNNFSKDNWSWYLAYSIPDTGESQIRKFSALARYEWQRGNYKQATFYLGEAMHYFGDIDTPYHPANVTAVDS
AGHVKFETFAERKEQYKINTVGCKTNEDFYADILKNKDFNAWSKEYARGFAKTGKSIYYSHASMSHSDWD
YAAKVTLANSQKGTAGYIYRFLHDVSEGNDP

>d1ak0_ a.124.1.2 (-) P1 nuclease {Penicillium citrinum}
WGALGHATVAYVAQHYVSPEAASWAQGILGSSSSYLASIASWADEYRLTSAGKWSASLHFIDAEDNPPTNCN
VDYERDCGSSGCISAIANYTQRVSDSSLSENHAEARFLVHFIGDMTQPLHDEAYAVGGNKINVTFDGYHDN
LHSDWDTYMPQKLIGGHALSDAESWAKTLVQNIESGNYTAQAIGWIKGDNISEPITTTRWASDANALVCTVV
MPHGAAALQTGDLYPTYYDSVIDTIELQIAKGGYRLANWINEIH

>d1f0ja_ a.125.1.1 (A:) Catalytic domain of cyclic nucleotide phosphodiesterase 4b2b {Human (Homo sapiens)}
SISRGVNTENEDHLAKELEDLNKWGLNIFNVAGYSHNRPLTCIMYAIFQERDLLKTRISSDTITYMMTLEDHY
HSDVAYHNSLHAADVQAQSTHVLSTPALDAVFTDLEIAlAAIFAAAHVDHPGVSNQFLINTSELALMYNDES
LENHHHLAVGFKLLQEEHCDIFMNLTKKQRQTLRKVMDVLTMSKHMSLLADLKTMVETKKVTSSGVLLD
NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDDKHTASVEKSQVGFI
DIYVHPLWETWADLVQPDAQDILDLEDNRNWYQSMIPQAPAPPLDEQNRDCQGLMEKFQF

>d1gnia1 a.126.1.1 (A:3-196) Serum albumin {Human (Homo sapiens)}
HKSEVAHRFKDLGEENFKALVLIQAFAQYLOQQCPFEDHVKLVNEVTEFAKTCVADESAENCDKSLHTLFGDKLCTV
ATLRETYGEMADCCAKQEPPERNECFLQHKDDNPNLPRLVRPEVDVMCTAFHDNEETFLKYLYEIARRHPYFYA
PELLFFAKRYKAAFECCQAADKAACLLPKLDELRDEGKASSAKQ

>d1gnia2 a.126.1.1 (A:197-388) Serum albumin {Human (Homo sapiens)}
RLKCASLQKFGERAFAVARLSQRFPKAFAEVSKLVTDLTVHTECCHGDLLECADDRADLAKYICENQDSI
SSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVKNYAEAKDVFLGMFLYEYARRHPDYSVLLL
RLAKTYETTLEKCCAAADPHECYAKVFDEFKPLVEEPQNL

>d1gnia3 a.126.1.1 (A:389-584) Serum albumin {Human (Homo sapiens)}
KQNCELFEQLGEYKFQNALLVRYTKKVPQVSTPTLVEVRNLGKGSKCCKHPEAKRMPCAEDYLSVVLNQLCV
LHEKTPVSDRTVKCCTESVNRRPCFSALEVDETYVPKEFNAETFTFHADICTLSEKERQIKKQTALVELVHKPKA
TKEQLKAVMDDAAFVEKCCACKDGETCFACEEGKKLVAASQAALG

>d1j78a1 a.126.1.1 (A:13-198) Vitamin D binding protein {Human (Homo sapiens)}
CKEFSHLGKEDFTSLVLSRKFPSGTFEQVSQLKEVVSLTECCAEGADPDCYDRTSALSASKCESNSPFPVH
PGTAECCTKEGLERKLCMAALKHQPKQFPTYVEPTNDEICEAFRKDPKEYANQFMWEYSTNYGQAPLSLLSYT
KSYLSMVGSCCTSASAPTVCFKLKERLQLKHLSSLTT

>d1j78a2 a.126.1.1 (A:199-386) Vitamin D binding protein {Human (Homo sapiens)}
LSNRVCSEQYAYGEKKSRLSNIKLAQKVPTADLEDVPLAEDITNILSKCCESASEDCMAKELPEHTVKLCDNLST
KNSKFEDCCQEKTAMDVFVCTYFMPAAQLPELPVELPTNKDVCDPGNTKVMKDYTFELSRRTHLPEVFLSKV
LEPTLKLGECCDVDSTTCFNAKGPLLKKELSSFDK

>d1j78a3 a.126.1.1 (A:387-457) Vitamin D binding protein {Human (Homo sapiens)}
GQELCADYSENTFTEYKKKLAERLKAKLPDATPTELAKLVNKRSDFASNCCSINSPPLYCDSEIDAEKLNI

>d1jswa_ a.127.1.1 (A:) L-aspartate ammonia lyase {Escherichia coli}
MSNNIRIEEDLLGTRVPADAYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKAAAMANKELQTIPKSVAN
AIIAACDEVLNNGKCMDQFPDVYQGGAGTSVNMTNEVLANIGLELMGHQKGEYQYLNPNPDHVNKCQST
NDAYPTGFRIAVYSSLIKLDAINQLREGFERKAVEFQDILKMGRTQLQDAVPMTLQGEFRAFSILLKEEVKNIQ

TAELLLEVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPAEDLIEATSDCGAYVMVHGALKRALVKMSKICN
DLRLSSGPRAGLNEINLPELQAGSSIMPAKVNPVPEVVNVQVCFKVGNDTTVTMAAEAGQLQLNVMEPVIG
QAMFESVHILTNACYNLLEKCINGITANKEVCEGYVYNSIGIVTYLNPFIGHHNGDIVGKICAETGKSREVVLER
GLLTEAELDDIFSV

>d1jswc_a.127.1.1 (C:) L-aspartate ammonia lyase {Escherichia coli}

IRIEEDLLGTREVPADAYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKAAAMANKELQTIPKSVANAIAC
DEVLNNGKCMDQFPDVYQGGAGTSVNMTNEVLANIGLELMGHQKGEYQYLNPNHDVNKCQSTNDAYP
TGFRIAVYSSLIKLDAINQLREGFERKAVEFQDILKMGRQLQDAVPMTLGQEFRASFILLKEEVKNIQRTEALL
EVNLGATAIGTGLNTPKEYSPLAVKKLAEVTGFPCVPAEDLIEATSDCGAYVMVHGALKRALVKMSKICNDLRLS
SGPRAGLNEINLPELQAGSSIMPAKVNPVPEVVNVQVCFKVGNDTTVTMAAEAGQLQLNVMEPVIGQAMF
ESVHILTNACYNLLEKCINGITANKEVCEGYVYNSIGIVTYLNPF

>d1fura_a.127.1.1 (A:) Fumarase {Escherichia coli}

VRSEKDSMGAIDVPADKLWGAQTQRSLEHFRISTEKMPTS LIHALALT KRAAKVNEDLGLLSEEKASAIRQAAD
EVLAGQHDDEFPLAIWQTGSGTQSNNMNEVLANRASELLGGVRGMERKVHPNDDVNKSQSSNDVFPTA
MHVAALLALRKQLIPQLKLTQTLNEKSRAFADIVKIGRTNLQDATPLTGQEISGWVAMLEHNLKHEYSLPHVA
ELALGGTAVGTGLNTHPEYARRVADELAVITCAPFVTAPNKFEALATCDALVQAHGALKGLAASLMKIANDVRW
LASGPRCGIGEISIPENEPEGSSIMPGKVNPTQCEALTMCCQVMGNDVAINMGGASGNFELNVFRPMVIHNFL
QSVRLLADGMESFNKHCAVGIEPNRERINQLNESLMLVTALNTHIGYDKAAEIKAHKEGTLKAAALALGYL
SEAEFD SWVRPEQM

>d1yfm_a.127.1.1 (-) Fumarase {Baker's yeast (Saccharomyces cerevisiae)}

SFRTE TDAFGEIHVPADKYWGAQTQRSFQNFKIGGARERMPPLVHAFGVLKSAAI VNESLGGDPKISKAIQ
QAADEVASGKLDHFPLVVFTQSGTQSNNMNEVISNRAIEILGGKIGSKQVHPNNHCNQSQSSNDTFPTV
MHIAASLQIQNELIPELTNLKNALEAKSKEFDHV KIGRTHLQDATPLTGQEFSGYVQQVENGIQRVAHSLKTL
FLAQGGTAVGTGLNTKPGFDV KIAEQISKETGLFQTAPNRFEALAAHDAIVECS GALNTLACSLFKIAQDIRYL
SGPRCGYHEMLPENEPEGSSIMPGKVNPTQNEALTQCVQVMGNAAITFAGSQGQFELNVFKPVMIANLL
NSIRLITDAAYSFRVHCVEGIKANEPRIHELLTKSLMLVTALNP KIGYDAASKVAKNAHKKGITLKESALELGVLTEK
EFDEWVVPEHML

>d1k62a_a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Human (Homo sapiens)}

GAVDPIMEKFNASIAYDRHLWEVDVQGSKAYSRGLEKAGLLTKAEMDQILHGLDKVAEEWAQGTFKLSNDE
DIHTANERRLKE LIGATAGKLHTGRSRNDQVVTDLRLWMRQTCSTLSLLWEI RTMVDRAEAERDVLFGYTH
LQRAQPIRWSHWILSHAVALTRD SERLLEVRKRINVPLGSGAIAGNPLGV DRELLRAELNFGAITLNSMDATSE
RDFVAEFLFWRSCLCMTHLSRMAEDLILYCTKEFSVQLSDAYSTGSSLMPRKKNPDSLEIRSKAGR VFGRCAGLL
MTLKGLPSTYNKDLQEDKEAVFEVSDTMSAVLQVATGVISTLQIHQENMGQALSPDMI LATDLAYYLVRKGMPF
RQAHEASGKAVFMAETKGVALNQLSLQELQTISPLFSGDVICVWDYRHSVEQY GALGGTARSSVDWQIRQVR
ALLQAQQA

>d1auwa_a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas platyrhynchos), delta-crystallin}

TD PIMEKLNSSIAYDQRLSEVDI QGS MAYAKALEKAGILT KTELEKILSGLEKISEEW SKGV FVVKQSDEDINTANE
RRLKE LIGDIAGKLHTGRSRNDQVVTDLKL FMKNSL SIISTHLLQ LIKT LVERAAIEIDV LPGY THLQKAQPIRWSQ
FLLSHAVALTRD SERLGEVKKRINVPLGSGALAGNPL DIDREMLRSELE FASISL NSMDAISERDFV VEFLSFATLL
MIHLSKMAEDLIIYSTSEFGFLTSDAFTGSSLMPKKNPDSLEIRSKAGR VFGRLASILMVLKGLPSTYNKDLQ
EDKEAVFDVVD TLA LQVATGVISTLQISKENMEKALTPEM IATL ALY LVRKGVPFRQAHTASGKAVH LAETK
GITINKL SLEDLK SISPQFSS DVSVQVFNFVN SVEQY TALGGTAKSSVTTQIEQLRELMKKQK

>d1dcnb_a.127.1.1 (B:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas

platyrhynchos), delta-crystallin}

DPIMAKLNSSIAYDQRLEVDIQGSMAYAKALEKAGILTTELAKILSGLEKISEEDIHTANERRLKEIGDIAGKLN
TGRSRNDQVVTDLKLFMKNLSIISTHLLQLIKTLVERAAIEIDVILPGYTNLQKAQPIRWSQFLLSHAVALTRDSE
LGEVKKRINVLPLGSGALAGNPLIDREMLRSELEFASISLNSMDAISERDFVVEFLSFATLLMIHLSKMAEDLIYS
TSEFGFLTLSPDSLEIRSKSGRVFGRLASILMVLKGLPSTYNKDLQEDKEAVFDVVDTLAVLQVATGVISTLQISKE
NMEKALTPEMLATDLALYLVRKGVPFRQAHTASGKAVHLAETKGITINNLSEDLKSIISPQFSSDVSVNFVNSV
EQYTALGGTAKSSVTTQIEQLRELMKKQK

>d1hy0a_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Domestic duck (Anas platyrhynchos), delta-crystallin}

DPIMQMLSTSISTEQRLEVDIQASIAYAKALEKAGILTTELEKILSGLEKISEELSKGVIVVTQSDEDIQTANERRL
KEIGDIAGKLHTGRSRNEQVVTDLKLFMKNLSIISTHLLQLIKTLVERAAIEIDVILPGYTHLQKAQPIRWSQFL
SHAVALTRDSERLGEVKKRINVLPLGSGALAGNPLIDREMLRSELEFASISLNSMDAISERDFVVEFLSVATLLIH
LSKMAEDLIYSTSEFGFLTLSADFSTGSSLMPQKKNPDSLEIRSKSGRVFGRLASILMVLKGLPSTYNKDLQEDK
EAVIDVVDTLTAVLQVATGVISTLQISKENMEKALTPEMLATDLALYLVRKGMPFRQAHTASGKAVHLAETKGIA
NNLTLEDLKSIPLFSSDVSVQVFNFVNSVEQYTALGGTAKSSVTTQIEQLRELMKKQK

>d1i0aa_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Turkey (Meleagris gallopavo), delta-crystallin}

GRFVGSDPIMEILSSISTEQRLEVDIQASMYAKALEKASILTTELEKILSGLEKISEESSKGVLVMTQSDEDIQ
TAIERRLKEIGDIAGKLQTGRSRNEQVVTDLKLLLKSSISVISTHLLQLIKTLVERAAIEIDIIMPGYTHLQKALPIRW
SQFLLSHAVALTRDSERLGEVKKRITVLPNGSVLAGNPLEIDRELLRSELDMTSITLNSIDAISERDFVVELISVATL
LMIHLSKLAEDLIIFSTTEFGFTLSDAYSTGSSLMPQKKNPDSLEIRSKAGR VFGRLAAILMVLKGIPSTFSKDLQE
DKEAVLDVVDTLTAVLQVATGVISTLQINKENMEKALTPELLSTDALYLVRKGMPFRQAHTASGKAVHLAETKG
TINNLITEDLKSIPLFASDVSVQFVVNSVEQYTAVGGTAKSSVTAQIEQLRELLKKQK

>d1c3ca_ a.127.1.1 (A:) Adenylosuccinate lyase {Thermotoga maritima}

VERYSLSPMKDLWTEEAKYRRWLEVELAVTRAYEELGMIPKGVTTERIRNNAIDVELFKIEEKTNHDVVAFVEG
IGSMIGEDSRFFHYGLTSSDVLDTANSALVEAGKILLESLKEFCDVWEVANRYKHTPTIGRTHGVHAEPSTFGL
KVLGWYSEMKRNVQRleraieevsygkisgavgnyanvppeveekalsylglkpepvstqvprdrhafylstl
AIVAAGIERIAVEIRHLQRTEVLEVEEPFRKGQRGSSAMPHKKNPITCERLTGLSRMMRAYVDPSENIALWHER
DISHSSVERYVFPDATQTLYYMIVTATNVVRNMKVNEERMKKNIDLTKGLVFSQRVLLKIEKGLTRKEAYDIVQR
NALKTWNSEKHFLLEYDEEVKKLVTKEELEELFDISYYLKHVDFERFEK

>d1dofa_ a.127.1.1 (A:) Adenylosuccinate lyase {Archaeon Pyrobaculum aerophilum}

HVSPFDWRYGSEEIRRIFTNEAIINAYLEVERALCAELGVAERGCCEVKVNKAWSADEVYRLERETGHDILSLV
LLLEQKSGCRYVHYGATSNDIIDTAWALLIRRALAAVKEKARAVGDQLASMARKYKTLEMVGRTHGQWAEPITL
GKFANYYYELYIACRQLALAEEFIRAKIGGAVGTMASWGEGLGEVRRVAAERLGLPHHVITTQVAPRESFAVLAS
ALALMAAVFERLAVEIRELSRPEIGEVVEGGGGSSAMPHKANPTASERIVSLARYVRALTHVAFENVALWHERD
LTNSANERVWIPEALLALDEILTSALRVLKNVYIDEERITENLQKALPYILTEFHMNRMKIGEGASRAEAYKKA
ALTFEYQKWPVERLIEDALSLKLC

>d1f1oa_ a.127.1.1 (A:) Adenylosuccinate lyase {Bacillus subtilis}

EMSAIWTDENRFQAWLEVEILACEAWAELGVIPKEDVKVMRENASFIDINRILEIEKDTRHDVVAFTRAVSES
EERKWVHYGLTSDVVTDLASYLLQANDILLKDLERFVDIIKEAKEHKYTVMGRTHGVHAEPPTFGLKLA
WHEEMKRNLERFKQAKAGIEVGKISGAVGTYANIDPFVEQYVCEKGLKA
TSIEKFAVEIRGLQKSETREVEEFFAKGQKGSSAMPHKRNP
SHSSAERIIPLDATIALNYMLNRSNIVKNLTVFPENMKRNMDRTLGLIYSQRVLLALIDTGLTREEAYDTVQPKA
MEAWEKQVPFRELVEAEKITSRLSPEKIACDFDNY

>d1gk2a_a.127.1.2 (A:) Histidine ammonia-lyase (HAL) {Pseudomonas putida}
TELTLKPGTLAQLRAIHAAPVRLQLDASAAPAIDASVACVEQIIAEDRTAYGINTGFGLLASTRIASHDLENLQRS
LVLSHAAGIGAPLDDDLVRLIMVLKINSLSRGFSGIRRKVIDALIALVNAEVYPHIPLKGSGDLAPLAHMSLV
LLGEKGKARYKGQWLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSVEAVLG
SRSPFDARIHEARGQRGQIDTAACFRDLLGDSSEVLSHKNADKVQDPYSLRCQPQVMGACLTQLRQAAEVLG
IEANAVSDNPLVFAAEVDVISGGNGHAEPVAMAADNLALALIAEIGSLSERISLMMDKHMSQLPPFLVENGGV
NSGFMIAQVTAAALASENKALSHPHSVDSLPTSANQEDHVSMAPAAGKRLWEWAENTRGVLAIWLGACQG
LDLRKGKTSALKERQALRSEVAHYDRDRFFAPDIEKAVELLAKGSLTGLPAGVLP SL

>d1uby_a.128.1.1 (-) Farnesyl diphosphate synthase {Chicken (Gallus gallus)}

SPVVVEREREFGVFFPQIVRDLTEDGIGHPEVGDAVARLKEVLQYNAPGGKCNRLTVAAAYRELSGPQKDA
ESLRCALAVGWCIELFQAASLVADDIMDQSLTRRGQLCWYKKEGVGLDAINDSFLLESSVYRVLKKYCRQRPYY
HLLELFQTYQTELGQMQLITAPVSKVDSLHFSEERYKAIVKYKTFYSFYLPVAAAMYMGIDSKEEHENAKA
ILLEMGEYFQIQDDYLCFGDPALTGAVGTDIQDNKCSWLVVQCLQRVTPEQRQLLEDNYGRKEPEKAVKEL
YEAVGMRAAFQQYEESYYRRLQELIEKHSNRLPKEIFLGLAQKIQKRQK

>d1ezfa_a.128.1.2 (A:) Squalene synthase {Human (Homo sapiens)}

NSLKTCYKYLNQTTSRSFAAVIQALGEMRNAVCIFYLVRALDTLEDDMTISVEKKVPLLHNFSFLYQPDWRF
MESKEKDRQVLEDFTISLEFRNLAEKYQTVIADICRRMGIGMAEFLDKHVTSEQEWDKYCHYVAGLVGIGLSR
LFSASEFEDPLVGEDTERANSMGLFLQKTNIRDYLEDQQGGREFWPQEWSRYVKKLGDFAKPENIDLAVQCL
NELITNALHHIPDVITYLSRLRNQSVNFCAIPQVMAIATLAACYNNQQVKGAVKIRKGQAVTLMDATNMP
AVKAIYQYMEEIYHRIPDSDPSSSKTRQIIRTQN

>d5eau_2 a.128.1.3 (221-548) 5-Epi-aristolochene synthase, C-terminal domain
{Tobacco (Nicotiana tabacum)}

KNNVLLRAKLDNFNLQMLHKQELAQVSRRWWKDLDFVTTLPYARDRVVECYFWALGVYFEPQYSQARVMLVK
TISMISIVDDTFDAYGTVKELEYTDIQRWDINEIDRLPDYMKISYKAILDLYKDYEKELSSAGRSHIVCHAIERM
KEVVRNNYNESTWFIEGYTPVSEYLSNALATTYYYLATTSYLGMKSATEQDFEWLSKNPKILEASVIICRVIDDT
ATYEVKSRGQIATGIECCMRDYGISTKEAMAKFQNMAETAWKDINEGLLRPTVSTEFLTPILNLARIVEVTYIH
NLDGYTHPEKVLKPHIINLLVDSIKI

>d1di1a_a.128.1.4 (A:) Aristolochene synthase {Fungus (Penicillium roqueforti)}

TPPPPTQWSYLCHPRVKEVQDEVGDYFLENWKPSFKAVRTFLDAKFSEVTCLYFPLALDDRIHFACRLLTVLFLID
DVLEHMSFADGEAYNNRLIPISRGDVLPDRTKPEEFILYDLWESMRAHDAELANEVLEPTFVFMRAQTDRARLS
IHELGHYLEYREKDVKGALLSALMRFMSGRLSADELQDMKALEANCAKQLSVVNDIYSYDKEEASRTGHKEG
AFLCSAVKVAEESKLGIPATKRVLWSMTREWETVHDEIVAEKIASPDGCSEAAKAYMKGLEYQMSGNEQWSK
TTR

>d1ps1a_a.128.1.4 (A:) Pentalenene synthase {Streptomyces sp., UC5319}

QDVDFHIPLPGRQSPDHARAEEQLAWPRSLGLIRSDAAAERHLRGGYADLASRFYPHATGADLDLGVDLMS
WFFLFDDLFDGPRGENPEDTKQLTDQVAAALDGPLPTAPPIAHGFADIWRRCTEGMTPAWCARSARHWRN
YFDGYVDEAESRFWNAPCDAAQYLAMRRHTIGVQPTVDAERAGRFEVPHRVFDSAVMSAMLQIAVDVNL
LLNDIASLEKEEARGEQNNMVMILRREHGWSKRSVSHMQNEVRARLEQYLLLESCLPKVGEIYQLDTAEREAL
ERYRTDAVRTVIRGSYDWHRSSG

>d1jfaa_a.128.1.5 (A:) Trichodiene synthase {Fusarium sporotrichioides}

MENFPTEYFLNTTVRLLEYIYRDSNYTREERIENLHYAYNKAHHFAQPRQQQLKVDPKRLQASLQTIVGMV
VYSWAKSKECMADLSIHYTTLVLDSDKDDPYPTMVNYFDDLQAGREQAHPWWALVNEHFPNVLRHFGPF
CSLNLRSTLDFEGCWIEQYNFGGPGSHDYPQFLRRMNGLGHCVGASLWPKEQFNERSLFLEITSIAQWMEN
WMVWVNDLMSFYKEFDDERDQISLVKNYVVSDEISLHEALEKLTDLHSSKQMVAVFSDKDPQVMMDTIECF

MHG YV TWHL CDRR YRL SEIYE KVKEE KTEDA QKFCKFYEQ AANVG AVSP SEWA YPPV AQLAN V
>d1oela1 a.129.1.1 (A:2-136,A:410-525) GroEL {Escherichia coli}
AAKDV KFGNDAGVKMLRGVNVLADAVKVT LGPKGRNVVLDKSGAPITKDGVSVAREIELEDKFENMGAQ MVKEVASKANDAAGDGT TATVLAQAIITEGLKAVAAGMNPMDLKRGIDKAVTV AVEELKAL SVXGVVAGGG VALIRVASKLADLRGQNEDQNVGIKVALRAMEAPLRQIVLNCGEEPSVVANTVKGGDGNYGYNAATEEYGNMI DMGILDPTKVTRSA LQYAASVAGL MITTECMVTDLP
>d1ioka1 a.129.1.1 (A:2-136,A:410-526) GroEL {Paracoccus denitrificans}
AAKEV KFNSDARDMLKGVNILADAVKVT LGPKGRNVVIDKSFGAPRITKDGVSVAKEIELSDKFENMGAQM VREVASRTNDEAGDGT TATVLAQAIIREGLKAVAAGMNPMDLKRGIDVATAKVVEAIKSAARXGIVVGGVAL VQGAKVLEG LSGANS DQDAGIAIIRRALEAPMRQIAENAGVDGAVVAGKVRESSDKAFGFNAQTEEYGD MFK FGVIDPAKVV RTALED AASVAGLLITTEAMIAEK P
>d1a6da1 a.129.1.2 (A:17-145,A:404-519) Thermosome {Archaeon Thermoplasma acidophilum}
REQGKNAQRNNIEAAKAIADAVRTTLGPKGMDKMLVDSIGDIISNDGATILKEMDVEHPTAKMIVEVSKAQD TAVGDGTTAVVLSGE LLKQAETLLDQGVHPTVISNGYRLAVNEARKIID EIAKSXFLWGGGAVEAELAMRLAK YAN SVGGREQLAIEAFAKALEIIPRTLAENAGIDPINTLKLKADDEKGRISVGVDLNNVGDMKA KG VVDPL R VKTHALESAVEVATMILRIDDVI
>d1a6db1 a.129.1.2 (B:20-144,B:404-521) Thermosome {Archaeon Thermoplasma acidophilum}
KDAMKENIEAAIAISNSVRSSLGPRGMDKMLVDSLGDIVITNDGV TILKEMDVEHPAAKMMVEVSKTQDSFVG DGTTTAVIIAGGLLQQAQGLINQNVHPTVISEGYRMASEEAKRVIDEISTKIXAYAAGGGATAAEIAFRLRSY AQK I GGRQQLAIEK FADAIEEIPR ALAENAGLDPIDILLKLRAEHAKGNKTYGINVFTGEIEDMVKNGVIEPI RVGKQ AIE SATEAAIMILRIDDVIA
>d1ecma_ a.130.1.1 (A:) Chorismate mutase domain of P-protein {Escherichia coli}
NPLLALREKISALDEKL ALLAERREL AVEVGKAKLLSHRPVRDIDRERDLLE RLITLGKAHHLD AHYITRLFQLII ED SVLTQQALLQQH
>d5csma_ a.130.1.2 (A:) Allosteric chorismate mutase {Baker's yeast (Saccharomyces cerevisiae)}
MDFTKPETVNLQNIRDELVRMEDSII FKFIERSHFATCP SYEANHPGLEIPNFKGSFLDWALS NLEIAHSRIRRF ESPDETPFFPDKIQKSFLPSINYPQILAPYAPEVNYNDKIKK VYIEKIIPLISKRDGDDKNNFGSVATRDIECLQSLR RIHFGKFVAEAKFQS DIPLYTKLI SKDVEGIMKNITNSAVEE KILERLT KAEVYGVDP TERRIERRISPEYLVKIYKE IVIPITKEVEVEYLLRRLEE
>d1pprm1 a.131.1.1 (M:1-156) Peridinin-chlorophyll protein {Dinoflagellate (Amphidinium carterae)}
DEIGDAAKKLG DASYAFAKEVDWNNGIFLQAPGKLQPLEALKAI DKMIVMGAAADPKLLKAAAEEAHHK AIGS IS GPNGVTSRADWDNVNAALGRVIASVPENMVMDVYDSVSKITDPKV PAYM KSLVNGADA EKAYEGFLAFKDV VKKSQVTSAAG
>d1pprm2 a.131.1.1 (M:157-312) Peridinin-chlorophyll protein {Dinoflagellate (Amphidinium carterae)}
PATVPSGD KIGVAAQQLSEASYPFLKEIDW LSDV YM KPLPGVSAQQSLKAI DKMIVMGAAQADGNALKAAA EA HHKAIGSIDATGVTSAADYAAVNAALGRVIASVPKSTVMDVYNA MAGVTDTSIPLNMFSKVNPLDANA AAKA FYTFKD VVQAAQ
>d1qq8a_ a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Human (Homo sapiens)}
PQDLSEALKEATKEVHTQAENA EFMRNFQKGQVTRDGFKLVMASLYHIYVALEEEIERNKESPVFAPVYFPEELH RKAAL EQD LAFWY GPRWQE VPYTPAMQRYVKRLHEVGRTEPELLVAHAYTRYLG DLSGGQVLKKIAQKALDL

PSSGEGLAFFTPNIASATFKQLYRSRMNSLEMPAVRQRVIEEAKTAFLNINQLFEELQELLTH
>d1dvga_ a.132.1.1 (A:) Heme oxygenase-1 (HO-1) {Rat (Rattus norvegicus)}
SQDLSEALKEATKEVHRAENSEFMRNFQKGQVSREGFKLVTASLYHIYTALEEEIERNKQNPVYAPLYFPEELHRR
AALEQDLAFWYGPWHQEAPIYPTPATQHYVKRLHEVGGTHPELLVAHAYTRYLGDSLGGQVLKKIAQKALALPSS
GEGLASFPTPSIDNPTKFKQLYRARMNTLELTPEVKHRVTEEAFTAFLNIELFEELQALLTE
>d1j77a_ a.132.1.2 (A:) Gram-negative bacterial heme oxygenase {Neisseria meningitidis}
ALTFAKRLKADTTAVHDSVDNLVMSVQPFVSKENYIKFLKLQSVFHKAVIDHIYKDAELNKAYPELEYMARYDAVT
QDLKDLGEEPYKFDKELPYEAGNKAIGWLCAEGSNLGAFLKHAQKLDYNGEHGARHLAPHPDGRGKHWR
AFVEHLNALNLTPEAEAAIQGAREAFAFYKVVLRETGLAADAEPAGMMPH
>d1knca_ a.152.1.1 (A:) Antioxidant defence protein AhpD {Mycobacterium tuberculosis}
SIEKLKAALPEYAKDIKLNLSITRSSVLDQEQLWGTLLASAAATRNPQVLADIGAEATDHSAAARHAALGAAAI
MGMMNNVFYRGRGFLEGGRYDDLPGRLRMNIIANPGIPKANFELWSFAVSAINGCSHCLVAHEHTLRTVGVDRE
AIFEALKAAAIVSGVAQALATIEALS
>d1poa_ a.133.1.2 (-) Snake phospholipase A2 {Taiwan cobra (Naja naja atra)}
NLYQFKNMIQCTVPSRSWWDFADYGCGYCGRGSGTPVDDLDRCQCVDNCYNEAEKISGCWPYFKTYSYEC
QGTLTCKGGNNACAAVCDCDRLAACIFAGAPYNDNDYNINLKARC
>d1pp2l_ a.133.1.2 (L:) Snake phospholipase A2 {Western diamondback rattlesnake (Crotalus atrox)}
SLVQFETLIMKIAGRSGLLWYSAYGCYCGWGGHGLPQDATDRCCFVHDCCYGKATDCNPKTVSYTYSEENGII
CGGDDPCGTQICECDKAAAICFRDNIPSYDNKYWLFPKDCREEPEPC
>d1bjja_ a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}
NLLQFNKMIKEETGKNAIPFYAFYGCYCGWGGQGKPKDGTDRCCFVHDCCYGRNVNCNTKSDIYSYLKEGYIT
CGKGTNCEEQICECDRVAACFRRNLDTYNNNGYMFYRDSKCTETSEEC
>d1jiaa_ a.133.1.2 (A:) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}
HLLQFRKMIKKMTGKEPVVSYAFYGCYCGSGGRGKPKDATDRCCFVHDCCYEKVTGCDPKWDDYTYSWKNG
TIVCGGDDPCKKEVCECDKAAAICFRDNLKYKKRYMAYPDILCSSKSEKC
>d1psj_ a.133.1.2 (-) Snake phospholipase A2 {Chinese water moccasin (Agkistrodon halys pallas), different isoforms}
SLIQFETLIMKVAKKSGMFWYSNYGCYCGWGGQGRPQDATDRCCFVHDCCYGKVTGCDPKMDVYSFSEENG
DIVCGGDDPCKKEICECDRAAAICFRDNLTLYNDKKYWAFGAKNCPQESEPC
>d1ppa_ a.133.1.2 (-) Snake phospholipase A2 {Eastern cottonmouth snake (Agkistrodon piscivorus)}
SVLELGKMLQETGKNAITSYGSYGCNCGWGHRGQPKDATDRCCFVHKCCYKKLDCNHKTDRYSYSWKNKAI
ICEEKNPCLKEMCECDKAVAICLRENLDTYNKKYKAYFKLKCKKPDT
>d1vapa_ a.133.1.2 (A:) Snake phospholipase A2 {Eastern cottonmouth snake (Agkistrodon piscivorus)}
NLFQFEKLIKKMTGKSGMLWYSAYGCYCGWGGQGRPQDATDRCCFVHDCCYGKVTGCNPKMDIYTYSVDNG
NIVCGGTNPCKKQICECDRAAAICFRDNLKYDSKYWKYPKKNCKEESEPC
>d1ijla_ a.133.1.2 (A:) Snake phospholipase A2 {Viper (Deinagkistrodon acutus)}

SLIQFETLIMKVVKKSGMFWYSAYGCYCGWGGHGRPQDATDRCCFVHDCCYGKVTGCDPKMDSYTYSEENG
DIVCGGDDPCKREICECDRVAADCFRDNLDTYNSDTWRYPRQDCEESPEPC
>d1fe7a_ a.133.1.2 (A:) Snake phospholipase A2 {Snake (Daboia russelli pulchella)}
SLLEFGKMIILEETGKLAIPSYSSYGCYCGWGGKGTPKDATDRCCFVHDCCYGNLPDCNPKSDRYKYKRVNGAIV
CEKGTCENRICECDKAAAICFRQNLNTYSKKYMLYPDFLCKGELKC
>d1ae7_ a.133.1.2 (-) Snake phospholipase A2 {Mainland tiger snake (Notechis scutatus scutatus), notexin}
NLVQFSYLIQCANHGKRPTWHYMDYGCYCGAGGSGTPVDELDRCCKIHDDCYDEAGKKGCFPKMSAYDYYCG
ENGPYCRNIKKCLRFVCDCDVEAACFAKAPYNNANWNIDTKKRCQ
>d2nota_ a.133.1.2 (A:) Snake phospholipase A2 {Mainland tiger snake (Notechis scutatus scutatus), notechis II-5}
NLVQFSYLIQCANHGRRPTRHYMDYGCYCGWGGSGTPVDELDRCCKIHDDCYSDAEKKGCPKMSAYDYYCG
ENGPYCRNIKKCLRFVCDCDVEAACFAKAPYNNANWNIDTKKRCQ
>d1qla_ a.133.1.2 (A:) Snake phospholipase A2 {Bothrops pirajai, Piratoxin-II (PRTX-II)}
SLFELGKAMILQETGKNAKSYGAYGCNCVLRGKPKDATDRCCVHKCCYKKLTGCNPKKDRYSYSWKDKTIV
CGENNPLKELCECDKAVAICLRENLTYNKKYRYHLKPFCKKADKC
>d1vip_ a.133.1.2 (-) Snake phospholipase A2 {Russell's viper (Vipera russelli)}
NLFQFAEMIVKMTGKNPLSSYSDYGCYCGWGGKGKPQDATDRCCFVHDCCYEVKVSCKPKLSLYSFQNGGI
VCGDNHSCKRAVCECDRVAATCFRDNLNTYDKYHNYPPSQCTGTEQC
>d1jta_ a.133.1.2 (A:) Snake phospholipase A2 {Sand viper (Vipera ammodytes meridionalis), vipoxin}
NLFQFGDMILQKTGKEAVHSYAIYGCYCGWGGQARAQDATDRCCFAQDCCYGRVNDNPKTATYTYSFENGDI
IVCGDNDLCLRAVCECDRAAAICLGENVNTYDKNEYYSISHCTEESEQC
>d1jtb_ a.133.1.2 (B:) Snake phospholipase A2 {Sand viper (Vipera ammodytes meridionalis), vipoxin}
NLFQFAKMINGKLGAFLSVNNYISYGCYCGWGGQGTPKDATDRCCFVHDCCYGRVRGCNPKLAIYSYSFKKGNI
VCGKNNNGCLRICECDRVAANCFHQNKNKYKFLSSSRCRTSEQC
>d1dpya_ a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (Bungarus caeruleus), different isoforms}
NLIQFKNMIIQCAGTRIWTAYVAYGCYCGKGGSGTPVDELDRCCTHDHCYNEAEKIPGCNPNIKTSYTCTQPN
LTCTDSADTCAQFLCECDRTAAICFASAPYNSNNIMLSSSTSCQ
>d1fe5a_ a.133.1.2 (A:) Snake phospholipase A2 {Indian krait (Bungarus caeruleus), different isoforms}
NLIQFKNMIIQCAGTRPWTAYVNYGCYCGKGGSGTPVDELDRCCTHDNCYNEAEKIPGCNPNIKTSYTCTEP
NLTCTDTADTCARFLCNCDRTAACIFASAPYNSNNVMISSSTNCQ
>d1kvoa_ a.133.1.2 (A:) Phospholipase A2 {Human (Homo sapiens), synovial fluid}
NLVNFRMILTTGKEAALSYGFYGCCHCGVGRGSPKDATDRCCVTHDCCYKRLEKRGCGTKFLSYKFSNSGSRTCAKQDSCRSQLCECDKAAATCFARNKTTYNKKYQYYSNKHCRGSTPRC
>d1g4ia_ a.133.1.2 (A:) Phospholipase A2 {Cow (Bos taurus), pancreas}
ALWQFNGMIKCKIPSSEPLDFNNYGCYCGLGGSGTPVDDLDRCQTHDNCYKQAKKLDSCKVLDNPYTNNYSYCSNNEITCSSENNACEAFICNCDRNAAACFSKVPYNKEHKNLDDKKNC
>d1hn4a_ a.133.1.2 (A:) Phospholipase A2 {Pig (Sus scrofa), pancreas}
GISSRALWQFRSMIKCAIPGSHPPLMDFNNGCYCGLGGSGTPVDELDRCCTHDNCYRDAKNLDSCFLVDNP
YTESYSYCSNTEITCNSKNNACEAFICNCDRNAAACFSKAPYNKEHKNLDTKKYC

>d5p2pa_a.133.1.2 (A:) Phospholipase A2 {Pig (Sus scrofa), pancreas}
ALFQFRSMIKCAIPGSHPLMDNNYGCYCGWGGSGTPVDELDRCCEHDNCYRDAKNLSCGCYPYTESYSSCS
NTEITCNSKNNACEAFICNCDRNAAACFSKAPYNKEHKNLDTKKC
>d1buna_a.133.1.2 (A:) beta2-bungarotoxin, phospholipase A2 chain {Many-banded krait (Bungarus multicinctus), elapid}
NLINFMEMIRYTIPCEKTWGEYADYGCGAGGSGRPIDALDRCCYVHDNCYGDAEKHKCNPKTQSYSYKLTK
RTIICYGAAGTCARIVCDCDRTAACFGNSEYIEGHKNIDTARFCQ
>d1goda_a.133.1.2 (A:) Myotoxin II {Bothrops godmani}
SMYQLWKMILQETGKNAVPSYGLYGCNCVGSRGPKDADRCVFHKCCYKKLTDCSPKTDSYSWKDGTI
VCGDNNPCLQEMCECDKAVAICLRENLDTNYKNYKIPKPLCKKADAC
>d1gmza_a.133.1.2 (A:) Myotoxin II {Snake (Bothrops pirajai), piratoxin III}
DLWQFGKMLKETGKLPFPYYVTGCYCGVGGRRGPKDADRCVFHDCCYGLTSCKPKTDRYPTSYSRKDGTV
CGENDPCRKEICECDKAAAVCFRENLDTNYKKYMSYLKSLCKXADD
>d1poc_a.133.1.1 (-) Phospholipase A2 {European honeybee (Apis mellifera)}
IIYPGTLWCGHGNKSSGPNEGRFKHTDACRTHDMCPDVMSSAGESKHGLNTASHTRLSCDCDDKFYDCLK
NSADTISSYFVGKMYFNLDTCYKLEHPVTGGERTEGRCLHYTVDKSKPKVYQWFDLRKY
>d1faza_a.133.1.3 (A:) Prokaryotic phospholipase A2 {Streptomyces violaceoruber}
APADKPQVLASFTQTASSQNAWLAANRNQSAWAAYEFDWSTDLCTQAPDNPFGFPFTACARHDFGYRNY
KAAGSFIDANKSRIIDSAFYEDMKRVCTGYGEKNTACNSTAWTYQQAVKIFG
>d1bxm_a.134.1.1 (-) beta-cryptogein {Phytophthora cryptogea}
RGTCTATQQTAAYHTLVSILSDASFNCSTDSGYMLTAKALPTTAQYKLMCASTACNTMIKKIVTLNPPNCDLT
VPTSGLVLNVSYANGFSNKCSSL
>d1g8qa_a.135.1.1 (A:) CD81 extracellular domain {Human (Homo sapiens)}
FVNKDQIAKDVQFYDQALQQAVVDDDANNAKAVVKTFHETLDCCGSTLTALTSVLKNNLCPSGSNIISNL
KEDCHQKIDDLFSGKH
>d1dvoa_a.136.1.1 (A:) Repressor of bacterial conjugation FinO {Escherichia coli}
PPKWVKKQKLAEKAAREAELTAKKAQARQALSIYLNPLTLDEAVNTLKWPWPGLFDGDTPRLLACGIRDV
DVAQRNIPLSHKKLRRAMKAITRSESYLCAMKAGACRYDTEGYVTEHISQEEEVYAAERLDKIRRQNRIK
AELQA
VLD
>d1jjsa_a.153.1.1 (A:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}
ALQDLLRTLKPSSPQQQQVNLNILKSNPQLMAAFIKQRTAKYVANQPGMQ
>d1kbhb_a.153.1.1 (B:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (Mus musculus)}
PNRSISPSALQDLLRTLKPSSPQQQQVNLNILKSNPQLMAAFIKQRTAKYVANQPGMQ
>d1kbha_a.153.1.1 (A:) Nuclear receptor coactivator ACTR {Human (Homo sapiens)}
EGQSDERALLDQLHLLSNTDATGLEEIDRALGIPELVNQGQALEPK
>d1ffky_a.137.1.1 (Y:) Ribosomal protein L39e {Archaeon Haloarcula marismortui}
GKKSKATKKRKAQLDNQNSRVPAYVMLKTREVQRNHKRRHWRRNDTDE
>d1jj21_a.137.1.1 (1:) Ribosomal protein L39e {Archaeon Haloarcula marismortui}
GKKSKATKKRKAQLDNQNSRVPAWVMLKTDEVQRNHKRRHWRRNDTDE
>d1g72b_a.137.2.1 (B:) Methanol dehydrogenase, light chain {Methylophilus methylotrophus, w3a1}
YDGQNCKEPGNCWENKPGYPEKIAGSKYDPKHDPELNKQEESIKAMDARNAKRIAN
>d4aab_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}
YDGTKCKAAGNCWEPKPGFPEKIAGSKYDPKHDPKELNKQADSIKQMEERNKKRVENFKKTGKFYDVAKISA
>d1gg2g_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}
SIAQARKLVEQLKMEANIDRIKVSKAAADLMAYCEAHAKEDPLLTPVPASENPF
>d1gotg_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}
LTEKDKLKMEVDQLKKEVTLEMLVSKCCEEFRDYVEERSGEDPLVKGIPEDKNPFKE
>d1tbge_ a.137.3.1 (E:) Transducin (heterotrimeric G protein), gamma chain {Cow (Bos taurus)}
APVINIEDLTEKDKLKMEVDQLKKEVTLEMLVSKCCEEFRDYVEERSGEDPLVKGIPEDKNPFKELK
>d1hfes_ a.137.4.1 (S:) Fe-only hydrogenase smaller subunit {Desulfovibrio desulfuricans}
VKQIKDYMLDRINGVYGADAKFPVRASQDNTQVKALYKSYLEKPLGHKSHDLLHTHWFDKSKGVKELTTAGKLP
NPRASEFEGPYPYE
>d1ef1c_ a.137.5.1 (C:) Moesin tail domain {Human (Homo sapiens)}
AEASADLRADAMAKDRSEEERTTEAEKNERVQKHLKALTSELANARDESKTANDMIHAENMRLGRDKYKTLR
QIRQGNTKQRIDEFESM
>d2prgc_ a.137.6.1 (C:) Nuclear receptor coactivator Src-1 {Human (Homo sapiens)}
QTSHKLVQLTTAEEQQLRHADIDTSCKDVLSCGTTSNSASANSSGGSCPSSHSSLTERHKILHRLLOEGSPSDIT
>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}
MNALVGCTTSFDPGWEVDAFGAVSNLCQPMEADLYGCADPCWXPAQVADTLNTYPNWSAGADDVMQDW
RKLQSVFPETK
>d1jmwg_ a.137.9.1 (G:) Quinohemoprotein amine dehydrogenase C chain {Pseudomonas putida}
AVAGCTATTDPGWEVDAFGVSSLQPMEADLYGCSDPCWXPAQVPDMMMSTYQDWNAQASNSAEDWRN
LGTVFVFKDK
>d1aqe_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}
TFEIPESVTMSPKQFEGYTPKKGDVTNFNASHMDIACQQCHHTVPTDTIESCMTEGCHDNIKERTEISSVERTF
HTTKDSEKSCVGCHRELKRQGPSDAPLACNSCHVQ
>d1i77a_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}
APAAPDKPLEFKGSQKTVMFPHAVHAKVECUTCHHQVDGKESFAKGCGSSGCHDDLAGKQGEKSLYYVVHTKK
ELKHTNCIGCHSKVVEGKPELKDLTACAKSKCHP
>d2cy3_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}
ADAPGDDYVIAPEGMKAKPKGDKGALQKTVPFPHKATVECVQCHHTLEADGGAVKKCTTSGCHDSLEF
RDKANAKDIKLVENAFHTQCIDCHKALKDKKPTGPTACGKCHTTN
>d3cyr_ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio desulfuricans, different strains}
APAVPNKPVEVKGSQKTVMFPHAPHEKVECVTCHHLVDGKESYAKCGSSGCHDDLTAKKGEKSLYYVVHAKGE
LKHTSCLACHSKVVAEKPELKKDLTGCAKSCKHP

>d2cdv__ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio vulgaris}
APKAPADGLKMDTKQPVFNHSTHKAVKCGDCHPVNGKENYQKCATAGCHDNMDKKDKSAKGYYHAM
HDKGTFKFSCVGCHLETAGADAACKKELTGCKGSKCHS

>d2ctha_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio vulgaris}
APKAPADGLKMEATKQPVFNHSTHKSVKCGDCHPVNGKEDYRKCGTAGCHDSMDKKDKSAKGYYHVMH
DKNTKFSCVGCHVEVAGADAACKKDLTGCKKSCKHE

>d1wad__ a.138.1.1 (-) Cytochrome c3 {Desulfovibrio gigas}
VDVPADGAKIDFIAGGEKNLTVFNHSTHKDVKCDDCHDPGDKQYAGCTTDGCHNILDKADKSVNSWYKV
HDAKGGAKPTCISCHKDKAGDDKELKKKLTGCKGSACHP

>d3caoa_ a.138.1.1 (A:) Cytochrome c3 {Desulfovibrio africanus}
EDMTHVPTDAFGKLERPAAVFNHDEHNEKAGIESCNACHHVVWVNGVLAEDEDVGTPCSDCHALEQDGDT
GLQDAYHQQCWGCGHEKQAKGPVMCGECHVKN

>d1hh5a_ a.138.1.1 (A:) Cytochrome c7 (cytochrome c551.5) {Desulfuromonas acetoxidans}
ADVVTYENKKGNVTFDHKHAEKLGCDACTEGTPAKIAIDKSAHKDACKTCHKSNNGPTKCGGCHIK

>d19hca_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}
AALEPTDSGAPSIAVMFPVGEKPNAKGAAAMKPAVFNLHEKKIADCETCHHTGDPVCSTCHTVEGKAEGDYI
TLDRAMHATDIAARAKGNTPTSCVSCHQSETKERRECAGCHAITPKDDEAWCATCHDITPSMTPSEMKGIA
GTLLPGDNEALAAETVLAETVAPVSPMLAPYKVVIDALADKYEPSDFTHRRHITSLMESIKDDKLAQAFHDKP
EILCATCHHRSPSLTPPKCGSCHTKEIDAADPGRPNLMAAYHLECMGCHKGMAVARPRTDCTTCHKAAA

>d1duwa_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 29577}
EPTDSGAPSIAVMFPVSAKPNPKGAAMKPAVFNLHEKKIANCETCHHTGDPVACSTCHTTEGKAEGNFVTL
DRAMHATNIAKRAKGNTPVSCVSCHQQTKERRECAGCHAIVTPKRDQAWCATCHNVTSSMTPEQMQQGI
KGKLPPDQNEALAAETVLNHPVQPLTAMQGPYKVSIDALADKYEPNSFTHRRHMASLIMERIKGDKLAEAFH
NKPETLCATCHHRSPSATPPKCGSCHTKEIDPANPNRPNLKAAYHLQCMGCHQGMNVGRPKNTDCTTCHKAA
RP

>d1dxrc_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit) {Rhodopseudomonas viridis}
CFEPPPATTQTGFRGLSMGEVLHPATVKAKKERDAQYPPALAAVKAEGPPVSQVYKNVKVLGNLTEAEFLRTM
TAITEWVSPQEGCTYCHDENNLASEAKPYVVARRMILEMTRAINTNWTQHVAQTGVTCTCHRGTPLPPYVR
YLEPTLPLNNRETPTHVERVETRSGYVVRALKYTAYSALNYDPFTMFLANDKRQVRVVPQTALPLVGVSRGKER
RPLSDAYATFALMMSISDSLGTNCTFCHNAQTFESWGKKSTPQRAIAWWGIRMVRLNMNYLAPLNASLPAS
RLGRQGEAPQADCRTCHQGVTKPLFGASRLKDYPELGPIK

>d1eysc_ a.138.1.2 (C:) Photosynthetic reaction centre (cytochrome subunit) {Thermochromatium tepidum}
CEGPPPGTEQIGYRGVMENYYVKRQRALSIQANQPVESLPAADSTGPKASEVYQSVQLKDLVGEFTRTMV
AVTTWVSPKEGCNYCHVPGNWASDDIYTKVVSRRMFELVRAANSWDWKAHVAETGVTCYTCHRGNPVPKYA
WVTDPGPKYPGKPTGQNYGSKTVAYASLPFDPLTPFLDQANEIRITGNAALAGSNPASLKQAEWTFGLMMN
ISDSLGVGCTSCHNTRAFNDWTQSTPKRTTAWYAIRHVRDINQNYIWPLNDLPASRKGPYGDPLRVSCMTCH
QAVNKPLYGAQMAKDYPGLYK

>d1fgja_ a.138.1.3 (A:) Hydroxylamine oxidoreductase, HAO {Nitrosomonas europaea}

DISTVPDETYDALKLDRGKATPKETYEAJVRYKDPAHGAGKGTMDYWEPIAISIYMDPNTFYKPPVSPKEVAE
RKDCVECHSDETPVVRAWKRSTHANLDKIRNLKSDDPLYYKKGLEEVENNLRSMGKLGEKETLKEVGCIDC
HVDVNKKDKADHTKDIRMPTADTCGTCHLREFAERESERDTMVWPNGQWPAGRPSHALDYTANIETTVWAT
MPQREVAEGCTMCHTNQNKCNDNCTRHEFSAAESRKPEACATCHSGVDHNNWEAYTMSKHGKLAEMNRD
KWNWEVRLKDAFSKGQQNAPTCAAACHMEYEGERHTNITRKTRWANYPFVPGIAENITSWDSEARLDSWVLT
CTQCHSERFARSYLDLMDKGTLLEGAKYQEANAIHVHMYEDGTLTGQKTNRPNPPEPEKPGFGIFTQLFWSKG
NNPASLELKLEMGENNLAKMHVGLAHVNPGGWTYTEGWGPMMRAYVEIQDEYTKMQELSALQARVN
>d1ft5a_a.138.1.3 (A:) Cytochrome c554 {Nitrosomonas europaea}
ADAPFEGRKKCSSCHKAQAQSWKDTAHAKAMESLKPNVKKEAKQKAKLDPAKDYTQDKDCVGCHVDGFGQ
KGGYTIESPKPMLTGVGESCHPGGRNFRGDHRKSGQAFEKSGKTPRKDLAKKGQDFHFEERCSACHLYEG
SPWKGAKAPYTPFTPEVDAKYTFKFDEMVKEVKAMHEHYKLEGVFEGEPEKFKFHDEFQASAKPAKKGK
>d1ddca_a.138.1.3 (A:) Dimeric di-heme split-soret cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}
RFDQVGGAFGWPHKLDPECAQVAYDGYWYKGFHCGFAGFYSIVGLMGEKYGAPYNQFPFAMLEANKGGI
SDWGTIYGALYGAATFSLFWGRKEVHPMVNELRWYEVTKLPIFNPQDAQGVKGDLPMASDSVLCHISVS
KWCYENKIEATSKRSERAGRILTADAQKAAEIINTKIDQGKDFKSTFPMQASVSSCGECHMTKGNDANWAKG
IMDCTPCHSGTAATQNKFVNH
>d1qdba_a.138.1.3 (A:) Cytochrome c nitrite reductase {Sulfurospirillum deleyianum}
GIAGKEKSEEWAKYYPRQFDWSKKTKEYDSFTDMLAKDPALVIAWSGYAFSKDYNNSPRGHYYALQDNVNSLRT
GAPVDAKTGPLPTACWTCKSPDVPRLIEEDGELEYFTGKWAKYGSQIVNVIGCANCHDDKTAELKVRVPHLNR
GLQAAGLKTFEESTHQDKRTLVCAQCHVEYYFKKTEWKDAKGADKTAMVVTLPWANGVGKDGNAGVEGMI
KYYDEINFSDWTHNISKTPMLKAQHPGEFWKSGIHGQKGVSCADCHMPYTQEGSVKYSDHQVKENPLDSM
DQSCMNCHRESESCLRGINHQKYERKEFLNKVAFDNIGKAHLETGKIAEAGASDEELKEVRKLIRHGQFKADM
AIAAHGNYFHAPEETLRLAAGSDDAQKARLLVKILAKHGVMDYIAPDFDTDKAQKLAKVDIAALAAEKMKF
KQTLEQEWKKEAKAKGRANPELYKDVTINDGKSSWNKK
>d1fs7a_a.138.1.3 (A:) Cytochrome c nitrite reductase {Wolinella succinogenes}
KTAHSQGIEGKAMSEEWARYYPRQFDWSKKTKESENITDMLKEKPALVVAWAGYPSKDYNAPRGHYYALQD
NINTLRTGAPVDGKGPLPSACWTCKSPDVPRIIEQDGELEYFTGKWAKYGEIVNTIGCYNCHDDKSAELKSK
VPYLDRLGLAAGFKTFAESTHQEKRSLVCAQCHVEYYFKKTEWKDDKGVDKTAMVVTLPWSKGISTEQMEAYY
DEINFADWTHGISKTPMLKAQHPDWELYKTGIHGQKGVSCADCHMPYTQEGAVKYSDHKGVNPLDNMDKS
CMNCNCHRESEQKLLDIVKQKFERKEFLQDIAFDNIGKAHLETGKAMELGATDAELKEIRTHIRHAQWRADMAIA
GHGSFFHAPEEVRLLLASGNNEAQKARIKLVKLAKYGAIDYVAPDFETKEKAQKLAKVDMEAFAEKLKFQTL
EQEWKKQAIKGRLNPESLKGVDKSSYYDKTKK
>d1e39a1_a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella frigidimarina}
ADNLAEFHVNQECDSCHTPDGELSNDLTYENTQCVSCHGTLAEVAETTKHEHYNASHFPGEVACTSCHS
AHEKSMIVYCDSCHSFDFNMPYAKKWLRE
>d1qo8a1_a.138.1.3 (A:2-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella frigidimarina}
TPDMGSFHADMGSQSCHAKPIKVTDSETHENAQCKSCHGEYAEELANDKLQFDPHNSHLGDINCTSCHKHGE
EPKFYCNECHSFDFIKPMPFSDAKKKKSWD
>d1d4ca1_a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella putrefaciens}

APEVLADFHGEMGGCDSCHVSDKGGVTNDNLTHENGQCVSCHGDLKELAAAAPDKVSPHKSHLIGEACTS
CHKGHEKSVAYCDACHSGFDMPFGGKWER
>d1neu_ b.1.1.1 (-) Myelin membrane adhesion molecule P0 {Rat (Rattus norvegicus)}
IVVYTDREVYGAVGSQLVTLHCSFWSSSEWVSDDISFTWRYQPEGGRDAISIFHYAKGQPYIDEVGTFKERIQWVG
DPSWKDGSIIVHNLDYSDNGTFTCDVKNPPDIVGKTSQVTLYVFE
>d1eaja_ b.1.1.1 (A:) Coxsackie virus and adenovirus receptor (Car), domain 1 {Human (Homo sapiens)}
FARSLSITTPPEEMIEAKGETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVVDQVIILYSGDKIYDDYYPDLKGRVHF
TSNDLKSGDASINVTNLQLSDIGTYQCKVKKAPGVANKKIHLVV
>d1qfoa_ b.1.1.1 (A:) N-terminal domain of sialoadhesin {Mouse (Mus musculus)}
TWGVSSPKNVQGLSGSCLLIPICFSYPADVPVSNGITAIWYYDYSRKQVVIHSGDPKLVDKRFRGRAELMGNM
DHKVCNLLLKDLKPEDSGTYNFRFEISDSNRWL DVKGTTVTVTT
>d1akjd_ b.1.1.1 (D:) CD8 {Human (Homo sapiens)}
SQFRVSPLDRTWNLGETVELKCQVLLSNPTSGCSWLFQPRGAAASPTFLYLSQNKPAAEGLDTQRFSGKRLG
DTFVLTSDLFRRENEGYYFCSALSNSIMYFHFVFPVFLPA
>d1bqh_ b.1.1.1 (G:) CD8 {Mouse (Mus musculus)}
KPQAPELRIFPKKMDAELGQKVDLVCEVLGSVSQGCSWLFQNSSLKPQPTFVYMASSHNKITWDEKLNSSK
LFSAMRDTNNKYVLTLNKFSKENEGYYFCVISNSVMYFSSVVPVLQKV
>d1cdy_1 b.1.1.1 (1-97) N-terminal domain of CD4 {Human (Homo sapiens)}
KKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKSPSKLNDRADSRRSLWDQGNFPLIIKNLKI
EDSDTYICEVEDQKEEVQLLV
>d1wioa2 b.1.1.1 (A:179-291) N-terminal domain of CD4 {Human (Homo sapiens)}
FQKASSIVYKKEGEQEVSFPLAFTVEKLTGSELWWQAERASSKSWITFDLKNKEVSVKRVQTQDPKLQMGKK
LPLHLTLQPALPQYAGSGNLTLDRGILYQEVLV
>d1cid_1 b.1.1.1 (1-105) N-terminal domain of CD4 {Rat (Rattus rattus)}
TSITAYKSEGESAESFPLNLGEESLQGELRWKAEKAPSSQSWITFSLKNQKVSVQKSTSNPKFQLSETLPLTLQIP
QVSLQFAGSGGNLTLDRGILYQEVLV
>d1hnf_1 b.1.1.1 (4-104) CD2, first domain {Human (Homo sapiens)}
TNALETWGALGQDINLDIPSQMSDDIDDIKWEKTSDDKKIAQFRKEKETFKEKDTYKLFNGTLKIKHLKTDDQ
DIYKVSIYDTKGKNVLEKIFDLKIQE
>d1hnga1 b.1.1.1 (A:2-99) CD2, first domain {Rat (Rattus norvegicus)}
DSGTVWGA GHGINLNIPNFQM TDDIDEVRWERGSTLVAEFKRKMKPFLKSGAFEILANGDLKIKNLTRDDSG
TYNVTVYSTNGTRILNKALDLRILE
>d1ccza1 b.1.1.1 (A:1-93) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}
FSQQIYGVVYGNVTFHVPNVPLKEVLWKKQKDVAELENSEFRAFSSFKNRVYLD TVSGSLTIYNLTSSDEDEYE
MESPNITDTMKFFLYVL
>d1qa9b_ b.1.1.1 (B:) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}
SSQQIYGVKYGNVTFHVPNSNQLKEVLWKKQKDVAELENSEFRAFSSFKNRVYLD TKGSLTIYNLTSSDEDEYE
MESPNITDSMKFFLYVGES
>d1dr9a1 b.1.1.1 (A:1-105) CD80, N-terminal domain {Human (Homo sapiens)}
VIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQKEKKMVLMMMSGDMNIWPEYKNRTIFDITNNLSIVIALRP
SDEGYTECVVLKYEKDAFKREH LAEVTLSVK
>d1i85a_ b.1.1.1 (A:) CD86 (b7-2), N-terminal domain {Human (Homo sapiens)}

MLKIQAYFNETADLPCQFANSQNQSLSELVVFWQDQEVLNEVYLGKEKFDSVHSKYMGRTSFDSDSWTLRL
HNLQIKDKGLYQCIHHKKPTGMIRIHQMNSELSVLA

>d1f97a1 b.1.1.1 (A:27-128) Junction adhesion molecule, JAM, N-terminal domain {Mouse (*Mus musculus*)}

KGSVYTAQSDVQVPENESIKLTCTYSGFSSPRVEWKFVQGSTTALVCYNSQITAPYADRVTFSSSGITFSSVTRKD
NGEYTCMVSEEGGQNYGEVSIHLTVL

>d1jmaa_ b.1.1.1 (A:) HSV glycoprotein D {Herpes simplex virus type 1}

KYALADASLKMADPNRFRGKDLPVLDQLTDPPGVRRVYHIQAGLPDPFQPPSLPITVYYAVLERACRSVLLNAPS
EAPQIVRGASEDVRKPYNLTIAWFRMGGNCAIPITVMEYTECSYNKSLGACPIRTQPRWNYYDSFAVSEDNL
GFLMHAPAFETAGTYLRLVKINDWTEITQFILEHRAKGSCSKYALPLRIPPSACLSPQAYQQGVTVDIGMLPRFIP
ENQRTVAVYSLKIAKGWHGPKAPYTSTLLPPELSE

>d1igta1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}

DIVLTQSPSSLSASLGDTITITCHASQNINVWSWYQQKPGNIPKLLIYKASNLTGVPSRFSGSGSGTGFTLTISLL
QPEDIATYYCQQGQSYPLTFGGGTKEIKR

>d1igtb1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}

EVKLQESGGGLVQPGGSLKLSCATSGFTFSDDYYMYWVQRTPKRLWEVAYISNGGGSTYYPPDTVKGRFTISRDN
AKNTLYLQMSRLKSEDTAMYCARHGGYYAMDYWGQGTTVSSA

>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}

KCAHTVSKSMSMSVGERTVLTCKASENVVTYVSWYQQKPEQSPKLLIYGASNRYTGVPDRFTGSGSATDFTLTIS
SVQAEDLADYHCGQGYSYPTFGGGTKEIK

>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}

VKLQESGAELARPGASVKMSCKASGYTFTTYTIHWIKQRPGQGLEWIGYINPSSVYTNYNQRFKDATALTRDRS
SNTANIHLSSLTSDDAVYYCVREGEVPYWGQGTTVSS

>d1hzhh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}

QVQLVQSGAEVKPGASVKVSCQASGYRFSNFVIHWVRQAPGQRFEWMGWINPYNGNKEFSAKFQDRVTFT
TADTSANTAYMELRSLSADTAVYYCARVGPySWDDSPQDNYYMDVWGKTTVIVSS

>d1hzhl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}

EIVLTQSPGTLSLSPGERATFSCRSSHSIRSRRVAWYQHKPGQAPRLVIHGVSNRASGISDRFSGSGSGTDFLTIT
RVEPEDFALYYCQVYGAASSYTFGQGKLERK

>d8fab1 b.1.1.1 (A:3-105) Immunoglobulin (variable domains of L and H chains) {Fab HIL (human), lambda L chain}

ELTQPPSVSPGQTARITCSANALPNQYAYWYQQKPGRAPVMVIYKDTQRPSGIPQRFSSTS GTTVTLTISGV
QAEDEADYYCQAWDNSASIFGGGTKLTV

>d8fabb1 b.1.1.1 (B:1-121) Immunoglobulin (variable domains of L and H chains) {Fab HIL (human), lambda L chain}

AVKLVQAGGGVVQPGRSRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAIWYNGSRTYYGDSVKGRFTISR
DNSKRTLYMQMNSLRTEDTA VYYCARDPDLTAFSF DYWGQGVLTVSS

>d7fabh1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and H chains) {Fab NEW

(human), lambda L chain}

AVQLEQSGPGLVRPSQTLSTCTVSGTSFDDYYWTWVRQPPGRGLEWIGYVFYTGTLLDPSLRGRVTMLVNT
SKNQFSLRLSSVTAADTAVYYCARNLIAGGIDVWGQGSLTVS

>d7fabl1 b.1.1.1 (L:1-103) Immunoglobulin (variable domains of L and H chains) {Fab NEW (human),
lambda L chain}

ASVLTQPPSVGAPGQRVTISCTGSSNIGAGHNVKWYQQLPGTAPKLLIFHNNARFSVSKSGTSATLAITGLQA
EDEADYYCQSYDRSLRVFGGGTKLTVR

>d1bafh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab ANO2
(mouse), kappa L chain}

DVQLQESGPGLVKPSQSLSLTCTVTGYSITSDYAWNWRQFPGNKLEWMGYMSYSGSTRYNPLRSRISITRDT
SKNQFFLQLKSVTTEDTATYFCARGWPLAYWGQGTQVSVE

>d1bafl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab ANO2
(mouse), kappa L chain}

QIVLTQSPAIMSASPGEKVTMTCASSSVYYMYWYQQKPGSSPRLLIYDTSNLASGVPVRFSGSGSGTSLTISR
MEAEDAATYYCQQWSSYPPITFGVGTKELEK

>d1a3rh1 b.1.1.1 (H:2-119) Immunoglobulin (variable domains of L and H chains) {Fab 8F5 (mouse),
kappa L chain}

VQLQQSGAELVRPGASVKLSCTTSGFNIDYIHWVKQRPEQGLEWIGRLDPANGYTKYDPKFQGKATITVDT
SNTAYLHLSSLTSEDTAVYYCDGYYSYDDMDYWGPGETVSSAKTTAP

>d1a3rl1 b.1.1.1 (L:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 8F5 (mouse),
kappa L chain}

DIVMTQSPSSLTVTTGEKVTMTCKSSQSLNSRTQKNYLWYQQKPGQSPKLLIYWASTRESGVPDFRTGSGSG
TDFTLSISGVQAEDLAVYYCQNNNYPLTFGAGTKLELKRAADAAPT

>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}

EVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWAKQKPEQGLEWIGYISPGNDDIKYNEFKKGKATLTADKS
SSTAYMQQLNSLTSEDSAVYFCKRSYYGHWGQGTTLVSSA

>d1bbjl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab B72.3
(mouse/human chimera), kappa L chain}

DIQMTQSPASLSVSGETVTITCRASENIYSNLAWYQQKQGKSPQLLYAATNLADGVPSRFSGSGSGTQYSLKI
NSLQSEDFGSYYCQHFWGTPYTFGGGTRLEIKRA

>d1hila1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 17/9 (mouse),
kappa L chain}

DIVMTQSPSSLTVTAGEKVTMCTSSQSLFNSGKQKNYLWYQQKPGQPPKVLIYWASTRESGVPDFRTGSGS
GTDFLTISVQAEDLAVYYCQNDYSNPLTFGGGTKELEK

>d1hilb1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 17/9 (mouse),
kappa L chain}

EVQLVESGGDLVKPGGSLKLSCAASGFSFSSYGMWSVRQTPDKRLEWVATISNGGYTYPDSVKGRFTISRDN
AKNTLYLQMSSLKSEDSAMYCCARRERYDENGFAYWGQGTLTVS

>d1dbbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab DB3
(mouse), kappa L chain}

QIQLVQSGPELKPGETVKISCKASGYAFTNYGVNWVKEAPGKELKWMGWINIYTGEPTYVDDFKGRFAFSLET
SASTAYLEINNLKNEDTATYFCTRGDYVNWYFDVWGAGTTVTVS

>d1dbbl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab DB3 (mouse),

kappa L chain}

DVVMTQIPLSLPVNLGDQASISCRSSQSLIHNGNTYLHWYLQKPGQSPKLLMYKVSNRFYGVPDFSGSGSG
TDFTLKISRVEAEDLGIYFCSQSSHVPPTFGGGTKLEIK

>d1dfbh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and H chains) {Fab 3D6 (human), kappa L chain}

EVQLVESGGGLVQPGRSLRLSCAASGFTFNDYAMHWVRQAPGKGLEWVSGISWDSSSIGYADSVKGRFTISRD
NAKNSLYLQMNSLRAEDMALYYCVKGRDYDGGYFTVAFDIWGQQGTMVTVSS

>d1dfbl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab 3D6 (human), kappa L chain}

DIQMTQSPSTLSASVGDRVTITCRASQSISRWLAWYQQKPGKVKLIIYKASSLESGVPSRFSGSGSGTEFTLTIS
SLQPDDFATYYCQQYNSYSFGPGTKVDIIRR

>d1igfh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab B13I2 (mouse), kappa L chain}

EVQLVESGGDLVKPGGSLKLSCAASGFTFSRCAMSWRQTPERKLEWVAGISSGGSYTFYPDTVKGRFIISRN
ARNTLSQMSSLRSEDTAIYYCTRYSSDPFYFDYWGQQGTTLVSS

>d1igfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab B13I2 (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASISCRSNQTTLSQDGDTYLEWYLQKPGQSPKLLIIYKVSNRFSGVPDFSGSGSGTD
FTLKISRVEAEDLGVYYCFQGSHPPTFGGGTKLEIK

>d1igja1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 26-10 (mouse), kappa L chain}

DVVMTQTPLSLPVSLGDQASISCRSSQSLHSNGNTYLNWYLQKAGQSPKLLIIYKVSNRFSGVPDFSGSGSGT
DFTLKISRVEAEDLGIYFCSQTTHVPPPTFGGGTKLEIK

>d1igjb1 b.1.1.1 (B:2-114) Immunoglobulin (variable domains of L and H chains) {Fab 26-10 (mouse), kappa L chain}

VQLQQSGPELVKPGASVRMSCKSSGYIFTDFYMNWVRQSHGKSLDYIGYISPYSGVTGYNQFKKGATLTVDKS
SSTAYMELRSLTSEDSAVYYCAGSSGNKWAMDYWGHHGASVTVSSA

>d1igmh _ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv POT (human) IgM, kappa L chain}

EVHLLESGGNLVQPGRSLRLSCAASGFTFNIFVMSWVRQAPGKGLEWVSGVFGSGNTDYADAVKGRFTITR
DNSKNTLYLQMNSLRAEDTAIYYCAKHRVSYLTGFDSWGQGTIVTSSGSASAPTL

>d1igml _ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv POT (human) IgM, kappa L chain}

DIQMTQSPSSLSASVGDRVTITCQASQDISNYLAWYQQKPGKAPELRIYDASNLETGVPSRFSGSGSGTDFTFTI
SSLQPEDIATYYCQQYQNPLTFGPGTKVDIKRTVAAPSV

>d1dq|h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv MEZ (human) IgM, kappa L chain}

EVQLVESGGGLVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWVAVISSLGGNKYYTDSVKGRFTISRN
DSKNLYLQMNSLRATEDTAVFYCARGNPPYSSGWGGGDYWGQQGTMVTVSS

>d1dq|l_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv MEZ (human) IgM, kappa L chain}

DIQMTQSPSSLSASVGDRVTITCRASQDIRNDLGWYQQKPGKAPKKLIYAASSLQSGVPSRFSGSGSGTDFTLT
SSLQPEDFATYYCLQQNSNWTFGQGTTKVDIK

>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}

EIVLTQSPATLSLSPGERATLSCGASQSVSSNYLAWYQQKPGQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTIS
RLEPEDFAVYYCQQYGSPLTFGGGTKEI

>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}

EVQLQQWGAGLLKPSETSLTCAVYGGSFSDYYWSWIRQPPGKGLEWIGEINHGSTNPNPSLKSRTVISVDT
KNQFSLKLSSVTAADTAVYYCARPPHDTSGHYWNWQGQGTLVTVSS

>d1indh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab Cha255 (mouse), lambda L chain}

EVTLVESGGDSVKPGGSLKLSCAASGFTLSGETMSWVRQTPEKRLEWVATTLSGGGFTFYSASVKGRFTISRDN
AQNNLYLQLNSLRSEDTALYFCASHRFVHWGHGTLVTVA

>d1faih1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Fab R19.9 (mouse), kappa L chain}

QVQLQQSGAELVRAGSSVKMSCKASGYTFTSYGVNVVKQRPGQGLEWIGYINPGKGYLSYNEKFKGKTTLV
DRSSSTAYMQLRSLTSEDAAVYFCARSFYGGSDLAVYYFDSWGQGTTLV

>d1fail1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab R19.9 (mouse), kappa L chain}

DIQMTQTTSSLASLGDRVTICRASQDISNYLNWYQQKPDGTVKLIYTSRLHSGVPSRFSGSGSGTDYSLTIS
NLEHEDIATYFCQQGSTLPRTFGGGTKLEIKR

>d2fb4h1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab KOL (human), lambda L chain}

EVQLVQSGGGVVQPGRSRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHYADSVKGRFTISRN
DSKNTLFLQMDSLRPEDTGVFYFCARDGGHGFCSSASCFGPDYWGQGTPTVSSA

>d2fb4l1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab KOL (human), lambda L chain}

QSVLTQPPSASGTPGQRVTISCGTSSNIGSSTNVWYQQLPGMAPKLLIYRDAMRPSGVPDFSGSKSGASASL
AIGGLQSEDETDDYCAAWDVSLNAYVFGTGTKVTVLG

>d2fbjh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and H chains) {Fab J539 (mouse), kappa L chain}

EVKLLESGGGLVQPGGSLKLSCAASGFDFSKYWMWSWVRQAPGKGLEWIGEIHPDSGTINYTPSLKDKFIISRDN
AKNSLYLQMSKVRSEDTALYYCARLHYYGNAYWGQGTLVTVSA

>d2fbjl1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab J539 (mouse), kappa L chain}

EIVLTQSPAITAASLGQKVITCSASSVSSLHWYQQKSGTSPKPWIYEISKLASGVPARFSGSGSGTSLINTME
AEDAAIYYCQQWTYPLITFGAGTKLELKRAD

>d1fgvh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab H52 (synthetic, humanised version), kappa L chain}

EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSYADSVKGRFTISV
DKSKNTLQMNLSRAEDTAVYYCARWRGLNYGFDVRYFDVWGQGTLVTVSS

>d1fgvl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab H52 (synthetic, humanised version), kappa L chain}

DIQMTQSPSSLSASVGDRVITCRASQDINNYLNWYQQKPGKAPKLLIYYTSTLESGVPSRFSGSGSGTDYTLTIS
SLQPEDFATYYCQQGNTLPPTFGAGTKVEIK

>d2fgwh1 b.1.1.1 (H:1-124) Immunoglobulin (variable domains of L and H chains) {Fab H52}

(synthetic, humanised version), kappa L chain}

EVQLVESGGGLVQPGGSLRLSCATSGYTFTEYTMHWMRQAPGKGLEWVAGINPKNGGTSHNQRFMDRFTIS
VDKSTSTAYMQMNSLRAEDTAVYYCARWRLNYGFVRYFDVWGQGTLTVSS

>d1mcph1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab MCPC603 (human), kappa L chain}

EVKLVESGGGLVQPGGSLRLSCATSGFTSDFYMEWVRQPPGKRLEWIAASRNKGNKYTTEYSASVKGRFIVSR
DTSQSILYLQMNALRAEDTAIYYCARNYYGSTWYFDVWGAGTTVTS

>d2imn__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Fab MCPC603 (human), kappa L chain}

DIVMTQSPSSLSVSAGERVTMSCKSSQSLLYKDGKNFLAWYQQKPGQPPKLIYGASTRESGVPDFRTGSIGT
DFTLTISSVQAEDLAVYYCQNDHSYPLTFGAGTKLELKR

>d1fvca_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Fab 4D5 (synthetic, humanised version), kappa L chain}

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLIYSASFYSGVPSRFSGSRSGTDFTLTIS
SLQPEDFATYYCQQHYTPPTFGQGTVKEIKRT

>d1fvcb_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Fab 4D5 (synthetic, humanised version), kappa L chain}

EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADT
SKNTAYLQMNSLRAEDTAVYYCSRWWGGDGFYAMDYWGQGTLTVSS

>d1ggbh1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 50.1 (mouse), kappa L chain}

QVQLQESGPGILQPSQTLSTLCFSFGSLSTYGMGVSWIRQPSGKGLEWLAHIFWDGDKRYNPSLKSRLKISKDT
SNNQVFLKITSVDTADTATYYCVQEGYIYWGQGTSVTS

>d1ggbI1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 50.1 (mouse), kappa L chain}

DIVLTQSPGSLAVSLGQRATISCRASESVDDDGSFLHWYQQKPGQPPKLIYRSSNLISGIPDRFSGSGSRDFT
LTINPVEADDVATYYCQQSNEDPLTFGAGTKLEIK

>d1ai1h1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 59.1 (mouse), kappa L chain}

QVKLQESGPAVIKPSQSLTICVSGFSITRTNYCWHIRQAPGKGLEWMGRICYEGSIYSPSIKSRSRSTISRDTS
NKFFIQLISVTNEDTAMYCSRENHMYETYFDVWGQGTTVTS

>d1ai1l1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 59.1 (mouse), kappa L chain}

DIVMTQSPASLVSLGQRATISCRASESVDSYGKSFMHWYQQKPGQPPKVLIIYIASNLESGVPARFSGSGSRDFT
TLTIDPVEADDATYYCQQNNEDPPTFGAGTKLEMRR

>d1mamh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab Yst9.1 (mouse), kappa L chain}

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMSWVRQPPGKALEWLGFIRNKADGYTTEYSASVKGRFTISR
DNSQSILYLQMNTLRAEDSATYYCTRDPYGPAAWGGQGTLTVSA

>d1maml1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab Yst9.1 (mouse), kappa L chain}

DIQMTQTTSSLASLGDRVTISCRASQDIYNYLNWYQQKPDGTVKLLIYTSLRHSGVPSRFSGSGSGTDYSLTIS
NLNQEDMATYICQQQNTLPFTFGSGTKLEIKR

>d1mfa_1 b.1.1.1 (1L-111L) Immunoglobulin (variable domains of L and H chains) {Fab SE155-4

(mouse), lambda L chain}

QIVVTQESALTTSPGETVLTCSRSTGTVTSGNHANWVQEKPDLFTGLIGDTNNRAPGVPARFSGSLIGDKAA
LTITGAQPEDEAIYFCALWSNNHWIFGGGTKLTVLGQ

>d1mfa_2 b.1.1.1 (251H-367H) Immunoglobulin (variable domains of L and H chains) {Fab SE155-4 (mouse), lambda L chain}

EVQVQQSGTVVARPGASVKMSCKASGYTFTNYWMHWIKQRPGQGLEWIGAIYPGNSATFYNHKFRAKTKLT
AVTSTTTAYMELSSLTSEDAVYYCTRGHHGYYGDYWGQGASLTVS

>d1nbvh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab BV04-01 (mouse), kappa L chain}

EVQPVETGGGLVQPK GSLKLSCAASGFSFTNAMNWVRQAPGKGLEWVARIRSKSNNYATYYADSVKDRFTIS
RDDSQNMLYLMQMNLLKTEDTAMYCVRDQTGTAWFAYWGQGTLTVSAA

>d1teth1 b.1.1.1 (H:1-112) Immunoglobulin (variable domains of L and H chains) {Fab TE33 (mouse), kappa L chain}

QIQLVQSGPELKTPGETVRISCKASGYTFTTYGMSWVKQTPGKGFKWGMGWINTYSGVPTYADDFKGRFAFSLE
TSASTAYLQINNLKNEDTATYFCARRSWYFDVWGTGTTVTS

>d1tetl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TE33 (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASISCKSSQSIVHSSGNTYFEWYLQKPGQSPKLLIYKVSNRSGVPDRFSGSGSGTD
FTLKISRVEAEDLGVYYCFQGSHPFTFGSGTKLEIK

>d1flrh1 b.1.1.1 (H:1-118) Immunoglobulin (variable domains of L and H chains) {Fab 4-4-20 (mouse), kappa L chain}

EVKLDETGGGLVQPGRPMKLCVVASGFTFS DYWMNWVRQSPKGLEWVAQIRNKPYNYETYYSDSVKGRFTI
SRDDSKSSVYLQMNLLRVEDMGIYYCTGSYYGMDYWGQGTSVTVSS

>d4fabl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 4-4-20 (mouse), kappa L chain}

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSQGNTYLRWYLQKPGQSPKVLIVKVSNRSGVPDRFSGSGSGT
DFTLKISRVEAEDLGVYFCQS QSTHVPWTFGGGTKLEIK

>d1jfqh1 b.1.1.1 (H:302-421) Immunoglobulin (variable domains of L and H chains) {Fab 36-71 (mouse), kappa L chain}

VQLQQSGVELVRAGSSVKMSCKASGYTFTSNGINWVKQRPGQGLEWIGYNPNPGNGYITYNEFKKGKTTLTVD
KSSNTAYMQLRSLTSEDAVYFCARSEYYGGSYKFDYWGQGTTLVSS

>d1jfql1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 36-71 (mouse), kappa L chain}

DIQMTQIPSSLSASLGDRVISCRASQDINNFLNWYQQKPDGTIKLLIYFTSRSGVPSRFSGSGSGTDYSLTISN
LEQEDIATYFCQQGNALPRTFGGGTKLEIKR

>d1gigh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab HC19 (mouse), lambda L chain}

QVQLKESGPGLVAPSQSLSITCTVSGFLLISNGVHWVRQPPGKGLEWLGVIWAGGNTNYNSALMSRVSISKDN
SKSQVFLKMKSLOQDDTAMYCCARDFYDYDVFYAMDYWGQGTSVT

>d2cgrh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Fab, anti-sweetener (mouse), kappa L chain}

RVQLLESGAELMKGASVQISCKATGYTFSEYWIEWVKERPGHGLEWIGEILPGSGRTNYREKFKGKATFTADTS
SNTAYMQLSSLTSEDAVYYCTRGYSSMDYWGQGTSVTVSA

>d2cgri1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab, anti-

sweetener (mouse), kappa L chain}

ELVMTQSPSLPVS LGDQASISCRPSQLVHSNGNTYLHWYLQKPGQSPKLLIYRVSNRFSGVPDRFSGSGSGTA
FTLKISRVEAEDLGVYFC SQGTHV PYTFGGGT KLELK

>d1fig1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 1F7 (mouse),
kappa L chain}

DVQLQQSGPELEKPGASVKISCKASGFSLPGHNINWIVQRNGKSLEWIGNIDPYGGTNFNPFKGKATLTVDK
SSSTLYMHLTS LQSEDSAVYYCARR RDGNYGFTYWGQGTLVTVA

>d1fig1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 1F7 (mouse),
kappa L chain}

ENVLTQSPA IM SASP GEKV T MACRASS VS STYLHWYQQKSGASP KLLIYSTS NLASGV PAR FSGSGSGT SYSLTI
SSVE AEDA AT YYC QQYSGYPLTF GAGTKLELKR

>d1frgh1 b.1.1.1 (H:218-336) Immunoglobulin (variable domains of L and H chains) {Fab 26/9
(mouse), kappa L chain}

EVLLVESGGDLV KPGFLKLSCA ASGFTFSSFGMSW VRHTPD KRLEW VAT ISNGGY TYQDSVKG RFT ISRD N
AKNTLFLEM TLKSE D AGLY CARR ERYDE KGFAY WGRG TLVT V S

>d1frgl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 26/9 (mouse),
kappa L chain}

DIVMTQSPS SLTV TAGE KV TM SCKSS QSL FN SGK RKN FLTW YHQ KPGQ PPK L IYWA STR ESGV PDR FSGSG SG
TDFTLTIT SVQA EDLAI YYC QNDY SHPLT FGAGT KLELK

>d1a2ya_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3 (mouse),
kappa L chain}

DIVLTQSPASLSASVGETVTITCRASGN IHN YLA WYQQKQGKSPQLLVYYTTLADGVPSRFSGSGSGTQ YSLK IN
SLQPEDFGSY YCQHF WSTP RTFGGGT KLEIK

>d1a2yb_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3 (mouse),
kappa L chain}

QVQLQESGP GLVAPS QSL SITCTVSGFS LTGYGVN WVRQPPGK GLEWL GM IWGDGNTD YNSALK SRLS ISKD N
SKSQVFLKM NSLHTDDTARYY CARER DYRLD YWGQ GTT LTVSS

>d1a7ql_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab D1.3 (mouse),
kappa L chain}

DIVLTQSPASLSASVGETVTITCRAG GN TH NYLA WYQQKQGKSPQLLVYYTTLA AGVPSRFSGSGSGTQ YSLK I
NSLPQDDFGSY YCQHF WSTP RSF GGGT KLEI

>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}

DIVMTQSHKF MSTS VGD RV SITCK ASQDV RI AVAWYQQKQGQSPKLLIYWA STR HTGV PDR FTGSGSG TDFTL
TISNVQSE DLADYFCQHC GSYPFTFGSGT KLEIK

>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}

QVQLQQPGSELVR PGASV KLS CKAS GY TFIS YWINWVK QRP GQGLEWIGNI YPGSGD SNYDEKFKSKATLTV
DTSSSTAYMQLSGL TSE DSAVYYC ARGLAFYFDHWGQ GTT LTVSS

>d1jhlh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv D11.15 (mouse),
kappa L chain}

QVQLQQSGA ELVR PGASV KLS CKAS GY TFIS YWINWVK QRP GQGLEWIGNI YPSDSY TNYNQFKDKATLTV
KSSSTAYMQLSSPTSE DSAVYYC TRDD NYGAMD YWGQ GTT LTV

>d1jhll_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv D11.15 (mouse),

kappa L chain}

DIELTQSPSYLVASPGETITINCRASKSISKSLAWYQEKGKTNNLLIYSGSTLQSGIPSRSFGSGSGTDFTLTISLEP
EDFAMYICQQHNEYWPWTFGGGTKLEIKR

>d1bqjh1 b.1.1.1 (H:2-116) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-5
(mouse), kappa L chain}

VQLQQSGAELMKPGASVKISCKASGYTFSDYWIEWVKQRPGHGLEWIGEILPGSGSTNYHERFKGATFTADT
SSSTAYMQLNSLTSEDSGVYYCLHGNYDFDGWGQGTTLVSS

>d1bql1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-5
(mouse), kappa L chain}

DIVLTQSPAAMSASPGEKVTMTCASSSVNYMYWYQQKSGTSPKRWIYDTSKLASGPVVRFSGSGSGTSYSLTIS
SMETEDAATYYCQQWGRNPTFGGGTKLEIKR

>d1ic7h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab HyHEL-10 (mouse),
kappa L chain}

DVQLQESGPSLVKPSQLSLTCVTGDSITSAYWSWIRKFPGNRLEYMGYVSYSGSTYYNPSLKSRSITRDTSKN
QYYLDLNSVTTEDTATYYCANWAGDYWGQGTLTVSAA

>d2jelh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab JE142
(mouse), kappa L chain}

QVLAQSGPELVRPGVSVKISCKASGYTFTTYAMHWVKQSHAKSLEWIGLISTYSGYTNYNQKFKGKATMTVD
KSSSTAYMELARLTSEDSAIYYCARVMGEQYFDVWGAGTTIVSS

>d1ncbh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab NC41
(mouse), kappa L chain}

QIQLVQSGPELKPKGETVKISCKASGYTFTNYGMNWVKQAPGKGLEWMGWINTNTGEPTYGEEFKGRFAFSL
ETSASTANLQINNLKNEDKATFFCARGEDNFGSLSDYWGQGTTLVSS

>d1ncbl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab NC41
(mouse), kappa L chain}

DIVMTQSPKFMSTVGDRVTITCKASQDVSTAVVWYQQKPGQSPKLLIYWASTRHIGVPDRFAGSGSGTDYTL
TISSVQAEDLALYYCQQHYSPPWTFGGGTKEIKR

>d1forh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 17-1a
(mouse), kappa L chain}

QGQLQQSGAELVRPGSSVKISCKASGYAFSSFWVNWKQRPGQGLEWIGQIYPGDGDNKYNGKFKGKATLTA
DKSSTAYMQLYSLTSEDAVYFCARSGNYPYAMDYWGQGTSVTVSSA

>d1forl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 17-1a (mouse),
kappa L chain}

QIVLTQSPAIMSAPGEGKVTITCSATSSVNYMHWFQQKPGTSPKLWIYSSNLASGPVPARFSGSGSGTSYSLTISR
MEAEDAATYYCQQRSSYPITFGSGTKLEIKR

>d1knoa1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Fab CNJ206
(mouse), kappa L chain}

QIQMTQSPSSLSASLGERVSLTCRASQEISGYLSWLQQKPDGTIKRLIYAASTLDSGVPKRFSRSRGSDYSLTISL
ESEDFADYYCLQYASSPYTFGGGTKEILR

>d1knob1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Fab CNJ206
(mouse), kappa L chain}

DVKLVESGGGLVQPGGSRKLSAACSGFTSSFGMHWRQAPEKGLEWVAYISSGSSTIYYADTVKGRFTISRDN
PKNTLFLQMTRLSEDTAMYCARGDYYGSRGAYWGQGTLTVSA

>d1eapb1 b.1.1.1 (B:1-124) Immunoglobulin (variable domains of L and H chains) {Fab 17E8

(mouse), kappa L chain}

EVQLQESGTELVKPGASVKISCKASGYISTDHAIHWVKQRPEQGLEWIGYISPGNGDIKYNEKFVVKATLTADQS
SSTAYMQLNSLTSEDSAVIDYFCKRSYYGSSYVDYWGQGTTLVSS

>d1mrdh1 b.1.1.1 (H:2-115) Immunoglobulin (variable domains of L and H chains) {Fab Jel 103
(mouse), kappa L chain}

VQLQQSGAELVKPGASVKLSCKASGYTFTSYWMQWVKQRPGQGLEWIGEIDPSDSYTNYNQFKGKATLTVD
TSSSTAYMQLSSLTSEDSAVIDYFCKRSYYGSSYVDYWGQGTTLVSSAK

>d1fbih1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab F9.13.7
(mouse), kappa L chain}

QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYWMHWVKQGPQGLEWIGEIDPSDSYPNYNEKFKGKATLT
DKSSSTAYMQLSSLTSEDSAVIDYFCKRSYYGSSYVDYWGQGTTLVSS

>d1fbil1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab F9.13.7
(mouse), kappa L chain}

DIQMTQTSSLSASLGDRVTISCRASQDISNYLNWYQKKPDGTVKLLIYYTSRLHSGVPSRFSGSQGTDYSLIR
NLEQEDIATYFCQQGYTLPYTFGGGTKEIK

>d1rmfh1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab R6.5
(mouse), kappa L chain}

QVQLQQSGPELVRPGVSVKISCKGSGYTFIDYAIHWVKESHAKSLEWIGVISAYSGDTNYNQFKGKATMTVDK
SSNTAYLELARLTSEDSAVIDYFCKRSYYGSSYVDYWGQGTTLVSS

>d1rmfl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab R6.5 (mouse),
kappa L chain}

DVVMTQSPLSLPVSLGDQASISCRSSQSLVHSNGNNYLHWYLQKSGQAPKLLIYKVSNRFSGVPDFSGSGSGT
DFTLKISRVEAEDLGVYFCSQSTHVPLTFGGGTKEIK

>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}

QVQLQQSGAELVRPGTSVKVSCKASGYAFTNYLIQWKQRPGQGLEWIGVINPGSGGTDYNANFKGKATLTAD
KSSSIVYMQLSSLTSDSAVIDYFCKRSYYGSSYVDYWGQGTTLVSS

>d1fptl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab C3,
neutralizing type 1 poliovirus, (mouse), kappa L chain}

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGKTYLHWYLQKPGQSPKLLIYKVSNRFSGVPDFSGSGSGT
FTLKISRVEAEDLGVYFCSQSTHVPTFGGGTKEIKR

>d1ikfh1 b.1.1.1 (H:1-126) Immunoglobulin (variable domains of L and H chains) {Fab, anti-
cyclosporin A, (mouse), kappa L chain}

EVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYWVRQNSEKRLEWVAFISNGGSAFYADIVKGRFTISRD
AKNTLYLQMSRLKSEDTAMYCTRHTLYDTLYGNYPVWFADWGQGTLTVSA

>d1ikfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab, anti-
cyclosporin A, (mouse), kappa L chain}

DIQMTQTSSLSASLGDRVTISCRASQDISTYLNWYQQKPDGTVKLLIIFYTSRLRGVPSRFSGSQGTDYSLISN
LEQEDIATYFCQQGSRIPPTFGGGTKEIL

>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}

VQLQQSGTELMKPGRSLKISCKTTGYIFSNWIEWVKQRPGHGLEWIGKILPGGGNTYNDFKGKATFTADTS
SNIAYMQLSSLTSEDSAVIDYFCKRSYYCARGEDYYAYWVLDYWGQGTTVSSGGGG

>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}

DIELTQSPLSLPVSLGDQASISCRSSQLVHSNGNTSLHWYLKKPGQSPKLLIYKVSTRFSGVPDRFSGSGSGTDF

TLKISRVEAEDLGVYFCSQSTHPFTFGSGTKLEK

>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}

DIELTQTPLSLPVSLGDQASISCRSSQSVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDF

TLKISRVEAEDLGVYCFQGSHVPYTFGGGTKEIKR

>d1igch1 b.1.1.1 (H:1-119) Immunoglobulin (variable domains of L and H chains) {Fab MoPC21 (mouse), kappa L chain}

DVQLVESGGGLVQPGGSRKLSAACSGFTFSSFGMHWVRQAPEKGLEWVAYISSGSSTLHYADTVKGRFTISRD

NPKNTLFLQMITSRSEDTGMYYCARWGNYPYYAMDYWGQGTSVTVS

>d1igcl1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab MoPC21 (mouse), kappa L chain}

NIVMTQSPKSMMSMSVGERVTLCKASENVVTYVSWYQQKPEQSPKLLIYGASNRTGVPDRFTGSGSATDFTLT
ISSVQAEDLADYHCGQGQNSPYTFGGGTKEIKR

>d1ibgh1 b.1.1.1 (H:2-113) Immunoglobulin (variable domains of L and H chains) {Fab 40-50 (mouse), kappa L chain}

VHLVQSGPGLVAPSQSLITCTVSGFSLTTYGHWFRQPPKGLEWLGLIWAGGNTDYNALMSRLSINKDNS
KSQVFLKMNSLQADDTAMYCARFRFASYDYAVDYWGQGTSVTVSS

>d1ibgl1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and H chains) {Fab 40-50 (mouse), kappa L chain}

IVLTQSPASLAvgQRATISCRASKSVSTGYSIHWHYQQKPGQPPKLLIYLASILESGVPARFSGSGSGTDFTLN
HPVEEDAATYYCQHSREYPLTFGAGTELEK

>d1mlbb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and H chains) {Fab D44.1 (mouse), kappa L chain}

QVQLQESGAEVMKPGASVKISCKATGYTFSTYIEWVKQRPGHGLEWIGEILPGSGSTYYNEFKKGKATFTADT
SSNTAYMQLSSLTSEDSAVYYCARGDGNYGYWGQGTTVSSAS

>d1a14h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fab NC10 (mouse), kappa L chain}

QVQLQQSGAELVKPGASVRMSCKASGYFTFTNMYWVKQSPGQGLEWIGIFYPNGDTSYNQFKDKATLT
ADKSSNTAYMQLSSLTSEDSAVYYCARGGSYRYDGGFDYWGQGTTVTV

>d1a14l_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab NC10 (mouse), kappa L chain}

DIELTQTTSSLSASLGDRVТИCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGSGSGTDYSLTIS
LEQEDIATYFCQQDFTLPFTFGGGTAA

>d1nmb1_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fab NC10 (mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVТИCRASQDISNYLNWYQQNPDGTVKLLIYYTSNLHSEVPSRFSGSGSGTDYSLTIS
NLEQEDIATYFCQQDFTLPFTFGGGTKEIRRA

>d1bm3h1 b.1.1.1 (H:1-125) Immunoglobulin (variable domains of L and H chains) {Anti-integrin Fab OPG2 (mouse), kappa L chain}

EVQLVQSGGGLVNPGRSKLCAASGFTFSSYGMSWVRQTPEKLEWVAISGGTYIHYPDSVKGRFTISRD
AKNNLYLQMSSLRSEDTALYYCTRHPFYRYDGGNYYAMDHWGQGTSVTVSA

>d1nsnh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab N10}

(mouse), kappa L chain}

DVQLQESGPLVKPSQLSLCTVTGYSITSDYAWNWRQFPGNKLEWMGYITYSGTTSYNPSLKSRSISRDTSK
NQFFMQLNSVTTEDTGTFYCTRGNGDWGQGTTLVSSA

>d1nsnl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab N10 (mouse),
kappa L chain}

DIVLTQSPSSLAVSLGQRATISCRASQSVSTSSFRYMHWYQQKPGQPPRLLIKYASNLESGVPARFSGSGSGTDFT
LNIHPVEEEDTATYYCQHSWEIPYTFGGGTKLEIK

>d1iaih1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Fab 730.1.4
(mouse), kappa L chain}

QIQLVQSGPELKPKGETVKISCKASGYTFTNYGMNWVKQAPGKGLKWMMAWINTYTGEPTYADDFKGRFAFL
ETSASTAYLQINNLKNEDTATYFCARDGYYENYYAMDYWGQGTSVTVSS

>d1ial1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab 730.1.4
(mouse), kappa L chain}

DIVMTQSHKFMSTSVGDRVSITCKASQDVSTAVAWYQQKPGQSPKLLIYSASYQYTGVPDFRTGSGSRDFTFT
INSVQAEDLAVYYCHQHYSTPFTFGSGTKLEIKR

>d1iaii1 b.1.1.1 (I:1-121) Immunoglobulin (variable domains of L and H chains) {Fab 409.5.3
(mouse), kappa L chain}

EVKLQESGGGLVQPGGSMKLSCVASGFTFNNYWMSWVRQSPEKGLEWVAEIRLNSDNFATHYAESVKGKFIIS
RDDSKSRLYLMQNSLRAEDTGIIYCVLRPLFYAVDYWGQGTSVTVSS

>d1iam1 b.1.1.1 (M:1-109) Immunoglobulin (variable domains of L and H chains) {Fab 409.5.3
(mouse), kappa L chain}

DIQLTQSPAFAASPGEKVTITCSVSSSISSNLHWYQQKSETSPKPWIYGTSNLASGVPVRFSGSGSGTSLTIS
SMEAEDAATYYCQQWNSYPYTFGGGTKEIKR

>d1plgh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Polysialic acid-
binding Fab (mouse), kappa L chain}

QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRPGEGLEWIGWIYPGSGNTKYNEFKKGATLTVDT
SSSTAYMQLSSLTSEDSAVYFCARGGKFAMDYWGQGTSVTVSS

>d1plgl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Polysialic acid-
binding Fab (mouse), kappa L chain}

DVVMTQTPLSLPVSLGDQASISCRSSQSLVHSNGNTLYWYLQKPGQSPKPLIYRVSNRFSGVPDRFSGSGSGT
DFTLKISRVEAEDLGVYFCFQGTHVPYTFGGGTRLEIK

>d1aj7h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 48G7
(mouse/human), kappa L chain}

QVQLQQSGAELVKPGASVKLSCTAGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITA
DTSSNTAYLQLSSLTSEDTAVYYCASYYGIYWQGTTLVSSA

>d1gafh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 48G7
(mouse/human), kappa L chain}

QVQLQQSGAELVKPGASVKLSCTAGFNIKDTYMHWVKQRPKQGLEWIGRIDPANVDTKYDPKFQDKATITAD
TSSKTTYQLSSLTSEDTAVYYCASYYGIYWQGTTLVSS

>d1gaf1 b.1.1.1 (L:1-109) Immunoglobulin (variable domains of L and H chains) {Fab 48G7
(mouse/human), kappa L chain}

DIQMTQSPSSLSASLGERVSLTCRASQEINGYLGWLQQKPDGTIKRLIYAASTLHSGVPKRSGSRSGSDYSLTISS
LESEDFADYYCLQYASYPRTFGGGTKVEIKRT

>d1vgeh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab TR1.9}

(mouse/human), kappa L chain}

QVKLLEQSGAEVKKPGASVKVSKASGYSFTSYGLHWVRQAPGQRLEWMWISAGTGNTKYSQKFRGRVTFTRDTSATTA
MGLSSLRPEDTAVYYCARDPYGGKSEFDYWQQGTLTVSS

>d1vgel1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TR1.9
(mouse/human), kappa L chain}

ELVMTQSPSSLSASVGDRVNIACRASQGISSALAWYQQKPGKAPRLLIYDASNLESGVPSRFSGSGSGTDFTLTIS
SLQPEDFAIYYCQQFNSYPLTFGGGTKEIK

>d1yuhb1 b.1.1.1 (B:1-118) Immunoglobulin (variable domains of L and H chains) {Fab anti-
nitrophenol (mouse), lambda L chain}

QVQFQQSGAELVKPGASVKLSCKASGYTFTSYLMHWIKQRPGRLWIGRIDPNNVTKFNEKFKSKATLTV
KPSSTAYMELSSLTSEDAVYYCARYAYCRPMFYWGQQGTTVTVSS

>d1ucbh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab CBR96
(mouse/human), kappa L chain}

EVNLVESGGGLVQPGGSLKVSCVTSGFTSDYYMYWVRQTPEKRLEWVAYISQGGDITDYPDTVKGRFTISRDN
AKNSLYLQMSRLKSEDTAMYYCARGLDDGAWFAYWGQQGTLTVSV

>d1ucbl1 b.1.1.1 (L:4-108) Immunoglobulin (variable domains of L and H chains) {Fab CBR96
(mouse/human), kappa L chain}

MTQIPVSLPVSLGDQASISCRSSQIIVHNNGNTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDFSGSGSGTDFTL
KISRVEAEDLGVYYCFQGSHPFTFGSGTKLEIKR

>d1dvfc_ b.1.1.1 (C:) Immunoglobulin (variable domains of L and H chains) {Fv E5.2 (mouse), kappa
L chain}

DIQLTQSPSSLSASLGDRVVTISCRASQDISNYLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGSGTDYSLTISN
LEQEDIATYFCQQGNTLPWTFGGGTKLEIK

>d1dvd_ b.1.1.1 (D:) Immunoglobulin (variable domains of L and H chains) {Fv E5.2 (mouse), kappa
L chain}

QVQLQQSGTELVKGASVKLSCTASGFNIKDTHMNWVKQRPEQGLEWIGRIDPANGNIQYDPKFRGKATITAD
TSSNTAYLQLSLTSEDTAVYYCATKVIYYQGRGAMDYWGQQGTTVSV

>d1ghfh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab GH1002
(mouse), kappa L chain}

VQLQQSGPELKPGETVKISCKLWYTFTDYGMMNWVKQAPGKGLKWMGWIQTNTEEPTYGAEFKGRFAFSLET
SAFTAYKQINNLKNEDMATYFCARVEAGFDYWAQGTTLVSS

>d1ghfl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab GH1002
(mouse), kappa L chain}

DIQMTQTTSSLSASLGDRVVTISCRSQDISNSLNWYQQKPDGTVKLLIYYTSRLHSGVPSRFSGSGTGT
DYSLTISNLEQEDFATYFCQQGNTLPYTFGGGTKEIK

>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}

QVKLQQSGPGLVQPSQLSITCTVSGFSITCYGVHWVRQSPGKGLEWLGVWSGGD
TDYNAAFISRLSITKDNSKSQVFFKMNSLQPNDR
AIYYCARRGGDFWGQQGTTVSV

>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}

DVVMTQTPLTLSVTIGQPASISCKSSQSL
LDSDGKTYLNWLLQRPQSPKRLIYLVSKLD
SGVPDFRTGSGSGTDFTLKISRVEAEDLGVYYCW
QGTHFPRTFGGGTKLEIK

>d1kelh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab 28B4

{mouse), kappa L chain}

EVKLVESGGGLGQPQPGSLRLSCATSGFTFTDYYFNWARQPPGKALEWLGFIRNKAKGYTTEYSASVKGRFTISR

DNSQGILYLQMNTLRAEDSATYYCARWGSYAMDYWQGQGTSV

>d1kell1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 28B4 (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASISCRFSQSIVHSNGNTYLEWYLQKSGQSPKLLIYKVSNRSGVPDRFSGSGSGTD
FTLKISRVEAEDLGVYYCFQGSHVPRTFGGGTKLEIK

>d1osph1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}

EVQLQESGPSLVKPSQTLSTCCTGEPISTGFWDWIRKFPGNKEFMGYIRYGGGTYYNPSLKSPISITRDTSKN
HYYLQLNSVVTEDTATYYCARSRDYYGSSGFAFWGEGLTVSA

>d1ospl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}

DIQMSQSSSFSVLGDRVITCKASEDIYSRLAWYQQKPGNAPRLLISGATSLETWVPSRFSGSDSGKDYTLSIT
SLQTEDVATYFCQQYWSPPPTFGGGTKLEIK

>d1fj1a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab LA-2 (mouse), kappa L chain}

DIQMTQSPSSLSATLGGKVITCKASQDINKYIAWYQHKPGKGPRLLIHYTSTLQPGNPSRFSGSGSGRDYSFSIS
NLEAEDIAIYYCLQYDNLQRTFGGGTKVEIK

>d1fj1b1 b.1.1.1 (B:1-114) Immunoglobulin (variable domains of L and H chains) {Fab LA-2 (mouse), kappa L chain}

QIQLVQSGPELKPGETVKISCKASGYTFDYSMYWWKQAPGKGLKRMGWINTETGEPTYADDFKGRFALSLD
TSASTAYLHISNLKNEDTATYFCARGLD SWGQGTSVTVSSA

>d1cloh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (mouse), kappa L chain}

EVKLVESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQPPGKALEWLGFIGNKANGYTTEYSASVKGRFTISR
DKSQSILYLQMNTLRAEDSATYYCTRDRGLRFYFDYWGQGTTLVSS

>d1clo1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (mouse), kappa L chain}

QTVLSQSPA ILSASPGEKVMTCRASSVTYIHWYQQKPGSSPKSWIYATSNLASGVPARFSGSGSGTSYSLTISR
VEAEDAATYYCQHWSSKPPTFGGGTKLEIK

>d1ad0a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (engineered human construct), kappa L chain}

QTVLTQSPSSLSVGDRVITCRASSVTYIHWYQQKPGLAPKSLIYATSNLASGVPSRFSGSGSGTDYTFISSL
QPEDIATYYCQHWSSKPPTFGQGTTKVEVKR

>d1ad0b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A5B7 (engineered human construct), kappa L chain}

EVQLLESGGGLVQPGGSLRLSCATSGFTFTDYYMNWVRQAPGKGLEWLGFIGNKANGYTTEYSASVKGRFTIS
RDKSKSTLYLQMNTLQAEDSAIYYCTRDRGLRFYFDYWGQGTTLVSS

>d1mimh1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab CHI621 (mouse), kappa L chain}

QLQQSGTVALRPGAVKMSCKASGYSFTRYWMHWIKQRPGQGLEWIGAIYPGNSDTSYNQKFEKGAKLTAV
TSASTAYMELSSLTHE DSAVYYCSRDYGYFD FWGQGTTLVSS

>d1mimi1 b.1.1.1 (L:1-105) Immunoglobulin (variable domains of L and H chains) {Fab CHI621

(mouse), kappa L chain}

QIVSTQSPAAMSASPGEKVTMTCASSSRSYM**WYQQKPGTSPKRW**IYDTSKLASGVPARFSGSGSGTSLTIS
SMEAEDAATYYCHQRSSYTGGGT**KLEIKR**

>d1afvh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Fab 25.3 (mouse),
kappa L chain}

QVQLQQPGSVLVRPGASVKLSCKASGYTFTSSWIHWAKQRPGQGLEWIGEIH**PNSGNTNYNEKFKGKATLTV**
DTSSSTAYVDLSSLTSEDSAVYYCARWRYGSPYYFDYW**GQGTTLVSS**

>d1afvl1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab 25.3 (mouse),
kappa L chain}

DIVLTQSPASLA**VSLGQRATISCRASESVDNYGISFMNWFQQKPGQPPKLLIYAASNLGSGVPARFSGSGSGTDF**
SLNIHPMEEEDTAMYFCQQSK**EVPLTFGAGTKVELKR**

>d2mpah1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Bactericidal
Fab MN12H2, (mouse), kappa L chain}

EVNLQQSGTVLARP**ASVRMSCKASGYSFTSYWLHWIKQRPGQGLEWIGGIYPGNRDTRYTQRFKD**KAKLTA
VTSANTAYMELSSLTNEDSAVYYCSIIYFDYADFIMDYWG**QGTTVSS**

>d2mpal1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Bactericidal Fab
MN12H2, (mouse), kappa L chain}

DIVMTQTPLSLPVSLGD**KASI**CRSSQALVHSNGNTYLHWYLQ**KPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDF**
FTLKISRVEA**EDLGVFFCSQSTHV**PRTFGGGT**KLEIK**

>d1qkzh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab MN14C11.6
(mouse), kappa L chain}

DVKLVESGGGLVKPG**RSLKLSCAASGFTFS**DYYMF**WVRQTP**EQRLEWVATISDG**GA**YTYY**PDSVKG**RFT**ISRD**N
AKNNLYLQMNSL**KSED**TGMYY**CARD**PLEYY**GMDY**WG**QGTS**AVSS

>d1qkzl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab MN14C11.6
(mouse), kappa L chain}

NIVMTQTPLSLPVSLGD**QASIS**CRSSQSLVHSNGNTYLHWYLQ**KPGQSPKLLIYTVSNRFSGVPDRFSGSGSGTDF**
FTLKISRVEA**EDLGVY**FCSQSTHFPTFGGGT**KLEIK**

>d1pskh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab against a
ganglioside (mouse), kappa L chain}

EVQLQQSGPELV**KPGASVKISCKTSGYIFTK**YTMHWVKQSHGKSLEWIGDINPNNGGT**NYNQKF**GTATL**TVH**
KSSTTAYMELRSLTSEDSAVYY**CTSKSF**DYWG**QGTT**LVSS

>d1pskl1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab against a
ganglioside (mouse), kappa L chain}

QIVLTQSPAAMSASP**GEKVT**CSASSVSNIHW**FQQKPGT**FPKL**WIYST**TLASGV**PGRFSGSGSGT**SLTISRM
GAEDAATYY**CQQRS**GYPFTFGGGT**KLEIK**

>d1yejh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.3 (mouse),
kappa L chain}

EMQLQQSGAELL**RPGTSV**KLSCKTSGYIFTSY**WIHWV**K**QRSQGLE**WIARIY**PGTG**STYY**NEKF**KGKATL**ADK**
SSSTAYMQLST**LKSE**DSAVY**FCTRWF**G**IPVREDYV**MDYWG**QGTL**TVSS

>d1yejl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab D2.3 (mouse),
kappa L chain}

DIVMTQSPLTLSVTIGQPASISCKSSQSLLYSNGKTYLNWLL**QPGQSPKRLIHLVSKLD**SGVPDRIT**GSGSGTDF**
LKISRVEA**ADLGVYY**CVQGTHFPYTFGGGT**KLEIL**

>d1yedb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.4

(mouse), kappa L chain}

AVKLQQSGPELVRPGTSVKLSCKTSGYIFTSYWIHWLKQSSGQGLEWIARIYPGTGGTYNEFKKGKATLTADKS
SSTAYMQLSSLKSEDSAVENTFCTRWGFTTVRENYYAMDYWGQGTLTVSS

>d1yeeh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab D2.5
(mouse), kappa L chain}

EVKLQESGAELVRPGASVKLSCKTSGYIFTSYWIHWVKQRAAAGLEWIARIYPGTGSSYYNVFKKGKATLTADKS
SSTAYMQLSSLKSDSAVYFCVRWGFIPVREDYVLDYWGQGTLTVSS

>d1cfvh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv 4155 (mouse),
kappa L chain}

QVQLQESGGGLVNLGGSMTLSCVASGFTNTYMSWVVRQTPEKTELVAAINS DGEPIYPDTLKGRVTISRDN
AKKTLYLQMSSLNFEDTALYYCARLN YAVYGM DYWGQGTTVTVSS

>d1cfvl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv 4155 (mouse), kappa
L chain}

DIELTQSPPSLPVSLGDQVSICRSSQLVSNNRRNYLHWYLQKPGQSPKLVYKVSNRSGVPDRFSGSGSGTDF
TLKISRVAEADLGLYFCSQSSHVPLFGSGTKLEIKR

>d1hyxh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 6D9 (mouse),
kappa L chain}

EVKLLESGGGLVKPGGSLKLSCAASGFTFSNYAMSWVVRQTPEKRLEWVVSISGGSIYLD SVKGRFTVSRDNA
RNILYLQM TSLRSEDTAMYFCARVSHYDGSRDWYFDVWGAGTSVTVSS

>d1hyxl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 6D9 (mouse),
kappa L chain}

ELVMTQTPLSLPVSLGDQASICRSSQTIVHSNGDTYLDWFLQKPGQSPKLLIYKVSNRSGVPDRFSGSGSGTDF
FTLKISRVEAEDLGVYYCFQGSHPPTFGGGT KLEIK

>d2hrph1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab F11.2.32
(mouse), kappa L chain}

DVQLVESGGGLVQP GGSRKLS CAASGFTFM RFGMHW VRQA PEKGLEW VAYISS GSSTI YYADTV KGRFT ISRD
NP KNTLFLQM TSLRSEDTALYYCARS GG IERYDG TYVMDYWGQG TS VTVSS

>d2hrpl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab F11.2.32
(mouse), kappa L chain}

DTVL TQSPASLA VSLGQRAT ISCRASE SVDYYGKSF MNWF QQKPGQPKL LIY AAS NQGS GP ARF SGSGSGTDF
FSLHIHPMEEDDSAMYFCQQSK EWPWT FGGGT KLEIK

>d2ap2a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {scFv C219, (mouse
sequence-based), kappa L chain}

FVRDIVMTQSPSSLTVTAGEKV TMSCSSQSLNSGNQKNLTWYQQKPGQPKL LIY WASTRESGV PDRFTG
SGSGTDFTLTISSVQAEDLAVYYCQNDYSYPLTFGAGTKLEP

>d2ap2b_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {scFv C219, (mouse
sequence-based), kappa L chain}

EVQLQQSGAE LVR PGAS VKLS CTAS GFNI KDD FMHW V KQRPE QGLE WIGRID PAND NT KYAP KF QDK ATIIAD
TSSNTAYLQLSSLT SEDT AVYY CARREV YSY SP LDV W GAGTT VTVPSG

>d1nfde1 b.1.1.1 (E:2-107) Immunoglobulin (variable domains of L and H chains) {Fab H57
(hamster), lambda L chain}

YELIQPSSASVT VGETVKITCSGDQLPKNFAYWFQQKSDKNILLIYMDNK RPSG IPERF SGST GTTATL TISGAQ
PEDEA AYYCLSSYGDNN DLVFGSGTQLTVLR

>d1nfdf1 b.1.1.1 (F:1-114) Immunoglobulin (variable domains of L and H chains) {Fab H57}

(hamster), lambda L chain}

EVYLVESGGDLVQPGSSLKVSCAASGFTSDFWMYWVRQAPGKGLEWVGRIKNIPNNYATEYADSVRGRFTIS
RDDSRNSIYLQMNRRLVDDTAIYYCTRAGRFDHFIDYWGQGTMVTVSSA

>d2h1ph1 b.1.1.1 (H:301-420) Immunoglobulin (variable domains of L and H chains) {Fab 2H1
(mouse), kappa L chain}

DVKLVESGGGLVKLGGSKLSCAASGFTFSSYFLSWVRQTPEKRLELVATINSNGDKTYHPDTMKGRFTISRDNA
KNTLYLQMSSLKSEDTALYYCARRDSSASLYFDYWGQGTTLVSS

>d2h1pl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 2H1 (mouse),
kappa L chain}

DVVMTQTPLSLPVSLGDPASICRSSSQLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRSGVPDKFSGSGSGT
DFTLKISRVEAEDQGVYFCSQSTHVPWTFGGGTKLEIKR

>d1aqkh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Fab B7-15A2
(human), lambda L chain}

EVQLVESGGVVQPGRSRLSCAASGFTFNNYAIHWVRQAPGKGLEWVAFISYDGSKNYYADSVKGRFTISRD
NSKNTLFLQMNSLRPEDTAIYYCARVLFQQLVLYAPFDIWGQGTMVTVSS

>d1aqkl1 b.1.1.1 (L:1-111) Immunoglobulin (variable domains of L and H chains) {Fab B7-15A2
(human), lambda L chain}

ENVLTQPPSVSGAPGQRTVTISCTGSNSNIGAGFTVHWYQHLPGTAPKLLIFANTNRPSGVPDFSGSKSGTSASL
AITGLQAEDAEADYYCQSYDSSLARFGGGTRLTVLG

>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)}

ELVLTQSPSSMYASLGERVTITCKASQDINSYLNWFQQKPGKSPKTLIYRTNRLVDGVPSRFSGSGSGQDYSLTIS
SLEYEDMGIYYCLQYDEFPYTFGSGTKLEIK

>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)}

QVQLQQSGAELMKPGASVKISCKATGYTFSSYWIIEWVKQRPGHGLEWIGEILPGSGSTNYNEFKKGKATFTAD
TSSNTAYMQLSSLTSEDSAVYYCARGHSYYFYDGDYWGQGTSVTVSS

>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)}

DIKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQQKPGKSPKTLIYRANRLVDGVPSRFSGSGSGQDYSLTIS
SLEYEDMGIYYCLQYDEFPYTFGSGTKLEIK

>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}

EVKLQESGGDLVQPGSSLKVSCAASGFTFSSYTMWSVRQTPEKRLEWVASINNGGRTYYPDTVKGRFTISRD
NAKNTLYLQMSSLKSEDTAMYYCVRHEYYYAMDYWGQGTTVTVSS

>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}

DIELTQTPVSLASVGETVTITCRASENIYSYLAWYQQKQGKSPQFLVYNAKTLGEGVPSRFSGSGSGTQFSLKINS
LLPEDFGSYYCQHHYGTPLTFGGGTKEIK

>d1ae6h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab CTM01
(mouse), kappa L chain}

QIQLQQSGPELVKPGASVKISCKASGYTFDYYINWMKQKPGQGLEWIGWIDPGSGNTKYNEFKKGKATLTVD
TSSSTAYMQLSSLTSEDTAVYFCAREKTTYYAMDYWGQGTSVTVSA

>d1ae6l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and H chains) {Fab CTM01

(mouse), kappa L chain}

DIVMTQAAPSVPVTPGESLSICRSSKSLLHSNGDTFLYWFQRLPGQSPQLIYRMSNLASGVPDFSGSGSGTA
FTLRSRVEAEDVGVYYCMQHLEYPFTFGAGTKLELK

>d1ad9a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab CTM01
(human construct), kappa L chain}

DIQMTQSPSTLSASVGDRVTITCRSSKSLLHSNGDTFLYWFQQKPGKAPKLLMYRMSNLASGVPSRFSGSGSGT
EFTLTISLQPDDFATYYCMQHLEYPFTFGQGTKVEVKK

>d1ad9b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab CTM01
(human construct), kappa L chain}

EIQLVQSGAEVKKGSSVKVSCKASGYTFTDYYINWMRQAPGQGLEWIGWIDPGSGNTKYNEKFGRATLTV
DTSTNTAYMELSSLRSEDTAFYFCAREKTTYYYAMDYWGQGTLTVSS

>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}

EIQLQQSGAELVRPGALVLSCKASGFNIKDYYMHWWKQRPEQGLEWIGLIDPENGNTIYDPKFQGKASITADT
SSNTAYLQLSLTSEDTAVYYCARDNSYYFDYWGQGTLTVSS

>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}

DIKMTQSPSSMYASLGERVTITCKASQDIRKYLWYQQKPKWSPKTLIYYATSLADGVPSRFSGSGSGQDYSLT
SSLESDDTATYYCLQHGESPYTFGGGTKEINR

>d1jpth1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-human
tissue humanised factor Fab D3H44}

EVQLVESGGGLVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGKGLEWVGLIDPEQGNTIYDPKFQDRATISAD
NSKNTAYLQMNSLRAEDTAVYYCARDTAAFYFDYWGQGTLTVSS

>d1jptl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-human tissue
humanised factor Fab D3H44}

DIQMTQSPSSLSASVGDRVTITCRASRDIKSYLNWYQQKPGKAPKVLIIYATSLAEGVPSRFSGSGSGTDYTLISS
LQPEDFATYYCLQHGESPWTFGQGTLKVEIK

>d1jrhh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab A6 (mouse),
kappa L chain}

AVKLQESGPGILKPSQTLSTCSFGSLTTYGMGVGWIRQSSGKGLEWLHAIWWDDDKYYNPSLKSRLTISKDT
SRNQVFLKITSVATADTATYYCARRAPFYGNHAMDYWGQGTTTVSS

>d1jrhl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab A6 (mouse),
kappa L chain}

SVEMTQSPSSFSVLGDRVTITCKASEDIYNRLAWYQQKPGNAPRLLISGATSLETEVPSRFSGSGSGKDYTLSITS
LQTEDVATYYCQQYWSTWTFGGGTKLEIK

>d1gpoh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab M41
(artificial design)}

EVKLQESGPGILKPSQTLSTCSVTGDSITSDFWSWIRQFPGNRLEYMGFVQYSGETAYNPSLKSRSITRDTSKN
QYYLDLNSVTTEDTAVYYCANWHGDYWGQGTTTVSS

>d1gpol1 b.1.1.1 (L:1-112) Immunoglobulin (variable domains of L and H chains) {Fab M41
(artificial design)}

DIELTQSPATLSVTPGNVSICRASQSLVNEDGNTYLFWYQQKSHESPRLLIKYASQSISGIPSRFSGSGSGTDFTL
SINSVETEDLAVYFCQQITDWPFTEFGGGTKLEIK

>d1kb5h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab Desire-1}

{mouse), kappa L chain}

EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWKQSQNGKSLEWIGNIDPYGGISYNQKFGRATLTV
KSSSTAYMQLSLTSEDSAVIDYFDYWGQGTTLVSS

>d1kb5I1 b.1.1.1 (L:1-108) Immunoglobulin (variable domains of L and H chains) {Fab Desire-1
(mouse), kappa L chain}

DIQMTQSPASLSASVGETVTITCRASKNIYSYLAWYQQKQGKSPQLVNAKTLGEGVPSRFSGSGSGTQFSLKI
NSLPEDFGSYYCQHHYGTPTFGGGTKLEIKR

>d1a4jb1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Diels alder
catalytic Fab (mouse), kappa L chain}

QVQLLESGPELKKPGETVKISCKASGYTFTNYGMNWKQAPGKGLKWMGWINTYTGEPTYADDFKGRFAFL
ETSASTAYLQINNLKNEDTATYFCVQAERLRTFDYWAGTTVSS

>d1a4ka1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and H chains) {Diels alder
catalytic Fab (mouse), kappa L chain}

ELVMTQTPLSLPVSLGDQASISCRSSQSLLHSNGNTYLHWYLQKPGQSPKLIYKVSNRFSGVPDFSGSGSGTD
FTLKISRVEAEDLGVYFCSQVTHVPPTFGGGTKLEIKRTVAA

>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}

QIQLVQSGPELKKPGETVKISCKASGYMFTNYGMNWKQAPGKALKLMGWINPYTGESTFADDFKGRFAFFL
ETSATTAYLQINNLKNEDMATYFCARGTTIVRAMDYWGQGTSLTVSSAKTPP

>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}

ELVMTQTPLSLPVSLGDQASISCRSSQSLLHSNGNTYLHWYLQKPGQSPKFLIYKVSNRFSGVPDFGGSGSGT
DFILKISRVEAEDLGVYFCFQSTHFFPTFGGGTKLEIKSADAA

>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}

EVQLEESGPELVRPGTSVKISCKASGYTFTNYWLGVVKQRPGHGFEWIGDIYPGGVYTTNEKFRGKAILTADT
SSSTAYMQLSSLTSEDSAVIDYFCARAGGYYTGGDYWGQGTSVTVSS

>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}

DIVLTQAFSNPVTLGASASISCRSSKSLLNSNGIIHMYWYLQKPGQSPQLIYQMSKLASGAPDRFSGSGSGTD
FTLRISRVEAEDVGVYYCAQNLELPYTFGGGTKLEIK

>d1ay1h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab TP7 (mouse),
kappa L chain}

EVQLQESGPGLVKPYQSLSLCTVTGYSITSYDYNWIRQFPGNKLEWMGYITYSGTTDYNPSLKSRSITRDTSK
NQFFLQLNSVTTEDTATYYCARYYYGYWYFDVWGQGTTLVSS

>d1ay1l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab TP7 (mouse),
kappa L chain}

DIQMTQSPAIMSASPGEKVTMTCASSSVSYMWWYQQKPGSSPRLLIYDSTNLASGVPDFSGSGSGTSLTIS
RMEAEDAATYYCQQWSTYPLTFGAGTKLEIK

>d1dsfh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anticancer Fv B1
(mouse)}

QLVESGGGLVKPGGSLKSCAASGFIFSDNYMYWVRQTPEKCLEWVATISDGTYIDYSDSVKGRFTISRDNAK
NNLYLQMSSLRSEDTGMYYCGRSPIYYDYAPFTYWGQGTLTVSA

>d1dsfl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anticancer Fv B1}

{mouse}}

DVVMTQTPLSLPVSLGDQASISCRSSQNLVHSDGKTYLHWFLQKPGQSPTLLIYKVSNRFSGPDRFSGSGSGT
DFILKISRVEAEDLGVYFCSQSTHVPLTFCGTKLELK

>d1a6ta1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab Mab1-IA
(mouse), kappa L chain}

QSVLSQSPAIALSASPGEKVIMTCSPSSVSYMWYQQKPGSSPKWIYSTSNLASGVPGRFSGGGSGTSFSLTIS
GVEAEDAATYYCQQYSSHPLTFGGGTKELEK

>d1a6tb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab Mab1-IA
(mouse), kappa L chain}

EVQLQQSGPDLVKPGASVKISCKASGYSFSTYYMHWWVKQSHGKSLEWIGRVDPDNGGTSFNQFKKGKAILTV
KSSSTAYMELGSLTSEDSAVYYCARRDDYYFDWFWGQGTSLTVSS

>d1a6wh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv B1-8 (mouse),
lambda L chain}

QVQLQQPGAEVLKPGASVKLSCKASGYTFTSYWMHWVKQRPGRLWEWIGRIDPNSSGTTKYNEKFKSKATLT
DKPSSTAYMQLSSLTSEDSAVYYCARYDYYGSSYFDYWQGQGTTVTVSS

>d1a6wl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv B1-8 (mouse),
lambda L chain}

AVVTQESALTTSPGETVTLTCRSSTGAVTTSNYANWVQEKPDLFTGLIGGTNNRAPGVPARFSGSLIGNKAALT
ITGAQTEDEAIYFCALWYSNHWVFGGGTKLTVLE

>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}

QVQLLESGAEVKKPGSSVKVSKASGDTFIRYSFTWVRQAPGQGLEWMGRIITILDVAHYAPHLQGRVTITADK
STSTVYLELRNLRSDDTAVYFCAGVYEGEADEGEYRNNGFLKHWGQGTLVTVSA

>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}

ELETQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPARFSGSGAEFTLT
LQSEDFAVYYCQQYNNWPPRYTFGQGTRLEIK

>d12e8h1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 2E8 (mouse),
kappa L chain}

EVQLQQSGAEVVRSGASVKLSCTAGFNIKDYIHWVKQRPEKGLEWIGWIDPEIGDTEYVPKFQGKATMTAD
TSSNTAYLQLSSLTSEDTAVYYCNAGHDYDRGRFPYWGQGTLTVSAA

>d12e8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 2E8 (mouse),
kappa L chain}

DIVMTQSQKFMSTSVGDRVSITCKASQNVTAVA
WYQQKPGQSPKLM
IYSASNRYTGVPDRFTGSGSGTDFT
LTISNMQSEDLADYFCQQYSSYPLTFGAGTKLELK

>d1adqh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {IgM rheumatoid
factor Fab (human), lambda L chain}

EVQLVESGGGLVQPGRLRLSCVTSGFTFDDYAMHWVRQSPGKGLEWVSGISWNTGTIIYADSVKGRFIISRD
AKNSLYLQMNSLRVEDTALYYCAKTRS
VVAEYYFHYWGQGILTVSS

>d1adql1 b.1.1.1 (L:2-107) Immunoglobulin (variable domains of L and H chains) {IgM rheumatoid
factor Fab (human), lambda L chain}

YVLTQPPSVVAPGQTARITCGGNNIGSKSVHWYQQKPGQAPVLVYDDSDRPPGIPERFSGNSGNTATLT
RVEAGDEADYYCQVWDSSSDHAVFGGGTKLT
VLG

>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}

DIQMTQTTSSLASLGDRVТИCSASQDISSYLNWYQQKPEGTVKLIIYTSSLHSGVPSAFSGSGSGTDYSLTISN
LEPEDFATYYCQQYSKFPWTFGGGTKLEIK

>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}

QITLKESGPGIVQPSQPFRLCTFSGFSLSTSGIGVTWIRQPSGKGLEWLATIWWDDDNRYNPSLKSRLTVSKDT
SNNQAFLNMMTVEADTAIYYCAQSAITVTDSAMDHWGQGTSVTVSS

>d1bvka_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Humanized anti-lysozyme Fv HuLys11 (mouse), kappa L chain}

DIQMTQSPSSLSASVGDRVТИCRASGNIHNYLAWYQQKPGKAPKLLIYYTTLADGVPSRFSGSGSGTDYTFI
SSLQPEDIATYYCQHFWSTPRTFGQGKTKEIKR

>d1bvkb_ b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Humanized anti-lysozyme Fv HuLys11 (mouse), kappa L chain}

QVQLQESGPGLVRPSQTLSTCTVSGFSLTGIGVNWRQPPGRGLEWIGMIWGDGNTDYNALKSRVTMLKD
TSKNQFSRLSSVTAADTAVYYCARERDYRLDYWGQGSLVTVSS

>d1a0qh1 b.1.1.1 (H:2-114) Immunoglobulin (variable domains of L and H chains) {Fab 29G11 (mouse), kappa L chain}

VQLQESDAELVKPGASVKISCKASGYFTDHVIHWVKQKPEQGLEWIGYISPGNGDIKYNEFKKGKATLTADKSS
STAYMQLNSLTSEDSAVYLCKRGYYGRSNVDYWGQGTTLVSSA

>d1a0ql1 b.1.1.1 (L:2-108) Immunoglobulin (variable domains of L and H chains) {Fab 29G11 (mouse), kappa L chain}

IELTQSPSSLSASLGGKVТИCKASQDIKKYIGWYQHKPGKQPRLLIHYTSTLLPGIPSFRGSGSGRDYSFSISNLEP
EDIATYYCLQYYNLRTFGGGTKLEIKR

>d1fnsh1 b.1.1.1 (H:215-336) Immunoglobulin (variable domains of L and H chains) {Fab NMC-4 (mouse), kappa L chain}

QVQLKESGPGLVAPSQSLSITCTVSGFSLTDYGVDWVRQPPGKGLEWLGMIWGDGSTDYNALKSRLSITKDN
SKSQVFLKMNSLQTDDTARYYCVRDPADYGYDYALDYWGQGTSVTVSS

>d1fnsl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab NMC-4 (mouse), kappa L chain}

DIQMTQSPSSLSASLGDRVТИCSASQDINKYLNWYQQKPDGAVKLLIFYTSSLHSGVPSRFSGSGSGTDYSLTIS
NLEPEDIATYYCQQYEKLPWTFGGGTKLEVK

>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}

QVQLQQPGAEVVRPGASVKLSCKASGYTLTTWMNWFQRPDGLEWIGRIDPYDSETHYNQFKDKAILTV
DRSSSTAYMQLSSLTSEDSAVYYCTRFLQITTIYGMDYWGQGTSVTVSS

>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}

QVQLQQSGAELMKPGPSVKISCKATGYSFSTYFIEWIRQRPGHGLEWIGEILPGSDNTNFNEKFDRATFTADT
PSNTAYMQLSSLTSEDSAVYYCARPTGRLWFSYWGQGTLVTVSA

>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}

QIILTQSPAIMSASPGEKVTMTCASSDISYMHWYQQKSDTSPKIWIYDTSKLASGVPARFSGSGSGTSYSLTIST
MEAEDAATYYCHQRSSYPTFGGGTKLEIK

>d35c8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab

5C8 (mouse), kappa L chain}

EVQLQQSGAELVKPGASV р KLSCTASGFNIKDTYMHWVKQKPEQGLEWIAQIDPANGNTKYDPKFQGKATITAD
TSSNTAYLHLSSLTSEDAVYYCAADPPYYGHGDYWGQGTTLVSS

>d35c8I1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 5C8
(mouse), kappa L chain}

DIVLTQSPAIMSASLGERVTMTCTASSSVSSNLHWYQQKPGSSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTI
SSMEAEDAATYYCHQYHRSPYTFGGGTKLEIK

>d1a5fh1 b.1.1.1 (H:1-120) Immunoglobulin (variable domains of L and H chains) {Anti-E-selectin
Fab (mouse), kappa L chain}

EVALQQSGAELVKPGASV р KLSCAASGFTIKDAYMHWVKQKPEQGLEWIGRIDSGSSNTNYDPTFKGKATITAD
DSSNTAYLQMSSLTSEDTAVYYCARVGLSYWYAMDYWGQGTVSS

>d1axth1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab
33F12 (mouse), kappa L chain}

EVKLEESGGGLVQPGGSMKLSCLV р VSGLTFSRFWMSWVRQSPEKGLEWVAEIRLKSDNYATHYAESVKGKFTISR
DDSKSRILQMNSLRTEDTGИYCKIYFYSFYWGQGTLTVSA

>d1axtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab
33F12 (mouse), kappa L chain}

ELVMTQTPLSLPVSLGDQASICRSSQLVHSYGNFLNWYLQKSGQSPKLLIYKVSNRFSGVPDRFSGSGSGTD
FTLKISRVEAEDLGVYFC SQGTHVPYTFGGGTKLEIK

>d1b2wh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Humanized and
chimeric anti-gamma-interferon Fab}

EVQLVQSGGGVVQPGRSLKLSCLASGYIFTSSWINWVKQRPGRGLEWIGRIDPSDGEVHYNQDFKDRFTISRD
KSKNTLYLQMNSLRPEDTAVYYCARGFLPWFA DWGQGTLTVSS

>d1b2wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Humanized and
chimeric anti-gamma-interferon Fab}

DIQMTQSPSTLSASVGDRVTITCKASENVDTYVSWYQQKPGKAPKLLIY GASNR YTGVPSRFSGSGSGTDFTLTI
SSLQPDDFATYYCGQSYNPFTFGQGTKVEVK

>d1b4jh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Humanized and
chimeric anti-gamma-interferon Fab}

EVQLQQPGADLVMPGAPV р KLSCLASGYIFTSSWINWVKQRPGRGLEWIGRIDPSDGEVHYNQDFKDKATLT
DKSSSTAYIQLNSLTSEDAVYYCARGFLPWFA DWGQGTLTVSA

>d1b4jl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Humanized and
chimeric anti-gamma-interferon Fab}

NIVMTQSPKSMYV р SIGERTLCKASENVDTYVSWYQQKPEQSPKLLIY GASNR YTGVPSRFRTGSGSATDFTLTI
SSVQAEDLADYHCGQSYNPFTFGSGTKLEIK

>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}

DIKMTQSPSFLSASVGDRVTLNCKASQNI р KLYN WYQQKLGE SPKLLIY NTNNL QTGIPS RFSGSGSGTDFTLTI
SLQPEDVATYFCLQHISRPRTFGTGTKEIK

>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}

EVKLLESGGGLVQPGGSMRLSCAGSGFTDFYMNWIRQPA GKAPEWLGFIRDKA KGYTTEYNPSVKGRTIS
RDNTQNMLYLQMNTLRAEDTATYYCAREGHTAAPFDYWGQGVMVTVSS

>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}

QVQLQESGPLVRPSQLTSLCTVSGFTFTDFYMNWVRQPPGRGLEWIGFIRDKAKGYTTEYNPSVKRVTML
VDTSKNQFSLRLSSVTAADTAVYYCAREGHTAAPFDYWQGQSLTVSS

>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}

DIQMTQSPSSLSASVGDRVTITCKASQNIKYLNWYQQKPGKAPKLLIYNTNNLQTGVPSRFSGSGSGTDFTFI
SSLQPEDIATYYCLQHISRPRTFGQGTKEIK

>d1bj1h1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {VEGF
neutralizing Fab-12 (mouse), kappa L chain}

EVQLVESGGGLVQPGGSLRLSCAASGYTFTNYGMNWVRQAPGKGLEWVGWINTYTGEPTYAADFKRRFTSL
DTSKSTAYLQMNSLRAEDTAVYYCAKYPHYGGSSHWFYFDVWGQGTIVTSS

>d1bj1j1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and H chains) {VEGF neutralizing
Fab-12 (mouse), kappa L chain}

DIQMTQSPSSLSASVGDRVTITCSASQDISNYLNWYQQKPGKAPKVLIVFTSSLHSGVPSRFSGSGSGTDFTLTIS
SLQPEDFATYYCQQYSTVPWTFQGTKEIK

>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}

DVLMTQTPVSLSVLDQASISCRSSQSIVHSTGNTYLEWYLQKPGQSPKLLIYKISNRSGVPDRFSGSGSGTD
TLKISRVEAEDLGVYYCFQASHAPRTFGGGTKLEIK

>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}

EVILVESGGGLVKPGGSLKLSCAASGFTFSSYTMWSVRQTPEKRLEWVATISSGGNTYYPDSVKGRFTISRDNA
KNNLYLQMSSLRSEDTALYYCARYRYEAWFASWGQGTIVTSA

>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}

DIKMTQSPSSMYTSLGERVTITCKASQDINSFLTWLQKPGKSPKLIYRANRLMIGVPSRFSGSGSGQTYSLTISS
LEYEDMGIYYCLQYDDFPLTFGAGTKLDLK

>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}

QDQLQQSGAELVRPGASVKLSCKALGYIFTDYIEHWVKQTPVHGLEWIGGIHPGSSGTAYNQFKKGATLTADK
SSTTAFMELSSLTSEDSAVIDYCTRKDYGQGTIVTSA

>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}

DVQLQQSGPDLVKPSQLTSLCTVTGYSITSQYSWHWIRQFPGNKLEWMGYIHYSAGTNYNPSLKSRSITRDT
KNQFFLQLNSVTTEDTATYYCAREEAMPYGNQAYYAMDCWGQGTIVTSS

>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}

DIVLTQSPASLAvgQRATISCKASQGVDFDGASFMNWYQQKPGQPPKLLIFAASTLESGIPARFSGRGSQTD
TLNIHPVEEDAATYYCQQSHEDPLTFGAGTKLELK

>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}

EVQLQQSGAELVKPGASVKLSCTASGFNIKDTYMHWVKQRPEKGLEWIGRIDPASGNTKYDPKFQDKATITAD
TSSNTAYLQLSSLTSEDTAVYYCAGYDYGNFDYWGQGTT

>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}

DIQMTQSPASLSASVGETVTITCRASGNINHNYLAWYQQKQGKSPQLLVNAKTLADGVPSRSGSGSGTQYSLK
INSLQPEDFGSYYCQHFWSTPWTFGGGTKEIK

>d1sbsh1 b.1.1.1 (H:1-123) Immunoglobulin (variable domains of L and H chains) {Anti-HCG Fab 3A2, (mouse), kappa L chain}

EVNLEESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVADIRLKSNNYATLYAESVKGRFTIS
RDDSKSSVYLQMNNLRAEDTGIYYCTRGAYRYDYAMDYWGQGTSVTVSS

>d1sbsl1 b.1.1.1 (L:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-HCG Fab 3A2, (mouse), kappa L chain}

DIVMSQSPSSLAVSVGEKVTMTCKSSQSLYSSNQMNLYLAWYQQKPGQSPKLLIYWASTRESGVPDFRTGS
GTDFTLTSSVEAEDLAVYYCQQYHSYPFTFGSGTKLEIK

>d1sm3h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Tumor-specific Fab SM3, (mouse), lambda L chain}

QVQLQESGGGLVQPGGSMKLSCVASGFTFSNYWMNWVRQSPEKGLEWVAEIRLKSNNYATHYAESVKGRFTI
SRDDSKSSVYLQMNNLRAEDTGIYYCTGVGFAYWGQGTTVSS

>d2pcpa1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 6B5, (mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQASICRSSQTIVHSNGNTYLEWYLQKPGQSPKLLIYKVTNRFSGVPDRFTSGSGSGTD
FTLKISRVEAEDLGVYYCFQGTHAPYTFGGGTKEIK

>d2pcpb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab 6B5, (mouse), kappa L chain}

EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYIHWNKQSHGKSLEWIGYIYPNNGGNGYNHKFKGKATLT
DKSSSTAYMDVRTLTSEDSAVIDYCFQGTHAPYTFGGGTKEIK

>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}

ELVMTQTPKFMSTTVGDRVSITCKASQNVGTPVAWYQQKPGQSPKLLIYSASNRYTGVPDRFTSGSGSGTDFTLT
ISNMQSEDLADYFCQQYSSYPLTFGGGTKEIK

>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}

QVQLLESGAELVKPGASVKLSCKASGYTFTSYWMHWVKQRPGRLWEWIGMIDPNSGGTKYNEKFKSKATLT
DKPSNTAYMQLSLTSEDSAVIDYCFQGTHAPYTFGGGTKEIK

>d1cf8h1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 19A4 (mouse), kappa L chain}

DVQLQESGPGLVKPGSQLSLTCTVGYSITSGYAWNIRQFPGNKLEWMGYIRYSGDTRYNPSLKSRSITRDTS
KNQFFLQLNSVTTEDTATYYCAIGYGNSDYWGQGTVSA

>d1cf8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 19A4 (mouse), kappa L chain}

DIVLTQSPTIMSVSPGEKVTLCASSSVSSNNVVYWYQQKPGSSPKVWIYSTSNLASGVPARFSGSGSGTSLTIS
SMEAEDAASYFCLQWSSFPYTFFGGGTKEIK

>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}

DIELTQSPSSMSVSLGDTVSITCHASQGISSNIGWLQQKPGKSFKGLIYHGTNLEDGVPSRSGSGSGADYSLTIS
SLESEDFADYYCVQYVQFPFTFGSGTKLEIK

>d1c12b1 b.1.1.1 (B:301-413) Immunoglobulin (variable domains of L and H chains) {Fab directed

againsts the musk odorant traseolide, (mouse), kappa L chain}

QVQLQESGPLVKPSQLSLCTVTGYSITSDYAWNWIRQFPGNKLEWMGYISYSGSTSPLKSRLSTRDTSK
NQFFLQLNSVTTEDATYYCVTSLTWLLRRKRSYWGQQGTTVTVSS

>d1dlfh_b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv, (mouse), kappa L chain}

EVKLEESGGGLVQPGGSMKLCATSGFTFSDAWMDWVRQSPEKGLEWVAEIRNKANNHATYYAESVKGRFTI
SRDDSKRVRVLQMNTLRAEDTGIYYCTGIYYHYPWFAYWGQGTLVTVS

>d1dlfl_b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anti-dansyl Fv, (mouse), kappa L chain}

DVVMTQTPLSLPVSLGNQASISCRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGPDRFGSGSGT
DFTLKISRVEAEDLGVYFCSQSTHPFTFGSGTKLEIKR

>d43c9a_b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and amidolytic Fv 43c9, (mouse), kappa L chain}

DVVMTQTSSLAMSVGQKVTMCKSSQSLLNISNQKNYAWYQQKPGQSPKLLVYFASTRESGVPDFIGSGS
GTDFTLTSSVQAEDQADYFCQQHYRAPRTFGGGTKEIK

>d43c9b_b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Sterolytic and amidolytic Fv 43c9, (mouse), kappa L chain}

GQVQLVESGPLVAPSQSLITCTVSGISLSRYNVHWRQSPGKGLEWLGMIWGGGSIEYNPALKSRLSISKDN
SKSQIFLKMNSLQTDMSAMYCVSYGYGGDRFSYWGQGTLVTVS

>d1bz7a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab R24, (mouse), kappa L chain}

DIQMTQITSSLVSLGDRVIICRASQDIGNFLNWYQQKPDGSLKLLIYYTSRLQSGVPSRFSGWGSGTDYSLTIS
NLEEDIATFFCQQGKTLPYTFGGGTKEIK

>d1bz7b1 b.1.1.1 (B:1-122) Immunoglobulin (variable domains of L and H chains) {Fab R24, (mouse), kappa L chain}

DVQLVESGGGLVQPGGSRKLSCAASGFTFSNFGMHWVRQAPEKGLEWVAYISSGGSSINYADTVKGRFTISRD
NPKNTLFLQMTSLRSEDTAIYYCTRGGTGTRSLYYFDYWQGQATLIVSS

>d1ct8a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 7C8, (mouse), kappa L chain}

ELVMTQTPATSLVTPGDSVSLSCRASQSVNKLHWYQQKSHESPRLLIKFASQSIPGIPSFRSGSGSDFTLSINS
VETEDFGIYFCHQTHGRPLTFGAGTKLEIK

>d1ct8b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 7C8, (mouse), kappa L chain}

QVKLLESGAVLVKGASVVKLSCKTSGFTFSSSYINWLKQKPGQSLEWIAWIYAGSGGTVYNQHFTDKARLTVD
SSSTAYMQFSSLTTEDSAIYYCARYRYDEGFAYWGQGTLVTVSA

>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}

DIQMTQSPPSLSASLGDKVTITCQASQDINKYIAWYQQKPGKAPRQLIRYTSILVLTGTPSRFGSGSGRDFSFIS
NVASEDIASYYCLQYGNLYTFGAGTKLEIK

>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}

EVKLLESGPLVQPSQTLSLCTVSGFPPTNGVSWVRQPPGKGLEWIAAISSGGSPYYNSALKSRLSINRDTSKS
QVFLKMNSLQTEDTAIYFCTREDGWNYFDYWGPGBTMVTVSS

>d1f3rb2 b.1.1.1 (B:139-257) Immunoglobulin (variable domains of L and H chains) {scFv MAB198,

(rat), kappa L chain}

DIKLTQSPSLLSASVGDRVTLSCKGSQLINNYLAWYQQKLGEAPKLIYNTNSLQTGIPSRSFGSGSGTDYTLISS
LQPEDVATYFCYQYNNGYTFGAGTKLEKAAEQKLISEEDLN

>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}

DIVLTQSPATLSVTGDSVSLSCRASQSISNNLHWYQQKSHESPRLLIKYASQSISSGIPSRFGSGSGTDFTLSINSV
ETEDFGMYFCQQSNSWPYTFGGGTKEIK

>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}

EVQLQESGPSLVKPSQTLSTCCTGDSVTSDYWSWIRKFPGNKLEYMGYISYSGSTYYHPSLKSRSITRDTSKN
QYYLQLNSVTTEDTATYYCASWGGDVWGAGTTTVSS

>d1ejoh1 b.1.1.1 (H:2501-2619) Immunoglobulin (variable domains of L and H chains) {Anti-FMDV Fab 4C4, (mouse), kappa L chain}

QMLVESGGDLVKPGGSLKLSCAASGFTFSSYTMWSVRQTPEKRLEWVATISGGAYTYPDSVKGRFTISDDNA
ESTLYLQMSSLRSEDTAMYCVRRAFDSDVGFASWHRTLTVSA

>d1ejol1 b.1.1.1 (L:2001-2111) Immunoglobulin (variable domains of L and H chains) {Anti-FMDV Fab 4C4, (mouse), kappa L chain}

DIVLTQSPASLAvgLQRATISCRASESVDSYGNFMHWYQQKPGQPPKLLIYRASNLESGIPARFSGSGSRTDFT
LTINPVEADDVATYYCQQSNEDPLTFGAGTKLELK

>d1cr9h1 b.1.1.1 (H:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-prion Fab 3F4, (mouse), kappa L chain}

KVKLQQSGAELVRSGAVKLSCTASGFNIKDYYIQWVWQQRPEQGLEWIGWIDPENGNSEYAPRFQGKATMTAD
TLSNTAYLQLSSLTSEDTAVYYCNADLHDYWGQGTTLVSS

>d1cr9l1 b.1.1.1 (L:1-106A) Immunoglobulin (variable domains of L and H chains) {Anti-prion Fab 3F4, (mouse), kappa L chain}

DVVMTQTPLSLSVTIGQPASICKSSQSLSDGKTYLIWVFQRPGQSPKRLIFLVSKRDSGVPDFTGSGSGTDF
TLKISRVEAEDVGVYYCWQGTHFPHTVGGGTKEIA

>d1qfwh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin alpha subunit] Fv, kappa L chain}

QLQQSGAELVKPGAVKLSCKASDFTSYWMHWVKQRPGQGLEWIGEINPTNGRTYYNEKFSKATLTVA
SASTAAMQASSLTSEDSA VYYCARRYGNFSFYWGQGTTTVSS

>d1qfwl_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin alpha subunit] Fv, kappa L chain}

DIELTQSPDSLAVSLGQRATISCRASESVDSYGNFMQWYQQKPGQPPKLLIYRASNLESGIPARFSGTGSRTDFT
LTINPVEADDVATYYCQQSDEYPYMYTFGGGTKEIKR

>d1qfwi_ b.1.1.1 (I:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin beta subunit] Fv, kappa L chain}

QVQLQESGGHLVKPGGSLKLSCAASGFAFSSFDMSWIRQTPEKRLEWVASITNVGTYTYPGSVKGRFSISRD
ARNTLNQMQSSLRSEDTALYFCARQGTAAQPYWYFDVWGAGTTTVS

>d1qfwm_ b.1.1.1 (M:) Immunoglobulin (variable domains of L and H chains) {Anti-[gonadotropin beta subunit] Fv, kappa L chain}

DIELTQSPKSMMSMSVGERTVLSCKASETVDSFVSWYQQKPEQSPKLLIFGASNRFSGVPDRFTGSGSATDFTLTIS
SVQAEDFADYHCGQTYNHPYTFGGGTKEIKR

>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}

DIVLTQSPASLAvgQRATISCRASKSVSTSGYGYMHWNQQKPGQPPRLLIYLVSNLESGVPARFSGSGSGTDF
TLNIHPVEEDAATYYCQHIREPLTFGGGTKEIK

>d32c2b1 b.1.1.1 (B:1-119) Immunoglobulin (variable domains of L and H chains) {Fab 32C2 against P450-arom, (mouse), kappa L chain}

DVQLQESGPGLVKPSQLSLCTVTGYSISSDYAWNWRQFPGNKLEWMGYISYSGSTSYNPSLKSRSITRDTSK
NQFFLQLSSVTTEDATYYCARGYYGSSHSPVGAGTTVTVSS

>d1dqdh1 b.1.1.1 (H:1-122) Immunoglobulin (variable domains of L and H chains) {Fab HGR-2 F6, (mouse), kappa L chain}

EVQLQESGPSLVKPSQLSLTCVTDGSITSGYWNWIRKFPGNKLEYMGYISYSGSTYYNPSLKSRLSITRDTSRN
QYYLQLKSVTPEDTATYYCASPPGYYGSGPYAMDYWGQGTSVTVSS

>d1dqd1 b.1.1.1 (L:1-106) Immunoglobulin (variable domains of L and H chains) {Fab HGR-2 F6, (mouse), kappa L chain}

DIVLSQSPAAMSASPGEKVITCSASSVSYMHWFFQQKPGTSPKLCIYTTSNLASGVPARFSGSGSGTSLISR
MEAEDAATYYCQQRSTYPPTFGSGTKLEIK

>d1deea1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}

DIQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFLTIS
LQPEDFATYYCQQSYSAPRTFGQGTVKVEIK

>d1deeb1 b.1.1.1 (B:501-621) Immunoglobulin (variable domains of L and H chains) {Fab of human IgM RF 2A2}

QVQLVESGGGVVQPGKSLRLSCAASGFTSGYGMHWVRQAPGKGLEWVALISYDESNKYYADSVKGRFTISRD
NSKNTLYLQMNSLRAEDTAVYYCAKVFKYDPTAPNDYWGQGTLTVSS

>d1qnzh_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fv 0.5B, (mouse), kappa L chain}

QVQLQQSGAELVKPGASVKMSCKASGYTFTTYPIEWMKQNHGKSLEWIGNFHPYSDDTNYNEKFKGAKLT
EKSSSTVYLEFSRLTSDDSAVYYCAIHGSAYAMDYWGQGTSVTVSS

>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}

EVQLEESGGGLVTGGSLRLSCAASGYVFSTYDMSWVRQTPEKRLEWVAFISSGGRTSYPTDVKGRFTISRDD
AKNTLYLQMSSLQSEDТАМYYCTRHFYAVLDYWGRTTLTVSS

>d1f4x1 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}

QAVVTQESALTTSPGETVTLCRSSTGTTSNYANWVQEKPDLHLFTGLIGATNNRAAGVPVRFSGSLIGGKAA
LTITGAQTEDEAIYFCALWYSGHWVFGGGTKLTVLG

>d1f11b1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Anti-Pres2 Fab F124, (mouse), kappa L chain}

EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTGYNQFKGKATLT
DKSSSTAYMQLNSLTSEDSAVYYCANDYGSTYGFAYWGQGTLTVSA

>d1f3dh1 b.1.1.1 (H:1-121) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}

EIQLQQSGPELVKPGASVKVSCKASGYSFDYNIHWVKQSHGKSLEWIGYIVPYSGGTFNQFKGKATLTVDKS
SSTAFMHLNSLTFEDSAVYYCANDYDGVYWGQGTTLVSS

>d1f3dj1 b.1.1.1 (J:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 4B2,

(mouse), kappa L chain}

DVLMTQTPLSLPVSLGDQVSICRSSQSIFHSDGKTYLEWHLQKPGQSPKLLIYKVSKRFSGVPDRFSGSGSGTD
FTLKISRVEAEDLGVYYCFQGSHPYTFGGGTKLEIK

>d1fh5h1 b.1.1.1 (H:4-120) Immunoglobulin (variable domains of L and H chains) {Fab MAK33, (human), kappa L chain}

SGGGLVKPAGSLKLSCAASGFTFSSYYMYWVRQTPDKRLEWVATISDGGSYTYYPDSVKGRFTISRDNAKNLY
LQMSSLKSEDTAMYYCARDAMDYWGGTTLVTVA

>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}

NIVLTQSPKSMSVGERVTLSCAKASENVDTYFWFQQKPDQSPKLLYGPSNRYTGVPDRFTGSGSTTDFTLTI
SSVQAEDLADYHCGQSYSPYTFGGGTKEIK

>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}

QVQLQQPGTELVRPGASVILSCKASGYTFTSYWINWVKQRPGQGLEWVGNIFPSDSYTNYNQFKDKATLTV
KSSSTAYMQVNAPTSEDAVYYCTRGARDTWFAYWGQGTLTVSV

>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)}

QVQLLEPGTELVKPGASVILSCKASGYTFTSYWMHWVKQRPGQGLEWIGLIDPSNGRTNFNDKFKS RATLTV
TSSSTAYMQLSSLTSEDAVYYCVRIAYWGQGTLTVSS

>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)}

EIQLTQSPSSLSASLGERVSLTCRTSQEISGYLSWLQQKPDGTIKRLIYDATKLDGAPKRFSGSRSGSDYSLISSLE
SEDFADYYCLQYASFPRTFGGGTKEIK

>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}

FAVVTQESALTTSPGETVTLTCRSTGAVTTSNYAIWVQEKPDLHLSGLIGGTNNRVPGVPARFSGSLIGDKAALT
VTGAQTEDEAIYFCALWYSNHWFGGGTLTVLG

>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}

QVTLKESGPGILQPSQTLSTCSFGSLSTSGMGVGWIRQPSGEGLEWLADIWWNDKKYYNPSLKSRLTVSKD
TSSNQVFLKITSVDTSDTATYHCARRTFSSYYGSSFYFDNWGQGTTLVSS

>d1emth1 b.1.1.1 (H:1-116) Immunoglobulin (variable domains of L and H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}

QVHLQESGPELVRPGASVKISCKTSGYVFSSWMNWVKQRPGQGLKWIGRIYPGNGNTNYNEFKKGATLTA
DKSSNTAYMQLSSLTSVDSAVIDFCATSSAYWGQGTLTVSA

>d1emtl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-C60 fullerene Fab, (mouse), kappa L chain}

DIQMTQTSSLSASLGDRVTFSCSASQDISNYLNWYQQKPDGTIKLLIYYTSSLRGVPSRFSGSGSGTDYSLTIN
NLEPEDIATYFCQQYSLPFTFGSGTKLEIK

>d1fl3a1 b.1.1.1 (A:2-116) Immunoglobulin (variable domains of L and H chains) {Blue fluorescent Fab 19G2, (mouse), kappa L chain}

AALLESGGGLVKPGGSLKLSCCTASGITFSRYIMSWVRQIPEKRLEWVASISGGITYYPDSVAGRFTISRDNRN
YLQMSSLRSEDTALYYCARGQGRPYWGQGTSVTVA

>d1fl3b1 b.1.1.1 (B:2-113) Immunoglobulin (variable domains of L and H chains) {Blue fluorescent

Fab 19G2, (mouse), kappa L chain}

AALTQSPVSNPVTLGTSAISCRSTKSLLHSNGITYLYWYLQKPGQSPQLIYQMSNLASGVPNRFSSSGSGTDFT
LRINTVEAEDVGVYYCAQNLELPPTFGAGTKLEKLR

>d1dzba1 b.1.1.1 (A:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}

QVKLQQSGAELVKPGASVLSCTASGFNIKDTYMHWVKQRPEQGLEWIGRIDPANGNTKYDPKFQGKATITAD
TSSNTAYLQLSSLTSEDTAVYYCARWDWYFDVGQGTTVTVSSG

>d1dzba2 b.1.1.1 (A:201-307) Immunoglobulin (variable domains of L and H chains) {Anti-lysozyme scFv 1F9, (mouse), kappa L chain}

DIELTQSPSSMYTSLGERVTITCKASQDINSYLRWFQQKPGKSPKTLIYYATSLADGVPSRFSGSQGDYSLTISSL
ESDDTTYYCLQHGESPYTFGGGTKEIK

>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}

QVKLQQSGAELVRSGTSVLSCTASGFNIKDSYMHWLRQGPSEQGLEWIGWIDPENGDTEYAPKFQGKATFTT
DTSSNTAYLQLSSLTSEDTAVYYCNEGTPGPYYFDYWQGTTVTVSSG

>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}

ENVLTQSPAAMSASPGEKVTITCSASSSVSYMHWFFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSLISR
MEAEDAATYYCQQRSSYPLTFGAGTKLEIK

>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}

EVQLQQSGAELARPGASVMSCKASGYTFTSYTMHWVKQRPGQGLEWIGYINPSSGYSNYNQFKDKATLTA
DKSSSTAYMQLSSLTSEDSAVIDYCSRPVVRGLYNFDYWQGSTLVSS

>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}

EIVLTQSPAITAASLGQKVITCSASSSVSYMHWYQQKSGTSPKPWIYEISKLASGVPARFSGSGSGTSLTISSM
EAEDAAIYYCQQWNYPFTFGSGTKLEIK

>d1d17h_ b.1.1.1 (H:) Immunoglobulin (variable domains of L and H chains) {Fv M3C65, (human), lambda L chain}

QVQLKESGPGLVAPSQSLITCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWGDGSTDYNSALKSRLNISKDK
SKSQVFLRMYSLQTDDTARYYCARDYGPYWGQGTLTVS

>d1d17l_ b.1.1.1 (L:) Immunoglobulin (variable domains of L and H chains) {Fv M3C65, (human), lambda L chain}

QAVVTQESALTTSPGETVTLCRSSTGAVTTSNYANWVQEKPDLHLFTGLIGGTKHRTPGAPARFSGSLIGDKAAL
TITGAQTEDEAIYFCALWYSNHWFGGGTKLTVL

>d1egjh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Fab against cytokyne receptor common beta chain domain 4, (mouse), kappa L chain}

EVQLQQSGPELVKPGTSVMSCKASGYTFTDYYMKWVKHSHGKSLEWIGDINPSNGGTLYNQFKKGATLTV
DKSSSTASMQLSRLTSEDSAVIDYCSRGDGIIHGGFAYWGQGTTVTVSS

>d1egjl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab against cytokyne receptor common beta chain domain 4, (mouse), kappa L chain}

NIVLTQSPASLAvgLQRATISCRANESVSYGDSFMHWYQQKPGQPPKLLIYLASNLASGVPARFSGSGSRTDF
TLTIDPVETDDAATYYCQQNNEDPWTFGGGTKLEIK

>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}

EVQLQQSGTVLARPGASVKMSCKASGYSFTSFWMHWVKQRPGQGLEWIGTIYPGNSDTSYNQFKGKAKLT
AVTSASTAYMEVSSLTNEDSAVYYCTRSGYKYYALDYWGQGTSVTSS

>d1fe8h1 b.1.1.1 (H:1-115) Immunoglobulin (variable domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

DVKLVQSGPGLVAPSQSLITCTVSGFSLTTYGVSWVRQPPGKGLEWLGVIWGDGNTTYHSALISRLSISKDNSR
SQVFLKLNSLHTDDATYYCAGNYYGMDYWQGQGTSVTSS

>d1fe8l1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

DIAMTQTSSLSASLGQKVTCRASQDIGNYLNWYQQKPDGTVRLLIYYTSRLHSGVPSRFSGSGSGTDYSLTIS
NLESEDIATYFCQNGGTNPWTFGGGTKLEV

>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}

EVKLQESGAGLVQPSQSLTCSVTGYSITSGYYWNWIRLFPGNKLEWVGYISNVGDNNYNPSLKDRLSITRDTIS
KNQFFLKLNSVTTEDTATYYCARSEYYSVTGYAMDYWQGQTTVSSAWRHP

>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}

DIELTQTPVSLAASLGDRVTCRASQDINNFLNWYQQKPDGTIKLLIYYTSRLHAGVPSRFSGSGSGTDYSLTISN
LEPEDIATYFCQHHIKFPWTFGAGTKLEIK

>d1il1a1 b.1.1.1 (A:3-121) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fab G3-519, (mouse), kappa L chain}

QLQQSGAELVRSGASVKLSCATSDFNIDYYIHWRQRPEQGLEWIGWLDPENGDTESAPKFQGKATMTADT
SSNTAYLQLSSLTSEASAVYYCNAISTTRDYALDYWGQGTSVTSS

>d1il1b1 b.1.1.1 (B:1-112) Immunoglobulin (variable domains of L and H chains) {Anti-HIV Fab G3-519, (mouse), kappa L chain}

DIVMSQSPSSLAVSVGEKVTMSCKSSQSLYSRNQMNLYSWYQQKPGQSPKLLIYWASTRESGVPDFRTGS
GTDFTLTISVKAEDLAVYYCQQYYHYRTFGGGTRLEIR

>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}

GVQLQESGPGLVKPSQSLTCTVTGYSITS DYAWN WIRL FPGN KLEW MG YITY SG STG YN PSL KRS ITRDTIS
KNQFFLKLNSVTTEDTATYYCAS YDDY TWFTYWGQ GTL VSA

>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}

DVQMTQPLTLSVTIGQPASISCESSQSLLYSNGKTYLNWLLQRPGQSPKR LIYLVSKLDGVPDFRTGS
GTDFTLTISVKAEDLAVYYCQQYYHYRTFGGGTRLEIK

>d1e4wh1 b.1.1.1 (H:1-110) Immunoglobulin (variable domains of L and H chains) {Anti-TGFalpha Fab TAB2, (mouse), kappa L chain}

QVQLQQPGAEVKGASVKLSCASGFTFTNYWMHWVKQRPGQGLEWIGEILPSNGRTNYNEKFKTATLTV
DKSSNTAYMQLSSLTSEDAVYYCARSPSDYWGQGTTLVSS

>d1e4wl1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-TGFalpha Fab TAB2, (mouse), kappa L chain}

DIQMTQTPSSLSASLGDRVTCRASQDISHYLNWFQQKPDGTVKLLIYTSTLHSGVPSRFSGSGSGTDYSLTIS
NLEEE DIAFYFCQ QGG ALPFTFGSGT KLA IK

>d1h8na1 b.1.1.1 (A:3-109) Immunoglobulin (variable domains of L and H chains) {Anti-ampicillin}

scFv, (mouse), kappa L chain}

KDIVLTQSHKFMSTVGDRVSITCKASQDVGTAVAWYQQKPGQSPKLLIYWASTRHTGVPDRFTGSGSGTDFTL
TISNVQSEDLADYFCQQYSSYPLTFAGTKLEI

>d1h8na2 b.1.1.1 (A:132-243) Immunoglobulin (variable domains of L and H chains) {Anti-ampicillin scFv, (mouse), kappa L chain}

QVQLQESGGELVRPGASVKLSCKASGYTFTSYWINWVKQRPGQGLEWIGNIYPSDSYTNYNQFKDKATLTV
KSSSTAYMQLSSLTSEDAVYFCARWGYWQQGTLTVSA

>d1i7za1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab GNC92H2, (mouse/human chimera), kappa L chain}

DLVLTQSPASLAWSLGQRATISCRASKSVSTSGYNMHWYQQKPGQPPKLLIYLASNLASGVPARFSGSGSGTD
TLNIHPVEEEADAATYYCLYSREFPPWTFGGGTKLEIK

>d1i7zb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Fab GNC92H2, (mouse/human chimera), kappa L chain}

QVQLQQSGPELKPGETVKISCKTSGYSFTNYGMNWVKQAPGKGLKWMGWINTYTGEPTYADDFRGRFAFS
LATASASTAYLQIINLNKNEDTATYFCETYDSDLGDYWGQQGTTVSS

>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}

IALTQSPGTLSSLSPGERATLSCRASQSFSSYLAWYQQKPGQAPRLLIYGASTRATGIPDRFSGSGSGTDFTLTISRL
EPEDFAVYYCQKYGTSAITFGQGTRLEIK

>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}

QVQLVQSGAEVKKPGASVKVSCKVSGYTLTELPVHWVRQAPGKGLEWVGSFDPESGESIYAREFQGSVTMTA
DTSTNIAYMELSSLRSDDTAVYYCAVPDPDAFDIWGQQGTMVTVSS

>d1fn4a1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Fab 198 against acetylcholine receptor, (rat)}

DIKLQTSPSLLSASVGDRVTLCKGSQNINNYLAWYQQQLGEAPKLLIYNTNSLQTGIPSRSRSGSGSGTDYTLTISS
LQPEDVATYFCYQYNNGYTFGAGTKLELKR

>d1fn4b1 b.1.1.1 (B:1-106) Immunoglobulin (variable domains of L and H chains) {Fab 198 against acetylcholine receptor, (rat)}

QVQLLESGPGLVRPSETLSLTCTVSGFSLTSFSVSWVRHPSKGPEWMGRMWYDGYTAYNSALKSRLSISRDTS
KNQVFLKMNSLQDDTGTYCTRDLYGGYPLGFWYDFWGP

>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}

QIQLVQSGPELKPGETVRISCKASDYSFMTSGMQWVQQMPGKGLKWIGWLNTQSGVPEYAEDFKGRFAFS
LETSATTAYLQINNLKNEDTATYFCATWGGSAYWGQQGTTVSS

>d1jp5a1 b.1.1.1 (A:1-112) Immunoglobulin (variable domains of L and H chains) {scFv 1695, (mouse), kappa L chain}

DILMTQTPLYLPVSLGDQASICRSSQTIVHNNGNTYLEWYLQKPGQSPQLLIYKVSNRSGVPDRFSGSGSGTD
FTLKISRVEADLGIVYCFQGSHFPPTFGGGTKLEIK

>d1jp5a2 b.1.1.1 (A:128-247) Immunoglobulin (variable domains of L and H chains) {scFv 1695, (mouse), kappa L chain}

EVQLQQSGPELKPGETVKISCKATNYAFTDYSMHVKQAPGGDLKYVGWINTETDEPTFADDFKGRFAFSLD
TSTSTAFLQINNLKNEDTATYFCVRDRHDYGEIFTYWGQQGTTVSS

>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} QVQLVESGGGLVQPGGSLRLSCATSGFTFDYMSWVRQPPGKALEWLGFIRNKANGYTTEYSASVKGRFTISR DNSQSILYLQMNTLRAEDSATYYCARDGSYAMDYWGQGTSVTSS >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} QVQLQQPGAEVKGASVQLSCKASGYTFTSDWIHWVKQRPGHGLEWIGEIIPSYGRANYNEKIQKKATLTADK SSSTAFMQLSSLTSEDSAVYYCARERGDGYFAVGAGTTVTSS >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} DILLTQSPAISVSPGERVSFSCRASQSIGTDIHWYQQRTNGSPRLLIKYASESISGIPSRSFGSGSGTDFTLSINSVE SEDIANYYCQQSNRWPFTFGSGTKLEIK >d1jguh1 b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain} EVKLVESRGGLVKPGGSQLQLSCAASGFTFSGYAMSWFRLPEKRLEWVASIYNGFRIHYLDVKGRFTISSDYARN ILYLQMSTLRSEDTAMYCSRGDAYSRYFDVWGAGTTVTSA >d1jgul1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain} EVVMTQSPSLPVSGLDQASICRSSQSLVHSNGNTYLHWYLQKPGQSPKLLIYKVSNRFSGPDRFSGSGSGT DFTLKISRVEAEDLGVYFCSQSTHVPPLTFGAGTKLELK >d1i8ma1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Anti ssDNA Fab, (mouse), kappa L chain} ELQMTQSPASLSASVGETVTITCRASENIYSYLAWYQQKQGKSPQLLVNAKTLAEGVPSRFSGSGSGTQFLKI NSLPEDFGSYYCQHHYGTPLTFGAGTKLELK >d1i8mb1 b.1.1.1 (B:1-113) Immunoglobulin (variable domains of L and H chains) {Anti ssDNA Fab, (mouse), kappa L chain} QVKLLESGPELVKGASVKMSCASGYTFTSYVMHWVKQKPGQGLEWIGYINPYNDGTYNEKFKGKATLTSD KSSSTAYMELSSLTSEDSAVYYCVRGGYRPYYAMDYWGQGTSVTSS >d1jv5b_b.1.1.1 (B:) Immunoglobulin (variable domains of L and H chains) {Anti-blood group A Fv, (human), kappa L chain} QVQLQQPGAEVKGASVQLSCKASGYNFTSYWINWVKLRPGQGLEWIGDIYPGSGITNYNEKFKSATLTVDT SSSTAYMQLSSLASEDSALYYCAGQYGNLWFAYWGQGTLTVS >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} QVQLQQPGAEVKGASVQLSCKASGYTFTSYWMQWVKQRPGQGLEWIGEIDPSDSYTNQFKKGKATLTIV DTSSSTAYMQLSSLTSEDSAVYYCARNRDYSNNWYFDVWTGTTVTSS >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} DIVLTQSPASLAWSLQQRATISCKASQSVDYDGDSYMNWYQQKPGQPPKLLIYAASNLESGIPARFSGSGSGTDF TLNIHPVEEDAATYYCQQSNEDPRTFGGGTKLEIK >d1jnha1 b.1.1.1 (A:1-108) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 10G6D6, (mouse), lambda L chain} QAVVTQESALTSPGETVLTCSRSSGAITTSYANWIQEKPDLFTGLISGTNNRAPGVPARFSGSLIGDKAALTI TGAQTEDEAIYICALWFSNQFIFSGSGTKVTV >d1jnhb1 b.1.1.1 (B:1-117) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol

Fab 10G6D6, (mouse), lambda L chain}

EVQLQQSGAELARPGASVKLSCRTSGYSFTTYWMQWVRQRPGQGLEWIAIYPGDDDARYTQKFKGKATLTA
DRSSSIVYLQLNLTSEDSAVYSSCRGRSLYYTMDYWGQGTSVTV

>d1jnlh1 b.1.1.1 (H:1-114) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}

EVQLQQSGAELVKPGASVRLSCSASGFNIKDTYMFVVKQRPEQGLDWIGRINPANGISKYDPRFQGKATLTAD
TSSNTAYLQLDNLTSEDTAVYYCAIEKDLPGQGTLTVSV

>d1jnll1 b.1.1.1 (L:1-107) Immunoglobulin (variable domains of L and H chains) {Anti-estradiol Fab 17E12E5, (mouse), kappa L chain}

QIVMTQTPASLSASVGETVTITCRASGNIYNLYAWYQQKQGKSPQLLVNAKTLVDGVPLRFSGSGSGTQYSLKI
NSLQPEDFGNYYCHHFVNTPYTFGGGTKEIK

>d1vhp__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {VH-P8 domain (human), camelized monomer}

EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKEREIVSAVSGSGSTYYADSVKGRFTISRDN
SKNTLYLQMNSLRAEDTAVYYCARLKYAFDYWGQGTLTVSS

>d1jtpa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-lysozyme antibody}

DVQLQASGGGSVQAGGSLRLSCAASGYTIGPYCMGWFHQAPGKEREVVAAINMGGGITYYADSVKGRFTISQ
DNAKNTVYLLMNSLEPEDTAIYYCAADSTIYASYYECGHGLSTGGYGYDSWGQGTQVTVSSRR

>d1bzqk_ b.1.1.1 (K:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-RNase A antibody}

QVQLVESGGGLVQAGGSLRLSCAASGYAYTYIYMGWFRQAPGKEREVVAAMDGGGGTLYADSVKGRFTISR
DKGKNTVYLQMDSLKPEDTATYYCAAGGYELRDRTYGQWGQGTQVTVSSRR

>d1f2xk_ b.1.1.1 (K:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), antibody cab-ca05}

QVQLVESGGGSVQAGGSLRLSCAASGYTVSTYCMGWFHQAPGKEREVATILGGSTYYGDSVKGRFTISQDNA
KNTVYLLQMNSLKPEDTAIYYCAGSTVASTGWCRLRPYDYHYRGQGTQVTVSS

>d1hcv__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), anti-gonadotropin alpha subunit VH domain}

VQLQESGGGLVQAGGSLRLSCAASGRTGSTYDMGWFRQAPGKERESVAAINWDSARTYYASSVRGRFTISRD
NAKKTVYLLQMNSLKPEDTAVYTCGAGEEGGTWDSWGQGTQVTVSS

>d1qd0a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), anti-RR6 VH domain}

QVQLQESGGGLVQAGGSLRLSCAASGRAASGHGHYGMGWFRQVPGKEREVAAIRWSGKETWYKDSVKGR
FTISRDNAKTTVYLQMNSLKGEDTAVYYCAARPVRVADISLPVGFDYWGQGTQVTVSS

>d1i3ua_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Llama (Lama glama), the dye RR1-binding VH domain}

VQLQESGGGLVQAGDSLKLSCAESGDSIGTYVIGWFRQAPGKERIYLATIGRNLVGPSDFYTRYADSVKGRFAVS
RDNAKNTVNLQMNSLKPEDTAVYYCAAKTTWGGNDPNNWNYWGQGTQVTV

>d1ivla_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {VL domain (kappa) of antibody M29B, dimer synthetic}

DIELTQSPATLSVTPGNSVISCRASQSIGNRLFWYQQKSHESPRLLIKYASQSISGIPSRFSGSGSGTDFTLSINSVE
TEDLAVYFCQQVSEWPFTFGGGTKLEIK

>d1bwwa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL}

(kappa) dimer REI (human)}

TPDIQMTQSPSSLSASVGDRVITCQASQDIKYLNWYQQKPGKAPKLLIYEASNLQAGVPSRSGSGSGTDYTF
TISSLQPEDIATYYCQQYQSLPYTFGQGKLTQLQT

>d2rhe__ b.1.1.1 (-) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (lambda)
dimer RHE (human)}

ESVLTQPPSASGTPGQRVTISCTGSATDIGNSNSVIWYQQVPGKAPKLLIYYNDLLPSGVSDRFSAKSCTSASLAIS
GLESEDEADYYCAAWNDSLDEPGFGGGTKLTVLGQPK

>d1bjma1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and H chains) {Bence-Jones
lambda L chain dimer LOC (human)}

ESVLTQPPSASGTPGQRVTISCGSSSNIGENSVTWYQHLSGTAPKLLIYEDNSRASGVSDRFSAKSCTSASLAIS
GLQPEDETDYYCAAWDDSLDVAVFGTGKTVLGL

>d1wtla_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL (kappa)
dimer WAT (human)}

DIQMTQSPSSLSASVGDRVITCrasQDITNYVNWFQQRPGQAPKVLiyGAsileTGVPSRSGSGSGTDFTFTI
SSLQPEDIATYYCQQYDTLPLTFGGGKVDIKR

>d1b0wa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL
(kappa) dimer BRE (human)}

DIQMTQSPSSLSASVGDRVITCQASQDISDYLIWYQQKLGKAPNLLIYDASTLETGVPSRSGSGSGTEYTFTI
LQPEDIATYYCQQYDDLPYTFGQGKVEIKR

>d1eeqa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL
(kappa) domain LEN (human)}

DIVLTQSPDSLAVSLGERATINCKSSQSVLDSSNSKNYLAwyQQKPGQPPKLLIyWASTRESGVPDFSGSGSGT
DFTLTISLQAEDVAVYYCQQYSHPYSFQGQGKLEIK

>d1lila1 b.1.1.1 (A:2-107) Immunoglobulin (variable domains of L and H chains) {Bence-Jones
lambda L chain dimer CLE (human)}

YEVTQPPSLSVSPGQTARITCSGEKLGDAYVCWYQQRPGQSPVVVIYQDNRRPSGIPERFSGSSSGNTATLTISG
TQTLDEADYYCQVWDSNASVVFGGGKLTVLG

>d1cd0a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL
(lambda) dimer JTO (human)}

NFMLNQPHSVSESPGKTVTISCTRSGNIDSNYVQWYQQRPGSAPITVIYEDNQRPSGVPDFAGSIDRSSNSA
SLTISGLKTEDEADYYCQSYDARNVVFGGGTRLTVLG

>d2cd0a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Bence-Jones VL
(lambda) dimer WIL (human)}

NFLLTQPHSVSESPGKTVTISCTRSGSIANNYVHWYQQRPGSSPTTVIFEDDHRRPSGVPDFSGSVDTSSNSAS
LTISGLKTEDEADYYCQSYDHNNQVFGGGKLTVLG

>d1b6da1 b.1.1.1 (A:1-107) Immunoglobulin (variable domains of L and H chains) {Bence-Jones
kappa L chain DEL (human)}

DIQMTQSPSSLSASVGDRVITCQASQDISSYLNWYQQKPGKAPKLLIHAASSLETGVPSRSGSGSGTDFTIS
SLQPEDLATYYCQQYDSLPLTFGGGKVEIK

>d1ek3a_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Kappa-4 VL REC
(human)}

DIVMTQSPDSLAVSPGERATINCKSSQNLLDSSFDNTLAWYQQKPGQPPKLLIyWASSRESGVPDFSGSGSG
TDFTLTISLQAEDVAVYYCQQYYPPTFGGGKVEIKR

>d1mcoh1 b.1.1.1 (H:1-117) Immunoglobulin (variable domains of L and H chains) {Intact antibody}

{lambda) MCG (human)}

PLVLQESGPGLVKPSEALSLTCTVSGDSINTILYYWSWIRQPPGKGLEWIGIYIYSGSTYGNPSLKSRTISVNTSK
NQFYSKLSSVTAAADTAVYYCARVPLVVNPWGQGTLTVSS

>d1dcla1 b.1.1.1 (A:1-111) Immunoglobulin (variable domains of L and H chains) {Lambda L chain dimer MCG (human)}

PSALTQPPSASGLQSVTISCTGTSSNVGGNYVSWYQQHAGKAPKVIYEVNKRPSGVPDFSGSKSGNTAS
LTVSGLQAEDADYYCSSLVEGSDNFVFGTGTKVTVLG

>d1mcww1 b.1.1.1 (W:1-111) Immunoglobulin (variable domains of L and H chains) {Heterologous L chain dimer MCG-WEIR hybrid (human)}

ESALTQPASVSGSPGQSITVSCAGHTSDVADSNSISWFQQHPDKAPKLLIYAVTFRPSGIPLRFSGSKSGNTASLTI
SGLLPDDEADYFCMSYLSDAFVFVFGSGTKVTVLR

>d1ac6a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

DSVTQTEGQVALSEEDFLTIHCNYSASGYPALFWYVQYPGEGPQFLFRASRDKEKGSSRGFEATYNKEATSFH
LQKASVQESDSA VYYCALSGGNNKLTFGAGTKLTIP

>d1b88a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

MQQVRQSPQSLTVWEGETAILNCSYEDSTFDYFPWYQQFPGE GPALLISILSVSNKKEDGRFTIFFNKREKKL
SLS HIADSPGDSATYFCAASASFGDNSKLIWGLGTSLVNP

>d1d9ka_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

QVRQSPQSLTVWEGETAILNCSYEDSTFDYFPWYQQFPGE GPALLIAISLVSNKEDGRFTIFFNKREKKL
SLS HITD SQPGDSATYFCAATGSFNKLTFGAGTRLA VSPY

>d1fo0a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

KVTQTQTSISVMEKTTVTMDCVYETQDSSYFLFWYKQTASGEIVFLIRQDSYKKENATVGHYSLNFQKP
KSSIGLI ITATQIEDSAVYFCAMRGDYGGSGNKLIFGTGTLLSVKP

>d1h5ba_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

GDQVEQSPSALSLHEGTD SALRCNFTTMRSVQWFRQNSRGSISLFLYLASGTKENGRLKSAFDSERARYSTL
HI RDAQLEDSGYFCAA EASSGSWQLIFGSGTQLTVMPVT

>d1i9ea_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

QSVTQPDARVTVSEGASLQLRCKYSATPYLFWYVQYPRQGLQLLLKYSGDPVVQGVNGFEAEFSKSNSSF
HL LRKASVHWSDSAVYFCAVSGFASALTFGSGTKVIVLPYIQN

>d1kb5a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

QQVRQSPQSLTVWEGETAILNCSYEDSTFNYFPWYQQFPGE GPALLISIRSVDKKEDGRFTIFFNKREKKL
SLS HITD SQPGDSATYFCAARYQGGRALIFGTGTTVSVPGSAD

>d1nfda1 b.1.1.1 (A:1-117) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

DSVTQTEGLVTTEGLPVKLNCNTYQTTYLTI AFFWYVQYLNEAPQVLLKSSTDNKTEHQGFHATLHKSSSF
HL QKSSAQLSDSALYYCALSEGGNYKYVFGAGTRLKIAH

>d1bd2d1 b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}

QKVQNSPSLSVQEGRISILNCDYTNSMFDYFLWYKKYPAEGPTFLISISSIKDNADGRFTVFLNKS
AKHLSLHIV PSQPGDSAVYFCAAMEGAQKLVFGQGTRLTINPN

>d1fytd1 b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}

QSVTQLGSHVSVSEGALVLLRCNYSSVPPYLFWYVQYPNQGLQLLLKYTS
AATLVKGINGFEAEFKKSETSFHLT KPSAHMSDAAEYFCAVSESPFGNEKLT
FGTGTTRLTIIPN

>d1qrnd1 b.1.1.1 (D:1-117) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}

KEVEQNNSGPLSVPEGAIASLNCTYSDRGSQSFFWYRQYSGK
SPELIMSIYSNGDKEDGRFTAQLNKASQYVSLI

RDSQPSDSATYLCAVTDSWGLQFGAGTQVVTPD
>d1bec_1 b.1.1.1 (3-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
AVTQSPRNKAVTGGKVTLSCQQTNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDI
PDKYKASRPSQE
FSLILELATPSQTSVYFCASGGGRGSYAEQFFGPGTRLT
VLE
>d1fo0b_ b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
VTLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTL
RSPGDKEVKSLPGADYLATRV
TDTELRLQVANMSQGRTLYCTCSADRGNTLYFGE
GSRLIV
>d1kb5b_ b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
VTLLEQNPRWRLVPRGQAVNLRCILKNSQYPWMSWYQQDLQKQLQWLFTL
RSPGDKEVKSLPGADYLATRV
TDTELRLQVANMSQGRTLYCTCSAAPDWGASAETLYFGSGTRLT
VLE
>d1nfdb1 b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
DSGVVQSPRHIIKEKGGRSVLTCIPISGHNSVVWYQQTLGKELKFLI
QHYEKVERDKGFLPSRFVQQFDDYHSE
MNMSALELEDSAMYFCASSLRWGDEQYFGPGTRLT
VLE
>d1tcrb1 b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}
EAAVTQSPRNKAVTGGKVTLSCNQTNNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDI
PDKYKASRPSQE
NFSLILELATPSQT
SVYFCASGGGTLYFGAGTRL
SVLE
>d1bd2e1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}
GVTQTPKFQVLKTGQSMTLQCAQDMNHEYMSWYRQDPGMGLRLI
HYSVGAGITDQGEVPNGYNVSRS
TTE
DFPLRLSAAPSQT
SVYFCASSY
PGGGFYEQYFGPGTRLT
VTE
>d1fyte1 b.1.1.1 (E:3-118) T-cell antigen receptor {Human (Homo sapiens), beta-chain}
KVTQSSRYLVKRTGEKV
FLECVQDMDHENMF
WYRQDPGLGLRLI
YFSYDV
KMKEKGDI
PEGYSVSREKKERF
S
ILESASTNQTS
MYLCASSST
GLPYGYTF
GSGTRLT
VVE
>d1hxma1 b.1.1.1 (A:1-120) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}
AIEVPEHQTV
PVISGPATL
RCSMKGE
AIGNYYIN
WYRKT
QGNTMT
FIYREK
DIYGP
GFKDN
FQGD
DIAKN
LA
VLKILAP
SERDE
GSYYCAC
DTLGM
GEYTD
KLIFG
KGTRV
TVEPR
>d1hxmb1 b.1.1.1 (B:1-123) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
AGHLEQP
QISST
KTL
SKTAR
LECV
VSG
ITISAT
SVY
WYR
ERP
GEVI
QFL
VISY
DGT
V
RKES
GIP
SGK
FEV
DRIP
ETST
STL
TIHN
VEK
QDIA
TYCAL
WEAQ
QEL
GKK
IKV
FGPG
TKLI
IT
>d1tvda_ b.1.1.1 (A:) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
DKVTQSSPD
QTV
V
AS
GSE
V
V
LLC
TY
DT
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Y
SN
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DL
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KA
FHL
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C
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>d1ah1_ b.1.1.1 (-) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}
AMHVAQPAV
VLASS
RGIA
SFVCEY
ASPG
KATE
VR
V
L
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Q
A
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>d1i8lc_ b.1.1.1 (C:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human (Homo sapiens)}
MHVAQPAV
VLASS
RGIA
SFVCEY
ASPG
KATE
VR
V
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P
>d1dqta_ b.1.1.1 (A:) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Mouse (Mus musculus)}
IQVTQPSV
VLASS
HGV
ASF
PCEY
SPSH
HNT
DEV
RV
T
V
L
R
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V
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K
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R

VNLTIQGLRAVDTGLYLCVELMYPPPYFVGGMGNGTQIYVIDP
>d3frua1 b.1.1.2 (A:179-269) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}
KEPPSMRLKARPGNSGSSVLCAAFSFYPPELKFRFLRNGLASGSGNCSTGPNGDGSFHAWSLLEVKGDEHH
YQCQVEHEGLAQPLTVDL
>d3frub1 b.1.1.2 (B:) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus norvegicus)}
IQKTPQIQVYSRHPPEKGPNFLNCYVSQFHPPQIEIELLKNGKKIPNIEMSDLSFSKDWSFYILAHTEFTPTETD
VYACRVKHVTLKEPKTVWDRDM
>d1bmg__ b.1.1.2 (-) Class I MHC, beta2-microglobulin and alpha-3 domain {Cow (Bos taurus)}
IQRPPKIQVYSRHPPEDGKPNYLNCVYGFHPPQIEIDLLKNGEKIKSEQSDLSFSKDWSFYLLSHAEFTPNSKDQ
YSCRVKHVTLEQPRIVKWDRDL
>d1i4fa1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-A2.1}
TDAPKTHMTHHAVSDHEATLRCWALSFYPAEITLTWQRDGEDQTQDTELVERPAGDGTQKWAADVPSG
QEQRYTCHVQHEGLPKPLTLRWE
>d1i4fb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-A2.1}
MIQRTPKIQVYSRHPAENGKSNFLNCVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDWSFYLLYYTEFTPTEK
DEYACRVNHVTLSQPKIVKWDRDM
>d1agda1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-B0801}
ADPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVERPAGDRTFQKWAADVPSGEE
QRYTCHVQHEGLPKPLTLRWE
>d1qqda1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-CW4}
AEHPKTHVTHHPVSDHEATLRCWALGFYPAEITLTWQWDGEDQTQDTELVERPAGDGTQKWAADVPSG
EEQRYTCHVQHEGLPEPLTLRW
>d1mhea1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), HLA-E}
LEPPKTHVTHHPISDHEATLRCWALGFYPAEITLTWQQDGEHTQDTELVERPAGDGTQKWAADVPSGEE
QRYTCHVQHEGLPEPVTLRW
>d1de4a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo sapiens), hemochromatosis protein Hfe}
QQPPLVKVTHVTTLCRALNYYPQNITMKWLKDQPMDAKEFEPKDVLPGDGTQGWITLAVPP
GEEQRYTCQVEHPGLDQPLIVIW
>d1fzka1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2KB}
TDSPKAHVTHHSRPEDKVTLRCWALGFYPADITLTWQLNGEELIQDMELVERPAGDGTQKWasVVVPLGKE
QYYTCHVYHQGLPEPLTLRW
>d1fzkb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2KB}
IQKTPQIQVYSRHPPEKGPNFLNCYVTQFHPPHIEIQMLKNGKKIPKVEMSDMSFSKDWSFYILAHTEFTPTET
DTYACRVKHDSMAEPKTVWDRDM
>d1jpfa1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus

musculus), H-2DB}

TDSPKAHVTHHPRSKGEVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTFQKWAASVVVPLGK
EQNYTCRVYHEGLPEPLTLRWE

>d1mhca1 b.1.1.2 (A:182-276) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2M3}

ADPPKAHVAAHPRPKGDVTLRCWALGFYPADITLTWQKDEEDLTQDMELVETRPSGDGTQKWAAVVPSG
EEQRYTCYVHHEGLTEPLALKWRS

>d1qo3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), H-2DD}

TDPPKAHVTHHRRPEGDVTLRCWALGFYPADITLTWQLNGEELTQEMELVETRPAGDGTQKWAASVVVPLGK
EQKYTCHVEHEGLPEPLTLRWG

>d1k8da1 b.1.1.2 (A:182-274) Class I MHC, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus), IB QA-2}

TDPPKAHVTHHPRSYGAVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTQKWAASVVVPLGK
EQNYTCHVNHEGLPEPLTLRW

>d1ed3a1 b.1.1.2 (A:182-275) Class I MHC, beta2-microglobulin and alpha-3 domain {Rat (Rattus norvegicus), RT1-AA}

SDPPEAHVTLHPRPEGDVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTQKWAASVVVPLGK
EQNYTCRVEHEGLPKPLSQRWE

>d1zaga1 b.1.1.2 (A:184-277) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}

QDPPSVVVTSHQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPELRGDVLHNGNGTYQSWVVAVPPQD
TAPYSCHVQHSSLAQPLVVPWEA

>d1hyrc1 b.1.1.2 (C:181-274) MHC I homolog {Human (Homo sapiens), Mic-a}

TVPPMVNVTRSEASEGNITVCRASGFYPWNITLSWRQDGVSLSHDTQQWGDVLPDGNQTYQTWVATRICQ
GEEQRFTCYMEHSGNHSTHPVPS

>d1c16a1 b.1.1.2 (A:181-276) MHC I homolog {Mouse (Mus musculus), t22}

RSDPPKAHVTRHPRPEGDVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGTQKWAASVVVPLG
KEQSYTCHVYHEGLPEPLILRWGG

>d1exua1 b.1.1.2 (A:177-267) MHC-related Fc receptor {Human (Homo sapiens)}

KEPPSMRLKARPSSPGFSVLTCSAFSFYPPELQLRFLRNGLAAGTGQGDFGPNSDGSFHASSSLTVKSGDEHHYC
CIVQHAGLAQPLRVEL

>d1igtb3 b.1.1.2 (B:236-361) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}

PCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWFVNNVEVHTAQQTQTHREDYN
STLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKG

>d1igtb4 b.1.1.2 (B:363-474) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a antibody Mab231 (mouse), kappa L chain}

SVRAPQVYVLPPPEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNTEPVLDSDGSYFMYSKLRVE
KKNWVERNSYSCSVVHEGLHNHHTTKSFSR

>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}

GCKPCICTVPEVSSVIFPPKPKDTLLITVTPKVTCCVVVDISKDDPEVQFSWFVDNVEVHTAQTPREEQFNSTF
RVVSALPIMHQDWLNGKEFKCRVNSAAFPAPIEKTKKG

>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}

KPRAPQVTIPPKEQMAKDKVSLCMITDFFPEDITVEWQSDGQAPENYKNTQPIMTDGSYFVYSKLNVQK
SNWEAGNTFTCSVHLHEGLHNHHTEKSLSH

>d1hh3 b.1.1.2 (H:236-359) Immunoglobulin (constant domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}

THTCPPCPAPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVGVEVHNAKTPREEQY
NSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTiska

>d8faba2 b.1.1.2 (A:106-208) Immunoglobulin (constant domains of L and H chains) {Fab HIL (human), lambda L chain}

LGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPIKAGVETTTSKQSNNKYAASSYLSLT
PEQWKSHRSYSCQVTHEGSTVEKTVAP

>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}

GSASAPTLFPLVSCENSPTSDTSSAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKGYAATSQVLLPSK
DVMAGTDEHVCKVQHPNGNKEKNVPLPV

>d2fb4l2 b.1.1.2 (L:110-214) Immunoglobulin (constant domains of L and H chains) {Fab KOL (human), lambda L chain}

QPKANPTVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADGSPVKAGVETTKPSKQSNNKYAASSYLSLT
EQWKSHRSYSCQVTHEGSTVEKTVAPTECS

>d2ig2h2 b.1.1.2 (H:120-231) Immunoglobulin (constant domains of L and H chains) {Fab KOL (human), lambda L chain}

STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPQPVTWSNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSLG
TQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC

>d2fbjh2 b.1.1.2 (H:119-220) Immunoglobulin (constant domains of L and H chains) {Fab J539 (mouse), kappa L chain}

ESARNPTIYPLTPALSSDPVIIGCLIHDYFPSGTMNVTWKGSKKDITTVNFPALASGGRTMSNQLTPAVEC
PEGESVKCSVQHDSNPVQELDVNCAG

>d1mfb1 b.1.1.2 (L:112-212) Immunoglobulin (constant domains of L and H chains) {Fab SE155-4 (mouse), lambda L chain}

PKSSPSVTLFPPSSEELETNKATLVCTITDFYPGVVTWDKVDGTPVTQGMETTQPSKQSNNKYM ASSYLT TAR
AWERHSSYSCQVTHEGHTVEKSLRA

>d1teth2 b.1.1.2 (H:113-213) Immunoglobulin (constant domains of L and H chains) {Fab TE33 (mouse), kappa L chain}

SAKTPPSVYPLAPGSGGQGNNSMVTLGCLVKGYFPEPVTVWNNSGSLSSGVHTFPAVLQSDLYT LSSVTPSSPRPSETVT
CNVAHPASSTKVDKKIVPR

>d2jelh2 b.1.1.2 (H:114-226) Immunoglobulin (constant domains of L and H chains) {Fab JE142 (mouse), kappa L chain}

AATTTPPSVYPLAPGSGGQGNNSMVTLGCLVKGYFPEPVTVWNNSGSLSSGVHTFPAVLAADLYTLSSVTPPSSP
RPSETVTCNVAHPASSTKVDKKIAPG

>d2jell2 b.1.1.2 (L:109-212) Immunoglobulin (constant domains of L and H chains) {Fab JE142 (mouse), kappa L chain}

ADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVWKWIGD GARQNGV LNSWTDQDSKDSTYSMSSTLT
KDEYERHNSYTCEATHKTSDSPIVKS FNRN

>d1eapb2 b.1.1.2 (B:125-221) Immunoglobulin (constant domains of L and H chains) {Fab 17E8}

(mouse), kappa L chain}

AKTTPPSVYPLAPGCGDGGSSVTLGCLVKGYFPESVTWNSGGLSSVHTFPALLQSGLYTMSSSVTVPAGG

WPSATVTCVAHPASSTVDKKL

>d1yuhb2 b.1.1.2 (B:119-218) Immunoglobulin (constant domains of L and H chains) {Fab anti-nitrophenol (mouse/human), lambda L chain}

AATTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNSGALSSGVHTFPAVLQSDLYTLSSSVTVPAST
WPSGTVCNVVAHPASSTAVDKKIVPR

>d1clzh2 b.1.1.2 (H:115-231) Immunoglobulin (constant domains of L and H chains) {Fab MBR96 (mouse), kappa L chain}

TTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQSGFYSLSLVTPSSTWPS
QTVICNVVAHPASKTELIKRIEPR

>d1nldh2 b.1.1.2 (H:113-215) Immunoglobulin (constant domains of L and H chains) {Fab 1583, against an epitope of gp41 of HIV-1, (mouse), kappa L chain}

SASTTAPSVYPLAPVSGDQTNSMVTLGCLVKGYFPEPVTLWNNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSPW
PSETITCNVAHPASSTKVDKKIEPRGC

>d1kelh2 b.1.1.2 (H:116-218) Immunoglobulin (constant domains of L and H chains) {Fab 28B4 (mouse), kappa L chain}

TVSSAKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVP
SSPRPSETVTCNVVAHPASSTKVDKKIVP

>d1osph2 b.1.1.2 (H:121-218) Immunoglobulin (constant domains of L and H chains) {Fab 184.1 (mouse), kappa L chain}

AKTTPPSVYPLAPGCGDGGSSVTLGCLVKGYFPESVTWNSGGLSSVHTFPALLQSGLYTMSSSVTVPSSTW
PSQTVTCVAHPASSTVDKKLE

>d1nfde2 b.1.1.2 (E:108-215) Immunoglobulin (constant domains of L and H chains) {Fab H57 (hamster), lambda L chain}

GPKSSPKVTVFPPSPEELRTNKATLVCLVNDFYPGSATVTWKANGATINDGVKTTKPSKQQNYMTSSYLSLT
DQWKSHNRVSCQVTHEGETVEKSLSPAECI

>d1nfdf2 b.1.1.2 (F:115-228) Immunoglobulin (constant domains of L and H chains) {Fab H57 (hamster), lambda L chain}

TTTAPSVYPLAPACDSTTSTDTVTLGCLVKGYFPEPVTVWNSGALSGVHTFPSVLHSGLYSLSSSVTVPSSTW
PKQPITCNVAHPASSTKVDKKIEPR

>d1aqkl2 b.1.1.2 (L:112-216) Immunoglobulin (constant domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}

QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVNAGVETTKPSKQSNNKYAASSYLSLTPE
QWKSHKSYSQVTHEGSTVEKTVAPAECI

>d1a4kh2 b.1.1.2 (H:120-211) Immunoglobulin (constant domains of L and H chains) {Diels alder catalytic Fab (mouse), kappa L chain}

SVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVWNSGALSGVHTFPAVLQSSGLYSLSVVTPSSSLGTQTYIC
NVNHKPSNTKVDKKV

>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}

SVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNSGSLSSGVHTFPAVLQSDLYTLSSSVTVPSSPRPSETV
CNVAHPASSTKVDKKIVPR

>d2hmic2 b.1.1.2 (C:108-214) Immunoglobulin (constant domains of L and H chains) {Fab 28

against HIV-1 RT (mouse), kappa L chain}

RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVAWAIDGSAANGVLNSWTDQDSKDSTYSMSSTLTL
TADEYEAAANSYTCAATHKTSTSPIVKSFNANE

>d1a5fh2 b.1.1.2 (H:121-217) Immunoglobulin (constant domains of L and H chains) {Anti-E-selectin Fab (mouse), kappa L chain}

AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNNSGLSSGVHTFPAVLQSDLYTLSSSVPTSTE
TVTCNVAHAPSSTKVDKKIVPR

>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}

RANAAPTVSIFPPSTEQLATGGASVVCLMNKFYPRDISVKWKIDGTERNGVLNSWTDQDSADSTYSMSSTLSLT
KADYQSHNLYTCQVVKHTSSSPVVAKNFNRNEC

>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}

AKTTAPSVYPLVPVCGGTTGSSVTLGCLVKGYFPEPVTLWNNSGLSSGVHTFPALLQSGLYTLSSVTTSNTWP
SQITCNVAHPASSTKVDKKIEPRV

>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}

LTVSSAETTPPSVYPLAPGTAALKSSMVTLGCLVKGYFPEPVTVWNNSGLSSGVHTFPAVLQSDLYTLSSVTVP
SSTWPSQTVCNVAHPASSTKVDKKIVPRNCGGDC

>d1sm3h2 b.1.1.2 (H:114-213) Immunoglobulin (constant domains of L and H chains) {Tumor-specific Fab SM3, (mouse), lambda L chain}

AKTTPPTVYPLAPGSNAASQSMVTLGCLVKGYFPEPVTVWNNSGLASGVHTFPAVLQSDLYTLSSVTVPSSST
WPSETVCNVAHPASSTKVDKIVPR

>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}

ASTKGPSVYPLAPGSKAAASMVTLGCLVKGYFPEPVTVWNNSGLSSGVHTFPAVLQSDLYTLSSVTVPSSPRP
SETVCNVAHPASSTKVDKKIVPE

>d1r24b2 b.1.1.2 (B:123-217) Immunoglobulin (constant domains of L and H chains) {Fab R24, (mouse), kappa L chain}

ATTTAPSVYPLVPGCSDTGSSVTLGCLVKGYFPGPVTVKWNYGALSSGVRTVSSVLQSGFYSLSSLTVPSSTWP
SQTVICNVAHPASKTDLIK

>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}

RADAAPTVSIFPPSTEQLATGGASVVCLMNNFYPDISVKWKIDGTERRDGVLDSTQDSKDSTYSMSSTLSLT
TKADYESHNLYTCEVVKHTSSSPVVKSFNANE

>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}

AQTTAPSVYPLAPGCGDTSSTVTLGCLVKGYFPEPVTVWNNSGALSSDVHTFPAVLQSGLYTLSSVTSSWT
QTVCNVAHPASSTKVDKKLERR

>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}

AKTTPPPVYPLVPGSLAQTNMVTLGCLVKGYFPEPVTVWNNSGLSSGVHTFPAVLQSDLYTLSSVTVPSSTW
PSETVCNVAHPASSTKVDKKIEP

>d1deeb2 b.1.1.2 (B:622-723) Immunoglobulin (constant domains of L and H chains) {Fab of human

IgM RF 2A2}

GSASAPTLFPLVSCENSNSSTAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGKGYAATSQVLLPSKD
VAQGTNEHVCKVQHPNGNKEKDVPL

>d1f3dh2 b.1.1.2 (H:122-223) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 4B2, (mouse), kappa L chain}

AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNNSGLSSGVHTFPALQSDLYTLSSSVTVPSS
WPSETVTCNVVAHPASSTKVDKKIVPRDC

>d1fh5h2 b.1.1.2 (H:121-215) Immunoglobulin (constant domains of L and H chains) {Fab MAK33, (human), kappa L chain}

AKTTPPSVYPLAVTLGCLVKGYFPEPVTVWNNSGLSSGVHTFPALQSDLYTLSSSVTVPSS
HPASSTKVDKKIVPR

>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)}

ASTKGPSVFPLAPSSKSTSGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSVVTVPSSL
GTQTYICNVNHKPSNTKVDKKVEPKC

>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)}

RTVAAPSVFIFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTTLS
KADYEKHKVYACEVTHQGLSPVTKSFRGEC

>d1fe8h2 b.1.1.2 (H:116-216) Immunoglobulin (constant domains of L and H chains) {Fab RU5, (mouse), kappa L chain}

AETTAPSVYKLEPVVSVTLGCLVKGYFPEPVTLTVWNNSGLSSGVHTFPALQSDLYTLSSSVTVPSS
VAHPASSTKVDKKIEPRG

>d1iqdb2 b.1.1.2 (B:115-212) Immunoglobulin (constant domains of L and H chains) {Fab BO2C11 against the C2 domain of factor VIII, (human), kappa L chain}

ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPALQSSGLYSLSVVTVPSSL
TATYTCNVDHKPSNTKVDKRV

>d1fn4b2 b.1.1.2 (B:107-208) Immunoglobulin (constant domains of L and H chains) {Fab 198 against acetylcholine receptor, (rat)}

TMVTVSSVFPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVWNNSGALSSGVHTFPALQSGLYLTSSSVTVPSS
WSSQAVTCNVVAHPASSTKVDKKIVPRDC

>d1jguh2 b.1.1.2 (H:114-212) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

AKTTAPSVYPLAPVCGDGGSSVTLGCLVKGYFPEPVTLTVWNNSGSLSSGVHTFPALQSDLYTLSSSVTVPSS
SQSITCNVAHPASSTKVDKKIEP

>d1jgul2 b.1.1.2 (L:108-214) Immunoglobulin (constant domains of L and H chains) {Catalytic Fab 1D4, (mouse), kappa L chain}

RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVWKWIDGSERQNGVLNSWTDQDSKDSTYSMSSTLT
TKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC

>d1mcoh2 b.1.1.2 (H:118-219) Immunoglobulin (constant domains of L and H chains) {Intact antibody (lambda) MCG (human)}

ASTKGPSVFPLAPSSKSTSGTAALGCLVKDYFPEPVTVWNNSGALTSGVHTFPALQSSGLYSLSVVTVPSSL
GTQTYICNVNHKPSNTKVDKRVAPEL

>d1adqa1 b.1.1.2 (A:238-341) Immunoglobulin (constant domains of L and H chains) {Fc (human)}

IgG1 class}

PSVFLPPPKDLMISRTPEVTCVVVDVSQEDPQVQFNWYVDGVQVHNNAKTPREQQFNSTYRVVSVLTVL
HQNWLGDKEYKCKVSNKGLPSSIEKTISKAKG

>d1dn2a1 b.1.1.2 (A:237-341) Immunoglobulin (constant domains of L and H chains) {Fc (human)}

IgG1 class}

GPSVFLPPPKDLMISRTPEVTCVVVDVSHENPEVKFNWYVDGVEVHNNAKTPREEQYNSTYRVVSVLTVL

HQDWLNGKEYKCKVSNKALPAPIEKTKAKG

>d1dn2a2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L and H chains) {Fc (human)}

IgG1 class}

QPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR
WQQGNVFSCSVMHEALHNHYTQKSSL

>d1fc2d1 b.1.1.2 (D:238-341) Immunoglobulin (constant domains of L and H chains) {Fc (human)}

IgG1 class}

PSVFLPPPKDLMISRTPEVTCVVVDVSHEDPQVKFNWYVDGVQVHNNAKTPREQQYNSTYRVVSVLTVLH
QNWLGDKEYKCKVSNKALPAPIEKTKAKG

>d1fp5a1 b.1.1.2 (A:336-438) Immunoglobulin (constant domains of L and H chains) {Fc (human)}

IgE}

VSAYLSRSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWI
EGETYQCRVTHPHLPRALMRSTTKSG

>d1fp5a2 b.1.1.2 (A:439-543) Immunoglobulin (constant domains of L and H chains) {Fc (human)}

IgE}

PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEQLPDARHSTTQPRKTKGSGFFFVFSRLEV
TRAWEQKDEFICRAVHEAASPSQTVQRAVSV

>d1i1ca1 b.1.1.2 (A:239-341) Immunoglobulin (constant domains of L and H chains) {Fc (rat) IgG}

SVFIFPPKTDVLGGGLTPKVTCVVVDISQNDPEVRFWFIDDVEVHTAQTHAPEKQSNSTLRVSELPIVERDW
LNGKTFKCKVNSGAFPAPIEKSKPEG

>d1i1ca2 b.1.1.2 (A:342-443) Immunoglobulin (constant domains of L and H chains) {Fc (rat) IgG}

TPRGPQVYTMAPPKEEMTQSQVSITCMVKGFYPPDIYTEWKMINGQPQENYKNTPPMTDGSYFLYSKLN
KKETWQQGNTFTCSVLHEGLENEHTEKSLSH

>d1pfc__ b.1.1.2 (-) Immunoglobulin (constant domains of L and H chains) {Fc (guinea pig)}

RTISKAKGPPRIPEVYLLPPRNELSKKVSLTCMITGFYPADINVWDSSEPSDYKNTPPVFDTDGSFFLYSRLKV
DTDAWNNGESFTCSVMHEALPNHVIQKSISRSPG

>d1cqka_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {Fc MAK33 (mouse)}

PAAPQVYTIPPLEQMAKDLVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMDTDGSYFVYSKLNQKS
NWEAGNTFTCSVLHEGLHNHHTEKSLSH

>d1g84a_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {C epsilon2 domain
from IgE (human)}

SRDFTPTVKILQSSSDGGGHFPPTIQLLCVSGYTPGTINITWLEDGQVMDVDLSTASTTQEGERLASTQSELTLS
QKHWLSDRTYTCQVTYQGHTFEDSTKKSA

>d1tcra2 b.1.1.2 (A:118-213) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

IQNPEPAVYALKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDATVLDMKAMDSKSNGAIAWSNQTSFTCQ
DIFKETNATYPSSDVPC

>d1bd2d2 b.1.1.2 (D:118-203) T-cell antigen receptor {Human (Homo sapiens), alpha-chain}

IQNPDPAVYQLRDSKSSDKSVCLTDFDSQTNVSQSKDSDVYITDKTVLDMRSMDFKNSAVAWSNKSDFACA

NAFNNSIIPEDTF

>d1bec_2 b.1.1.2 (118-246) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

DLRQVTPPKVSLFEPSKAEIANKQKATLVCLARGFFPDHVELSWWVNGKEVHSGVSTDPAQYKESNYSYCLSSRLRVSATFWHNPRNHFRCQVFHGLSEEDKWPEGSPKPVTQNISAEAWGRAD

>d1bd2e2 b.1.1.2 (E:119-247) T-cell antigen receptor {Human (Homo sapiens), beta-chain}

DLKNVFPPAVEVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVSTDPLKEQPALNDSRYALSSRLRVSATFWQDPRNHFRCQVFYGLSENDEWTQDRAKPVQTQIVSAEAWGRAD

>d1hxma2 b.1.1.2 (A:121-206) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}

SQPHTKPSVFVMKNGTNVACLVKEFYPKDIRINLVSSKKITEFDPAIVISPSGKYNNAVKLGYEDSNVTCSVQHDNKTVHSTDDE

>d1hxmb2 b.1.1.2 (B:124-230) T-cell antigen receptor {Human (Homo sapiens), delta-chain}

KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLEKFFPDVIIHWEEKSNTILGSQEGNTMKTNDTYSMKFSWLTPEKSLDKEHRCIVRHENNKGVDQEIIFPPI

>d1cd1a1 b.1.1.2 (A:186-279) CD1, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus)}

QEKPVAWLSSVPSSAHGHRQLVCHVSGFYPKPVWWMMWRGDQEQQGTHRGDFLPNADETWYLQATLDVEAGEEAGLACRVKHSSLGGQDIILYW

>d1hdma1 b.1.1.2 (A:94-196) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}

SRGFPIAEVFTLKPLEFGKPNTLVCVSNLFPPMLTVNWHDHSVPGPFTVSAVDGLSFQAFSYLNFTPEPSDIFSCIVTHEPDRTAIAYWVPRNALPS

>d1hdmb1 b.1.1.2 (B:88-185) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}

TRPPSVQVAKTPFNTREPVMLACYVWGFYPAEVITWRKNGKLVMHSSAHKTAQPNGDWTYQTLSHALTPEYGDTYTCVVEHIGAPEPILRDWTPG

>d1aqdb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR1}

RRVEPKTVYPSKTQPLQHHNLLCVSGFYPGSIEVRWFRNGQEEKAGVVSTGLIQNGDWTFQTLVMLETPVRSGEVYTCQVEHPSVTSPLTVEWRA

>d1fv1a1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

ITNPPEVTVLTNSPVELREPNVLICFIDKFTPPVNVTWLRNGKPVTTGVSETVFLPREDHLFRKFHYLPFLPSTE DVYDCRVEHWGLDEPLLKHWEFD

>d1fv1b1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}

RRVEPKTVYPARTQTLQHHNLLCVNGFYPGSIEVRWFRNSQEEKAGVVSTGLIQNGDWTFQTLVMLETPVRSGEVYTCQVEHPSVTSPLTVEWRA

>d1d5zb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR4}

RRVYPEVTVYPAKTQPLQHHNLLCVNGFYPGSIEVRWFRNGQEEKTGVVSTGLIQNGDWTFQTLVMLETPVRSGEVYTCQVEHPSLTSPLTVEWRA

>d1jk8a1 b.1.1.2 (A:85-181) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}

EVPEVTVFSKSPVTLGQPNTLICLDVNIFPPVVNITWLSNGHSVTEGVSETFLSKSDHSFFKISYLTFLPSDDEIYD
CKVEHWGLDEPLLKHWEPE

>d1jk8b1 b.1.1.2 (B:95-192) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}

VEPTVTISPSRTEALNHNLVCVTDFYPAKVFRNDQEETTGVVSTPLIRNGDWTFQILVMLEMTPQRG
DVYTCHVEHPSLQNPIIVEWRAQS

>d1iaka1 b.1.1.2 (A:82-181) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}

ATNEAPQATVFPKSPVLLGQPNTLICFDVNIFPPVINITWLRNSKSVTDGVYETSFFVRDYSFHKLSYLTIPSDD
DIYDCKVEHWGLEEPVLKHWEPE

>d1iakb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}

RLEQPSVVISLSRTEALNHNTLVCSVTDFYPAKIKVFRNGQEETVGVSSTQLIRNGDWTFQVLVMLEMTP
RRGEVYTCHVEHPSLTSPITVEWRA

>d1fnnga1 b.1.1.2 (A:82-182) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

DANVAPEVTVLSRSPVNLGEPNILICFIDKSPPVVNVTLRNGRPVTEGVSETVFLPRDDHLFRKFHYLTFLPST
DDFYDCEVDHWGLEEPLRKHWEFEE

>d1fnrgb1 b.1.1.2 (B:93-188) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

RRVEPTVTYPTKTQPLEHHNLLVCVSDFYPGNIEVRWFRNGKEEKTGIVSTGLVRNGDWTFQTLVMLETVP
QSGEVYTCCQVEHPSLTDPVTVEW

>d2iada1 b.1.1.2 (A:83-186) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AD}

TNEAPQATVFPKSPVLLGQPNTLICFDVNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHSFKLSYLTIPSDDD
IYDCKVEHWGLEEPVLKHWEPEISSADLVR

>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)}

TNEAPQATVFPKSPVLLGQPNTLICFDVNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHSFKLSYLTIPSDDD
IYDCKVEHWGLEEPVLKHWS

>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)}

RLEQPNAISLSRTEALNHNTLVCSVTDFYPAKIKVFRNGQEETVGVSSTQLIRNGDWTFQVLVMLEMTP
HQGEVYTCHVEHPSLKSPITVEWS

>d1k8ia1 b.1.1.2 (A:93-191) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

VSRLPVAEVFTLKPITLEFGKPNTLVCFISNLFPPTLTNVWQLHSAPVEGASPTSIADVGLTFQAFSYLNFTPEPF
LYSCTVTHEIDRYTAIAYWVPQ

>d1k8ib1 b.1.1.2 (B:95-190) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

APSVRVAQTTPFNTREPVMLACYVWGFYPADVTITWMKNGQLVPSHSNKEKTAQPNGDWTYQTYSYLA
TPEPFD SYGDVYTCVVQHSGTSEPIRGDWTP

>d1vcaa1 b.1.1.3 (A:91-199) Second domain of vascular cell adhesion molecule-1 (VCAM-1) {Human (Homo sapiens)}

FPKDPEIHLGPLEAGKPITVKCSVADVYPFDRLEIDLLKGDHLMKSQEFLEDADRKSLETKSLEVTFPTVIEDIGKV
LVCRAKLHIDEMDSVPTVRQAVKELQVYISP

>d1iam_1 b.1.1.3 (83-185) Second domain of intercellular cell adhesion molecule-1 (ICAM-1)
{Human (Homo sapiens)}

YWTPERVELAPLPSWQPVGKQLTLRCQVEGGAPRAQLTVLLRGEKELKREPAVGEPAEVTTVLVRRDHHGA
QFSCRTELDLRPQGLELFENTSAPYQLQTF

>d1ic1a1 b.1.1.3 (A:83-190) Second domain of intercellular cell adhesion molecule-1 (ICAM-1)
{Human (Homo sapiens)}

YWTPERVELAPLPSWQPVGKNLTLRCQVEGGAPRANLTVVLLRGEKELKREPAVGEPAEVTTVLVRRDHHGA
NFSCRTELDLRPQGLELFENTSAPYQLQTFVLPAT

>d1zxq_1 b.1.1.3 (87-192) Second domain of intercellular cell adhesion molecule-2 (ICAM-2)
{Human (Homo sapiens)}

PPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAPQEATATFNSTADREDGHRN
FSCLAVLDLMSRGGNIFHKHSAPKMLEIY

>d1cdy_2 b.1.1.3 (98-178) CD4 {Human (Homo sapiens)}

FGLTANSDTLLLQQSQLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLQDSGTWTCTVLQNQKKVEFKI
DIVVLA

>d1wioa4 b.1.1.3 (A:292-363) CD4 {Human (Homo sapiens)}

MRATQLQKNLTCEVWGPTSPKMLSLKLENKEAKVSKREKAVWVNPEAGMWQCLLSDSGQVLLESNIKVLP

>d1cid_2 b.1.1.3 (106-177) CD4 {Rat (Rattus rattus)}

VMKVTQPDSENTLCEVMGPTSPKMRLILKQENQEAVSRQEKVIQVQAPEAGVWQCLLSEGEEVKMDSKIQV

>d1hnf_2 b.1.1.3 (105-182) CD2, second domain {Human (Homo sapiens)}

RVSXPKISWTCINTTLCEVMNGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFCTAGNKVSKESSVEPVSC
PEK

>d1ccza2 b.1.1.3 (A:94-171) CD2-binding domain of CD58, second domain {Human (Homo sapiens)}

EMVSKPMIYWECSNATLCEVLEGTDVELKLYQGKEHLRSLRQKTMYSQWTNLRAPFKCKAVNRVSQESEME
VVNCPE

>d1dr9a2 b.1.1.3 (A:106-200) CD80, second domain {Human (Homo sapiens)}

ADFPTPSISDFEIPTSNIRRIICSTGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLFNMNTNHSFMC
LIKYGHLRVNQTFNWNTA

>d1vcaa2 b.1.1.4 (A:1-90) N-terminal domain of vascular cell adhesion molecule-1 (VCAM-1)
{Human (Homo sapiens)}

FKIETTPESRYLAQIGDSVSLTCSTTGCESPFFSWRTQIDSPLNGKVTNEGTTSTLMNPVSFGNEHSYLCTATCES
RKLEKGQIVIYS

>d1iam_2 b.1.1.4 (1-82) N-terminal domain of intracellular adhesion molecule-1, ICAM-1 {Human (Homo sapiens)}

QTSVSPSKVILPRGGSVLTCSTCDQPKLLGIETPLPKKELLPGNNRKVYELSNVQEDSQPMCYSNCPDGQST
AKTFLTV

>d1zxq_2 b.1.1.4 (1-86) N-terminal domain of intracellular adhesion molecule-2, ICAM-2 {Human (Homo sapiens)}

KVFEVHVRPKKLAVERPKGSLEVNCSTTCNQPEVGGLETSNKILLDEQAQWKHYLVSNIHDTVQCHFTCSKG
QESMNSNVSYQ

>d1epfa1 b.1.1.4 (A:1-97) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}

LQVDIVPSQGEISVGESKFFLCQVAGDAKDDISWFSPNGEKLSPNQQRISVVWNDSSLTIYNANIDDAGI

YKCVVTAEDGTQSEATNVVKIFQ

>d1epfa2 b.1.1.4 (A:98-189) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}
KLMFKNAPTPQEFKEGEDAVIVCDVVSSLPTIIWKHKGRDVILKKDVRFIVLSNNYLQIRGIKKTDEGTYCEGRI
LARGEINFKDIQVIV

>d1ie5a_ b.1.1.4 (A:) Neural cell adhesion molecule (NCAM) {Chicken (Gallus gallus)}
GKDIQVIVNVPPSVRARQSTMNATANLSQSVTLACDADGFPEPTMTWTKDGEPIEQEDNEEKYSFNYDGSELII
KKVDKSDEAEYICIAENKAGEQDATIHLKVFAK

>d1gsma1 b.1.1.4 (A:1-90) Mucosal addressin cell adhesion molecule-1 (MADCAM-1) {Human (Homo sapiens)}

VKPLQVEPPEPVVAVALGASRQLTCRLACADRGASVQWRGLDTSLGAVQSDTGRSVLTVRNASLSAAGTRVCV
GSCGGRTFQHTVQLLVY

>d1gsma2 b.1.1.4 (A:91-206) Mucosal addressin cell adhesion molecule-1 (MADCAM-1) {Human (Homo sapiens)}

AFPNQLTVSPAALVPGDPEVACTAHVTPVDPNALSFSLVGGQELEGAQALGPEVQEEEEEPQGDDEVLFRTV
ERWRLPPLGTPVPPALYCQATMRLPGLELSHRQAIPVIEGR

>d1fhga_ b.1.1.4 (A:) Telokin {Turkey (Meleagris gallopavo)}
AEEKPHVKPYFTKTILDMEVVEGSAARFDCKVEGYPDPEVMWFKDNPVKESRHFQIDYDEEGNCSLTISEVC
GDDDAKYTCKAVNSLGEATCTAELLVETM

>d1g1ca_ b.1.1.4 (A:) Titin {Human (Homo sapiens), different modules}

SMEAPKIFERIQSQTVQGQSDAHFRVRVVGKPDPECEWYKNGVKIERSDRIYWYWPEDNVCELVIRDVTGEDS
ASIMVKAINIAGETSSHAFLVQAK

>d1nct_ b.1.1.4 (-) Titin {Human (Homo sapiens), different modules}

SKTTLAARIITKPRSMTVYEGESARFSCDTDGEPVPTVWLKGQVLSTSARHQVTTTKYKSTFEISSVQASDEG
NYSVVVENSEGKQEAFTLTIQK

>d1koa_1 b.1.1.4 (6265-6361) Twitchin {Nematode (Caenorhabditis elegans)}

QPRFIVKPYGTEVGEQSANFYCRVIASSPPVVTWHKDDRELKQSVKYMKRYNGNDYGLTINRVKGDDKGEYT
VRAKNSYGTKEEIVFLNVTRHSEP

>d1wiu_ b.1.1.4 (-) Twitchin {Nematode (Caenorhabditis elegans)}

LKPKILTASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGDSGAALAPELLVDAKSSTSIFFPSAKRADSGNYKLKV
KNELGEDEAIFEVIVQ

>d1tiu_ b.1.1.4 (-) Twitchin {Human (Homo sapiens), Ig repeat 27}

LIEVEKPLYGVVFVGETAHFEIELSEPDVHGQWKLKGQPLTASPDCEIIEDGKKHILILHNCQLGMTGEVSFQAA
NAKSAANLKVKEI

>d1iray1 b.1.1.4 (Y:1-101) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

DKCKEREKIIILVSSANEIDVRPCPLNPNEHKGTITWYKDDSKTPVSTEQASRIHQHKEKLWFVPAKVEDSGHY
CVVRNSSYCLRIKISAKFVENEPNL

>d1iray2 b.1.1.4 (Y:102-204) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

YNAQAIKFQKLPVAGDGLVCPYMEFFKNENNELPKLQWYKDCPLLDNIHFSGVKDRILVMNVAEKHRGNY
TCHASYTYLGKQYPITRVIEFITLEENKPT

>d1iray3 b.1.1.4 (Y:205-311) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

RPVIVSPANETMEVDLGSQIQLICNVTGQLSDIAYWKWNGSVIDEDDPVLGEDYYSVENPANKRRSTLITVLNIS
EIESRFYKHPFTCFAKNTHGIDAAYIQLIYPV

>d1cvsc1 b.1.1.4 (C:149-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}

MPVAPYWTSPEKMEKKLHAVPAAKTVFKCPSSGTPQPTLRWLKNGKEFPDHRIGGYKVRYATWSIIMDSVV
PSDKGNYTCIVENEYGSINHTYQLDVVER

>d1cvsc2 b.1.1.4 (C:251-359) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR1}

SPHRPILQAGLPANKTVALGSNVEFMCKVYSDPQPHIQWLKHIEVNGSKIGPDNLPYVQILTAGVNNTDKEM
EVLHLRNVSFEDAGEYTCAGNSIGLSHSAWLTVL

>d1ev2e1 b.1.1.4 (E:150-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR2}

NKRAPYWTNTEKMEKRLHAVPAANTVKFRCPAGGNPMPTMRWLKNGKEFKQEHRIGGYKVRNQHWSLIM
ESVVPSDKGNYTCVVENEYGSINHTYHLDVVE

>d1ev2e2 b.1.1.4 (E:251-360) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens), FGFR2}

RSPHRPILQAGLPANASTVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPGLPYLKVLKAAGVNNTDKEI
EVLYIRNVTFEDAGEYTCAGNSIGISFHSAWLTVL

>d1biha1 b.1.1.4 (A:5-98) Hemolin {Moth (Hyalophora cecropia)}

KYPVLKDQPAEVLFRENNPTVLECIIEGNDQGVKYSWKKDGKSYNWQEHNAALRKDEGLVFLRPQASDEGH
YQCFAETPAGVASSRVISFRKT

>d1biha2 b.1.1.4 (A:99-209) Hemolin {Moth (Hyalophora cecropia)}

YLIASPAKTHEKTPIEGRPFQLDCVLPNAYPKPLTWKKRLSGADPNADVTDFDRITAGPDGNLYFTIVTKEDVS
DIKYVCTAKNAAVDEEVVLVEYEIKGVTKDNNSGY

>d1biha3 b.1.1.4 (A:210-306) Hemolin {Moth (Hyalophora cecropia)}

KGEPVHQVSKDMMMAKAGDVTMIYCMYGSNPMGYPNYFKNGKDVGNGNPEDRITRHNRSGKRLFKTTLPE
DEGVYTCVDNGVGKPQKHSILKLTVV

>d1biha4 b.1.1.4 (A:307-395) Hemolin {Moth (Hyalophora cecropia)}

SAPKYEQKPEKVIVVKQGQDVTPCKVTGLPAPNVVSHNAKPLSGGRATVTDGLVIKGVKNGDKYYGCRA
TNEHGDKYFETLVQVN

>d1cs6a1 b.1.1.4 (A:7-103) Axonin-1 {Chicken (Gallus gallus)}

RSYGPVFEEQPAHTLFPEGSAEEKVTLTCRARANPPATYRWKMNGTELKMGPDSDRYRLVAGDLVISNPVKAKD
AGSYQCVATNARGTVVSREASLRF

>d1cs6a2 b.1.1.4 (A:104-208) Axonin-1 {Chicken (Gallus gallus)}

GFLQEFSAEERDPVKITEGWGMFTCSPPPYPALSYRWLLNEFPNFIPADGRRFVSQTGNLYIAKTEASDLGN
YSCFATSHIDFITKSFSKFSQLSAAEDA

>d1cs6a3 b.1.1.4 (A:209-299) Axonin-1 {Chicken (Gallus gallus)}

RQYAPSIAKFPADTYALTGQMVTLECAFGNPVPQIKWRKLDGSQTSKWLSSEPLLHIQNVDFEDEGTYECEA
ENIKGRDTYQGRIIIHA

>d1cs6a4 b.1.1.4 (A:300-388) Axonin-1 {Chicken (Gallus gallus)}

QPDWLDVITDTEADIGSDLRWSCVASGKPRPAVRWL RDGQPLASQNRIEVSGGELRFSKLVLEDGMYQCVA
ENKHGTVYASAELTVQA

>d1gl4b_ b.1.1.4 (B:) Perlecan Ig3 domain {Mouse (Mus musculus)}

PIMVTVEEQRSQS VRPGADVTICTAKSKSPAYTLVWTRLHNGKLPSRAMDFNGILTIRNVQPSDAGTYVCTGS
NMFAMDQGTATLHVQ

>d1f97a2 b.1.1.4 (A:129-238) Junction adhesion molecule, JAM, C-terminal domain {Mouse (Mus musculus)}

VPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPEYSWFKD GISMLTADAKKTRAFMNSSFTIDPKSGDLIFDPVTA

FDSGEYYCQAQNGYGTAMRSEAAHMDAELNVGG
>d1fltx_ b.1.1.4 (X:) Second domain of the Flt-1 receptor {Human (Homo sapiens)}
GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIISNATYKEIGLLTCEATV
NGHLYKTNYLTHRQT
>d1he7a_ b.1.1.4 (A:) NGF binding domain of trkA receptor {Human (Homo sapiens)}
SHMPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLRLNQPTHV
NNGNYTLLAANPFGQASASIMAAFMMDNPFEFNPE
>d1wwwx_ b.1.1.4 (X:) NGF binding domain of trkA receptor {Human (Homo sapiens)}
VSFPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVRHGCLRLNQPTHV
NNGNYTLLAANPFGQASASIMAAFMMDNP
>d1wwbx_ b.1.1.4 (X:) Ligand binding domain of trkB receptor {Human (Homo sapiens)}
VHFAPTITFLESPTSDHHWCIPFTVKGNPKPALQWFYNGAILNESKYICTKIHTVNHTHEYHGCLQLDNPTHMNN
GDYTIAKNEYGKDEKQISAHFMGWPGID
>d1wwca_ b.1.1.4 (A:) NT3 binding domain of trkC receptor {Human (Homo sapiens)}
TVYYPPRVVSLEEPELRLEHCIEFVVRGNPPPTLHWLHNGQPLRESKIIHVEYYQEGEISEGCLLFNKPTHYNNGN
YTIAKNPLGTANQTINGHFLKEPFPVDE
>d1fcga1 b.1.1.4 (A:4-88) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIa}
APPKAVALKLEPPWINVLQEDSVTLCQGARSPESDSIQWFHNGNLIPTHTQPSYRFKANNNDSGEYTCQTGQT
SLSDPVHDTVLF
>d1fcga2 b.1.1.4 (A:89-174) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIa}
EWLVLQTPHLEFQEGETIMLRCHSWDKPLVKVTFFQNGKSQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTL
FSSKPVTITVQV
>d2fcba1 b.1.1.4 (A:6-90) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIb}
APPKAVALKLEPQWINVLQEDSVTLCRGTHSPESDSIQWFHNGNLIPTHTQPSYRFKANNNDSGEYTCQTGQT
SLSDPVHDTVLS
>d2fcba2 b.1.1.4 (A:91-178) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), IIb}
EWLVLQTPHLEFQEGETIVLRCHSWDKPLVKVTFFQNGKSQKFSRSDPNFSIPQANHSHSGDYHCTGNIGYTL
YSSKPVTITVQAPA
>d1fnla1 b.1.1.4 (A:3-86) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), III}
EDLPKAVVFLEPWYSVLEKDSVTLKCQGAYSPEDNSTQWFHNESLISSQASSYFIDAATVNDSGEYRCQTNLST
LSDPVQLEV
>d1fnla2 b.1.1.4 (A:87-175) Fc gamma receptor ectodomain (CD32) {Human (Homo sapiens), III}
HIGWLLQAPRWVFKEEDPIHLRCHSWKNTALHKVTYLQNGKDRKYFHHNSDFHIPKATLKDSGSYFCRGLVG
SKNVSETVNITITQA
>d1f2qa1 b.1.1.4 (A:4-85) IgE high affinity receptor alpha subunit {Human (Homo sapiens)}
KPKVSLNPPWNRIFGENVTLCNGNNFFEVSSKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNES
EPVYLEVFS
>d1f2qa2 b.1.1.4 (A:86-174) IgE high affinity receptor alpha subunit {Human (Homo sapiens)}
DWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIVYYKDGEALKYWYENHNISITNATVEDSGTYCTGKVW
QLDYESEPLNITVIKAPR
>d1efxd1 b.1.1.4 (D:4-103) Killer cell inhibitory receptor {Human (Homo sapiens), kir2dl3}
VHRKPSLLAHPGRLVKSEETVILQCWSDVRFEHFLHREGFKDTLHLIGEHHDGVSKANFSIGPMMQDLAGTY
RCYGSVTHSPYQLSAPSDPLDIVITG
>d1efxd2 b.1.1.4 (D:104-200) Killer cell inhibitory receptor {Human (Homo sapiens), kir2dl3}

LYEKPSLSAQPGPTVLAGESVTLCSSRSSYDMYHLSREGEAHECRFSAGPKVNGTFQADFPLGPATHGGTYRCF
GSFRDSPYEWNSSDPLLVSI

>d1nkr_1 b.1.1.4 (6-101) Killer cell inhibitory receptor {Human (Homo sapiens), p58-cl42 kir}
RKPSLLAHPGPLVKSEETVIQCWSVMFEHFLHREGMFNDTLRLIGEHHDGVSKANFSISRMTQDLAGTYRC
YGSVTHSPYQVSAPSDPLDIV

>d1nkr_2 b.1.1.4 (102-200) Killer cell inhibitory receptor {Human (Homo sapiens), p58-cl42 kir}
IGLYEKPSLSAQPGPTVLAGENVTLCSSRSSYDMYHLSREGEAHERRLPAGPKVNGTFQADFPLGPATHGGTYR
CFGSFHDSPYEWSKSSDPLLVSVT

>d1g0xa1 b.1.1.4 (A:2-97) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}
HLPKPTLWAEPGSVITQGSPVTLRCQGGQETQEYRLYREKKTAPWTRIPQELVKKQFPIPSITWEHAGRYRCY
YGSDTAGRSESSDPLELVTG

>d1g0xa2 b.1.1.4 (A:98-198) Ligand binding domain of lir-1 (ilt2) {Human (Homo sapiens)}
AYIKPTLSAQQPSPVVNSGGNVTLCDSQAFDGFIILCKEGEDEHPQCLNSQPHARGSSRAIFSGPVSRRW
WYRCYAYDSNSPYEWSLPSDLLELLVLG

>d1f42a1 b.1.1.4 (A:1-87) The p40 domain of interleukin-12 (IL-12 beta chain), N-terminal domain
{Human (Homo sapiens)}
IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGE
VLSHSLLLLHKKD

>d1jbja1 b.1.1.4 (A:101-186) CD3 gamma chain ectodomain fragment {Mouse (Mus musculus)}
KKDGSQTNKAKNLVQVDGSRGDGSVLLTCGLTDKTIKWLKDGSIIISPLNATKNTWNLGNNAKDPRGTYQCQG
AKETSNPLQVYYRM

>d1jbja2 b.1.1.4 (A:1-100) CD3 epsilon chain ectodomain fragment {Mouse (Mus musculus)}
DDAENIEYKVSISGT SVELCPLSDDENLKWEKNGQELPKHDKHLVLQDFSEVEDSGYYVCYTPASNKNTYLYL
KARVGSADDAAKKDAAKKDDAKKDDA

>d1k3ia1 b.1.1.5 (A:538-639) Galactose oxidase, C-terminal domain {Fungi (Fusarium spp)}
GNLATRPKITRTSTQSVKVGGGRITISTDSSISKASLIRYGTATHTVNTDQRRIPLTNNGGNSYFQVPSDSGVALP
GYWMLFVMNSAGVPSVASTIRVTQ

>d1qba_1 b.1.1.5 (781-885) Bacterial chitobiase, c-terminal domain {Serratia marcescens}
GETHFVDTQALEKDWLRFANILGQRELAKLDKGGVAYRLPVPGARVAGGKLEANIALPGLIEYSTDGGKQWQ
RYDAKAKPAVSGEVQVRSVSPDGKRYSAEKV

>d1svb_1 b.1.1.5 (303-395) Envelope glycoprotein, domain III (C-terminal) {Tick-borne
encephalitis virus}
TYTMCDKTKFTWKRAPTDGHDTVMEVTFSGTKPCRIPVRAVAHGSPDVNVAMLITPNPTIENNGGFIE
QLPPGDNIIYVGELSHQWFQK

>d1cgt_1 b.1.1.5 (495-579) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans, different
strains}
ETTPTIGHVGPVMGKPGNVVTIDGRGFGSTKGTVYFGTTAVTGAAITSWEDTQIKVTIPSVAAGNYAVKVAASG
VNSNAYNNFTI

>d1kcla1 b.1.1.5 (A:496-581) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans,
different strains}
TATPTIGHVGPMMAKPGVTITIDGRGFSSKGTVYFGTTAVSGADITSWEDTQIKVKIPAVAGGNYNIVANAA
GTASNVYDNFEV

>d1cyg_1 b.1.1.5 (492-574) Cyclodextrin glycosyltransferase, domain E {Bacillus
stearothermophilus}

ESTPIIGHVGPMMGQVGHQVTIDGEGFTNTGTVKFGTTAANVWSNNQIVVAVPNVSPGKYNITVQSSSG
QTSAAYDNFEV

>d1qhoa1 b.1.1.5 (A:496-576) Cyclodextrin glycosyltransferase, domain E {Bacillus stearothermophilus, maltogenic alpha-amylase}

ASAPQIGSVAPNMGIPGNVVTIDKGKGFTTQGTVFGGTATVKSWTSNRIEVYVPNMAAGLTDVKVTAGGV
SSNLYSYNI

>d1pama1 b.1.1.5 (A:497-582) Cyclodextrin glycosyltransferase, domain E {Bacillus sp., strain 1011}

TTPIIGNVGPMMAKPGVTITDGRGFSGKGTVYFGTTAVTGADIVAWEDTQIQVKIPAVPGGIYDIRVANAAG
AASNLYDNFEVL

>d1ciu_1 b.1.1.5 (496-578) Cyclodextrin glycosyltransferase, domain E {Thermoanaerobacterium thermosulfurigenes, EM1}

SNSPLIGHVGPTMTKAGQTITDGRGFSGQVLFGSTAGTIVSWDDTEVKVKVPSVTPGKYNISLKTSSGATS
NTYNNINI

>d1smaa1 b.1.1.5 (A:1-123) Maltogenic amylase, N-terminal domain {Thermus sp.}

MRKEAIHHRSTDNFAYAYDSETLHLRLQTKNDVDHVELLFGDPYEWDGAWQFQTMPMRKTGSDGLFDY
WLAEVKPPYRRLRYGFVLRAGGEKLVYTEKGFYHEAPSDDTAYYFCFPFLHRV

>d1bvza1 b.1.1.5 (A:1-120) Maltogenic amylase, N-terminal domain {Thermoactinomyces vulgaris, TVAII}

MLLEAIFHEAKGSYAYPISETQLRVRLRAKKGDVVRCEVLYADRYASPEEELAHALAGKAGSDERFDYFEALLECST
KRVKYVLLTGPQGEAVYFGETGFSKAERSKAGVFQYAYIHRSE

>d1eh9a1 b.1.1.5 (A:1-90) Glycosyltrehalose trehalohydrolase, N-terminal domain {Archaeon Sulfolobus solfataricus, km1}

TFAYKIDGNEVIFTLWAPYQKSVKLVLEKGLYEMERDEKGYFTITNNVKVRDRYKYVLDASEIPDPASRYQPE
GVHGPSQIIQESKE

>d1bf2_1 b.1.1.5 (1-162) Isoamylase, N-terminal domain {Pseudomonas amylofera}

AINSMSLGASYDAQQANITFRVYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVWAVTPVSSIKAAGITGAVY
YGYRAWGPNPWPYASNWGKGSQAGFVSVDANGDRFNPNKLLDPYAQEVSQDPLNPSNQNGNVFASGAS
YRTTDSGIYAPKGVVVL

>d1lla_3 b.1.1.5 (380-628) Hemocyanin, C-terminal domain {Horseshoe crab (Limulus polyphemus)}

PYDHDLNFPDIQVQDVTLHARVDNVVHTFMREQELELKGINPGNARSIKARYYHLDHEPFSYAVNVQNNS
ASDKHATVRIFLAPKYDELGNEIKADELRTAIELDKFTDLHPGKNTVVRHSLSSVTLHQPTFEDLLHGVLN
EHKSEYCSCGWPSPHLLVPKGNIKGMEYHLFVMLTDWDKDKVDGSESACDAVSYCGARDHKYPDKPMGF
PFDRPITHEISDFLTNNMFIKDIKIKFHE

>d1hc2_3 b.1.1.5 (399-653) Hemocyanin, C-terminal domain {Spiny lobster (Panulirus interruptus)}

PPYTHDNLEFSGMVVNGVAIDGELITFFDEFQYSLINAVDGENIEDVEINARVHRLNHNEFTYKITMSNNNDG
ERLATFRIFLCPIEDNNGITLTLEARWFCIELDKFFQKVPSGPETIERSSKDSSVTPDMPSFQLKEQADNAV
GGHDLDSLAYERSCGIPDRMLLPKSKPEGMEFNLYVAVTDGDKDTEGHNGGHDYGGTHAQC GVHGEAYPDN
RPLGYPLERRIPDERVIDGVSNIKHVVVKIVHHL

>d1js8a2 b.1.1.5 (A:2792-2892) C-terminal domain of octopus hemocyanin {Giant octopus (Octopus dofleini)}

EDRVFAGFLRTIGQSADVNFVCTKDGECTFGGTFCILGGEHEMF WAFDRLFKYDITSLKHLRLDAHDDFDIK
VTIKGIDGHVLSNKYLSPPTVFLAPA

>d1clc_2 b.1.1.5 (35-134) CelD cellulase, N-terminal domain {Clostridium

thermocellum}

IETKVSAAKITENYQFDSRIRLN SIGFIPNHSKKATIAANCSTFYVVKEDGTIVYGTATSMFDNDTKETVYIADFSS
VNEEGTYYLAVPGVGKSVNFKI

>d1f1sa2 b.1.1.5 (A:171-248) Hyaluronate lyase precatalytic domain {Streptococcus agalactiae}
SEHPQPVTQIEKSNTALNKNYVFNKADYQYTLNPSLGKIVGGILYPNATGSTTVKISDKSGKIIKEVPLSVTAST

>d1edqa1 b.1.1.5 (A:24-132) Chitinase A, N-terminal domain {Serratia marcescens}

AAPGKPTIAWGNTKFAIVEVDQAA TAYNNLVKVKA DVS VSWNLWNGDTGTTAKVLLNGKEAWSGPSTGS
SGTANFKVNKGGRYQMQLVALCNADGCTASDATEIVVAD

>d1f13a1 b.1.1.5 (A:5-190) Transglutaminase N-terminal domain {Human (Homo sapiens)}
RTAFGRRRAVPPNNSNAAEDDLPTVELQGVVPRGVNLQEFLNVTSHLFKERWDTNKVDHHTDKYENNKLIV
RRGQSFYVQIDFSRPYDPRRDLFRVEYVIGRYPQENKGTYIPVPIVSELQSGKWGAKIVMREDRSVRLSIQSSPKC
IVGKFRMYVAVWTPYGVLRSRNPETDTYILFNPWCED

>d1g0da1 b.1.1.5 (A:6-140) Transglutaminase N-terminal domain {Red sea bream (Chrysophrys major)}

GLIVDVNGRSHENNLAHRTREIDRERLIVRRGQPFSTLQCSDSLPPKHHLELVHLGKRDEVVIKVQKEHGARD
KWWFNQQGAQDEILLTLHSPANAVIGHYRLAVLMSPDGHIVERADKISFHMLFNPWCRD

>d1eut_1 b.1.1.5 (403-505) Sialidase, "linker" domain {Micromonospora viridifaciens}

GICAPFTIPDVALEPGQQVTVPAVTNQSGIAVPKPSLQLDASP DWQVQGSVEPLMPGRQAKGQVTITVPAGT
TPGRYRVGATLRTSAGNASTTFTVTVGLLD

>d1ksr__ b.1.1.5 (-) F-actin cross-linking gelation factor (ABP-120), one repeat (ROD 4) {Slime mold (Dictyostelium discoideum), different domains}

ADPEKSYAEGPGLDGGECFQPSKFKIH AVDPDG VHRTDGGDGFVVTIEGPAPVDPVMVDNGDGT YDVEFEPK
EAGDYVINL TDGD NVNGFPKTVVKPA

>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}

KPAPSAEH SYAEGEGLV KVF DNAPAEFTIFAVDTKG VARTDGGDPFEVAINGPDGLVVDAK VTDNN DGT YGVV
YDAPVEGN YNVNVN VTLRG NPIKNM PIDVK CIE

>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}

GANGEDSSFGSFTFTVAAKNKKG EVKTYGGDKF E SIT GPAEE ITL DAIDN QDG TYTA AYSLVG NGRF STGV KLN
GKHIEGSPFKQVLGNPGKKNPEVKSFTT RTAN

>d1ds6b_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
GNYKPPPQKSLKELQEMDKDDESLIK YKKTLLGDGPV VTDPKAPNVV VTR LTV CESAPGPITMDLTGD LEALKK
ETIVLKEGSEYRVKIHFKVN RDIVS GLKYVQHTYRTGV KV DKAT FMV GS YG PRPEEY EFL TP VEEAPKGMLARGT
YHN KSFFT DDDKQDHLSWEWNLSIKKEWG

>d1fsoa_ b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
MVPNVV VTGL TLV CSSA PGPLE DLT GDLES FK QSF VLKE GVEY RI KIS FR VN RE I VSG M KYI QHTY RAG VAI DA
TDY MVG S YG PRAEE Y EFL TP VEE AP KGML ARG SY SI K SR FT D DD KTD HLSWE WNFT IKK DWK

>d1hh4e_ b.1.1.5 (E:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
HSV NYK PPAQ KSI QI EQI QEL DK D E SLR KY KE ALL GRV A VAS ADP NVP VV VTGL TLV CSSA PGPLE DLT GDLES FK
KQS FVLKE GVEY RI KIS FR VN RE I VSG M KYI QHTY RKG V KID KTD YMVG S YG PRAEE Y EFL TP VEE AP KGML ARG
SY SI K SR FT D DD KTD HLSWE WNFT IKK DWK

>d1rhoa_ b.1.1.5 (A:) Rho GDP-dissociation inhibitor 1, RhoGDI {Human (Homo sapiens)}
VA VAS ADP NVP VV VTGL TLV CSSA PGPLE DLT GDLES FK QSF VLKE GVEY RI KIS FR VN RE I VSG M KYI EHTY RK

GVKIDKTDYMGSGYGPRAEYEFLTPVEEAPKMLARGSYSIKSRFTDDDKTDHLSWEWNLTICKDWK
>d1ajw__ b.1.1.5 (-) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}
AVSADPNVPNVVTRTLVCSTAPGLELDLTGDLESFKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGV
VKIDKTDYMGSGYGPRAEYEFLTPMEEAPKMLARGSYNIKSRTDDRTDHLSWEWNLTICKEWKD
>d1doab_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (Bos taurus)}
EPTAEQLAQIAAENEDEHSVNYKPPAQKSIQEIQELDKDDESLRKYKEALLGRVAVSADPNVPNVVTRTLVC
STAPGLELDLTGDLESFKQSFVLKEGVEYRIKISFRVNREIVSGMKYIQHTYRKGVKIDKTDYMGSGYGPRAE
YEFLTPMEEAPKMLARGSYNIKSRTDDRTDHLSWEWNLTICKEWKD
>d1ayra2 b.1.1.5 (A:183-368) Arrestin {Cow (Bos taurus), visual arrestin}
DMGPQPRAEASWQFFMSDKPLRLAVSLSKIEIYYHGEPIPVTVAVTNSTEKTVKKIKVLVEQVTNVVLYSSDYYIK
TVAAEEAQEKVPPNSSLTKTTLVPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDKTVMGILVSQIKVKLT
SGLLGE LTSSEVATEVPFRLMHPQPEDPDTAKA
>d1cf1a1 b.1.1.5 (A:10-182) Arrestin {Cow (Bos taurus), visual arrestin}
HVIFKKISRDKSVTIYLGKRDYIDHVERVEPVDPGVVLVDPELVKGKRVYVSLCAFRYGQEDIDVMGLSFRRDLYFS
QVQVFPPVGASGATTRLQESLIKLGANTYPFLTFPDYLPCSVMLQPAPQDVKGSCGVDFEIKAFATHSTDVEE
DKIPKKSSVRLLIRKVQHAPR
>d1cf1a2 b.1.1.5 (A:183-393) Arrestin {Cow (Bos taurus), visual arrestin}
DMGPQPRAEASWQFFMSDKPLRLAVSLSKIEIYYHGEPIPVTVAVTNSTEKTVKKIKVLVEQVTNVVLYSSDYYIK
TVAAEEAQEKVPPNSSLTKTTLVPLLANNRERRGIALDGKIKHEDTNLASSTIIKEGIDKTVMGILVSQIKVKLT
SGLLGE LTSSEVATEVPFRLMHPQPEDPDTAKESFQDENFVFEEFARQNLKDAGEYKE
>d1g4ma1 b.1.1.5 (A:5-175) Arrestin {Cow (Bos taurus), beta-arrestin 1}
GTRVFKKASPNGKLTVYLGK RDFVDHIDLVEPVDPGVVLVDPEYLKERRVYVTLTCFRYGRELDLVGLTFRKDLF
VANVQSFPPAPEDKKPLTRLQERLIKLGHEAYPFTFEIPPNLPCSVTLQPGPEDTGKACGVDYEVKAFC
KIHKRNSVRLVIRKVQYAP
>d1g4ma2 b.1.1.5 (A:176-393) Arrestin {Cow (Bos taurus), beta-arrestin 1}
ERPGPQPTAETTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVNNTNKTVKKIKISVRQYADICLFNTAQYKC
PVAMEEADDTVAPSSTFCKVYLTPLFLANNREKRGALADGKLKHEDTNLASSTLLREGANREILGIIVSYKV
VVSRGGLLGDASSDVAELPFTLMPKPKEEPPHREVPEHETPVDTNLIELDTNDDDIVFEDFAR
>d1a02n1 b.1.1.5 (N:577-678) Transcription factor NFATC, C-terminal domain {Human (Homo sapiens)}
LPMVERQDTDSCLVYGGQQMILTQGNFTSESKVVTEKTTDGQQIWEMEATVDKDKSQPNMLFVEIPEYRNK
HIRTPVKVNFYVINGKRKRSQPQHFTYHPV
>d1imhc1 b.1.1.5 (C:368-468) Transcription factor TONEBP, C-terminal domain {Human (Homo sapiens)}
VPEILKKSLHCSVKGEEEVFLIGKNFLKGTVIFQENVSDENSWKSEAEIDMELFHQNHLIVKVPPYHDQHITLP
VSVGIYVVTNAGRSHDVQPFTYTPD
>d1bfs__ b.1.1.5 (-) p50 subunit of NF-kappa B transcription factor, C-terminal domain {Mouse (Mus musculus)}
ASNLKIVRMDRTAGCVTGGEEIYLLCDKVQKDDIQIRFYEEEENGWEGFGDFSP TDVHRQFAIVFKTPKYKD
VNITKPASVVFQLRRKSDLETSEPKPFLYYPE
>d1a3qa1 b.1.1.5 (A:227-327) p52 subunit of NF-kappa B (NFKB), C-terminal domain {Human (Homo sapiens)}
NLKISRMDKTAGSVRGGDEVYLLCDKVQKDDIEVRFYEDDENGWQAFGDFSP TDVHKQYAIVFRTPPYH
KMKI
ERPVTVFLQLKRKGGSVDSKQFTYYP

>d1bfta_ b.1.1.5 (A:) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Mouse (Mus musculus)}

TAEKICRVNRNSGSCGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTPPYADPSLQAP
VRVSMQLRRPSDRELSEPMEFQYLPD

>d1ikna1 b.1.1.5 (A:192-303) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Mouse (Mus musculus)}

AELKICRVNRNSGSCGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTPPYADPSLQAP
VRVSMQLRRPSDRELSEPMEFQYLPDTDDRHRRIEEKRK

>d1nfia1 b.1.1.5 (A:190-314) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Human (Homo sapiens)}

NTAELKICRVNRNSGSCGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFSQADVHRQVAIVFRTPPYADPSLQA
PVRVSMQLRRPSDRELSEPMEFQYLPDTDDRHRRIEEKRKRTYETFKSIMK

>d1ahm__ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides farinae), Der f 2}

DQVDVKDCANNEIKKVMVDGCHGSDPCIIRGKPFITLEALFDANQNTKTAKEIKASLDGLEIDVPGIDTNACH
FVKCPLVKQQYDIKYTWNVPKIAPKSENVVTVKLIGDNGVLACAIATHGKIRD

>d1a9v__ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides pteronyssinus), Der p 2}

SQVDVKDCANHEIKKVLVPGCHGSEPCIIHRGKPFQLEAVFEANQNTKTAKEIKASIDGLEVDVPGIDPNACHY
MKCPLVKQQYDIKYTWNVPKIAPKSENVVTVKLIGDNGVLACAIATHAKIRD

>d1soxa1 b.1.1.5 (A:344-466) Sulfite oxidase, C-terminal domain {Chicken (Gallus gallus)}

ELPVQSAVTQPRPGAAVPPGELTVKGYAWSGGGREVVDRVSDGGRTWKVARLMGDKAPPGRRAWAWAL
WELTVPEAGTELEIVCKAVDSSYNQPDSVAPIWNLGVLSAWHRVRVSQD

>d1cvra1 b.1.1.5 (A:351-432) Gingipain R (RgpB), C-terminal domain {Porphyromonas gingivalis}

PTEMQVTAPANISASAQTFEVACDYNGAIATSLDDGDMVGTAIVKDGKAIKLNESIADETNLTLTVVGYNKVTVI
KDKVKE

>d1h6ta1 b.1.1.6 (A:241-321) Internalin B {Listeria monocytogenes}

ECLNKPINHQSNLVPNTVKNTDGLS廖TPEIISDDGDYEKPNVKWHLPEFTNEVSFIFYQPVТИKAKARFHGRV
TQPLKE

>d1h6ua1 b.1.1.6 (A:263-343) Internalin H {Listeria monocytogenes}

TITNQPVFYNNNLVVPNVVKGPSGAPIPATISDNGTYASPNTWNLTFSINNVSYTFNQSFTKNTTVPFSGTV
TQPLTE

>d1ehxa_ b.1.1.6 (A:) Cellulosomal scaffoldin protein CipC, module x2.1 {Clostridium cellulolyticum}

MQDPTINPTSISAKAGSFADTKITLTPNGNTFNGISELQSSQYTKGTNEVTLASYLNTLPENTTKTLTFDFGVGTT
NPKLTITVLPKDIPGLE

>d1im3d_ b.1.1.6 (D:) Cytomegalovirus protein US2 {Human cytomegalovirus}

PWFQIEDNRCYIDNGKLFARGSIVGNMSRFVDPKADYGGVGENLYVHADDVEFVPGESLKWNVRNLDVMP
FETLALRLVLQGDVILWLRCPPEL

>d1jjua3 b.1.1.6 (A:274-351) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}

AAPQVLAVAPARLKIGEETQLRVAGTGLGSDLTLPEGVAGSVESAGNGVTVLKLTATGTPGPVSLELGGQKVDLV
AYD

>d1jjua4 b.1.1.6 (A:352-489) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}

RPDRISIVPDLTIARIGGNGGPIPKVPAQFEAMGWLNGPDGQPGTGDIALGAFPASWATDNFDEEAEMQD
AKYAGSIDDTGLFTPAAEAGPNPERPMQTNNAGNLKVIATVDAEGEPLSAEAHLYATVQRFVDAPIR
>d1jmx3 b.1.1.6 (A:282-363) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
{*Pseudomonas putida*}
GKARLLAVQPAFIKAGGESEITLVSGSLAGKPDLGAGVEVTEVLEQTPTLVRLKARAAADAKPGQREAVGTLKG
VNLAVID
>d1jmx4 b.1.1.6 (A:364-494) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5
{*Pseudomonas putida*}
KVEEVKVVPAFSIARIGENGASVPKVQGRFEAEAWGKDANGQPLRIGYLPASWKVEPFNERAVEDEDVKFAGK
MQADGVFVPGGAGPNPERKMMTNNAAGNLKVIATLADGGQTGEGHMIVTVQRWNPPPLP
>d2hft_1 b.1.2.1 (1-106) Extracellular region of human tissue factor {Human (Homo sapiens)}
SGTTNTVAAYNLTWKSTNFK TILEWEPKPVNQVYTVQISTKSGDWKS KCFYTTDECDLTDEIVKDVQTYLARV
FSYPAGNVESTGSAGEPLYENSPEFTPYLET
>d2hft_2 b.1.2.1 (107-211) Extracellular region of human tissue factor {Human (Homo sapiens)}
NLGQPTIQSFEQVGTKNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYWKS S QEKGEFRSGKKTAKTNTNE
FLIDVDKGENYCF SVQAVIPSRTVNRKSTDSPV ECMG
>g1dan.1 b.1.2.1 (T:,U:91-106) Extracellular region of human tissue factor {Human (Homo sapiens)}
TVAAYNLTWKSTNFK TILEWEPKPVNQVYTVQISTKSGDWKS KCFYTTDECDLTDEIVKDVQTYLARVFSYPA
XEPLYENSPEFTPYLET
>d1a21a1 b.1.2.1 (A:4-106) Extracellular region of human tissue factor {Rabbit (Oryctolagus cuniculus)}
TGRAYNLTWKSTNFK TILEWEPKSIDHVYTVQISTRLENWKS KCF LTAE TECDLTDEVVKDVGQTYMARVLSYPA
RNGNTTGFPEEPPFRNSPEFTPYLDTNL
>d1a21a2 b.1.2.1 (A:107-208) Extracellular region of human tissue factor {Rabbit (Oryctolagus cuniculus)}
GQPTIQSFEQVGTKLNVTVQDARTLVRRNGTFLSLRAVFGKDLNYTLYW RASSTGKKTATTNTNEFLIDVDKGE
NYCFSVQAVIPS RKR KQR SPESLTECT
>d1fn a__ b.1.2.1 (-) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
RDLEVVAATPTSLISWDAPAVTVRYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVDYTITVYAVTGRGDSP
ASSKPISINYRTEI
>d1fnf_1 b.1.2.1 (1142-1235) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
PLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRITTTNGQQGNSLEEVVHADQSSCTFDNLSPGLEYNVS
VYTVKDDKESVPISDTIIPA
>d1fnf_2 b.1.2.1 (1236-1326) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
VPPPTDLRFTNIGPDTMRVTWAPPSIDL TNFLVRYSPVKNEEDVAELSI PSDNAVVLTNLLPGTEYVVSVSSVY
EQHESTPLRGRQK T G
>d1fnf_3 b.1.2.1 (1327-1415) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
LDSPTGIDFS DITANSFTVHWIAPRATITGYRIRHHPEHFS GRPREDRVPHSRNSITLTN LPGTEYVV SIVALNGR
EESPLLIGQQST
>d1fnha1 b.1.2.1 (A:3-92) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
PAP TDLKFTQVTPTLSAQWT PPNVQLTGYRVRVTPKEKT GPMKEINLAPDSSVV VSGLMVATKYEVSVYALK
DTLTSRPAQGVVTTLE
>d1fnha2 b.1.2.1 (A:93-182) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
NVSPPRRARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKPDVRSYITGLQPGTDYKIYLYTLNDN

ARSSPVVIDASTA

>d1fnha3 b.1.2.1 (A:183-271) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
IDAPSNLRLATTPNSLLWSWQPPRARITGYIICKYEPGSPPREVPRPRPGVTEATITGLEPGTEYTIYVIALKNNQ
KSEPLIGRKKT

>d1j8ka_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
NIDRPKGIAFTDVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELPAPDGEEDTAELQGLRPGSEYTVSVAL
HDDMESQPLIGTQSTAIPA

>d2fnba_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
MRGSEVPQLTDLSFVDITDSSIGLRWTPLNSSTIIGYRITVVAAGEGIPIFEDFVDSSVGYYTGTLEPGIDYDISVIT
LINGGESAPTTLTQQT

>d2mfn_1 b.1.2.1 (1-92) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}
GLDSPTGFDSSDITANSFTVHWVAPRAPITGYIIRHHAHSVGRPRQDRVPPSRNSITLNLNPGETYVVSIAVN
GREESPPLIGQQATVS

>d2mfn_2 b.1.2.1 (93-184) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}
DIPRDLEVIASTPTSLISWEPPAVSVRYRITYGETGGNSPVQEFTVPGSKSTATINNIKPGADYTITLYAVTGRGD
SPASSKPVSINYKT

>d1qr4a1 b.1.2.1 (A:1-87) Tenascin {Chicken (Gallus gallus)}
DNPKDLEVSDPTETTLWRWRPVAKFDRYRLTYVSPSGKKNEMEIPVDSTSFLRGLDAGTEYTISLVAEKGRHK
SKPTTIKGSTV

>d1qr4a2 b.1.2.1 (A:88-175) Tenascin {Chicken (Gallus gallus)}
VGSPKGISFSDITENSATVSWTPRSRVDSYRVSYVPITGGTPNVVTDGSKRTKLVLVPGVDYNVNIIISVKGF
EESEPISGILKT

>d1ten__ b.1.2.1 (-) Tenascin {Human (Homo sapiens)}
RLDAPSQIEVKDVTDTTALITWFKPLAEIDGIELTYGIKDVGDRTTIDLTEDENQYSIGNLKDTEYEVSLSRRGD
MSSNPAKETFTT

>d1cfb_1 b.1.2.1 (610-709) Neurogian, two amino proximal Fn3 repeats {Drosophila melanogaster}
IVQDVPNAPKLTGITCQADKAEIHWEQQGDNRSPILHYTIQFNTSFTPASWDAAYEVKVPNTDSSFVVQMSWA
NYTFRVIAFNKIGASPPSAHSDSCTTQ

>d1cfb_2 b.1.2.1 (710-814) Neurogian, two amino proximal Fn3 repeats {Drosophila melanogaster}
PDVPFKNPDNVVGQGTEPNNLVISWTPMPEIEHNAPNFHYYVSWKRDIPAAWENNINFDWRQNNIVIAD
QPTFVKYLIKVVAINDRGESNVAEEEVGVSGEDR

>d1qg3a1 b.1.2.1 (A:1126-1217) Integrin beta-4 subunit {Human (Homo sapiens)}
DLGAPQNPNAKAAGSRKIHFNWLPMSGKPMGYRVKYWIQGDSESEAHLDSKVPSVELTNLYPYCDYEMKVC
AYGAQGEGPYSSLVSCRTHQ

>d1qg3a2 b.1.2.1 (A:1218-1320) Integrin beta-4 subunit {Human (Homo sapiens)}
EVPSEPGRLAFNVVSSVTQLSWAEPAEITNGEITAYEVCYGLVNDNRPIGPMKKLVDPNPKNRMLLIENLRES
QPYRYTVKARNGAGWGPEREAIINLATQP

>d1axib1 b.1.2.1 (B:32-130) Growth hormone receptor {Human (Homo sapiens)}
EPKFTKCRSPERETFSCHWTDEVHHGKNEGPIQLFYTRRNTQEWWTQEWKECPDYVSAGENSCYFNSSFTSIAI
PYCIKLTNGGTVDLKCFSVDEIVQ

>d1axib2 b.1.2.1 (B:131-236) Growth hormone receptor {Human (Homo sapiens)}
PDPPIALNWTLNVSLTGIHADIQVRWEAPRNADIQKGWMVLEYLQYKEVNETKWKMMDPILTSVPVYSL
KVDKEYEVVRVRSKQRNSGNYGEFSEVLYVTLPMQ

>d1eerb1 b.1.2.1 (B:8-116) Erythropoietin (EPO) receptor {Human (Homo sapiens)}

DPKFESKAALLAARGPEELLCFTERLEDLVCWEEAASAGVGPGQYSFSYQLEDEPWKLRLHQAPTARGAVRF
WCSLPTADTSSFPVPLRVTAASGAPRYHRVIHIN
>d1erb2 b.1.2.1 (B:117-220) Erythropoietin (EPO) receptor {Human (Homo sapiens)}
EVVLLDAPVGLVARLADES GHVVLRWLPPPETPMTSHIRYEVDSAGQGAGSVQRVEILEGRTECVLSNLRGRT
RYTFAVRARMAEPSFGFWSEWSEPVSLLT
>d1bp3b1 b.1.2.1 (B:202-300) Prolactin receptor {Human (Homo sapiens)}
LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSLTYHREGETLMHECPDYITGGPNSCHFGKQYTSMWRT
YIMMVNATNQMGSFSDELYVDVTYI
>d1bp3b2 b.1.2.1 (B:301-404) Prolactin receptor {Human (Homo sapiens)}
VQPDPGLEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWEIHFAGQQTEFKILSLHPGQ
KYLVQVRCKPDHGYSWAWSPATFIQIPS
>d1f6fb1 b.1.2.1 (B:5-100) Prolactin receptor {Rat (Rattus norvegicus)}
GKPEIHKCRSPDKETFTCWWNP GTDGGLPTNYSLTYSKEGEKTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVN
ATNQMGSSSSDPLYVDVTYI
>d1f6fb2 b.1.2.1 (B:101-203) Prolactin receptor {Rat (Rattus norvegicus)}
VEPEPPRNLTLEVKQLDKKTYLWVKWSPPTIDVKTGWFTMEYEIRLKPEEAEEWEIHFTGHQTQFKVFDLYP
GQKYLVQTRCKPDHGYSWAWSQESSVEMP
>d1iarb1 b.1.2.1 (B:1-96) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}
FKVLQEPTCVSDYMSISTCEWMNGPTNCSTELRLLYQLVFLSEAHTCIPENNGGAGCVCHLLMDDVVSADN
YTLDLWAGQQQLWKGSKPKSEHV
>d1iarb2 b.1.2.1 (B:97-197) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}
KPRAPGNLT VHTN VSDT LLLTWSNPYPPDNYLYNHLYAVNIWSENDPADFRIYNVTYLEPSLRIA STLKSGISY
RARVRAWAQAYNTTWSEWSPSTKWH
>d1egja_ b.1.2.1 (A:) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}
IQMAPPSLNVT KDGDSYSLRWETMKMRYEHIDHTFEI QYRKDTATWKDSKTETLQNAHSMALPAEPSTRYW
ARVRVRTSRTGYNGIWSEWSEARSWDTE
>d1gh7a1 b.1.2.1 (A:1-103) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}
EETIPLQLRCYNDYTS HITCRWADTQDAQRLVN TLI RVNEDLLEPVSCDLSDDMPWSACPHPRCVPRRCV
PCQSFVVT D VDFYFSFQPD RPLGTRLT VTL
>d1gh7a2 b.1.2.1 (A:104-217) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}
TQHVQPPEPRDLQISTDQDHFLTWSVALGSPQSHWLSPGDLEFEVYKRLQDSWEDAAILLSNTSQATLGPE
HL MPSSTYVARVTR LAPGSRLSGRPSKWSPEVCWDSQPGD
>d1gh7a3 b.1.2.1 (A:218-316) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}
EAQPQNLECFDGA AVLSCSWE VRKEVASSV SFGFYKPSPDAGSAVLLREECSPVLREGL GSLHTRH CQIPV
PDPATHGQYIVSVQPRRAEKHIKS
>d1cd9b1 b.1.2.1 (B:1-107) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse (Mus musculus)}
AGYPPASPSNLSC LMH LTTNSLVCQW EPGPETHLPTS FILKSFRSRADCQYQGDTIPDCVAKKRQNNCSIPRKNL
LLYQYMAIWVQAE NMLGSSES PKLCLDPMDVV
>d1cd9b2 b.1.2.1 (B:108-213) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse}

{Mus musculus)}

KLEPPMLQALDIGPDVVSHQPGCLWSWKWPWKPSEYMEQECELRYQPQLKGANWTLVFLPSSKDQFELCGL
HQAPVYTLQMRCIRSSLPGFWSPWSPGLQLRPTM

>d1fyhb1 b.1.2.1 (B:12-109) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}
VPTPTNVTIESYNMNPIVYWEYQIMPQPVFTEVKNYGVKNSEWIDACINISHHYCNISDHGDPSNSLWVR
VKARVGQQKESAYAKSEEFAVCRDGK

>d1fyhb2 b.1.2.1 (B:110-223) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}
IGPPKLDIRKEEKQIMIDIFHPSVFVNGDEQEVYDPETTCYIRVYNVYRMNGSEIQYKILTQKEDDCDEIQCQL
AIPVSSLNSQYCVSAEGVLHVWGVTEKSKEVCITFN

>d1bqua1 b.1.2.1 (A:5-99) Cytokine receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

GLPPEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPSCTVDYSTVYFVNIEV
WVEAENALGKVTSVDHINFDPV

>d1bqua2 b.1.2.1 (A:100-214) Cytokine receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

YKVKPNPPHNLSVINSEELSSILKLTWTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDASTRSSFTVQDLKPFTEY
VFRIRCMKEDGKGWSDWSEEASGITYEDRPSKEPSF

>d1i1ra1 b.1.2.1 (A:2-101) Cytokine receptor gp130 cytokine-binding domains {Human (Homo sapiens)}

LLDPCGYISPESPVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINRTASSVTFTDIASLNIQ
LTCNILTFGQLEQNYYGITIISG

>d1j7vr1 b.1.2.1 (R:2-100) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}

GTELPSPPSVWFEAEFFHHILHWTPPIPQQESTCYEVALLRYGIESWNSISQCSQTLSYDLTAVTLDLYHSNGYRA
RVRAVDGRHSQWTVNTNTRFSVD

>d1j7vr2 b.1.2.1 (R:101-206) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}

EVTLTVGSVNLEIHNGFILGKIQLPRPKMAPAQDTYESIFSHFREYEIAIRKVPQFTFHKVKHEQFSLLTSGEV
GEFCVQVKPSVASRSNKGWMSKEECISLT

>d1bpv_ b.1.2.1 (-) Type I titin module {Human (Homo sapiens)}

SPIDPPGKPVPLNITRHTVTLWAKPEYTGGFKITSYIVEKRDLNGRWLKANFSNILENEFTVSGLTEDAAYEFR
VIAKNAAGAISPPSEPSDAITCRDDVEA

>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)}

GIWSTDILKDQKEPKNKTFLCEAKNYSGRFTCWVWLTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD
NKEYEYSVECQEDSACPAEESLPIEVMVDAVHKLKYENYTSSFFIRDII

>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)}

KPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASIV
RAQDRYYSSSWSEWASVPCS

>d1b4ra_ b.1.3.1 (A:) Polycystein-1, PKD-1 {Human (Homo sapiens)}

ATLVGPHGPLASGQLAAFHIAAPLPVTATRWDFGDGSAEVDAAGPAASHRYVLPGRYHVTAVLALGAGSALLG
TDVQVEA

>d1jz8a1 b.1.4.1 (A:220-333) beta-Galactosidase, domains 2 and 4 {Escherichia coli}

TQISDFHVATRFNDFSRAVLEAEVQMCGELRDYLRTVSLWQGETQVASGTAPFGGEIIDERGGYADRVTRL
NVENPKLWSAEIPNLYRAVVELHTADGTIEAEACDVGFR

>d1jz8a2 b.1.4.1 (A:626-730) beta-Galactosidase, domains 2 and 4 {Escherichia coli}
FFQFRLSGQTIEVTSEYLFRHSDNELLHWMVALDGKPLASGEVPLDVAPQGKQLIELPELPQPESAGQLWLT
VVQPNATAWSEAGHISAWQQWRLAENLSVT
>d1bhga1 b.1.4.1 (A:226-328) beta-Glucuronidase {Human (Homo sapiens)}
TYIDDTITTSVEQDSGLVNYQISVKGSNLFKLEVRLDAENKVVANGTGTQGQLKPGVSLWWPYLMHERPAY
LYSLEVQLTAQTSLGPVSDFYTLPGVIRT
>d1f13a2 b.1.5.1 (A:516-627) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}
SNVDMDFEVENAVLGKDFKLSITFRNNSHNRYTITAYLSANITFYTGVPKAEFKKETFDVTLEPLSFKEAVLIQAG
EYMGQMLEQASLHFFVTARINETRDVLAKQKSTVL
>d1f13a3 b.1.5.1 (A:628-728) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}
TIPEIIIKVRGTQVGSDMTVTVEFTNPLKETLRNVVHLDGPGVTRPMKKMFREIRPNSTVQWEEVCRPWV
SGHRKLIASMSSDSLHVYGEVDVQIQRR
>d1g0da2 b.1.5.1 (A:472-583) Transglutaminase, two C-terminal domains {Red sea bream
(Chrysophrys major)}
RLQLSIKHAQPVFGTFDVIDEVKNEGGRDAHAQLTMLAMAVTYNSLRRGECQRKTISVTPAHKAHKEVMRL
HYDDYVRCVSEHHILIRVKALLDAPGENGPIMTVANIPLS
>d1g0da3 b.1.5.1 (A:584-684) Transglutaminase, two C-terminal domains {Red sea bream
(Chrysophrys major)}
TPELLVQVPGKAVVWEPLTAYVSFTNPLPVPLKGGVFTLEGAGLLSATQIHVNGAVAPSGKVSVKLSFSPMRTGV
RKLLVDFDSRDLKVGVTTVVHKK
>d1ncia_ b.1.6.1 (A:) N-cadherin (neural) {Mouse (Mus musculus)}
GSDWVIPPINLPENSRGFPFPQELVRISGRDKNLSLRYSVTGPGADQPPTGIFIINPISGQLSVTKPLDREIARFH
LRAHAVDINGNQVENPIDIVINVID
>d1ncja2 b.1.6.1 (A:102-215) N-cadherin (neural) {Mouse (Mus musculus)}
NDNRPEFLHQVWNNGSVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRIVSQAPTPSPNMFTINNETGDIIT
VAAGLDREKVQQYTLIIQATDMEGNPTYGLSNTATAVITVD
>d1edha1 b.1.6.1 (A:3-101) E-cadherin (epithelial) {Mouse (Mus musculus)}
VIPPISCPENEKGEEPKNLVQIKSNRDKETKVFYSITGQGADKPPGVFIIERETGWLKVTQPLDREIAKYILYSHA
VSSNGEAVEDPMEIVITVTDQ
>d1edha2 b.1.6.1 (A:102-213) E-cadherin (epithelial) {Mouse (Mus musculus)}
NDNRPEFTQEVFEGSVAEGAVPGTSVMKVSATDADDVNNTYNAIAYTIVSQDPELPHKNMFTVNRTGVIS
VLTSGLDRESYPTYTLVQAADLQGEGLSTTAKAVITVKD
>d2mcm_ b.1.7.1 (-) Macromycin {Streptomyces macromomyceticus}
APGVTVTPATGLSNGQTVTVSATGLPGTVYHVGQCAVVEPGVIGCDATTSTDVTADAAGKITAQLKVHSSFQA
VVGADGTPWGTVNCKVVSCAGLSDSGEGAAQAITFA
>d1noa_ b.1.7.1 (-) Neocarzinostatin {Streptomyces carzinostaticus}
AAPTATVTPSSGLSDGTVVKVAGAGLQAGTAYDVGQCAWVDTGVLACNPADFSSVTADANGSASTSLTVRRSF
EGFLFDGTRWGTVDCTAACQVGLSDAAGNGPEGVAISFN
>d1acx_ b.1.7.1 (-) Actinoxanthin {Actinomyces globisporus, number 1131}
APAFSVPASGASDGQSWSVAAAGETYYIAQCAPVGGQDACNPATATSFTTDASGAASFSTVRKSYAGQTP
SGTPVGSVDCATDACNLGAGNSGLNLGHVALTFG
>d1hzka_ b.1.7.1 (A:) Antitumor antibiotic C-1027 apoprotein {Streptomyces
globisporus}
APAFSVPASGLSDGQSWSVSGAAAGETYYIAQCAPVGGQDACNPATATSFTTDASGAASFVVRKSYTGST

PEGTPVGSVDCATAACNLGAGNSGLDLGHVALTFG

>d1akp__ b.1.7.1 (-) Kedarcidin (apo form) {Actimomycete, strain L585-6}

ASAAVSVPATGLADGATVTSASGFATSTSATALQCAILADGRGACNVAEFHDFSLSGGEGTTSVVRRSFTGY
VMPDGPEVGAVIDCDTAPGGCEIVVGGNTGEYGNAAISFG

>d1cbja_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Cow (Bos taurus)}

ATKAVCVLKGDPVQGTIHFEAKGDTVVVTGSITGLTEGDHGFHVHQFGDNTQGCTSAGPHFNPLSKKHGGP
KDEERHVGDLGNVTADKNGVAIVDIVDPLISLSGEYSIIGRTMVVHEKPDDLGRGGNEESTKTGNAGSRLACGV
IGIAK

>d1azva_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Human (Homo sapiens)}

ATKAVCVLKGDPVQGIINFEQKESNGPVKVGSIKRLTEGLHGFHVHEFGDNTAGCTSAGPHFNPLSRKHGG
PKDEERHVGDLGNVTADKDGVADVSIEDSVISLSDHCIIIGRTLVVHEKADDLGKGGNEESTKTGNAGSRLACGV
VIGIAQ

>d1xsoa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {African clawed frog (Xenopus laevis)}

VKAVCVLAGSGDVKGVVHFEQQDEGAVSVEGKIEGLTDGLHGFHIHVFGDNTNGCMSAGSHFNPNENKNHGA
PGDTDRHVGDLGNVTAEggVAQFKITDSLISLKGPNsIIGRTAVVHEKADDLGKGGNDESLKTGNAGGRLACGV
IGYSP

>d1srda_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Spinach (Spinacia oleracea)}

ATKKAVAVLKGTSNVEGVVTLTQEDDGPTTVNRISGLAPGKHGFHLHEFGDTTNGCMSTGPHFNPDKKTHG
APEDEVRHAGDLGNIVANTDGVAEATIVDNQIPLTPNSVGRALVVHELEDDLGKGGHELSPTTGNAGGRLA
CGVVGLTPV

>d1jcv__ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Baker's yeast (Saccharomyces cerevisiae)}

VQAVAVLKGDAGVSGVVKFEQASESEPTVSYEAGNSPNAERGFHIHEFGDATNGCVSAGPHFNPFKKTHGA
PTDEVVRHVGDMGNVKTDENGVAKGSFKDSLIKIGPTSVVGRSVVIHAGQDDLGKGDTEESLKTGNAGPRPAC
GVIGLTN

>d1yaia_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Photobacterium leiognathi}

QDLTVKMTDLQTGKPGVTIELSQNKYGVVFTPTELADLTPGMHGFIHQNGSCASSEKDGVVLGGAAGGHYD
PEHTNKHGFPWTDDNHKGDLPALFVSANGLATNPVLAPRRTLKEKGHAIMIHAGGDNHSDMPKALGGGG
RVACGVIQ

>d1eso_ b.1.8.1 (-) Cu,Zn superoxide dismutase, SOD {Escherichia coli}

ASEKVEMNLVTSQGVGQSIGSVTITDKGLEFSPDLKALPPGEHGFHIHAKGSCQPATKDGKASAESAGGHL
DPQNTGKHEGPAGHLGDLPALVVNNNDGKATDAVIAPRLKSLDEIKDKALMVHVGDNMSDQPPLGGGG
ERYACGVIK

>d1eqwa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Salmonella typhimurium}

NTLTVKMNDALSSGTGENIGEITVSETPYGLLFTPMLNGLTPGIHGFHVHTNPSCMPGMKDGEVPMAGG
HLDPEKTGKHLGPYNDKGHLGDLPLGVVNADGTATYPLAPRLKSLSELKGHSLMIHKGGDNYSDKPAPLGGGG
ARFACGVIE

>d2apsa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Actinobacillus pleuropneumoniae}

EKLVVQVQLDPVKGNKDVGTVITESAYGLVFTPMLHGLAQGLHGFHIHQNPSCEPKEKDGLVAGLGAGGH
WDPKETKQHGYPWSDNAHLGDLPLALFVEHDGSATNPVLAPRLKKLDEVKGHSLMIHEGGDNHSDHPAPLGG
GGPRMACGVIK

>d1ej8a_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

SSAVAILETFQKYTIDQKKDTAVRGLARIVQVGENKTLFDITVNGVPEAGNYHASIHEKGDVSKGVESTGKVWHK

FDEPIECFNESDLGKNLYSGKTFSLAPLPTWQLIGRSFVISKSLNHPENEPPSSVKDYSFLGVIAR
>d1jk9b1 b.1.8.1 (B:74-245) Copper chaperone for superoxide dismutase, C-terminal domain
{Baker's yeast (Saccharomyces cerevisiae)}
GKPNSSAVAILTFQKYTIDQQKDTAVRGLARIVQVGENKLFITVNGVPEAGNYHASIHEKGDVSKGVESTGK
VWHKFDEPIECFNESDLGKNLYSGKTFSLAPLPTWQLIGRSFVISKSLNHPENEPPSSVKDYSFLGVIARSAGVWE
NNKQVCACTGKTWEEERKDALA
>d1do5a_ b.1.8.1 (A:) Copper chaperone for superoxide dismutase, C-terminal domain {Human
(Homo sapiens)}
QNLGAAVAILGGPGTVQGVVRFLQLTPERCLIEGTIDGLEPGLHGLHVHQYGLTNNCNSCGNHFPDGASHG
GPQDSDRHRGDLGNVRADADGRAIFRMEDEQLKVVWDVIGRSLIIDEGEDDLRGHHPLSKITGNSGERLACGI
IARSAGLF
>d1d7ca_ b.1.9.1 (A:) Cytochrome domain of cellobiose dehydrogenase {Fungus (Phanerochaete
chrysosporium)}
ESASQFTDPTTGFQFTGITDPVHDVTYGFVFPLATSGAQSTEFIGEVVAPIASKWIGIALGGAMNNNDLLVAWA
NGNQIVSSTRWATGYVQPTAYTGTATLTLPETTINSTHWKWFRCQGCTEWNGGIDVTSQGVLAWFSN
VAVDDPSDPQSTFSEHTDFGFFGIDYSTAHSANYQNYLNGDSG
>d1i8aa_ b.1.9.2 (A:) Xylanase 10A {Thermotoga maritima}
MVATAKYGTPVIDGEIDEIWNTTEEETKAVAMGSLDKNATAKVRVLWDENLYVLAIVKDPVLNKDNNSNPWE
QDSVEIFIDENNHTGYYEDDAQFRVNFMNEQTFGTGGSPRFKTAVKLIEGGYIVEAAIKWTKIPTPNTVIG
FNIQVNDANEKGQRVGIISWSDPTNNSWRDPSKFGNLRLIK
>d1qtsa1 b.1.10.1 (A:692-824) Alpa-adaptin AP2, N-terminal subdomain {Mouse (Mus musculus)}
GSPGIRLGSSEDNFARFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFLNFTPLICADDLQTNL
NLQTKPVDPVDGGAQVQQVVNIECISDFTEAPVLDIQFRYGGTFQNVSVKLPI TLNK
>d1e42a1 b.1.10.1 (A:705-824) Beta2-adaptin AP2, N-terminal subdomain {Human (Homo
sapiens)}
GGYVAPKAVWLPAVKAKGLEISGTFTHRQGHYMEMNFTNKALQHMTDFAIQFNKNSFGVIPSTPLAIHTPLM
PNQSIDVSLPLNTLGPVMKMEPLNNLQAVKNNIDVFYFSCLIPNV
>d1jv2a1 b.1.15.1 (A:439-598) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo
sapiens)}
PVITVNAGLEVYPSILNQDNKTCSPGTALKVSCFNVRFCLKADGKGVLPKLNQVELLLDKLKQKGAI RRALFL
YSRSPSHSKNMTISRGGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAADTTGLOPILNQFTPANISRQAH
ILLDCGE
>d1jv2a2 b.1.15.1 (A:599-737) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo
sapiens)}
DNVCKPKLEVSDQDKKIYIGDDNPLTLIVKAQNQGEGAYEAEIIVSIPLQADFIGVVRNNEALARLSCAFKTEN
QTRQVVCVLGNPMKAGTQLLAGLRFVHQQSEMDTSVKFDLQIQSSNLFDKVSPVVSHKV DLA
>d1jv2a3 b.1.15.1 (A:738-956) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (Homo
sapiens)}
VLA AVEIRGVSSPDHVFLPIPWNWEHKENPETEEDVGPVVQHIYELRNNGPSSFSKAMLHLQWPYKYNNTLLYI
LHYDIDGPMNCTS DMEINPLRIKISSLQTTKNDTVAGQGERDHЛИKRD LASEGDIHTLGCGVAQCLKIVCQV
GR LDRGKSAILYVKSLWTETFMNKENQHSYSLKSSASFNVIEFPYKNLPIEDITNSTLVTTNVTWGIQ
>d1jv2b1 b.1.15.1 (B:55-106,B:355-434) Hybrid domain of integrin beta {Human (Homo sapiens)}
EFPVSEARVLEDRLPLSDKGSGDSSQVTQVSPQRIALRLRPDDS K NFSIQVRQXVELEVRDLPEELSLFNATCLNN
EVIPGLKSCMGLKIGDTVSFSIEAKVRGCPQEKEKSFTIKPVGFKDSLIVQVTFDCD

>d1qpxa1 b.1.11.1 (A:1-124) Pilus chaperone PapD, N-domain {Escherichia coli}
AVSLDRTRAVFDGSEKSMTLDISNDNKQLPYLAQAWIENENQEIKITGPVIATPPVQRLLPGAKSMVRLSTTPDI
SKLPQDRESLFYFNLREIPPRSEKANVVQIALCTIKLFYRPAAIKTRP

>d1quna1 b.1.11.1 (A:1-121) Periplasmic chaperone FimC {Escherichia coli}
GVALGATRVYYPAGQKQVQLAVTNNDENSTYLIQSWWENADGVKDGRFIVTPPLFAMKGKKENTLRILDATNN
QLPQDRESLFWMNVKAIPSMDKSKLTENTLQLAIISRIKLYYRPAKLA

>d1mspa_ b.1.11.2 (A:) Major sperm protein, alpha isoform (recombinant), ph 4.6
{Pig roundworm (*Ascaris suum*)}
SVPPGDINTQPSQKIVFNAPYDDKHTYHIKITNAGGRRIGWAIKTTNMRRLSVDPPCGVLDPKEKVLMAVSCD
TFNAATEDLNNDRITIEWTNTPDGAAKQFRREWFGDGMRKRKNLPIEYNL

>d4kbpa1 b.1.12.1 (A:9-120) Purple acid phosphatase, N-terminal domain {Kidney bean (*Phaseolus vulgaris*)}
RDMPLDSDVFRVPPGYNAPQQVHITQGDLVGRAMIISWVTMDEPGSSAVRYWSEKNGRKRIAKGKMSTYRF
FNYSSGFIHHTTIRKLKYNTKYYEVGLRNTTRRFSFITPP

>d1dqja_ b.1.13.1 (A:) Superoxide reductase (SOR) {Archaeon *Pyrococcus furiosus*}
MISETIRSGDWKGEKHVPVIEYEREGELVKVKVQVGKEIPHNTTEHHIRYIELYFLPEGENFVYQVGRVEFTAHG
ESVNGPNTSDVYTEPIAYFVLTKKKGKLYALSYCNIHGLWENEVTLE

>d1dfx_1 b.1.13.1 (37-125) Desulfoferrodoxin C-terminal domain {Desulfovibrio desulfuricans}
VEGSTDGAMEKHPVIEKVDDGGYLIKVGGSVPHPMEEKHWIEWIELLADGRSYTKFLKPGDAPEAFFAIDASKVT
AREYCNLGHGHWKAEN

>d1f00i1 b.1.14.1 (I:658-752) Intimin {Escherichia coli}
ASITEIKADKTTAVANGQDAITYTVKVMKGDKPVSNQEVTTLGKLSNSTEKTDTNGYAKVTLSTTPGKSLVS
ARVSDVAVDVKAPEVEFFT

>d1f00i2 b.1.14.1 (I:753-841) Intimin {Escherichia coli}
TLTIDDGNIEIVGTGVKGKLPFWLQYGQVNLSASGGNGKYTWRSANPAIASVDASSGQVTLKEKGTTTISVISS
DNQTATYTIATPNS

>d1cwva1 b.1.14.1 (A:503-596) Invasin {Yersinia pseudotuberculosis}
LTLTAAVIGDGAPANGKTAITVEFTVADFEKGPLAGQEVVITNNNGALPNKITEKTDANGVARIALNTTDGVT
VTAEEVGQRQSVDFHVKG

>d1cwva2 b.1.14.1 (A:597-692) Invasin {Yersinia pseudotuberculosis}
TIAADKSTLAAVPTSIADGLMASTITLELKDTYGDPAQANVAFDTTLGNMGVITDHNDGTYSAPLTSTLGVA
TVTVKVDGAAFSVPSVTVNFT

>d1cwva3 b.1.14.1 (A:693-795) Invasin {Yersinia pseudotuberculosis}
ADPIPDAGRSSFTVSTPDILADGTMSSLSFVPDFKNGHFISGMQGLSFTQNGVPVISPIEQPDSYTATVGN
SVGDTVITPQVDTLILSTLQKKISLFPV

>d1cwva4 b.1.14.1 (A:796-886) Invasin {Yersinia pseudotuberculosis}
PTLTGILVNGQNFATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSRSSFTPNVSNDQGQVTITYQTYSEVAV
TAKSKKFPSYSVSYRFYP

>d1f0la1 b.2.1.1 (A:381-535) Diphtheria toxin, C-terminal domain {Corynebacterium diphtheriae}
SPGHKTQPFLHDGYAVSWNTVEDSIIRTGFQGESGHDIKITAENTPLPIAGVLLPTIPGKLDVNKSKitTHISVNGRK
RMRCRAIDGDVTFCRPKSPVYVGNGVHANLHAFHRSSEKIHSNEISSDSIGVLGYQKTVDHTKVNSKLSLFFE
IKS

>d1exh__ b.2.2.1 (-) Exo-1,4-beta-D-glycanase (cellulase, xylanase), cellulose-binding domain, CBD

{Cellulomonas fimi}

ASSGPAGCQVLWGVNQWNTGFTANVTVKNTSSAPVDGWTLTFSFPSGQQVTQAWSSTVTQSGSAVTVRNA
PWNGSIPAGGTAQFGFNGSHTGTNAAPTAFLSLNGTPCTVG

>d1e5ba_ b.2.2.1 (A:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas fimi}
TGCSVATRAEEWSDFGNVTYSVSGSSAWTVNLALNGSQTIQASWNANVTGSGSTRTVTPNGSGNTFGVTV
MKNGSSTTPAACAGS

>d1hejc_ b.2.2.1 (C:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas fimi}
TGSCSVAVRGEEWADRFNVTVSGSSWVVTLGLNGGQSVQSSWNAALTGSSGTVTARPNGSGNSFGVTF
YKNGSSATPGATCATG

>d1nbca_ b.2.2.2 (A:) Cellulosomal scaffolding protein A, scafoldin {Clostridium thermocellum}
NLKVEFYNSNPSDTNSINPQFKVTNTGSSAIDLSSLKLRLYYYTVDGQKDQTFWCDHAAIIGSNGSYNGITSNVK
GTFVKMSSSTNNADTYLEISFTGGTLEPGAHHQIQGRFAKNDWSNYTQSNDYSFKSASQFVEWDQVTAYLNG
VLVWGKEP

>d1g43a_ b.2.2.2 (A:) Cellulosomal scaffolding protein A, scafoldin {Clostridium cellulolyticum}
AGTVVSVQFNNGSPASSNSIYARFKVTNTSGSPINADLKLRLYYYTQDADKPLTFWCDHAGYMSGNSNYIDAT
SKVTGSFKAVSPAVENTNADHYLEVALNSDAGSLPAGGSIEIQTRFARNDWSNFDQSNDWSYTAAGSYMMDWQKI
SAFVGGTLAYGSTP

>d1tf4a2 b.2.2.2 (A:461-605) Endo/exocellulase:cellobiose E-4, C-terminal domain
{Thermomonospora fusca}

PEIFVEAQINTPGTTFTEIKAMIRNQSGWPARMEDKGTFRYWFTLDEGVDPADITVSSAYNQCATEPDVHHVS
GDLYYVEIDCTGEKIFPGGQSEHRREVQFRIAGPGWDPSNDWSFQGIGNELAPAPYIVLYDDGVPVWGTAP

>d1anu_ b.2.2.2 (-) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

VVVEIGKVTGSVGTTEIPVYFRGVPSKGIANCDFVFRYDPNVLEIIGIDPGDIIVDPNPTKSFDATIYPDRKIIVFLF
AEDSGTGAYAITKDGVFAKIRATVKSSAPGYITFDEVGGFADNDLVEQKVSFIDGGVNV

>d1aoha_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}
AVRIKVDTVNAKPGDTVIPVRSGIPSKGIANCDFVSYDPNVLEIIEPGEIIVDPNPTKSFDATVYPDRKMIVF
LFAEDSGTGAYAITEDGVFATIVAKVKSGAPNGLSVIKFVEVGGFANNLVEQKQTQFFDGGVNVG

>d1g1ka_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}
ASLKVTGVTANGKPGDTVTPVTFAADVAKMKNVGTCNFYLGYDASLLEVSVSDAGPIVKNAAVNFSSASNGTI
SFLFLDNTITDELITADGVFANIKFKLKSVTAKTTPVTFKDGGAFGDTMSKIASVTKTNGSVTIDPG

>d1qba_2 b.2.2.3 (28-200) Bacterial chitobiase, n-terminal domain {Serratia marcescens}

DQQLVDQLSQLKLNVKMLDNRAGENGVDCAALGADWASCNRVLFTLSNDGQAIDGKDWWIYFHSPRQTLR
VDNDQFKIAHLTGDLYKLEPTAKFSGFPAGKAVEIPVVAEYWQLFRNFLPRWYATSGDAKPMLANTDTENL
DQFVAPFTGDQWKRTKDDKNILMTPASRFV

>d1amx_ b.2.3.1 (-) Collagen-binding domain of adhesin {Staphylococcus aureus}

TSSVFYYKTGDMILPEDTHVRWFNLINNEKSYVSKDITIKDQIQQGQQQLDLSTLNINVGTGTHSNYYSGQSAITDF
EKAFCPGSKITVDNTKNTIDVTIPQGYGSYNFSINYKTKITNEQQKEFVNNSQAWYQEHGKEEVNGKSFNHTVN
N

>d1qunb1 b.2.3.2 (B:1-158) Mannose-specific adhesin FimH {Escherichia coli}

FACKTANGTAIPGGGSANVYVNLAPVVNVGQNLVDSLSTQIFCHNDYPETITDYVTLQRGSAYGGVLSNFSGT
VKYSGSSYPFPTTSETPRVVYNSRTDKPWPVALYLPVSSAGGVAIKAGSLIAVLIRQTNNYNSDDFQFWNIYA
NNDDVVVPT

>d1qunb2 b.2.3.2 (B:159-279) Mannose-specific adhesin FimH {Escherichia coli}
GGCDVSARDVTVDYDYPGSVPIPLTVYCAKSQNLGYYLSGTTADAGNSIFTNTASFSPAQGVGVQLTRNGTI
NNTVSLGAVGTSAVSLGLTANYARTGGQVTAGNVQSIIGVTFVYQ

>d1pdkb_b.2.3.2 (B:) PapK pilus subunit {Escherichia coli}
LLDRPCHVSGDSLHKVVFKTRASRDFWYPPGRSPTESFIRLENCHATAVGKIVTLFGTEEAALPGHLKVTG
VNAGRLGIALLDTDGSSLLKPGTSHNKQQGEKVTGNSLELPFGAYVATPEALRTKSVPGDYEATATFELTYR

>d1j8ra_b.2.3.3 (A:) PapG adhesin receptor-binding domain {Escherichia coli}
WNNIVFYSLGDVNSYQGGNVITQRQPQFITSWRPGIATWNQCNGPEFADGFWAYREYIAWVFVPKVM
TQNGYPLFIEVHNKGWSSEENTGDNDSYFFLKGYKWDERAFDAGNLCQKPGEITRLTEKFDDIIFKVALPADLPL
GDYSVKIPYTSQMQRHFASYLGARFKIPYNVAKTPRENEMLFLFKNIGG

>d1edya_b.2.4.1 (A:) alpha-1-macroglobulin {Rat (Rattus norvegicus)}
EAPFTLKVNTPNFDKAEEHRKFQIHINVSYIGERPNSNMVIVDVKMVSGFIPVKPSVKKLQDQSNIQRTEVN
TNHVLIYIEKLTNQTMGFSFAVEQDIPVKNLKPAPVKVYDYYETDEFAIEEYSAPFSSDS

>d1bv8a_b.2.4.1 (A:) alpha-2-macroglobulin {Human (Homo sapiens)}
EEFPFALGVQTLQTCDEPKAHTSFQISLSVSYIGSRPASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRT
EVSNHVLIYLDKVSNQTLSSLFTVLQDVPVRDLKPAIVKVVYDYYETDEFAIAEYNAPCSKDLGNA

>d1ayoa_b.2.4.1 (A:) alpha-2-macroglobulin {Cow (Bos taurus)}
EFPALEVQTLQTCDEPKAHTSFQISLSVSYIGSRPASNMAIVDVKMVSGFIPLKPTVKMLERSNV
SRTEVSNHVLIYLDKVTNETLTLFTVLQDIPVRDLKPAIVKVVYDYYETDEFAVAEYSAPCS

>d1ycsa_b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Human (Homo sapiens)}
VPSQKTYQGSYGFRLGFLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTRV
RAMAIYKQSQHMT
EVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLD
DRNTFRHSVVV
PYEPPEVGSDCTT
IHNYMCNSS
CMGGMNRRP
ILTIITLEDSSGNLLGRNSFEVRVCACPGRDRR
TEEE

>d1hu8a_b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Mouse (Mus musculus)}
TYQGNYGFHLGFLQSGTAKSVMCTYS
PPLNKLFCQLAKTCPVQLWVSATPPAGSR
RAMAIYKKSQHMTEV
RCPHHERCSDGDGLAPPQHLIRVE
GNLAPEYLED
RQTRHSVV
PYEPPEAGSE
YTTIHYK
YMCNSSCMGG
NRRP
ILTIITLEDSSGNLLGRDSFEVRVCACPGRDRR
TEEE

>d1a02n2 b.2.5.1 (N:399-576) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}
WPLSSQSGSYELRIEVQPKPHRAHYETEGSRGAVKAPTGGHPVVQLHGY
MENKPLGLQFIGTADERILKPHAFYQVHRITGKTV
TTSYEKIVGNTKVLEIP
LEPKNNMRATIDCAGILKLRNADIELRKGETD
IGRK
NTRVRLVFRVH
IPESSGRIVSLQTASNP
IECSQRS
AHE

>d1a66a_b.2.5.1 (A:) Transcription factor NFATC, DNA-binding domain {Human (Homo sapiens)}
MKDWQLPSHSGPYELRIEVQPKSHHRARYETEGSRGAVKASAGGH
PIVQLHG
YLENEPLMLQLFIGTADD
RPHAFYQVHRITGKTV
STSHEA
ILSNTKVLEIP
LLPENS
MRA
VIDCAGILKLR
NSD
IELRKGETD
IGRK
NTRV
RLV
RVH
VPQPSGRT
LSLQVASN
PIECS
QRS
AHE

>d1imhc2 b.2.5.1 (C:188-367) Transcription factor TONEBP, DNA-binding domain {Human (Homo sapiens)}
KKSPMLCGQYPVKSEGKELKIVVQPETQH
RARYL
TEGS
RG
SV
KD
RT
QQG
F
PTV
KLEG
H
NE
PV
V
LQ
V
FG
ND
SG
RV
KPH
GF
Y
QAC
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KHCEDGVCTVAGPKDMVVGFANLGLHVTKKVFETLEARMTEACIRGYNPGLLVHSDLAYLQAEGGGDRQL
TDREKEIIRQAAVQQTKEMDLSVVRLMFTAFLPDSTGSFTRRLEPVVSDAIYDSKAPNASNLKI

>d1a3qa2 b.2.5.1 (A:37-226) p52 subunit of NF-kappa B (NFKB), N-terminal domain {Human (Homo sapiens)}

GPYLVIVEQPKQRGFRFRYGCCEGPGSHGLPGASSEKRKTYPTVKICNYEGPAKIEVDLVTHSDPPRAHAHSLVG
KQCSELGICAVSGPKDMTAQFNNLGVLHVTKNMMGTMIQKLQRQRLSRPQGLTEAEQRELEQEAKELKK
VMDLSIVRLRFSALRSLPLKPVISQPIHDSKSPGAS

>d1ikna2 b.2.5.1 (A:19-191) p65 subunit of NF-kappa B (NFKB), N-terminal domain {Mouse (Mus musculus)}

PYVEIIEQPKQRGMFRYKCEGRSAGSIPGERSTDCKTHPTIKINGYTGPGTVRISLVTKDPPHRPHELVGKD
CRDGYYEADLCPDRSIHSFQNLGIQCVKKRDLEQAISQRIQTNNNPFHVPIEEQRGDYDLNAVRLCFQVTVRDP
AGRPLLTPVLSHIPIFDNRAPNT

>d1nfia2 b.2.5.1 (A:20-189) p65 subunit of NF-kappa B (NFKB), N-terminal domain {Human (Homo sapiens)}

YVEIIEQPKQRGMFRYKCEGRSAGSIPGERSTDCKTHPTIKINGYTGPGTVRISLVTKDPPHRPHELVGKDC
RDGFYEAELCPDRCIHSFQNLGIQCVKKRDLEQAISQRIQTNNNPFHVPIEEQRGDYDLNAVRLCFQVTVRDP
GRPLRLPPVLPHPIFDNRAPNT

>d1bvoa_b.2.5.1 (A:) Dorsal homologue Gambif1 {African malaria mosquito (Anopheles gambiae)}

PYVEITEQPHPKALRFRYECEGRSAGSIPGVNTTAEQKTFPSIQVHGGRGRAVVVSCVTKEGPEHKPHPHNLV
GKEGCKKGVCVTEINSTTMSYTFNNLGIQCVKKKDVEEALRQEIRVDPFRTGFGHAKEPGSIDLNAVRLCFQV
FLEGQQQRGRFTEPLTPVVSIDIYDKK

>d1xbra_b.2.5.1 (A:) T domain from Brachyury transcription factor {African clawed frog (Xenopus laevis)}

ELKVSLEERDLWTRFKELTNEMIVTKNGRRMFPVLKVSMGLDPNAMYTVLLDFVAADNHRWKYVNGEWVP
GGKPEPQAPSCVYIHPDSPNFGAHWMKDPVSFSKVKLTKNMNGGGQIMNSLHKYEPRIHVVGQTQRMI
TSHSFPEAQFIAVTAYQNEEITALKIKHNPFAKFLDAKERN

>d1bf5a2 b.2.5.1 (A:317-568) STAT-1, DNA-binding domain {Human (Homo sapiens)}

FVVERQPCMPTHPQRPLVLKTGVQFTVKLRLLVKLQELNYNLKVVLFDKVNERNTVKGFRKFNILGTHTKV
MNMEESTNGSLAAEFRHLQLKEQKNAGTRTNEGPLIVTEELHLSLFETQLCQPGVIDLETTSPVVVISNVSQ
PSGWASILWYNMLVAEPRNLSFFLTPPCARWAQLSEVLSWFQSSVTKRGlnVDQNLMLGEKLLGPNASPDGLI
PWTRFCKENINDKNFPFWLWIESILELIKHH

>d1bg1a2 b.2.5.1 (A:322-575) STAT3b {Mouse (Mus musculus)}

VVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTKVMN
MEESNNNGSLAEFKHHTLREQCGNGGRANCADASLIVTEELHLITFETEVYHQGLKIDLEHSLPVVVISNICQM
PNAWASILWYNMLTNNPKNVNFFTAKPIGTWDQVAEVLSWFQSSVTKRGlsIEQLTTLAEKLLGPVNYSGCQ
ITWAKFCKENMAGKGFSFWVLDNIIDLVKKY

>d1e50q_b.2.5.1 (Q:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}

LVRTDSPNFLCSVLPHTWRCNKLPIAFKVALGDVPDGTIVTMAGNDENYSAELRNATAAMKNQVARFND
LRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVD

>d1h9da_b.2.5.1 (A:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}

VLADHPGELVRTDSPNFLCSVLPHTWRCNKLPIAFKVALGDVPDGTIVTMAGNDENYSAELRNATAAMK
NQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGPREPRR

>d1hcz_1 b.2.6.1 (1-167,231-250) Cytochrome f, large domain {Turnip (Brassica rapa)}

YPIFAQQNYENPREATGRIVCANCHLASKPVDIEVPQAVLPDTVFEAVVKIPYDMQLKQVLANGKKGALNVGA
VLILPEGFELAPPDRISPEMKEKIGNLSFQNYRPNNKILVIGPVGQKYSEITFPILAPDPATNKDVHFLKYPIYVG
GNRGRGQIYPDGSKSXPNVGGFGQGDAEIVLQDPLR

>d1e2wa1 b.2.6.1 (A:1-168,A:233-251) Cytochrome f, large domain {Chlamydomonas reinhardtii}

YPVFAQQNYANPREANGRIVCANCHLAQKAVEIEVPQAVLPDTVFEAVIELPYDKQVKQVLANGKKGDLNVG
MVLILPEGFELAPPDRVPAEIKEVGNLYYQPYSPEQKNILVVGPGKKYSEMVVPILSPDPAKNKNVSYLKYPI
FGGNRGRGQVYPDGKKSFXNVGGFGQAETEIVLQNPART

>d1ci3m1 b.2.6.1 (M:1-169,M:232-249) Cytochrome f, large domain {Phormidium laminosum}

YPFWAQQNYANPREATGRIVCANCHLAQKPAEIEVPQAVLPDSVFKA VVKIPYDH SVQQVQADGSKGPLNVG
AVLMLPEGFTIAPEDRIPEEMKEEVGPSYLFQPYADDKQNIVLGPLGDEYE EIVFPVILSPNPATNKSVAFGKYSI
HLGANRGRGQIYPTGEKSNNXNVGGFGQKDTEIVLQSPN

>d1i31a_b.2.7.1 (A:) Second domain of Mu2 adaptin subunit (ap50) of ap2 adaptor {Rat (Rattus norvegicus)}

IGWRREGIKYRRNELFLDVLESVNLLMSPQGQVLSAHSGRVVMKS YLSGMPECKFGMNDKIVIEKQGKGTAD
ETSKSGKQ SIAIDDCTFHQCVRSLKFDSERSIS FIPP DGEFELMRYRTKDIILPFRVIPLVREVGRTKLEVKKVVIKS
FKPSLLAQKIEVRIPTPLNTSGVQVICMKGKAKYKASENAIVW KIKR MAGM KESQ ISAEIELLPTNDKKKWARPP
ISMNF EVPFAPSGLKV RYLKV FEPKLNYS DHDV IKW VRY IGRSGI YETRC

>d1cgt_2 b.3.1.1 (580-684) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}

LTGDQVTVRFVVNNASTTLGQNL YTGNVAELGNWSTGSTAIGPAFNQVIHQYPTWYYDVSVPAGKQLEFKFF
KKNGSTIWESGSNHTFTPASGTATVTVNWQ

>d1kcla2 b.3.1.1 (A:582-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus circulans, different strains}

LSGDQVS VRFVVNNATT ALGQNV LTGSV SELGNW DP AKAIGPMYNQV VYQYPN WYYD VSVPAGKTIEFKFL
KKQGSTV TWE GGSN HNT F TAPSSGTATINV NWQ P

>d1cyg_2 b.3.1.1 (575-680) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus}

LTNDQVS VRFVVNNATT NLGQNIYIVGNVYELGNW DTSKAIGPMFNQV VSYPTWYIDVSVP EGK TIEFKFIKK
DSQGNVTWESGSN HVYTTPTNTGKII DVWQN

>d1qhoa2 b.3.1.1 (A:577-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus, maltogenic alpha-amylase}

LSGTQTSV VFTV KSAPPTNLGDKIYLTGNIPELGNWSTD TS GAVN NAQGPL LAPN YPDWFYV FS VPAGKTIQFK
FFIKRADGT IQWENG SNHV ATTPTG ATGN ITV TWQ N

>d1pama2 b.3.1.1 (A:583-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus sp., strain 1011}

TGDQVTVRFVINNATT ALGQNV LTGNV SELGNW DP NNAIGPMYNQV VYQYPTWYYD VSVPAG QTIEFKFLK
KKGSTV TWE GGSN HNT VPS STGTATV NWQ P

>d1ciu_2 b.3.1.1 (579-683) Cyclodextrin glycosyltransferase, C-terminal domain {Thermoanaerobacterium thermosulfurigenes, EM1}

LTGNQICVRFVVNNASTVYGENVYLTGNVAELGNW DTSKAIGPMFNQV VYQYPTWYYD VSVPAGTTIQFKFIK
KNGNTITWEGGSNHTYTVPSSTGTIVNWQQ

>d1acz_b.3.1.1 (-) Glucoamilase, granular starch-binding domain {Aspergillus niger}

CTTPTAVAVTFDLTATTTYGENIYLVGSISQLGDWETSDGIALSADKYTSSDPLWYVTVTL PAGESFEYKFIRIESDD

SVEWESDPNREYTVPQACGTSTATVTDTW

>d1cqya_ b.3.1.1 (A:) beta-amylase {Bacillus cereus}

TPVMQTIVVKNPPTTIGDTVYITGNRAELGSWDTKQYPIQLYYDSHSNDWRGNVVLPAERNIEFKAFIKSKDGT
VKSWQTIQQSBNPVLKTTSHSSW

>d1h8la1 b.3.2.1 (A:305-383) Carboxypeptidase D, a regulatory domain {Crested duck (Lophonetta specularioides)}

GIWGFVLDATDGRGILNATISVADINHPVTTYKDGYWRLVQGTYKVTASARGYDPVKTVEVDSKGKVQVN
FTLSRT

>d1vcbc_ b.3.3.1 (C:) VHL {Human (Homo sapiens)}

LRSVNSREPSQVIFCNRSPRVLPVWLNFGEPPQPYPTLPPGTGRRIHSYRGHLWFRDAGTHDGLLNQTELF
VPSLNVDGQPIFANITLPVYTLKERCLQVVRSLVKPENYRRLDIVRSLYEDLEDHPNVQKDLERLTQE

>d1f86a_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (Homo sapiens)}

CPLMVKVLDAVRGSPAINVAHVFRKAADDTWEPFASGKTSESSELHGLTTEEEFVEGIYKVEIDTKSYWKALGI
SPFHEHAEVVFTANDSGPRTIAALLSPYSYSTMAVVTN

>d1ttba_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Human (Homo sapiens)}

GPTGTGESKCPLMVKVLDAVRGSPAINVAHVFRKAADDTWEPFASGKTSESSELHGLTTEEEFVEGIYKVEIDT
KSYWKALGISPFHEHAEVVFTANDSGPRTIATLLSPYSYSTAVVTNPKE

>d1gkea_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Rat (Rattus norvegicus)}
SKCPLMVKVLDAVRGSPAVDVAVKFKKADGSWEFPASGKTAESSELHGLTDEKFTEGVYRVELDTKSYWKA
LGISPFHEYAEVVFTANDSGHRHYTIAALLSPYSYSTAVVSNPQN

>d1tfpa_ b.3.4.1 (A:) Transthyretin (synonym: prealbumin) {Chicken (Gallus gallus)}

CPLMVKVLDAVRGSPAANAVKVFKAADGTWQDFATGKTTEFGEIHELTTEEQFVEGVYRVEFDTSYWKGL
GLSPFHEYADVFTANDSGHRHYTIAALLSPFSYSTAVVS

>d1d2oa1 b.3.5.1 (A:535-624) B repeat unit of collagen binding surface protein (cna)
{Staphylococcus aureus}

ETTSSIGEKVWDDKDNQDGKRPEKVSVNLLANGEVKVTLVTSETNWKYEFKDPKYDEGKKIEYTVDHVK
DYTTDINGTTITNKYTP

>d1d2oa2 b.3.5.1 (A:625-721) B repeat unit of collagen binding surface protein (cna)
{Staphylococcus aureus}

GETSATVKNWDDNNNQDGKRPEIKAELYQDGKATGKTAILNESNNWHTWTGLDEKAKGQQVKYTVEELT
KVKGYTTHDNNNDMGNLITTNKYTP

>d1dmha_ b.3.6.1 (A:) Catechol 1,2-dioxygenase {Acinetobacter calcoaceticus}

VKIFNTQDVQDFLRVASGLEQEGGNPRVKQIIHRVLSLDYKAIEDLNITSDEYWAGVAYLNQLGANQEAGLLSPG
LGFHYLDMRMDAEDAALGIENATPRTIEGPLYVAGAPESVGYARMDDGSDPONGHTLHGTTFADGKPLPN
AKVEIWHANTKGFYSHDPTGEQQAFNMRRSIITDENGQYRVRTILPAGYGCPEGPTQQLLNQLGRHGNRPA
HIHYFVSADGHRKLTTQINVAGDPYTYDDFAYATREGLVVDAVEHTDPEAIKANDVEGPFAEMVFDLKLTRLVD
GVDNQVVDRPRLAV

>d3pcca_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Pseudomonas aeruginosa}

PIELLPETPSQTAGPYVHIGLAEEAGNPRDQEIWNLAKPDAPGEHILLGQVYDGNNGHLVRDSLEVWQAD
ANGEYQDAYNLENANFSFGRTATTFDAGEWTLHTVKPGVVNNAAAGVPMAPHINISLFARGINIHLHTRLYFDD
EAQANAKCPVLNLIEQPQRRETLIAKRCEVDGKTAYRFDIRIQGEGETVFFDF

>d1eo9a_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Acinetobacter calcoaceticus,
adp1}

ELKETPSQTGGPYVHIGLLPKQANIEVFEHNLDNNLVQDNTQGQRIRLEGQVFDSLPLRDVLIEIWQADTNG

VYPSQADTQGKQVDPNFLWGRTGADFGTGFWSFNTIKPGAVPGRKGSTQAPHISLIIFARGINIGLHTRVYFD
DEAEANAKDPVLNSIEWATRRQTLVAKREERDGEVVYRFDIRIQGENETVFFDI

>d3pccm_b.3.6.1 (M:) Protocatechuate-3,4-dioxygenase, beta chain {Pseudomonas aeruginosa}
PAQDNSRFVIRDRNWHPKALPDYKTSIARSPRQALVSIPQSISETTGPNFSHLGFAHDHDLLNFNNGLPIG
ERIIVAGRVDQYGKPVNLTLEMWQANAGGRYRHKNDRYLAPLDPNFGGVGRCLTDGYYSFRTIKPGPYP
WRNGPNDWRPAHIHFGISGPSIATKLITQLYFEGDPLIPMCPIVKSIANPEAVQQLIAKLDMNNANPMDCAYR
FDIVLRGQRKTHFE

>d1eo9b_b.3.6.1 (B:) Protocatechuate-3,4-dioxygenase, beta chain {Acinetobacter calcoaceticus,
adp1}
IIWGAYAQRNTEDHPPAYAPGYKTSVLSPKNALISIAETLSEVTAPHFSADKFGPKDNDLILNYAKDGLPIGERVI
VHGVRDQFGRPVKNALVEWWQANASGRYRHPNDQYIGAMDPNFGGCGRMLDDNGYYVFRTIKPGPYP
WRNRINEWRPAHIHFSLIADGWAQRLISQFYFEGDTLIDSCPILKTIPSEQQRRALEDSNFIEADSRCYRFDI
TLRGRRATYFENDLT

>d1c3ga1 b.4.1.1 (A:180-259) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}

ETVQVNLPVSLEDLFVGKKKSFKIGRKPHGASEKTQIDIQLKPGWKAGTKITYKNQGDYNPQTGRRKTLQFVI
QEKSHP

>d1c3ga2 b.4.1.1 (A:260-349) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}

NFKRDGDDLIYTPLSFKESLLGFSKTIQTIDGRTLPLSRVQPVQPSQTSTYPGQGMPTPKNPSQRGNLIVKYKVD
YPISLNDAQKRAID

>d1hd8a1 b.105.1.1 (A:263-356) Penicillin-binding protein 5, C-terminal domain {Escherichia coli}

FETVNPLKVGKEFASEPFWFGSDRASLGVDKVLTIPRGRMKDLKASYVLSSELHAPLQKNQVVGTTINFQL
DGKTIQRPLVVLQEIPEGN

>d1hoe_b.5.1.1 (-) alpha-Amylase inhibitor tendamistat {Streptomyces tendae}
DTTVSEPA PSCVTLYQSWRYSQADNGCAETVTVKVYEDDTEGLCYAVAPGQITTVGDGYIGSHGHARYLARCL

>d1aac_b.6.1.1 (-) Amicyanin {Paracoccus denitrificans}

DKATIPSESPFAAAEVADGAIIVDIAKMKYETPELHVKGDTVTWINREAMPHNVHFVAGVLGEAALKGPMM
KKEQAYSLTFTEA GTYDYHCTPHPFMRGKVVVE

>d1id2a_b.6.1.1 (A:) Amicyanin {Paracoccus versutus (Thiobacillus versutus)}

QDKITVTSEKPVAADVPADAVVVGIEKMKYLTPETIKAGETVYWNNGEVMPHNVAFKKGIVGEDAFRGEM
MTKDQAYAITFNEAGSYDYFCTPHPFMRGKVVVE

>d1plc_b.6.1.1 (-) Plastocyanin {Poplar (Populus nigra), variant italicica}

IDVLLGADDGSLAFVPSEFSISPGEKIVFKNNAGFPNIVFDEDSIPSGVDASKISMSEEDLLNAKGETFEVALSNK
GEYSFYCSPHQGAGMVGVKTVN

>d9pcy_b.6.1.1 (-) Plastocyanin {French bean (Phaseolus vulgaris)}

LEVLLGGDDGLVFSPSSFTVAAGEKITFKNNAGFPNIVFDEDEIPAGVDAVKISMPEELLNAPGETYVVTLD
TKGTYSFYCSPHQGAGMVGVKTVN

>d1pla_b.6.1.1 (-) Plastocyanin {Parsley (Petroselinum crispum)}

AEVKLGSDGGLVSPSSFTVAAGEKITFKNNAGFPNIVFDEDEIPAGVNAEKISQPEYLNAGETYEVLTKE
GTYKFYCEPHAGAGMKGEVTVN

>d1ag6_b.6.1.1 (-) Plastocyanin {Spinach (Spinacia oleracea)}

VEVLLGGDDGSLAFLPGDFSVASGEEIVFKNNAGFPNIVFDEDEIPSGVDAAKISMSEEDLLNAPGETYKVTLT

EKGTYKFYCSHQGAGMVGKVTVN

>d1bypa_ b.6.1.1 (A:) Plastocyanin {White campion (*Silene pratensis*)}
AEVLLGSSDGLAFVPSDLIASGEKITFKNNAGFPNHLFDKKEVPAGVDVTKISMPEEDLLNAPGEEYSVTLTE

KGTYKFYCAPHAGAGMVGKVTVN

>d1iu_ b.6.1.1 (-) Plastocyanin {Sea lettuce (*Ulva pertusa*)}
AQIVKLGGDDGSLAFVPSKISVAAGEAIEFVNNAGFPNIVFDEDAVPAGVDADAISYDDYLNKGGETVVRKLST

PGVYGVYCEPHAGAGMKMTITVQ

>d2plt_ b.6.1.1 (-) Plastocyanin {Green alga (*Chlamydomonas reinhardtii*)}
DATVKLGADSGALEFPKTLIKSGETVNFFNNAGFPNIVFDEDAVPAGVDADAISYDDYLNKGGETVVRKLTA
AGEYGYYCEPHQGAGMVGKIVQ

>d7pcy_ b.6.1.1 (-) Plastocyanin {Green alga (*Enteromorpha prolifera*)}
AAIVKLGGDDGSLAFVPPNITVGAGESIEFINNAGFPNIVFDEDAVPAGVDADAISYDDYLNKGQTVVRKLTT
PGTYGVYCDPHSGAGMKMTITVQ

>d1kdj_ b.6.1.1 (-) Plastocyanin {Fern (*Adiantum capillus-veneris*)}
AKVEVGDEVGNFKFYPDSITVSAGEAVEFTLVGETGHNIVFDIPAGAPGTVASELKAASMDENDLSEDEPSFKA

KVSTPGTYTFYCTPHKSANMKGLTVK

>d1nin_ b.6.1.1 (-) Plastocyanin {Anabaena variabilis}
ETYTVKLGSDKGLVFPEPAKLTIKPGDTVEFLNNKVPPHNVVFDAALNPAKSADLA
KSLSHQQLMSPGQSTTTPADAPAGEYTFYCEPHRGAGMVGKITVAG

>d1bawa_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (*Phormidium laminosum*)}
ETFTVKMGADSGLLQFEPANVTVHPGDTVKWVNNKLPPHNILFDDKQVPGASKELADKLHSQLMFSPGESY
EITFSSDFPAGTYYYCAPHRGAGMVGKITVEG
>d1pcs_ b.6.1.1 (-) Plastocyanin {Cyanobacterium (*Synechocystis* sp.), pcc 6803}
ANATVKMGSDSGALVFEPESTVTIKAGEEVKWVNNKLSPHNIVFDAGVPADTA
KLSHKGLLFAAGESFTSTFTEPGTYTYCEPHRGAGMVGKVVVE

>d1bxva_ b.6.1.1 (A:) Plastocyanin {Cyanobacterium (*Synechocystis* sp.), pcc 7942}
QTVAIKMGADNGMLAFEPSTIEIQAGDTVQWVNNKLAPHNVVVEGQPELSHKD
LAFSPGETFEATFSEPGTYTYYCEPHRGAGMVGKIVVQ

>d2b3ia_ b.6.1.1 (A:) Plastocyanin {Photosynthetic prokaryote (*Prochlorothrix hollandica*)}
ASVQIKMGTDKYAPLYEPKALSI
SAGDTVEFVMNKVGPHNIFDKVPAGESAPALSNTKLA
IAPGSFYSVTLGPTGTYSFYCTPHRGAGMVGKTITVE

>d1paz_ b.6.1.1 (-) Pseudoazurin {Alcaligenes faecalis, strain s-6}

ENIEVHMLNKGAE GAMVFEPA
YIKANPGDTVTIFPVDKGHNV
ESIKDMIPEGA
EKF
FSK
KIN
EN
YV
LT
V
T
Q
P
G
AY
LV
K
C
T
P
H
Y
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B
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X
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>d1pm_ b.6.1.1 (-) Pseudoazurin {Methylobacterium extorquens, strain am1}
DEVAVKMLNSPGGMMVFDPALVRLKPGDSIKFLPTDKHN
VETIKGM
APDGADYV
KTTVGQEAVV
KFD
KE
GVYGF
K
C
A
P
H
Y
M
M
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E
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F
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Q

>d1bqk_ b.6.1.1 (-) Pseudoazurin {Achromobacter cycloclastes}

ADFEVHMLNKGKD
GAMVFEPA
SLK
V
A
P
G
D
T
F
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P
T
D
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>d1adwa_ b.6.1.1 (A:) Pseudoazurin {Thiosphaera pantotropha}

ATHEVHMLNKG
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>d2cbp__ b.6.1.1 (-) Plantacyanin {Cucumber (Cucumis sativus)}

AVYVVGSGGWTFNTESWPKGKRFRAGDILLFNYNPSMHNVVVNQGGFSTCNPAGAKVYTSRDQIKLP
KGQSYFICNFPGHCGSGMKIAVNAL

>d1f56a_ b.6.1.1 (A:) Plantacyanin {Spinach (Spinacia oleracea)}

AVYNIGWSFNVNGARGKSFRAGDVLVFKYIKGQHNVAVNGRGYASCSAPRGARTYSSGQDRIKLTGQNYFI
CSFPGHCGGGMKIAINAK

>d1azca_ b.6.1.1 (A:) Azurin {Alcaligenes denitrificans}

AQCEATIESNDAMQYNLKEMVVDKSKCKQFTVHLKHVGKMAVKAMGHNWVLTEADKQGVATDGMNAGLA
QDYVKAGDTRVIAHTKVIGGESDSVTFDVSKLTPGEAYAYFCSPFGHWAMMKGTLKLSN

>d1dyza_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015), different isoforms}

AQCEATVESNDAMQYNVKEIVVDKSKCKQFTMHLKHVGKMAVKAMGHNVLTKDADKQAVATDGMGAGLA
QDYVKAGDTRVIAHTKVIGGESDSVTFDVSKIAAGENYAYFCSPFGHWAMMKGTLKLS

>d1rkra_ b.6.1.1 (A:) Azurin {Alcaligenes xylosoxidans, NCIMB (11015), different isoforms}

AECSVDIAGNDGMQFDKKEITVSKSKCKQFTVNLKHPGKLAKNVMGHNWVLTKQADMQGAVNDGMAAGLD
NNYVKKDDARVIAHTKVIGGETDSVTFDVSKLAAGEDYAYFCSPFGHFALMKGVLKLV

>d1cc3a_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}

AECSVDIQGNDQMWFNTNAITVDKSKCKQFTVNLSPGNLPKNVMGHNWVLSTAADMQGVVTDGMASGL
DKDYLKPDDSRVIAHTKLIGSGEKDSVTFDVSKLKEGEQYMFFCSELCGINHALMKGTTLK

>d1jzga_ b.6.1.1 (A:) Azurin {Pseudomonas aeruginosa}

AECSVDIQGNDQMWFNTNAITVDKSKCKQFTVNLSPGNLPKNVMGHNWVLSTAADMQGVVTDGMASGL
DKDYLKPDDSRVIAHTKLIGSGEKDSVTFDVSKLKEGEQYMFFCTPGHSALMKGTTLK

>d1joi_ b.6.1.1 (-) Azurin {Pseudomonas fluorescens}

AECKVTVSTDQMSFNTKAIEIDKSCKTFTVELTHSGSLPKNVMGHNWLSSAADMPGIASDGMAAGIDKNY
LKEGDTRVIAHTKIIGAGEKDSVTFDVSKLAAAGTDYAFFCSFGHISMMKGTVTVK

>d1nwpa_ b.6.1.1 (A:) Azurin {Pseudomonas putida}

AECKVTVSTDQMSFNTKDIAIDKSCKTFTVELTHSGSLPKNVMGHNWLSSAADMPGIASDGMAAGIDKQYLN
DGDARVIAHTKVIGAGEKDSVTFDVSKLAAAGEKYGFCSFGHISMMKGTVTLK

>d1cuoa_ b.6.1.1 (A:) Azurin {Methylomonas sp. j}

ASCETTVTSGDTMTYSTRSISVPASCAEFTVNFEHKHMPKTGMGHNWVLAKSADVGDVAKEGAHAGADN
NFVTPGDKRVIATPIIGGGEKTSVFKFVSALKDEAYTYFCSYPGHFSMMRGTLKLEE

>d1qhqa_ b.6.1.1 (A:) Auracyanin {Chloroflexus aurantiacus}

ANAPGGSNVNETPAQTVEVRAAPDALAFAQTSLSPANTVVRDFVNQNNLGVQHNWVLVNGGDDVAAA
VNTAAQNNADALFVPPPDTPNALAWTAMLAGESGSVTFRTPAPGTYLYICTFGHYLAGMKGTTLVTP

>d1e30a_ b.6.1.1 (A:) Rusticyanin {Thiobacillus ferrooxidans}

LDTTWKEATLPQVKAMLEKDTGKVSGDTVTSGKTVHVAAVLPGFPPSFEVHDKNPTLEIPAGATDVTF
INTNKGFHGSFDITKKGPPYAVMPVIDPIVAGTGFSPVPKDGKFGYTNTFWHPTAGTYYVCQIPGHAATGQFG
KIVVK

>d1jer__ b.6.1.1 (-) Stellacyanin {Cucumber (Cucumis sativus)}

MQSTVHIVGDNTGWSVPSSPNFYSQWAAGKTFRVGDSLQFNFPANAHHVHEMETKQSFACNFVNSDNDV
ERTSPVIERLDELGMHYFVCTVGHCSNGQKLSINVVAAN

>d1ibya_ b.6.1.4 (A:) Red copper protein nitrosocyanin {Nitrosomonas europaea}

EHNFnVVINAYDTTIPELNVEGTVKNIRAFNLNEPETLVVKKGDAVKVVENKSPIEGFSIDAFGVQEVIKAG
ETKTISFTADKAGAFTIWCQLHPKNIHLPGLTNVVE

>d1qnia1 b.6.1.4 (A:451-581) Nitrous oxide reductase, C-terminal domain {Pseudomonas nautica}

KIYERNDPYFASCRAQAEKDGVTLSENKVRDGKVRVYMTSAPQYGMDFVKKEGDEVTVYITNLDMVE
DVTHGFCMVNHGSMEISPQQTASVTFTAGKPGVYWYYCNWFCHALHMEMVGRMLVEAA
>d1fwxa1 b.6.1.4 (A:452-581) Nitrous oxide reductase, C-terminal domain {Paracoccus denitrificans}
SVWDRNDPMWAETRAQAEADGVIDNWTEEVIRDGNKVRVYMSSVAPSFSIESFTVKEGDEVTVINTNLDEI
DDLHGFTMGNYGVAMEIGPQMTSSVTVAANPGVYWYYCQWFCHALHMEMRGRMLVEPK
>d1cyx_ b.6.1.2 (-) Quinol oxidase (CyoA) {Escherichia coli}
KPITIEVVSMWDWKWFFIYPEQGIATVNEIAFPANTPVFKVTSNSVMHSFFIPRLGSQIYAMAGMQTRLHLIANE
PGTYDGCAEICGPGHSGMKFKAIATPDRAFDQWAKAKQSPNTMSDMAAFEKLAAPSEYNQVEYFSNVKP
DLFADVINKFM
>d1fftb1 b.6.1.2 (B:118-283) Quinol oxidase (CyoA) {Escherichia coli}
KPLAHDEKPITIEVVSMWDWKWFFIYPEQGIATVNEIAFPANTPVFKVTSNSVMNSFFIPRLGSQIYAMAGMQT
RLHLIANEPGTYDGISASYSGPGFSGMKFKAIATPDRAFDQWAKAKQSPNTMSDMAAFEKLAAPSEYNQV
EYFSNVKPDLFADVINKFMA
>d1ocrb1 b.6.1.2 (B:91-227) Cytochrome c oxidase {Cow (Bos taurus)}
NNPSLTVKTMGHQWWSYEYTDYEDLSFDSYMIPTSELKPGELRLLEVDNRVLPMEMTIRMLVSSEDVLHS
WAVPSLGLKTDAIPGRLNQTTLMSSRPGLYYGQCSEICGSNHSFMPIVLELVPLKYFEKWSASML
>d1ar1b1 b.6.1.2 (B:108-252) Cytochrome c oxidase {Paracoccus denitrificans}
NDPDLVIKAIGHQWWSYEYPNDGVAFDALMLEKEALADAGYSEDEYLLATDNPVVVPVGKKVLVQVTATDVI
HAWTIPAFAVKQDAVPGRIAQLWFSVDQEGVYFGQCSELGINHAYMPIVVKAVSQEKYEAWLAGAKEFFAA
>d2cuaa_ b.6.1.2 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}
AGKLERVDPTTVRQEGPWADPAQAVVQTGPNCYQTCGKQVTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE
GTNINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE
>d2cuab_ b.6.1.2 (B:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}
AYTLATHTAGVIPAGKLERVDPTTVRQEGPWADPAQAVVQTGPNCYQTCGKQVTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE
TSPDVIHGFHVEGTINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLGHQNMFGTIVVKE
>d1nif_1 b.6.1.3 (8-166) Nitrite reductase, NIR {Achromobacter cycloclastes}
DISTLPRVKVDLVKPPFVHAHDQVAKTGPVVEFTMTIEEKKLVIDREGTEIHAMTFNGSVPGPLMHHENDYV
ELRLINPDTNTLLHNIDFHAATGALGGGALTQVNPGEETTLRFKATKPGVFVYHCAPGMVPWHVTSGMNGA
IMVLPRDGLKDEK
>d1nif_2 b.6.1.3 (167-340) Nitrite reductase, NIR {Achromobacter cycloclastes}
GQPLTYDKIYYVGEQDFYVPKDEAGNYKKYETPGEAYEDAVKAMRTLPTHIVFNGAVGALTGDHALTAAVGER
VLVVHSQANRDTRPHLIGGHGDDYVWATGKFRNPPDLDQETWLIPGGTAGAAFYTFRQPGVYAYVHNHNLIEAF
ELGAAGHFVTKGEWNDLMTSVVKPASM
>d1j9qa1 b.6.1.3 (A:4-166) Nitrite reductase, NIR {Alcaligenes faecalis, strain s-6}
ATAAEIAALPRQKVVELDPFVHAHSQVAEGGPKVVEFTMVIEEKKIVIDDAGTEVHAMAFNGTVPGPLMVHV
QDDYLELTLINPETNTLMHNINFHAATGALGGGLTEINPGEKTIILRFKATKPGVFVYHCAPGMVPWHVVSG
MNGAIMVLPREGLHDGK
>d1j9qa2 b.6.1.3 (A:167-339) Nitrite reductase, NIR {Alcaligenes faecalis, strain s-6}
GKALTYDKIYYVGEQDFYVPDENGKYKKYEAAPGDAYEDTVKVMRTLPTHVFNGAVGALTGDKAMTAAVG
EKVLIVHSQANRDTRPHLIGGHGDDYVWATGKFNTPPDVDQETWFIPGGAAGAAFYTFQQPGIYAYVHNHNLIEA
FELGAAAHFKVTGEWNDLMTSVLAPSG
>d1gs7a1 b.6.1.3 (A:1-159) Nitrite reductase, NIR {Alcaligenes xylosoxidans}
QDADKLPHTKVTLVAPPQVHPHEQATKSGPKVVEFTMTIEEKKMVIDDKGTTLQAMTFNGSMPGPTLVVHEG

DYVQLTLVNPATNAMPHNVDFHGATGALGGAKLTNVNPGEQATLRFKADRSHTFVYHCAPEGMVPWHVVS
GMSGTLMVLPRDGLKDP

>d1gs7a2 b.6.1.3 (A:160-336) Nitrite reductase, NIR {Alcaligenes xylosoxidans}
QGKPLHYDRAYTIGEFDLIYPKGPDKYKDYLTAESYGDTVQVMRTLTPSHIVFNGKVGALTGANALTAKVGET
VLLIHSQANRDTRPHLIGGFDWWWTGKFANPPQRDLETWFIRGGSAGAALYTFKQPGVYAYLNHNHNLIEAFE
LGAAGHIKVEGKWNDLMKQIKAPAPIPR

>d1ndsa1 b.6.1.3 (A:11-166) Nitrite reductase, NIR {Alcaligenes xylosoxidans}
GLPRVAVDLVAPPLVPHSQVAAGAPKVVQFRMSIEKKMVADDGTTAQAMTFNGSVPGPTLVVHEGYIE
LTIVNPATNSMPHNVDFHAATGALGGAGLTQVVPGQEAVLRFKADRSHTFVYHCAPIAGMVPWHVSGMNG
ALMVLPRDGLRDAA

>d1ndsa2 b.6.1.3 (A:167-340) Nitrite reductase, NIR {Alcaligenes xylosoxidans}
GAALAYDRVYTIGESDLVYVKAADGNYSDFPALASAYADTVAVMRTLTPSHAVFNGAVGALTGANALTAAVGES
VLIIHSQANRDSRPHLIGGHDWWWTGKFANPPQLNMETWFIPGGSAAAALYTFKQPGTYAYLSHNLIEAM
ELGAAAQQASVEGWQWDDLMTSVAAPGPA

>d1kbva1 b.6.1.3 (A:13-163) Nitrite reductase, NIR {Neisseria gonorrhoeae, AniA}
ELPVIDAVTTHAPEVPPAIDRDYPAKVRVKMETVEKTMKMDGVEYRYWTFDGDVPGRMIRVREGDTVEVEF
SNPPSSTVPHNVDFHAATGQGGAAATTAPGRSTFSFKALQPGLYIYCAVAPVGMHIANGMYGLILVEPK
EGLPKV

>d1kbva2 b.6.1.3 (A:164-314) Nitrite reductase, NIR {Neisseria gonorrhoeae, AniA}
DKEFYIVQGDFYTKGKKGAGQLQPFDMDKAVAEQPEYVVFNGHVGALTGDNALAKAGETVRMYVGNGGP
NLVSSFHIGEIFDKVYVEGGKLINENVQSTIVPAGGSAIVEFKVDIPGNYTLVDHSIFRAFNKGALGQLKVEGAE
NPEIM

>d1kv7a1 b.6.1.3 (A:31-170) multi-copper oxidase CueO {Escherichia coli}
RPTLPPIPDLTTDARNRIQLTIGAGQSTFGGKTATTWGYNGNLLGPAVKLQRGKAVTVDIYNQLTEETTLHWHL
EVPGEVDGPGQGIIPPGGKRSTLNVDQPAATCWFPHQHGKTGRQVAMGLAGLVIEDDEILKL

>d1kv7a2 b.6.1.3 (A:171-335) multi-copper oxidase CueO {Escherichia coli}
MLPKQWGIDDVPVIVQDKKFSADGQIDYQLDVMTAAGWFGDTLLNGAIYPQHAAPRGWLRLRLNGCNA
RSLNFATSDNRPLYVIASDGLLPEPVKSELPMGERFEVLVEVDNKPFDLVTPVSQMGMAIAPFDKPHP
VMRIQPIAISASGALPDTLS

>d1kv7a3 b.6.1.3 (A:336-516) multi-copper oxidase CueO {Escherichia coli}
SLPALPSLEGTVRKQLQLSMDPMLDMMMGMQMLMEKYGDQAMAGMDHSQMMGHMGHGNMNHMNH
GGKFDFHHANKINGQAFDMNKPMFAAAKGQYERWVISGVGDMMLHPFHIHGQTFRILSENGKPPAAHRAG
WKDTVKEGNVSEVLVKFNHDAPKEHAYMAHCHLEHEDTGMMMLGFTV

>d1aoza1 b.6.1.3 (A:1-129) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}
SQIRHYKWEVEYMFWAPNCNENIVMGINGQFPGPTIRANAGDSVVELTNKLHTEGVVIWHGILQRGTPW
ADGTASISQCAINPGETFFYNFTVDNPGTFFYHGHLMQRSAAGLYGSLIVDPPQGKKE

>d1aoza2 b.6.1.3 (A:130-338) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}
PFHYDGEINLLSDWWHQSIHKQEVGLSSKPIRWIGEPQTILLNGRGQFDCSIAKYDSNLEPCKLKGSESCAPYI
FHVSPKKTYRIRIASTTALAALNFAIGNHQLLVEADGNYVQPFYTSIDYSGESYVLITTDQNPSENWVSVG
TRARHPNTPPLTLLNYLPNSVSKLPTSPPPQTPAWDDFDRSKNFTYRITAAMGSPK

>d1aoza3 b.6.1.3 (A:339-552) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}
PPVKFNRRIFLLNTQN VINGYVKAINDVSLALPPTYLGAMKYNLLHAFDQNPPPEVFPEDYDIDTPPTNEKT
RIGNGVYQFKIGEVV DVLQNA NM KEN LSET HPWHLHDFWVLGYGDGK FSAEEESSNLKNPPLRNTV
VIFPYGWTAIRFVADNPGVWA FHCHIEPHLHMGMGVVFAEGVEKVGRIPTKALACGGTAKSLINNPKNP

>d1hfua1 b.6.1.3 (A:1-131) Laccase {Inky cap fungus (*Coprinus cinereus*)}
AIVNSVDTMTLTNAVSPDGFRAGILVNGVHGPLIRGGKNDNFELNVVNDLNPTMLRPTSIHWHLFQRG
TNWADGADGVNQCPISPGHAFLYKFTPAGHAGTFWYHSHTFGTQYCDGLRGPMVIYDDND
>d1hfua2 b.6.1.3 (A:132-303) Laccase {Inky cap fungus (*Coprinus cinereus*)}
PHAAALYDEDDENTIITLADWYHIPAPSIQGAAQPDATLINGKGRYVGGAELSIVNEQGKKYRMRLISLCDP
NWQFSIDGHETLIIEVDGELTEPVDRQLIFTGQRYSFVLDANQPVDNYWIRAQPNKGRNGLAGTFANGVNS
AILRYAGAANADPTTSANPNPAQL
>d1hfua3 b.6.1.3 (A:304-503) Laccase {Inky cap fungus (*Coprinus cinereus*)}
NEADLHALIDPAAPGIPTGAADVNLRFQLGFSGGRFTINGTAYESPVPTLLQIMSGAQSAQDLPAGSVYELP
RNQVVELVPAGVLGGPHPFLGHAFSVRSAGSSTYNFNPVKRDVSLGVTGDEVTIRFVTDNPGPWFF
HCHIEFHLMNGLAIVFAEDMANTVDANNPPVEAQLCEIYDDLPPEATSIQT
>d1kcw_1 b.6.1.3 (1-192) Ceruloplasmin {Human (*Homo sapiens*)}
KEKHYYIGIETTDYASDHGEKKLISVDTEHSNIYLQNGPDRIGRLYKKALYLYQYDFTFRTTIEKPVWLGFGLP
KAETGDKVYVHLKNLASRPYTFHSHGITYKEHEGAIYPDNTDFQRADDKVYPGEQYTYMLLATEEQSPGEGD
GNCVTRIYHSHIDAPKDIASGLIGPLICKKDSLKEKEK
>d1kcw_2 b.6.1.3 (193-338) Ceruloplasmin {Human (*Homo sapiens*)}
HIDREFVVMFSVVDENFSWYLEDNIKYCSEPEKVDKDNEFQESNRMYSVNGYTFGSLPGLSMCAEDRVKW
YLFGMGNEVDVHAAFFHGQALTNKNYRIDTINLFPATLFDAYMVAQNPGEWMLSCQNLNLKAGLQAFFQV
QEC
>d1kcw_3 b.6.1.3 (347-553) Ceruloplasmin {Human (*Homo sapiens*)}
IRGKHVRHYYIAAEIIWNYAPSGIDIFTKENLTAPGSDSAVFFEQQTTRIGGSYKKLVREYTDASFTNRKERGPE
EEHLGILGPVIWAEVGDTIRVTFHNGAYPLSIEPIGVRFNKNNEGTYYSPNYPQSRSVPPSASHVAPTTFTYE
WTPKEVGPTNADPVCLAKMYYSAVDPTKDIFTGLIGPMKICKGSLHANGRQK
>d1kcw_4 b.6.1.3 (554-705) Ceruloplasmin {Human (*Homo sapiens*)}
DVDKEFYLFPTVFDENESLLLEDNIRMFTTAPDQVDKEDEDFQESNKMHSMNGFMYGNQPGLTMCKGDSVV
WYLFSGNEADVHGIYFSGNTYLWRGERRDTANLFPQTSLTLMWPDTEGTFNVECLTDHYTGGMKQKYTV
NQCRRQSED
>d1kcw_5 b.6.1.3 (706-884) Ceruloplasmin {Human (*Homo sapiens*)}
STFYLGERTYYIAAVEVEWDYSPQREWEKELHHLQEQQNSNAFLDKGEFYIGSKYKKVVYRQYTDSTFRVPVER
KAEEEHLGILGPQLHADVGDKVKIIFKNMATTRPSIHAHGVQTESSTVTPLGETLTYVWKIPERSGAGTEDSA
CIPWAYYSTVDQVKDLYSGLIGPLIVCR
>d1kcw_6 b.6.1.3 (892-1040) Ceruloplasmin {Human (*Homo sapiens*)}
RRKLEFALLFLVDENESWYLDDNIKYSDHPEKVNKDDEFIESNKMHAINGRMFGNLQGLTMHVGDEVNW
YLMGMGNEIDLHTVHFHGSFQYKHRGVYSSDVFDIFPGTYQTLFPRTPGIWLLHCHVTDHIHAGMETTY
TVLQN
>d1qasa2 b.7.1.1 (A:626-756) PI-specific phospholipase C isozyme D1 (PLC-D1), C-terminal domain {Rat (*Rattus norvegicus*)}
WRPERLRVRIISGQQLPKVNKNKNSIVDPKVIVEIHGVGRDTGSRQTAITNNNGNPRWDMEFEFETVVPDLA
LVRFMVEDYDSSSKNDFIGQSTIPWNSLQGYRHVHLLSKNGDQHPSATLFVKISIQD
>d1rlw_ b.7.1.1 (-) Domain from cytosolic phospholipase A2 {Human (*Homo sapiens*)}
SSHKFTVVVLRATKVTGAFGDMILDTPDPYVELFISTTPDSRKTRHFNNNDINPVWNNETFFILDPNQENVLEIT
LMDANYVMDETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMSLEVASS
>d1d5ra1 b.7.1.1 (A:188-351) Pten tumor suppressor (Phosphoinositide phosphatase), C-terminal domain {Human (*Homo sapiens*)}
A

YRPVALLFHKMMFETIPMFSGGTCPQFVVCQLVKVIFYSSNSG PTRREDKF MYFEFPQPLPVCGDIKVEFFHKQ
NKMLKKDKMFHFWVNTFFIPGPEEVNDKEYVLTLKNDLDKANKDKANRYFSPNFVKLYFTKTV
>d1e8xa2 b.7.1.1 (A:357-522) Phosphoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}
CDRKFRVKIRGIDIPVLPRTADLTVFVEANIQYGQQVLCQRRTSPKPTEEVLWNVWLEFSIKIKDLPKGALLNLQI
YCGKAPALSGKTS AEMPS PESKGKAQ LYYVNLLIDHRFLRHGEYVLHMWQLSGKG EDQGSFNADKLTSATN
PDKENSMSISILLDN
>d1e8ya2 b.7.1.1 (A:357-522) Phosphoinositide 3-kinase (PI3K) {Human (Homo sapiens)}
CDRKFRVKIRGIDIPVLPRTDLTVFVEANIQHGQQVLCQRRTSPKPTEEVLWNVWLEFSIKIKDLPKGALLNLQ
IYCGKAPALSSKASAESPSS ESKGKVRLLYVNLLIDHRFLLRGEYVLHMWQISGKG EDQGSFNADKLTSATN
DKENSMSISILLDN
>d1bdya_ b.7.1.1 (A:) Domain from protein kinase C delta {Rat (Rattus norvegicus)}
MAPFLRISFNSYELGLSQAEDDASQPFCAVKMKEALTTDRGKTLVQKKPTMYPEWKSTFDAHIYEGRVIQIVLM
RAAEDPMSEVTGVSVLAERCKKNNGKA EF WLDLQPQAKVLMC VQYFLE
>d1gmia_ b.7.1.1 (A:) Domain from protein kinase C epsilon {Rat (Rattus rattus)}
MVVFNGLLKIKICEAVSLKPTAWSLRDAVGPRPQTFLDPYIALNVDDSRIGQTAKQKTNSPAW HDEFVTDVC
NGRKIELAVFHDAPIGYDDFVANCTIQFEELLQNGSRHFEDWIDLEPEGKVVII DLSGSSG
>d1byna_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}
EKLGKLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVKVFLPDKKKFETKVHRKTLNPV FNEQFTFKV
PYSELGGKTLVMAVYDFDRFSKHDIIIGEFKVPMNTVDFGHVTEEW RDLSQSAEK
>d1dqa1 b.7.1.2 (A:295-424) Synaptogamin I {Rat (Rattus norvegicus)}
GAPCGRISFALRYLYGSDQLVVRILQALDLPAKDSNGFSDPYVKIYLLPDRKKFQTKVHRKTLNPV FNETFQFSVP
LAELAQRKLHFSVYDFDRFSRHD LIGQVVL DNLLEAEQPPDRPLWRDILEGG
>d1dqa2 b.7.1.2 (A:425-569) Synaptogamin I {Rat (Rattus norvegicus)}
SEKADLGELNFSLCYLPTAGLLVTI IKASNLKAMDLTGFSDPYVKASLISEGRRKKRKT SIKNTLNPTYNEALVF
DVAPESVENVGLSIAVVDYDCIGHNEVIGVCRVGPEAADPHGREHWAEM LANPRKPVEHW HQLVEEK
>d1k5wa_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}
KLG DICFSLRYVPTAGKLTVVILEAKNLKKMDVGGLSDPYVKIHLMQNGKRLKKKTTIKKNTLN PYYNESFSFEV
PFEQIQKVQVVTVLDYD KIGKND AIGKVFGYNSTGAELRHWS DMLANPRRPIAQWHTLQVEEEV DAMILA
V
>d1rsy_ b.7.1.2 (-) Synaptogamin I {Rat (Rattus norvegicus)}
GGGILD SMVEKEEPKEEKL GKLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVKVFLPDKKKFETKV
HRKTLNPV FNEQFTFKVPYSELGGKTLVMAVYDFDRFSKHDIIIGEFKVPMNTVDFGHVTEEW RDLSQSA
>d1dsya_ b.7.1.2 (A:) C2 domain from protein kinase c (alpha) {Rat (Rattus norvegicus)}
TEKRGRIYLKA EVTDEKLHVTVRDAKNLIPMDP NGLSDPYVKLKLIPDPK NESQKTKTIRSTLN P QWNESFTFKL
KPSDKDRRLSVEIWDWDRTRNDFMGSLSGVSELMKMPASGWYKLLNQEEGEYYN VPipe
>d1a25a_ b.7.1.2 (A:) C2 domain from protein kinase c (beta) {Rat (Rattus norvegicus)}
ERRGRIYIQA HIDREV LIVV VRDAKNLVPMDP NGLSDPYVKLKLIPDPK SESQKTKT ICKSLNPEWNETFRFQLK
ESDKDRRLSVEIWDWDLTSRNDFMGSLSGVSELMKMPASGWYKLLNQEEGEYYN VPipe
>d3rpba_ b.7.1.2 (A:) C2b-domain of rabphilin {Rat (Rattus norvegicus)}
RGKILVSLMYSTQQGGLIVGIIRC VHLAAMDANGYSDPFV KLWLKPDMGKKAKHKTQIKKKT LNPEFNEEFFYD
IKHSDLAKKSLDISVWDY DIGKSNDYIGGCQLGISA GERLKHWYECLKNKDKKIERWHQLQNE NH
>d1qpxa2 b.7.2.1 (A:125-215) PapD {Escherichia coli}
NEVWQDQLILNKVSGGYRIENPTPYYVTIGLGGSEKQAE EG FETV M LSPRSEQ TVKSANYNTPYLSYINDY G
GRPVLSFICNGSRC SVK

>d1quna2 b.7.2.1 (A:122-205) FimC {Escherichia coli}
LPPDQAAEKLFRRSANSLTINPTPYLTTELNAGTRVLENALVPPMGEAVKLPSDAGSNITYRTINDYGALT
PKMTGVME

>d1who__ b.7.3.1 (-) Pollen allergen PHL P 2 {Timothy grass (Phleum pratense)}
VPKVTFTEVKGNEKHLAVLVYEGDTMAEVELREHGSDEWVAMTKGEGGVWTFDSEEPLQGPNFRLTEK
GMKNVFDDVVPEKYTIGATYAP

>d1dcea2 b.7.4.1 (A:241-350) Rab geranylgeranyltransferase alpha-subunit, insert domain {Rat (Rattus norvegicus)}
PHDVLCVHSREEACLSVCFSRPLTVGSRMGTLLMVDEAPLSVEWRTPDGRNRPSHVWLCDLPAASLNDQ
LPQHTFRVIWTGSDSQKECVLLKDRPECWCRDSATDEQ

>d1cza1 b.8.1.1 (A:350-501) TNF receptor associated factor 2 (TRAF2) {Human (Homo sapiens)}
YDGVIWIKISDFPRKRQEAVGRIPAIIFSPAFTSRYGYKMCLRIYLNGDGTGRGTHLSLFFVMKGPNDAALLRW
PFNQKVTLMLLDQNNREHVIDAFRPDVTSSFQRPVNDMNIASGCPLFCPVSKEAKNSYVRDDAIFIKAIVDL
TGL

>d1flka1 b.8.1.1 (A:350-504) TNF receptor associated factor 3 (TRAF3) {Human (Homo sapiens)}
YNGVLIWKIRDYKRRKQEAVMGKTLQLYSQPFTGYFGYKMCARVYLNQDMGKGTHSLFFVIMRGHEYDALL
PWPFKQKVTLMLMDQGSSRRHLGDAFKPDPNSSFKPTGEMNIASGCPVFVAQTVLENGTYIKDDTIFIKIV
DTSDLPPD

>d1k2fa_ b.8.1.2 (A:) SIAH, seven in absentia homolog {Mouse (Mus musculus)}
SVLFPCKYASSGCEITLPHTEKAEEHEELCEFPRYSCPCPGASCKWQGSLDAVMPHLMHQHKSIITLQGEDIVFLA
TDINLPGAVDWVMMQSCFGFHFMILVLEKQEKYDGHQQFFAIVQLIGTRKQAENFAYRLELNGHRRRLTWEAT
PRSIHEGIATAIMNSDCLVFDTSIAQLFAENGNLGINVTISM

>d2bn2a_ b.9.1.1 (A:) Neurophysin II {Cow (Bos taurus)}
AMSDLELRQCLPCPGGGKGRCFGPSICCGDELGCFVGTAEALRCQEENYLPSPCQSGQKPCGSRRCAAAGIC
CNDESCVTEPEC

>d1kvp__ b.10.1.1 (-) Bacteriophage capsid proteins {Bacteriophage phi-X174}
SNIQTGAERMPHDLSHLGFLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPRRGLAIDSTVDIFTFYVPHRH
YGEQWIKFMKDGVNATPLTVNTTGIDHAFLGTINPDTNKIPKHLFQGYLNIYNNYFKAPWMPDRTEAN
NELNQDDARYGFRCCHLKNIWTAPLPPETELSRQMTTSTGMAPVTTKFRDVPNLSGTPLIFRDNKGRTIKTQ
GIGPVDAGFLVAQNTAQANGERAIPSNLWADLSNATSIDIMGLQAAYANLHTDQERDYFMQRYRDVISSFG
KTSYDADNRPLLVMRSNLWASGYDVGDGTDTQSLQFSGRVQQTYKHSVPRFFVPEHGTMFTLALVRFPTATK
EIQYLNAGALTYTDIAGDPVLYGNLPPREISMKDVFVFRSGDSSKKFKIAEGQWYRYAPSYVSPAYHLLEGFPFIQE
PPSGDLQERVLIRHHYDQCFQSVQLLQWNSQVKFNVTYRNLPTRDSIMTS

>d2bpa1_ b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage phi-X174}
SNIQTGAERMPHDLSHLGFLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPRRGLAIDSTVDIFTFYVPHRH
YGEQWIKFMKDGVNATPLTVNTTGIDHAFLGTINPDTNKIPKHLFQGYLNIYNNYFKAPWMPDRTEAN
NELNQDDARYGFRCCHLKNIWTAPLPPETELSRQMTTSTSIDIMGLQAAYANLHTDQERDYFMQRYRDVISS
FFGKTSYDADNRPLLVMRSNLWASGYDVGDGTDTQSLQFSGRVQQTYKHSVPRFFVPEHGTMFTLALVRFPP
TATKEIQYLNAGALTYTDIAGDPVLYGNLPPREISMKDVFVFRSGDSSKKFKIAEGQWYRYAPSYVSPAYHLLEGFP
FIQEPPSGDLQERVLIRHHYDQCFQSVQLLQWNSQVKFNVTYRNLPTRDSIMTS

>d2bpa2_ b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage phi-X174}
MFQTFISRHNSNFFSDKLVLTSVPASSAPVLQTPKATSSSTLYFDSTVNAGNGGFLHCIQMDSVNAANQVVS
GADIAFDADPKFFACLVRFESSIONVPTLPTAYDVYPLNGRHGGYYTVKDCVTIDVLPRPGNNVYVGFMVWS
NFTATKCRGLVSLNQVIKEIIICLQPLK

>d1gff1_b.10.1.1 (1:) Bacteriophage capsid proteins {Bacteriophage G4}
VPHDLHLVFEAGKIGRLKTISWTPVAGDSFECDMVGAIRSLRGLAVDSRVDIFSYIIPHRHIYQQQWINF
MKDGVNASPLPPVTCSGGWDSAAYLGTIPSSTLKPKFLHQGYLNLYNNYFKPPWSDDLTANPSNMPSEDYK
WGVRVANLKSITAPLPPDTRTSENMTTGTTIDIMGLQAAYAKLHTEQERDYFMTRYRDIMKEFGGHTSYD
GDNRPLLMRSEFWASGYDVGDQSSLQFSGRVQQTNFHKVPRFYVPEHGVIMTLAVTRFPPTHEMEMH
YLVGKENLTYTDIACDPALMANLPPREVSLEFFHSSPDSAKFKIAEGQWYRTQPDRAFPYNALDGFPFYSALP
STDLKDRVLVNTNNYDEIFQSMQLAHWNMQTKFNIINVYRHMPTRDSIMTS

>d1gff2_b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage G4}
MFQKFISKHNAPINSTQLAATKTPAVAAPVLSVPNLSRSTILINATTAVTTHSGLCHVVRIDETNPNTHHALSIAG
SLSNVPADMIAFAIRFEVADGVVPTAVPALYDVYPIETFNNGKAISFKDAVTIDSHPRTVGNDVYAGIMLWSNA
WTASTISGVLSVNQNVRATVLQPLK

>d1stma_b.10.1.2 (A:) SPMV coat protein {Satellite panicum mosaic virus}
AAATSLVYDTCYVTLTERATTSFQRQSFPTLKGMDRAFQVVAFTIQGVSAAPLMYNARLYNPGDTDSVHATG
VQLMGTVPRTVRLTPRGQNNWFFGNTEEAETILAIDGLVSTKGANAPSNTVIVTGCFLAPSELQSS

>d1a34a_b.10.1.2 (A:) STMV coat protein {Satellite tobacco mosaic virus}
TGDNSNVVTMIRAGSYPKVNPPTWVRAIPFEVSVQSGIAFKVPVGSLSANFRDTSFTSVTMSVRAWTQLT
PPVNEYSFVRLKPLFKTDSTEEFGRASNINTRASVGYRIPTNLRQNTVAADVCEVRSNCRQVALVISCCFN

>d2stv_b.10.1.2 (-) STNV coat protein {Satellite tobacco necrosis virus}
TMRAVKRMINTHLEHKRFALINSGNTNATAGTVQNLNGIIQGDDINQRSGDQVRIVSHKLHVRGTAITVSQTF
RFIWFRDNMNRRGTTPTVLEVINTANFMSQYNPITLQQKRFTILKDTLNCSLTGESIKDRIINLPGQLVNYNGAT
AVAASNGPGAIFMLQIGDSLVGLWDSSYEAVYTDA

>d1smva_b.10.1.2 (A:) SMV coat potein {Sesbania mosaic virus}
GAITVLHCELTAEIGVTDSIVSSELVMPYTVGTWLRGVADNWSKYSWLSVRYTYIPSCPSSTAGSIHMGFQYD
MADTVPVSVNKLSNLRGYVSGQVWSGSAGLCFINNSRCSDTSTAISTLDVSELGKKWYPYKTSADYATAVGVD
VNIATDLVPARLVIALLDGSSSTAVAAGRIYDTYTIQMIEPTASALNL

>d1smvc_b.10.1.2 (C:) SMV coat potein {Sesbania mosaic virus}
QAGISMAPSAQGAMVRIRNPNAVSSSRGAITVLHCELTAEIGVTDSIVSSELVMPYTVGTWLRGVADNWSKYS
WLSVRYTYIPSCPSSTAGSIHMGFQYDMADTVPVSVNKLSNLRGYVSGQVWSGSAGLCFINNSRCSDTSTAIST
TLDVSELGKKWYPYKTSADYATAVGVDVNIATDLVPARLVIALLDGSSSTAVAAGRIYDTYTIQMIEPTASALNL

>d1f2na_b.10.1.2 (A:) RYMV capsid protein {Rice yellow mottle virus}
LSSNTWPLHSVEFLADFKRSSTSADATTYDCVPNLPRVWSLARCYSMWKPTRWDVYLPEVSATVAGSIEMC
FLYDYADTIPRYTGKMSRTAGFVTSSWYGAEGCHLLSGGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVV
NTILPARLAVRSSIKPTVSDTPGKLYVIASMVLRDPVDPLNT

>d1f2nc_b.10.1.2 (C:) RYMV capsid protein {Rice yellow mottle virus}
AEPQLQRAPVAQASRISGTVGPLSSNTWPLHSVEFLADFKRSSTSADATTYDCVPNLPRVWSLARCYSMWK
PTRWDVYLPEVSATVAGSIEMCFLYDYADTIPRYTGKMSRTAGFVTSSWYGAEGCHLLSGGSARNAVVASM
DCSRVGWKRVTSSIPSSVDPNVVNTILPARLAVRSSIKPTVSDTPGKLYVIASMVLRDPVDPLNT

>d1bmv1_b.10.1.2 (1:) BPMV coat protein {Bean pod mottle virus}
SISQQTVWNQMATVRTPLNFDSKQSFQFSV DLLGGGISVDKTGDWITLVQNSPISNLLRVAAWKKGCLMVK
VVMSGNAAVKRSDWASLVQVFLNSNSTEHFDACRWTKSEPHSWELFPIEVCGPNNGFEMWSSEWANQTS
WHLSFLVDNPKQSTTFDVLLGISQNFEIAGNTLMPAFSVPQ

>d1bmv2_b.10.1.2 (2:) BPMV coat protein {Bean pod mottle virus}
METNLFKLSDDVETPKGSMLDLKISQSKIALPKNTVGGTILRS DLLANFLTEGNFRASV_DLQRTHR IKGMIKMV
ATVGIPENTGIALACAMNSSIRGRASSDIYTICSQDCELWNPACTKAMTMSFNPNPCSDAWSLEFLKRTGFHCD

IICVTGWTATPMQDVQVTIDWFISSQECVPRTYCVLNPQNPFLNRWMGKLTFPQGTSRSVKRMPLSIGGGA
GAKSAILMNMPNAVLSMWRYFVGDLFEVSKMTSPYIKCTVSFFIAFGNLADDTINFEAFPHKLVQFGEIQEKV
VLKFSQEELTAWSTQVRPATTLLADGCPLYAMVHDSSVSTIPGDFVIGVKLTIIENMCAYGLNPGISGSRLLGTI
PQ

>d1a6ca1 b.10.1.2 (A:1-176) TRSV capsid protein {Tobacco ringspot virus}

AVTVVPDPTCCGTLFSFKVPKDAKKGKHLGTFDIRQAIMDYGGLHSQEWCAGIVNPTFTVRMHAPRNAFAGL
SIACTFDDYKRIDLPAKGNECPPSEMELPTKVFMLKDADVHEWQFNYGELTGHGLCNWANVATQPTLYFFVA
STNQVTMAADWQCIVTMHVDMGPVIDRFELN

>d1a6ca2 b.10.1.2 (A:177-348) TRSV capsid protein {Tobacco ringspot virus}

PTMTWPIQLGDTFAIDRYYEAKEIKLDGSTSMSISYNFGGPVKHSKKHAISYSRAVMSRNLGWSGTISGSVKSV
SSLFCTASFVIFPWECEAPTLRQVLWGPHQIMHGDGQFEIAKTRLHSAATTEEGFGRGLILPLSGPIAPDAHV
GSYEFIVHINTWRPDSQVHPPM

>d1a6ca3 b.10.1.2 (A:349-513) TRSV capsid protein {Tobacco ringspot virus}

FSSSELYNWFTLTNLKPANTGVNFIDPGYIHDFASKDATVTLASNPLSWLVAATGWHYGEVDLCISWSRSKQ
AQAAQEGSVSITTNYRDWGAYWQGQARIYDLRRTEAEIPIFLGSYAGATPSGALGKQNYVRISIVNAKDIVALRVC
LRPKSIKFWGGRSATLF

>d4sbva_ b.10.1.2 (A:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}

SSMDVTILSHCELSTELAVTVTIVTSELVMPFTVGTWLRGVAQNWSKYAWVAIRYTYLPSCPTTSGAIHMGF
QYDMAADTLPVSVNQLSNLKGYVTGPVWEGQSGLCFVNNTKCPDTSRAITIALDTNEVSEKRYPFKTATDYATAV
GVNANIGNILVPARLVTAMEGGSSKTAVENTGRLYASYTIRLIEPIAAALNL

>d4sbvc_ b.10.1.2 (C:) SBMV coat protein {Southern bean mosaic virus, cow pea strain}

QAGVSMAPIAQGTMVKLRPPMLRSSMDVTILSHCELSTELAVTVTIVTSELVMPFTVGTWLRGVAQNWSKY
AWVAIRYTYLPSCPTTSGAIHMGFQYDMAADTLPVSVNQLSNLKGYVTGPVWEGQSGLCFVNNTKCPDTSRAI
TIALDTNEVSEKRYPFKTATDYATAVGVNANIGNILVPARLVTAMEGGSSKTAVENTGRLYASYTIRLIEPIAAALNL

>d2tbva_ b.10.1.2 (A:) TBSV coat protein {Tomato bushy stunt virus}

GGVTVTSHREYLTVNNSSGFVVNGGIVGNQLNPNPSNGTLFSWLPALASNFDQYSFNSVVDYVPLCGTTEV
GRVALYFDKDSQDPEPADRVELANFGVLKETAPWAEAMLRIPTDKVKRYCNDSDATVDQKLIDLGQLGIATYGGA
GADAVGELFLARSVTLYFPQPTNTLSSKRLDTGSLADATGPGYLVTRPTVLTHTFRATGTFNLSGGRLCLTSLT
LGATGAVVINDILAIDNVGTASDYFLNCTVSSLPATVFTVSGVAAGILLVGRARANVVNLL

>d2tbvc_ b.10.1.2 (C:) TBSV coat protein {Tomato bushy stunt virus}

IIHGTVGGSIMAPVAVSRQLVGSKPKFTGRTSGGTVTSHREYLTVNNSSGFVVNGGIVGNQLNPNPSNGT
LFSWLPALASNFDQYSFNSVVDYVPLCGTTEVGRVALYFDKDSQDPEPADRVELANFGVLKETAPWAEAMLRI
PTDKVKRYCNDSDATVDQKLIDLGQLGIATYGGAGADAVGELFLARSVTLYFPQPTNTLSSKRLDTGSLADATGP
GYLVLRPTVLTHTFRATGTFNLSGGRLCLTSLGATGAVVINDILAIDNVGTASDYFLNCTVSSLPATVFTVSG
VAAGILLVGRARANVVNLL

>d1cwpb_ b.10.1.2 (A:) Cowpea chlorotic mottle virus {Host: cowpea (Vigna unguiculata), (L.)}

KAIKAWTGYSVSKWTASCAAAEAKVTSAITISLPNELSSERNKQLKGRVLLWLGLPSVSGTVKSCVTETQTTAA
ASFQVALAVADNSKDVAAMYPEAFKGITLEQLAADLTIYLYSSAALTEGDVIVHLEVEHVRPTFDDSTPVY

>d1c8na_ b.10.1.2 (A:) TNV coat protein {Tobacco necrosis virus}

NSTVVSNSELILNLTPIALAYTVQLPLIATQPAWLGTIADNYSKWRWVSLRIIYSPKCPTTSGTVAMCLSYDRND
VAPGSRVQLSQTYKAINFPPYAGYDGAAILNTDVTPTSAIYVDVDVTRFDKAWYSTIGTAAFAALTAFDQNQFCP
CTVHIGSDGGPAVPPGDIFFKYVIELIEPINPTMN

>d1c8nc_ b.10.1.2 (C:) TNV coat protein {Tobacco necrosis virus}

GVSRAGGFVTAPVIGAMVTRPTVPRFGMRGNSTVVSNSELILNLTPIALAYTVQLPLIATQPAWLGTIADNYSK

WRWVSLRIIYSPKCPTTSGTVAMCLSYDRNDVAPGSRVQLSQTYKAINFPPYAGYDGAAILNTDVPTSAYVD
VDVTRFDKAWYSTIGTAFAALTAFDQNQFCPCTVHIGSDGGPAVAVPPGDIFFKYVIELIEPINPTMN
>d1auya_b.10.1.2 (A:) TYMV coat protein {Turnip yellow mosaic virus}
SPLTIKQPFQSEVLFLAGTKDAEASLTIANIDSVSTLTFYRHASLESLWVTIHPTLQAPTFTVGVCWVPAQSPVT
PAQITKTYGGQIFCIGGAIQTLSPPLIVKCPLLEMMQPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTLMHSP
LITDTST
>d1auyb_b.10.1.2 (B:) TYMV coat protein {Turnip yellow mosaic virus}
MEIDKELAPQDRTVTATVLPAPVPGPSPLTIKQPFQSEVLFLAGTKDAEASLTIANIDSVSTLTFYRHASLESLWVTI
HPTLQAPTFTVGVCWVPAQSPVTPAQITKTYGGQIFCIGGAIQTLSPPLIVKCPLLEMMQPRVKDSIQYLDSPKL
LISITAQPTAPPASTCIITVSGTLMHSPLITDTST
>d1e57a_b.10.1.2 (A:) PHMV coat protein {Physalis mottle virus}
SPAIVLPFQFEATTFGTAETAAQVSLQTADPITKLTAPYRHAQIVECKAILPTDLSAVSNPLTVYLAWPANSPATPT
QILRVYGGQSFVLGGAISAAKTIEVPLNLDNVNRMLKDSVYTDTPKLLAYSRAPTNPSKIPTASIQISGRIRLSKP
MLIAN
>d1e57b_b.10.1.2 (B:) PHMV coat protein {Physalis mottle virus}
VVVKVKQASIPAPGSILSQNPTEQSPAIVLPFQFEATTFGTAETAAQVSLQTADPITKLTAPYRHAQIVECKAILPTD
LAVSNPLTVYLAWPANSPATPTQILRVYGGQSFVLGGAISAAKTIEVPLNLDNVNRMLKDSVYTDTPKLLAYSRA
APTNPSSKIPTASIQISGRIRLSKPMLIAN
>d1ddla_b.10.1.2 (A:) DYMV coat protein {Desmodium yellow mottle tymovirus}
MEQDKILAHQASLNTKPSLLPPPVGNNPPVISYPFQITLASLGTEADAADSVISIASNSVLATYTALYRHAQLKHLKAT
IHPTYMAPKYPTSVALWVPANSTATSTQVLDTYGGLHFCIGGSVNSVKPIDVEANLTNLNPIIKASTTFTDTPKLL
YYSKAQATAPTSPTYLTIQGQIELSSPLLQASS
>d1f15a_b.10.1.2 (A:) CMV coat protein {Cucumber mosaic virus, strain fny}
ERCRPGYTFITSILKPPKIDRGSSYYGKRLLLPSVTEYDKKLVSRLQIRVNPLPKFDSTVVWTVRKVPASSDLVAII
SAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIGDMRKYAVLVYSKDDALETDELVLHVDIEHQRIPTS
GVLPV
>d1f15b_b.10.1.2 (B:) CMV coat protein {Cucumber mosaic virus, strain fny}
DANFRVLSQQQLSRLNKTLAAGRPTINHPTFVGSERCRPGYTFITSILKPPKIDRGSSYYGKRLLLPSVTEYDKKLVS
RLQIRVNPLPKFDSTVVWTVRKVPASSDLVAIIISAMFADGASPVLVYQYAASGVQANNKLLYDLSAMRADIG
DMRKYAVLVYSKDDALETDELVLHVDIEHQRIPTSGVLPV
>d2bbva_b.10.1.3 (A:) Nodavirus capsid protein {Black beetle virus}
LTRLSQPLAFLKCAFAPPDFNTDPKGKIPDRFEGKVTRKDVLNQSINFNTANRDTFILIAPTGVAYWWADVPA
GTFPISTTFNAVNFPGFNSMFGNAAASRSRDQVSSFRYASMNVGIYPTSNLMQFAGSITVWKCPVKLSNVQFP
VATTPATSALVHTLGLDGVLAVGPDNFSESFIKGVFSQVCNEPDFEFSDILEGIQTLPPANVTATSGQPFNLAA
GAEAVSGIVGWGNMDTIVIRVSAPTGAVNSAILKTWACLEYRPNPNAIMLYQFGHDSPPCDEVALQEYRTVARS
LPVAVIAAQN
>d2bbvc_b.10.1.3 (C:) Nodavirus capsid protein {Black beetle virus}
TQTAPVPQQNVPKQPRRRRNARRNRRQGRAMNMIGALTRLSQPLAFLKCAFAPPDFNTDPKGKIPDRFEG
KVVTRKDVLNQSINFNTANRDTFILIAPTGVAYWWADVPGTFPISTTFNAVNFPGFNSMFGNAAASRSRDQVS
SFRYASMNVGIYPTSNLMQFAGSITVWKCPVKLSNVQFPATTPATSALVHTLGLDGVLAVGPDNFSESFIKGV
FSQVCNEPDFEFSDILEGIQTLPPANVTATSGQPFNLAAGAEAVSGIVGWGNMDTIVIRVSAPTGAVNSAILK
TWACLEYRPNPNAIMLYQFGHDSPPCDEVALQEYRTVARSLPVAVIAAQN
>d1nova_b.10.1.3 (A:) Nodavirus capsid protein {Nodamura virus}
NMLKMSAPGLDFLKCAFASPDFSTDPKGKIPDKFQGLVLPKKHCLTQSITFTPGKQTMLLVAPIPGIACLKAEN

VGASFSGVPLASVEFPGFDQLFGTSATDTAANVTAFRYASMAAGVYPTSNLMQFAGSIQVYKIPLKQVLNSYSQ
TVATVPPTNLAQNTIAIDGLEALDALPNNNYSGSFIEGCYSQSVCNEPEFEFHPIMEGYASVPPANVTNAQASM
FTNLTFSGARYTGLGMDAIAILVTTPTGAVNTAVLKVWACVEYRPNPNSTLYEFARESPANDEYALAAYRKIAR
DIPIAVACKDN

>d1novc_b.10.1.3 (C:) Nodavirus capsid protein {Nodamura virus}

RRRAAPRQQQRQQSNRASNQPRRRARRTRRQQRMAATNNMLKMSAPGLDFLKCAFASPDFSTDPKGIP
DKFQGLVLPKKHCLTQSITFTPQKQTMILLAPIPGIACLKAEANVGASFSGVPLASVEFPGFDQLFGTSATDTAAN
VTAFRYASMAAGVYPTSNLMQFAGSIQVYKIPLKQVLNSYSQTVATVPPTNLAQNTIAIDGLEALDALPNNNYS
GSFIEGCYSQSVCNEPEFEFHPIMEGYASVPPANVTNAQASMFTNLTFSGARYTGLGMDAIAILVTTPTGAVN
TAVLKVWACVEYRPNPNSTLYEFARESPANDEYALAAYRKIARDIPIAVACKDN

>g1f8v.1 b.10.1.3 (A:,D:) Nodavirus capsid protein {Pariacoto virus}

NRRNKARKVVSRSRALVPMAPASQRTGPAPRKPRKRNRNQALVRNPRLTAGLAFLKCAFAAPDFSVDPGKGIPD
NFHGRTLAIKDCNTTSVFTPNTDTYIVVAPVPGFAYFRAEVAVGAQPTTFVGVPYPTYATNFGAGSQNGLPAV
NNYSKFRYASMACGLYPTSNNMQFSGSVQWRVDLNLEAVNPAVTAITPAPGVFANFVDKRINGLRGIRPLA
PRDNYSGNFIDGAYTAFDKSTDWEWCDVRSLEFSESNVLGAAATAMKLLAPGGTDTTLGLGNVNTLVYKIST
PTGAVNTAILRTWNICIELQPYTDSALFQFSGVSPPFDPLALECYHNLKMRFPVAVSSRENXSKFWEGVLRVLNQI
SGTLSVIPGPVGTISAGVHQLTGMYM

>g1f8v.2 b.10.1.3 (B:,E:) Nodavirus capsid protein {Pariacoto virus}

NPRLTAGLAFLKCAFAAPDFSVDPGKGIPDNFHGRTLAIKDCNTTSVFTPNTDTYIVVAPVPGFAYFRAEVAV
GAQPTTFVGVPYPTYATNFGAGSQNGLPAVNNSYKFRYASMACGLYPTSNNMQFSGSVQWRVDLNLEAV
NPAVTAITPAPGVFANFVDKRINGLRGIRPLAPRDNYSGNFIDGAYTAFDKSTDWEWCDVRSLEFSESNVLGAA
ATAMKLLAPGGTDTTLGLGNVNTLVYKISTPTGAVNTAILRTWNICIELQPYTDSALFQFSGVSPPFDPLALECY
HNLKMRFPVAVSSRENXSKFWEGVLRVLNQISGTLSVIP

>d1dnv_b.10.1.3 (-) Galleria mellonella densovirus capsid protein {Wax moth (Galleria mellonella), densovirus}

YIIIPRFSNFGKKLSTYTKSHKFMIFGLANNVIGPTGTGTTAVNRLTTCLAEIPWQKLPLYMNQSEFDLLPPGS
RVVECNVKVFRTNRIAFETSSTVKQATLNQISNVQTAIGLNKLGWINRAFTAFQSDQPMIPTATTAPKYEPVT
GDTGYRGMIADEYYGADSTNDTAFGNAGNYPHHQVSSFTFLQNYYCMYQQTNQGTGGWPCLAELQQFDISK
TVNNQCLIDVTYKPKMGLIKSPLNYKIIGQPTVKGTISVGDNLVNMRGAVVTNPPEATQNVAEsthNLTRNFPA
DLFNIYSDIEKSQVLHKGPWGHENPQIQPSVHIGIQAVPALTTGALLINSSPLNSWTDSMGYIDVMSSCTVMEA
QPTHFPFSTEANTNPGNTIYRINLTPNSLTSAFNGLYNGNGATLGN

>d1b35a_b.10.1.3 (A:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (*Teleogryllus commodus*)}

VMGEDQQIPRNEAQHGVPISIDTHRISNNWSPQAMCIGEKVVSRQLIKRFGIFGDANTLQADGSSFVVAPF
TVTSPTKLTSTRNYTQFDYYYYLYAFWRGSMRIKMVAETQDGTGTPRKKTNFTWFVRMFNSLQDSFNLISTS
SSAVTTVLPSTGTINMGPSTQVIDPTVEGLIEVEPYNNISHITPAVTIDDGTPSMEDYLKGHSPPCLLTFSRDSIS
ATNHIIASFMRALGDDFSFMYLLGVPPLVNVARA

>d1b35b_b.10.1.3 (B:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (*Teleogryllus commodus*)}

ENSHIENEDKRLTSEQKEIVHFSEGVPSTTALPDIVNLSTNYLDKNTREDRIHSIKDFLSRPIIIATNLWSVSDPVE
KQLYTANFPEVLISNAMYQDKLKGFGVGLRATLVVKVQVNSQPFQQGRLMLQYIPYAQYMPNRVTLINETLQGR
SGCPRTDLELSVGTEVEMRIPYVSPHLYNLITGQGSFGSIYVVVYSQLHDQVSGTGSIEYTVWAHLEDVDVQYP
TGANIFTGNEAYIKGTSRYDAAQKAHAA

>d1b35c_b.10.1.3 (C:) Cricket paralysis virus (CRPV) {Host: australian black field

cricket (*Teleogryllus commodus*)}

SKPTVQGKIGECKLRGQGRMANFDGMDMSHKMALSSTNEIETNELAGTSLDVMDSRVLSIPNYWDRFTW
KTSDVINTVLWDNYVSPFKVKPYSATITDRFRCTHMGKVANAFTYWRGSMVYTFKFVTQYHSGRLRISFIPYY
YNTTISTGTPDVSRRTQKIVVDLRTSTAVSFTVPYIGSRPWLYCIRPESSWLSKDNTDGALMYNCVSGIVRVEVNL
QLVAAQNVFSEIDVICEVNGGPDLFAGPTCPRYVPYAGDFTLADTRKIEAERTQEYNNED

>d1sida_b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

KACPRPAPVPKLLIKGGMEVLDLVTPDSVTEIEAFLNPRMGQQPTPESLTEGGQYYGWSRGINLATSDTEDSP
GNNTLPTWSMAKLQLPMLNEDLTCCTLQMWEAVSVKTEVVGSGLLDVHGFNKPTDTVNTKGISTPVEGSQ
YHVFAVGGEPLDLQGLVTDARTKYKEEGVVTIKTITKKDMVNKDQVLPNISKAKLDKDGMYPVEIWHPDPAKN
ENTRYFGNYTGGTTPPVLFNTLTVLLDENGVGPLCKGEGLYLSCVDIMGWRVTRNYDVHHWRGLPRYFK
ITLRKRWVKNPYPMASLISSLFNNMLPQVQGQPMEGENTQVEEVRYDGETEPVPGDPDMTRYVDRFGKTKT
VFPG

>d1vpsa_b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

GGMEVLDLVTPDSVTEIEAFLNPRMGQQPTPESLTEGGQYYGWSRGINLATSDTEDSPGNNTLPTWSMAKL
QLPMLNEDLTCCTLQMWEAVSVKTEVVGSGLLDVHGFNKPTDTVNTKGISTPVEGSQYHVFAVGGEPLDLQ
GLVTDARTKYKEEGVVTIKTITKKDMVNKDQVLPNISKAKLDKDGMYPVEIWHPDPAKNENTRYFGNYTGGTT
TPPVLFNTLTVLLDENGVGPLCKGEGLYLSCVDIMGWRVTRNYDVHHWRGLPRYFKITLRKRWVK

>d1fmd1_b.10.1.4 (1:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTTGESADPVTTVENYGGETQVQRRHHTDVAFVLDRFVKVTVSDNQHTLDVMQAHKDNIVGALLRAATYY
FSDLEIAVTHTGKLTWVPGAPVSALNNTTNPTAYHKPVTRLALPYTAPHRLATAYTGTYYTASARGDLAHL
TTTHAAHLPTSFNFGAJAVAETITELLVRMKRAELYCPRPILPIQPTGDRHKQPLVAPAKQ

>d1fmd2_b.10.1.4 (2:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

DKKTEETTLLEDRLTTRNGHTTQSSVGVTGYATAEDSTGPNTSALETRVHQAEFFKMAFLDWVPSQN
FGHMHKVVLPHPKGVGGLVKSAYMRNGWDVEVTAVGNQFNNGCLLVALVPEMDISDREKYQLTLYPH
QFINPRTNMTAHITVPYVGVRDYDQYKQHRPWTLVMMVVAPLITNTAGAQQIKVYANIAPTNVHVAGELPSK
E

>d1fmd3_b.10.1.4 (3:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

GIFPVACSDGYGNMVTDPKTADPAYGKVYNPPRTALPGRFTNYLDVAEACPTFLMFENVPYVSTRTDGQRLL
AKFDVSLAAKHSNTYLAGLAQYTQYTGTINLHFMTGPTDAKARYMVAYVPPGMDAPDNPEEAHCIAHE
WDTGLNSKFTFSIPIYISAADYTYTASHEAETTCVQGWVCVYQITHGKADADALVVSASAGKDFELRLPVDARQQ
>d1qqp1_b.10.1.4 (1:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTSAGESADPVTTVENYGGETQIQRQHTDVSFIMDRFKVTPQNQINILDLMQVPSHTLVGALLRASTYYFS
DLEIAVKHEGDLTWVPGAPEKALDNNTNPTAYHKAPLTRLALPYTAPHRLATVYNGECRYSRNAVPNLRGDL
QVLAQKVARTLPTSFNYGAIKATRVTELLYRMKRAETYCPRPLLAIHPTEARHKQKIVAPVK

>d1qqp2_b.10.1.4 (2:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

DKKTEETTLLEDRLTTRNGHTTQSSVGVTGYATAEDFVSGPNTSGLETRVVQAERFFKTHLFDWVTSDF
GRCHLLELPTDHKGVYGS LTD SYAMRNGWDVEVTAVGNQFNNGCLVAMVPELCSIQKRELYQLTLFPHQFIN

PRTNMTAHITVPFGVNRYDQYKVHKPWTLLVMVVAPLTVNTEGAPQIKVYANIAPTNVHVAGEFPSKE
>d1qqp3_ b.10.1.4 (3:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}
GIFPVACSDGYGGLVTTDPKTADPVYGKVFNPPRNQLPGRFTNLLDVAEACPTFLRFEGGVPYVTTKTDSDRVL
AQFDMSLAAKHMSNTFLAGLAQYYTQYSGTINLHFMTGPTDAKARYMVAYAPPGMEEPKTPEAAAHCIAHE
WDTGLNSKFTFSIPYLSAADYTASDVAETTNVQGWVCLFQITHGKADGDALVVLASAGKDFELRLPVDARAE
>d1c8da_ b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host: dog (Canis familiaris)}
GVGISTGTFNNQTEFKFLENGWVYITANSSRLVHLNMPESENYRRVVNNMDKAVNGNMALDDIHAEVTP
WSLVDANAAGVWFNPWDQQLIVNTMSELHLVSFEQEIFNVVLKTVESATQPPTKVYNNDLTASLMVALDSN
NTMPFTPAAMRSETLGFPWKPTIPTPWRYYFQWDRTLIPSHTGSGTPTNIYHGTDPPDVQFYTIENSPVH
LLRTGDEFATGTFFFDCPKCRLHTWQTNRALGLPPLNSLPQSEGDTNGDIGVQQDKRRGVQMGNNTYIT
EATIMRPAEVGYSAPYYSEASTQGPFKTPIAAGRGAQTDENQAADGNPRYAFGRQHGQKTTTGETPERFT
YIAHQDTGRYPEGDWIQNINFNLPTNDNVLLPTDPIGGKTGINYTNIFNTYGPLTALNNVPPVYPNGQIWDE
FDTDLKPRLVNAPFVCQNNCPGQLFVKVAPNLTNQYDPDASANMSRIVTYSDFWWKGKLVFKAKLRASHT
WNPIQQMSINVDNQFNYPSENIGGMKIVYEKSQALPRKLY
>d1k3va_ b.10.1.4 (A:) Parvovirus (panleukopenia virus) capsid {Host: pig (Sus scrofa)}
GVGVSTGTFNNQTEFQYLGEGLVRITAHASRLIHLNMPEHETYKRIHVLNSESGVAGQMVQDDAHTQMVTP
WSLIDANAAGVWFNPADWQLISNNMTEINLVSFEQEIFNVVLKTITESATSPPTKIYNNDLTLASLMVALDTNNT
LPYTPAAPRSETLGFPWLPTKPTQYRYYLSCIRNLNPPTYTGQSQQITDSIQTGLHSDIMFYTIENAVPIHLLRTG
DEFSTGIYHFDTKPLKLTHSWQTNRSLGLPPKLLTEPTTEGDDQHPTLPAANTRKGYHQTINNSYTEATAIRPAQV
GYNTPYMNFEYSNGGPFLTPIVPTADTQYNDDEPNGAIRFTMDYQHGHLTSSQELERYTFNPQSKCGRAPKQ
QFNQQAPLNLENTNNGTLLPSDPIGGKSNMHMNTLNTYGPLTALNNTAPVFPNGQIWDEKELTDLKPRLV
TAPFVCKNNPPGQLFVKIAPNLDDFNADSPQQPRIITYSNFWWKGTLFTAkmrssnmwnpiqqhttaen
IGNYIPTNIGGIRMFPEYSQQLPRKLY
>d1mvma_ b.10.1.4 (A:) MVM coat protein {Murine minute virus, strain i}
GVGVSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDSVKGNAKDDAHEQIWTP
WSLVDANAAGVWLQPSDWQYICNTMSQLNLVSLDQEIFNVVLKTVEQDSGGQAIIYNNDLTACMMVAV
DSNNILPYTPAANSMETLGFPWKPTIASPYRYYFCVDRDLSVTYENQEGTIEHNVMGTPKGGMNSQFFTIENT
QQITLLRTGDEFATGTYYFDTNPVKLHTWQTNRQLGQPPLSTFPEADTDAGTLTAQGSRHGATQMEVNWV
SEAIRTRPAQVGFCQPHNDFEASRAGPFAAPKVPADVTQGMDREANGSVRYSYGKQHGENWAHGPAPER
TWDETNFGSGRDRDGFIQSAPLVPPPLNGILTANPIGTKNIDIFHSNVFNSYGPLTFSHPSPVYPQGQIW
KELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQYDPNGATLSRIVTYGTFFWKGKLTMRALKRANTTW
NPVYQVSVEDNGNSYMSVTKWLPTATGNMQSVPLTRPVARNTY
>d1hxs1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}
GSSSTDNTVRETVGAATSRDALPNTAESGPTHHSKEIPALTAVENTGATNPLVPSDTVQTRHVVQHRSSESSIESFF
ARGACVTIMTVDPNAPSTTNKDKLFAVWKITYKDTVQLRRKLEFTTYSRFDMELTFTVVTANFTETNNGHALNQV
YQIMYVPPGAPVPEKWDDYTWTSSNPSIFYTYGTAPARISVPYVGISNAYSHFYDGFSKVPLKDQSAALGDSLY
GAASLNDFGILAVRVVNDHNPTKVTSKIRVYLKPKHIRVWCPRPPRAVAYYGPVDYKDGTLPSTKDLTTY
>d1hxs2_ b.10.1.4 (2:) Poliovirus {Poliovirus type 1, strain Mahoney}
ACGYSDRVNLQLTGNSTITTQEAANSVAVGRWPEYLRDSEANPVDQPTEPDVAACRFYTLDTVSWTKESRGW
WWKLPDALRDMLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSNTTMHTSYQN
ANPGEKGFTGTFPDNNQTSPARRFCPVDYLLNGTLLGNAFVPHQIINLRTNNCATLVPVNSLSIDS
KHNNWGIAILPLAPLNFAESSPEIPITLTIAPMCCFNGLRNITLPRLIQ
>d1hxs3_ b.10.1.4 (3:) Poliovirus {Poliovirus type 1, strain Mahoney}

GLPMNTPGSNQYLADNFQSPCALPEFDVTPPIDIPGEVKNMELAEIDTMIPFDLSATKNTMEMYRVRLS
DKPHTDDPILCLSPLSPASDPRLSHTMLGEILNYYTHWAGSLKFTLFCGSMMATGKLLSYAPPGADPPKRKEA
MLGTHVIWDIGLQSSCTMVPWISNTTYRQTIDDSFTEGGYISVFYQTRIVVPLSTPREMDILGFVSACNDFSVR
LLRDTTHIEQKA

>d1pov0_b.10.1.4 (0:) Poliovirus {Poliovirus type 1, strain Mahoney}

GAQVSSQKVGAHENSNRAYGGSTINYTTINYYRDSASNAASKQDFSQDPSKTEPIKDVLIKTAPMLNSPNIEAC
GYSDRVQLTLGNSTITTQEAANSVAVGRWPEYLRDSEANPVDQPTEPDVAAACRFYTLDTVSWTKESRGWW
WKLPDALRDMGLFGQNMYYHYLGRSGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSNTTMHTSYQNA
NPGEKGHTFTGTFTPDDNNQTSPARRFCPVYLLGNGTLLGNAFVFPHQIINLRTNNCATLVPYVNSLSIDSMVK
HNNWGIAILPLAPLNFASESSPEIPITLTIAPMCCEFNGLRNITLPRLQ

>d1pov1_b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}

QHRSRSESSIESFFARGACVTIMTVDPNAPSTTNKDKLFAWKITYKDTVQLRKLEFFTYSRFDMELTFVVTANFT
ETNNNGHALNQVQIMYVPPGAPVPEKWDYTWTQTSNPSIFYTYGTAPARISVPYVGISNAYSHFYDGFSKVPL
KDQSAALGDSLYGAASLNDFGILAVRVVNDHNPTKVTSKIRVYLPKHIRVWCPRPPRAVYYGPGVDYKDGL
TPLSTKDLTTY

>d1eah1_b.10.1.4 (1:) Poliovirus {Poliovirus type 2, strain Lansing}

ANNLPDTQSSGPAHSKETPALAVETGATNPLVPSDTVQTRHVIQKRTRSESTVESFFARGACVAIIEVDNDAPTK
RASKLFSVWKITYKDTVQLRKLEFFTYSRFDMEFTFVVTTSNYTDANNGHALNQVQIMYIPPGAPIPGKWND
YTWTQTSNPSVFYTYGAPPARISVPYVGIANAYSHFYDGFAKVPLAGQASTEGDSLYGAASLNDFGSLAVRVV
DHNPTKLTISKIRVYMKPKHVRVWCPRPPRAVYYGPGVDYKDGLAPLPGKGLTTY

>d1eah2_b.10.1.4 (2:) Poliovirus {Poliovirus type 2, strain Lansing}

SVRVMQLTGNSTITTQEAANSVAVGRWPEYIKDSEANPVDQPTEPDVAAACRFYTLDTVWRKESRGWWW
KLPDALRDMGLFGQNMFYHYLGRAGYTVHVQCNASKFHQGALGVFAVPEMCLAGDSTHMFTKYENANPG
EKGGEFKGSFTLDTNATNPARNFCPVYLLFGSGVLAGNAFVYPHQIINLRTNNCATLVPYVNSLSIDSMTKHN
NWGIAILPLAPLDFATESSTEIPITLTIAPMCCEFNGLRNITVPRTRQ

>d1eah3_b.10.1.4 (3:) Poliovirus {Poliovirus type 2, strain Lansing}

GLPVNTPGSNQYLADNYQSPCAIPEFDVTPPIDIPGEVRNMELAEIDTMIPLNLTNQRKNTMDMYRVELN
DAAHSDTPILCLSPLSPASDPRLAHTMLGEILNYYTHWAGSLKFTLFCGSMMATGKLLSYAPPGAEAPSRKEA
MLGTHVIWDIGLQSSCTMVPWISNTTYRQTINDSFTEGGYISMFYQTRIVVPLSTPRKMDILGFVSACNDFSV
VRLLRDTTHISQEA

>d1pvc1_b.10.1.4 (1:) Poliovirus {Poliovirus type 3, strain Sabin}

QDSLPTKASGPAHSKEVPAHTALAVETGATNPLAPSNDTQTRHVVQRRSRSESTIESFFARGACVAIIEVDNEQPTT
RAQKLFAMWRITYKDTVQLRKLEFFTYSRFDMEFTFVVTANFTNANNGHALNQVQIMYIPPGAPTPKSWD
DYTWQTSNPSIFYTYGAAPARISVPYVGLANAYSHFYDGFAKVPLTDANDQIGDSLYSAMTVDDFGVLAVRV
VNDHNPTKVTSKVRIYMKPKHVRVWCPRPPRAVYYGPGVDYRNNDPLSEKGLTTY

>d1pvc2_b.10.1.4 (2:) Poliovirus {Poliovirus type 3, strain Sabin}

ACGYSDRVQLTGNSTITTQEAANSVAVGRWPEFIRDDEANPVDQPTEPDVATCRFYTLDTVMWGKESKG
WWWKLPDALRDMGLFGQNMFYHYLGRSGYTVHVQCNASKFHQGALGVFAIPEYCLAGDSDKQRYTSYANA
NPGERGGKFYSQFNKDNAVTSPKREFCPVYLLGCVLLGNAFVYPHQIINLRTNNSATIVLPYVNALAIDSMV
KHNNWGIAILPLSPLDFAQDSSVEIPITVTIAPMCCEFNGLRNVTAPKFQ

>d1pvc3_b.10.1.4 (3:) Poliovirus {Poliovirus type 3, strain Sabin}

GLPVNTPGSNQYLSDNHQSPCAIPEFDVTPPIDIPGEVKNMELAEIDTMIPLNLESTKRNTMDMYRVTLS
SADLSQPILCLSPLSPAFDPRLSHTMLGEVLYYTHWAGSLKFTLFCGSMMATGKILVAYAPPQAQPPTSKEAM
LGTHVIWDIGLQSSCTMVPWISNTYRQTTQDSFTEGGYISMFYQTRIVVPLSTPKMSMLGFVSACNDFSV

RLLRDTTHISQSA

>d4rhv1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 14}

TVASIISGPKHTQKVPILTANETGATMPVLPDSIETRTTYMHNGSETDVECFLGRAACVHVTIEIQNKDATGID
NHREAKLFNDWKINLSSLVQLRKLELFTYVRFDSEYTILATASQPDSANYSSNLVQAMIVPPGAPNPKEWDD
YTWSASNPSVFFKVGDTSRFSVPYVGLASAYNCFYDGYSHDDAETQYGITVLNHMGMSMAFRIVNEHDEHKT
VKIRVYHRAKHVEAWIPRAPRALPYTSIGRTNYPKNTEPVIKKRGDIKSY

>d4rhv2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 14}

GYSDRVQQITLGNSTITTQEAAANAVVCYAEWPEYLPVDASDVNKTSKPDTSCRFYTLDSKTWTGSKGWC
WKLPDALKDMGVFGQNMFFHSLGRSGYTVHQCNATKFHSGCLLVIPIEHQLASHEGGNVSVKYTFTHPG
ERGIDLSSANEVGGPVKDVLYNMNGTLLGNLLIFPHQFINLRTNNTATIVIPYINSVPIDSMTRHNNVSLMVIPIA
PLTVPTGATPSLPIVTIAPMCTEFSGIRSKSIVPQ

>d4rhv3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 14}

GLPTTLPMSGQFLTTDRQSPSALPNEYEPTPRIHPGVHNLLIEIQVDTLIPMNNTHTKDEVNSYLIPLNANRQ
NEQVFGTNLFIGDGVFKTLLGEIVQYYTHWSGSLRFLMYTPALSSAKLILAYTPPGARGPQDRREAMLGTH
VVWDIGLQSTIVMTIPWTSGVQFRTDPDTYTSAGFLSCWYQTSLIPPETTGQVYLLSFISACPDFKLRLMKDT
QTISQTVALTE

>d1aym1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 16}

NPVERYVDEVLNEVLPNINQSHPTTSNAAPVLDAETGHTNKIQPEDTIETRYVSSQTLDEMSVESFLGRS
GCIHESVLDIVDNYNDQSFTKWNINLQEMAQIRRKFEMFTYARFDSEITMVPSPAACKDHIGHIVMQYMYVP
PGAPIPTTRDDYAWQSGTNASVFWQHGQPFPFRSLPFLSIASAYYMFYDGYDGDYKSRYGTVVNTDMGTL
SRIVTSEQLHKVKVVTIYHKAKHTKAWCPRPPRAVQYSHTHTNYKLSSEVHNDVAIRPRTNLTTV

>d1aym2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 16}

SDRIIQITRGDSTITSQDVANAVVGYGVWPHYLTPQDATAIDKPTQPDTSNRFYTLDSKMWNSTSKGWWWK
LPDALKDMGIFGENMFYHFLGRSGYTVHQCNASKFHQGTLLVMIPEHQLATVNKGNVNAGYKYTHPGEA
GREVGTQVENEKQPSDDNWLNFDGTLLGNLLIFPHQFINLRSNNSATLIVPYVNAVPMDSMVRHNNWLSVIIP
VCQLQSNNNISNIVPITVSISPMCAEFSGARAKTVVQ

>d1aym3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 16}

GLPVYITPGSGQFMTTDDMQSPCALPWYHPTKEIFIPGEVKNLIMCQVDTLIPINSTQSNIGNVSMYTVTLSP
QTKLAEEIFAIKVDIASHPLATTLIGEIASYFTHWTGSLRFSFMFCGTANTTLKVLLAYTPPGIGKPRSKEAMLGT
HVWDVGLQSTVSLVVPWISASQYRFTTPDTYSSAGYITCWYQTNFVPPNTPNTAEMLCFVSGCKDFCLRM
ARDTDLHKQTGPITQ

>d1r1a1_b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 1A}

NYIDEVLNEVLPNIKESHHTTSNSAPLLDAETGHTSNVQPEDAIETRYVITSQTRDEMSIESFLGRSGCVHIS
RIKVDYTDYNGQDINFQKWLQEMAQIRRKFELFTYVRFDSEITLVPICIAGRGGDDIGHIVMQYMYVPPGAPIP
SKRNDFSWQSGTNMSIFWQHGQPFPFRSLPFLSIASAYYMFYDGYDGDNTSSKGTVTNDGTCRIVTEK
QKLSVITTHIYHKAKHTKAWCPRPPRAVPTYHTSHVTNYMPETGDTVTAIVRRNTITTA

>d1r1a2_b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 1A}

DRIMQITRGDSTITSSDDVANAVVGYGVWPHYLTPQDATAINKPTQPDTSNRFYTLESKHWNGSSKGWWWK
LPDALKDMGIFGENMYYHFLGRSGYTVHQCNASKFHQGTLLVAMIPEHQLASAKHGSVTAGYKLTHPGEAG
RDVSQERDASLRQPSDDSWLNFDGTLLGNLLIFPHQFINLRSNNSATLIVPYVNAVPMDSMLRHNNWCLVIPI
SPLRSETTSSNIVPITVSISPMCAEFSGARAKNIQ

>d1r1a3_b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 1A}

GLPVYITPGSGQFMTTDDMQSPCALPWYHPTKEISIPGEVKNLIMCQVDTLIPVNNVGNVGNVSMYTVQL
GNQTGMAQKVFSIKVDIRSTPLATTLIGEIASYYTHWTGSLRFSFMFCGTANTTLKLLAYTPPGIDEPTTRKDAM

LGTHVVWDVGLQSTISLVPW/VSASHFRLTADNKYSMAGYITCWYQTNLVPPSTPQTADMILCFVSACKDFCL
RMARDTDLHIQSGPIEQ

>d1fpn1_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 2}
LVVPNISSNPTTSNSAPALDAETGHTSSVQPEDVIETRYVQTSQLDEMLESFLGRSGCIHESKLEVTLANYN
KENFTVWAINLQEMAQIRRKFELFTYTRFDSEITLVPICISALSQDIGHITMQYMYVPPGAPVPNSRDDYAWQSG
TNASVFWQHGQAYPRFLSVASAYYMFYDGYDEQDQNYGTANTNNMGSLSRIVTEKHIHKVHIMTRIYH
KAKHVKAWCPRPPRALEYTRAHRTNFKIEDRSIQTAVTRPIITTA

>d1fpn2_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 2}
RIIQITRGDSTSQDVANAIVAYGVWPHYLSSKDASAIDKPSQPDTSNRFTLRSVTWSSSKGWWWKLPDA
LKDMGIFGENMFYHYLGRSGYTIHVQCNASKFHQGTLIVALIPEHQIASALHGNVNVGNYTHPGETGREVKA
ETRLNPDLQPTEEYWLNFDTLLGNITIPHQFINLRSNNSATIIAPYVNAVPMDSMRSHNNWSLVIIPCLETS
SAINTIPIESISPMCAEFGARAKRQ

>d1fpn3_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 2}
GLPVFITPGSGQFLTTDDFQSPCALPWYHPTKEISIPGEVKNLVEICQVDSLVPINNTDTYINSENMSVVLQSSI
NAPDKIFSIRTDVASQPLATTIGEISSYFHTWTGSLRFSFMFCGTANTTVKLLAYTPPGIAEPTTRKDAMLGTHV
IWDVGLQSTISMVVPWISASHYRNTSPGRSTSGYITCWYQTRLVIPPQTPTARLLCFVSGCKDFCLRMARDTN
LHLQSGAIAQ

>d1rhi1_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 3}
QLASVSSGPKHTQSVPALNETGATLPRPSDNVETRTTYMHNGSETDVEFLGRAACVHTEIKNNAAG
LDNHRKEGLFNDWKINLSSLVQLRKKLELFTYVRFDSEYTILATASQPEASSYNNLTQAMYVPPGAPNPKEWD
DYTWQSASNPSVFFKVGGETSRFSVPFVGIASAYNCFYDGYSHDDPDTPYGITVLNHMGMSMAFRVVNEHDVHT
TIVKIRVYHRAKHVEAWIPRAPRALPYVSIGRTNYPRDSKTIVKKRTNIKY

>d1rhi2_ b.10.1.4 (2:) Rhinovirus coat protein {Human rhinovirus 3}
GYSDRVQQITLGNSTITTQEARNAAIVCYAEWPEYLSNDNDASDVNKTSKPDISVCRFTLDSKTWKATSKGWCW
KLPDALKDMGVFGQNMFYHSLGRTGYTIHVQCNATKFHSGCLLVIPEHQLASHEGGTVSVKYKYTHPGDR
GIDLDTVEAGGPTSDAIYNMDGTLGNNLFPHQFINMRTNNTATIVPYINSVPIDSMTRHNNVSLMVPIA
PLNAPTGSSPTLPVTVTIAPMCTEFTGIRSRSIVPQ

>d1rhi3_ b.10.1.4 (3:) Rhinovirus coat protein {Human rhinovirus 3}
GLPTTTLPGSGQFLTTDDRQSPSALPSYEPTPRIHIPGKVRNLLEIIQVGTIPMNNNTGNDNVNTYLIPLHADRQ
NEQIFGKLYIGDGVFKTLLGEIAQYYTHWSGLRISLMYTGPALSSAKIILAYTPPGTRGPEDKKEAMLGTHVV
WDIGLQSTIVMTIPWTSGVQFRYTDPTYTSAGYLSCWYLTSLIIPQTSQGVYLLSFISACPDFKRLMKDTQTI
SQTDALTE

>d1bev1_ b.10.1.4 (1:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}
QAAGALVAGTSTSTHSVATDSTPALQAAETGATSTARDESMIETRTIVPTHGIHETSVESFFGRSSLVGMPLLATG
TSITHWRIDREFVQLRAKMSWFTYMRFDVEFTIIATSSTGQNVTEQHTTYQVMYVPPGAPVPSNQDSFQW
QSGCNPSPFADTDGPPAQFSVPMSSANAYSTVYDGYARFMDDPDRYGILPSNFLGFMYFRTLEAAHQVRF
RIYAKIKHTSCWIPRAPRQAPYKKRYNLVSGDSDRICSNRASLTSY

>d1bev2_ b.10.1.4 (2:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}
EACGYSRVAQLTLGNSTITTQEAAANICVAYGCWPAKLSDTDATSVDKPTEPGVSADRFTLRSKPWQADSKG
WYWKLPLDANNTGMFGQNAQFHYLYRGGWAVHVQCNATKFHQGTLVLAPEHQIATQECPAFDRTMPGS
EGGTFQEPFWLEDGTSGLNSLIYPHQWINLRTNNSATLILPYVNAIPMDSAIRHSNWTLAIIPVAPLKAAETTPL
VPITVTIAPMETEYGLRRAIASNQ

>d1bev3_ b.10.1.4 (3:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}
GLPTKPGPGSYQFMTTDEDSPCILPDFQPTPEIFIPGKVNNLLEIAQVESILEANNREGVEGVVERYVIPVSQDA

LDAQIYALRLELGGSGPLSSLLGTLAKHYTQWSGSVEITCMFTGTFMTTGKVLAYTPPGDMPRNREEAMLG
THVIWDFGLQSSITLVIPWISASHFRGVSNDDVLNYQYYAAGHVTIWYQTNMVIPPGFPNTAGIIMMIAAQPN
FSFRIQKDREDMTQTAILQ

>d2mev1_b.10.1.4 (1:) Mengo virus {Host: monkey brain; middle size plaque variant}

GVENAEKGVTENTDATADFVAQPVYLPEQTKVAFFYDRSSPIGAFAVKSGSLESGFAPFSNKACPNSVILTPGP
QFDPAYDQLRPQRLTEIWGNNGNEETSEVFPLKTQDYSFCLFSPFVYYKCDLEVTSPHTSGAHGLLVRWCPTGT
PTKPTTQLHEVSSLSEGRTPQVSAGPGTSNQISFVVPYNPLSVPAWYNGHKRFDNTGDLGIAPNSDFGT
LFFAGTKPDIKFTVYRLYKNMRVFCRPTVFFPWPTSGDKIDMT

>d2mev2_b.10.1.4 (2:) Mengo virus {Host: monkey brain; middle size plaque variant}

ENLSDRVSDTAGNTVTNTQSTVGRIVGYGTVHDGEHPASCADTASEKILAVERYYTFKVNNDWTSTQKPFEYIRI
PLPHVLSGEDGGVFGATLRRHYLVKTGWRVQVQCNASQFHAGSLLVFMAGEYPTLDVFAMDNRWSKDNLNP
GTRTQTNRKGPFAAMDHQNFWQWTLYPHQFLNLRTNTVDLEVYVNIAPTSSWTQHASWTLVIAVVAPLTYS
TGASTSLDITASIQPVRPVFNGLRHEVLSRQ

>d2mev3_b.10.1.4 (3:) Mengo virus {Host: monkey brain; middle size plaque variant}

SPIPVTIHAGTWYSTLPDSTVPIYGKTPVAPANYMVGEYKDFLEIAQIPTFIGNKVVPNAVPYEASNTAVKTQPL
AVYQVTSCSCLANTFLAALSRNFAQYRGSLVYTFVFTGTAMMKGFIAVTPPGAGKPTSRDQAMQATYAIW
DLGLNSSYSFTVPFISPTHFRMVGTDQANITNDGWVTVWQLTPLTYPPGCPTSAKLTMVSAGKDFSLKMPIS
PAPWSPQ

>d1cov1_b.10.1.4 (1:) Coxsackievirus B3 {Host: human (Homo sapiens)}

RVADTVGTGPTNSEAIPALTAETGHTSQVPSDTMQTRHVKNYHSRSESTIENFLCRSACVYFTEYENSGAKRY
AEWVITPRQAAQLRRKLEFFTIVRFDLELTIVITSTQQPSTTQNQDAQILTHQIMYVPPGGPVPDKVDSYVWQ
TSTNPSVFWTEGNAPPRMSVPFLSIGNAYSNFYDGWSEFSRNGVYGINTELNNMGTLYARHVNAGSTGPIKSTI
RIYFKPKHVKAWI PPPRLCQYEKAKNVNFQPSGVTTTRQSITTMNT

>d1cov2_b.10.1.4 (2:) Coxsackievirus B3 {Host: human (Homo sapiens)}

GYSDRVRISITLGNSTITTQECANVVVGYGVWPDYLKDEATAEDQPTQPDVATCRFYTLDSVQWQKTSPGWW
WKLPDALSNLGLFGQNMQYHYLGRGTGYTIHVQCNASKFHQGCLLVCVPEAEMGCATLNNTPSSAELLGGDT
AKEFADKPVASGSNKLVQRVYNAGMGVGVGVLNTIFPHQWINLRTNNSATIVMPYNSVPMNDNMFRHNNV
TLMVIPFVPLDCPGSTTYVPITVTIAPMCAEYNGLRLAGHQ

>d1cov3_b.10.1.4 (3:) Coxsackievirus B3 {Host: human (Homo sapiens)}

GLPTMNTPGSCQFLTSDDFQSPSAMQPQYDVTPEMRIPGEVKNLMEIAEVDSVPVQNVGEKVNSMEAYQIPV
RSNEGSGTQVFGPLQPGYSSVFSRTLLGEILNYYTHWSGISIKLTFMFCGSAMATGKFLLAYSPPGAGAPTKRVD
AMLGTHVVWDVGLQSSCVLCIPWISQTHRYVASDEYTAGGFITCWYQTNIVVPADAQSSCYIMCFVSACNDF
SVRLLKDTPFISQENFFQ

>d1d4m1_b.10.1.4 (1:) Coxsackievirus A9 {Host: human (Homo sapiens)}

GDVEEAIERAVHVADTMRGPSNSASVPALTAVETGHTSQVTPSDTMQTRHVKNYHSRSESTVENFLGRSAC
VYMEYKTTDNDVNKKFVAWPINTKQMVQMRRKLEMFTYLRFDMEVTFVITSRQDPGTTLAQDMPVLTQH
MYVPPGGPIAKVDDYAWQTSTNPSIFWTEGNAPARMSIPFISIGNAYSNFYDGWSNFDQRGSYGYNTLNNL
GHIYRVHVGSSPHITSTIRVYFKPKHTRAWVPRPPRLCQYKKAFSVDFTPTITDTRKDINTVTT

>d1d4m2_b.10.1.4 (2:) Coxsackievirus A9 {Host: human (Homo sapiens)}

SDRVRISITLGNSTITTQECANVVVGYGRWPTYLRDDEATAEDQPTQPDVATCRFYTLDSIKWEKGSVGWWK
FPEALSDMGLFGQNMQYHYLGRAGYTIHVQCNASKFHQGCLLVCVPEAEMGGAVVGQAFSATAMANGDK
AYEFTSATQSDQTKVQTAIHAGMGVGVGVLNTIYPHQWINLRTNNSATIVMPYINSVPMNDNMFRHYNFTLM
VIPFKLDYADTASTYVPITVAPMCAEYNGLRLAQAO

>d1d4m3_b.10.1.4 (3:) Coxsackievirus A9 {Host: human (Homo sapiens)}

GLPTMNTPGSTQFLTSDDFQSPCALPQFDVTPSMNIPGEVKNLMEIAEVDSVPVNNVQDTTDQMEMPFRIP
VTINAPLQQQVFGLRLQPGLDSVFKHTLLGEILNYYAHWSGSMKLTFCGSAMATGKFLIAYSPPGANPPKTR
KDAMLGTHIIWDIGLQSSCVLCVPWISQTHYRLVQQDEYTSAGYVTCWYQTGMIVPPGTPNSSIMCFASACN
DFSVRMLRDTPFISQDNKLQ

>d1ev11_b.10.1.4 (1:) Echovirus type 1 {Host: human (Homo sapiens)}

GDVQNAVEGAMVRVADTVQTSATNSERVPNLTAVETGHTSQAVPGDTMQTRHVINNHVRSESTIENFLARSA
CVFYLEYKTGTKEDENSFNNWITTRVAQLRRKLEMFTYLRFDMEITVVITSSQDQSTSQNQNAPVLTHQIMY
VPPGGPIPVSVDDYSWQTSTNPSIFWTEGNAPARMSIPFISIGNAYSNFYDGWSHFSQAGVYGFTLNNMGQ
LFFRHVNKPNAITSVARIYFKPKHVRAWVPRPPRLCPYINSTNVNFEPKPVTEVRTNIITT

>d1ev12_b.10.1.4 (2:) Echovirus type 1 {Host: human (Homo sapiens)}

GYSDRVRISITLGNSTTQCANEVNVGYGEWPEYLSNEATAEDQPTQPDVATCRFYTLDSVQWENGSPGWW
WKFPDALRDMGLFGQNMYYHYLGRAGYTIHVQCNASKFHQGCILVVCVPEAEMGSAQTSGVVNYEHISKGEI
ASRFTTTTAEDHGVQAAVWNAGMGVGVLGNLTIPHQWINLRTNNSATIVMPYVNSVPMNDNMYRHHNFTL
MIIPFVPLDFSAGASTYVPITVTVAPMCAEYNGLRLAGHQ

>d1ev13_b.10.1.4 (3:) Echovirus type 1 {Host: human (Homo sapiens)}

GLPTMNTPGSNQFLTSDDFQSPSAMQPFDVTPEMHIPGEVRNLMEIAEVDSVMPINNDSAALKVSSMEAYRV
ELSTNTNAGTQVFGFQLNPGAESVMNRTLMGEILNYYAHWSGSIKITFVFCGSAMTTGKFLLSYAPPGAGAPK
TRKDAMLGTHVWWDVGLQSSCVLCIPWISQTHYRFVEKDPYTNAQFVTCWYQTSVSPASNQPKCYMMCM
VSACNDFSVRMLRDTKFIEQTSFYQ

>d1tme1_b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

GSDNAEKGVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNIESTFVYQENDLRLNCLLTP
SFCPDSTSGPVTKAPVQWRWVRSGGTTNFPLMTKQDYAFLCSPFTYYKCDLETVSALGTDVASVLRWAP
TGAPADVTDLIGYTPSLGETRNPHMWLVGAGNTQISFVVPYNSPLSVLPAAWFNGWSDFGNTKDFGVAPN
ADFGRLWIQGNTSASVRIRYKKMKVFCPRPTLFFPWV

>d1tme2_b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

DRVASDKAGNSATNTQSTVGRLCGYGEAHHGEHPASCADTATDKVLAAYERYTIDLASWTTQEAFSHIRIPLP
HVLAGEDGGVFGATLRRHYLCKTGWRVQVQCNASQFHAGSLVFMAPEFYTGKGTKTGDMEPDFTMDTT
WRAPQGAPTGYRYDSRTGFFAMNHQNQWQWTVYPHQILNLRNTTVDLEVPYVNIAPTSSWTQHANWTL
VVAVFSPLQYASGSSSDVQITASIQPVNPVFNGLRHETVIA

>d1tme3_b.10.1.4 (3:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

SPIAVTVREHKGFYSTNPDTTVPIYGKTISTPNDYMCGEFSDLLECLKPTFLGNPNSNNKRYPYFSATNSVPTTS
LVDYQVALSCSCMCNSMLAAVARNFNQYRGSLNFLVFTGAAMVKGKFLIAYTPPGAGKPTTRDQAMQATYA
IWDLGLNSSFVFTAPFISPTHYRQTSYTSATIASVDGWVTVWQLTPLTYPGTPVNSDILTVSAGDDFTLRMPIS
PTKWVPQ

>d1tmf1_b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

GVDNAEKGVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNMETTFNYQENDYRLNCLLTP
LPSFCPDSSSGPQKTKAPVQWRWVRSGGVNGANFPLMTKQDYAFLCSPFTFYKCDLETVSALGTDVASVL
RWAPTGAPADVTDLIGYTPSLGETRNPHMWLVGAGNSQVSFVVPYNSPLSVLPAAWFNGWSDFGNTKDF
GVAPNADFGRLWIQGNTSASVRIRYKKMKVFCPRPTLFFPWPTPTTKINADNPVPILELE

>d1tmf2_b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine

encephalomyelitis virus, strain da}

DQNTEEMENLSDRVASDKAGNSATNTQSTVGRLCGYGKSHGEHPASCADTATDKVLAAYERYTIDLASWTT
QEAFSHIRIPLPHLAGEDGGVFGATLRRHYLCKTGWRVQVQCNASFHAGSLVFMAPEFTGKGTKTGME
PSDPFTMDTEWRSPQGAPTYRYDSRTGFFATNHQNQWQWTVYPHQILNLRTNTVDLEVPVNVAPSS
WTQHANWTLVVAVLSPHQYATGSSPDVQITASLQPVNPVFNGLRHETVIAQ

>d1sva1_b.10.1.4 (1:) Simian virus 40 (SV40) coat protein {Simian virus 40}

PKKPKEPVQVPKLVKGIEVLGVKTGVDSTEVCFNLPQMGNPDEHQKGLSKSAAEKQFTDDSPDKEQLPC
YSVARIPLPNINEDLTCGNILMWEAVTVKTEIGVTAMLNLHSGTQKTHENGAGKPIQGSNFHFFAVGGEPLEL
QGVLANYRTKYPQTVPKNAATVDSQQMNTDHKAVALDKDNAYPVECWVPPDSKNENTRYFGTYTGGENVPP
VLHITNTATTVLLDEQGVGPLCKADSLYSAVDICGLFTNTSGTQQWKGLPRYFKITLRKRSVKNPYPIFLLSDLI
NRRTQRVDGQPMIGMSQVEEVRVYEDTEELPGDPDMIRYIDEFGQTTTRMQ

>d1dzla_b.10.1.4 (A:) L1 protein {Human papillomavirus type 16}

KVVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIKKPNNNKILVPKVSGLQYRVFRIHLPDPNKFGFPDTSFYNPDT
QRLVWACVGVEVGRGQPLGVGISGHPLLNLKDDTENASAYAANAGVDNRECISMODYKQTQLCLIGCKPPIGEH
WGKGSPCTQAVQPGDCPPELEINTVIQDGDMVDTGFGAMDFTLQANKSEVPLDICTSICKYPDYIKMVSEP
YGDSSLFFYLREQMFVRHLFNRAVTGENVPDDLYIKGSGSTANLASSNYFPTPSGSMVTSDAQIFNKPWYLQ
RAQGHNNNGICWGNQLFVTVVDTTRSTNMSLCAAISTSETTYKNTNFKENYDLQFIFQLCKITLTADVM
TYIHSMNSTILEDWNFGLQPPPGTLEDTYRFVTSQAIACQKHTPPAPKEDPLKKYTFWEVNLEKEKFSADLDQF
PLGRKFLLQLGL

>d1ihma_b.10.1.4 (A:) Calicivirus capsid protein {Norwalk virus}

DPLAMDPVAGSSTAVATAGQVNIDPWIIINNFVQAPQGEFTISPNNTPGDVLFDSLGPHLNPFLHLSQMYN
GWVGNMRVRIMLAGNAFTAGKIIVSCIPPGFGSHNLTIAQATLFPVIADVRTLDPIEVPLEVRNVLFHNNDR
NQQTMRLVCMLYTPLRTGGGTGDSFVVAAGRVMTCSPDFNFLFLVPPTEEQKTRPFTLPNLPLSSLSNSRAPLPI
SSMGISPDNVQSVQFQNGRCTLDGRLVGTPVSLSHVAKIRTSNGTVINLTELGDGTPFHPFEGPAPIGFPLGG
CDWHINMTQFGHSSQTQYDVDTTPDTFVPHLGSIQANGIGSGNYGVLSWISPPSHPSGSQVDLKIPNYGS
SITEATHLAPSVPYPPGFGEVLFVFFMSKMPGPGAYNLPCLLPQEYISHLASEQAPTVEAALLHYVDPTGRNLGE
FKAYPDGFLTCVPNGASSGPQQLPINGVFVFWVSFRYQLKPVGTAS

>d1amm_1 b.11.1.1 (1-85) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GKITFYEDRGFQGHCYECSSDCPNLQPYFSRCNSIRVDSGCWMLYERPNYQGHQYFLRRGDYPDYQQWMGF
NDSIRSCLRLIPQHT

>d1amm_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GTFRMRIYERDDFRGQMSEITDDCPSLQDRFHLETVHSLNVLEGSWVLYEMPSYRGRQYLLRPGEYRRYLDWG
AMNAKVGSLRRVMDFY

>d1elpa1 b.11.1.1 (A:1-85) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}

GKITFYEDRGFQGRHYECSSDHSLNQPYLGRCNSRVDSGCWMIYEQPNYLGPQYFLRRGDYPDYQQWMGL
NDSIRSCLIPHAG

>d1elpa2 b.11.1.1 (A:87-174) gamma-Crystallin {Cow (Bos taurus), isoform IIIb (D)}

SHRLRLYEREDYRGQMIEITEDCSSLQDRFHNEIHSLNVLEGSWVLYELPNYRGRQYLLRPGEYRRYHDWGAM
NAKVGSLRRVIDIY

>d1a7ha_b.11.1.1 (A:) gamma-Crystallin {Cow (Bos taurus), isoform S}

MYKIQIFEKGDFNGQMHETTEDCPSSIMEQFHMREVHSCKVLEGAWIFYELPNYRGRQYLLDKKEYRKPVDWG
AASPAVQSFRRIVE

>d1ha4a_b.11.1.1 (A:) gamma-Crystallin {Human (Homo sapiens)}

GQYKIQIFEKGDFSGQMYETTEDCPSSIMEQFHMREIHSCKVLEGWIFYELPNYRGRQYLLDKKEYRKPIDWGA

ASPAVQSFRRIVE

>d1a45_1 b.11.1.1 (1-84) gamma-Crystallin {Cow (Bos taurus), isoform F}

GKITFYEDRGFQGRHYECSSDHNSNLQPYFSRCNSIRVDSCWCWMLYEQPNFQGPQYFLRRGDYPDYQQWMGL
NDSIRSCRLIPHT

>d1a45_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform F}

GSHRLRIYEREDYRGQMVEITEDCSSLHDRFHSEIHSFNVLEGWWVLYEMTNYGRQYLLRPGDYRRYHDW
GATNARVGSLRAVDFY

>d2bb2_1 b.11.1.1 (-2-85) beta-Crystallin {Cow (Bos taurus)}

LNPKIIIFEQENFQGHSHELNGPCPNLKETGVEKAGSVLVQAGPWVGYEQANCKGEQFVFEKGEYPRWDSWT
SSRRTDSLSSLRPIKVDS

>d2bb2_2 b.11.1.1 (86-175) beta-Crystallin {Cow (Bos taurus)}

QEHKITLYENPNFTGKKMEVIDDVPSFHAGHQEKVSSVRVQSGTWVGYQYPGYRGLQYLLEKGDYKDSGDF
GAPQPQVQSVRRIRDMQW

>d1a5da1 b.11.1.1 (A:1-84) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

GKITFYEDRGFQGRHYECSTDHSNLQPYFSRCNSRVDSGCWCWMLYEQPNFTGCQYFLRRGDYPDYQQWMGF
SDSVRSCRLIPHS

>d1a5da2 b.11.1.1 (A:85-174) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

SSHRIIYEREDYRGQMVEITDDCPHLQDRFHFSDFHSFHVMEGYWVLYEMPNYGRQYLLRPGEYRRYHDW
GAMNARVGSLRRIMDFY

>d1bd7a_b.11.1.1 (A:) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

EHKIILYENPNFTGKKMEIVDDDVPSPFHAGHQEKVSSVRVQSGTWVGYQYPGYRGLQYLLEKGDYKDNSDFG
APHPQVQSVRRIRDMQGNPKIIIFEQENFQGHSHELSGPCPNLKETGMEKAGSVLVQAGPWVGYEQANCKG
EQFVFEKGEYPRWDSWTSSRRTDSLSSLRPIK

>d1npsa_b.11.1.1 (A:) Protein S {Myxococcus xanthus}

ANITVFYNEDFQGKQVDLPPGNYTRAQLAALGIENNTISSVKVPPGVKAILYQNDGFAGDQIEVVANAELGPL
NNNVSSIRVISPV

>d1prr_2 b.11.1.1 (91-173) Protein S {Myxococcus xanthus}

PRARFFYKEQFDGKEVDLPPGQTQAELEYRIDNNNTISSVKPQGLAVVLFKNDNFSGDTLPVNSDAPTLGAM
NNNTSSSIRIS

>d1hdfa_b.11.1.1 (A:) Spherulin 3a (S3a) {Slime mold (Physarum polycephalum)}

SVCKGVSGNPAKGEVFLYKHVNFGDSWKVTGNYDFRSVSGLNDVVSSVKVGPNTKAFIFKDDRFNGNFIRL
EESSQVTDLTRNLNDAISSMIVATFE

>d1wkt_b.11.1.2 (-) Yeast killer toxin {Williopsis mrakii}

GDGYLIMCKNCDPTNGSCDWKQNNTCVGIGANHWMVTGGSTDGKQGCATIWEWSGCVGRSTTMCCP
ANTCCNINTGFYIRSYRRVE

>d1bhu_b.11.1.3 (-) Streptomyces metalloproteinase inhibitor, SMPI {Streptomyces nigrescens}

APSCPAGSLCTYSGTGLSGARTVIPASDMEKAGTDGVKLPSARSFANGTHFTLRYPARKVTCVRFCYQYATV
GKVAPGAQLRSLPSPGATVTVGQDLGD

>d1f53a_b.11.1.4 (A:) Killer toxin-like protein SKLP {Streptomyces sp.}

IDHVPCKRGGENFLKIWSHSGGQQSVDCYANRGRIDFGWWWDKISTGNNDLIYYDANGDSVRVDRWHIDTY
PNRPPKVNSIEIL

>d1g6ea_b.11.1.6 (A:) Antifungal protein AFP1 {Streptomyces tendae, tu901}

MINRTDCNENSYLEIHNEGRDTLCFANAGTMPVAIYGVNWVESGNVVTQFQRNLSDPRLETITLQKWGS
WNPGHIHEILSIRIY

>d1c01a_ b.11.1.5 (A:) Plant antimicrobial protein MIAMP1 {Macadamia nut (Macadamia integrifolia)}

SAFTVWSGPGCNNRAERYSKCGCSAIHQKGGYDFSYTGQTAALYNQAGCSGVAHTRFGSSARACNPFGW/KSIFIQC

>d1f8na2 b.12.1.1 (A:6-149) Plant lipoxygenase {Soybean (Glycine max), isozyme L1}

HKIKGTVVLMPKNELEVNPDGSAVDNLNAFLGRSVSLQLISATKADAHGKGKVGKDFTLEGINTSLPTLGAGESAFNIHFEDGSMGIPGAFYIKNYMQVEFFLKSLTLEAISNQGTIRFCNSWVYNTKLYKSVRIFFANHTY

>d1ik3a2 b.12.1.1 (A:9-167) Plant lipoxygenase {Soybean (Glycine max), isozyme L3}

GHKIKGTVVLMRKNVLDVNSVTSGGIIGQGLDLVGSTLDTLTAFLGRSVSLQLISATKADANGKGLGKATFLEGIIITSPLTGAGQSAFKINF EWDDGSGIPGAFYIKNFMQTEFFLVSLEDIPNHGSIHFCNSWIYNAKLFKSDRIFFANQTY

>d1lox_2 b.12.1.1 (2-112) 15-Lipoxygenase {Rabbit (Oryctolagus cuniculus)}

GVYRVCVSTGASIYAGSKNKVELWLVGQHGEVELGSCLRPRTRNKEEEFKVNVS KYLGSLLFVRLRKHHFLKEDA WFCNWISVQALGAAEDKYWFPCYRWVVGDGVQSLPVG

>d1hpla1 b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain {Horse (Equus caballus)}

RWRYRVDVTLSGKKVTGHVLVSLFGNKGNSRQYEIFQGTLKP DNTSNEFDSDVEVGDLQKVFKFIWYNNVINLTLPKVGASKITVERNDGSVFNFCEETVREDVLLTAC

>d1letha1 b.12.1.2 (A:337-448) Pancreatic lipase, C-terminal domain {Pig (Sus scrofa)}

ARWRYKVS VTL SGKKVTGHILVSLFGNEGNSRQYEIYKGTLPDNTHSDEF DSDVEVGDLQKVFKFIWYNNVINPTLPRVGASKITVERNDGK VYDFCSQETVREEVLLTLP C

>d1gpl_1 b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain {Guinea pig (Cavia porcellus)}

RWRYKVS VTL SGKKVTGHILVSLFGNKGNSKQYEIFKGTLPDNTHSNEFDSDDV DVGDLQMVVKFIWYNNVINPTLPRVGASKIIVETNVGKQFNFCSPETVREEVLLTLP C

>d1rp1_1 b.12.1.2 (337-449) Pancreatic lipase, C-terminal domain {Dog (Canis familiaris)}

RWRYGV SITLSGKRATGQAKVALFGSKGNTHQFNIFKGILKPGSTSNEFDAKLDVG TIEKVFKFLWNNNNPTFPKVGA AKITVQKGEEKTVHSFCSEETVREDVLLTLP C

>d1bu8a1 b.12.1.2 (A:337-449) Pancreatic lipase, C-terminal domain {Rat (Rattus norvegicus)}

RWRYKVS VTL SGAKKLSGYILVALYGNNGNSKQYEIFKGSLKPEARHVRDIDV DINVGEIQKVFKFLWNNNKVINLF RPTLGASQITVQSGVDGKEYNFCSSDTVREDVLQSLYP C

>d1ca1_2 b.12.1.3 (250-370) Alpha-toxin, C-terminal domain {Clostridium perfringens}

SVGKNV KELVAYISTSGEK DAGTDDYMF GIKTKDGKTQEWE MDNPGNDFMTGSKDTYTFKLKDENLKIDD IQNMWIRKRKYTA FPDAYKPE NIKVIANGKVVVDKDINEWISGNSTYNIK

>d1k5ja_ b.13.3.1 (A:) Nucleoplasmin core {Xenopus laevis}

VSLIWGC E LNEQNKT FEFKVEDDEEKCEHQLALRTVCLGD KAKDEFHIVEI VTQEEGA EKSVPIATLKPSILPMATMVGIELTPPVTFRLKAGSGPL YISGQHVA

>d1pgs_1 b.13.1.1 (4-140) Peptide:N-glycosidase F, PNGase F {Flavobacterium meningosepticum}

DNTVNIKTFDKVKA FG DGLSQSAEGTTF PADVTTVKT I KMF IKNECPNKT CDEWDRYANVYVKNKTTGEWYEIGRFITPYWVGTEKLRGLEIDVTDFKSLLSGNTELKIYTETWLAKGREYSVDFDIVYGT PDY

>d1pgs_2 b.13.1.1 (141-314) Peptide:N-glycosidase F, PNGase F {Flavobacterium meningosepticum}

KYSAVVPVIQYNKSSIDGV PYGKAHTLGLKKNIQLPTNTEKAYLRTTISGWGHAKPYDAGSRGCAEWCFRTHTIA INNANTFQHQLGALGCSANPINNQSPGNWTPDRAGWCPGM AVPTRIDVLNNSLTG STFSYEYKFQS WTNN G

TNGDAFYAISSFVIKSNTPISAPVVTN

>d1phm_1 b.13.1.2 (45-198) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (Rattus norvegicus)}

NECLGTIGPVTPLDASDFALDIRMPGVTPKESDTYFCMSMRLPVDEEAVIDFKPRASMDTVHHMLLFGCNM
PSSTGSYWCDEGCTDKANILYAWARNAPPTRLPKGVGFRVGGETGSKYFVLQVHYGDISAFRDNHKDCSGV
SVHLTRVPQ

>d1phm_2 b.13.1.2 (199-354) Peptidylglycine alpha-hydroxylating monooxygenase, PHM {Rat (Rattus norvegicus)}

PLIAGMYLMMSVDTVIPPGEKVVNADISCQYKMYPMHVFAYRVHTHHLGKVSGYRVRNGQWTLIGRQNP
QLPQAFYPVEHPVDVTFGDILAARCVFTGEGRTEATHIGGTSSDEMCLNLYIMYYMEAKYALSFMTCNVAPD
MFRTIPAEANIPI

>d1hx6a1 b.13.2.1 (A:15-244) Coat protein p3 {Bacteriophage prd1}

LRNQQAMAANLQARQIVLQQSYPIQQVETQTDFPANRSVFDVTANVGIVKGFLVKVTAITNNHATEAVAL
TDFGPANLVQRVIYYDPDNQRHTETSGWHLHFVNATAQGAPFLSSMVTDSPIKYGDVMNVIDAPATIAAGATG
ELTMYYWVPLAYSETDLTGAVLANVPQSKQRLKLEFANNNTAAVGANPLEAIYQGAGAADCEFEISYTVYQ
SYLDQLPVGQ

>d1hx6a2 b.13.2.1 (A:245-384) Coat protein p3 {Bacteriophage prd1}

NGYILPLIDLSTLYNLENSAQAGLTPNVDFVVQYANLYRYLSTIAVFDFDNGGSFNAGTDINYLSQRTANFSDRKLD
PKTWAAQTRRRRIATDFPKGVYYCDNRDKPIYTLQYGNVGFVNPKTVNQNARLLMGYEYFTSRT

>d1dhx_1 b.13.2.2 (44-650) Adenovirus hexon {Human adenovirus type 2}

FRNPTVAPTHDVTTDRSQRRTLRFIPVDRDFTASYKARFTLAVGDNRVLDMASTYFDIRGVLDRGPTFKPYSGT
AYNALAPKGAPNSCEWEQTEDSGRAVAEDEEEEEEDEEEEEEEQNARDQATKKTHVYAQAPLSGETITKGLQI
GSDNAETQAKPVYADPSYQPEPQIGESQWNEADANAAGGRVLKKTPMKPCYGSYARPTNPFGGQSVLPD
EKGVPLPKVDLQFFSNTSLNDRQGNATPKVVLYSEDVNMETPDTHLSYKPGKDENSKAMLGQQSMPNRP
NYIAFRDNFIGLMMYNSTGNMGVLAGQASQLNAVVDLQDRNTELSYQLLDSIGDRTRYFSMWNLQAVDSYDP
DVRIIENHGTEDELPNYCFPLGGIGVTDYQAIKANGNGSGDNGDTTWTKDETFACTRNEIGVGNNFAMEINLN
ANLWRNFLYSNIALYLPDKLKYNPTNVEISDNPNTYDYMNKRVVAPGLVDCYINL GARWSLDYMDNVNPFNH
HRNAGLRYRSMLLNGNGRYVPFHIQVPQKFFAIKNLLPGSYTYEWNFRKDVMVLQSSLGNDLRVDGASIKF
DSICLYATFFPMAHNTASTLEAMLR

>d1ruxa1 b.13.2.2 (A:5-636) Adenovirus hexon {Human adenovirus type 5}

MMPQWWSYMHISGQDASEYLSPLGLVQFARATETYFSLNNKFRNPTVAPTHDVTTDRSQRRTLRFIPVDRDFTAY
SYKARFTLAVGDNRVLDMASTYFDIRGVLDRGPTFKPYSGTAYNALAPKGAPNPCEWDEAATALEINLEEDDD
NEDEVDEQAEQQKTHVFGQAPYSGINITKEGIQIGVEGQTPKYADKTFQPEPQIGESQWYETEINHAAGRVLK
KTTPMKPCYGSYAKPTNENGQGILVKQQNGKLESQVEMQFFSTTEATAGNDNLTPKVVLYSEDVDIETPDT
HISYMPTIKEGNSRELMGQQSMPNRPNYIAFRDNFIGLMMYNSTGNMGVLAGQASQLNAVVDLQDRNTELS
YQLLDSIGDRTRYFSMWNLQAVDSYDPDVRIIENHGTEDELPNYCFPLGGVINTELTKVPKTGQENGWEKD
ATEFSDKNEIRVGNNFAMEINLNANLWRNFLYSNIALYLPDKLKYSPSNVKISDNPNTYDYMNKRVVAPGLVDC
YINL GARWSLDYMDNVNPFNHHRNAGLRYRSMLLNGNGRYVPFHIQVPQKFFAIKNLLPGSYTYEWNFRKD
VN MV LQSSLGNDLRVDGASIKFDSICLYATFFPMAHNTASTLEAMLRND

>d1ruxa2 b.13.2.2 (A:637-946) Adenovirus hexon {Human adenovirus type 5}

TNDQSFNDYLSAANMLYPIPANATNVPISPSRNWAARFGWAFTRLKTKETPSLGSYDPYYTSGSIPYLDGTF
YLNHTFKKVAITFDSSVSPGNDRLLTPNEFEIKRSVDGEGYNVAQCNMTKDWFLVQMLANYNIGYQGFYIPE
SYKDRMYSFFRNQPMRSRQVDDTKYKDYQQVGLHQHNNSGFGVGYLAPTMREGQAYPANFPYPLIGKTAVD
SITQKKFLCDRTLWRIFFSNFMSMGALTDLGQNLLYANSAHALDMTEVDPMDDEPTLLYVLFEVFDVVRVHRP

HRGVIETVYLRTPFSA

>d1kful2 b.14.1.1 (L:356-514) Calpain large subunit, middle domain (domain III) {Human (Homo sapiens)}

WKLTKMDGNWRRGSTAGGCRNYPNTFWMNPQYLIKLEEEDEDEEDGESGCTFLVGLIQQKHHRRRQRKMGED
MHTIGFGIYEVPEELSGQTNIHL SKNFFLTNRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPNKDGDFCIRVFS
EKKADYQAVDD

>d1df0a2 b.14.1.1 (A:356-514) Calpain large subunit, middle domain (domain III) {Rat (Rattus norvegicus)}

WKLTKMDGNWRRGSTAGGCRNYPNTFWMNPQYLIKLEEEDEDEDGERGCTFLVGLIQQKHHRRRQRKMGED
MHTIGFGIYEVPEELTGQTNIHL SKNFFLTTRARERSDTFINLREVLNRFKLPPGEYILVPSTFEPHKNGDFCIRVFS
EKKADYQTVDD

>d1f35a_ b.94.1.1 (A:) Olfactory marker protein {Mouse (Mus musculus)}

AEDGPQQKQLEMPVLQDLTQQMQLRVESLQKQRGEKKQDGEKLRPAESVYRLDFIQQQKLQFDHWNVVLD
KPGKVTITGTSQNWTPLTNLMTRQLLDPAIFWRKEDSDAMDWNEADALEFGERLSLAKIRKVMYFLITFG
EGVEPANLKASVVFNL

>d1shsa_ b.15.1.1 (A:) Small heat shock protein {Archaeon Methanococcus jannaschii}

TGIQISGKGFMPIISIEGDQHIKVIAWLPVNKEIDIILNAVGDTLEIRAKRSPLMITESERIIYSEIPEEEEYRTIKLPA
TVKEENASAKFENGVLVLPKAESSIKKGINIE

>d1gmea_ b.15.1.1 (A:) Small heat shock protein {Wheat (Triticum aestivum)}

SIVRRSNVFDPFADLWADPDFTRSVPAISGGGSETAAFANARMDWKETPEAHVFKA DLPGVKKEEVKVEVE
DGNVLVSGERTKEKEDKNDKWHRVERSSGKFVRRFRLLDAKVEEVKAGLENGVLTVPKAEVKKPEVKAI
QISG

>d1gmbe_ b.15.1.1 (B:) Small heat shock protein {Wheat (Triticum aestivum)}

NARMDWKETPEAHVFKA DLPGVKKEEVKVEVEDGNVLVSGERTKEKEDKNDKWHRVERSSGKFVRRFRLL
DAKVEEVKAGLENGVLTVPKAEVKKPEVKAIQISG

>d1ejfa_ b.15.1.2 (A:) Co-chaperone p23 {Human (Homo sapiens)}

MQPASAKWYDRRDYVFIEFCVEDSKDVNVNFKEKS KLTFSCLGGSDNFKHLNEIDLHICIDPNDSKHKR DRSILC
CLRKGESGQS WPRLT KERAKLNWL SVDFNNWKDWE

>d1ezsa_ b.16.1.1 (A:) Ecotin, trypsin inhibitor {Escherichia coli}

PYPQAEGKGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGAAAAYYVFDKVSSPVSTRM
ACPDGKKEKKFVTAYLGDAGMLRYNSKLP I VYTPDNVDV KYRVWKAEEKIDNAVVR

>d1slua_ b.16.1.1 (A:) Ecotin, trypsin inhibitor {Escherichia coli}

IAPYPQAEGKGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGYDYYVFDKVSSPVST
MMHCPDGKKEKKFVTAYLGDAGMLRYNSKLP I VYTPDNVDV KYRVWKAEEKIDNAVVR

>g1fi8.1 b.16.1.1 (C;D:) Ecotin, trypsin inhibitor {Escherichia coli}

PLEKIAPYPQAEGKGMKRQVIQLTPQEDESTLKVELLIGQTLEVDCNLHRLGGKLENKTLEGWGYDYYVFDKVSSP
IEPDXKFVTAYLGDAGMLRYNSKLP I VYTPDNVDV KYRVWKAEEKIDNAVVR

>d1 beha_ b.17.1.1 (A:) Phosphatidylethanolamine binding protein, PEBP {Human (Homo sapiens)}
VDLSKWSGPLSLQEVDERPQHPLHVTYAGAAVDELGVLTPTQVKNRPTSISWDGLDSGKLYTLVLTDPDAPSR
KDPKYREW HHFLVVNMKGNDI SSGTVLS DYVGSGPPKG TGLHRYVWL VYEQDRPLKCDEPILSNSRGDH RGKF
KVASFRKKYELRAPVAGTCYQAEWDDYVPKLYEQLSG

>d1a44_ b.17.1.1 (-) Phosphatidylethanolamine binding protein, PEBP {Cow (Bos taurus)}

PVDLSKWSGPLSLQEVDERPQHPLQVKYGGAEVDELGVLTPTQVKNRPTSITWDGLDPGKLYTLVLTDPDAPS

RKDPKYREWHHFLVVNMKGNNIISGTVLSDYVGSGPPKGTLHRYVWLVEQEGPLKCDEPILSNRSGDHRG
KFKVASFRKKYELGAPVAGTCYQAEWDDYVPKLYEQLSG
>d1qoua_b.17.1.1 (A:) Centroradialis protein Cen {Garden snapdragon (Antirrhinum majus)}
GRVIGDVVDHFTSTVKMSVIYNSNNSIKHVYNGHELPASVTSPRVEHGGMRSFTLIMTDPDVPGPSDP
YLREHLHWIVTDIPGTTDSSFGKEVSYEMPRPNIGHRFVFLFKQKKRGQAMLSPPVCRDGFNTRKFTQEN
ELGLPVAAVFFNCQRET
>d1fjja_b.17.1.2 (A:) Hypothetical protein YbhB {Escherichia coli}
AMKLISNDLRDGDKLPHRHVFNGMGYDGDNISPFLAWDDVPAGTKSFVTCYDPDAPTGSWWWHVVVN
LPADTRVLPQGFGSGLVAMPDGVLQTRTDFGKTGYDGAAPPKGETHYIFTVHALDIERIDVDEGASGAMVGF
NVHFHSLASASITAMFS
>d1fuxa_b.17.1.2 (A:) Hypothetical protein YbcL {Escherichia coli}
EFQVTSNEIKTGEQLTTSHVSGFGCEGGNTSPSLTWSGVPEGTKSFAVTYDPAUTGSGWWWHWTVVNIPAT
VTYLPVDAGRRDGTKLPTGAVQGRNDFGYAGFGGACPPKGDKPHHYQFKVWALKTEKIPVDSNSSGALVGYM
LNANKIATAEITPVYEIKLE
>d1g13a_b.95.1.1 (A:) Ganglioside M2 (gm2) activator {Human (Homo sapiens)}
SSFSWDNCDEGKDPAIRSLTEPDPIIVPGNVTLSVMGSTVPLSSPLKVDLVEKEAGLWIKIPCTDYIGSCTF
EHFCDVLDMLIPTGEPCPEPLRTYGLPCHCPFKEGTYSLPKSEFVVDLPSWLTGNYRIESVLSSGKRLGCIKI
AASLKGI
>d1i9ba_b.96.1.1 (A:) Acetylcholine binding protein (ACHBP) {Great pond snail (Lymnaea stagnalis)}
FDRADILYNIRQTSRPDVIPTQRDRPVAVSLSKFINILEVNEITNEVDVVFWQQTTWSRTLAWNNSHSPDQV
SVPISSLWVPDLAAYNAISKPEVLTPLARVVSDGEVLYMPSIRQRFSCDVSGVDTESGATCRIKIGSWTHHSREI
SVDPTTENSDDSEYFSQYSRFEILDVTQKKNSVTYSCCPEAYEDVEVSLNFRKKG
>d1k3ia2 b.18.1.1 (A:-12-150) Galactose oxidase, N-terminal domain {Fungi (Fusarium spp)}
IPEGSLQFLSLRASAPIGSAISRNNAWVTCDSAQSGNECNKAIDGNKDTFWHTFYGANGDPKPPHTYTIDMKT
TQNNGNLMLPRQDGQNQNGWIGRHEVYLSSDGTNWGPVAGSWFADSTTKYSNFETRPARYVRLVAITEA
NGQPWTSIAEINVFQASS
>d1eut_2 b.18.1.1 (506-647) Sialidase, C-terminal domain {Micromonospora viridifaciens}
QARMSIADVSEETAREDGRASNVIDGNPSTFWHTEWSRADAPGYPHRISLDLGGHTISGLQYTRRQNSAN
EQVADYEIYTSNGLTTWDGPVASGRFTTSLAPQRAVFPARDARYIRLVALSEQTGHKYAAVAELEVEGQR
>d1czsa_b.18.1.2 (A:) C2 domain of factor V {Human (Homo sapiens)}
GCSTPLGMENGKIENKQITASSFKKSWGDYWEPRFRARLNAQGRVNAWQAKANNNKQWLEIDLKIKKITAI
TQGCKSLSEMVKSYTIHYSEQGVEWKPYRLKSSMVDKIFEGNTNTKGHVKNFFNPPIISRFIRVIPKTWNQSI
TLRLELFGCDIY
>d1d7pm_b.18.1.2 (M:) C2 domain of factor VIII {Human (Homo sapiens)}
LNSCSMPLGMESKAISDAQITASSYFTNMIFATWSPSKARLHLQGRSNAWRPQVNNPKEWLQVDFQKTMKV
GVTTQGVKSLLTSMYVKEFLISSQDGHQWTLFFQNGKVKVFQGNQDSFTPVNCLDPLLTRYLRIHPQSWV
HQIALRMEVLGCEAQ
>d1jhja_b.18.1.9 (A:) APC10/DOC1 subunit of the anaphase-promoting complex {Human (Homo sapiens)}
ATPNKTPPGADPKQLERTGTREIGSQAVVSLSSCKPGFGVDQLRDDNLETYWQSDGSQPHLVNIQFRRKTT
VKTLCIYADYKSDESYTPSKISVRVGNNFHNLQEIRQLELVEPSGWIHVPLTDNHKKPTRTFMIQIAVLANHQNG
RDTHMRQIKIYTPV
>d1dlc_1 b.18.1.3 (500-644) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis}

tenebrionis, CRYIIIA (BT13)}

FFNMIDSKKITQLPLVKAYKLQSGASVVAGPRFTGGDIQCTENGSAATIYVTPDVSYSQKYRARIHYASTSQITFT
LSLDGAPFNQYYFDKTINKGDTLTYSNFSNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIPVN

>d1ji6a1 b.18.1.3 (A:503-652) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis, CRY3bb1}

FFNTIDAEEKITQLPVVKAYALSSGASIIEGPGFTGGNLLFLKESSNSIAKFVTLNSAALLQRYRVRIRYASTTNLRLF
VQNSNNDFLVYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPVQL

>d1ciy_1 b.18.1.3 (462-609) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis, CRYIA (A)}

NNIIPSSQITQIPLTKSTNLGSGTSVVKPGPGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRIRYASTTNLQFHTSI
DGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAHVFNSGNEVYIDRIEFVPAEV

>d1i5pa1 b.18.1.3 (A:473-633) delta-Endotoxin, C-terminal domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}

NIYAAANENGTMIHLAPEDYTGFTISPIHATQVNNQTRFISEKFGNQGDSLRFEQSNTARYTLRGNGNSYNLYL
RVSSIGNSTIRVTINGRVYTVSNVNTTNNDGVNDNGARFSDINIGNIVASDNTNVTL DINVTLNSGTPFDLMN
IMFPVPTNLPPLY

>d1nuka_b.18.1.4 (A:) Ligand-binding domain of the ephb2 receptor tyrosine kinase {Mouse (Mus musculus)}

EETLMDSTTATAELGWMVHPPSGWEEVSGYDENMINTIRTYQVCNVFESSQNNWLRTKIRRRGAHRIHVEM
KFSVRDCSSIPSVPGSCKETFNLYYEADFDLATKTFPNWMENPWVVKVDTIAADESFSQVDLGGRVMKINTEV
RSFGPVSRNFGYLAQDYGGCMSLIAVRVFYR

>d1jz8a3 b.18.1.5 (A:13-219) beta-Galactosidase {Escherichia coli}

RRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQQLRSLNGEWRFAWFPAPEAVPESWLECDLPEADT
VVVPSNWQMHGVDAPITYTNVTPITVNPPFVPTENPTGCYSLTFNVDESWLQEGQTRIIFDGVN SAFHLWCN
GRWVGYGQDSRLPSEFDLSAFLRAGENRLAVMVLWRWSDGSYLEDQDMWRMSGIFRDVSLLHKPT

>d1bhga2 b.18.1.5 (A:22-225) beta-Glucuronidase {Human (Homo sapiens)}

GLQGGMLYPQESPNSRECKELDGLWSFRADFSDNRGGFEEQWYRRLWESGPTVDMPPVSSFNDISQDWRL
RHFVGWWYEREVILPERWTQDLRTRVLRIGSAHSYAIWVNGVDTLEHEGGYLPFEADISNLVQVGPLPSR
LRITIAINNTLPTTLLPPGTIQYLTDTSKYPKGYFVQNTYFDFNYAGLQRSVLLYTTPT

>d1cx1a_b.18.1.6 (A:) Cellulose-binding domain {Cellulomonas fimi}

ASLDSEVELLPHTSFAESLGPWSLYGTSEPVFADGRMCVDPGGQGNPWDAGLVNGVPVGEGESYVLSFTAS
ATPDMPVRVLVGEPPPRTAFEQGSAPLTGEPATREYAFTSNLTFPPDGADPGQVAFHGKAGAYEFCISQVSL
TTSAT

>d1ulo_b.18.1.6 (-) Cellulose-binding domain {Cellulomonas fimi}

ASPIGEGETFDDGPEGWVAYGTDGPLDTSTGALCVAVPAGSAQYGVVNLNGVAIEEGTTYTLRYTATASTDVTV
RALVGQNGAPYGTVLDTSPALTSEPRQVTETFTASATYPATPAADDPEGQIAFQLGGFSADA WLCLDDVALDSE
VEL

>d1gmma_b.18.1.10 (A:) Carbohydrate binding module from xylanase U {Clostridium thermocellum}

FSKIEEEYNSLKSSTIQTIGTSDGGSGIGYIESGDYLVFNKINFNGANGANSFKARVASGADPTPTNIQLRLGSPTGTLI
GTLTVASTGGWNYYEKSCSITNTTGQHDLYLVSGPVNIDYFIFDSN

>d1gnya_b.18.1.11 (A:) Xylan-binding module from xylanase 10c {Pseudomonas cellulosa}

GNVIEVDMANGWRGNASGSTSHSGITYSADGVTFAALGDGVGAVIDARPTTLEDAVIAMVVNVSAEFKAS
EANLQIFAQLKEDWSKGEWDCLAGSSELTADTDLTCTIDEDEDDKFNQTARDVQVGIQAKGTPAGTITIKSVTIT

LAQEA

>d1j83a_ b.18.1.12 (A:) Endo-1,4-beta glucanase EngF {Clostridium cellulovorans}
QPTAPKDFSSGFWDNDGTTQGFGVNPDSPIAINVENANNALKISNLNSKGSNDLSEGNFWANVRISADIW
GQSINIYGDTKLTMDVIAPTPVNVSIAAIPQSSTHGWNPTRAIRVWTNNFVAQTDGTYKATLTISTNDSPNFN
TIATDAADSVVTNMILFGSNSDNISLDNIKFTK
>d1dyoa_ b.18.1.7 (A:) Xylan-binding domain {Clostridium thermocellum}
PDAGYYYHDTFEGSVGQWTARGPAEVLLSGRTAYKGSESLLVRNRTAAWNGAQRALNPRTFVPGNTYCFVVA
SFIEGASSTTFCMQLQYVDGSGTQRYDTIDMKTVGPNQWVHLYNPQYRIPSDATDMYVYVETADDTINFYIDE
AIGAVAGTVI
>d1xnaa_ b.18.1.8 (A:) N-terminal domain of xrcc1 {Human (Homo sapiens)}
MPEIRLRHVSCSSQDSTHCAENLLKADTYRKWRAAKAGEKTISSVLQLEKEEQIHSVDIGNDGSAFVEVLGS
SAGGAGEQDYEVLLVTSSFMSPSESRSGSNPNRVRMFGPDKLVRAAAEEKRWDRVKIVCSQPYSKDSPFGLSFV
RFHS
>d1ju3a1 b.18.1.13 (A:352-574) Bacterial cocaine esterase C-terminal domain {Rhodococcus sp.
mb1}
PLPDTAYTPFYLGSGAANTSTGGTLSTSISGTESADTYLYDPADPVPSLGGTLLFHNGDNGPADQRPIHDRDD
VLCYSTEVLTDPEVTGTVSARLFVSSSAVTDFTAQLVDVFPDGRAIALCDGIVRMRYRETLVNPTLIEAGEIYEV
AIDMLATSNVFLPGHRIMVQVSSNFPKYDRNSNTGGVIAREQLEEMCTAVNRIHRGPEHPSHIVLPIIKR
>d1bvp12 b.19.1.1 (1:121-254) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain
{Bluetongue virus}
PARQPYGFFLETEETFQPGRWFMRQAQAVTAVVCGPDMIQVSLNAGARGDVQQIFQGRNDPMIYLVWRR
IENFAMAQGNSQQTQAGVTVSVGGVDMRAGRIIAWDGQAALHVHNPTQQNAMVQIQVVFYISMD
>d1ahsa_ b.19.1.1 (A:) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {African horse
sickness virus}
TGPYAGAVEVQSQSGRYYVPQGRTRGGYINSNIAEVCMDAGAAGQVNALLAPRRGDAVMIYFVWRPLRIFCDP
QGASLESAPGTFVTDGVNVAAGDVAWNTIAPVNPGARRSILQFEVLWYT
>d1qhda2 b.19.1.1 (A:149-332) vp6, the major capsid protein of group A rotavirus {Bovine rotavirus}
GFTFHKNIFPYSASFTLNRSQPAHDNLMTMWLNAGSEIQVAGFDYSCAINAPANTQQFEHIVQLRRVLTTAT
ITLLPDAERFSFPRVITSADGATTWYFNPVILRPNNVEIEFLNGQIINTYQARFGTIIARNFDTIRLSFQLMRPPN
MTPAVAALFPNAQPFEEHATVGLTLRIESAVCE
>d1jsda_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
DKICIGYQSTNSTETVDTLTETNVPVTHAKELLHTSHNGMLCATNLGHPLIILDCTIEGLIYGNPSCDLLGGREW
SYIVERPSAVNGMCYPGNVENLEELRLFSSASSYQRIQIFPDTIWNVSYSGTSSACSDSFYRSMRWLTQKNAY
PIQDAQYTNNRGKSILFMWGINHPPTDTVQTNLYTRDTTSVTTEDINRTFKPVIGPRPLVNGLHGRIDYYWS
VLKPGQTLRVRSGNLIAPWYGHILSGESHGRILKTDLNSGNCVVCQCTERGLNTLPFHNVSKYAFGNCPKY
VGVKSLKLAVGLRNVPAR
>d1jsma_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}
DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDNGVKPLILRDCSAGWLLGNPMCDEFNV
PEWSYIVEKDNPVNGLCYPENFNDYEELKHLLSSTNHFEKIRIIPRSSWSNHASSGVSSACPYNGRSSFRNVV
WLIKKNNAZPTIKRSYNNTNQEDLLLWGIHHPNDAEAEQTKLYQNPTTYVSGTSTLNQRSVPEIATPKVNGQ
SGRMEFFWTILKPNDAINFESNGNFIAPEYAYKIVKKGGSAIMKSGLEYGNCNTKCQTPMGAINSSMPFHNIHP
LTIGECPKYVKSGRLVATGLRNVP
>d2visc_ b.19.1.2 (C:) Hemagglutinin {Influenza A virus, different strains}
VQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTL

EFITEGFTWTGVIQNGGSNACKRGPGSGFFSRLNWLTKGSTYPVLNVTPNNDNFKLYIWGIHHPSTNQE
QTSLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGLSSRISIYWTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSI
MRSDAPIIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYV

>d2viua_b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}

STATLCGHAVPNGTLVKITDDQIEVTNATELVQSSSTGKICNNPHRILDGIDCTLIDALLGDPHCDVFQNETW
DLFVERSKAFSNCYPDVDPYASLRSLVASSGTLEFITEGFTWTGVIQNGGSNACKRGPGSGFFSRLNWLTSGS
TYPVLNVTPNNDNFKLYIWGIHHPSTNQEQTSLYVQASGRVTVSTRRSQQTIIPNIGSRPWVRGLSSRISIY
WTIVKPGDVLVINSNGNLIAPRGYFKMRTGKSSIMRSDAPIIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYV
KQNTLKLATGMRVNPEKQT

>d1flca1 b.19.1.3 (A:151-306) Hemagglutinin domain of
haemagglutinin-esterase-fusion glycoprotein HEF1 {Influenza C virus}
CMSLVNALDKTIPLQVTAGTAGNCNNFLKNPACYTQEVKPSENKGKENLAFFTLPTQFGTYECKLHLVASCYFI
YDSKEVYNKRGCDNYFQVIYDSFGKVVGGLDNRVSPYTGNSGDPTMQCDMLQLKPGRYSVRSSPRFLLMPE
RSYCFDMK

>d1ao1_b.20.1.1 (-) F-MuLV receptor-binding domain {Friend murine leukemia virus}
QVYNITWEVTNGDRETVWAISGNHPLWTWWPVLPDLCMLALSGPPHWGLEYQAPYSSPPGPPCCSGSSGS
SAGCSRDCDEPLTSLTPRCNTAWNRLKLDQVTHKSSEGFYVCPGSHRPREAKSCGGPDASFYCASWGCETTGRV
YWKPSSWDYITVDNNLTTSQAVQVCKDNKWCNPLAIQFTNAGKQVTSWTGHYWGLRLYVSGRDPLTFGI
RLRYQNLGPRVP

>d1knb_b.21.1.1 (-) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 5}

NDKLTLWTPAPSPNCRLNAEKDAKTLVLTKCGSQLATVSVLAVKGSLAPISGTVQSAHLIIRFDENGVLLNNSF
LDPEYWNFRNGDLTEGTAYTNAVGFMPNLSAYPKSHGKTAKSNIQSQVYLNGDKTPVTLITLNGTQETGDTT
PSAYSMSFSWDWSGHNYINEIFATSSYTFSYIAQE

>d1qhva_b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 2}

AITIGNKNDDKLTLWTPDPSPNCRIHSNDCKFTLVLTKCGSQLATVAALAVSGDLSSMTGTVASVISFLRFDQ
NGVLMENSSLKKHYWNFRNGNSTANPYTNAVGFMPLNLLAYPKTQSQTAKNNIVSQVYLHGDKTPMILIT
LNGTSESETSEVSTYSMSFTWSWESGKYTTETFATNSYTFSYIAQE

>d1h7za_b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 3}

KNNTLWTGPKEANCIIEYGKQNPDSKLTLLVKNGGIVNGYVTLMGASDYVNTLFKNKNVSINVELYFDATGHI
LPDSSLKTDLELKQKTADFSARGFMPSTTAYPFVLPNAGTHNENYIFGQCYYKASDGALFPLETVMLNKRLP
DSRTSYVMTFLWSLNAGLAPETTQATLITSPFTFSYIREDD

>d1kaca_b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 12}

TPYDPLTWTPDPNNCSLIQELDAKTLCLTKNGSIVNGIVSLGVVKGNLLNIQSTTTVGVLVDEQGRLITS
TPTALVPQASWGYRQGQSVSTNTVTNGLGFMPNVSAYPRPNASEAKSQMVSLTYLQGDTSKPITMKVAFNGI
TSLNGYSLTFMWSGLSNYINQPFSTPSCFSYITQE

>d1kke1_b.21.1.2 (A:250-312) Reovirus attachment protein sigma 1 {Reovirus}

EQSYVASAVTPLRLNSSTKVLDMLIDSSTLEINSSGQLTVRSTSPNLRYPIADVSGGIGMSPN

>d1aly_b.22.1.1 (-) Extracellular domain of CD40 ligand {Human (Homo sapiens)}

GDQNPQIAAHVISEASSKTTSVLQWAEGYYTMSNNLVTLENGKQLTVKRQGLYYIYAQVTFCNSREASSQAPFI
ASLCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFELQPGASVFNVTDPSSQVSHGTGFTSFGLKL

>d1c28a_b.22.1.1 (A:) 30 kd adipocyte complement-related protein {Mouse (Mus musculus)}
MYRSAFSVGLETRTVNPVPIRFTKIFYNQQNHYDGSTGKFYCNIPGLYYFSYHITVYMKDVKVSLFKDKAVLFT
YDQYQEKNVDQASGSVLLHLEVGDQVW/LQVYGDGDHNGLYADNVNDSTFTGFLLYHDT
>d1tnra_b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}
KPAAHЛИGDP SKQNSLLWRANTDRAFLQDGFSLSNSLLVPTSGIYFVYSQVFSGKAYSPKATSSPLYLAHEVQL
FSSQYPFHVP LLSSQKMVYPGLQEPWLHS MYHGAAFQLTQGDQLSTHTDGIPH LVLS P STVFFGAFAL
>d4tsva_b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}
DKPVAHV VANPQAEGQLQWSNRRANALLANGVELRD NQLV VPIEGLFL IYSQVL FK GQGCPSTH VLLT HISRI
AVSYQT KVNLLSAIKSPC QRETPEGAEAKPW YEPI YLGGV FQ LEKG DRLS A EINRP DYLDFA ESGQ VYFGII AL
>d2tnfa_b.22.1.1 (A:) Tumor necrosis factor (TNF) {Mouse (Mus musculus)}
SDKPVAHV VANHQVEEQLEWLSQRAN ALLANGMDLKDNQLV VPAD GLYLV S QVLF KGQGCPD YVLLT HTVS
RFAISYQE KVNL LSAV KSPCPKD TPEGAEAKP WYEPI YLGGV FQ LEKG DQLS AEVNLP KYLDFA ESGQ VYFGVIAL
>d1dg6a_b.22.1.1 (A:) Apoptosis-2 ligand, apo2l/TRAIL {Human (Homo sapiens)}
QRVA AHITGTRGRSNTLSSPN SKNE KALGRK IN SWESSR SGH FSNL HLRN GELVI HEKG FYYI YSQTYFRFQEEI
KENTKNDKQMVQYIYKYTSYPAPILL MKSARN SCSW KSDAEY GLYI YQGGI FELK END RIFV SVTNEH LIDMDHE
ASFFGAFLVG
>d1jtzx_b.22.1.1 (X:) TRANCE/RANKL cytokine {Mouse (Mus musculus)}
QPFAHL TINA ASI PGS SHKV TLSSWYHD RGWAK ISN MTL SNGK LRVN QDG FYY LYANIC FRH HETGS VPTDYL
QLM VYV VKTS IKS PSSH NLM KGG STKN WSGN SE FH YSIN VGG FFKL RAGE E EISI QVS NPS LLD PDQ DATY FGAF
KVQ DID
>d1jh5a_b.22.1.1 (A:) Soluble part of TALL-1, sTALL-1 {Human (Homo sapiens)}
VTQDCLQLI ADSETPTI QKG SYTF VPWLL SFKRG SALE EKEN KILV KETGY FFYI GQVLY TDKT YAM GH LI QR KK VH
VFG DELS LVT L FRCI QNMP ETLP NNCS Y SAGIA KLEEG DEL QL AIPRE NAQ I SLD GDV TFFG AL KLL
>d1gr3a_b.22.1.1 (A:) Collagen X NC1 trimerisation domain {Human (Homo sapiens)}
MPVSAFTVILSKAYPAIGTPIPFDK ILYNRQQHYD PRTGIFT CQIPGI YYFSYHV HVKG THV VV GLYK NGTP VMYT
YDE YT KG YLDQ ASGS AII DL TEND QV W LQLPNA E NSNGL YSE YV HSS FSG FLV AP M
>d1sfp__b.23.1.1 (-) Acidic seminal fluid protein (ASFP) {Cow (Bos taurus)}
LPRNTNCGGILKEESGVIA TYGP KTCV WTLQVDPK YKLL SIPL NLTCGKEY VEVLEGAPGSKSLG KFC EGLS IL
MDYRSS GSIM TVKY I REPEH PASFY EVLY FQDP QA
>d1sppa_b.23.1.1 (A:) Major seminal plasma glycoprotein PSP-I {Pig (Sus scrofa)}
LDYHACGGRLTDYGTIFTYKGPKTECVWTLQVDPK YKLL SIPL NLTCGKEY VEVLEGAPGSKSLG KFC EGLS IL
NRGSSG MVT KYKR DSGH P ASPY EIIFL RD SQG
>d1sppb_b.23.1.1 (B:) Major seminal plasma glycoprotein PSP-II {Pig (Sus scrofa)}
ARINGPDEC GRV I KDT SG SIS NTDRQ KNL CTWT LMKPDQ KV RMAI PYLN LACG KEY VEVFDG LLSG PSY GKL C
AGAAIVFL STANTMTI KYNRIS GNSSPFLI YFYGSSP
>d1cb8a2_b.24.1.1 (A:600-700) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}
PKVLANTNQLQAVYHQQLDMVQAIFYTAGKLSVAGIEIETDKPCAVLIKHINGKQVIWAADPLQKEKTA VLSIRD
LKTGKTN RVKIDFPQQEFAGATVELK
>d1egua2_b.24.1.1 (A:815-893) Hyaluronate lyase {Streptococcus pneumoniae}
SSLIENNETLQSVYDAKQGVWGIVKYDDSVSTISNQFQVLKRGVY TIRKEGDEYKIA YYN PETQESAPDQE VFKK
LEQH
>d1f1sa3_b.24.1.1 (A:920-984) Hyaluronate lyase {Streptococcus agalactiae}
SKQQVIYDKNSQTWAVIKHDNQESL INNQFK MNKAGLYLVQKV GNDYQNVYYQP QTMTKDQ LAI

>d1iaza_b.97.1.1 (A:) Equinatoxin II (eqtII, tenebosrin C) {European sea anemone (Actinia equina)}

AGAVIDGASLSFDILKTVLEALGNVKRKIAVGVDNESGKTWTALNTYFRSGTSDIVLPHKVPHGKALLYNGQKDR

GPVATGAVGVLAYLMSDGNTLAVLFSPYDYNWYSNWWNVRIYKGKRRADQRMYEELYNLSPFRGDNGW

HTRNLGYGLKSRGFMNSSGHAILIEHVSKA

>d1aun_b.25.1.1 (-) Pathogenesis-related protein 5d {Common tobacco (Nicotiana tabacum)}

SGVFEVHNCPYTVWAAATPVGGGRRLERGQSWWFWAPPGTMARIWGRTNCNFDGAGRGCQTCGDC

GGVLECKGKGPKPPNTLAEYALNQFSNLDFWDISVIDGFNIPMSFGPTKPGPKCHGIQCTANINGECPGSLRV

PGGCNNPCTTFGGQQYCCTQGPGCPTELSRWFQRCPDAYSYPQDDPTSTFTCTS威TTDYKVMFCPYG

>d1du5a_b.25.1.1 (A:) Zeatin {Maize (Zea mays)}

AVFTVVNQCPFTVWAASVPVGGGRQLNRGESWRITAPAGTTAARIWARTGCKFDASGRGSCRTGDCGGVLQ

CTGYGRAPNTLAEYALKQFNNDFFDISLIDGFNVPMSFLPDGGSGCSRGPRCAVDVNARCPAELRQDGVCNN

ACPVFKDEYCCVGSANDCHPTNSRYFKGQCPDAYSYPKDDATSTFTCPAGTNKYKVVF

>d1thw_b.25.1.1 (-) Thaumatin {Ketemfe (Thaumatococcus daniellii)}

ATFEIVNRCSTVWAAASKGDAALDAGGRQLNNGESWTINVEPGTKGGKIWARTDCYFDDSGSGICKTGDCG

GLLRCKRKGPRPTTAEFSLNQYQKDYIDISNIKGFNVPMDSFPTTRGCRGVRAADIVGQCPAKLAPGGC

DACTVFQTSEYCCTGKGCGTEYSRFFKRLCPDAFSYVLDKPTTVTCPGSSNYRVTFCPTA

>d1dd1a_b.26.1.1 (A:) Smad4 tumor suppressor C-terminal domain {Human (Homo sapiens)}

NGHLQHHPPMPPHPGHYWPVHNELAFQPPISNHPAPEYWCSIAYFEMDVQVGETFKVPSSCPIVTVDGYV

PSGGDRFCLGQLSNVRTEAIERARLHIGKGVQLECKGEGDVWVRCLSDHAVFVQSYYLDREAGRAPGDAVH

KIYPSAYIKVFDLRQCHRQMQQQAATAQAAAAAQAAVAGNIPGPGSVGGIAPAISLAAAGIGVDDLRLCIL

RMSFVKKGWGPDYPRQSIKETPCWIEIHLHRALQLLDEVLHTMPI

>d1ygs_b.26.1.1 (-) Smad4 tumor suppressor C-terminal domain {Human (Homo sapiens)}

APEYWCSIAYFEMDVQVGETFKVPSSCPIVTVDGYVDPGGDRFCLGQLSNVRTEAIERARLHIGKGVQLECK

GEGDVWVRCLSDHAVFVQSYYLDREAGRAPGDAVHKIYPSAYIKVFDLRQCHRQMQQQAATAQAAAAAQAA

AAVAGNIPGPGSVGGIAPAISLAAAGIGVDDLRLCILRMSFVKKGWGPDYPRQSIKETPCWIEIHLHRALQLLD

EVLHTM

>d1khxa_b.26.1.1 (A:) Smad2 MH2 domain {Human (Homo sapiens)}

PTYSEPAFWCSIAYYELNQRVGETFHASQSLTVDGFTDPSNNRFCLGLLSNVNRNATVEMTRRHIGRGRVLY

YIGGEVFAECLSDSAIFVQSPNCNQRYGWHPATVCKIPPGCNLKIFNNQEFAALLAQSVNQGFEAVYQLTRMCT

IRMSFVKKGWGAEYRRQTVTSTPCWIELHLNGPLQWLKDVKLTQMGSPSVRCSSMS

>d1khua_b.26.1.1 (A:) Smad1 {Human (Homo sapiens)}

PKHWCSIVYYELNNRVGEAFHASSTSVLDGFTDPSNNKNRFCLGLLSNVNRNSTENRRHIGKGVHLYVGG

EVYAECLSDSSIFVQSRNCNYHHGFHPTTVCKIPSGCSLKIFNNQEFAQLLAQSVNHGFETVYELTKMCTIRMSF

VKGWGAEYHRQDTSTPCWIEIHLGPLQWLKDVKLTQMGSPPHNPSSVS

>d1dmza_b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

GNGRFLTLPDSIIQESLEIQQGVNPFFIGRSEDCNCKIEDNRLSRVHCFIFKKRHAVGKSMYESPAQGLDDIW

YCHGTGTVSYLNNNRMIQGTTKFLQDGDEIKIIWDKNNKFVIGFKVEINDTGLFNEGLMLQEQRVVLKQTAEEKDLVKKL

>d1g6ga_b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}

GENIVCRVICTTGQIPIRDLISADISQVLKEKRSIKVWTGRNPACDYHLGNISRLSNKFQILLGEDGNLLNDIS

TNGTWLNGQKVEKNSNQLSQGDEITVGVGVESDILSIVFINDKFKQCL

>d1k3ja_b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast}

(*Saccharomyces cerevisiae*)}

ATQRFLIEKFSQEIQIGENIVCRVICTTGQIPIRDLSDLISQLKEKRSIKKVWTFGRNPACDYHLGNISRLSNKHFQI
LLGEDGNLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVGVGVESDILSVIFINDFKQCLEQNKVDRIR
>d1qu5a_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (*Saccharomyces cerevisiae*)}

EAETREQKLLHSNNNTENVKSSKKKGNGRFLTLKPLPDSIIQESLEIQQGVNPFFIGRSEDCNCIEDNRSLRVHCFI
FKKRHAVGKSMYESPAQGLDDIWYCHTGTNVSYLNNNRMIQGTKFLLQDGDEIKIIWDKNNKFVIGFKVEIND
TTGLFNEGLGMLQEQRVVLQTAEEKDLVKKL

>d1cq3a_ b.27.1.1 (A:) Soluble secreted chemokine inhibitor, VCCI {Cowpox virus}

SFSSSSCTEEENKHHMGIDVIKVTQKDQPTNDKICQSVTEVTESEDESEEVKGDPPTYTVGGGLTMDFG
FTKCPKISSISEYSDGNTVNARLSSVSPGQGKDSPAIRREEALSMIKDCEMSINIKCSEEKDSNIKTHPVLGSNISH
KKVSYEDIIGSTIVDTKCVKNLEISVRIGDMCKESSELEVKGDFKYYVDGSASEDAADDTSLINSAKLIACV

>d1p35a_ b.28.1.1 (A:) Paculovirus p35 {Nuclear polyhedrosis virus (*Autographa californica*), ACMNPV}

CVIFPVEDVSQTIIRDQCVDKQTRELVYINKIMNTQLTPVLMMFNISGPIRSVTRKNNNLDRRIKSVDQFDQ
LERDYSMDQMDGFHDSIKYFKDEHYSVSCQNGSVLKSFKAKILKSHDYTDKKSIEAYEKYCLPKLVDERNDYYVAVC
VLKPGFENGNSNQVLSFEYNPIGNKVIVPFAHEINDTGLYEYDVVAYVDSVQFDGEQFEFVQSLILPSSFKNSEKV
LYYNEASKNSMIYKALEFTTESSWGKSEKYNWKIFCNGFIYDKKSKVLYVKLHNVTSALNKNVILNTIKA

>d1nls_ b.29.1.1 (-) Concanavalin A {Jack bean (*Canavalia ensiformis*)}
ADTIVAVELDTYPNTDIGPSYPHIGIDIKSRSKKTAKWMQNGKVGTAIIYNSVDKRLSAVVSPNADSATV

SYDVLDNVLPFWRVGLSASTGLYKETNTILSWSFTSKLKSNSTHETNALHFMFNQFSKDQKDLILQGDATTG
TDGNLELTRVSSNGSPQGSSVGRALFYAPVHIWESSAVVASFEATFTFLIKSPDSHPADGIAFFISNIDSSIPSGSTG
RLLGLFPDAN

>d2cna_ b.29.1.1 (-) Concanavalin A {Jack bean (*Canavalia ensiformis*)}
ADTIVAVELDTYPNTDIGPSYPHIGIDIKSRSKKTAKWMQNGKVGTAIIYNSVDKRLSAVVSPNADSATV

SYDVLDNVLPFWRVGLSASTGLYKETNTILSWSFTSKLKSNSTHETNALHFMFNQFSKDQKDLILQGDATTG
TDGNLELTRVSSNGSPQGSSVGRALFYAPVHIWESSATVSAFEATFAFLIKSPDSHPADGIAFFISNIDSSIPSGSTG
RLLGLFPDAN

>g2ltn.1 b.29.1.1 (A;B:) Legume lectin {Garden pea (*Pisum sativum*)}

TETTSFLITKFSPDQQNLIFQGDGYTTKEKLTAKVNTVGRALYSSPIHIWDRGNVANFVTSFTVINAPNSY
NVADGFTFFIAPVDTKPQTGGGYLGVFNSAEYDKTTQTVAVEFDTFYNAAWDPSNRDRHIGIDVNSIKSVNTKS
WKLQNGEANVVIAFNAATNVLTSLTPNXVTSYTLSDVVSLKDVVPEWVRIGFSATTGAEYAAHEVLSWSFH
SELSG

>g1len.1 b.29.1.1 (A;B:) Legume lectin {Common lentil (*Lens culinaris*)}
TETTSFSITKFSPDQQNLIFQGDGYTTKGKLTAKVNTVGRALYSTPIHIWDRGNVANFVTSFTVIDAPSSY

NVADGFTFFIAPVDTKPQTGGGYLGVFNSKEYDKTSQTVAVEFDTFYNAAWDPSNKERHIGIDVNSIKSVNTKS
WNLQNGERANVVIAFNAATNVLTSLTPNXVTSYTLNEVVPLKDVVPEWVRIGFSATTGAEFAAQEVHSWSF
NSQLG

>d1led_ b.29.1.1 (-) Legume lectin {West-central african legume (*Griffonia simplicifolia*)}
ENTVNFTYPDFWSYSLKNGTEITFLGDATRIPGALQLTKTDANGNPVRSSAGQASYSEPVFLWDSTGKAASFYTS

FTFLLNKGAPTADGLAFFAPVDSSVKDYGGFLGLFRHETAADPSKNQVVAVEFDTWINKDWNDPPYPHIGID
VNSIVSVATRWENDDAYGSSIATAHITYDARSKILTVLLEYHGRDYILSHVVDLAKVLPQKVIGFSAGVGYDEV
TYILSWHFFSTLDGTNK

>d1hqla_ b.29.1.1 (A:) Legume lectin {*Griffonia simplicifolia*, lectin I-b4}

SVSFTFPNFWSDVEDSIIFQGDANTTAGTLQLCKTNQYGTPLQWSAGRALSMDPVQLWDNKTESVASFYTEFTF
FLKITGNGPADGLAFFLAPPDSVDKAGEYLGLFNKSTATQPSKNQVVAVEFDWTNPNTPEPSYRHIGINVNSI
VSVATKRWEDSDIFSGKIATARISYDGSAEILTVVLSYPDGSYILSHSVDMRQNLPESRVGISASTGNQNQFLTVY
ILSWRFSSNL

>d1ax0_ b.29.1.1 (-) Legume lectin {Coral tree (Erythrina corallodendron)}
VETISFSFSEFEPGNDNLTLQGAALITQSGVLQLTKINQNGMPAWDSTGRPLYAKPVHIWDMTTGTASFETRF
SFSIEQPYTRPLPADGLVFFMGPDKPAQGYGYLGIFNNSKQDNSYQTLGVFDTFSNPWDPPQVPHIGIDVN
SIRSIKTQPFQLDNGQVANVVIKYDASSKILHAVLVYPSSGAIYTAIEIVDVVKQLPEWVDVGLSGATGAQRDAAE
THDVYSWSFQASLP

>d1wbfa_ b.29.1.1 (A:) Legume lectin {Winged bean (Psophocarpus tetragonolobus), basic agglutinin}
KTISFNFNQFHQNEEQLKLQRDARISSNSVLELTKVVNGVPTWNSTGRALYAKPVQVV/DSTTGNVASFETRF
SIRQPFPFRPHPADGLVFFIAPPNTQTGEGGGYFGIYNPLSPYPFVAVEFDTFRNTWDPQVPHIGIDVNSVISTK
PFTLDNGGIANVVIKYDASTKILHVVLVFPSSLTIYTIAIDVDLKQVLPEVNFGSAATGDPGKQRNATEHDIL
SWSFSASLPG

>d1f9ka_ b.29.1.1 (A:) Legume lectin {Winged bean (Psophocarpus tetragonolobus), acidic lectin}
ETQSFNFDHFEEINSKELNLQRQASIKSNGVLELTKLTKNGVPVW/KSTGRALYAEPIKIWDSTTGNVASFETRF
NITQPYAYPEPADGLTFFMVPPNSPQGEDGGNLGVFKPPEGDNAFAVEFDTFQNTWDPQVPHIGIDVNSIVSS
KTLHFQLENGGVANVVIKYDSPTKILNVVLAFLHSVGTVTLSNIVDLKQEFPNSEWVNVLGSLATTGYQKNAVET
HEIISWSFTSSL

>g1loe.1 b.29.1.1 (A:,B:) Legume lectin {Lathyrus ochrus, isolectin I}
TETTSFSITKFGPDQQNLIFQGDGYTTKERLTLTKAVRNTVGRALYSSPIHIWDSKTGNVANFVTSFTVIDAPNS
YNVADGFTFIAPVDTKPQTGGGYLGVFNSKDYDKTSQTVAVEFDTFYNTAWDPSNGDRHIGIDVNSIKSINTK
SWALQNGKEANVVIAFNAATNVLTVSLTPXTSYTLNEVVLKEFVPEWVRIGFSATTGAFAAHEVLSWYFHSE
LA

>d2pela_ b.29.1.1 (A:) Legume lectin {Peanut (Arachis hypogaea)}
AETVSFNFSFSEGNPAINFQGDVTVLNGNIQLTNLNKVNNSVGRVLYAMPVRIWSSATGNVASFLTSFSFEMK
DIKYDPADGIIFIAPEDTQIPAGSIGGGTLGVSDTKGAGHFGVFEFDTYSNSEYNDPPTDHVGIDVNSVDSVK
TVPWNSVSGAVVKVTVIYDSSTKTLSAVTNDNGDITTAQVVDLKAKLPERVKFGSASGSLGGRQIHLIRSWS
FTSTLITT

>d1g9fa_ b.29.1.1 (A:) Legume lectin {Soybean (Glycine max)}
AETVSFSWNKFVPKQPNMILQGDAIVTSSGKLQLNKVDENGTPKSSLGRALYSTPIHIWDKETGSVASFAASF
NFTFYAPDTKRLADGLAFFLAPIDTKPQTHAGYLGFLNENESGDQVVAVEFDTFRNSWDPPNPHIGINVNSIRSI
KTTSWDLANNKAVKLITYDASTSLLVSYVPSQRTSNILSDVVDLKTSLPEWVRIGFSATGLDIPGESHDVLS
WSFASNLPHASSNIDPLDLTSFVLHE

>g1qmo.1 b.29.1.1 (A:,E:) Legume lectin {Field bean (Dolichos lab lab), Fril}
AQSLSFSTKFDPNQEDLIFQGHATSTNNVLQVTKLDAGNPVSSAGRVLYSAPRLWEDSAVLTSFTIINFEIS
TPYTSRIADGLAFFIAPPDSVISYHGGFLGLFPNANXSNNVAVEFDTYLNPDYGDPMYIHIGIDVNSIRSKVTAKW
DWQNGKIATAHISYNSVSKRLSVTSYYAGSKPATLSYDIELHTVLPEWVRVGLSASTGQDKERNTVHSWSFTSSL
WTN

>d1g7ya_ b.29.1.1 (A:) Legume lectin {Horse gram (Dolichos biflorus), different isoforms}
ADIQSFNFNNSSSFILQGDATVSSSKLRLTKVKGNGLPTLSSLGRAFYSSPIQIYDKSTGAVASWATSFANIFAP
NKSSSADGIAFALVPVGSEPKNSGFLGVFDSDVYDNAQTVAVEFDTFSNTWDPTSRHIGIDVNSIKSIRTAS
WGLANGQNAEILITYNAATSLVAVSLVHPSSRTSYIVSERVDITNELPEYVSIGFSATTGLSEGYTETHDVLWSFA

SKLPDDSTTEPLDIASYLVRNVL

>d1lu1_ b.29.1.1 (-) Legume lectin {Horse gram (*Dolichos biflorus*), different isoforms}

ANIQSFSFKNFNSPSFILQGDATVSSGKLQLTKVKENGIPTPSSLGRAFYSSPIQIYDKSTGAVASWATSVKISAP SKASFADGIAFALPVGSEPRRNGGYLGVDSDVYNNSAQTVAVEFDTLSNSGWPSMKHIGIDVNSIKSIATVS WDLANGENAEILITYNAATSLLVASLVHPSRTSYILSERVDITNELPEYVGFSATTGLSEGYIETHDVLWSFAS KLPDDSTAEPPLDLASYLVRNVL

>d1h9wa_ b.29.1.1 (A:) Legume lectin {Duke (*Dioclea guianensis*)}

ADTIVAVELDSPNTDIGDSPYPHIGIDIKSIRSKSTARWNMQTGKVTGHISYNSVAKRLSAVVSYTGSSTTVSY DVDLNNVLPEWVRVGLSATTGLYKETNTILSWSFTSKLKNTSIADANSLHFSFNQFSQNPKDLILQGDATTDSDG NLELTKVSSSGDPQGSSVGRALFYAPVHIWEKSAVVASFDATFTFLIKSPDRDPADGITFFIANTDTSIPSGGGRL LGLFPDAN

>d1fx5a_ b.29.1.1 (A:) Legume lectin {Furze (*Ulex europaeus*), UEA-I}

SDDLSFKFKNFNSQNGKDLSFQGNASVIETGVQLQNKVGNNLPDETGGIARYIAPIHIWCNTGELASFITSFSFF METSANPKAATDGLTFLAPPDSPLRRAGGYFGLFNDTKCDSSYQTVAVEFDTIGSPVNFWDPGFPHIGIDVNC VKSINAERWNKRYGLNNVANVEIIYEASSKTLTASLTYPSDQTSISVTSIVDLKEILPEWVSGFSGSTYGRQATHE VLNWYFTSTFINT

>d1qnwa_ b.29.1.1 (A:) Legume lectin {Furze (*Ulex europaeus*), UEA-II}

SDDLSFNFDKFVPNPKNIIFQGDASVTTGVLQVTKSKPTTSIGRALYAAPIQIWDSITGKVASFATSFSFVKA DKSDGVGVLGAAFLAPANSQIPSGSSAGMFLFSSSDSKSSNQIIAVEFDTYFGKAYNPWDPDFKHIGIDVNSIKI KTVKWDWRNGEADVITYRAPTKSLTVCLSYPSDGTSNIITASVDLKAILPEWVSGFSGGVGNAAEFETHDV LSWYFTSNLE

>d1dbna_ b.29.1.1 (A:) Legume lectin {Maackia amurensis, leukoagglutinin}

SDELSFTINNFVPNEADLLFQGEASVSTTGVQLQTKVENGQPQKYSVGRALYAAPVRIWGNTTGSASFSTSFTF VVKAPNPDTISDGLAFYLAPPDSQIPSGSVSKYGLFNNNSNSDSSNNQIVAVEFDTYFAHSYDPWDPNRYRHIGIDV NGIESIKTVQWDWINGGVAFATITYLAPNKTIALVYPSNQTTFSVAASVDLKEILPEWVVGFSATGYPTEVE THDVLWSFTSTL

>d1fnya_ b.29.1.1 (A:) Legume lectin {Black locust (*Robinia pseudoacacia*)}

TGSLSFSPKFAPNQPYLINQGDAVTSTGVLQLTNVNVNGPSSKSLGRALYAAPFQIWDTGNTGVASFSTSFTFII QAPNPATTADGLAFLAPVDTQPLDLGGMLGIFKDGYFNKSQIVAVEFTFSNGDWDPKGRHLGINVNSIESI KTPWNWTNGEVANVFISYEASTKSLTASLVYPSLETSFIIDAIVDVKIVLPEWVRFGSATTGIDKGYVQTNDVLS WSFESNLPG

>d1avba_ b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (*Phaseolus vulgaris*)}

SNDASFNVETFNKTNLILQGDATVSSEGHLNTNVKGNEEDSMGRAFYAPIQINDRTIDNLASFSTNFTFRINAK NIENSAYGLAFALPVGSRPKLKGRLGFLNTNYDRDAHTVAVVFDTVSNRIEIDVNSIRPIATESCNFGHNNGE KAEVRITYDSPKNDLRVSLLYPSSEEKCHVSATVPLEKEVEDWVSVGFSATSGSKKETTETHNVLSWSFSSNFI

>d1dhkb_ b.29.1.1 (B:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (*Phaseolus vulgaris*)}

ATETSFIIIDAFNKTNLILQGDATVSSNGNLQLSYNSYDSMSRAFYAPIQIRDSTTGNVASFDTNFTMNIRTHRQ ANSAVGDFVLVPVQPESKGDTVTEFDTFLSRISIDVNNNDIKSVPWDVHDYDGQNAEVRTYNSSTKVFVSL SNPSTGKSNVNSTTVELEKEVYDWVSVGFSATSGAYQWSYETHDVLWSFSSKF

>d1g8wa_ b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (*Phaseolus vulgaris*)}

SNDIYFNFQRFNETNLILQRDASVSSSGQLRLTNLNGNGEPRV GSLGRAFYAPIQIWDTNTGTVASFATSFTFNI QVPNNAGPADGLAFAVPVGSQLPKDKGGFLGLFDGSNSNFHTVAVEFDTLYNKDWDPTERHIGIDVNSIRSIKT

TRWDFVNGENAEVLITYDSSTNLLASLVPSQKTSFIVSDTVDLKSVLPEWVSVGFSATTGINKGNVETNDVLS
WSFASKLS

>d1ioaa_b.29.1.1 (A:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (*Phaseolus vulgaris*), G02771, arcelin-5a}

ATETSFNFNFHTDDKLILQGNATISSKGQLQLTGVGSNELPRVDSLGRAFYSDPIQIKDSNNVASFNTNFTIIRA
KNQSISAYGLAFALVPVNSPPQQKKQEFLGIFNTNNPEPNARTVAVVFNTFKNRIDFDKNFIKPYVNENCDFHKYN
GEKTDVQITYDSSNNDLRVFLHFTVSQVKCSVSATVHLEKEVDEWVSVGFSPTGLTEDTTETHDVLWSFSSKF
R

>d1gbg__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus licheniformis}

QTGGSFYEPFNNYNTGLWQKADGYSNGNMFNCTWRANNVSMTSLGEMRLSLTSPSYNKFDCEGENRSVQTY
GYGLYEVNMKPAKNVGIVSSFFTGTGPTDGTWDEIDIEFLGKDTTKVQFNYTNGVGNHEKIVNLGFDAANSY
HTYAFDWQPNSIKWVVDGQLKHTATTQIPQTPGKIMMNLWNGAGVDEWLGSYNGVTPLYAHYNWVRYTKR
>d2ayh__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Hybrid protein: residues 1-16 from Bacillus amyloliquefaciens and Bacillus macerans}

QTGGSFPEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNKFDCAEYRSTNIYGY
GLYEVSMKPAKNTGIVSSFFTGTGPAHGTQWDEIDIEFLGKDTTKVQFNYTNGVGGHEKVISLGFDASKGFHTY
AFDWQPGYIKWVVDGVLKHTATANIPSTPGKIMMNLWNGTGVDWLGSYNGANPLYAEYDWVVKYTSN

>d1ajka_b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

NTGIVSSFFTGTGPAHGTQWDEIDIEFLGKDTTKVQFNYTNGVGGHEKVISLGFDASKGFHTYAFDWQPGYIK
WYVDGVLKHTATANIPSTPGKIMMNLWNGTGVDWLGSYNGANPLYAEYDWVVKYTSNQTGGSFPEPFNSYN
SGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNKFDCAEYRSTNIYGYGLYEVSMKPAK

>d1ajoa_b.29.1.2 (A:) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

GHEKVISLGFDASKGFHTYAFDWQPGYIKWVVDGVLKHTATANIPSTPGKIMMNLWNGTGVDWLGSYNGA
NPLYAEYDWVVKYTSNQTGGSFPEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAY
NKFDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTGTGPAHGTQWDEIDIEFLGKDTTKVQFNYTNG

>d1cpm__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTGTGPAHGTQWDEIDIEFLGKDTTKVQFNYTNGVGGHEK
VISLGFDASKGFHTYAFDWQPGYIKWVVDGVLKHTATANIPSTPGKIMMNLWNGTGVDWLGSYNGANPLYA
EYDWVVKYTSNQTGGSFPEPFNSYNSGTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSSAYNA

>d1cpn__ b.29.1.2 (-) Bacillus 1-3,1-4-beta-glucanase {Bacillus macerans}

FDCAEYRSTNIYGYGLYEVSMKPAKNTGIVSSFFTGTGPAHGTQWDEIDIEFLGKDTTKVQFNYTNGVGGHEK
VISLGFDASKGFHTYAFDWQPGYIKWVVDGVLKHTATANIPSTPGKIMMNLWNGTGVDWLGSYNGANPLYA
EYDWVVKYTSNGSVFWEPKSYFNPSTWEKADGYSNGGVFNCTWRANNVNFTNDGKLKLGLTSS

>d1dypa_ b.29.1.2 (A:) kappa-Carrageenase, catalytic
{*Pseudoalteromonas carrageenovora*}

SMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQTENYGVWSWKNEATVSKGKLKLTTKRESHQRTFWDG
CNQQQVANYPLYYTSGVAKSRATGNYGYEARIKGASTFPGVSPAFWMYSTIDRSLTKEGDVQYSEIDVVELTQK
SAVRESDHDLHNIVVKNGKPTWMRPGSFPQTNHNGYHLPFDRNDFHTYGVNVTDKITWYVDGEIVGEKD
NLYWHRQMNLTSQGLRAPHTQWKCNQFYPNSANKSAEGFPTSMEVDYVRTWVKV

>d1sita_b.29.1.3 (A:) S-lectin, different isoforms {Cow (*Bos taurus*)}

CGLVASNLNLKPGECLRVRGEVAADAKSFLNLGKDDNNLCLHFNPRFNAHGDVNTIVCNSKDAGAWGAEQR
ESAFTPQPGSVVEVCISFNQTDLTIKLPDGYESFKFPNRLNLEAINYLSAGGDFKIKCVAFE

>d1bkza_b.29.1.3 (A:) S-lectin, different isoforms {Human (*Homo sapiens*)}

SNVPHKSSLPEGIRPGTVLIRGLVPPNASRFHVNLCCGEEQGSDAALHFNPRLDTSEVFNSKEQGSWGREER

GPGVPFQRGQPFEVLIIASDDGFKA VVGDAQYHHFRHLPLARVRLVEVGGDVQLDSVRIF
>d1hlca_b.29.1.3 (A:) S-lectin, different isoforms {Human (Homo sapiens)}
ELEVKNMMDMKPGSTLKITGSIADGTDGFVINLGQTDKLNLFNPRFSESTIVCNSLDGSNWGQEQR DHLCF
SPGSEVKFTVTFESDKFKVLPDGHELTFPNRLGHSHLSYLSVRGGFNMSFFKLKE
>d1qmja_b.29.1.3 (A:) S-lectin, different isoforms {Chicken (Gallus gallus)}
QGLVVTQLDVQPGECKVKGKILSDAKGFSVN VGDSSMLHFNP RDCHGDVNTVCNSKEDGTWGEED
RKADFPPQQGDKVEICISFDAAEVKVKVPEVEFEPNRLGMEKIQYLA VEGDFKVKAIFK
>d1a78a_b.29.1.3 (A:) S-lectin, different isoforms {Toad (Bufo arenarum)}
ASAGVAVTNLNLKPGHCVEIKGSIPPDCKGFAVN LGEDASN FLLHFNARFDLHG DVN KIVCNSKEADAWGSEQ
REEVFPPQQGAEMVC FEYQTQKIIKFSSGDQFSFPVRKVLP SIPFLSLEGLAFKSITTE
>d1hdka_b.29.1.3 (A:) Charcot-Leyden crystal (CLC) protein {Human (Homo sapiens)}
SLLPV PYTEAASLSTGSTVTIKGRPLVCFLNEPYLQVD FHTEMKEESDIVFH FQV CFGRRV VMNSREYGAWKQQ
VESKNMPFQDGQEFELSISVLPDKYQVMVNGQSSYTFDHRIKPEAVKMVQVWRDISLTKFNVSYL
>d1a3k_b.29.1.3 (-) Galectin-3 CRD {Human (Homo sapiens)}
LIVPYNLPPLPGGVVPRMLITILGTVKPNANRIALDFQRGNDVA FH FNPRF NENNRRVIV CNTKLDNNWG REER
QS VFPFESGKPFKIQV LVEPDHF KVAVNDAHLLQYNHRVKKLNEISK LGISGDIDLT SASYTM
>d1c1la_b.29.1.3 (A:) Congerin I {Conger eel (Conger myriaster)}
GG LQVKNF DFTV GKFL TVGGFIN NSPQR FS VNV GES MNSL HLDH RFN YGAD QNTIV MNSTLKG DNG WET
EQRSTNFTLSAGQYFEITLSYDINKFYIDILDGP NLEFPN RYSKEFLPFLSLAGDARLT LVKLE
>d1d2sa_b.29.1.4 (A:) Sex hormone-binding globulin {Human (Homo sapiens)}
PPAVHLSNGPGQEPIAVMTFDLT KITKTSSFEVRTWDPEGVIFYGDTNPKDDWFMLGLRDGRPEIQLHNHW
AQLTVGAGPRLDDGRWHQVEVKMEGDSVLLEV DGE EVLRLRQVSGHPIMRIALGGLLFPASNLRLPLV PALDG
CLRRDSWLDKQAEISASAPTSLRSC
>d1dyka1_b.29.1.4 (A:2744-2932) Laminin alpha2 chain {Mouse (Mus musculus)}
HGPCVAESEPALLTGSKQFGLSRNSHIAIAFDDTKVKNRLTIE VRTEAESGLLFYMARINHAD FATVQLRNGFP
YFSYDLGSGDTSTMPIKINDGQWHKIKIVRVKQEGILYVDDASSQTISP KKADILDVVGILYVGGL PINY TTRIG
PTVYSLDGCVRNLHMEQAPVLDQPTSSFHVGTCFA
>d1dyka2_b.29.1.4 (A:2933-3117) Laminin alpha2 chain {Mouse (Mus musculus)}
NAESGTYFDGTGFAKAVGGFKVGLDLLVEF EFRTRPTGVLLGVSSQKMDGMGIEMIDEKLMFHV DNGAGR
TAIYDAEIPGHMCNGQWHKV TAKKIKNRLELV DGNQVDAQSPNSASTSADTNDPVFVG FP GGLNQFGLTT
NIRFRGCIRSLKLTGKPLEVNFAKALELRGVQPVSCPT
>d1c4ra_b.29.1.4 (A:) Ligand-binding domain of neurexin 1beta {Rat (Rattus norvegicus)}
HAGTTYIFSKGGGQITYKWP PNDPSTRADRLAIGFSTVQKEAVLVRV DSSS GLGDYLELHIHQGKIGVKFN VGT
DDIAIEESN AINDGKYH VVRF TRSGGNATLQVDSWPVIERYPAGRQLTIFNSQATIIIGGKEQGQPFQGQLSGLY
YNGLKVLNMAAENDANIAIVGNVRLVGEV
>d1saca_b.29.1.5 (A:) Serum amyloid P component (SAP) {Human (Homo sapiens)}
HTDLSGKV FVFPRESV TDHVNLITPLEKPLQNF TLCFRAYSDLSRAYS LFSYNTQGRDNELLVYKERVGEYSLYIGR
HKVTSK VIEKFPAPVHICV SWESSGIAEFWINGTPLVKKGLRQGYFVEAQPKIVLGQE QDSYGGKFD RSQSFVG
EIGDLYMWDSVLP PENILSAYQGTPLPANILDWQALNYEIRGYVIKPLVWW
>d1b09a_b.29.1.5 (A:) C-reactive protein (CRP) {Human (Homo sapiens)}
QTDM SRKAFVFPKESDT SYVSLKAPLTKPLKAFTVCLHFYTELSS TRGYSIFS YATKRQDNEILIFWSKD IGY SFTVG
GSEILFEVPEVT VAPVHICTSWESASGIVEFWVDGKPRVRKSLKKGYTVGA EASI ILGQE QDSFGGNFEGSQSLV
GDIGNVNMWDFVLPDEINTIYLGGPFSPNVLNWRALKYEVQGEVFTKPKQLWP
>d1jhna1_b.29.1.12 (A:61-262) Calnexin {Dog (Canis familiaris)}

YKAPVPSGEVYFADSFDRGTLSGWILSKAKKDDTDDEIAKYDGKWEVDEMKTLPDKGLVLMRAKHHAIS
AKLNKPFLFDTKPLIVQYEVNQNGIECGGAYVKLLSKTPELNLDQFHDKPTIMFGPDKGEDYKLHFIFRHK
NPKTGVYEEKHAKRPDADLKYFTDKTHLYTLINPdnsFEILVDQSIVNSGN
>d1jhna2 b.29.1.12 (A:412-458) Calnexin {Dog (Canis familiaris)}
LEPFKMTPTFSAIGLEWSMTSDIFFDNFIVCGDRRVDDWANDGWGL
>d1a8d_1 b.29.1.6 (1-247) Tetanus neurotoxin {Clostridium tetani}
MKNLDCWVDNEEDIDVILKKSTILNLDINNDIISDISGFNSSVITYPDAQLVPGINGKAIHLVNNESSEVIVHKAM
DIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSIISMKKHSLSIGSGWSVSLKGNNLIWTLKDSAGEVRQ
ITFRDLPPDKFNAYLANKWVFITITNDRLSSANLYINGVLMGSAEITGLGAIREDNNITLKLDRCNNNNQYVSIDKF
RIFCKALNPKEIEKLYTSYL
>d3bt aa1 b.29.1.6 (A:872-1078) Botulinum neurotoxin {Clostridium botulinum, serotype A}
IINTSILNLRYESNHLIDLRSRYASKINIGSKVNFDPIDKNQIQLFNLESSKIEVILKNAIVYNSMYENFSTFWIRIPKY
FNSISLNNEYTIINC MENNSGWKVSLNYGEIIWTLQDTQEIKQRVVFKYSQMINISDYINRWIFVTITNNRLNN
KIYINGRLIDQKPISNLGNIHASNНИMFKLDGCRDTHRYIWIKYFNLFDKEL
>d1epwa1 b.29.1.6 (A:862-1079) Botulinum neurotoxin {Clostridium botulinum, serotype B}
IIILNLRYKDNNLIDL SGYGAKEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFLDFSVFWIRIPKYKM
DGIQNYIHNEYTIINC MKNNSGWKISIRGNRIIWTLIDINGKTKSVFFEYNIREDISEYINRWFFVTITNNLNNAKI
YINGKLESNTDIKDIR EVIANGEIIFKLDGIDRTQFIWMKYFSIFNTELSQSNI EERYKIQSY
>d1ikpa1 b.29.1.7 (A:2-251) Exotoxin A, N-terminal domain {Pseudomonas aeruginosa}
EEAFDLWNECAKACVLDLKDGV RSSRMSVDPAIADTNGQGVLYHSMVLEGGNDALKLAIDNALSITS DGLTIRL
EGGVEPNKPVRYSYTRQARGSWSLNWLPIGHEKPSNIKVFIHELNAGNQLSHMSPIYTIEMGDELLAKLARDA
TFFVRAHESNEMQPTLAISHAGVS VMAQAQPRREKRWSE WASGKVLC LLDQ LDGV NYLAQ QRCN LDDT
WEGKIYRVLAGNPAKHDLDIKPTVISHRLHFP
>d1kit_1 b.29.1.8 (25-216) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}
ALFDYNATGDTEFDSPA KQGW M QDN TNN GSVL TNADGMPA WL VQ GIGG RAQW TYSL STNQ HAQASS FG
WRMTTEMKVLSGGMITNYYANGTQRVLPIISLDSSGNLV FEGQTGR TVLATGTAATEYHKFELVFLPGSNPS
ASFYFDGKLIRDNIQPTASKQNMIVWGNGSSNTDGVAA YRD IKF EI QGD
>d1kit_2 b.29.1.8 (347-543) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}
DVTDQVKERSFQIAGWGGSELYRRNTLSNSQQDWQSNAKIRIVDGAANQIQVADGSRKYVVTLSIDESGGLVA
NLNGVSAPII LQSEHAKVHSFHDYELQYSALNHTTLFVDGQQITT WAGEV SQENN I QFGNADAQIDGRLHVQ
KIVLTQQGHNLVEFDAFYLAQQTPEVEKDL EKLGWT KIKTGNTMSLYGNAS
>d2sli_1 b.29.1.9 (81-276) Leech intramolecular trans-sialidase, N-terminal domain {North american leech (Macrobdella decora)}
IPEGILMEKNNVDIAEGQGYSLDQEAGAKYVKAMTQGTIILSYKSTSENGIQSLFSVGNSTAGNQDRHFHIYITN
SGGIGIELRNTDGVNFYTLDRPASV RALYKGERVFNTVALKADAANKQCRLFANGELLATLDKDAFKFISDITGVD
NVTLGGT KRQGKIA PFGGTIGDIKVYSNALSDEELI QTGVTTY
>d6cel__ b.29.1.10 (-) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma reesei, Cel7A}
ESACTLQSETHPPLTWQKCSSGGTCTQQTGSVVIDANWRWTHATNSSTNCYDGNTWSSTLCPDNETCAKNC
CLDGAA YASTYGVTTSGN SLSIDFVTQSAQKNVGARLYLMASD TT YQEFTLLGNEFSFDV DVS QLPC GLNG ALYF
VSMDADGGVSKYPTNTAGAKYGTGYCDSQCPRDLKFINGQANVEGWE PSSNNANTGIGGHGSCCSQMDI W
EANSISEALTPHPCTTVGQEICEGDCGGT YSDNRYGGTCDPDGCDWNPYRLGNTSFYGP GSSFTLDT KKLT

VTQFETSGAINRYVQNGVTQQPNAELGSYSGNELNDDYCTAEEAEFGGSSFDKGGLTQFKKATSGGMVLV
MSLWDDYYANMLWLDSYPTNETSSTPGAVRGSCSTSSGVPAQVESQSPNAKVTFSNIKFGPIGSTGNPSG
>d1eg1a_b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma reesei, Endoglucanase I}
EQPGTSTPEVHPKLTYKCTKSGGCVAQDTSVLDWNYRWMHDANYNSCTVNGGVNTTLCPDEATCGKNCF
IEGVDYAASGVTTGSSLTMNQYMPSSGGYSSSPRLYLLSDGEYVMLKLNQELSFDVDLSALPCENGSL
YLSQMDENGGANQYNTAGANYGSGYCDACPQTWRNGTLNTSHQGFCCNEMDILEGNSRANALPHSCT
ATACDSAGCGFPYGYKSYYGPGDTVDTSKFTIITQFNDNGSPSGNLVSITRKYQQNGVDIPSAQPGGDTI
SSCPASASYGLATMGKALSSGMVLVFSIWNDNSQYMNWLDSGNAGPCSTEGRNPSNILANNPNTHVVFSNI
RWGDIGSTT
>d3ovwa_b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Fusarium oxysporum}
ETPDKAQEHPKLETYRCTKASGCKKQTNIVADAGIHGIRQKNGAGCGDWGQKPNAACPDEASCAKNCILS
GMDSNAYKNAGITSGNKRLQQLINNQLVSPRVYLLEENKKYEMLHLTGTEFSFDVEMEKLPCGMNGALYL
SEMPQDGKSTSRSNKAGAYYGAGYCDAQCYVTPFINGVNIKGQGVCCNELDIWEANSRATHIAPHPCSKP
GLYGCTGDECSSGICDKAGCGWNHNRINVTDFYGRGKQYKVDSLRTKFTVTSQFVANKQGDLIELHRHYIQDN
KVIESAVVNISGPPKINFINDKYCAATGANEYMRLGGTKQMGDAMSRGMVLAMSVWWSEGDFMAWLQDG
VAGPCDATEGDPKNIVKVQPNPEVTSNIRIGEIGSTSSV
>d1dyma_b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Humicola insolens, Cel7b}
EKPGETKEVHPQLTFRCTKRGGCKPATNFIVLDSLHPIHRAEGLPGGCGDWGNPPPKDVCVDVESCACNCI
MEGIPDYSQYGVTTNGTSLRLQHILPDGRVPSPRVYLLDKTRRYEMLHLTGFEFTFDVDATKLPCGMNSALYLS
EMHPTGAWSKYNPGGAYGTGYCDAQCFVTPFINGLGNIEKGKSCCNAMDIWEANSRASHVAPHTCNKKGLY
LCEGEECAFEGVCDKNGCGWNNNYRVNVTDYYGRGEFKVNTLKPFVVTQFLANRRGKLEKIHRFYVQDGKVI
ESFYTNKEGPYTNMIDDEFCEATGSRKYMELGATQGMGEALTRGMVLAMSIWWDQGGNMEWLDHGEA
GPCAKGEGAPSNIQVEPFPEVYTNLRWGEIGSTY
>d1gpia_b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Phanerochaete chrysosporium, Cel7d}
EQAGTNATAENHPQLQSQQCTTSGGCKPLSTKVLDNSWRWVHSTSGYTCYNEWDTSLCPDGKTCAN
CALDGADYSGYGITSTGTALTLPVFTGSNVGSRVYLMADDTHYQLLKNQEFTEVDMSNLPCGLNGALYLS
AMDADGGMSKYPGNKAGAKYGTGYCDSQCPKDIKFINGEANVGNWTETGSNTGTGSYGTCCSEMDIWEAN
NDAAAFTPCTTGQTRCSGDDCARNTGLCDGDFNSFRMKGDKTFLKGKGMVTDTSKPFVVTQFLTND
NTSTGTLSEIRRIYIQNGKVIQNSVANIPGVDPVNSITDNFCAQQKTAFGDTNWFAQKGGLKQMGEALNGM
VLALSIWDDHAANMLWLSDYPTDKDPSAPGVARGTCATTSGVPSDVESQVPSQVFSNIKFGDIGSTSGT
S
>d1xnb_b.29.1.11 (-) Xylanase II {Bacillus circulans}
ASTDYWQNWTGGGIVNAVNGSGGNYSVNWSNTGNFVGKGWTTGSPFRTINYAGVWAPNGNGYLTY
GWTRSPLIEYYVVDWSWGTYRPTGTYKGTVKSDGGTYDIYTTTRYNAPSIDGRTTFTQYWSVRQSKRPTGSNAT
ITFTNHVNAWKSHGMNLGSNWAYQVMATEGYQSSGSSNVTW
>d1qh7a_b.29.1.11 (A:) Xylanase II {Bacillus agaradhaerens}
EIVTDNSIGNHDGYDYEFWKDSGGSGTMILNHGGTSAQWNNVNNILFRKGKKFNETQTHQQVGNMSINYG
ANFQPNAYLCVYGVTVDPVLEYIVDSWGNWRPGATPKGTTVDGGTYDIYETLRVNQPSIKGIATFKQY
WSVRRSKRTSGTISVSNHFRAWENLGMNMGKMYEVALTVEGYQSSGSANVYSNTRLINGNPLS
>d1hixa_b.29.1.11 (A:) Xylanase II {Streptomyces sp. s38, xyl1}

ITTNQTGTNNGYYYFWTDGGGSVSMNLASGGSYGTSWTNCNFVAGKGWANGARRTVNYSGSFNPSGN
AYLTLYGWTANPLVEYYIVDNWGTYRPTGYKGTVDGGTYDVYQTRVNAPSVEGTKTFNQYWSVRQSKRT
GGSITAGNHFDAWARYGMPLGSFNYYMIMATEGYQSSGSSSIS
>d1xnd_ b.29.1.11 (-) Xylanase II {Trichoderma harzianum}
QTIGPGTGYSNGYYYWNDGHAGVTYNGGGGSFTVNSNSGNFVAGKGWQPGTKNKVINFGSYNPNG
NSYLSIYGWSRNPLIEYYIVENFGTNPSTGATKLGEVTSDDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNHS
SGSVNTANHFNAWASHGLTLGTMQIVAVEGYFSSGSASITVS
>d1xyn_ b.29.1.11 (-) Xylanase II {Trichoderma reesei, xynI}
ASINYDQNYQTGGQVSYSPSNTGFSVNWNTQDDFVVGWTTGSSAPINF GGFSVNSGTGLLSVYGWSTN
PLVEYYIMEDNHNPQAQGTVKGTVTSDDGATYTIWENTRVNEPSIQGTATFNQYISVRNSPRTSGTVQNHFN
AWASLGLHLGQMNYQVVAEGWGGSASQSVSN
>d1enxa_ b.29.1.11 (A:) Xylanase II {Trichoderma reesei, xynII}
ETIQPGTGYNNGYFYSWNDGHGGVTYNGPGQFSVNSNSGNFVGGKGWQPGTKNKVINFGSYNP
GNSYLSVYGVSRNPLIEYYIVENFGTNPSTGATKLGEVTSDDGSVYDIYRTQRVNQPSIIGTATFYQYWSVRRNHS
RSSGSVNTANHFNAWAQQGLTLGTMQIVAVEGYFSSGSASITVS
>d1yna_ b.29.1.11 (-) Xylanase II {Thermomyces lanuginosus}
ETTPNSEGWHDGYYYSWSDGGAQATYTNEGGTYEISWGDDGNLVGGKGWNPGLNARAIHFEVYQPN
GNSYLA VYGVTRNPLVEYYIVENFGTDPSSGATDLGTVCDGSIYRLGKTRVNAPSIDGTQTFDQYWSVRQD
KRTSGTVQTGCHFDAWARAGLNVNGDHYYQIVATEGYFSSGYARITVADVG
>d1bk1_ b.29.1.11 (-) Xylanase II {Aspergillus kawachii}
AGINYYQNYNGNLGDFTYDESAGTFSMYWEDGVSSDFVVLGWTGSSNAITYSAEYSASGSSSYLAVYGVW
NYPQAEYYIVEDYGDYNPCSSATSLGTVYSDGSTYQVCTDRTNEPSITGTSTFTQYFSVRESTRSGTVTVANHF
NFWAQHGFGNSDFNYQVMAVEAWSGAGSASVTIS
>d1pvxa_ b.29.1.11 (A:) Xylanase II {Paecilomyces variotii bainier}
GTTPNSEGWHDGYYYSWSDGGDSTYTNNSSGTYEITWGNGGNLVGGKGWNPGLNARAIHFTGVYQPN
GTSYLSVYGVTRNPLVEYYIVENFGSSNPSSGSTD LGTVSCDGSTYLGQSTRYNAPSIDGTQTFNQYWSVRQD
KRSSGTVQTGCHFDAWASAGLNVTGDHYYQIVATEGYFSSGYARITVADVG
>d1f5ja_ b.29.1.11 (A:) Xylanase II {Dictyoglomus thermophilum}
ALTSNASGTFDGYYELWKDTGNTTMTVYTQGRFSCQWSNINNALFRTGKKYNQNWLQLTIRITYSATYNP
NGNSYLCIYGVWSTNPLVEFYIVESWGNWRPPGATSLGQVTIDGGTYDIYRTTRVNQPSIVGTATFDQYWSVRTS
KRTSGTVTVTDHFRAWANRGLNLGTIDQITLCVEGYQSSGSANITQNTFSQSS
>d2nlra_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain
{Streptomyces lividans, CelB2}
DTTICEPF GTT IQGRYVVQNNRWGSTAPQCVTATDTGFRVTQADGSA PTNGAPKS YPSV FNGCHY TNCS PGT
DLPVRLDTVSAAPSSISYGFV DGA VYNASYDIWLDPTARTDGVNQTEIMIWFNRVGPIQPI GSPVGTAS VGG RT
WEVWSGGNGSNDVLSFVAPSAISGWSFDVMDFVRATVARGLAENDWYLT SVQAGFEPWQNGAGLAVNSFS
STVET
>d1h8va_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain
{Trichoderma reesei, Cel12A}
ETSCDQWATFTGNGYTVSNNLW GASAGSGFGCVTA VSLGGASWHADWQWSGGQNNVKS YQNSQIAIPQ
KRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVTYSGDYELMIWL GKYG D IGPIGSSQGT NVGG Q
SWT LYGYNGAMQVYSFVA QTNTT NYSGDVKNFFNYLRDNKG YNAAGQV VLSYQFGTEPFTGSGT LNV ASW
TASIN
>d1jz8a4 b.30.1.1 (A:731-1023) beta-Galactosidase, domain 5 {Escherichia coli}

PAASHAIPHLLTSEMDFCIELGNKRWQFNQRSGFLSQMWIGDKKQLLPLRDQFTRAPLDNDIGVSEATRIDP
NAWVERWKAAGHYQAEALLQCTADTLADAVLITTAHAWQHQGKTLFISRKYRIDGSGQMAITVDVEVASD
TPHPARIGLNCQLAQVAERVNWGLGPQENYPDRLTAACFDRWLPLSDMYTPYVFPSENGLRCGTRELNYG
PHQWRGDFQFNISRYSQQQLMETSHRHLLHAEEGTWLNIIDGFHMGIGGDDSWSPSVAEFQLSAGRYHYQL
VWCQK

>d1oaca1 b.30.2.1 (A:301-724) Copper amine oxidase, domain 3 (catalytic) {Escherichia coli}

PAVKPMQIIPEGKNYTITGDMIHWRNWFHLSMNSRVGPMISTVTYNDNGTKRKVMYEGSLGGMIVPYGD
PDIGWYFKAYLDSGDYGMGTLTSPIARGKDAPSNAVLLNETIADYTGPMEIPRAIAVFERYAGPEYKHQEMGQ
PNVSTERRELVRWISTVGNADYIFDWIFHENGTIGIDAGATGIEAVKGVKAKTMHDEAKDDTRYGTLIDHNIV
GTTHQHIYNFRLLDLDVGGENNSLVAMDPVKPNTAGGPRSTMQVNQYNIGNEQDAAQKFDPGTIRLLSNP
NKENRMGNPVSQIIPYAGGTHPVAKGAQFAPDEWIYHRLSFMDKQLWVTRYHPGERFPEGKYPNRSTHDTG
LGQYSKDNESLDNTDAVVWMTTGTTHVARAEWPIMPTEWVHTLLKPWNFFDETPTLGALK

>d1ksia1 b.30.2.1 (A:207-647) Copper amine oxidase, domain 3 (catalytic) {Pea seedling (*Pisum sativum*)}

VSKQSPPFGPKQHSLTSHQPQPGFQINGHSVSWANWKFHIGFDVRAGIVISLASIYDLEKHKSRVLYKGYISE
LFVPYQDPTEEFYFKTFDSGEFGFGLSTVSLIPNRDCPPHAQFIDTYVHSANGTPILLKNAICVFEQYGNIMWR
HTENGIPNESIEESRTEVNLLIVRTIVTGNADNVIDWEFKASGSIKPSIALSGILEIKGTONIKHKDEIKEDLHGKLVA
NSIGIYHDHFYIYYLDFDIDGTHNSFEKTSLKTVRIKGSSKRKSYWTETQTAKTESDAKITIGLAPAEVVNPNI
KTAVGNEVGYRLIPAPIAHPLTEDDYQPQIRGAFTNYNVWVTAYNRTEKWAGGLYDHSGRDDTLAVWTQKQR
EIVNKDIVMWHVVGHHVPAQEDFPIMPLLSTSFEIPLPTNFFERNPVLKTLSPRDVAWPGC

>d1av4_1 b.30.2.1 (212-628) Copper amine oxidase, domain 3 (catalytic) {Arthrobacter globiformis}
PLRTTQKPISTQPEGPSFTVTGGNHIEWEKWSLDVGFDVREGVVLHNIAFRDGDRRLPIINRASIAEMVVPG
DPSPIRSWQNYFDTGEYLVGQYANSLELGCDCLGDIYLSPVISDAFGNPRERNGICMHEEDWGILAKHSDLW
SGINYTRRNRRMVISFFTIGNADYGFYWLYLDGTIEFEAKATGVVFTSAFPEGGSNDISQLAPGLGAPFHQHI
FSARLDMAIDGFTNRVEEEDVVRQTMGPGNERGNAFSRKRTVLTRESEAVREADARTGRTWIISNPESKNRLN
EPVGYKLHAHNQPTLLADPGSSIARRAAFATKDLWVTRYADDERYPTGDFVNQHSGGAGLPSIAQDRDIDGQ
DIVVWHTFGLTHFPRVEDWPIMPVDTVGFKLRPEGFFDRSPVLDV PAN

>d1a2va1 b.30.2.1 (A:237-672) Copper amine oxidase, domain 3 (catalytic) {Yeast (*Hansenula polymorpha*)}

PEAPPINVTPPEGVSFKMTGNVMEWSNFKFHIGFNYREGIVLSDVSYNDHGNVRPIFHRISLSEMIVPYGSPEF
PHQRKHADIGEYAGYMTNPLSLGCDCKGVIHYLDAHFSDRAGDPITVKNAVCIHEEDDGLFKHSDFRDNF
ATSLVTRATKLVSQIFTAANAEYCLYWVFMQDGAIQLDIRLTGILNTYILGDDEAGPWGTRVYPNVNAHNHQ
HLFLSLRIDPRIDGDGNSAACDAKSSPYPLGSPENMYGNAFYSEKTTKTVKDSLNTYESATGRSWDIFNPNKV
NPYSGKPPSYKLSTQCPLLAKE GSLVAKRAPWASHSVNVPYKDNRLLYPSGDHVPQWSGDGVRGMREWI
GDGSENIIDNTDILFFHTFGITHFPAPEDFPLMPAEPITMLRPRHFFTENPGLDIQPSYAMTTSEAKRAV

>d1cb8a3 b.30.3.1 (A:336-599) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}

IEPYHHQFWNGDYVQHLRPAYSFNVRMVKRTRRSSEGKENCNLLGRYLSGATNIQLRGPEYYNIMPVWEWD
KIPGITSRDYLTDPLTKLWGEQGSNDFAGGVSDGVY GASAYALDYDSLQAKKAWFFFDEIVCLGAGINSNAPE
NITTLNQSWLNGPVISTAGKTGRGKITTFAQGQFWLLHDAIGYYFPEGANLSLTSQKGNWFHINNSHSK
DEVSGDVFKLWINHGPENAQYAYIVLPGINKPEEIKKYNGTA

>d1egua3 b.30.3.1 (A:541-814) Hyaluronate lyase {Streptococcus pneumoniae}

TSYLSAFNKM DKTAMYNAEKGF GFLSFSSRTLNYEHMNKENKRGWYTS DGMF YLYNGDLSHYSDGYWPT

VNPYKMPGTTETDAKRADSDTGKVLPASFVGTSKLDDANATATMDFTNWNTQTLTAHKSWFMLKDKIAFLGS
NIQNTSTDATTIDQRKLESSNPYKVYVNDKEASLTEQEKDYPETQSVFLESSDSKKNIGYFFFKKSSISMSKALQ
KGAWKDINEQSDKEVENEFLTISQAHKQNGDSYGYMLIPNVDRATFNQMIKELE
>d1f1sa4 b.30.3.1 (A:620-919) Hyaluronate lyase {Streptococcus agalactiae}
LKSNLSTFNSMDRLAYNAKKDFGFAISLHSKRTLNYESGMNDENTRGWYTGDGMFYIYNQDQSHYSNHFWP
TVNPYKMGATTEKDAKREDTTKEFMSKHSKDAKEKTGQVTGTSDFVGSVKLNDHFALAAAMDFTNWDRTLTA
QKGWVILNDKIVFLGSNIKNTNGIGNVSTTIDQRKDDSKTPYTTVNGKTIDLQASSQQFTDTKSFLESKEPG
RNIGYIFFKNSTIDIERKEQTGTWNSINRTSKNTSIVSNPFITISQKHDKGDSYGYMMVPNIDRTSFDFKLANSKE
VELLENS
>d1h54a2 b.30.4.1 (A:1-268) Lactobacillus maltose phosphorylase, N-terminal domain
{Lactobacillus brevis}
MKRIFEVQPWNVITHTFDPDKRQLQESMTSLGNGYMGMRGDFFEGYSGDSLQGIYLGGVWYPDKTRVGW
WKNGYPKYFGKVVNAVNFIKLPIEINGEPVDLAKDKISDFTLDLMHQGVLNRSFVERGAVALNFQRFLSV
AQPELSVQKVTVKNLSDAEVDVTLKPSIDADVMNEEANYDERFWDVLATDQQADRGSIVAKTPNPFGTPRF
TSGMEMRLVTDLKNAITQPNEKEVTTAYTGKLAQASAELEKRVIVVTSRDY
>d1hs6a2 b.98.1.1 (A:1-208) Leukotriene A4 hydrolase N-terminal domain {Human (Homo sapiens)}
PEIVDTCASPVCRTHKHLHRCVDFTRRLTGTAALTQSQEDNLRSVLDTKDLTIEKVVINGQEVKYALGE
RQSYKGSPMEISLPIALSQNQEIVIEISFETSPKSSALQWLPEQTSGKEHPYLFSQCQAIHCRAILPCQDTPSVKLT
YTAEVSVPKELVALMSAIRDGETPDPEDPSRKIYKFIQKVPIPCYLIALLVGA
>d1es6a_b.31.1.1 (A:) EV matrix protein {Ebola virus}
GDTPSNPLRPPIADDTIDHASHTPGVSSAFILEAMVNVISGPVLMKQIPIW/LPLGVADQKTYSDSTAAIMLA
SYTITHFGKATNPLVRVNRGLPGIPDHPLRLLRIGNQAFLQEFVLPPVQLPQYFTFDLTALKLITQPLPAATWTDDT
PTGSNGALRPGISFHPKLRPILLPNKSGKKGNSADLTSPEKIQAIMTSLQDFKIVPDKNIMGIEVPETLVLKLTG
KKVTSKNGQPIIPVLLPKYIGLDPVAPGDLTMVITQDCDTCHSPASLP
>d1qexa_b.32.1.1 (A:) gp9 {Bacteriophage T4}
MFIQEKKLIDTGEIGNASTGDIIFDGGNKINSDFNAIYNAFGDQRKMAVANGTADGQIIHATGYYQKHSITE
YATPVKVGTRHDIDTSTGVVKVIIERGELGDCVEFINSGNSISVTNPLTIQAIIDSIGVSGNLVVTSPYSKVTLCISS
DNSTS VVNYSIESMFGQKESPAEGTWNISTSGVDIPLFHRTEYNMAKLLVTCQSVDGRKIKTAEINILVDTVNS
EVISSEYAVMRVGNETEEDEIANIAFSIKENYVTATISSTVGMRRAVKVIATQKIGVAQ
>d1rie_b.33.1.1 (-) ISP subunit of the mitochondrial cytochrome bc1-complex, watersoluble
domain {Cow (Bos taurus)}
AMSKIEIKLSDIPEGKNMAFKWRGKPLFVRHRTKKEIDQEAAVEVSQLRDPQHDLERVKKPEWVILIGVCTHLG
CVPIANAGDFGGYYCPCHGSHYDASGRIRKGPAVLLEVPSYEFTSDDMVIVG
>d1ezve1 b.33.1.1 (E:87-215) ISP subunit of the mitochondrial cytochrome bc1-
complex, watersoluble domain {Baker's yeast (Saccharomyces cerevisiae)}
DVLAMAKVEVNLAAPLGNVVVKWQGKPVFIRHRTPHEIQEANSVDMMSALKDPQTDADRVKDPQWLIMLG
ICTHLGCVPIGEAGDFGGWFCPCHGSHYDISGRIRKGPAVLNLEIPAYEFDGDKIVVG
>d1rfs_b.33.1.1 (-) ISP subunit from chloroplast cytochrome bf complex {Spinach (Spinacia
oleracea)}
TIAKDALGNDVIAAEWLKTHAPGDRTLTQGLKGDPYLVVESDKTLATFGINAVCTHLGCVVPFNAEENKFICPC
HGSQYNNQGRVVRGPAPLSSLALAHCDVDDGKVFVFWTETDFRTGEAPWWSA
>d1g8kb_b.33.1.1 (B:) Arsenite oxidase Rieske subunit {Alcaligenes faecalis}
RTTLAYPATAVSVAKNLAANEPEVSFTYPDTSSPCVAVKLGAPVPGGVGPDDDIVASVLCVTHMGCPSTSVDSSKT
FSCPCCHTEFDAEKAGQMICGEATADLPRVLLRYDAASDALTAVGVDGLIYGRQANVI

>d1fqta_ b.33.1.1 (A:) Rieske-type ferredoxin associated with biphenyl dioxygenase {Burkholderia cepacia}
MKFTRVCDRRDVPEGEALKVESGGTSVAIFNVDGELFATQDRCTHGDWSLSDDGGYLEGDVVECSLHMGKFCV
RTGKVKSPPPCEALKIFPIRIEDNDVLVDFEAGYLAP

>d1eg9a1 b.33.1.2 (A:1-154) Naphthalene 1,2-dioxygenase alpha subunit, N-domain {Pseudomonas putida}
MNYNNKILVSEGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVISRQNDGSIR
AFLNVCRHRGKTLVSVEAGNAKGFCVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHGFIY
GCFDQ

>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}
NPIPGLDELGVGNSDAAAPGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITL
SHNGKDVELLDDLAHTIRIEEL

>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}
PGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGSEVEIVDRDGHITLHNGKDVELLDDLAHTIRI
EE

>d1fx7a3 b.34.1.2 (A:145-230) Iron-dependent regulator IdeR {Mycobacterium tuberculosis}
GADDANLVRTELPGSPVAVVRQLTEHVQGIDIDLTRLKDAGVVPNARVTVETTPGGGVTIVIPGHENVTL
HEMAHAVKVEKV

>d1igqa_ b.34.1.3 (A:) Transcriptional repressor protein KorB {Escherichia coli}
KKAIQVEHDERPARLILNRRPPAEGYAWLKYEEDGQFEANLADVKLVALIEG

>d1igub_ b.34.1.3 (B:) Transcriptional repressor protein KorB {Escherichia coli}
PDPLKLKAIVQVEHDERPARLILNRRPPAEGYAWLKYEEDGQFEANLADVKLVALIEG

>d1ckaa_ b.34.2.1 (A:) C-Crk, N-terminal SH3 domain {Mouse (Mus musculus)}
AEYVRALFDNGNDEEDLPFKKGDLRIRDKPEEQWWNAEDSEGKRGMIPVPYVEKY

>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)}
TAGKIFRAMYDYMAADADEVSKFDGDAIINVQAIDEGWMYGTVQRTGRTGMLPANYVEAI

>d1bbza_ b.34.2.1 (A:) Abl tyrosine kinase, SH3 domain {Human (Homo sapiens)}
NLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNGQGWVPSNYITPVNS

>d2abl_1 b.34.2.1 (75-139) Abl tyrosine kinase, SH3 domain {Human (Homo sapiens)}
MGPSENDPNLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNGQGWVPSNYITPVN

>d1pht_ b.34.2.1 (-) Phosphatidylinositol 3-kinase (p85-alpha subunit, pi3k), SH3 domain {Human (Homo sapiens)}
AEGYQYRALYDYKKEREEDIDLHLGDIITVNKGSLVALGFSDGQEARPEEIGWLNGYNETTGERGDFPGTYVEI

GRKKISPP

>d1g2ba_ b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
MDRQGFVPAAYVKKLDGTGKELVLALYDYQEKPSPREVTMKKGDILTLNNSTNKDW/WKVEVN
>d1pwt_ b.34.2.1 (-) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
MGTGKELVLALYDYQEKPSPREVTMKKGDILTLNNSTNKDW/WKVEVNDRQGFVPAAYVKKLD
>d1qkwa_ b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
KELVLALYDYQEKPSPREVTMKKGDILTLNNSTNKDW/WKVEVGDRQGFVPAAYVKKLD
>d1tuc_ b.34.2.1 (-) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
MGPSPREVTMKKGDILTLNNSTNKDW/WKVEVNDRQGFVPAAYVKKLDGTGKELVLALYDYQE
>d1awj_ b.34.2.1 (-) IL-2 inducible T-cell (ltc) kinase {Mouse (Mus musculus)}
KKPLPPTPEDNRRSFQEPEETLVIALYDYQTNDPQELALCDEEYYLLDSSEIHWWWRVQDKNGHEGYAPSSYLVE
KS
>d1bu1a_ b.34.2.1 (A:) Hemopoetic cell kinase Hck {Human (Homo sapiens)}
IIVVALYDYEAIIHHEDLSFQKGDQMVMVLEESGEWWKARSLATRKEGYIPSNYVARVD
>d1qcfa1 b.34.2.1 (A:80-145) Hemopoetic cell kinase Hck {Human (Homo sapiens)}
SGIRIIVVALYDYEAIIHHEDLSFQKGDQMVMVLEESGEWWKARSLATRKEGYIPSNYVARVDSLET
>d1cska_ b.34.2.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}
GTECIAKYNFHGTAEQDLPFCKGDVLTIVAVTKDPNWYKAKNKVGREGIIPANYVQKR
>d1fmk_1 b.34.2.1 (82-145) c-src tyrosine kinase {Human (Homo sapiens)}
MVTTFVALIDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLSTGQTGYIPSNYVAPSDSIQA
>d1nloc_ b.34.2.1 (C:) c-src tyrosine kinase {Chicken (Gallus gallus)}
TFVALIDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLTTGQTGYIPSNYVAPS
>d1awx_ b.34.2.1 (-) Bruton's tyrosine kinase {Human (Homo sapiens)}
GSMSTSELKKVVALIDYDMPMNANDLQLRKGDNEYFILEESNLPWWRARDKNGQEGYIPSNYVTEAEDS
>d1qlya_ b.34.2.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}
LKKVVALIDYDMPMNANDLQLRKGDNEYFILEESNLPWWRARDKNGQEGYIPSNYVTEAE
>d1gl5a_ b.34.2.1 (A:) tyrosine kinase tec {Mouse (Mus musculus)}
GSEIVVAMYDFQATEAHLRLERGQEYIILEKNDLHWWRARDKYGSEGYIPSNYVTGKKSNNLDQYD
>d1gcqa_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}
STYVQALFDQDPQEDGELGFRRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPV
>d1gr1a1 b.34.2.1 (A:1-56) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}
MEAIKYDFKATADDELSFKRGDILKVLNEECQNWWYKAELNGKDGFIPKNYIEMKPHPEFIVTD
>d1gr1a2 b.34.2.1 (A:157-217) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Human (Homo sapiens)}
QPTYVQALFDQDPQEDGELGFRRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPVNRNV
>d1gbra_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Mouse (Mus musculus)}
GSRRASVGSMEAIAKYDFKATADDELSFKRGDILKVLNEECQNWWYKAELNGKDGFIPKNYIEMKPHPEFIVTD
>d1sema_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains {Caenorhabditis elegans, SEM-5}
ETKFVQALDFNPQESGELAFKRGDVITLINKDDPNWWEGQLNNRRGIFPSNYVCPYN
>d2hsp_ b.34.2.1 (-) Phospholipase C, SH3 domain {Human (Homo sapiens)}

GSPTFKCAVKALFDYKAQREDELTIFIKSAIIQNVEKQEGGWWRGDYGGKKQLWFPSNYVEEMVNPEGIHRD
>d1h92a_ b.34.2.1 (A:) p56-lck tyrosine kinase, SH3 domain {Human (Homo sapiens)}
GSPLQDNLIVIALHSYEPSHDGLGFEKGEQLRILEQSGEWWKAQSLTTGQEGFIPFNFVAKAN
>d1lcka1 b.34.2.1 (A:63-116) p56-lck tyrosine kinase, SH3 domain {Human (Homo sapiens)}
DNLVIALHSYEPSHDGLGFEKGEQLRILEQSGEWWKAQSLTTGQEGFIPFNFV
>d1ycsb2 b.34.2.1 (B:457-519) 53BP2 {Human (Homo sapiens)}
IMNKGVIVYALWDYEPQNDDELPMKEGDCMTIIHREDEDEIEWWWARLNDKEGYVPRNLLGLYP
>d1bb9_ b.34.2.1 (-) Amphiphysin 2 {Rat (Rattus norvegicus)}
TTGRLDLPPGMFMKVQAQHDYTATDTDELQLKAGDVVLVIPFQNPEEQDEGWLMGVKESDWQNQHKELEKCR
GVFPENFTERVQ
>d1i07a_ b.34.2.1 (A:) EPS8 SH3 domain {Mouse (Mus musculus)}
KKYAKSKYDFVARNSSELSVMKDDVLEILDDRQWWKVRNASGDSGFVPNNILDIMRTP
>d1gcqc_ b.34.2.1 (C:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}
GSHMPKMEVFQEYYGIPPPPAGFPFLRNPGDIVELTKAEEAHNWWEGRNTATNEVGWPCNRVHPYV
>d1k1za_ b.34.2.1 (A:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}
RAQDKKRNELGLPKMEVFQEYYGIPPPPAGFGFLRNPGDIVELTKAEEAHNWWEGRNTATNEVGWPCN
RVHPYVH
>d1i1ja_ b.34.2.1 (A:) Melanoma inhibitory activity protein {Human (Homo sapiens)}
GPMPKLADRKLCAEQCSHPISMAVALQDYMADPDCRFLTIRGQVVYFSKLKGRGRLFWGGSVQGDYYGDL
AARLGYPSSIVREDQTLKPGKVDVKTDKWDFY
>d1kjwa1 b.34.2.1 (A:430-525) Psd-95 {Rat (Rattus norvegicus)}
GFYIRALFDYDKTKDCGFLSQALSFRFGDVLVIDAGDEEWQARRVHSDSETDDIGFIPSKRRVERREWSRLK
AKDWGSSSGSQGREDSVLSYET
>d1br2a1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain {Chicken (Gallus gallus),
pectoral muscle}
LVWVPSEKHGFEAAASIKEKGDEVTVLQENGKKVTLSKDDIQKMN
>d2mysa1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain {Chicken (Gallus gallus),
pectoral muscle}
AKSSVFVHPKQSFVKGTIQSKEGGKVTVKTEGGETLTVKEDQVFS
>d1b7ta1 b.34.3.1 (A:29-76) Myosin S1 fragment, N-terminal domain {Bay scallop (Aequipecten
irradians)}
DGKKNCWVPDEKEGFASAEIQSSKGDEITVKIVADSSTRVKKDDIQS
>d1jwya1 b.34.3.1 (A:36-79) Myosin S1 fragment, N-terminal domain {Slime mold (Dictyostelium
discoideum)}
FKLTVDKRYIWYNPDPKERDSYECGEIVSETSDSFTFKTVGDQ
>d1lvk_1 b.34.3.1 (34-79) Myosin S1 fragment, N-terminal domain {Slime mold (Dictyostelium
discoideum)}
YIWYNPDPKERDSYECGEIVSETSDSFTFKTSQDGQDRQVKKDDANQ
>d1g5va_ b.34.9.1 (A:) Survival motor neuron protein 1, smn {Human (Homo sapiens)}
QQWKVGDKCSAIWSEDCIYPATIASIDFKRETCVVVTGYNREEQNLSDLSP
>d1khca_ b.34.9.2 (A:) DNA methyltransferase DNMT3B {Mouse (Mus musculus)}
TEYQDDKEFGIGDLVGKIKGFSWWPAMVVSWKATSQRQAMPGMRWVQWFQDGKFSEISADKLVALGLFS
QHFNLATFNKLVSYRKAMYHTLEKARVRAKGTFSSSPGESLEDQLKPMLEWAHGGFKPTGIEGLKPN
>d1vie_ b.34.4.1 (-) R67 dihydrofolate reductase {Escherichia coli, plasmid PL1}

PSNATFGMGDRVRKKSGAAW/QQQIVGWYCTNLPEGYAVESEAHPGSVQIYPVAALERIN
>d1psf__ b.34.4.2 (-) Photosystem I accessory protein E (PsaE) {Cyanobacterium (Synechococcus sp.), pcc 7002}
AIERGSKVKILRKESYWYGDVGTVASIDKSGIIYPVIVRFNKVNNGFSGSAGGLNTNNFAEHELEVVG
>d1qp2a_ b.34.4.2 (A:) Photosystem I accessory protein E (PsaE) {Cyanobacterium (Nostoc sp.), strain pcc8009}
MVQRGSKVRLRPESYWFDVGTAVSDQSGIKYPVIVRFEKVNYSGINTNNFAEDELVEAPEAKPKK
>d1jb0e_ b.34.4.2 (E:) Photosystem I accessory protein E (PsaE) {Synechococcus elongatus}
VQRGSKVILRPESYWNEVGTVASVDQTPGVKYPVIVRFDKVNYTGYSASGVNTNNFALHEVQEVA
>d1dj7b_ b.34.4.3 (B:) Ferredoxin thioredoxin reductase (FTR), alpha (variable) chain {Synechocystis sp.}
MNVGDRVRVTSSVVYHHPEHKKTAFLQGMGEVAAVLTEWQGRPISANLPVLVKFEQRFKAHFRPDEVTLLI
>d2ahjb_ b.34.4.4 (B:) Nitrile hydratase beta chain {Rhodococcus erythropolis}
MDGVHDLAGVQGFGKVPHTVNADIGPTFHAEWEHLPYSLMAGVAELGAFSVDERYVVERMEPRHYMM
TPYYERYVIGVATLMVEKGILTQDELESLAGGPFLSRPSESEGRPAPVETTFEVGQRVRDEYVPGHIRMPAY
CRGRVGTISHRTTEWPFPDAIGHGRNDAGEEPTYHVKAEEELFGSDTDGGSVVVDLFEGYLEPA
>d1jj2s_ b.34.5.1 (S:) Ribosomal proteins L24 (L24p) {Archaeon Haloarcula marismortui}
SKQPDKQRKSQRRAPLHERHKQVRATLSADLREYGQRNVRVNAGDTVEVLRGDFAGEEGEVINVLDKAVIH
VEDVTLEKTDGEEVPRPLDTSNVRVTDLDEKREARLESEDDSA
>d1jj2p_ b.34.5.1 (P:) Ribosomal proteins L21e {Archaeon Haloarcula marismortui}
PSSNGPLEGTRGKLKNKPRDRGTSPPQRAVEEFDDGEKVHLKIDPSVPNGRHFPRFDGQTGTVEGKQGDAYKV
DIVDGGKEKTIIVTA AHLRRQE
>d2eifa1 b.34.5.2 (A:1-73) N-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Methanococcus jannaschii}
VIIMP GTQNVGSLKVGQYVMIDGP CPEIVDISVSKPGKHGGAKARVVGIGIFEKVKEFVAPTSSKVEVPI
>d1bkb_1 b.34.5.2 (4-74) N-terminal domain of eukaryotic initiation translation factor 5a {Archaeon Pyrobaculum aerophilum}
KWVMSTKYVEAGELKEGSYVVIDGEPCRVVEIEKSKTGKHGSAKARI AVGVFDGGKRTLSPVDAQVEVP
>d1rl2a1 b.34.5.3 (A:126-195) C-terminal domain of ribosomal protein L2 {Bacillus stearothermophilus}
GNALPLEIPGVTLVHNIELKPGRGQLVRAAGTSAQVLGKEGKYVIVRLASGEVRMILGKCRATVGEVG
>d1jj2a1 b.34.5.3 (A:91-237) C-terminal domain of ribosomal protein L2 {Archaeon Haloarcula marismortui}
GNTLPLAEIPGVPCNVESSPGDGK FARASGVNAQLLHDRNVAVVKLPSGEMKRLDPQC RATIGVVG
GRTDKPFVKAGNKKHMKARGTKWPNVRGVAMNAVDHPFGGGRQHPGKPKSISRNAPPGRKV
GDIASK RTGRGG
>d3vub__ b.34.6.1 (-) CcdB {Escherichia coli}
MQFKVYTYKRESRYRLFVDVQSDIIDTPGRRMVIPLASARLLSDKVSRELYPVVHIGDESWRMMTTDMASVPV
SVIGEEVADLSHRENDIKNAINLMFWGI
>d1hyoa1 b.34.8.1 (A:1-118) Fumarylacetacetate hydrolase, FAH, N-terminal domain {Mouse (Mus musculus)}
MSFIPVAEDSDFPIQNLPYGVFSTQSNPKRIGVAIGDQILDLSVIKHLFTGPALS KHQHVFD ETTLNNFMGLGQ
AAWKEARASLQNLLSASQARL RDDKELRQRAFTSQASATMHL P

>d1ex4a1 b.34.7.1 (A:223-270) DNA-binding domain of retroviral integrase {Human immunodeficiency virus type 1}
FRVYYRDSRNSLWKGPAKLLWKGEAVVIQDNSDIKVVPRRKAKIIRD

>d1ihva_b.34.7.1 (A:) DNA-binding domain of retroviral integrase {Human immunodeficiency virus type 1}
MIQNFRVYYRDSRDPWKGPALKGEAVVIQDNSDIKVVPRRKAKIIRD

>d1c0ma1 b.34.7.1 (A:217-269) DNA-binding domain of retroviral integrase {Rous sarcoma virus (RSV, avian sarcoma virus)}
VLTEGPPVKIRIETGEWEKGWNVLVWGRGYAAVKNRDTDKVIWVPSRKVKPDI

>d1c6vx_b.34.7.1 (X:) DNA-binding domain of retroviral integrase {Simian immunodeficiency virus}
KNSKFKNFRVYYREGRDQLWKGPGELLWKGEAVLLKGTDIKVVPRRKAKIIRD

>d1aono_b.35.1.1 (O:) Chaperonin-10 (GroES) {Escherichia coli}
MNIRPLHDRVIVKRKEVETKSAGGIVLTGSAAKSTRGEVLAVGNGRILENGEVKPLDVKGDIVIFNDGYGVKS
EKIDNEEVLIMSESDILAIVEA

>d1jh2a_b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium tuberculosis}
AKVNIKPLEDKILVQANEAEETTASGLVIPDTAKEKPQEGTVVAVGPGRWDEDGEKRIPLDVAEGDTVIYSKYGG
TEIKYNGEEYLILSARDVLA VVSK

>d1lepa_b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium leprae}
AKVKIKPLEDKILVQAGEAETMTPSGLVIPENAKEKPQEGTVVAVGPGRWDEDGA KRIPLDVSEGDIVIYSKYGG
TEIKYNGEEYLILSARDVLA VVSK

>d1g31a_b.35.1.1 (A:) GP31 co-chaperonin {Bacteriophage T4}
QQLPIRAVGEYVILVSEPAQAGDEEVTESGLIIGKRVQGEVPELCVVHSVGPDVPEGFCEVGDLTSLPVGQIRNV
PHPFVALGLKQPKEIKQKFVTCHYKAIPCLY

>d1heta1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Horse (Equus caballus)}
STAGKVIKCKAAVLWEEKKPF SIEEVAPPKAHEVRIKMVATGICRSDDHVSGTLVPLVIAGHEAAGIVESIG
EGVTTVRPGDKV IPLFTPQCGKCRVCKHPEGNFCLKNDLSMPRTMQDGT SRFTCRGKPIHHFLGTSTFSQYT
VVDEISVAKIDAASPLEKVCLIGCXKDSVPKLADFMAKKFALDPLITHVLPFEKINEGF DLLSGESIRTLF

>d1d1ta1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}
GTAGKVIKCKAAVLWEQKQPF SIEEVAPPKTKEVRIKILATGICRTDDHVKGTMVSKFPVIVGHEATGIVESIGE
GVTTVKPGDKV IPLFLPQCRCNA CRNPDGNCIRSDITGRGV LADGTT RFTCRGKPVHHFLNTSTFTEYTVVDE
SSVAKIDDAAPPEKVCLIGCXRDDVPKLVTEFLAKKF DLDQLITHVLPFKKISEGFELLNSGQSIRT VLT

>d1hsoa1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}
STAGKVIKCKAAVLWELKKPF SIEEVAPPKAHEVRIKMVAVGICGTDDHVSGTMVTPLPVILGHEAAGIVES
VGEGVTTVKPGDKV IPLFLPQC CGKCRICKNPESNYCLKNDVSNPQGTLQDGTRRFTCRGKPIHHFLGTSTFSQYT
VVDENAVAKIDAASPLEKVCLIGCXKECVPKLADFMAKKFSL DALITHVLPFEKINEGF DLLHSGKSIRTILMF

>d1hsza1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}
STAGKVIKCKAAVLWEVKKPF SIEDVEVAPPKAYEVRIKMVAVGICRTDDHVSGNLVTPLPVILGHEAAGIVESV
GEGVTTVKPGDKV IPLFTPQCGKCRVCKNPESNYCLKNDLG N PRTMQDGT RRFTCRGKPIHHFLGTSTFSQYT
VVDENAVAKIDAASPLEKVCLIGCXKEGIPKLVADFMAKKFSL DALITHVLPFEKINEGF DLLHSGKSIRT VLT

>d1ht0a1 b.35.1.2 (A:1-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}

STAGKVIKCKAAVLWELKKPFSIEEVEVAPPKAHEVRIKMAAGICRSDEHVVSGNLVTPLPVILGHEAAGIVESV
GEGVTTVKPGDKVPLFTPQCGKCRICKNPESNYCLKNDLGNPRGTLQDGTRRFTCSGKPIHHFVGVSTFSQYTV
VDENAVAKIDAASPLEVKCLIGCXKESVPKLVADFMACKFSLDALTNVLPEFEKINEGFDFLLRSGKSIRTVLTF
>d1teha1 b.35.1.2 (A:3-174,A:325-374) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}
ANEVIKCKAAVAWEAGKPLSIEEIEVAPPKAHEVRIKIIATAVCHTDAYTSLGADPEGCFPVILGHEGAGIVESVGE
GVTKLKAGDTVIPLYIPQCGECKFCLNPKTNLCKIRVTQGKGLMPDGTSRFTCKGKTLHYMGTSTFSEYTVVA
DISVAKIDPLAPLDKVCLLGCXVESVPKLVSEYMSKKIKVDEFVTHNLSFDEINKAFELMHSGKSIRTVVKI
>d1e3ia1 b.35.1.2 (A:1-174,A:325-376) Alcohol dehydrogenase {Mouse (Mus musculus), class II}
GTQGKVIKCKAAIAWKTGSPLCIEEIEVSPPKACEVRIQVIATCVCPTDINATDPKKKALFPVVLGHECAGIVESVG
PGVTNFKPGDKVIPFFAPQCKRCKLCLSPLTNLCGKLRFNKYPTIDQELMEDRTSRFTCKGRSIYHFMIVSSFSQY
TVVSEANLARVDDEANLERVCXKSVDSPNLVSDYKNKKFDLLVTHALPFESINDAIDLMKEGKSIRTLTF
>d1cdoa1 b.35.1.2 (A:1-175,A:325-374) Alcohol dehydrogenase {Cod (Gadus callarias)}
ATVGKVIKCKAAVAWEANKPLVIEEIEVDVPHANEIRKIIATGVCHTDLYHLFEGKHKGDPVVLGHEGAGIVESV
GPGVTEFQPGEKVIPLFISQCQCGECRFCQSPKTNQCVKGWANESPDMSPKETRFTCKGRKVLOFLGTSTFSQYT
VVNQIAVAKIDPSAPLDTVCLLGCXKDGVPKMVKAYLDKKVKLDEFITHRMPLESVNDAIDLMKHGKCIRTVLSL
>d1keva1 b.35.1.2 (A:1-150,A:315-351) Bacterial secondary alcohol dehydrogenase {Clostridium beijerinckii}
MKGFAMLGINKLGWIEKERPVAGSYDAIVRPLAVSPCTSDIHTVFEGALGDRKNMILGHEAVGEVVEVGSEVK
DFKPGDRVIVPCPTPDWRSLVQAGFQQHSNGMLAGWKFSNFKDGVFGEYFHVNNDADMNLAILPKDMPLE
NAVMITDXDLSKLVTHVYHGFDHIEEALLLMKDKPKDLIKAVVIL
>d1ykfa1 b.35.1.2 (A:1-150,A:315-352) Bacterial secondary alcohol dehydrogenase {Thermoanaerobacter brockii}
MKGFAMLSIGKVGWIEKEKPAPGPFDIVRPLAVAPCTSIDIHTVFEGAIGERHNMILGHEAVGEVVEVGSEVKD
FKPGDRVVVPAITPDWRTSEVQRGYHQHSGGMLAGWKFSNVKDGVFGEFFHVNDADMNL AHLPKEIPLEA
AVMIPDXDPSKLVTHVFRGFDNIEKAFMLMKDKPKDLIKPVVILA
>d1e3ja1 b.35.1.2 (A:4-150,A:314-351) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}
DNLSAVLYKQNDLRLEQRPIPEPKEDEVLLQMAVGICSDVHYEHGRIADFIVKDPMVIGHEASGTVVKGK
NVKHLKKGDRVAVEPGVPCRRCQFCKEGKYNLCPDLTCATPPDDGNLARYVHAADFCHKLPDNVSLEEGAL
XNVKQLVTHSKLEQTVDafeaARKKADNTIKVMISCRQ
>d1qora1 b.35.1.2 (A:2-135,A:266-327) Quinone oxidoreductase {Escherichia coli}
ATRIEFHKHGGPEVLQAVEFTPADPAENEIQVENKAIGINFIDTYIRSGLYPPPSLPSGLGTEAAGIVSKVGSGVKHI
KAGDRVYQAQSALGAYSSVHNIIADKAAILPAAISFEQAAASFLKGLTVYLLRKTXLQGYITTREELTEASNELFSLI
ASGVIKVDVAEEQQKYPLKDAQRAHEILESRATQGSSLIP
>d1auua_ b.35.2.1 (A:) SacY {Bacillus subtilis}
MKIKRILNHNAIVVKDQNEEKILLGAGIAFNKKNDIVDPSKIEKTFIRKDTPDY
>d1pdr_ b.36.1.1 (-) Discs large protein homolog {Human (Homo sapiens)}
ITREPRKVVLRGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRGDRIISVNSVDLRAASHEQAAAALKNA
GQAVTIVAQYRPEEYSRQHA
>d1kwaa_ b.36.1.1 (A:) Cask/Lin-2 {Human (Homo sapiens)}
RSRLVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMIHRQGTLHVGDEIREINGISVANQTVEQLQKMLRE
MRGSITFKIVPSYREF
>d1be9a_ b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}

FLGEEDIPREPRRIVIHRGSTGLGFNIIGGEDGEFIFISFILAGGPADLSGELRKGDQILSVNGVDLRNASHEQAAI
ALKNAGQTVTIIAQYKPEEYSRFEANSRVNSSGRIVTN
>d1qlca_ b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (Rattus norvegicus)}
AEKVMEIKLIKPKGLGFSIAGGVGNQHIPGDNISIYVTKIIEGGAHKDGRLQIGDKILAVNSVGLEDVMHEDAV
AALKNTYDVVYLKAVAKPSNA
>d1qava_ b.36.1.1 (A:) Syntrophin {Mouse (Mus musculus)}
GSLQRRRTVRKADAGGLGISIKGGRENKMPILISKIFKGLAADQTEALFGDAILSVNGEDLSSATHDEAVQALK
KTGKEVVLEVVKYMK
>d1b8qa_ b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}
GSHMIEPNVISVRLFKRKVGGFLVKERVKPPVIISDLIRGGAAEQSGLIQAGDIIILAVNDRPLVDLSYDSALEV
LRGIASETHVVLILRGPEGFTTHELETTFTGDGTPKTIRVTQPLGPPTKAV
>d1qaua_ b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (Rattus norvegicus)}
NVISVRLFKRKVGGFLVKERVKPPVIISDLIRGGAAEQSGLIQAGDIIILAVNDRPLVDLSYDSALEVLRGIASET
HVVILRGPEGFTTHELETTFTGDGTPKTIRVTQP
>d3pdza_ b.36.1.1 (A:) Phosphatase hPTP1e {Human (Homo sapiens)}
PKPGDIFEVELAKNDNSLGISVTGGVNTSVRHGGIYVKAVIPQGAAESDGRIHKGDRVLA VNGVSLEGATHKQA
VETLRNTGQVHVLLKGQSPT
>d1g9oa_ b.36.1.1 (A:) Na+/H+ exchanger regulatory factor, NHERF {Human (Homo sapiens)}
RMLPRLCCLEKGPNNGYGFHLHGEKGKLGQYIRLVEPGSPAEKAGLLAGDRLVEVNGENVEKETHQQVVSIRAA
LNAVRLLVDPETDEQL
>d1ihja_ b.36.1.1 (A:) Inad {Fruit fly (Drosophila melanogaster)}
GELIHMTLDKTGKKSFGICIVRGEVKDSPNTKTTGIFIKGIVPDSPAHLCGRLKGDRILSNGKDVRNSTEQAVI
DLIKEADFKIELEIQTF
>d1fc6a3 b.36.1.3 (A:157-248) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}
AGSVTGVGLEITYDGGSGKDVVVLTPAPGGPAEKAGARAGDVITVDGTAVKGMSLYDSDLQGEADSQEV
VLHAPGAPSNTRTLQLTRQ
>d1k32a1 b.36.1.3 (A:763-853) Tricorn protease {Archaeon Thermoplasma acidophilum}
GRIACDFKLDGDHYVVAKAYAGDYSNEGEKSPIFEYGIDPTGYLIEDIDGETVGAGSNIYRVLSEKAGTSARIRLSG
KGGDKRDLMDIDL
>d1i16_ b.36.1.2 (-) Interleukin 16 {Human (Homo sapiens)}
MPDLNSSTDAAASASAASDVSVESTAEATCTVTLKMSAGLGSLEGGKGSLHGDKPLTINRIFKGAASEQSET
VQPGDEILQLGGTAMQGLTRFEAWNIIKALPDGPVTIVIRRKSLQSKETTAAGDS
>d1g3p_1 b.37.1.1 (1-65) N-terminal domains of the minor coat protein g3p {Bacteriophage M13}
AETVESCLAKSHTENSFTNVWKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIP
>d1g3p_2 b.37.1.1 (91-217) N-terminal domains of the minor coat protein g3p {Bacteriophage M13}
EYGDTPIPGYTYINPLDGTYPGPTEQNPANPNPSLEESQPLNTFMQNNRFRNRQGALTIVTGTQGTDPVK
TYYQYTPVSSKAMYDAYWNGKFRDCAFHSGFNEDIFVCEYQQQSSDLPQPPVNA
>d1fgp_ b.37.1.1 (-) N-terminal domains of the minor coat protein g3p {Bacteriophage fd}
ETVESCLAKPHTENSFTNVWKDDKTLDRYANYEGCLWNATGVVVCTGDETQCYGTWVPIGLAIPENAAAH
>d1b34a_ b.38.1.1 (A:) D1 core SNRNP protein {Human (Homo sapiens)}
KLVRFLMKLSHETVTIELKNGTQVHGTTGVDVSMNTHLKAVKMTLNREPQLETLSIRGNNIRYFILPDSLPLD
TLLV

>d1b34b_b.38.1.1 (B:) D2 core SNRNP protein {Human (Homo sapiens)}
TGPLSVLTQSVKNNTQVLINCRNNKKLLGRVKA FDRHCNMVLENVKEMWTEVPKSGKGKKSKPVNKDRYISK
MFLRGDSVIVVLRNPLIAGK

>d1d3ba_b.38.1.1 (A:) D3 core SNRNP protein {Human (Homo sapiens)}
GVPIKVLHEAEGHVTCETNTGEVYRGK LIEAEDNMNCQMSNITVTYRDGRVAQLEQVYIRGCKIRFLILPD

>d1d3bb_b.38.1.1 (B:) B core SNRNP protein {Human (Homo sapiens)}
SKMLQHIDYRMRCILQDGRIFIGTFKA FDKHMNLILCDCDEFRKIKPKNSKQAEREEKRVGLVLLRGENLVSMT
VEGPPP

>d1d3bl_b.38.1.1 (L:) B core SNRNP protein {Human (Homo sapiens)}
TVGKSSKMLQHIDYRMRCILQDGRIFIGTFKA FDKHMNLILCDCDEFRKIKPKNSKQAEREEKRVGLVLLRGEN
LVSMTVEGPPP KDTG

>d1i81a_b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium thermoautotrophicum}
RVNVQRPLDALGNLSLNSPVIILKGDREFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGDNIVYISP

>d1jria_b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium thermoautotrophicum}
QRPLDALGNLSLNSPVIILKGDREFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLGTVLIRGDNIVYISRGK

>d1i8fa_b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Pyrobaculum aerophilum}
ATLGATLQDSIGKQVLVKLRDSHEIRGILRSFDQHVNLLEDAEIIDGNVYKR GTMVVRGENVLFISPVP

>d1i4k1_b.38.1.1 (1:) Archaeal homoheptameric Sm protein {Archaeon Archaeoglobus fulgidus}
PPRPLDVNRSLKSPVIVRLKGGREFRGTLGYDIHMNLVLLDAEEIQNGEVVRKVGSVIRGDTVVFVSPA

>d1h5pa_b.99.1.1 (A:) Nuclear autoantigen Sp100b {Human (Homo sapiens)}
MDENINFHQSELPTCGEVKGTLYKERFKQGT SKKCIQSEDKKWFTPREFEIEGDRGASKNWKL SIRC GGYTLKV
LMENKFLEPEPPSTRKKVTIK

>d1whi_b.39.1.1 (-) Ribosomal protein L14 {Bacillus stearothermophilus}
MIQQESRLKVADNSGAREV LVIKVLGGSGRRYANIGDVV VATVKDATPGGVVKKGQVVKA VVVRTKRGVRRP
DGSYIRFDENACVI RDDKSPRGTRIFGPVARELRDKDFMKIISLAPEVI

>d1jj2j_b.39.1.1 (J:) Ribosomal protein L14 {Archaeon Haloarcula marismortui}
MEALGADVTQGLEKGS LITCADNTGARELKVISVHGSGT KRNHPKAGLGDKITV S VTKGTPEMRRQVLEAVV
VRQRKPI RPDGTRVKFEDNA AIVDENEDPRGTELKGPI AREVAQRFGS VASAATMIV

>d1ez6a_b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}
LHKEPATLIKAIDGDTV KLMYKGQPMVF RLLLVDIPETKHPKKGV EKGPEAAAFTKKMVENAKKIEVEFDKGQ
RTDKYGRGLAYIYADGK MVNEALVRQGLAKVAYVYKGNNTHEQLLRKA EAQAKKEKLNIWS

>d1joqa_b.40.1.1 (A:) Staphylococcal nuclease {Staphylococcus aureus}
ATSTKKLHKEPATLIKAIDGDTV KLMYKGQPMTF RLLLVDTPETKHPKKGV EKGPEASAF TKKMVENAKKIEVE
FDKGQRTDKYGRGLAYIYADGK MVNEALVRQGLAKVAYVYKPNNTHEQLLRKA EAQAKKEKLNIWS EDNADS
GQ

>d1sty_b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}
KLHKEPATLIKAIDGDTV KLMYKGQPMTF RLLLVDTPETKHPKKGV EKGPEASAF TKKMVENAKKIEVEFDKG
QRTDKYGRGLAYIYADGK MVNEALVRQGLAKVAYVYKPNNTHEQLLRKA EAQAKKEKLNIWS

>d2sob_b.40.1.1 (-) Staphylococcal nuclease {Staphylococcus aureus}
ATSTKKLHKEPATLIKAIDGDTV KLMYKGQPMTF RLLLVDTPETKHPKKGV EKGPEASAF TKKMLENAKKIEVEF
DKGQRTDKYGRV LAYIYADGK MVNEAL

>d1djrd_b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}

APQTITELCSEYRNTQIYTINDKILSYTESMAGKREMVIIKFSGETFQVEVPGSQHIDSQQKAIERMKDTLRITYLT
ETKIDKLCVWNNKTPNSIAISMKN

>d1ltrd_b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}

APQSITELCSEYHNTQIYTINDKILSYTESMAGKREMVIIKFSGATFQVEVPGSQHIDSQQKAIERMKDTLRITYL
TETKIDKLCVWNNKTPNSIAISMKEKLYAGA

>d1tiid_b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IIB}

GASQFFKDNCNRTTASLVEGVELTKYISDINNNTDMGYVSVSSTGGVWRISRAKDYPDNVMTAEMRKIAMA
LSGMRVNMCASPASPVNIWAIELEA

>d3chbd_b.40.2.1 (D:) Cholera toxin {Vibrio cholerae}

TPQNITDLCAEYHNTQIHTLNDKIFSITESLAGKREMAIITFKNGATFQVEVPGSQHIDSQQKAIERMKDTLRIAY
LTEAKVEKLCVWNNKTPRAIAISMAN

>d1c4qa_b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}

TPDCVTGKVEYTKYNDDDFTVKVGDKELATNRANLQLSLLSAQITGMTVTIKTNACHNGGFSEVIFR

>d2bosa_b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}

ADCAKGKIEFSKYNEEDNTFTVKVSGREYWTRWNLQPLQSAQLTGMTVTIISNTCSSSGFAEVQFN

>d1prtb1_b.40.2.1 (B:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain
{Bordetella pertussis}

TTRNTGQPATDHYSNVTATRLSSTSRLCAVFVRSGQPVIGACTSPYDGKYWSMYSRLKMLYLIYVAGISVR
VHVSKEEQYYDYEDATFETYALTGISICNPGLOSSC

>d1prtc1_b.40.2.1 (C:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain
{Bordetella pertussis}

TIYKTGQPAADHYSKVTATRLLASTNSRLCAVFVRDGQSIVACASPYEGRYRDMYDALRRLLYMIYMSG
VHVSKEEQYYDYEDATFQTYALTGISLCNPAAASIC

>d1prtd_b.40.2.1 (D:) Pertussis toxin S4 subunit {Bordetella pertussis}

DVPYVLVKTNMVVTSVAMKPYEVTPTRMLVCGIAAKLGAAASSPDAHPFCFGKDLKRGSSPM
MQQRPLRMFLGPQLTFEGKPALELIRMVCESGKQDCP

>d1prtf_b.40.2.1 (F:) Pertussis toxin S5 subunit {Bordetella pertussis}

LPTHLYKNFTVQELALKKGKNQECLTAFMSGRSLVRACLDAGHEHDTWFDTMLGFAISAYALKSRIALT
VEDSPYPGTPGDLLELQICPLNGYCE

>d1esfa1_b.40.2.2 (A:1-120) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}

SEKSEEINEKDLRKSELOQGTALGNLKQIYYYNEAKTENKESHDQFLQHTILFGFTDHSWYNDLLDFDSKDI
VDKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT

>d1i4pa1_b.40.2.2 (A:1-120) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}

ESQPDPTPDELHKSSEFTGTMGNMKYLYDDHYVSATKMSVDKFLAHDLIYNISDKKLKNYDKV
KKYKDEVVDVYGSNNYVNCYFSSKDNVGKVTGGKTCMYGGITKHEG

>d3tss_1_b.40.2.2 (5-93) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}

NIKDLLDWYSSGSDTFTNSEVLDNSLGSMSRIKNTDGSISLIIFPSPYSPAFTKGEKVDLNTKRIKSQHTSEG
HFQISGVTNTEK

>d1sebd1_b.40.2.2 (D:2-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

SQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLISIKDTYDNVRVEFKNKDLADKYKDK
YVDVFGANYYYQCYFSKKKTCMYGGVTEH

>d3seb_1_b.40.2.2 (1-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

ESQPDPKPDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDIYSIKDTKLGNYDNVRVEFKNKDLAD
KYKDVKYDVGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGVTEH
>d1jckb1 b.40.2.2 (B:1-121) Staphylococcal enterotoxin C3, SEC3 {Staphylococcus aureus}
ESQPDPMPPDDLHSSEFTGTMGNMKYLDDHYVSATKVKSVDKFLAHDLIYNINDKLNNDKVKTELLNEDL
ANKYKDEVVDVYGSNYYVNCYFSSKDNVGKVTSGKTCMYGGITKHEGN
>d1enfa1 b.40.2.2 (A:2-101) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}
DLHDKSELTDALANAYGQYNHPFIKENIKSDEISGEKDLIFRNQGDGNDLRVKFATADLAQKFKKNKNVDIYGA
SFYYKCEKISENISECLYGGTTLNS
>d1an8_1 b.40.2.2 (3-95) Streptococcal superantigen Spe-C {Streptococcus pyogenes}
KKDISNVKSDLLAYTITPYDYKDCRVNFSTHTLNIDTQKYRGKDYYISSEMSYEASQKFKRDDHVDVGLFYILN
SHTGEYIYGGITPAQN
>d1et9a1 b.40.2.2 (A:1-95) Streptococcal superantigen Spe-H {Streptococcus pyogenes}
NSYNTTNRHNLESYKHDNSNLIEADSIKNSPDIVTSHMLKYSVKDKNLSVFFEKDWISQEFDKEVDIYALSAQEV
CECPGKRYEAFGGITLTNS
>d1eu3a1 b.40.2.2 (A:2A-96) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}
GLEVDNNSSLRNIYSTIVYEYSDIVDFKTSHNLVTKKLDVRDARDFFINSEMDEYAANDFKTGDKIAVFSPFDW
NYLSKGKVTAYTYGGITPYQK
>d1bxta1 b.40.2.2 (A:1-119) Streptococcal superantigen SSA {Streptococcus pyogenes}
SSQPDPTPEQLNKSSQFTGVGMNLRCYDNHFVEGTNRSTGQLQHDLIFPIKDLKLKNYDSVKTEFNSKDLA
TKYKNKDVDIFGSNYYNCYYSEGNNSCKAKKTCMYGGVTEHHRN
>d1fnua1 b.40.2.2 (A:1-107) Streptococcal pyrogenic exotoxin A1 {Streptococcus pyogenes}
QQDPDPSLHRSSLVKNLQNIYFLYEGDPVTHENVKSVDQLLSDHLIYNVSGPNYDKLKTELKNQEMATLFKDK
NVDIYGVEYYHLCYLCENAERSACIYGGVTNHE
>d1d2ba_b.40.3.1 (A:) TIMP-1 {Human (Homo sapiens)}
CTCVPPHPQTAFCNSDLVIRAKFVGTPEVNQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCYFH
RSHNRSEELIAGKLQDGLLHITTCSFVAPWNSLSAQRRGFTKTYTVGCEE
>d1ueab_b.40.3.1 (B:) TIMP-1 {Human (Homo sapiens)}
CTCVPPHPQTAFCNSDLVIRAKFVGTPEVAQTTLYQRYEIKMTKMYKGFQALGDAADIRFVYTPAMESVCYFH
RSHARSEELIAGKLQDGLLHITTCSFVAPWNSLSAQRRGFTKTYTVGCEE
QLLQGSEKGFQSRHLACPREPLCTWQLRS
>d1br9__b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}
CSCSPVHPQQAFNCADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIIFIYTAPSSAVCGVSL
DVGGKKEYLIAGKAEGDGKMHITLCDFIVPWDLSTTQKSLNHRYQMGCECKITRCPMIPCYISSPDECLWM
DWVTEKNINGHQAKFFACIKRSDGSCAWYRGAA
>d2tmp__b.40.3.1 (-) TIMP-2 {Human (Homo sapiens)}
CSCSPVHPQQAFNCADVVIRAKAVSEKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPEKDIIFIYTAPSSAVCGVSL
VGGKKEYLIAGKAEGDGKMHITLCDFIVPWDLSTTQKSLNHRYQMGCE
>d1bqqt_b.40.3.1 (T:) TIMP-2 {Cow (Bos taurus)}
CSCSPVHPQQAFNCADIVIRAKAVNKKEVDSGNDIYGNPIKRIQYEIKQIKMFKGPDQDIEFIYTAPAAAVCGVSL
DIGGKKEYLIAGKAEGNGNMHITLCDFIVPWDLSATQKSLNHRYQMGCECKITRCPMIPCYISSPDECLWM

DWVTEKNINGHQAKFFACIKRSDGSCAWYRGAAPP
>d1jb3a_ b.40.3.2 (A:) The laminin-binding domain of agrin {Chicken (Gallus gallus)}
ELQRREEEANVLTGTVEEIMNVDPVHHTYSCKVRVWRYLKGKDITHEILLDGGNKVVIGGFGDPLICDNQVS
TGDTRIFFVNPAWPQMWPAPRNELMLNSSLMRITLRNLEEVEHCVEEHRKLLA
>d1k28a1 b.40.8.1 (A:6-129) Tail-associated lysozyme gp5, N-terminal domain {Bacteriophage T4}
NNLNWFVGVEDRMDPLKLGRVRVRVGLHPPQRAQGDVMGIPTEKLPWMSVIQPITSAMSGIGGSVTG
PVEGTRVYGHFLDKWTNGIVLGTYGGIVREKPNRLEGFSDDPTGQYPTRLGNNT
>d1eova1 b.40.4.1 (A:71-204) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}
AKDNYGKLPLIQRSDRTGQKRVKFVDLDEAKDSKEDKEVLFRARVHNTRQQGATLAFTLRQQASLIQGLVKAN
KEGTISKNMVKWAGSLNLESIVLVRGIVKKVDEPIKSATVQNLEIHITKIYTSETPEAL
>d1b8aa1 b.40.4.1 (A:1-103) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus kodakaraensis}
MYRTHYSSEITEELNGQKVVKVAGWWWEVKDLGGIKFLWIRDRDGIVQITAPKKVDPELFKLIPKLRSEDVVAVE
GVVNFTPKAHLGFEILPEKIVVLRNRAET
>d1c0aa1 b.40.4.1 (A:1-106) Aspartyl-tRNA synthetase (AspRS) {Escherichia coli}
MRTEYCGQLRLSHVGQQVTLCGWVNRRRLGSLIFIDMRDREGIVQVFFDPDRADALKASELRNEFCIQVTG
TVRARDEKNINRDMATGEIEVLASSLTIIINRAD
>d1g51a1 b.40.4.1 (A:1-104) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}
MRRTHYAGSLRTHVGEEVVLEGWVNRRRLGGLIFLDLDRDREGIVQVLPQLVAHPASPAYATAERVRPEWVVRAKG
LVRLRPEPNPRLATGRVEVELSALEVLAEAK
>d1bbua1 b.40.4.1 (A:11-154) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}
VVDLNNELKTRREKLANLREQGIAFPNDFRDHTSDQLHAEFDGKENEELEALNIEVAVAGRMMTRRIMGKA
SFVTLQDVGGRIQLYVARDDLPEGVYNEQFKKWDLGDLGAKGKLFKTGTGELSIHCTELRLLTКАLRPLPD
>d1krs_ b.40.4.1 (-) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}
FRRDHTSDQLHAEFDGKENEELEALNIEVAVAGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDLPEGVYNE
QFKKWDLGDILGAKGKLFKTGTGELSIHCTELRLLTKA
>d1e1oa1 b.40.4.1 (A:11-153) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysU}
AIDFNDELNRNREKLAALRQQGVAFPNDFRRDHTSDQLHEEFDAKDNQELESNIEVSVAGRMMTRRIMGKA
SFVTLQDVGGRIQLYVARDSLPEGVYNDQFKKWDLGDIIGARGTLFKTGTGELSIHCTELRLLTКАLRPLP
>d1gm5a2 b.40.4.9 (A:106-285) RecG "wedge" domain {Thermotoga maritima}
CSGEEVDSLTDIQYAKGVGPNRKKLKKLGIETLRDLLEFFPRDYEDRRKIFKLNDLLPGEKVTQGKIVSVERKKF
QNMNILTAVLSDGLVHVPLKWFNQDYLQTYLKQLTGKEVFVTGTVKSNAUTGQYEIHNAEVTPKEGEYVRRILPI
YRLTSGISQKQMRKIFEENIPSLCCSLK
>d1cuk_3 b.40.4.2 (1-64) DNA helicase RuvA subunit, N-terminal domain {Escherichia coli}
MIGRLRGIIIIEKQPPLVLIEVGGVGYEVHMPMTCFYELPEAGQEAIVFTHFVVREDAQLLYGFn
>d1bvs4 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}
LERSLNRVHLLGRVGQDPVLRQVEGKNPVTIFSLATNEMWRSGDSEVYQLGDVSQKTTWHRISVFRPGLRDVA
YQYVKKGSRIYLEGKIDYGEYMDKNNVRRQATTIIADNIIFL
>d1kawa_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}

RGVNKVLVGNLQDPEVRYMPNGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAEVASEYLRKG
SQVYIEGQLRTRKWTDSQGQDRYTTEVVNVGGTMQML
>d1qvca_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}
ASRGVNKVLVGNLQDPEVRYMPNGAVANITLATSESWRDKATGEMKEQTEWHRVVLFGKLAEVASEYLR
KGSQVYIEGQLRTRKWTDSQGQDRYTTEVVNVGGTMQMLGGRQGGAPAGGNIGGGQPQGGWGQPQ
QPQGGN
>d1ewia_ b.40.4.3 (A:) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}
MVGQLSEGAIAAIMQKGDNTIKPILQVINIRPITTGNSPPRYRLLMSDGLNTLSSFMLATQLNPLVEEQQLSSNC
VCQIHRFIVNTLKDGRRVILMELEVLSAEAVGVKIGN
>d1fgua1 b.40.4.3 (A:181-298) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}
MSKVVPPIASLTPYQSKWTICARVTNKSQIRTWSNSRGEKLFSELVDGESGEIRATAFNEQVDKFFPLIEVNKVYY
FSKGTLKIANKQFTAVKNDYEMTFNNETSVMPCEDDHHLPTV
>d1fgua2 b.40.4.3 (A:299-426) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}
QFDFTGIDDLENKSKDSLVDIIGICKSYEDATKITVRSNNREVAKRNIYLMDTSGKVVTATLGEDADKFDGSRQ
PVLAIGARVSDFGGRSLVSSSTIIANPDIPEAYKLRGWFDAEGQALDGVS
>d1quqa_ b.40.4.3 (A:) Replication protein A 32 KDa subunit (RPA32) fragment {Human (Homo sapiens)}
HIVPCTISQLLSATLVDEVFRIGNVEISQVTIVGIIRHAEKAPTNIVYKIDDMTAAPMDVRQWVDTDDTSSENTV
VPPETYVKVAGHLRSFQNKKSLVAFKIMPLEDMNEFTTHILEVINAHMVLSK
>d1quqb_ b.40.4.3 (B:) Replication protein A 14 KDa (RPA14) subunit {Human (Homo sapiens)}
DMMDLPRSRINAGMLAQFIDKPVCVGRLEKIHTGKMFILSDGEGKNGTIELMEPLDEEISGIVEVVGRVTAK
ATILCTSYVQFKEDSHPDFDLGLYNEAVKIIHDFPQFYPLG
>d1jb7a1 b.40.4.3 (A:36-204) Telomere end binding protein alpha subunit {Oxytricha nova}
YEYVELAKASLTSAQPQHFYAVVIDATFPYKTNQERYICSLKIVDPTLYLKQQKGAGDASDYATLVLAKRFEDLPII
HRAGDIIRVHRATLRLYNGQRQFNANVFYSSSWALFSTDKRSVTQEINNQDAVSDTPSFSSKHATIEKNEISIL
QLNRKWANQYFSSYS
>d1jb7a2 b.40.4.3 (A:205-328) Telomere end binding protein alpha subunit {Oxytricha nova}
VISSDMYTALNKAQAQKGDFDVVAKILQVHELDEYTNELKLKDASGQVFYTLSKLKFPHVRTGEVVRIRSATYD
ETSTQKKVLILSHYSNIITFIQSSKLAKELRAKIQDDHSVEASLKKN
>d1jb7a3 b.40.4.3 (A:329-495) Telomere end binding protein alpha subunit {Oxytricha nova}
SLNAVVLTEVDKKHAALPSTSQQDLFHADSDKELQAQDTFRQFYVTKIEPSDVKEWVKGYDRTKKSSLKG
ASGKGDNIFQVQFLVKDASTQLNNNTYRVLLYTQDGLGANFFNVKADNLHKNADARKKLEDSAELLTKFNSYV
DAVVERRNGFYLIKDTKLI
>d1k8ga2 b.40.4.3 (A:205-315) Telomere end binding protein alpha subunit {Oxytricha nova}
VISSDMYTALNKAQAQKGDFDVVAKILQVHELDEYTNELKLKDASGQVFYTLSKLKFPHVRTGEVVRIRSATYD
ETSTQKKVLILSHYSNIITFIQSSKLAKELRAKIQD
>d1jb7b_ b.40.4.3 (B:) Core domain of telomere end binding protein beta subunit {Oxytricha nova}
QQQSAFKQLYTELFNNNEGDFSKVSSNLKKPLCYKESYPHFLVTDGYFFVAPYFTKEAVNEFHAKFPNVNIVDLT
DKVIVINNWSLELRRVNSAEVFTSYANLEARLIVHSFKPNLQERLNPTRYPVNLFRDDEFKTTIQHFRHTALQAAI
NKTVKGDNLVDISKVADAAGKKGVDAVKGKVDAGIVKASASKGDEFSDSFKEGNTATLKIADIFVQEKG
>d1jjcb3 b.40.4.4 (B:39-151) Domain B2 of PheRS-beta, PheT {Thermus thermophilus (Thermus

aquaticus)}

FPIPRGVVFARVLEAHPIPGTRLKRLVLDAGRTVEVSGAENARKGIGVALALPGTELPGLGQKVGERVIQGVRS
FGMALSPRELGVGEYGGGLLEFPEDALPPGTPLSEAWP

>d1fl0a_ b.40.4.4 (A:) EMAP II {Human (Homo sapiens)}

IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVSGLVNVHVPLEQMQRNMVILLCNLPAKMRGVLSQ
AMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPDKELNPKKIWEQIQPDLHTNDECVATYKGVPFEVKGK
GVCRAQTMSNSGIKL

>d1gd7a_ b.40.4.4 (A:) CsaA {Thermus thermophilus}

MTPLEAFQILDLRVGRVLRAEPHEKARKPSYKLWVDLGPLGVQSSAQITELYRPEDLVGRLVVCAVNLAKRVA
GFLSEVLVLGVPDEAGRVVLLAPDREVPLGGKVF

>d1mjc_ b.40.4.5 (-) Major cold shock protein {Escherichia coli}

SGKMTGIVKWFNADKGFGFITPDDGSKDVFHFSAIQNDGYKSLDEGQKVSTIESGAKGPAAGNVTLS

>d1csp_ b.40.4.5 (-) Major cold shock protein {Bacillus subtilis}

MLEGKVKWFNSEKGFGFIEVEGQDDVFVHFSAIQGEGFKTLEEGQAVSFEIVEGNRGQPQAANVTKEA

>d1c9oa_ b.40.4.5 (A:) Major cold shock protein {Bacillus caldolyticus}

MQRGKVKWFNNEKGYGFIIEVEGGSDFVHFTAIQGEGFKTLEEGQEVSFEIVQGNRGQPQAANVVKL

>d1g6pa_ b.40.4.5 (A:) Major cold shock protein {Thermotoga maritima}

MRGKVKWFDSKKGYGFITKDEGGDVFHWSAIMEGFKTLKEGQVVEFEIQEGKKGPQAAHVKVVE

>d1h95a_ b.40.4.5 (A:) Y-box protein 1 cold shock domain (YB1-CSD) {Human (Homo sapiens)}

MKKVIATKVLGTVKWFNVRNGYGFINRNDTKEDVFVHQTAIKNNPRKYLRSVGDGTEVFDFVVEGEKGAEAA
ANVTGPG

>d1sro_ b.40.4.5 (-) S1 RNA-binding domain of polyribonucleotide phosphorylase, PNPase
{Escherichia coli}

AEIEVGRVTGKVTRIVDFGAFVAIGGGKEGLVHISQIADKRVEKVTDYLQMGQEVPVKLEVDRQGRIRLSIKE
A

>d1e3pa2 b.40.4.5 (A:656-717) S1 RNA-binding domain of polyribonucleotide
phosphorylase, PNPase {Streptomyces antibioticus}

GSVVKTTTFGAFVSLLPGKDGLLHISQIRKLAGGKRVENVEDVLGVGQKVQVEIAEIDSRGK

>d1hh2p1 b.40.4.5 (P:127-198) S1 domain of NusA {Thermotoga maritima}

FEKYSELKGTVTTAEVIRVMGEWADIRIGKLETRLPKKEWIPGEEIKAGDLVKVYIIDVVKTTKGPKILVSR

>d1k0ra1 b.40.4.5 (A:108-183) S1 domain of NusA {Mycobacterium tuberculosis}

STREGEIVAGVIQRDSRANARGLVVVRIGTETKASEGVIPAAEQVPGESYEHGNRLCYVVGVTGAREPLTLSR

>d1go3e_ b.40.4.5 (E:) RNA polymerase II subunit RBP4 (RpoE) {Archaeon Methanococcus jannaschii}

MYKILEIADVVKVPPEFGKDLKETVKKILMEKYEGRLDKDVGFLSIVDVKD1GEGKVVHGDGSAYHPVVFETL
VYIPEMYELIEGEVVDVVEFGSFVRGLGPLDGLIHSVQIMDDYVSYDPKREAIIKGKTVLEIGDYVRARIVAISLK
AERKRGSKIALTMRQPYLGKLEWIEEKAKKQ

>d1ah9_ b.40.4.5 (-) Translational initiation factor 1, IF1 {Escherichia coli}

AKEDNIEMQGTVLETLPNTMFRVELENGHVVTAHISGKMRKNYIRILTGDKVTVELTPYDLSKGRIVFRSR

>d1hr0w_ b.40.4.5 (W:) Translational initiation factor 1, IF1 {Escherichia coli}

AKEKDTIRTEGVVTEALPNATFRVKLDGSGPEILAYISGKMRMHYIRILPGDRVVVEITPYDPTRGRIVYRK

>d1jt8a_ b.40.4.5 (A:) Archaeal initiation factor-1a, aIF1a {Archaeon Methanococcus jannaschii}

MAEQQQEQQIRVIRPRKEENEILGIIEQMLGASRVVRCLDGKTRLGRIPGRLKNRIWVREGDVVIVKPWEVQ
GDQKCDIIWRYTKTQVEWLKRKGYLDELL

>d1d7qa_b.40.4.5 (A:) Translation initiation factor-1a, eIF1a {Human (Homo sapiens)}
PKNKGKGGKNRRRGKNENESEKRELVFKEQYAQVIKMLGNGRLEAMCFDGVKRLCHIRGKLKKVVINT
SDIILVGLRDYQDNKADVLKYNADEARSLKAYGELPEHAKINETDTFGPGDDDEIQFDDIGDDDEDIDDI
>d1a62_2 b.40.4.5 (48-125) Rho termination factor, RNA-binding domain {Escherichia coli}
DIFGDGVLEILQDGFGFLRSADSSYLAGPDDIVSPSQIRRFNLRTGDTISGKIRPPKEGERYFALLKVNEVNFDP
E
>d2eifa2 b.40.4.5 (A:74-132) C-terminal domain of eukaryotic initiation translation
factor 5a {Archaeon Methanococcus jannaschii}
IDRRKGQVLAIMGDMVQIMDLQTYETLELPIPEGIEGLEPGGEVEYIEAVGQYKITRVI
>d1bkb_2 b.40.4.5 (75-139) C-terminal domain of eukaryotic initiation translation factor 5a
{Archaeon Pyrobaculum aerophilum}
IIEKFTAQILSVDVQLMDMRDYKTIEVPMKYVEEEAKGRLAPGAEVEVWQILDRYKIIRVKG
>d1rl2a2 b.40.4.5 (A:60-125) N-terminal domain of ribosomal protein L2 {Bacillus
stearothermophilus}
QYRIIDFKRDKDGPGRVATIEYDPNRSANIALINYADGEKRYIIAPKNLKVGMEIMSGPDADI
>d1jj2a2 b.40.4.5 (A:1-90) N-terminal domain of ribosomal protein L2 {Archaeon Haloarcula
marismortui}
GRRIQGQRRGRGTSTFRAPSHRYKADLEHRKVEDGDIVAGTVVDIEHDPARSAPVAAVEFEDGDRLILAPEGV
GVGDELQVGVDIAEIA
>d1fjgl_b.40.4.5 (L:) Ribosomal protein S12 {Thermus thermophilus}
PTINQLVRKGREKVRKSKVPALKGAPFRRGVCTVVRTVTPKKPNSALRKVAKVRLTSGYEVTAYIPGEGHNLQE
HSVVLIRGGRVKDLPGVRYHIVRGVYDAAGVKDRKKSRSKYGTKKPKEAA
>d1fjqq_b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}
PKKVLTVVVSDKMQKTVTVLVERQFPHPLYGKVIKRSKKYLAHDPEEKYKLGDVVEIIESRPISKRKFRVRLVE
SGRMDLVEKYLIRRQNYQSLSKRGGKA
>d1i94q_b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}
PKKVLTVVVSDKMQKTVTVLVERQFPHPLYGKVIKRSKKYLAHDPEERYKVGDVVEIIEARPISKRKFRVRLV
EEGRLLDVEKYLIRRQNYQSLSKRGGKA
>d1rip__ b.40.4.5 (-) Ribosomal protein S17 {Bacillus stearothermophilus}
QRKVYVGRVVSDFKMDKTITVLVETYKKHPLYGKRVKYSKKYAHDEHNEAKVGDIVKIMETRPLSATKRFRVRLVE
VEKAVR
>d1ckma1 b.40.4.6 (A:239-327) RNA guanylyltransferase (mRNA capping enzyme) {Chlorella virus,
PBCV-1}
THHTIDFIIMSEDGTIGIFDPNLRKNVPVGKLDGYYNKGSIVECGFADGTWKYIQGRSDKNQANDRLTYEKTLLN
IEENITIDELLDLF
>d1a0i_1 b.40.4.6 (241-349) ATP-dependent DNA ligase {Bacteriophage T7}
PENEADGIIQGLVWGTGLANEKGKVIGFEVLLESGRLVNATNISRALMDEFTEVKEATLSQWGFFSPYIGDN
DACTINPYDGWACQISYMEETPDGSLRHPSFVMFR
>d1fvia1 b.40.4.6 (A:190-293) ATP-dependent DNA ligase {Chlorella virus, PBCV-1}
FKDAEATIISMTALFKNTNTKDNFGYSKRSTHKSGKVEEDVMGSIEVDYDGVVFSIGTGFDADQRRDFWQN
KESYIGKMKVFKYFEMGSKDCPRFPVFIGIR
>d1dgsa2 b.40.4.6 (A:315-400) NAD+-dependent DNA ligase {Thermus filiformis}
AEEKETRLLDVVFQVGRTGRVTPGVLEPVFIEGSEVSRTLHNESYIEELDIRIGDWVLVHKAGGVIEPEVRLVLK
ERRTGKERPI

>d1gvp__ b.40.4.7 (-) Gene V protein {Filamentous bacteriophage (f1, M13)}

MIKVEIKPSQAQFTTRSGVSRQGKPYSLNEQLCYVDLGNEYPVLVKITLDEGQPAYAPGLYTvhLSSFKVGQFGSL
MIDRLRLVPAK

>d1pfsa_ b.40.4.7 (A:) Gene V protein {Pseudomonas bacteriophage pf3}

MNIQITFTDSVRQGTSAKGNPYTFQEGFLHLEDKPHPLQCQFFVESVIPAGSYQVPRINVNNGRPELA FDKA
MKRA

>d1gpc_ b.40.4.7 (-) Gene 32 protein (gp32) core {Bacteriophage T4}

GFSSEDKGEWKLKLDNAGNGQAVIRFLPSKNDEQAPFAILVNHGFKKNGKWYIETCSSTHGDYDSCPVCQYISK
NDLYNTDNKEYSLVKRKTSYWANILVVKDPAAPENEGKVFKYRGKKIWDKINAMIAVDVEMGETPVDVTCP
WEGANFVLKVQVSGFSNYDESKFLNQSAIPNIDDEFQKELFEQMVDLSEMTSKDKFKSFEELNTKFGQVM

>d1je5a_ b.40.4.7 (A:) gp2.5 {Bacteriophage T7}

MAKKIIFTSALGTAEPYAYIAKPDYGNEERGFGNPRGVYKVDLTIPNKDPRCQRMVDEIVKCHEEAYAAVEEYE
NPPAVARGKKPLKPYEGDMPPFDNGDGTTFKFKCYASFQDKKTETKHINLVVDSKGKKMEDVPIIGGGSKL
KVKYSLVPYKWNTAVGASVQLQLESVMLVELATFGGGEDDWADVEEN

>d1i50h_ b.40.4.8 (H:) RNA polymerase subunit RBP8 {Baker's yeast (Saccharomyces cerevisiae)}

SNTLFDDIFQVSEVDPGRYNKVCRIAAS TTQDQCKLTDINVELFPVAAQDSLTVTIASSLNLEDTPANDSSATRS
WRPPQAGDRSLADDYDYVMYGTAYKFEEVSKDLIAVYYSGGLLMRLEGNYRNLNNLKQENAYLLIRR

>d1e9ga_ b.40.5.1 (A:) Inorganic pyrophosphatase {Baker's yeast (Saccharomyces cerevisiae)}

TYTTRQIGAKNTLEYKVIEKDGPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEITKEETLNPIIQDTKKGKL
RFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPIDVLEIGETIAYTGQVKQVKALGIMALLDEGE
TDWKVIAIDINDPLAPKLNDIEDVEKYFPGLLRATNEWFRIYKIPDGK PENQFAFSGEAKNKKYALDIKETHDSW
KQLIAGKSSDSKGIDLTNVLPDTPTYSKAASDAIPPASL KadAPIDKSIDKWFFISG

>d1qeza_ b.40.5.1 (A:) Inorganic pyrophosphatase {Archaeon Sulfolobus acidocaldarius}

KLSPGK NAPDVNVLVEIPQGSNIKYEYDDEEGVIK VDRVLYTSMNYPFNYGFIPGTLEEDGDPLDVLVITNYQLY
PGSVIEVRPIGILYMKDEEGEDAKIVAVPKDKTDPSFSNIKDINDLPQATKNKIVHFFEHYKELEPGKYVKISGWGS
ATEAKNRQIQLAIKRVSG

>d1i40a_ b.40.5.1 (A:) Inorganic pyrophosphatase {Escherichia coli}

SLLNPAGKDLPE DIYV VIEIPANADPIKYEIDKESGALFVDRFMSTAMF YPCNYGYINHTSLGDGPVDVLVPTP
YPLQPGSVTRCRPVGVLMKTDEAGEDAKLVAVPHSKLSKEYDH KDVNDLPELLKAQIAHFFEHYKDLEKGK
KVEGWENAEAAKAEIVASFERAKNK

>d2prd_ b.40.5.1 (-) Inorganic pyrophosphatase {Thermus thermophilus}

ANL KSLPVGDKAPEV VHMVIEPRGSGN KYEYDPE DPGD LGA IKL DRV LPG A QF YPG DY G FIP STLA EGD PLD GLV
L STYPLLPGVVVE RVV VG LLL MEDE KGG DAK VIG VVA ED QRL DH IQD IGV PEG VK QEI QH FF ETY KALEAKKGK
WV KV TG W RDR KA A LE EV RACIARYKG

>d1fr3a_ b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {Sporomusa ovata}

MKISGRNKLEATVKEIVKGTVMAKIVMDYKGTELVAITIDSVALDLVPGDKVTALVKATEMEVLK

>d1guta_ b.40.6.1 (A:) Molybdate/tungstate binding protein MOP {Clostridium pasteurianum, MOP II}

SISARNQLKGKVVG LKKGVVTAEVVLEIAGGNKITSIISLDSVEELGVKEGAELTAVVKSTDVMILA

>d1h9ma1 b.40.6.2 (A:1-73) Cytoplasmic molybdate-binding protein ModG {Azotobacter vinelandii}

MKISARNVFKGTVS ALKEGAVNAEV DILLGGGDKLA AVVTLESARSLQ LAAGKEVVA VVKAPWVLLMTDSSGY

>d1h9ma2 b.40.6.2 (A:74-141) Cytoplasmic molybdate-binding protein ModG {Azotobacter vinelandii}

RLSARNILTGTVKTIETGAVNAEVTLALQGGTEITSMVTKEAVAEGLKLPGASASAVIKASNVLGV
>d1h9ra1 b.40.6.2 (A:123-199) C-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}
MQTSARNQWFGTITARDHDDVQQHVDVLLADGKTRLKVAITAQSGARLGLDEGKEVLILLKAPWVGITQDEA
VAQNA
>d1h9ra2 b.40.6.2 (A:200-261) C-terminal domain of molybdate-dependent transcriptional regulator ModE {Escherichia coli}
DNQLPGIISHIERGAEQCEVLMALPDGQTLCATVPVNEATSLQQGQNVTAYFNADSVIIATL
>d1g2913 b.40.6.3 (1:241-301) Maltose transport protein MalK, C-terminal domain {Archaeon Thermococcus litoralis}
GSPPMNFLDAIVTEDGFVDFGEFRLKLLPDQFEVLGELGYVGREVFIRPEDLYDAMFAQ
>d1g2914 b.40.6.3 (1:302-372) Maltose transport protein MalK, C-terminal domain {Archaeon Thermococcus litoralis}
VRVPGENLVRAVVEIVENLGSERIVRLRVGGTFVGSFRSERVREGVEVDVVFDMMKKIHIFDKTTGKAIF
>d1b3qa2 b.40.7.1 (A:540-671) Histidine kinase CheA, C-terminal domain {Thermotoga maritima}
TLAIICALLVKVNNLVYAPIANIDTILSKEDIQRVQDRDVIVIRGEVIPVYRLWEVLQIEHKEELEEMEAIVVRVG
NRKYGIVVDDLLGQDDIVIKSLGKVFSEVKEFSGAAILGDGSIALINVSGIV
>d1k0sa_ b.40.7.1 (A:) Chemotaxis protein CheW {Thermotoga maritima}
MKTLDALKEFEVLSFEIDEQALAFDVEDNIEMVIEKSDITPVPKSRHFVEGVINLRGRRIIPVVNLAKILGISFDEQK
MKSIIIVARTKDVEVGFVLDRVLGVLRITENQLDTNVSDKFGKKSKGLVKTDGRLIIYLDIDKIIEITVKEGV
>d1dxrh1 b.41.1.1 (H:37-258) Photosynthetic reaction centre {Rhodopseudomonas viridis}
RREGYPLVEPLGLVKLAPEDGQVYELPYPKTFVLPHGGTVTPRRPETRELKLAQTDGFEGAPLQPTGNPLVDA
VGPASYAERAEEVVDATVDGKAKIVPLRVATDFSIAEGDVDPRGLPVVAADGVEAGTVTDLWVDRSEHYFRYLEL
SVAGSARTALIPLGFCDVKDKIVVTSILSEQFANVPRLQSRDQITLREEDKVSAYYAGGLYATPERAESLL
>d1qovh1 b.41.1.1 (H:36-250) Photosynthetic reaction centre {Rhodobacter sphaeroides}
MREGYPLENEDGTPAACQGPFPPLPKPKTFILPHGRGTLTVPGPESEDRPIALARTAVSEGFPHAPTGDPMKDGV
GPASWVARSDLPELDGHGHNKIKPMKAAAGFHVSAGKNPIGLPVRGCDLEIAGKVVDIWVDIPEQMARFLEV
ELKDGSTRLPMQMVKVQSNRVHVNALSSDLFAGIPTKSPEVTLLEEDKICGYVAGGLMYAAPKRKS
>d1eysh1 b.41.1.1 (H:59-259) Photosynthetic reaction centre {Thermochromatium tepidum}
PDLPDPKTFVLPHNGGTVVAPRVEAPVAVNATPFSPAPGSPLVNGDPMILSGFGPAASPDFRKHCDLTFEGLPK
IVPMRVAKEFSIAEGDPDPRGMVVGLDGEVAGTVSDVVDRSEPQIRYLEVEVAANKKVLLPIGFSRFDKKA
RKVKVDAIAAHFANVPTLSNPDQVTLYEEDKVCAYYAGGKLYATAERAGPLL
>d1bfg_ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}
DPKRLYCKNGGFFLRIHPDGRVDRKSDPHIKLQLQAEERGVSIKGVSANRYLAMKEDGRLLASKSVTDEC
FFFERLESNNYNTYRSRKYTWSYVALKRTGQYKLGSKTGPGQKAILFLPMSA
>d1bla_ b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}
MAEGEITTPALPEDGGSGAFFPPGHFKDPKRLYCKNGGFFLRIHPDGRVDRKSDPHIKLQLQAEERGVVSICK
GVSANRYLAMKEDGRLLASKSVTDECFFERLESNNYNTYRSRKYTWSYVALKRTGQYKLGSKTGPGQKAILFLP
MSAKS
>d1bara_ b.42.1.1 (A:) Acidic FGF (FGF1) {Cow (Bos taurus)}
PKLLYCSNGGYFLRILPDGTVDGTKDRSDQHQIQLQLAAESIGEVYIKSTETGQFLAMTDGLLYGSQTPNEECLFL

ERLEENGYNTYISKKHAEKHWFVGLKKNGRSKLGPRTHFGQKAILFLPLPV
>d1jqza_b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}
HHHHFNLPPGNYKKPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHQIQLQLSAESVGEVYIKSTETGQYLAMD
GLLYGSQTPNEECLFLERLEENHYNTYISKKHAEKWNWFVGLKKNGSCKRGPRTHYGQKAILFLPLPV
>d2afga_b.42.1.1 (A:) Acidic FGF (FGF1) {Human (Homo sapiens)}
KPKLLYCSNGGHFLRILPDGTVDGTRDRSDQHQIQLQLSAESVGEVYIKSTETGQYLAMD
GLLYGSQTPNEECLFLERLEENHYNTYISKKHAEKWNWFVGLKKNGSCKRGPRTHYGQKAILFLPLPV
>d1fmms_b.42.1.1 (S:) Acidic FGF (FGF1) {Eastern newt (Notophthalmus viridescens)}
QKPKLLYCSNGGYFLRIFPDGKVDGTRDRSDPYIQLQFYAESVGEVYIKSLETGQYLAMD
SDGQLYASQSPSEECLFLERLEENNYNTYKSKVHADKDWFVGKIKKNGKTKPGSRTHFGQKAILFLPLPVSSD
>d1ijta_b.42.1.1 (A:) Fibroblast growth factor 4 (FGF4) {Human (Homo sapiens)}
GIKRLRRLYCNVGIGFHQLQALPDGRIGGAHADTRDSLLELSPVERGVVSIFGVASRFFVAMSSKGKLYGSPFFTDE
CTFKEILLPNNNAYESYKYPGMFIALGKNGKTKKGNRVSPTMKVTHFLPRL
>d1qqka_b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus norvegicus)}
DIRVRRLCRTQWYLRIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIKGVESEYYLAMNKEGKLYAKKECNE
DNFKELILENHNTYASAKWTHSGGEMFVALNQKGLPVKGKKTKEQKTAHFLPMAIT
>d1qqla_b.42.1.1 (A:) Keratinocyte growth factor, FGF7 {Rat (Rattus norvegicus)}
DIRVRRLCRTQWYLRIDKRGKVKGTQEMRNSYNIMEIRTVAVGIVAIKGVESEYYLAMNKEGKLYAKQTPNEEC
LFLERLEENHYNTYISKKHAEKWNWFVGLKKNGSCKRGPRTHYGQKAILFLPLPVSS
>d1ihka_b.42.1.1 (A:) Fibroblast growth factor 9, FGF9 {Human (Homo sapiens)}
TDLDHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRGILEFISIAVGLVSIRGVDSGLYLG
MNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGTPREGTRTKRHQKFTHFL
PRPVDPDKVPELYKDISQS
>d1i1b_b.42.1.2 (-) Interleukin-1beta {Human (Homo sapiens)}
VRSLNCTLRDSQQKSLVMSGPYELKALHLQGQDMEQQQVFSMSFVQGEESNDKIPVALGLKEKNLYLSC
VLKD
DKPTLQLESVDPKNYPKKMEKRFVFNKIEINNKLEFESAQFPNWYISTSQAENMPVFLGGTKGGQDITDF
TMQFVSS
>d8i1b_b.42.1.2 (-) Interleukin-1beta {Mouse (Mus musculus)}
QLHYRLRDEQQKSLVSDPYELKALHLNGQNINQQVIFSMSFVQGEPSNDKIPVALGLKGK
NLYLSCVMKDGTPTLQLESVDPKQYPKKMEKRFVFNKIEVKS
KVEFESAEPNWYISTSQA
EHNPKVFLGNNSGQDIIDFTMESV
>d1ilr1_b.42.1.2 (1:) Interleukin-1 receptor antagonist protein {Human (Homo sapiens)}
SKMQAFRIWDVNQKTFYLRNNQLVAGYLQGPNVN
LEE
KIDVVPIE
PHALFLGIHGGKMCLSC
VKSGDET
RLQEA
VNITDLSEN
RKQDKRFA
FIRSD
SGPTTS
FESA
ACP
GWFL
CTAME
ADQP
VSLTN
MPDEGV
MVTK
FYFQE
DE
>d2ila_b.42.1.2 (-) Interleukin-1alpha {Human (Homo sapiens)}
NVKYNFMR
IIKYEF
ILNDAL
NQSI
IRANA
AQYL
TAA
LHN
DEAV
KFDM
GAY
KSS
KDD
AKIT
VIL
RISK
TQL
YV
TAQD
EDQP
VLL
KEM
PEI
PKT
ITG
SET
NLL
FFW
ETH
GT
KNY
FTS
VA
H
P
NL
FIAT
K
QD
Y
W
V
C
LAG
GPP
SIT
DFQ
I
LE
>d2aaib1_b.42.2.1 (B:1-135) Plant cytotoxin B-chain (lectin) {Castor bean (Ricinus communis), Ricin}
ADVCMDPEPI
RIVGRNGL
CVRD
GRFH
NGNA
IQL
WP
CKS
NTD
AN
QL
WTL
KRD
NT
IRS
NG
KCL
TT
GY
SPG
VY
V
MI
YDC
NTA
AT
D
TRW
QI
WD
NGT
I
I
N
P
RSS
L
LA
AT
SG
NS
G
TT
L
T
V
QT
NI
Y
AV
SQ
GW
L
PTN
>d2aaib2_b.42.2.1 (B:136-262) Plant cytotoxin B-chain (lectin) {Castor bean (Ricinus communis), Ricin}
NTQPFVTTIV
GLY
GLC
LQAN
SGQ
VW
IED
CS
SE
KA
EQ
QW
AL
YAD
GS
IR
P
QQ
N
R
D
N
C
L
T
S
D
N
I
R
E
T
V
V
K
I
L
S
C
G
P
ASS
GQR
WMF
KND
GT
I
LN
L
Y
S
G
L
V
L
D
V
R
A
S
D
P
S
L
K
Q
I
I
Y
P
L
H
G
D
P
N
Q
I
W
L
P
L
F
>d1abrb1_b.42.2.1 (B:1-140) Plant cytotoxin B-chain (lectin) {Abrus precatorius}

IVEKSICSSRYEPTVRIGGRDGMCSVYDNGYHNGNRIIMWKCKDRLEENQLWTLKSDKTIRSNGKCLTYGY
APGSYVMIYDCTSVAEATYWEIWDNGTIINPKSALVSAESSSMGGTLTVQTNEYLMRQGWRTGN
>d1abrb2 b.42.2.1 (B:141-267) Plant cytotoxin B-chain (lectin) {Abrus precatorius}
NTSPFVTISGYSIDLCKMQAQGSNVWMADCDSNKKEQQWALYTDGSIRSVQNTNNCLTSKDHKGSTILLMG
CSNGWASQRWVFKNDSIISLYDDMVMDVKGSDPSLKQILWPYTGKPNQIWLTLF
>d1ce7b1 b.42.2.1 (B:1-133) Plant cytotoxin B-chain (lectin) {European mistletoe (Viscum album)}
CSASEPTVRIVGRNGMNVDVRDDDFHDGNQIQLWPSKSNNDPNQLWTIKRGDTIRSNGSCLTTYGVTAGVYV
MIFDCATAVGEATVWQIWGNGTIINPRSNLVAASSGIKGTTLVQTLDYTLGQGWLAGND
>d1ce7b2 b.42.2.1 (B:134-255) Plant cytotoxin B-chain (lectin) {European mistletoe (Viscum album)}
TAPREVTIYGFNDLCMESGGGSVTETCSSGKADKWALYGDGSIRPEQNQAQCLTSGGDSVAGVNIVSCGAA
SGQRWVFTNEGAILNLKNGLAMDVANPGGGRIIYPATGKPNQMWLWLF
>d1hwmb1 b.42.2.1 (B:3-135) Plant cytotoxin B-chain (lectin) {Sambucus ebulus, ebulin}
ETCAIPAPFTRRIVGRDGLCVDVRNGYDTDGTPQLWPCGTQRNQQWTFYNDKTIRSMGKCMTANGLNSGSY
IMITDCSTAAEDATKWEVLIDGSIINPSSGLVMTAPSGASRTLLENNIHAASQGWTVSN
>d1hwmb2 b.42.2.1 (B:136-266) Plant cytotoxin B-chain (lectin) {Sambucus ebulus, ebulin}
DVQPIATLIVGYNEMCLQANGENNVMEDCDVTSVQQQWALFDDRTIRVNNSRGLCVTSNGYVSKDLIVI
RKCQGLATQRWFFNSDGSVVNLKSTRVMDVKESDVSLQEVIIFPATGNPNQQWRTQVPQI
>d1xyfa1 b.42.2.1 (A:313-436) Endo-1,4-beta-xylanase C-terminal domain {Streptomyces olivaceoviridis}
GQIKGVGSGRCLDVPNASTTDGTQVQLYDCHSATNQQWTYTDAGELRVYGDKCLDAAGTGNGTKVQIYSCW
GGDNQKWLNSDGSIVGVQSGLCLDAVGGBTANGTLIQLYSCNSGSNQRWTRT
>d1dqga_ b.42.2.2 (A:) Mannose receptor {Mouse (Mus musculus)}
DARQFLIYNEDHKRCVDALSAISVQTATCNPEAESQKFRWVSDSQIMSVAFKLCLGVPSKTDWASVTLYACDSK
SEYQKWECKNDTFLFGIKGTELYFNQYGNRQEKNIKLYKSGGLWSRWKVYGTDDLCRSGYE
>d1jlxa1 b.42.3.1 (A:1-153) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}
AGLPVIMCLKSNNHQYLRYQSDNIQQYGLLQFSADKILDPLAQFEVEPSKYDGLVHIKSRTNKLVRWSPN
HYWITASANEPMENKSNWACTLFKPLYVEEGNMKKVRLHVQLGHYTQNYTVGGSFVSYLFAESSQIDTGSKD
VFHVID
>d1jlxa2 b.42.3.1 (A:154-299) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}
WKSIFQFPKGYVTFKGNNNGKYLGVITINQLPCLQFGYDNLNDPKVAHQMFVTSNGTICKSNYMNKFWRSLTD
DWILVDGNDPRETNEAAALFRSDVHDFNVISLLNMQKTFIKRFTSGKPGFINCMNAATQNVDETAILEIIL
>d1wba__ b.42.4.1 (-) Winged bean albumin 1 {Goa bean (Psophocarpus tetragonolobus)}
DDPVYDAEGNKLVRGKYTIVSFSDGAGIDVVATGNENPEDPLSIVKSTRNIMYATSISSEDKTPPQPRNILENM
RLKINFATDPKGDVWSVDFQPDGQQQLLAGRYPNQVKGAFTIQKGSNTPRTYKLLFCPVGSPCKNIGISTDP
EGKKRLVVSYQSDPLVVKFHRH
>d1tie__ b.42.4.1 (-) Erythrina caffra trypsin inhibitor {Erythrina caffra}
VLLDGNGEVVQNGGTYLLPQVWAQGGGVQLAKTGEETCPLTVQSPNELSDGKPIRIESRLRSAFIPDDDKV
RIGFAYAPKCAPSPWTVVEDEQEGLSVKLSEDESTQFDYPFKFEQVSDQLHSYKLLYCEGKHEKCASEGINRDQ
KGYRRLVVTEDYPLTVVLKKDE
>d1eyla_ b.42.4.1 (A:) chymotrypsin inhibitor WCI {Winged bean (Psophocarpus

tetragonolobus)}

EFDDDLVDAEGNLVENGGTYLLPHIWAHGGIETAKTGNNEPCPLTVVRSPNEVSKGEPIRISSQFLSFLPRGSLV
ALGFANPPSCAASPWTVDSPQGPALKSQQLPEKDILVFKEKVSHSNIHVYKLLYCQHDEEDVKCDQYIG
IHRDRNGNRRLVVTEENPLEVLKLAKS

>d1avwb_b.42.4.1 (B:) Soybean trypsin inhibitor {Soybean (Glycine max)}

DFVLDNEGPNLENGGTYILSDITAFGGIRAAPTGNERCPLTVVQSRNELDKIGTISSPYRIRFIAEGHPLSLKFD
SFAVIMLCVGIPTEWSVVEDLPEGPAVKIGENKDAMDGFRLERVSEFNNYKLVFCPQDKCGDIGISIDHDDGT
RRLVVSKNKPLVVQFQKLD

>d1avac_b.42.4.1 (C:) Amylase/subtilisin inhibitor {Barley (Hordeum vulgare), seed}

ADPPPWHDTDGHELRADANYVLSANRAHGGGLTMAGPHGRHCPLFVSQLDPNGQHDGFPVRITPYGVAPSD
KIIRLSTDVRISFRAYTTCLQSTEWHIDSELAAGRRHVITGPVKDPSPSGRENAFRIEKYSGAEVHEYKLMSCGDW
CQDLGVFRDLKGGAWFGLATEPYHVVVFKKAPPA

>d1a8d_2 b.42.4.2 (248-452) Tetanus neurotoxin {Clostridium tetani}

ITFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYMILTNAPSNTNGKLNIIYRRLYNGLFIIKRYTPNNEIDS
FKVSGDFIKLYVSYNNEHIVGPKDGNFNNLDRILRVGYNAPIPLYKKMEAVKLRLKTYSQLKLYDDKNA
SLGLVGTHNGQIGNDPNRDILIASNWYFNHLKDKILGCDWYFVPTDEGWTND

>d3bt aa2 b.42.4.2 (A:1079-1295) Botulinum neurotoxin {Clostridium botulinum, serotype A}

NEKEIKDLYDNQSNSGILKDFWDYDYLQYDKPYMLNLYDPNKYVVDVNNVGIRGYMYLKGRGSVMTTNIYLN
SLYRGTKFIKKYASGNKDNIVRNNDRVYINVVVKNKEYRLATNASQAGVEKILSALEIPDVG-NLSQVVVMKSKN
DQGITNKCKMNLQDNNGNDIGFIGHFQFNNIAKLVASNWYNRQIERSSRTLGCSWEFIPVDDGWGERPL

>d1epwa2 b.42.4.2 (A:1080-1290) Botulinum neurotoxin {Clostridium botulinum, serotype B}

SEYLKDFWGNPLMYNKEYMFNAGNKNYSIKLKKDSPVGEILTRSKYNQNSKYINYRDLYIGEKFIIRKNSNSQSI
NDDIVRKEDYIYLDFFNLNQEWRVYTYKYFKKEEKLFAPISDSDEFYNTIQKEYDEQPTYSQQLFKDEESTD
EIGLIGIHRFYESGIVFEEYKDYFCISKWLKEVKRKPYNLKGNCNWQFIPKDEGWTE

>d1dfca1 b.42.5.1 (A:1008-1140) Fascin {Human (Homo sapiens)}

EAVQIQGLINCGNKYLTAEAFGFVNASSLKKQIWTLTQPPDEAGSAAVCLRSHLGRYLAADKDGNVTCE
REVPGPDCRFLIVAHDDGRWSLQSEAHRRYFGGTEDRLSCFAQTSPAEKWSVHIAMHP

>d1dfca2 b.42.5.1 (A:1141-1259) Fascin {Human (Homo sapiens)}

QVNIYSVTRKRYAHLARPADEIAVDRDVPWGVDLSLTAFQDQRYSVQTADHRFLRHDGRLVARPEPATGYTLE
FRSGKVAFRDCEGRYLAPSGPSGTLKAGKATKVGKDELFALEQS

>d1dfca3 b.42.5.1 (A:1260-1382) Fascin {Human (Homo sapiens)}

CAQVVLQAANERNVSTRQGMDSLANSQDEETDQETFQLEIDRDTKKCAFRTHTGKYWLTATGGVQSTASSKN
ASCYFDIEWRDRRITLRASNGKFVTSKKNGQLAASVETAGDSEFLMKLIN

>d1dfca4 b.42.5.1 (A:1383-1493) Fascin {Human (Homo sapiens)}

RPIIVFRGEHGFIGCRKVTGTLANRSSYDVFQLEFDGAYNIKDSTGKYWTVGSDSAVTSSGDTPVDFEEFCD
YNKVAIKVGGRKLKGDHAGVLKASAETVDPASLWEY

>d1hcd_b.42.5.2 (-) Histidine-rich actin-binding protein (hisactophilin)
{Dictyostelium discoideum}

MGNRAFKSHGHFLSAEAEAVKTHHHHDHHFHVENHGGKVALKTHCGKYL SIGDHKQVYLSHHLGD
HSLFLEHHGGKVSIGHHHHYISADHHGHVSTKEHHHDHTTFEEIII

>d1i8da1 b.43.4.3 (A:1-93) Riboflavin synthase {Escherichia coli}

MFTGIVQGTAKLVSIDEKPNFRTHVVELPDHMLDGETGASVAHNGCCLTVTEINGNHVSFDLMKETLRITNLG
DLKVGDWVNVERAAKFSDE

>d1i8da2 b.43.4.3 (A:94-206) Riboflavin synthase {Escherichia coli}

IGGHLMMSGHIMTTAEVAKILTSENNRQIWFKVQDSQLMKYILYKFIGIDGISLTVGEVTPTRFCVHLIPETLERTT
LGKKKLGARVNIEIDPQTQAVVDTVERVLAARENAM
>d1fnc_1 b.43.4.2 (19-154) Ferredoxin reductase (flavodoxin reductase) N-terminal domain
{Spinach (*Spinacia oleracea*)}
HSKKMEEGITVNFKPKTPYGRCLLNKITGDDAPGETWHMVFSHEGEIPIYREGQSVGVIPDGEDKNGKPHK
LRLYSIASSALGDFGDAKSVCVKRLIYTNDAGETIKGVCSNFLCDLKPGAEVKLTGPVGKE
>d1qfza1 b.43.4.2 (A:1-153) Ferredoxin reductase (flavodoxin reductase) N-terminal domain
{Garden pea (*Pisum sativum*)}
QVTTEAPAKVVKHSDKQDENIVVNFKPKEPYGRCLLNKITGDDAPGETWHMVFSTEGERPYREGQSIGIVP
DGIDKNGKPHKLRLYSIASSAIGDFGDSKTVSLCVKRLVYTNDAGEVVKGVCSNFLCDLKPGSEVKITGPVGKEM
LMPK
>d1fb3a1 b.43.4.2 (A:67-207) Ferredoxin reductase (flavodoxin reductase) N-terminal domain
{Paprika (*Capsicum annuum*)}
ISKKQDEGVVVNKFRPKEPYIGRCLLNKITGDDAPGETWHMVFSTEGERPYREGQSIGVIADGVDANGKPHKL
RLYSIASSALGDFGDSKTVSLCVKRLVYTNDKGEEVKGVCSNFLCDLKPGADVKITGPVGKEMLMPK
>d1gawa1 b.43.4.2 (A:11-156) Ferredoxin reductase (flavodoxin reductase) N-terminal domain
{Maize (*Zea mays*), leaf isoform}
PATAKAKKESKKQEEGVVTNLYKPKEPYGRCLLNKITGDDAPGETWHMVFSTEGERPYREGQSIGVIADGVD
KNGKPHKVRRLYSIASSAIGDFGDSKTVSLCVKRLIYTNDAGEIVKGVCSNFLCDLQPGDNVQITGPVGKEML
>d1jb9a1 b.43.4.2 (A:6-162) Ferredoxin reductase (flavodoxin reductase) N-terminal domain
{Maize (*Zea mays*), root isoform}
SRSKVSVAPLHLESAKEPLNTYKPKEPTATIVSVELVGPKAPGETCHIVIDHGGNVPYWEGQSYGVIPPGENP
KKPGAPQNVRRLYSIASTRYGDNFDRGRTGSLCVRRAYYDPETGKEDPSKNGVCSNFLCNSKPGDKIQLTGPSGKI
MLLPEE
>d1que_1 b.43.4.2 (1-141) Ferredoxin reductase (flavodoxin reductase) N-terminal domain
{Cyanobacterium (*Anabaena* sp.), pcc 7119}
TQAKAKHADVPVNLYRPNAPFIGKVISNEPLVKEGGIGIVQHIFDLTGGNLKYIEGQSIGIIPPGVDKNGKPEKLR
LYSIASTRHGDVDDKTISLCVRQLEYKHPESGETVYGVCASTYLTHIEPGSEVKITGPVGKEML
>d1fdr_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain
{Escherichia coli}
ADWVTGKVTKVQNWTDALFSLTVHAPVLPTAGQFTKLGLEIDGERVQRAYSYVNSPDNPDLEFYLVTVPDGK
LSPRLAALKPGDEVQVVSEAAGFFVL
>d1a8p_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain
{Azotobacter vinelandii}
SNLNVERVLSVHHWNDTLFSFKTTRNPSLRFENGQFVMIGLEVDRPLMRAYSIASPNYEEHLEFFSIKVQNGP
LTSRLQHLKEGDELMVSRKPTGTLV
>d1qfja1 b.43.4.2 (A:1-97) NAD(P)H:flavin oxidoreductase {Escherichia coli}
TTLSCKVTSVEAITDTVYRVIRVPDAFSFRAGQYLMVVMDERDKRPFMSASTPDEKGFIELHIGASEINLYAKAV
MDRILKDHQIVVDIPHGEAWL
>d2cnd_1 b.43.4.2 (11-124) Nitrate reductase core domain {Corn (*Zea mays*)}
GRIHCRLVAKKELS RDVRLFRSLPSPDQVLGLPIGHIFVCATIEGKLCMRAYPTSMVDEIGHFDLLVKVYFKNE
HPKFPNGGLMTQYLDLSPVGSYIDVKGPLGHVEYTGR
>d1ndh_1 b.43.4.2 (3-125) cytochrome b5 reductase {Pig (*Sus scrofa*), liver}
PAITLENPDIKYPLRLIDKEVVNNHDTRRFRALPSPEHILGLPVGQHIYLSARIDGNL VIRPYTPVSSDDDKGFVDLV

IKVYFKDTHPKFPAGGKMSQYLESMKIGDTIEFRGPNGLLVYQGK
>d1i7pa1 b.43.4.2 (A:29-153) cytochrome b5 reductase {Rat (Rattus norvegicus)}
HHHMITLENPDIKYPLRLIDKEILSHDTRRFRALPSQPHILGLPIGQHIYLSTRIDGNLIRPYTPVSSDDDKGFVD
LVVKVYFKETHPKFPAGGKMSQYLEMNIGDTIEFRGPNGLLVYQGK
>d2pia_1 b.43.4.2 (1-103) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}
TTPQEDGFLRLKIASKEKIARDIWSFELDPQGPLPPFEAGANLTAVAPNGSRRTYSLCNDSQERNRYVIAVKR
DSNGRGGSISFIDDSEGDAVEVSLPRN
>d1ep3b1 b.43.4.2 (B:2-102) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}
SQLQEMIMTVVSQREVAYNIFEMVLKGTLVDEMDLPQFLHLAVPNGAMLLRRPISISSWDKRAKTCTILYRIG
DETTGTYKLSKLESGAKVDMGPLGNGF
>d1cqxa2 b.43.4.2 (A:151-261) Flavohemoglobin, central domain {Alcaligenes eutrophus}
WKGWRTFVIREKRPESDVITSFILEPADGGPVNFEPGQYTSVAIDVPALGLQQIRQYSLSDMPNGRTYRISVKR
EGGGPQPPGYVSNLHDHVNVGDQVKLAAPYGSFH
>d1ja1a1 b.43.4.1 (A:240-518) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}
SSIRQYELVVHEDMDVAKVYTGEMGRKSYENQKPPFDAKNPFLAAVTANRKLNQGTERHLMHLELDISDSKIR
YESGDHVAVYPANDSALVNQIGEILGADLDVIMSLNNLDEESNKHKPFPCPTTYRTALTYYLDITNPPRTNVLYEL
AQYASEPSEQEHLHKMASSSGEGKELYLSWVVEARRHILAILQDYPSLRPPIDHLCELLPRLQARYYAIASSSKVHP
NSVHICAVAVEYEAKSGRVNKGVATSWLRAKEPAGENGGRALVPMFVRKSQF
>d1ddga1 b.43.4.1 (A:226-446) Sulfite reductase flavoprotein {Escherichia coli}
IHTSPYSKDAPLVASLVNQKITGRNSEKDVRHIEIDLGDGLRYQPGDALGVWYQNDPALVKELVELLWLKGDE
PVTVEGKTLPLNEALQWHFELTVNTANIVENYATLRSSETLLPLVGDKAKLQHYATTPIVDMVRSPAQLDAEAL
INLLRPLTPRLYIASSQAEVENEVHVTGVVRYDVEGRARAGGASSFLADRVEEGEVRFIEHNDNFR
>d1f20a1 b.43.4.1 (A:963-1232) Neuronal nitric-oxide synthase FAD/NADP+ domain {Rat (Rattus norvegicus)}
SWKRNKFRLTVAEAPDLTQGLSNVHKKRVSAARLLSRQNLLQSPKSSRSTIFVRLHTNGNQELQYQPGDHLGVF
PGNHEDLVNALIERLEDAPPANHVVKMEMLEERNTALGVISNWKDESRLLPCTIFQAFKYYLDITTPPTPLQLQQ
FASLATNEKEKQRLVLSKGLQEYEEWKWGKNPTMVEVLEEPSIQMPATLLTQLSLLQPRYYSISSSPDMYPDE
VHLTVAIVSYHTRDGEGPVHHGVCSSWLNRIQADDVPCFVRGAP
>d1fua1 b.43.2.1 (A:356-591) L-fucose isomerase, C-terminal domain {Escherichia coli}
AQVFADVRTYWSPEAIERVTVGHKLDGLAEHGIHLINSGSAALDGSCQRDSEGNPTMKPHWEISQQEADACL
AATEWCPAIHEYFRGGGYSSRFLTEGGVPFTMTRVNIKGLGPVLQIAEGWSVELPKDVHDILNKRTNSTWPTT
WFAPRLTGKGPFTDVSVMANWGANHGVLIGHVGADFITLASMLRIPVMHNVEETKVYRPSAWAHGM
DIEGQDYRACQNYGPLYKR
>d1efca1 b.43.3.1 (A:205-296) Elongation factor Tu (EF-Tu), domain 2 {Escherichia coli}
AIDKPFLPIEDVFSISGRGTVTGRVERGIICKVGEVEIVGIKETQKSTCTGVEMFRKLLDEGRAGENVGVLLRGI
KREEIERGQVLAKPG
>d1exma1 b.43.3.1 (A:213-312) Elongation factor Tu (EF-Tu), domain 2 {Thermus thermophilus}
PVRDVDPKFLMPVEDVFTITGRGTATGRIERGKVKVGDEVEIVGLAPETRKTVTGVEMHRKTLQEGIAGDN
VGVLLRGVSREEVERGQVLAKPGSITP
>d1d2ea1 b.43.3.1 (A:251-348) Elongation factor Tu (EF-Tu), domain 2 {Cow (Bos taurus), mitochondrial}
TRDLEKPFLPVESVYSIPGRGTVTGTLERGILKKGDECEFLGHHSKNIRTVTGIEMFHKSLSRAEAGDNLGALV

RGLKREDLRRGLVMAKPGSIQP

>d1f60a1 b.43.3.1 (A:241-334) Elongation factor eEF-1alpha, domain 2 {Baker's yeast (Saccharomyces cerevisiae)}

DKPLRLPLQDVYKIGGIGTVPGVRVETGVIKPGMVVTFAPAGVTTEVKSVEMHHEQLEQGVPGDNVGFNKN
VSVKEIRRGNCVGDAKNDPPKG

>d1jnya1 b.43.3.1 (A:228-322) Elongation factor eEF-1alpha, domain 2 {Archaeon Sulfolobus solfataricus}

PVDKPLRIPIQDVYSISGVGTVPGRVESGVLKVGDKIVFMPAGKVGEVRSIETHHTKMDKAEPGDNIGFNVRG
VEKKDIKRGDVVGHPNNPPTV

>d1dar_1 b.43.3.1 (283-400) Elongation factor G (EF-G), domain II {Thermus thermophilus}

PLDIPPIKGTTPEGEVVEIHDPNGPLAALAFKIMADPYVGRLTFRVSGTLTGSYVYNTTKGRKERVARLLRM
HANHREEEELKAGDLGAVVGLKETITGDTLVGEDAPRVILE

>d1g7sa1 b.43.3.1 (A:228-328) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

EDSPARGTILEVKEETGLGMTIDAVIYDGILRKDDTIAMMTSKDVISTRIRSSLKPRPLEEMRESRKKFQKVDEVV
AAAGIKIVAPGIDDVMAGSPLRVVT

>d1g7sa2 b.43.3.1 (A:460-587) Initiation factor IF2/eIF5b, domains 2 and 4 {Archaeon Methanobacterium thermoautotrophicum}

IIKPASIRLIPKLVFRQSKPAIGGVELTGVIRQGYPLMNDGETVGTVESMQDKGENLKSASRGQKVAMAIKDA
VYGKTIHEGDTLYVDIPENHYHILKEQLSGDLTDEELDLMKDIAEIKRKKNPD

>d1d1na_b.43.3.1 (A:) Initiation factor IF2/eIF5b, domains 2 and 4 {Bacillus stearothermophilus}
YEEKVIGQAERVQTFKVSKGVTIAGCYTDGKITRDSKVRЛИRQGIVVYEGEIDLKRYKDDVREVAQGYECGLTI
KNFNDIKEGDVIEAYVMQEVARA

>d1jj2b_b.43.3.2 (B:) Ribosomal protein L3 {Archaeon Haloarcula marismortui}

PQPSRPRKGSLGFGRKRSTSETPRFNSWPSDDGQPGVQGFAGYKAGMTHVVLVNDEPNSPREGMEETVPV
TVIETPPMRAVALRAYEDTPYQQRPLTEVWTDEFHSELDRTLDVPEHDHPDAAEQIRDAHEAGDLGLRLITH
TVPDAVPSVPKKPDVMETRVGGGSVSDRLDHADIVEDGGEHAMNDIFRAGEYADVAGVTKGKGTQGPVK
RGVQKRKGKHARQGWRRIGNLGPWNPSRVRSTVPQQGQTGYHQRTELNKRLIDIGEGDEPTVDGGFVN
YGEVDGPYTLVKGSPGPDKRLVFRPAVRPNQDQPRLDPEVRYVSNESNQG

>d1efca2 b.44.1.1 (A:297-393) Elongation factor Tu (EF-Tu) {Escherichia coli}

TIKPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEMVMPGDNIKMVVTLIHPIAMDD
GLRFAIREGGRTVGAGVVAKVL

>d1exma2 b.44.1.1 (A:313-405) Elongation factor Tu (EF-Tu) {Thermus thermophilus}

HTKFEASVYVLKKEEGGRHTGFFSGYRPQFYFRTTDVTGVVQLPPGVEMVMPGDNIKMVVTLIHPIAMDD
AIREGGRTVGAGVVTKILE

>d1d2ea2 b.44.1.1 (A:349-451) Elongation factor Tu (EF-Tu) {Cow (Bos taurus), mitochondrial}

HQKVEAQVYILTKEEGGRHKPFVSHMPVMFSLTWDMACRIILPPGKELAMPGEDLKLTLRQPMILEKGQRF
TLRDGNRTIGTGLVTDTPEAMTEEDKNIKW

>d1f60a2 b.44.1.1 (A:335-441) Elongation factor eEF-1alpha, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

CASFNATVIVLNHPGQISAGYSPVLDCHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSGDAALVKFVPSKPMC
VEAFSEYPPPLGRFAVRDMRQTVAVGVIKSVDK

>d1jnya2 b.44.1.1 (A:323-429) Elongation factor eEF-1alpha, C-terminal domain {Archaeon Sulfolobus solfataricus}

ADEFTARIIVVWHPTALANGYTPVLHVHTASVACRVSELVKLDPRTGQEAENPQFLKQGDVAIVKFPIKPLC
VEKYNEFPPLGRFAMRDMGKTVGVGIIVDVKP
>d1flma_b.45.1.1 (A:) FMN-binding protein {Desulfovibrio vulgaris, strain Miyazaki F}
MLPGTFFEVLKNEGVVAIATQGEDGPHLVNTWNSYLKVLGNNRIVVPVGGMHKTEANVARDERVLMTLGSR
KVAGRNGPGTGFLIRGSAAFRTDGPEFEAIARFKWARAALVITVSAEQTL
>d1ci0a_b.45.1.1 (A:) Pyridoxine 5'-phoshate oxidase (PNP oxidase) {Baker's yeast (Saccharomyces cerevisiae)}
FTLNEKQLTDDPIDLFTKWFNEAKEDPRETLPEAITFSSAELPSGRVSSRILLFKELDHRGFTIYSNWGTSRKAHD
ATNPNAIAVFFWKDLQRQVRVEGITEHVNRETSEYFKTRPRGSKIGAWASRQSDVIKNREELDELTQKNTER
KDAEDIPCPDYWGGLRIVPLEIEFWQGRPSRLHDRFVYRRKTENDPWKVVR LAP
>d1dnla_b.45.1.1 (A:) Pyridoxine 5'-phoshate oxidase (PNP oxidase) {Escherichia coli}
GGLRRRDLPADPLTLFERWLSQACEAKLADPTAMVVATVDEHGQPYQRIVLLKHYDEKGMVFYTNLGSRKA
QIENNPRVSLLFPWHTLERQVMVIGKAERLSTLEVMKYFHSRPRDSQIGAWVSKQSSRISARGILESKFLELKQK
FQQGEVPLPSFWGGFRVSLEQIEFWQGGEHRLHDRFLYQRENDAWKIDRLAP
>d1ejea_b.45.1.2 (A:) FMN-binding protein MTH152 {Archaeon Methanobacterium thermoautotrophicum}
GSQAAHMMSMDFEDFPVESAHRLTPRPTVMVTTVDEEGNINAAPFSFTMPVSIDPPVVAFASAPDHHTARN
IESTHEFVININITPADIIERMWVTARDIPAGENELEAAGLAWTSSRRVKPPRIVEAPGHLECELLRMFEVGDHNLT
GSVVSASVRSGAVKEGLLDVESVKPVLHVGGNKFVVGHDHVRHE
>d1i0ra_b.45.1.2 (A:) Ferric reductase {Archaeon Archaeoglobus fulgidus}
MDVEAFYKISYGLIVTSESNGRKCGQIANTVFQLTSKPVQIAVCLNKENDTHNAVKESGAFGVSVLELETPMEFI
GRFGFRKSSEFEKFDGVEYKTGKTGVPLVTQHAVAVIEAKVVKECDVGTHTLFVGEAVDAEVLKDAEVLYADYH
LMKKKGKTPRT
>d1k28d1_b.106.1.1 (D:4-200) Baseplate structural protein gp27 {Bacteriophage T4}
LQRPGYPNLSQLVLFDSYDAWSNNRFVELAATITLTMRDSLGRNEGMLQFYDSKNIHTKMDGNEIIQISVANA
NDINNVKTRIYGCKHFSVSDSKGDNIIAIELGTIHSIENLKFGRPF DAGESIKEMLGVIYQDRTLLPAINAINAY
VPDIPWTSTFENYLSYVREVALAVGSDKFVFWQDIMGVNMMDY
>d1k28d2_b.106.1.1 (D:201-376) Baseplate structural protein gp27 {Bacteriophage T4}
DMMINQEPPMIVGEPSLIGQFQELKYPLAYDFVWLTKSNPHKRDP MKNATIYAH SFLDSSIPMITTGKGensi
VVSRSRGAYSEMTYRNGYEEAIRLQTMAQYDGYAKCSTIGNFNLTPGVKIIFNDSKNQFKTEFYVDEVIHELSNNN
SVTHLYMFTNATKLETIDPVKVKN EF
>d1fmta1_b.46.1.1 (A:207-314) Methionyl-tRNAfmet formyltransferase, C-terminal domain
{Escherichia coli}
LSKEEARIDWLSAAQLERCIRAFNPWPMSWLEIEGQPVKVWKASVIDTATNAAPGTILEANKQGIQVATGDGI
LNLLSLQPAGKKAMSAQDLLNSRREWVPGNRLV
>d1ewna_b.46.1.2 (A:) 3-methyladenine DNA glycosylase (AAG, ANPG, MPG) {Human (Homo sapiens)}
HLTRLGLEFFDQPAVPLARAFLGQVLVRRPNGTELGRIVETQAYLGPEDEAAHSRGGRQTPRNRMFMKPG
TLYVIIYGMYFCMNISSQGDGACVLLRALEPLEGLETMRQLRSTLRKGTA SVRLKDRELCSGPSKLQCALAINKS
FDQRDLAQDEAVWLERGPLEPSEPAVVAARVGVGHAGEWARKPLRFYVRGSPWVSVVDRVAE QD
>d1arb_b.47.1.1 (-) Achromobacter protease {Achromobacter lyticus, strain m497-1}
GVSGSCNIDVVCPEGDGRDIIRAVGAYSKSGTLACTGSLVNNTANDRKMYFLTAHC GMGTASTAASIVYW
NYQNSTCRAPNTPASGANGDGSMSQTQSGSTVKATYATSDFTLLENNNAANPAFNLFWAGWDRRDQNYPG
AIAIHHPNVAEKRISNSTSPTSFVAWGGAGTTHLNVQWQPSGGVTEPGSSGSPISPEKRLVQLHGGPSSC

SATGTNRSDQYGRVFTSWTGGGAAASRLSDWLDPASTGAQFIDGLDS
>d1qq4a_ b.47.1.1 (A:) alpha-Lytic protease {Lysobacter enzymogenes, 495}
ANIVGGIYE SINNASLCSVGF SVTRGATKG FVTAGHCGTVNATARI GGAVV GTFAARVFPGN DRAWVSLT SAQT
LLPRVANGSSF VTVRGSTEAAVGAAVCHSGRTTG YQCGTITAKNVTANYAEGAVRGLTQSACMGRGDSGGS
WITSAGQAQGVMSGGNVQSNGNNCGIPASQRSSLFERLQPILSQYGLSLVTG
>d2sga__ b.47.1.1 (-) Protease A {Streptomyces griseus, strain k1}
IAGGEAITTGGSRCSLGFNVSVNGVAHALTAGHCTNISASWSIGTRGTSFPNDYGIIRHSNPAAADGRVYLYN
GSYQDITTAGNAFGQAVQRSGSTTGLRSGSVTGLNATVNYGSSGIVYGMIQTNVCAQPGDSGGSLFAGSTAL
GLTSGGSGNCRTGGTTFYQPVTEALSAYGATVL
>d1hpg a_ b.47.1.1 (A:) Glutamic acid-specific protease {Streptomyces griseus}
VLGGGAIYGGGSRC SAAFNVTKG GARYFVTAGHCTNISANWSASSGSVVGVR EGTSPTNDYGIIVRYTDGSS
PAGTV DLYNGSTQDISSAANAVVGQAIKKSGSTTKV TSGTVTAVNVTVNYGDGPVYNMVRTTACSAGGD SGG
AHFAGSVALGIHSGSSGCSGTAGSAIHQPVTEALSAYGATVY
>d1sgt__ b.47.1.1 (-) Trypsin {Streptomyces griseus, strain k1}
VVGGTRA AQGEFPFMVRLSMICGGALYA QDVLTA AHCVSGSGNNTSITATGGVVDLQSGAAVKRSTKVLQ
APGYNGTGKD WALIKLAQPNQPTLK IATT TAYNQGFTVAGWGANREGGSQQRYLLKANVPFVSDAACRSAY
GNELVANEEICAGYPDTGGV DTCQGDSSGPMFRKDNADEWIQVGIVSWGYGCARPGYPGVYEVSTFASAIA
SAARTL
>d2sfa__ b.47.1.1 (-) Serine proteinase {Streptomyces fradiae}
IAGGEAIYAAGGGRC SLCGFNVRSSSGATYALTAGHCTEIA STWYTNSGQTSLLGTRAGTSFPNDYGLIRHSNAS
AADGRVYLYNGSYRDITGAGNAYVGQTVQRSGSTTGLHSGRV TGLNATVNYGGDIVSGLIQTNVCAEPGD SGG
GALFAGSTALGLTSGGSGNCRTGGTTFFQPVTEALSAYGVSIL
>d1sgpe_ b.47.1.1 (E:) Protease B {Streptomyces griseus, strain k1}
ISGGDAIYSSTGRCSLGFNVRS GSTYYFLTAGHCTDGATTWWANSARTV LGTSGSSFPNDYGIIVRYTNTTIP
KDGTVGGQD ITSAANATVGM AVTRRGSTTGTHSGSVT ALNATVNYGGDVVYGMIRT NVCAEPGD SGGPLY
SGTRAIGLTSGGSGNCSSGGTFFQPVTEALVAYGVSY
>d1agja_ b.47.1.1 (A:) Epidermolytic (exfoliative) toxin A {Staphylococcus aureus}
EVSAEEIKKHEEKWNKYYGVNAFNL PKELFSVDEKDRQKPYNTIGNVFVKGQTSATGV LIGKNTV LNRHI AK
FANGDPSKVSFRPSINTDDNGNTETPYGEYEVKEILQEPFGAGV DLA LIRLKP DQNGVSLGD KISPAKIGTSNDLK
DGDKLELIGYPFDHKVNQMHRSEIELTLSRGLRYYGFVPGNSGSGIFNSNGELVGIHSSKVSHLDREHQINYG
VGIGNYVKR INEKNE
>d1qtfa_ b.47.1.1 (A:) Exfoliative toxin B {Staphylococcus aureus}
KEYSAEEIRKLQKFEVPP TD KELYTHITDNARSPYNSVGT VFVKGST LATGV LIGKNTIV TNHV AREA AKNPSNI
IFTPAQN RDAEKN EFP TYGK FEAEEIKES PYGQQLDLAI IKLKPNEK GESAGD LIQ PANIPDHIDIA KGD KYSLLGY
PYNYSAYS LYQS QIEMF NDSQYFGY TEVG NSG SGIF NLKG ELIGI HSGK GGQH NLPIGV FFNR KISS LYSV DNTFG
DTLGNDLKKRAKLDK
>d1ezxc_ b.47.1.2 (C:) Trypsin(ogen) {Cow (Bos taurus)}
CGGSLINSQWVVAH CYKSGI QVRLGEDNINVVEGNEQFISASKSIVHPSYNSNTLNDIMLIKLKAASLNSR
VASISLPTSCASAGTQCLISGWGNTKSSGT SYPDVLKCLKAPI LSDSSCKSAYPGQITSNMFCAGYLEG GK DSCQG
DSGGPVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN
>d1hj9a_ b.47.1.2 (A:) Trypsin(ogen) {Cow (Bos taurus)}
IVGGYTCGANTV PYQVSLNSGYHFCGGSLINSQWVVAH CYKSGI QVRLGEDNINVVEGNEQFISASKSIVHP
SYNSNTLNDIMLIKLKAASLNSRV ASISLPTSCASAGTQCLISGWGNTKSSGT SYPDVLKCLKAPI LSDSSCKS
YPGQITSNMFCAGYLEG GK DSCQG DS GG PVVCSGKLQGIVSWGSGCAQKNKPGVYTKVCNYVSWIKQTIASN

>d1mcta_b.47.1.2 (A:) Trypsin(ogen) {Pig (Sus scrofa)}

IVGGYTCAANSIPYQVSLNSGSHFCGGLINSQWVVAACYKSRIQVRLGEHNIDVLEGNEQFINAAKIITHPN
FNGNTLDNDIMIILKLSSPATLNSRVATVSLPRSCAAAGTECLISWGNTKSSSSPSLLQCLKAPVLSNSSCKSSY
PGQITGNMICVGFLQGGKDSCQGDGGPVVCNGQLQGIVSWGYGCAQKNKPGVYTKVCNYVNWIQQTIAA
N

>d1f7za_b.47.1.2 (A:) Trypsin(ogen) {Rat (Rattus norvegicus)}

IVGGYTCQENSVPYQVSLNSGYHFCGGLINDQWVVAACYKSRIQVRLGEHNINVLEGNEQFVNAAKIHKHP
NFDRKTLNNDIMIILKLSSPVKLNARVATVALPSSCAPAGTQCLISWGNTLSSGVNEPDLLQCLDAPLLPQADCE
ASYPGKITDNMVCVGFLEGGKDSCQGDGGPVVCNGQLQGIVSWGYGCAQKNKPGVYTKVCNYVDWIQDTI
AAN

>d1trna_b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens)}

IVGGYNCEENSPYQVSLNSGYHFCGGLINEQWVVSAGHCYKSRIQVRLGEHNIEVLEGNEQFINAAKIIRHP
QYDRKTLNNDIMIILKLSSRAVINARVSTISLPTAPPATGTKCLISWGNTASSGADYPDELQCLDAPVLSQAKCEA
SYPGKITSNMFCVGFLEGGKDSCQGDGGPVVCNGQLQGIVSWGDGCAQKNKPGVYTKVYNYVKWIKNTI
AANS

>d1h4wa_b.47.1.2 (A:) Trypsin(ogen) {Human (Homo sapiens), trypsin IV (brain isoform)}

IVGGYTCEENSLPYQVSLNSGSHFCGGLISEQWVVSAAHCYKTRIQVRLGEHNIKVLEGNEQFINAVKIIIRHPKY
NRDTLDNDIMIILKLSSPAVINARVSTISLPTAPPAGTECLISWGNTLSFGADYPDELKCLDAPVLTQAECKASYP
GKITNSMFCVGFLEGGKDSCQRDSGGPVVCNGQLQGIVSWGHCawanRPGVYTKVYNYVDWIKDTIAAN
S

>d1a0ja_b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo salar)}

IVGGYECKNSASYQASLQSGYHFCGGSILSTWVVAACYKSRIQVRLGEHNIAVNEGTEQFIDSVKVIMHPS
YNSRNLDNDIMIILKSXPASLNSYVSTVALPSSCASSGTRCLVSGWGNLSGSSNYPDTLRCLDLPILSSSCNSAY
PGQITSNMFCAGFMEGGKDSCQGDGGPVVCNGQLQGIVSWGYGCAQRNKPGVYTKVCNYRSWISSTMS
SN

>d1hj8a_b.47.1.2 (A:) Trypsin(ogen) {North atlantic salmon (Salmo salar)}

IVGGYECKNSASYQASLQSGYHFCGGSILSTWVVAACYKSRIQVRLGEHNIKVTEGSEQFISSSRVIRHP
NYSSYNIDNDIMIILKSXPATLNTYVQPVALPTSCAPAGTMCTSGWGNTMSSTADSNLQCLNIPILSYSDCNN
SYPGMITNAMFCAGYLEGGKDSCQGDGGPVVCNGELQGIVSWGYGCAEPGNPGVYAKVICIFNDWLTSTM
ASY

>d1gdna_b.47.1.2 (A:) Trypsin(ogen) {Mold (Fusarium oxysporum)}

IVGGTSASAGDFPFIVSISRNGGPWC GGSLNNANTVTAACVSGYAQSGFQIRAGSLRTSGGITSSLSSVRVH
PSYSGNNNDLAILKLSTSIPSGGNIGYARLAASGSDPVAGSSATVAGWGATSEGGSTPVNLLKTVPIVS RATCR
AQYGTSAITNQMFCAGVSSGGKDSCQGDGGPIVDSSNTLIGAVSWGNGCARPNYSGVYASVGALRSFIDTYA

>d1pytd_b.47.1.2 (D:) (alpha,gamma)-chymotrypsin(ogen) {Cow (Bos taurus)}

CGAPIFQPNLSARVVGGEDAIPHSPWQISLQYLRDNTWRHTCGTLITPNHVLTAAHCISNTLTYRVALGKN
NLEVEDEAGSLYVGVDTIFVHEKWNFLVRNDIALIKLAETVELGDTIQVACLPSEGSLPPQDYPFCVTGWGRLYT
NGPIAAELQQGLQPVVVDYATCSQRDWWGTTVKETMVCAGGDGVISACNGDGGPLNCQADGQWDVRGIV
SFGSGLSCNTFKKPTVFRVSAYIDWINQKLQL

>g1gg6.1 b.47.1.2 (A:,B:,C:) (alpha,gamma)-chymotrypsin(ogen) {Cow (Bos taurus)}

CGVPAIQPVLXIVNGEEAVPGSWPWQVSLQDKTGFHFCGGLINENWVTAACGVTTSDVVAGEFDQGS
SSEKIQKLKIAKVFKN SKYNSLTINNDITLLKSTAASFQTVSAVCLPSASDDFAAGTTCVTGWLTRYXANTPD
RLQQASLPLSNTNCKKYWGT KIKDAMICAGASGVSSCMGDGGPLVCKNGAWTLVGIVSWGSSCSTSTP
GVYARVTA LVNWVQQT LAAN

>d1eq9a_ b.47.1.2 (A:) (alpha,gamma)-chymotrypsin(ogen) {Red fire ant (Solenopsis invicta)}

IVGGKDAPVGKPYQVSLRLSGSHRCGASILDNNNVLTAAHCVDGLSNLNRLKVHVGTNYLSEGDVDVEDA
VVNKNYDDFLRNDVALVHLTNPIKFNDLVQPKLSTNDEDLESNPCTLTGWGSTRLGGNTPNALQEIELVHPQ
KCERDQWRVIDSHICLTKRGEACHGDSGGPLVANGAQIGIVSGSPCALGEPDVYTRVSSFVSWINANLKK

>d1npma_ b.47.1.2 (A:) Neuropsin {Mouse (Mus musculus)}

ILEGRECIPHSQPWQAALFQGERLICGGVLVGDRWLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQVAQSIQ
HPCYNNSNPEDHSHDIMLIRLQNSANLGDKVKPVQLANLCPKVGQKCIISGWGTVTSPQENFPNTLNCAEVKI
YSQNKCERAYPGKITEGMVCAGSSNGADTCQGDGGPLVCDGMLQGITSWGSDPCGKPEKPGVYTKICRYTT
WIKKTMD

>d1azza_ b.47.1.2 (A:) Crab collagenase {Atlantic sand fiddler crab (Uca pugilator)}

IVGGVEAVPNSPHQAALFIDDLYFCGGS LISPEWILTAAHCMDGAGFVDVVLGAHNIREDEATQVTIQSTDF
TVHENYNSFVISNDIAVIRLPVPVTAAITAVGLPSTDVGVTGVPTGWGLPSDSALGISDVLRQDVPIMSN
ADCDAVYGIVTDGNICIDSTGGKGTCNGDGGPLNYNLTYGITSFGAAAGCEAGYPDAFTRVTYFLDWIQTQT
GITP

>d2hlca_ b.47.1.2 (A:) HL collagenase {Common cattle grub (Hypoderma lineatum)}

IINGYEAYTGLFPYQAGLDITLQDQRVWCAGSLIDNKWILTAAHCVHDAVVVYLGSAVQYEAEVVNSERII
SHSMFNPDPTYLNDVALIKIPHVEYTDNIQPIRLPSGEELNNKFENIWATVSGWGQSNTDTVILQYTYNLVIDNDR
CAQEYPPGIIVESTICGDTSDGKSPCFGDSGGPFVLSDKNLLIGVVSFVSGAGCESGKPVGFSRVTSYMDWIQQ
NTGIKF

>g1h8d.1 b.47.1.2 (L;H:) Thrombin {Human (Homo sapiens)}

EADCGLRPLFEKKSLEDKTERELLESYISXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAHCLL
YPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLRDIALMKKKVAFSDYIHPVCLPD
RETAASLLQAGYKGRVTGWGNLKETGQPSVLQVNLPIVERPVCKDSTRIRITDNMFAGYKPDEGKRGDACE
GDSGGPFVMKSPFNNRWYQMGIVSWGEGCDRGKYGFYTHVFRKKWIQKVIDQFGCSSVLIVVC

>g1jou.1 b.47.1.2 (A;,B;) Thrombin {Human (Homo sapiens)}

SEYQTFFNPRTFGSGEADCGLRPLFEKKSLEDKTERELLESYIDGXIVEGSDAEIGMSPWQVMLFRKSPQELLCG
ASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLRDIALMKL
KKPVAFSDYIHPVCLPDRETAASLLQAGYKGRVTGWGNLKETWTANVGKGQPSVLQVNLPIVERPVCKDSTR
RITDNMFAGYKPDEGKRGDACEGDAGGPFVMKSPFNNRWYQMGIVSWGEGCDRGKYGFYTHVFRKKWIQKVID
WIQKVIDQFGE

>g1vr1.1 b.47.1.2 (L;H:) Thrombin {Human (Homo sapiens)}

ADCGLRPLFEKKSLEDKTERELLESYIXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAHCLL
CLLYPPWDKNFTENDLLVRIGKHSRTRYERNIEKISMLEKIYIHPRYNWRENLRDIALMKKKVAFSDYIHPVC
LPDRETAASLLQAGYKGRVTGWGNLKETWTANVGKGQPSVLQVNLPIVERPVCKDSTRIRITDNMFAGYKP
DEGKRGDACEGDGGPFVMKSPFNNRWYQMGIVSWGEGCDRGKYGFYTHVFRKKWIQKVID

>g2hnt.1 b.47.1.2 (L;,C;,E;,F;) Thrombin {Human (Homo sapiens)}

ADCGLRPLFEKKSLEDKTERELLESYIDXIVEGSDAEIGMSPWQVMLFRKSPQELLCGASLISDRWVLTAHCLLY
PPWDKNFTENDLLVRIGKHSXEKISMLEKIYIHPRYNWRENLRDIALMKKKVAFSDYIHPVCLPDRETAASLL
QAGYKGRVTGWGXPSVLQVNLPIVERPVCKDSTRIRITDNMFAGYKPDEGKRGDACEGDGGPFVMKSPF
NNRWYQMGIVSWGEGCDRGKYGFYTHVFRKKWIQKVIDQ

>g1etr.1 b.47.1.2 (L;H:) Thrombin {Cow (Bos taurus)}

TFGAGEADCGLRPLFEKKQVQDQTEKEFESYIEGRXIVEGQDAEVGLSPWQVMLFRKSPQELLCGASLISDRW
VLTAAHCLLYPPWDKNFTVDDLLVRIGKHSRTRYERKVEKISMIDKIIYIHPRYNWKENLRDIALKLKRPIELSDY
IHPVCLPDQTAKLLHAGFKGRVTGWGNRRETWTVAEVQPSVLQVNLPLVERPVCKASTRIRITDNMF

AGYKPGEGKRGDACEGDSGGPFVMKSPYNNRWYQMGIVSWGEGCDRDGYGFYTHVFRKKWIQKVIDRL
GS

>d1fona_b.47.1.2 (A:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (Bos taurus)}
SWSWQVSLQYEKDGAHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGEYDRSVLEGSEQVIPINAGDLFVHP
LWNSNCVACGNALVKLSRSAQLGDKVQLANLPPAGDILPNEAPCYISGWGRLYTGGPLPDKLQQALLPTVDY
EHCSQWDWWGITVKKTMVCAGGDTRSGCNGDSGGPLNCPAADGSWQVHGVTFSVAFGCNTIKKPTVFT
RVSAFIDWIDETIASN

>d1pytc_b.47.1.2 (C:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (Bos taurus)}
SRPSSRVVNGEDAVPYSWSQVSLQYEKDGAHHTCGGSLIAPDWVVTAGHCISTSRTYQVVLGEYDRSVLQ
GSEQVIPINAGDLFVHPLWNSNCVACGNALVKLSRSAQLGDKVQLANLPPAGDILPNEAPCYISGWGRLYTG
GPLDKLQEALLPVVDEHCSQYDWWGITVKKTMVCAGGDTRSGCNGDSGGPLNCPAADGSWQVHGVTSF
VSAFGCNTIKKPTVFTRVSAFIDWINETIASN

>d1ppfe_b.47.1.2 (E:) Elastase {Human (Homo sapiens)}

IVGGRRARPHAWPFMVSQQLRGGHFCGATLIAPNFVMSAAHCVANVNRAVRVVLGAHNLSRREPTRQVFA
VQRIFENGYDPVNLLNDIVLQLNGSATINANQVAQLPAQGRRGNGVQCLAMGWGLLGRNRGIASVLQEL
NVTVVTSLCRSNVCTLVRGRQAGVCFGDSGSPLVCNGLIHGIASFVRGGCASGLYPDAFAPVAQFVNWIDSII
Q

>d1brup_b.47.1.2 (P:) Elastase {Pig (Sus scrofa)}

VVGGEDARPNSWPWQVSLQYDSSGQWRHTCGTLVDQSWVLTAAHCISSSRTYRVVLGRHSLSTNEPGSLA
VKVSKLVVHQDWNSNQLSNGNDIALLKLAQPSLTDKIQLGCLPAAGTILPNNYVCYVTGWGRILQTNASPDIIL
QQGQLLVVDYATCSKPGWWGSTVKTNMICAGGDGISSCNGDSGGPLNCQGANGQWQVHGIVSFGSSLGC
NYYHKPSVFTRVSNYIDWINSVIANN

>d1qnja_b.47.1.2 (A:) Elastase {Pig (Sus scrofa)}

VVGGTEAQRNNSWPSQISLQYRSGSSWAHTCGTLIRQNWVMTAAHCVDRELTFRVVVGEHNLNQNDGTEQ
YVGVQKIVVHPYWNTDDVAAGYDIALRLAQSVTLNSYVQLGVLPAGTILANNSPCYITGWGLRTNGQLAQ
TLQQAYLPTVDYAISSSSYWGSTVKNSMVCAGGDGVRSGCQGDGGPLHCLVNGQYAVHGVTFSVRLGCN
VTRKPTVFTRVSAYISWINNVIASN

>d1elt_b.47.1.2 (-) Elastase {Salmon (Salmo salar)}

VVGGGRAQPNSWPWQISLQYKSGSSYYHTCGSLIRQGWVMTAAHCVDARTWRVVLGEHNLNTNEGKEQ
IMTVNSFIHSGWNSDDVAGGYDIALRLNTQASLNSAQLAALPPSNQILPNNNPCYITGWKTSTGGPLSD
SLKQAWLPSVDHATCSSGWWGSTVKTTMVCAGGGANSGCNGDSGGPLNCQVNGSYVHGVTSFVSSSGC
NASKKPTVFTRVSAYISWMNGIM

>d1ekbb_b.47.1.2 (B:) Enteropeptidase (enterokinase light chain) {Cow (Bos taurus)}

IVGGSDSREGAWPWVVALYFDDQQVCGASLVS RDWLVSAAHCVYGRNMEPSKWAVGLHMASNLTPQIE
TRLIDQIVINPHYNKRRKNNDIAMMHLEMKVNYTDYIQPICLPEENQVFPPGRICSIAGWGALIYQGSTADVLQ
EADVPLLSNEKCQQQMPEYNITENMVCAGYEAGGVDSLQGDGGPLMCQENNWRLLAGVTSFGYQCALPN
RPGVYARVPRTEWIQSFLH

>d1a7s_b.47.1.2 (-) Heparin binding protein, HBP {Human (Homo sapiens)}

IVGGRKARPRQFPFLASIQNQGRHFCGGALIHFVMTAACFPVGSTVVLGAYDLRRRERQSRQTFISSMSE
NGYDPQQNLNDLMLQLDREANLTSSVTILPLPLQNATVEAGTRCQVAGWGSQRSGGRLSRFPRFVNVTVTP
EDQCRPNNVCTGVLRGGICNGDGTPLVCEGLAHGVASFSLGPCRGPDFTRVALFRDWIDGVLNNGPG
GPA

>d1a0la_b.47.1.2 (A:) beta-Tryptase {Human (Homo sapiens)}

IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDKLAAALRVQLREQHLYYQDQ

LLPVSRIVHPQFYTAQIGADIALLELEEPVKVSSHVHTVLPPASETFPPGMPCWVTGWGDVDNDERLPPPFL
KQVKVPIMENHICDAKYHLGAYTGGDVRIRDDMLCAGNTRRDSCQGDSGGPLVKVNGTWLQAGVVSWG
EGCAQPQRPGIYTRVTYYLDWIHHYVPKK

>d1cgha_b.47.1.2 (A:) Cathepsin G {Human (Homo sapiens)}

IIGGRESRPHSRPYMAYLQIQSPAGQSRCGGFLVREDFVLTAAHCGSNINVTLGAHNIQRRENTQQHITARRA
IRHPQYNQRTIQNDIMLLQLSRRVRRNRNVNPVALPRAQEGLRPGTLCTVAGWGRVSMRRGTDLREVQLRV
QRDRQCLIFGSYDPRRQICVGDRRERKAFKGDGGPLLCNNVAHGIVSYGKSSGPVEVFTRSSFLPWIRT
TMRS

>d1danh_b.47.1.2 (H:) Coagulation factor VIIa {Human (Homo sapiens)}

IVGGKVC PKGECPWQVLLLNGAQLCGGTINTIWWVSAAHCFDKIKNWRNLIAVLGEHDLS EHDGDEQSRRV
AQVIIPSTYVPGTTNHDIALLRLHQPVLT DHHVPLCLPERTFSERTLA FVRFSLVSGWGQLLDRGATALEMV
VPR LMTQDCLQQRKVGDS P NITEYMFCAG YSDGSKDSCKGDSGGPHATHYRG TWYLTGIVSWGQGCATVG
HFGVYTRVSQYIEWLQKLMRSEPRPGVLLRAPFP

>d3rp2a_b.47.1.2 (A:) Chymase (Proteinase II) {Rat (Rattus rattus)}

IIGGVESIPHSRPYMAHLDIVTEKGLRVC CGGFLISRQFVLTAAHC KGREITVILGAHDVRKRESTQQKIKVEKQIH
ESYNSVPNLHDIMLLKLEKKVELTPAVNVVPLPSPSDFIHPGAMCWAAGWGKTGVRDPTSYTLREVELRIMDE
KACVDYRYYEYKFQVCVGSPTTLRAAFMGDSGGPLLCAGVAH GIVSYGH PDAKPPAIFTRVSTYV PWINA
VIN

>d1klt_b.47.1.2 (-) Chymase (Proteinase II) {Human (Homo sapiens)}

IIGGTESKPHSRPYMAYLEIVTSNGPSKFCGGFLIRRNFVLTAAH CAGRSITVTLGAHNITEEEDTWQKLEV
I QFR HPKYNTSTLHHDIMLLKLKEKASLT LAVGTLPFPSQFNFVPPGRMCRVAGWGRTGVLKPGSDTLQEV
KLRLMD PQACSHFRDFDHNLQLCVGNPRKTKSAFKGDGGPLLCAGVAQGIVSYGRSDAKPPAVFTRISHYR
PWINQILQ AN

>g2pka.1 b.47.1.2 (A;B:) Kallikrein A {Pig (Sus scrofa)}

IIGGRECEKN SHPWQVAIYHYSSFQC GGVLVNP KWVL TAAHC KNDNYEVWLGRHNL FENENTAQFFGVTADF
PHPGFNL SXADGKD YSHDLMLLRLQSPA KITDA KVLELPTQEPELG STCEAS GWG SIEPGPDDFE FPDEIQC
VLTLLQNTFCADAHPDKVTE SMLCAGYLPGKDT CMGDSGGPLCNGMWQ GIT SWGHTPCGSANKPSIYT
KLFYLDWIDDTITENP

>d1ton_b.47.1.2 (-) Tonin {Rat (Rattus rattus)}

IVGGYKCEKNSQPWQVAVINEYLCGGVLIDPSWVITAHC YSN NYQVLLGRNNLFKDEPFAQRRLVRQSFRHP
DYIPLIVTNDTEQPVHDHSNDLMLLHLSEPADITGGVKVIDLPTKEPKVG STCLASGWGSTNPSEM VVSHDLQC
VNIHLLSNEKCIETYKDNVTDVMLCAGEMEGGKDT CAGDSGGPLCDGV LQGITSGGATPCAKPKT PAIYAKLIK
FTSWIKKVMK ENP

>d1sgfa_b.47.1.2 (A:) 7S NGF protease subunits {Mouse (Mus musculus)}

NSQPWHVAVYRFNKYQCGGVLLDRNWVLTAAHCYNDKYQVWL GKN NFLEP SDQHRLVSKAIPHPDFNM
SLLNEHTPQPEDDYSNDLMLLRLSKPADITDVVKPITLPTEEPKLG STCLASGWGSTTPIKYPDDLQCVNLKLLPN
EDCDKAHEMKVTDAMILCAGEMDGGSYTCEHD SGGPLICDGILQGIT SWGPEPCGEPEPSVYTKLIK FSSWIR
ETMANNP

>d1sgfg_b.47.1.2 (G:) 7S NGF protease subunits {Mouse (Mus musculus)}

IVGGFKCEKNSQPWHVAVYR YTQYLCGGVLLDPNWVLTAAHCYDDNYKVWL GKN NL FKDEPSAQH RFVSKAI
PHPGFNMSLMRFLEYDYSNDLMLLRLSKPADITDTVKPITLPTEEPKLG STCLASGWGSTTPIKYPFTDDLYCVNL
KLLPNEDCAK AIEKVT DAMLCAGEMDG GKDT CKGD SGGPLICDGVLQGIT SWGHTPCGEPD MPG VYTKLN
KFTSWIKDTMAKNP

>d1dlea_b.47.1.2 (A:) Factor B {Human (Homo sapiens)}

ADPDESQSLSLCGMVWEHRKG TDYHKQPWQAKISVIRPSKGHESCMGAVVSEYFVLTAAHCFTVDDKEHSIKV

SVGGEKRDLEIEVVLFHPNYNINGKKEAGIPEFYDYDVALIKLKNKLKYGQTIRPICLPCETGTRALRLPPTTCQ
QQKEELLPAQDIKALFSEEEKKLTRKEVYIKNGDKKGSCERDAQYAPGYDKVKDISEVVTPRFLCTGGVSPYADP
NTCRGDGGPLIVHKRSRFIQVGVISWGVVDVCKNQKRQKQVPAHARDFHINLFQVLPWLKEKLQDEDLGFL
>d1bio__ b.47.1.2 (-) Factor D {Human (Homo sapiens)}
ILGGREAEAHRPYMASVQLNGAHLCGGVVAEQWVLSAAHCLEADAADGKVQVLLGAHSLSQPEPSKRLYDV
LRAVPHPDSPQDTIDHDLQLSEKATLGPAVRPLWQRVDRDVAPGTLCDVAGWGIVNHAGRRPDSLQHVL
LPVLDLRTACNRRTHDGAITERLMCAESNRRDSCKGDSGGPLVCGGVLEGVVTSGSRVCGRKKPGIYTRVAS
YAAWIDSVLA
>g1rtf.1 b.47.1.2 (A;B;) Two-chain tissue plasminogen activator (TC)-T-PA {Human (Homo sapiens)}
TCGLRQYSIKGGLFADIASHPWQAAIFAKHRRSPGERFLCGGILISSCWILSAAHCFQERFPPHHLTVILGRTYRV
VPGEQQKFEVEKYIVHKEFDDDTYNDIALLQLKSDDSRCAQESSVVRTVCLPPADLQLPDWTECELSGYGKHE
ALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVDNMILCAGDTRSGGPQANLHDACQGDSGGPLVCLNDGRM
TLVGIISWGLCGQKDVPGVYTKVTNYLDWIRDNMRP
>d1a5ia_ b.47.1.2 (A:) Single chain tissue plasminogen activator {Vampire bat (Desmodus rotundus)}
TCGLRKYKEPQLHSTGGLFTDITSHPWQAAIFAKQNRRSSGERFLCGGILISSCWVLTAACFQESYLPDQLKVVL
GRTYRVKPGEEEQTFKVKKYIVHKEFDDDTYNNNDIALLQLKSDDSRCAQESSVVRTVCLPPADLQLPDWTECELS
GYGKHKSSEPFYSEQLKEGHVRLYPSSRCAPKFLFNKTVTNMILCAGDTRSGEYIPNVHDACQGDSGGPLVCM
NDNHMTLLGIISWVGCGEKDVPGVYTKVTNYLGWIRDNMHL
>d1bqya_ b.47.1.2 (A:) Plasminogen activator from snake venom, TSV-PA {Chinese green tree viper (Trimeresurus stejnegeri)}
VFGGDECNINEHRSLVVLFNSNGFLCGTLINQDWVVTAAHCDSNNFQLLFGVHSKKILNEDEQTRDPKEKFF
CPNRKKDDEVDKDIMALIKLDSVSNSEHIAPLSLSSPPSVSCRIMWGKTIPTKEIYPDVPHCANINILDHAV
CRTAYSWRQVANTTLCAGILQGGRDTCHFDGGPLICNGIFQGIVSWGHHPCGQPGEPGVYTKVFDYLDWIKS
IIAGNKDATCPP
>d1ao5a_ b.47.1.2 (A:) Kallikrein-13 {Mouse (Mus musculus)}
VVGGFNCEKNSQPWQVAVYYQKEHICGGVLLDRNWVLTAAHYDQYEVWLGNKLFQEEPSAQHRLVSKS
FPHPGFNMSLLMLQTIPPGADFSDDLMLLRLSKPADITDVVKPIALPTKEPKPGSKCLASGWGSITPTRWQKPD
DLQCVFILPNENCAKVLQKVTDMILCAGEMGGGKDTCRDDSGGPLICDGILQGTTSYGPVPCGKPGVPAI
YTNLIKFNSWIKDMMKNA
>d1pxc_ b.47.1.2 (C:) Coagulation factor IXa, protease domain {Pig (Sus scrofa)}
IVGGENAKPGQFPWQVLLNGKIDAFCGGSIINEKWVVTAAHCIEPGVKITVAGEYNTEETEPTEQRRNVIRAIP
HHSYNATVNKYSHDIALLELDEPLTLSYVTPICIADKEYTNIFLKFGSGYVSGWGRVFNRGRSATILQYLKVPLVD
RATCLRSTKFTIYSNMFCAGFHEGGKDSCQGDGGPHVTEVEGTSFLTGIISWGEECAVKGKYGIYTKVSRYVN
WIKEKTKL
>d1rfna_ b.47.1.2 (A:) Coagulation factor IXa, protease domain {Human (Homo sapiens)}
VVGGEDAKPGQFPWQVVLNGKVDACGGSIVNEKWVVTAAHCETGVKITVAGEHNIEETEHTEQKRNVIRI
IPHHNYNAINKYHDIALLDEPLVLSYVTPICIADKEYTNIFLKFGSGYVSGWGRVFHKGRSALVLQYLRVPL
VDRATCLRSTKFTIYNNMFCAGFHEGGRDSCQGDGGPHVTEVEGTSFLTGIISWGEECAMKGKYGIYTKVSRY
VNWIKEKTKL
>d1fjsa_ b.47.1.2 (A:) Coagulation factor Xa (Chrismas factor), protease domain {Human (Homo sapiens)}
IVGGQECKDGECPWQALLINEENEGFCGGTILSEFYILTAACLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVI

KHNRFTKETYDFDIAVRLKTPITFRMNVAAPACLPERDWAESTLMTQKTGIVSGFGRTHEKGRQSTRLKMLEVP
YVDRNSCKLSSFIITQNMFCAGYDTKQEDACQGDGGPHVTRFKDTYFVTGIVSWGEGCARKGKYGIYTKVTA
FLKWIDRSMKT

>d1kigh_b.47.1.2 (H:) Coagulation factor Xa (Chrismas factor), protease domain {Cow (Bos taurus)}
IVGGRDCAEGECPWQALLVNEENEGFCGGTILNEFYVLAAHCLHQAKRFTVRVGDRNTEQEEGNEMAHEVE
MTVKHSRFVKETYDFDIAVRLKTPIRFRRNVAPACLPEKDWAETLMTQKTGIVSGFGRTHEKGRLSSTLKMLE
VPYVDRSTCKLSSFTITPNMFCAGYDTQPEDACQGDGGPHVTRFKDTYFVTGIVSWGEGCARKGKFGVYTK
VSNFLKWIDKIMKARAGAAGS

>d1fxya_b.47.1.2 (A:) Coagulation factor Xa-trypsin chimera {Synthetic, based on
Homo sapiens sequence}

IVGGYNCKDGEPWPQALLINEENEGFCGGTILSEFYILTAAHCLYQAKRFKVRVGDRNTEQEEGGEAVHEVEVVI
KHNRFTKETYDFDIAVRLKTPITFRMNVAAPASLPTAPPATGTKLISWGNTASSGADYPDELQCLDAPVLSQA
KCEASYPGKITSNMFCVGLEGKDKSCQGDGGPVVCNGQLQGVVSWGDGCAQKNKPGVYTKVYNYVKWI
KNTIAANS

>d1elva1_b.47.1.2 (A:410-668) Complement C1S protease, catalytic domain {Human (Homo
sapiens)}

CGVPREPFEEKQRIIGGSADIKNFPWQVFFDNPWAGGALINEYWVLTAAHVVEGNREPTMYVGSTSQTSL
LAKSKMLTPEHVFHPGWKLLAVPEGRTNFDNDIALVRLKDPVKMGPTVSPICLPGTSSDYNLMDGDLGLISG
WGRTEKRDRAVRLKAARLPVAPLRKCDEVKVEKPTADAЕAYVFTPNMICAGGEKGMDSKGDGGAFAVQDP
NDKTFYAAGLVSWGPQCCTYGLYTRVKNYVDWIMKTMQENS

>d1autc_b.47.1.2 (C:) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}
LIDGKMTRRGDSPWQVVLDSKKLACGAVALHPSWVLTAAHCMDESKLLVRLGEYDLRRWEKWELLDIKE
VFVHPNYSKSTTDNDIALLHLAQPATLSQTIVPICLPSGLAERELNQAGQETLVTGWGYHSSREKEAKRNRTFV
LNFIKIPVVPHNECSEVMSNMVSENMLCAGILGDRQDACEGDSGGPMVASFHGTWFLVGLVSWGEGCGLLH
NYGVYTKVSRYLDWIHGHIRD

>d1fuja_b.47.1.2 (A:) Myeloblastin, PR3 {Human (Homo sapiens)}

IVGGHEAQPHSRPYMASLQMRRGNPGSHFCGGTLIHPSFVLTAAHCLRDIPQRLVNVVLGAHNVRTQEPTQQH
FSVAQVFLNNYDAENKLNDILLQLSSPANLSASVATVQLPQQDQPVPHGTQCLAMGWGRVGAHDPPAQVLQ
ELNVTVVTFFCRPHNICTFVPRRKAGICFGDSGGPLICDGIIQGIDSFVIWGCATRLFDPFFTRVALYVDWIRSTLR
>g1c5y.1_b.47.1.2 (A:,B:) Urokinase-type plasminogen activator (LMW U-PA), catalytic domain
{Human (Homo sapiens)}

LKFQCGQKTXIIGGEFTTIENQPWFAAIYRRHRGGSVTYVCGSLMSPCWVISATHCFIDYPKKEDYIVYLGRSRL
NSNTQGEMKFEVENLILHKDYSADTLAHHNDIALLKIRSKEGRCAQPSRTIQTICLPSMYNDPQFGTSCITGFG
KEASTDYLYPEQLKMTVVKLISHRECQQPHYYGSEVTTKMLCAADPQWKTDSCQGDGGPLVCSLQGRMTLT
GIVSWGRCALKDPGVYTRVSHFLPWIRSHTKEE

>d1ddja_b.47.1.2 (A:) Plasmin(ogen), catalytic domain {Human (Homo sapiens)}

SFDGKPKQVEPKKCPGRVGGCVAHPHSWPWQVSLTRFGMHFCGGTLISPEWVLTAAHCLEKSPRPSSYKVI
LGAHQEVNLEPHVQEIEVSRLFLEPTRKDIALLKLSSPAVITDKVIPACLPSPNYVVADRTECFITGWGETQGTFGA
GLLKEAQLPVENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDAGGPLVCFCFKDKYILQGVTSWGLCAR
PNKPGVYVVRVSRFVTWIEGVMRNN

>d1fi8a_b.47.1.2 (A:) Granzyme B {Rat (Rattus norvegicus)}

IIGGHEAKPHSRPYMAYLQIMDEYSGSKKCGFLIREDFVLTAAHCSGSKIQVTLGAHNIKEQEKMQQIIPVVKII
PHPAYNSKTISNDIMLLKLKSAKRSSAVKPLNPRRNVKVKPGDVCYAGWGKLGPMGKYSDTLQEVELTVQE
DQKCESYLKNYFDKANEICAGDPKIKRASFRGDSGGPLVCKVAAAGIVSYGQNDGSTRAFTKVSTFLSWIKKT

MKK

>d1iaua_b.47.1.2 (A:) Granzyme B {Human (Homo sapiens)}

IIGGHEAKPHSRPYMAYLMIWDQKSLKRCGGFLIRDFVLTAAHCGSSINVTLGAHNIKEQEPTQQFIPVKRPI
PHPAYNPKNFSNDIMLLQLERKAKRTRAVQPLRLPSNKAQVKPGQTCSAGWGQTAPLGKHSHTLQEVKMTV
QEDRKCESDLRHYYDSTIELCVGDPEIKKTSFKGDGGPLVCNKVAQGIVSYGRNNGMPRACTKVSSFVHWIK
KTMKR

>d1eufa_b.47.1.2 (A:) Duodenase {Cow (Bos taurus)}

IIGGHEAKPHSRPYMAFLFKTSKGSHICGGFLVREDFVLTAAHCLGSSINVTLGAHNIMERERTQQVIPVRRPIP
HPDYNDETLANDIMLLKLTRKADITDKVSPINLPRSLAEVKPGMMCSVAGWGRGVNMMPSTDKLQEVDLEVQ
SEEKCIARFKNYIPFTQICAGDPSKRKNSFSGDGGPLVCNGVAQGIVSYGRNDGTTPDVYTRISSFLSWIHSTM
R

>g1fiw.1 b.47.1.2 (L;A:) Beta-acrosin {Sheep (Ovis aries)}

TTCDGPCGVFRQNIXIIGGQDAAHGAWPVMVSLQIFTYHNNRRYHCGSLLNSQWLTAACFRKKVTD
DWRLIFGAKEVEWGTNKPVKPPLQERYVEKIIHEKYSASSEANDIALMKITPPVTCGHFIGPGCLPQFRAGPPR
VPQTCWVAGWGFLQENARRTSPMLQEARVLDLIDLGLCNSTRWYNGRIRSTNVCA
GYP
LMCKDSAENSYVVVGITSWVGVCARAKRPGVYTSTWSYLNWIASKIGSTAVHMIQLPT

>g1fiz.1 b.47.1.2 (L;A:) Beta-acrosin {Pig (Sus scrofa)}

ATCDGPCGLRFRQXVVGMSAEPGA
WPWMVSLQIFMYHNNRRYHTCGILLNSHWVLTAAHC
CFKNKKVTD
DWRLIFGANEVVWGSNKPVKPPLQERFVE
IIIHEKYVSGLEINDIALIKITPPVPCGPFIGPGCLPQFKAGPPR
APC
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>d1eaxa_b.47.1.2 (A:) Matriptase MTSP1 {Human (Homo sapiens)}

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APGVQERRLKRIISHPFNDFTFDYDIALLELEKPAEYSSMVRP
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>d1svpa_b.47.1.3 (A:) Viral capsid protein {Sindbis virus}

ALKLEADRLFDVKNEDGDVIGHALAMEGKVMKPLHV
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>d1vcpa_b.47.1.3 (A:) Viral capsid protein {Semliki forest virus}

CIFEVKHEGKVTGYACLVGDKVMKPAHV
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>d1a1qa_b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

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>d1cu1a1_b.47.1.3 (A:705-720,A:3-186) NS3 protease {Human hepatitis C virus (HCV), different isolates}

GSVVIVGRIILSGSGSXITAYSQQTRGLLGCII
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>d1dxwa_b.47.1.3 (A:) NS3 protease {Human hepatitis C virus (HCV), different isolates}

TGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPIQMYTNVDQDLVGWQAPPGA
RSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSSLSPRPVSYLGSSGGPLLCPGHAVGIFRAAVCTRGVAKAV
DFVPVESMETTMRASKKKK
>g1a1r.1 b.47.1.3 (A.;C;) NS3 protease {Human hepatitis C virus (HCV), different isolates}
VEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPAPQGSRSLTPCTCGS
SDLYLVTRHADVIPVRRRGDSRGSSLSPRPISYLGSSGGPLLCPTGHAVGLFRAAVCTRGVAKAVDFIPVENLETT
MRXGSVVIVGRIVLSGKPA
>g1a1r.2 b.47.1.3 (B.;D;) NS3 protease {Human hepatitis C virus (HCV), different isolates}
PITAYAQQTTRGLLGCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTN
VDQDLVGWPAPQGSRSLTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSSLSPRPISYLGSSGGPLLCPTGHAVG
LFRAAVCTRGVAKAVDFIPVENLETTMRXGSVVIVGRIVLSGKPAIIPK
>g1dy9.1 b.47.1.3 (A.;C;) NS3 protease {Human hepatitis C virus (HCV), different isolates}
APITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVLSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPIQMYTN
YTNVNDQDLVGWPAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSSLSPRPVSYLGSSGGPLLCPSG
HVVGIFRAAVCTRGVAKAVDFIPVESMXGSVVIVGRIILS
>g1ns3.1 b.47.1.3 (A.;C;) NS3 protease {Human hepatitis C virus (HCV), different isolates}
ITAYSQQTRGLLGCIITSLTGRDKNQVEGEVQVVSTATQSFLATCVNGVCWTVYHGAGSKTLAGPKGPIQMYT
NVDQDLVGWQAPPGARSMTPCTCGSSDLYLVTRHADVIPVRRRGDSRGSSLSPRPVSYLGSSGGPLLCPSGHA
VGIFRAAVCTRGVAKAVDFIPVESMETTMRXGSVVIVGRIILS
>d1befa_ b.47.1.3 (A;) NS3 protease {Dengue virus serotype 2}
WDVPSPPVGKAELEDGAYRIKQKGILGYSQIGAGVYKEGTFTHTMWHVTRGAVALMHKGKRIEPSWADVKKDL
VSCGGGWKLEGWEWKEGEEVQVLAEPGKNPRAVQTKPGLFKTNAGTIGAVSLDFSPGTSGSPIIDKKGVVGIY
GNGVVTRSGAYVSAIAQTEKSIEDNPEIEDD
>d1cqqa_ b.47.1.4 (A;) 3C cysteine protease (picornain 3C) {Human rhinovirus type 2}
GPEEEFGMSLIKHNCSVITTENGKFTGLGVYDRFVVVPTHADPGKEIQVDGITTVIDSYDLYNKNGIKLEITVLK
LDRNEKFRDIRRYIPNNEDDYPNCLALLANQPETIINVGDVVSYGNILLSGNQTARMLKYSYPTKSGYCGGVL
YKIGQVLGIHVGGNGRDGFSAMLLRSYFT
>d1hava_ b.47.1.4 (A;) 3C cysteine protease (picornain 3C) {Human hepatitis A virus}
STLEIAGLVRKNLVQFGVGEKNGSVRWVMNALGVKDDWLLVPSHAYKFEKDYEEMMEFYFNRRGGTYSISAGN
VVIQSLDVGFDQVVLMKVPTIPKFRDITQHFIIKKGDVPRALNRLATLVTVNNGTPMLISEGPLKMEEKATYVHKK
NDGTTVDLTDQAWRGKGEGLPGMCGGALVSSNQSIQNAILGIHVAGGNSILVAKLVTQEMFQNIKKI
>d2hrva_ b.47.1.4 (A;) 2A cysteine proteinase {Human rhinovirus 2}
GPSDMYVHVGNIYRNHLFNSEMHEISILVSYSSDLIYRTNTVGDDYIPSCDCTQATYYCKHKNRYFPITVTSHD
WYEIQESEYYPKHQYNLLIGEGPCEPGDCGGKLLCKHGIVIGITAGGDNHVAFIDLRFHCA
>d1bco_1 b.48.1.1 (481-560) mu transposase, C-terminal domain {Bacteriophage mu}
TEEQKRMLLLPAEAVNVSRKGEFTLKVGSSLKGAKNVYYNMALMNAGVKVVVFDPQLHSTVYCYTLDR
FICEAECL
>d1e79a2 b.49.1.1 (A:19-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase
{Cow (Bos taurus)}
ADTSVDLEETGRVLSIGDGIARVHGLRVQAEMVEFSSGLKGMSLNLEPDNVGVVVFGNDKLIKEGDIVKRT
GAI
>d1e79d2 b.49.1.1 (D:9-81) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Cow
(Bos taurus)}
TTGRIVAVIGAVVDVQFDEGLPPILNALLEVQGRETRLVLEVAQHLGESTVRTIAMDGTEGLVRGQKVLDGAP

>d1maba2 b.49.1.1 (A:10-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (*Rattus norvegicus*)}
SSILEERILGADTSVDLEETGRVLSIGDGIARVHGLRVQAEEMVEFSSGLKGMSLNLEPDNVGVVFGNDKLIK
EGDIVKRTGAI

>d1mabb2 b.49.1.1 (B:1-81) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (*Rattus norvegicus*)}
SAAPKAGTATGQIVAVIGAVDVQFDEGLPPIALNEVQGRESRLVLEVAQHLGESTVRTIAMDGTEGLVRGQKVLDSGAP

>d1skyb2 b.49.1.1 (B:21-95) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}
SQIQVSDVGTVIQVGDGIARAHGLDNVMSGEAVEFANAVMGMALNLEENNVGIVILGPYTGIKEGDEVRTGRIM

>d1sky2 b.49.1.1 (E:1-82) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}
MTRGRVIQVMGPVVDVKFENGHLPAIYNALKIQHKARNENEVDIDLTEVALHLGDDTVRTIAMASTDGLIRG
MEVIDTGAP

>d1fx0a2 b.49.1.1 (A:25-96) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (*Spinacia oleracea*), chloroplast}
KVVNTGTVLQVGDGIARIHGLDEVMAGELVFEEGTIGIALNLESNNVGVVLMDGLMIQEGSSVKATGRIA

>d1fx0b2 b.49.1.1 (B:19-97) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Spinach (*Spinacia oleracea*), chloroplast}
NLGRIAQIIGPVNLNAFPPGKMPNIYNALIVKGRDTAGQPMNVTCEVQQLLGNRRAVAMSATDGLTRGME
VIDTGAP

>d1bd0a1 b.49.2.1 (A:2-11,A:245-382) Alanine racemase {Bacillus stearothermophilus}
NDFHRDTWAEXFSLHSRLVHVKKLQPGEKSYGATYTAQTEEWIGTIPIGYADGWLRRLQHFHVLDGQKAPIV
GRICMDQCMIRLPGPLPGTKVTLIGRQGDEVISIDDVARHLETINYEVPCISYRVPRIFRHKRIMEVRNAIG

>d1d7ka1 b.49.2.1 (A:7-43,A:284-427) Eukaryotic ornithine decarboxylase {Human (*Homo sapiens*)}
EEFDCHFLDEGFTAKDILDQKINEVSSDDKDAFYVAXFTLAVNIIAKKIVLKEQTGSDDDESSEQTFMYYVNDG
VYGSFNCLYDHAVKPLLQKRKPDERYYSSIWGPTCDGLDRIVERCDLPEMHVGDWMLFENMGAYTVAA
ASTFNGFQRPTIYYYMSGPAWQLMQQFQNPDFPP

>d7odca1 b.49.2.1 (A:2-43,A:284-418) Eukaryotic ornithine decarboxylase {Mouse (*Mus musculus*)}
SSFTKDEFDCILDEGFTAKDILDQKINEVSSDDKDAFYVAXFTLAVNIIAKKTWKEQPGSDDDESNEQTFM
YYVNDGVYGSFNCLYDHAVKALLQKRKPDEKYSSSIWGPTCDGLDRIVERCNLPEMHVGDWMLFENMG
AYTVAAASTFNGFQRPNIYYYMSRPMWQLMK

>d1f3ta1 b.49.2.1 (A:14-43,A:284-422) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}
RFLEGFNTRDALCKKISMNTCDEGDPFFVAXFTLAVNVIACKVTPGVQTDVGAHAESNAQSFMYYVNDGVYG
SFNCILYDHAVVRPLPQREPIPNEKLYPSSVWGPCTCDGLDQIVERYYLPEMQVGEWLLFEDMGAYTVVGTSFN
GFQSPTIYYYVSGLPDHVVRELKS

>d2toda1 b.49.2.1 (A:37-43,A:284-410) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}
GDPFFVAXFTLAVNVIACKVTPGVQTDVGAHAESNAQSFMYYVNDGVYGSFNCLYDHAVVRPLPQREPIPNE

KLYPSSVWGPTCDGLDQIVERYLPEMQVGEWLLFEDMGAYTVVGTSFNGFQSPTIYVV
>d1b6la_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWKRPLVTIRGGQLKEALLDTGADDTVIEEMNLPGKWPKMIGGIGGFIVRQYDQIPVEIXGHKAIGTV
LVGPTPVNIIGRNLLTQIGCTLNF
>d1bdqa_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWQRPLVTIKIGGQLKEALLDTGADDSIVAGIELPGRWPKPVMGGIGGFIVRQYDQILIEICGHKAIGTV
VGPTPINIIGRNLLTQIGCTLNF
>d1c6ya_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWQRPVVTIKIGGQLMEALIDTGADDTVLEEMDLPGRWPKPVIIGGIGGFIVRQYDQIPIEICGHKVIGTV
LVGPTPTNIIGRNLLTQIGCTLNF
>d1dazc_ b.50.1.1 (C:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWKRPLVTIKIGGQLKEALLDTGADDTVIEEMSLPGRWPKPIMIGGIGGFIVRQYDQIIIIEAGHKAIGTV
VGPTPVNIIGRNLLTQIGATLNF
>d1difa_ b.50.1.1 (A:) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWPKPMMIGGIGGFIVRQYDQILIEICGHKAIGTV
VGPTPVNIIGRNLLTQIGCTLNF
>d1hvc_ b.50.1.1 (-) Human immunodeficiency virus type 1 protease {Human immunodeficiency virus type 1}
PQITLWQRPLVTIRGGQLKEALLDTGADDTVLEEMNLPGKWPKMIGGIGGFIVRQYDQILIEICGHKAIGTV
LVGPTPVNIIGRNLLTQIGCTLNFQGGSGPQITLWQRPLVTIKIGGQLKEALLDTGADDTVLEEMSLPGRWPKPMM
IGGIGGFIVRQYDQILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNF
>d1idaa_ b.50.1.1 (A:) Human immunodeficiency virus type 2 (HIV-2) protease {Human immunodeficiency virus type 2}
PQFSLWKRPVVTAYIEGQPVEVLLDTGADDSIVAGIELGNNSPKIVGGIGGFINTKEYKNVEIEVLNKKVRATIM
TGDTPINIFGRNLLTALGMSLNL
>d1az5_ b.50.1.1 (-) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}
PQFHLWKRPVVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVEVEVLGKRIKGTM
TGDTPINIFGRNLLTALGMSLNF
>d1k6va_ b.50.1.1 (A:) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}
PQITLWKRPLVTIRGGQLKEALLDTGADDTVLEEMNLPGRWPKPMMIGGIGGFIVRQYDQIPIEICGHKAIGTV
LVGPTPTNVIGRNLLTQIGCTLNF
>d1siva_ b.50.1.1 (A:) Simian immunodeficiency virus (SIV) protease {Simian immunodeficiency virus, different strains}
PQFSLWRRPVVTAHIEGQPVEVLLDTGADDSIVTGIELGPHYTPKIVGGIGGFINTKEYKNVKIEVLGKRIKGTM
GDTPINIFGRNLLTALGMSLNL
>d4fiv_ b.50.1.1 (-) Feline immunodeficiency virus (FIV) protease {Feline immunodeficiency virus}
VGTTTLEKRPEILIFVNGYPIKFLLDTGADITLNRRDFQVKNSIENGRQNMIGVGGKRGTNYINVHLEIRDEN

YKTQCIFGNVCVLEDNSLIQPLLGRDNMIKFNIRLVM

>d1baia_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}

LAMTMEHKDRPLVRVILNTGSHPVKQRSVYITALLDTGADDTVISEEDWPTDWPVMEAANPQIHIGGGIPV
RKS RD MIELGVINRDGSLERPLLFPLVAMTPVNILGRDCLQGLGLRLTNL

>d2rspa_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}

LAMTMEHKDRPLVRVILNTGSHPVKQRSVYITALLDSGADITIISEEDWPTDWPVMEAANPQIHIGGGIPM
RKS RD MIELGVINRDGSLERPLLFPAVAMVRGSILGRDCLQGLGLRLTNL

>d1fmb_ b.50.1.1 (-) EIAV protease {Equine infectious anemia virus}

VTYNLEKRPTTIVLINDTPLNVLLDTGADTSVLTTAHYNRLKYRGRKYQGTGIGGVGGNVENTFSTPVTKKKGRHI
KTRMLVADIPVTILGRDILQDLGAKLVL

>d2er7e_ b.50.1.2 (E:) Endothiapepsin {Chestnut blight fungus (Endothia parasitica)}

STGSATTPIDSLLDAYITPVQIGTPAQTLNLDFDTGSSDLWVFSSETTASEVDGQTIVTPSKTTAKLLSGATWSIS
YGDGSSSSGDVYTDTVVGGLTVGQAVESAKVSSSFTEDSTIDGLLGAFSTLNTVSPTQQKTFDNAKASLD
SPVFTADLGYHAPGTYNFGFIDTTAYGSIYTAVSTKQGFWEWTSTGYAVGSGTFKSTSIDGIADTGTLLYPAT
VVSAYWAQVSGAKSSSVGGYVFPCSATLPSFTFGVGSARIVPGDYIDFGPISTGSSCFGGIQSSAGIGINIFGD
VALKA AFVVFN GATT PTLGFASK

>d1bxoa_ b.50.1.2 (A:) Acid protease {Fungus (Penicillium janthinellum),
penicillopepsin}

AASGVATNTPTANDEEYITPVТИGGTTLNLNFDTGSADLWVFS TEL PASQSQSGHSVYNPSATGKE LSGYTWSISY
GDGSSASGNVFTDSVTVGVT AHGQAVQAAQQISAQFQ QDTNN DGLLGAFSSINTVQPQSQTFFDTVKSS
LAQPLFAVALKHQQPGVYDFGFIDSSKYTGSLTYTGVDNSQGFWSFN VDSYTAGSQSGDG FSGIADTGTLLL
DDSVVSQYYSQVSGAQQQDSNAGGYVFDCSTNLPDFSVSISGYTATVPGSLINYGPSGDGSTCLGGIQSNSGIGFS
IFGDIFLKSQYVVFDSDGPQLGFAPQA

>d1ibqa_ b.50.1.2 (A:) Acid protease {Fungus (Aspergillus phoenicis), aspergillopepsin}

SKGS AVTTPQNNDEEYLTPVTVGKSTLHLDFDTGSADLWVFSDELPSEQTGHDL YTPSSATKLSGYSWDISYG
DGSSASGDVYRDTVTGGVTTNKQAVEAASKISSEFVQDTANDGLLGAFSSINTVQPKAQTTFFDTVKSQLDS
PLFAVQLKHDAPGVYDFGYIDDSKYTGSIYTDADSSQGYWGSTDGYSIGDGSSSSGFSAIADTGTLLILLDEI
VSAYYEQVSGAQESYEAGGYVFSCSTLDPFTVIGDYKAVVPGKYINYAPVSTGSSTCYGGIQSNSGLGLSILGD
VFLKSQYVVFNSEGPKLGFAAQA

>d2apr_ b.50.1.2 (-) Acid protease {Bread mold (Rhizopus chinensis)}

AGVGTVPMTDYGNDIEYYGQVTIGTPGKKFNLDFTGSSDLWI ASTLCTNC SGQTKYDPNQSSTYQADGRT
WSISYGDGSSASGILAKDNVNLLGGLIKGQTI ELAKREAASFASGPNDLLGFDTITTVRGVKT PMDNLISQG
LISRPIFGVYLGAKNGGGGEYIFGGYDSTKFKGS LTTV PIDNSRGWWGITVDRATVGTSTVASSFDGILD GTTL
LILPNNIAASVARAYGASDNGDGTYTISC DTS AFKPLV FSINGASFQVSPDSL VFEFQGQCIAGFGYGNWGFAII
GDTFLKN NYVVFNQGVPEVQIAPVAE

>d2asi_ b.50.1.2 (-) Acid protease {Rhizomucor miehei}

GSVDT PGYYDFDLEEYAI PV SIGTPGQDFLLFDTGSSDTWPHKGCTKSEGCVGSRFFDPSASSTFKATNYNLNI
TYGTGANGLYFEDSIAIGDITVTKQIAYDVNRGPTAEQSPNADIFLDGLFGAA YPDNTAMEAEYGSTYNTVHV
NLYKQGLISSPLFSVYMNTNSGTGEVVF GGVNNTLLGGDIAYTDVMSRYGGYYWDAPVTG ITVDGSAAVRFS
RPQAFTIDTGTNFFIMPSSAASKIVKAALPDATE TQ QGWV VPCASYQNSKSTISIVMQKSGSSSDTIEISPVSK
MLLPVDQSNETCMFIILPDGGNQYIVGNLFLRFFVN VYDFGNNRIGFAPLASAYENE

>d1eaga_ b.50.1.2 (A:) Acid protease {Yeast (Candida albicans)}

QAVPVT LHNEQV TYAADITV GSNNQ KLNIV DTGSSDLWV PDV NVDCQV TS DQTA DFCKQKG TYDPSGSSA
SQDLNTPFKIGYGDGSSSQGTLYKDTVGF GGVS IKNQV LADVD STSIDQG ILGVGYKT NEAGGSYD NVPV TLKK

QGVIAKNAYSLYLNSPDAATGQIIFGGVDNAKYSGLIALPVTSRDLRISLGSVEVSGKTINTDNDVLLSGTTI
TYLQQDLADQIIKAFNGKLTQDSNGNSFYEVDCNLSGDVVFNFSKNAKISVPASEFAASLQGDDGQPYDKCQLL
FDVNDANILGDNFLRSAYIVYDLDDEISLAQVKYTASSISALT

>d1j71a_b.50.1.2 (A:) Acid protease {Yeast (*Candida tropicalis*)}

SDVPTTLINEGPSYAADIVVGSNQQKQTVIDTGSSDLWVVDTDACEQVTVSGQTNNFCKQEGTFDPSSSSA
QLNLNQDFSIEYGDLTSSQGSFYKDTVGFGGISIKNQQFADVTTSVDQGIMGIGFTADEAGYNLYDNVPVTLKK
QGIINKNAYSLYLNSEDASTGKIIFGGVDNAKYTGTLALPVTSVELVHLGSINFDGTSVSTNAVVLDSGTTIT
YFSQSTADKFARIVGATWDSRNEIYRLPSCDLSGDAVFNFQGVKITVPLSELILKDSDSSICYFGISRNDANILGD
NFLRRAYIVYDLDKTISLAQVKYTSSDISAL

>d1dpja_b.50.1.2 (A:) Acid protease {Baker's yeast (*Saccharomyces cerevisiae*), proteinase A}
GGHDVPLTNYLNAQYYTDITLGTTPQNFKVILDGTSSNLWVPSNECGSLACFLHSKYDHEASSSYKANGTEFAIQ
YGTGSLEGYISQDTLSIGDLTIPKQDFAEATSEPGTFAFGKFDGILGLGYDTISVDKVVPPFYNAIQQDLLDEKRFA
FYLGDTSKDTENGGEATFGGIDESFKGDTWLPVRRKAYWEVKFEGIGLGDEYAELESHGAAIDTGTSLITLPSG
LAEMINAEIGAKKGWTGQYTLCNCNRDNLPDLIFNFNGYNFTIGPYDYTLEVSGSCISAITPMDFPEPVGPLAIV
GDAFLRKYYSIYDLGNNAVGLAKAI

>g1b5f.1 b.50.1.2 (A:,B:) Plant acid proteinase, phytepsin {*Cynara cardunculus*}

GSAVVALTNDRTSYFGEIGIGTPPKFTVIFDTGSSVLWVPSKACRAHSMYESSDSSTYKENGTFGAIY
GTGSITGFFSQDSVTIGDLVKEQDFIEATDEADNVFLHRLFDGILGLSQTISVPWYNMLNQGLVKERRFSFW
LNRNVDEEEGGELVFGGLDPNHFGRGDHTYVPVTYQYYWQFGIGDVLIQDKSTGFCAQFCAGGCAAIDS
TAIVTQINHAIGANXEELQVDCNTLSSMPNVSFTIGGKKFGLTPEQYILKVGKGEATQCISGFTAMDATLLGPLWI
LGDVFMRPYHTVFDYGNLLVGFAEAA

>d1qdma2 b.50.1.2 (A:2-247,A:248-338) Plant acid proteinase, phytepsin {Barley (*Hordeum vulgare*)}

EEEGDIVALKNYMNAQYFGEIGVGTPPKFTVIFDTGSSNLWVPSAKCYFSIACYLHSRYKAGASSTYKNGKPA
AIQYGTGSIAGYFSEDSVTVGDLVVKDQEIEATKEPGITFLVAKFDGILGLGFEISVGKAVPVWYKMIEQGLVSD
PVFSFWLNRHVDEEGGEIIFGGMDPKHYVGEHTYVPVTQKGWQFDMDVLLGGKSTGFCAAGGAAIADS
GTSLLAGPTAIITEINEKIGAAGXSPMGESAVDCGSLGSMPDIEFTIGGKKFALKPEEYILKVGEGAAAQCISGFTA
MDIPPRGPLWILGDVFMPYHTVFDYKLRIGFAKAA

>d3psg_b.50.1.2 (-) Pepsin(ogen) {Pig (*Sus scrofa*)}

LVKVLVRKKSLRQNLIKDGKLDFLKHKNPASKYFPEAAALIGDEPLENYLDTEYFGTIGIGTPAQDFTVIFDT
GSSNLWVPSVYCSSLACSDHNQFNPDSSSTFEATSQELSITYGSMTGILGYDTVQVGGISDTNQIFGLSETEP
GSFLYYAPFDGILGLAYPSIASGATPVFDNLWDQGLVSQDLFSVYLLSSNDDSGSVVLLGGIDSSYYGSLNWVPV
SVEGYWQITLDSITMDGETIACSGGCQAIVDTGSLTGPTSAIANIQSDIGASENSDGEVMVISCSSIDSLPDIVFT
IDGVQYPLSPSAYILQDDDSCTSGFEGMDVPTSSGELWILGDVFIRQYYTVFDRANNKVG LAPVA

>d4pep_b.50.1.2 (-) Pepsin(ogen) {Pig (*Sus scrofa*)}

IGDEPLENYLDTEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACSDHNQFNPDSSSTFEATSQELSITYGT
GSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSIASGATPVFDNLWDQGLVSQDLFSV
YLSNDDSGSVVLLGGIDSSYYGSLNWVPVSVEGYWQITLDSITMDGETIACSGGCQAIVDTGSLTGPTSAI
ANIQSDIGASENSDGEVMVISCSSIDSLPDIVFTIDGVQYPLSPSAYILQDDDSCTSGFEGMDVPTSSGELWILGDV
FIRQYYTVFDRANNKVG LAPVA

>d1psoe_b.50.1.2 (E:) Pepsin(ogen) {Human (*Homo sapiens*), 3A}

VDEQPLENYLDMEYFGTIGIGTPAQDFTVIFDTGSSNLWVPSVYCSSLACTNHNRNPEDSSTYQSTSETVSITY
GTGSMTGILGYDTVQVGGISDTNQIFGLSETEPGSFLYYAPFDGILGLAYPSISSGATPVFDNIWNQGLVSQDLF
SVYLSADDQSGSVVIFGGIDSSYYGSLNWVPVTVEGYWQITVDSITMNGEAIACAEGCQAIVDTGSLTGPTS

PIANIQS DIGASENS DGD MVVCSA ISSLP DIVFTINGVQYPVPPSAYILQSEGSCISGFQGMNLPTESGELWILG
DV FIRQYFTV FDR ANNQ VGLAPVA

>g1htr.1 b.50.1.2 (P;B:) Pepsin(ogen) {Human (Homo sapiens), progastricsin (pepsinogen C)}

AVVKVPLKKFKSI RETMKEKGLLGEFLRTHKYDPAWKYRGDLXSVTYEPMA YMADAAYFGEISIGTPPQNFLVLF
DTGSSNLWVPSVYC SQACTSHSRFNPSE SS TNGQTFSLQYGSGLTGFFGYDTLT VQSIQVPNQEFG LSEN
EPGTNFVYAQFDGIM GLAYPAL SDE ATTAMQGMVQEGALTSPVFSVYL SNQQGSSGGAVVFGGV DSSL YTG
QIYWAPVTQELYWQIGIEFLIGGQASGW CSEG CQAIVDTGTSLLTV PQQYMS ALLQATGAQ EDEY QFLVNC
NSIQNLPSLTFIINGVEFPLPPSSYILSNNGYCTVGVEPTYLSSQNGQPLW ILGDVFLRSY SVYD LGNN RVGFATA
A

>d1am5__ b.50.1.2 (-) Pepsin(ogen) {Atlantic cod (Gadus morhua)}

RVTEQM KNEADTEYYGVISIGTPPESFKVIFDTGSSNLWVSSHC SAQACSNHNKF KPRQSSTYVETGKTVD LT
GTGGMRGILQ DTVS VGGSDPNQELGESQTEPGPFQAAAPFDGILG LAYPSIAAAGAVPVFDNMGSQSL VE
KDLFSFYLSGGGANGSEVMLGGVDNSHYTGSIH WIPVTAEKY WQVALD GITVNGQTAACEGCQAIVDTGTSKI
VAPV SALANIMKD IGA SENQ GEMMG NCAS VQLP DITFTINGVK QPLP PSAYIEGDQAFCTSGLGSSG VPS NT
SELWIFGDVFLRN YYTIYDRTNNKVGFA PAA

>d1mpp__ b.50.1.2 (-) Pepsin {Mucor pusillus}

GSV DTPG LYDFD LEE YAI PV SIGTPG QDFY LLFDTGSS DTWV PHKGCDN SEGV GKRFF DPSS STFK ET DYN LNI
TYGTGGANGIYFRDSITV GGATV KQQTLAYVDNVSGPTAEQSPDSELF DGI FGAAYPDNTAMEA EYGD TYNTV
HV NLYKQGLI SS PVF SVY MNTNDGGQV VFGGVNNTLGGDIQYTDVLKSRGGYFFWDAPVTGV KIDGSD AV
SFDGAQ AFTID GTNFFI APSSFAE KVKA ALP DATES QQGY TVPC SKY QDSKTTF SLV LQKGSS SDT IDV SVP IS
KM LLP DV KSG ETCMFIVLPDGGNQFIVGNLFLRFFVN VYDFGKNRIGFAPLA SGYEND

>g1lyb.1 b.50.1.2 (A:,B:) Cathepsin D {Human (Homo sapiens)}

GPIE VLKNYMDA QYYGEIGIGTPPQCFTV VFDTGSSNLWVPSI HCKL LDIACWI HHKYN SDKS STYV KNGT SFD
IH YGSGSLSGYLSQDTVSPCQXGGVKVERQVFG EATK QPGITFIAAKFDGILGMAY PRISV NNLPVFDN LMQ
QKLVDQNI FS FYLSRDPDAQPGGELMLGGTDSKYYKGSLSYLN VTRKAYWQVHLDQVEV ASGLT CKEG CEA IV
DTG TSLMVGPVDEVRELQKAIGAVPLI QGEYMIPCEKVSTLPAITLK LGGKGYK LSPEDY TLK VSQAGK TLCLSGF
MGMDI PPPS GPLW ILGDV FIG RY YTF DRDN NRVG FAE AA

>d3cms__ b.50.1.2 (-) Chymosin (synonim: renin) {Cow (Bos taurus)}

GEVASVPLTN YLDSQYFGK IYLG TPPQE FTVL FDTGSS DFV WVPSI CKS NACK NHQR FDPR KS STFQ NLG KPL SIH
YGTGSMQGILG YDTV TVSNIV DIQ QT VGLSTQ EP GD FFTYAE FDG ILGMAY PSLASEY SIVF DNMM NRHL VA
QDLF SVYMD RNGQ ESMI LTG AIDP SYT GSLH WVPV TQ QYWQ FTV DSVT ISGV VV ACEGGC QAI LDGT SK
LV GPSSD IL NIQQ AIGAT QNQY GEFDID CDN LS YMPTVV FEING KMYPL P S AY TSQD QGF CTSGF QSE NH SQK
W ILGDV FIRE YYS VFD RANN LV GLAKAI

>d1hrna_ b.50.1.2 (A:) Chymosin (synonim: renin) {Human (Homo sapiens)}

GN TTSS VIL TNYMDTQYYGEIGIGTPPQTFK VV FDTGSS NVW VPSS KCS RL YTACV YHKL FDAS DSSY KHNG TE
LT LRYST GTV SGFL SQDI ITV GG ITV TQ MFGEV TEMPAL PFM LAE FDGV VMGF IEQA IGRV TP IFD NIIS QGV LK
EDV FSF YYNR DSE NSQ SLGG QIVL GGSDP QHYEG NFHY IN LIK TGV WQI QMKG VSGS STLL CEDG CLA LVD TG
ASYISGSTSSIEKLMEALGAKKRLFDYV VKCNEGPTLPDISFH LGGKEY TLTSADYV FQESYSSKKL CTLAI HAMDIP
PPTGPTW ALGATFIRK FYTEFDR RNNRIGFALAR

>d1smra_ b.50.1.2 (A:) Chymosin (synonim: renin) {Mouse (Mus musculus)}

TD LIS PVLT NYL NSQ YYGEIGIGTPPQTFK VIFDTG SANLW VPST KCS RL YAC GIHS LYESSD SSY MENG DDFTI
HYGSGRVKGFLSQDSVTVGGITV TQTFGEV TQLPLIP FM LAQFDGV LGM GFPAQAVGGVTPVFDHILSQGV LK
EKVFSVYYNRGP HLLG GEV VLG SDP QHYQGDFHYV SLSK TD SWQIT MKGV SVGS STLL CEEG CEV VV DTG SS

FISAPSSLKLIQMQLGAKEKRLHEYVVSCSQVPTLPDISFNLGGRAYTLSSTDYVLQYPNRRDKLCTVALHAMDI
PPPTGPVVVLGATFIRKFYTEFDRHNNRIGFALAR
>d1fkna_ b.50.1.2 (A:) beta-secretase (memapsin) {Human (Homo sapiens)}
RRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNILVDTGSSNFAVGAAPHFLHRYYQRQLSSTYRDLRKGV
YVPYTQGKWEGLGTDLVSIPHGPNTVRANIAAITESDKFFINGSNWEGILGLAYAEIARPDDSLPFFDSLVKQ
THVPNLFLSQLCGAGFPLNQSEVLASVGGSMIIGGIDHSLYT GSLWYTPIRREWYYEVIVRVEINGQDLKMDCK
EYNYDKSIVDSGTTNLRPKVFEEAVKSIAASSTEKFDPGFWLGEQLVCWQAGTPWNIFPVISLYLMGEVT
NQSFRITILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRAKRIGFAVSACHVDEFRT
AAVEGPFVTLDMEDCGYN
>d1pfza_ b.50.1.2 (A:) Plasmeprin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}
HLTIGFKVENAHDRIKTIKTHKLKNYIKESVNFLNSGLTKTNYLGSNDNIELVDFQNIMFYGDAEVGDNQQPFT
FILDTSANLWVPSVKCTTAGCLTKHLYDSSKSRTYEKDGTKVEMNYVSGTSGFFSKDLTVGNLSLPYKFIEVI
DTNGFEPTYTASTFDGILGLGWKDL SIGSVDPIVVELKNQN KIENALFTFYLPVHDKHTGFLTIGGIEERFYEGPLT
YEKLNHDLYWQITLDAHVGNI MLEKANCIVDSGTSAITVPTDFLNKMLQNL DVIKVPFLPFYVTL CNNSKLPTFE
FTSENGKYTLEPEYYLQHIEDVPGGLCMLNIIGLDFPVPTFILGD
>d1smea_ b.50.1.2 (A:) Plasmeprin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}
SSNDNIELVDFQNIMFYGDAEVGDNQQPFTFILDTSANLWVPSVKCTTAGCLTKHLYDSSKSRTYEKDGTKVE
MNYVSGTSGFFSKDLTVGNLSLPYKFIEVIDTNGFEPTYTASTFDGILGLGWKDL SIGSVDPIVVELKNQN KIE
NALFTFYLPVHDKHTGFLTIGGIEERFYEGPLTYEKL NHDLYWQITLDAHVGNI MLEKANCIVDSGTSAITVPTDF
LNKMLQNL DVIKVPFLPFYVTL CNNSKLPTFEFTSENGKYTLEPEYYLQHIEDVPGGLCMLNIIGLDFPVPTFILGD
PFMRKYFTVFDYDNHSV GIALAKKNL
>d1qs8a_ b.50.1.2 (A:) Plasmeprin ii (a hemoglobin-degrading enzyme) {Plasmodium vivax}
SENDVIELDDVANIMFYGEGEVGDNHQKFMLIFDTGSANLWVPSKKCNSSGCSIKNLYDSSKS SKSYEKDGKVD
ITYGSGTVKGFFSKDLVTLGHLSMPYKFIEVIDTDDLEPISSVEFDGILGLGWKDL SIGSIDPIVVELKNQN KIDNA
LFTFYLPVHDVHAGYL TIGGIEEKFYEGNITYEKL NHDLYWQIDLDVHFGKQTMEKANVIVDSGTTTAPSEFLN
KFFANLNVIKVPFLPFYVTTCDNKEMPTLEFKSANNTY TLEPEYYMNPILEVDDTLCMITMLPVIDSNTFILGDP
FMRKYFTVFDYDKE SVGFAIAKN
>d1ile_2 b.51.1.1 (198-386) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}
KEIQDPSVYVRFPLKEPKKLGLEKASLLIWTTPWTLPGNVAAAVHPEYTYAAFQVGDEALILEEGLGRKLLGE GT
QLKTFPGKALEGLPYTPPYPOALEKGYFVVLADYVSQEDGTGIVHQAPA FGAEDLETARVYGLPLLKVDEEGK
LLVEPKGLYFREANRAILRDLRGRLLFKEESYLSHY
>d1ffya2 b.51.1.1 (A:201-394) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}
HDKRSASIYVAFNVKDDKGVV DADAKFI IWTTPW TIPS NVAITV HPELK YGQY NVNG EKII AEALSD AVEA AL
DWDKASIKLEKEYTGKELEWVVAQHPFLDRESLVINGDHVTT DAGTGC VHTAPGHGEDDYIVGQQYELPVISPI
DDKGVFTEEGGQFEGMFYDKANKAVTDLTEKGALLKLD FITHSY
>d1gaxa2 b.51.1.1 (A:190-342) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}
TEPTPGKLYTLRYEVEGGGFIEIATVRPETVFADQAIAVHPEDERYHLLGKRARIPLTEVWIPIADPAVEKDFGT
GALKVTPAHDPLDYEIGERHGLKPVSVINLEGRM EGERVPEALRGLDRFEARRKA VELFREAGHLVKEE DY TIA
A
>d1gmua1 b.107.1.1 (A:1-70) Urease metallochaperone UreE, N-terminal domain {Klebsiella aerogenes}
MLYLTQRLEIPAAATASVLPIDVRVKS RVKVTLNDGRDAGLLPRGLL RGGDVL SNEEGTEFVQVIAA
>d1eara1 b.107.1.1 (A:1-74) Urease metallochaperone UreE, N-terminal domain {Bacillus pasteurii}
MVITKIVGHIDDL SHQIKKVDWLEVEWEDLNKRILRKETENGTDIAIKLENSGTLRYGDVLYESDDTLIAIRTK

>d2eng__ b.52.1.1 (-) Endoglucanase V {Humicola insolens}
ADGRSTRYWDCCKPSCGWAKKAPVNQPVFSCNANFQRITDFDAKSGCEPGGVAYSCADQTPWAVNDDAL
GFAATSIAGSNEAGWCCACYELTFTGPVAGKKMVVQSTSTGGDLGSNHFDLNIPGGVGIFDGCTPQFGGLP
GQRYGGISSRNECDRFPDALKPGCYWRFDWFKNADNPSFSFRQVQCPAELVARTGCRRNDDGNFPAV
>d1bw3__ b.52.1.2 (-) Barwin {Barley (*Hordeum vulgare*)}
EQANDVRATYHYYRPAQNNWDLGAPAVSAYCATWDASKPLSWRSKYGTAFCGPAGPRGQAACGKCLRVT
NPATGAQITARIVDQCANGGLDWDTVFTKIDTNGIGYQQGHLNVNYQFVDCRD
>g1aw8.1 b.52.2.1 (A:,B:) Pyruvoyl dependent aspartate decarboxylase, ADC {Escherichia coli}
MIRTMILQGKLHRVKVTHADLHYEGXCAIDQDFLDAAGILENEAIDIWNVNTNGKRFSTYAI_AERGSRIISVNG
AAAHCASVGDIVIIASFVTMPDEEARTWRPNVAYFEGDNEMIK
>d1eu1a1 b.52.2.2 (A:626-780) Dimethylsulfoxide reductase (DMSO reductase)
{Rhodobacter sphaeroides}
ERLGGAGAKYPLHVVASHPKSRLHSQLNGLTSRDLYAVAGHEPCLINPADAAARGIADGDVLRVFNDRGQILVG
AKVSDAVMPGAIQIYEGGWYDPLDPSEEGTLKYGDVNVLSDLVGTSKLAQGNCGQTILADVEKYAGAPVT
VFDTPKGAA
>d1dmr_1 b.52.2.2 (626-781) Dimethylsulfoxide reductase (DMSO reductase)
{Rhodobacter capsulatus}
ERLDGPGAKYPLHIAASHPFNRLHSQLNGLTVLREGYAVQGHEPCLMHPDDAARGIADGDVVRVHNDRGQIL
TGVKVTDAVMKGVIQIYEGGWYDPSDVTEPGTLKYGDVNVLSDIGTSKLAQGNCGQTVLAEVEKYTGPAVT
LTGFVAPKAAE
>d1aa6_1 b.52.2.2 (565-715) Formate dehydrogenase H {Escherichia coli}
PIDKLTDEYPMLSTVREVGHYSRSMGNCAALAALADEPGYAQINTEDAKRLGIEDEALVVHSRKGKIITRA
QVSDRPNKGAIYMTYQWWIGACNELVTENLSPITKPEYKCAVRVEPIADQRAAEQYVIDEYNKLKTRLREAA
LA
>d1tmo_1 b.52.2.2 (632-798) Trimethylamine N-oxide reductase {Shewanella massilia}
ERSHGGPGSDKHPIWLQSCHPDKRLHSQMCSREYRETYAVNGREPVYISPVDAKARGIKDGDIVRVFNDRGQ
LLAGAVVSDNFPKGIVRIHEGAWYGPVGKDGSTEGGAEVGALCSYGDPNTLTDIGTSKLAQACSAYTCLVEFEK
YQGKVPKVSSFDGPIEVEI
>d1g8ka1 b.52.2.2 (A:683-825) Arsenite oxidase large subunit {Alcaligenes faecalis}
LPATVQQQKDKYRFWLNNGRNNEVWQTAYHDQYNSLMQERYPMAYIEMNPDDCKQLDVTGGDIVEVYND
FGSTFAMVYPVAEIKRGQTFMLFGYVNGIQGDVTTDWTDRDIIPYYKGTWGD_{DIRKVG}SMSEFKRTVSFKSRRF
G
>d2napa1 b.52.2.2 (A:601-723) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}
AAEEPDAEYPLYLTSMRVIDHWHTATMTGKVEPELQKANPIAFVEINEEDAARTGIKHGDSVIVETRRDAMELPA
RVSDVCRPLIAVPPFDPKLVLNKLF DATDPVSREPEYKICAARVRKA
>d1qcsa1 b.52.2.3 (A:0-85) N-terminal domain of NSF-N, NSF-Nn {Hamster (*Cricetulus griseus*)}
NMAGRSMQAARCPTDELSNC_{AVV}SEKDYQSGQHVIVRTSPN_HKYIFTL_RTHPSV_VPGSVA_FSLPQRKWAGL
SIGQEIEVALYSF
>d1cr5a1 b.52.2.3 (A:26-107) N-terminal domain of NSF-N, NSF-Nn {Baker's yeast (*Saccharomyces cerevisiae*), sec18p}
TRHLKVSNCPNNSYALANVAAVSPNDFPNNIYIIDNLVFTTRHSNDIPP_GTIGFNGNQRTWGGWSLNQDVQ
AKAFDLFKY
>d1cz4a1 b.52.2.3 (A:1-91) N-terminal domain of VAT-N, VAT-Nn {Archaeon *Thermoplasma acidophilum*}

MESNNIILRVAEANSTDPGMSRVRLDESSRRLLDAEIGDVVEIEKVRKTGRVYRARPEDENKGIVRIDSVMR
NNCGASIGDKVKVRKVR

>d1e32a1 b.52.2.3 (A:21-106) Membrane fusion atpase p97 N-terminal domain , P97-Nn {Mouse (Mus musculus)}

NRPNRLIVDEAINEDNSVVSLSQPKMDELQLFRGDTVLLGKKREAVCIVLSDDTCSDKIRMNRVVRNNLRV
RLGDVISIQPCP

>d1dfup_ b.53.1.1 (P:) Ribosomal protein L25 {Escherichia coli}

MFTINAEVRKEQGKGASRRLRAANKFPAAIYGGKEAPLAIELDHDKVMNMQAKAEFYSEVLTIVVDGKEIKVKA
QDVQRHPYKPKLQHIDFVRA

>d1feua_ b.53.1.1 (A:) Ribosomal protein TL5 (general stress protein CTC) {Thermus thermophilus}

MEYRLKAYYREGEKPSALRAGKLPGLMYNRHLNRKVYVDLVEFDKVFHQASIHHVILELPDGQLPTLVRQV
NLDKRRRPEHVDFVLSDEPVEMYVPLRFVGTPAGVRAGGVLQEIHARDILVKVSPRNIPEFIEVDVSGLEIGDSL
HASDLKLPPGVELAVSPEETIAAVVPPEDVEKLAE

>d1gtra1 b.53.1.2 (A:339-547) Gln-tRNA synthetase (GlnRS), C-terminal (anticodon-binding) domain {Escherichia coli}

APRAMAVIDPVKLVIENYQGELEMVTMPNHPNKPEMGSRQVFSGEIWIDRADFREEANKQYKRLVLGKEVR
LRNAYVIKAERVEKDAEGNITTIFCTYDADTLSKDPADGRKVKGVIHWVSAAHALPVEIRLYDRLFSVPNPGAAD
DFLSVINPESLVIKQGFAEPSLKDAVAGKAFQFEREGYFCLDSRHSTAEPVFVNRTVGLRDT

>d1h9db_ b.54.1.1 (B:) Core binding factor beta, CBF {Human (Homo sapiens)}

PRVVPDQRSKFENEFFRQLSRECEIKYTGFRDRPHEERQARFQNAACRDGRSEIAFVATGTNLSIQFFPASWQG
EQRQTPSREYVDLEREAGKVYLKAPMILNGVCVIKGWIDLQRLDMGCLEFDEERAQQE

>d1mai_ b.55.1.1 (-) Phospholipase C delta-1 {Rat (Rattus norvegicus)}

GLQDDPDLQALLKGSQLLKVKSSSWRRERFYKLQEDCKTIWQESRKVMRSPEQLFSIEDIQEVRMGHRTGLE
KFARDIPEDRCFSIVFKDQRNTLDLIAPSPADAQHWVQGLRKIIH

>d1btn_ b.55.1.1 (-) beta-spectrin {Mouse (Mus musculus), brain}

MEGFLNRKHWEAHNKKASSRSWHNVYCVINNQEMGFYKDAKSAASGIPYHSEVPVSLKEAICEVALDYKKK
KHFVFLRLSDGNEYLFQAKDDEEMNTWIQAISSA

>d1dro_ b.55.1.1 (-) beta-spectrin {Fruit fly (Drosophila melanogaster)}

GSGTGAGEGHEGYVTRKHEWDSTTKASNRSWDKVYMAAKAGRISFYKDQKGYKSNELTFRGEPSYDLQNA
AIEIASDYTKKHKVLRVKLANGALFLQAHDDTEMSQWVTSKQAQSDSTA

>d1dyna_ b.55.1.1 (A:) Dynamin {Human (Homo sapiens)}

ILVIRKGWLTINNIGIMKGGKEYWFVLTAENLSWYKDDEEKEKKYMLSDNLKLRDVEKGFMSSKHIFALFNTE
QRNVYKDYRQLELACETQEEVDSWKASFLRAGVYPERV

>d1btk_ b.55.1.1 (A:) Bruton's tyrosine kinase {Human (Homo sapiens)}

AAVILESIFLKRSQLKKKTSPLNFKKCLFLTVHKLSYYEYDFERGRGSKKGSIDVEKITCVETVPEKNPPPERQIP
RRGEESSEMEQISIIERFPYPFQVYDEGPLYVFSPEELRKWRHQLKNVIRYNSDLVQKYHPCFWIDGQYLCCS
QTAKNAMGCQILEN

>d1pls_ b.55.1.1 (-) Pleckstrin, N-terminal domain {Human (Homo sapiens)}

MEPKIREGYLVKKGSVFNTWKPMWWVLLLEDGIEFYKKSDNSPKGMIPLKGSTLTSPCQDFGKRMFVFKITTT
KQQDHFFQAAFLEERDAWRDINKAIKCIEGLEHHHHHH

>d1dbha2 b.55.1.1 (A:418-550) Son of sevenless-1 (sos-1) {Human (Homo sapiens)}

AIKKMNEIQKNIDGWEGKDIGQCCNEFIMEGTLTRVGAHERHIFLDGLMICCKSNHGQPRLPGASNAEYRL
KEKFFMRKVQINDKDDTNEYKHAFEIILKDENSIVSAKSAEKNWMAALISLQYRSTL

>d1foea2 b.55.1.1 (A:1240-1401) GEF of TIAM1 (T-Lymphoma invasion and metastasis indusing

protein 1) {Mouse (Mus musculus)}

EFGAVFDQLIAEQTGEKKEVADLSMGDLLLHTSVIWLNPASLGKWKPELAAFVFKTAVVLVYKDGSKQKKK
LVGSHRLSIYEWDPFRFRHMIPEALQVRALPSADALEANAVCEIVHVKSSEGRPERVFHLCCSSPESRKDFLKS
VHSILRDKHRRQ

>d1bak_ b.55.1.1 (-) G-protein coupled receptor kinase 2 (beta-adrenergic receptor kinase 1) {Human (Homo sapiens)}

GSHMGKDCIMHGYSMSKGNGPFLTQWQRRYFYLFPNRLEWRGEAPEQSLLTMEEIQSVEETQIKERKCLLKI
RGKKQFILQCDSDPELVWKELRDAYREAQQLVQRVPKMKNKPRS

>d1faoa_ b.55.1.1 (A:) Dual adaptor of phosphotyrosine and 3-phosphoinositides DAPP1/PHISH {Human (Homo sapiens)}

PSLGTKEGYLTQGGLVKTWKTRWFTLHRNELKYFKDQMSPEPIRILDTECSAVQFDYSQERVNCFLVFPFRT
FYLCAKTGVEADEWIKILRWKLSQI

>d1fgya_ b.55.1.1 (A:) Grp1 {Mouse (Mus musculus)}

TFNPDREGWLLKLGGRVKTWKRRWFILTDNCLYYFEYTTDKEPRGIIPLENLSIREVLDPRKPNCFELYNSHKG
QVIKACKTEADGRVVEGNHVVYRISAPSPEEKEWMKSIKASISRDPFYDM

>d1fhoa_ b.55.1.1 (A:) UNC-89 {Nematode (Caenorhabditis elegans)}

MGDTGKLGRIIRHDAFQVWEGDEPPKLRVFLFRNKIMFTEQDASTSPSYTHYSSIRLDKYNIRQHTTDEDTIV
LQPQEPLPSFRIPKDFETSEYVRKAWLRIAEEQEKYAAERD

>d1aqca_ b.55.1.2 (A:) X11 {Human (Homo sapiens)}

MEDLIDGIIFAANYLGSTQLSDKTPSKNRMMQAQEAVSRKMAQKLAKSRRKAPEGESQPMTEVDLFIITQR
IKVLNADTQETMMDHPLRTISYIADIGNIVLMARRIPRSNSQENVEASHPSQDGKRQYKMICHVFESEDAQ
LIAQSIGQAFSVAYQEFLR

>d1qqga1 b.55.1.2 (A:12-114) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

DVRKVGYLRKPMSMHKRFFVLRASEAGGPARLEYENEKKWRHKSSAPKRSIPLESFCNINKRADSKNHLVAL
YTRDEHFAIAADSEAEQDSWYQALLQLH

>d1qqga2 b.55.1.2 (A:159-262) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

AFKEVWQVILPKGLGQTNLIGIYRLCLTSKTISFVKLNSEAAAVLQLMNIRRCGHSENFFFIEVGRSAVTGPG
EFWMQVDDSVVAQNMHETILEAMRAMSD

>d1shca_ b.55.1.2 (A:) Shc adaptor protein {Human (Homo sapiens)}

GSHMGQLGEEWTRHGSFVNKPTRGWLHPNDKVMGPGVSYLVRYMGCVEVLQSMRALDFNTRTQVTREA
ISLVEAVPGAKGATRRRKPCSRPLSSILGRSNLKFAGMPITLTNSTSSLNLMAADCKQIIANHHMQSISFASGGD
PDTAEYVAYVAKDPVNQRACHILECPEGLAQDVISTIGQAFELRFKQYLR

>d1ddma_ b.55.1.2 (A:) Numb {Fruit fly (Drosophila melanogaster)}

HQWQAEEAVRSATCSFSVYKLYCDEVFESRGMQVCEEALKVLRQSRRPVRGLLHVSGDGLRVVDDETKGLI
VDQTIEKVSFCAPDRNHERGFSYICRDGTRRWMCCHGFLACKDSGERLSHAVGCAFACVLER

>d1rrpb_ b.55.1.3 (B:) Nuclear pore complex protein Nup358 {Human (Homo sapiens)}

HFEPVVPLPDKIEVKTGEDEEEFFCNRAKLFRFDVESKEWKERGIGNVKILRHKTSGKIRLLMRREQVLKICANH
YISPDMKLPNAGSDRSFVHALDYADELPKPEQLAIRFKTPPEAAFKCKFEEAQSI

>d1k5db_ b.55.1.3 (B:) Ran-binding protein 1, Ranbp1 {Human (Homo sapiens)}

NHDPQFEPIVSLPEQEIKTLEEDEEELFKMRAKLFRFASENDLPEWKERGTGDVKLLKHKEKGAIIRLLMRREQDKTL
KICANHYITPMMEKPNAGSDRAWVNTHADFADECPKPELLAIRFLNAENAQKFKTFEECRKEIEEREK

>d1evha_ b.55.1.4 (A:) Enabled {Mouse (Mus musculus)}

SEQSICQARAAMVYDDANKWVPAGGSTGFSRVHIYHHTGNNTFRVGRKIQDHQVVINCAIPKGLKYNQA
TQTFHQWRDARQVYGLNGSKEDANVFASAMMHALEVNL

>d1qc6a_b.55.1.4 (A:) Ena/vasp-like protein {Mouse (Mus musculus)}
MSEQSICQARASVMVYDDTSKKWVPIKPGQQGFSRINIYHTASSTFRVVGVLQDQQVVINYSIVKGLYNQ
ATPTFHQWRDARQVYGLNFASKEATTFSNAMLFALNIMN
>d1egxa_b.55.1.4 (A:) Vasodilator-stimulated phosphoprotein (VASP) {Human (Homo sapiens)}
MSETVICSSRATVMLYDDGNKRWLPAGTGPQAFSRVQIYHNPTANSFRVVGRKMQPDQQVVINCAIVRGVKY
NQATPNFHQWRDARQVWGLNGSKEDAAQFAAGMASALEALEG
>d1ddwa_b.55.1.4 (A:) Homer {Rat (Rattus norvegicus)}
MGEQPIFSTRAHVFQIDPNTKKNWVPTSCHKAVTVSYFYDSTRNVYRIISLDGSKAIINSTITPNMTFTKTSQKFG
QWADSRANTVYGLGFSSEHHLSKFAEKFQEKFKEAAR
>d1i7aa_b.55.1.4 (A:) Homer {Mouse (Mus musculus), 2b/vesl 2}
EQPIFTTRAHVFQIDPSTKKNWVPTSCHKAVTVSYFYDSTRNVYRIISLDGSKAIINSTITPNMTFTKTSQKFGQW
ADSRANTVFGLGFSSELQLTKFAEKFQEVRREAAR
>d1e5wa2 b.55.1.5 (A:199-346) Moesin {Human (Homo sapiens)}
EMYGVNYFSIKNKKGSELWLVGDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVYAPRL
RINKRILALCMGNHELYMRRRKPDTEVQQMKAQAREEKHQKQMERAMLENEKKREMAEKEKEKIEREKEE
>d1ef1a2 b.55.1.5 (A:199-297) Moesin {Human (Homo sapiens)}
EMYGVNYFSIKNKKGSELWLVGDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVYAPRL
RINKRILALCMGNHELYMRRRKPD
>d1gc7a2 b.55.1.5 (A:199-297) Radixin {Mouse (Mus musculus)}
EMYGVNYFEIKNKKGTELWLVGDALGLNIYEHDDKLTPKIGFPWSEIRNISFNDKKFVIKPIDKKAPDFVYAPRL
RINKRILALCMGNHELYMRRRKPD
>d1gg3a2 b.55.1.5 (A:188-279) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
GVDLHKAKDLEGVDIILGVCSSGLLVYDKLRLINRFPWPKVLKISYKRSSFFIKIRPGEQEQQESTIGFKLPSYRAAK
KLWKVCVEHHTFFR
>d1h4ra2 b.55.1.5 (A:215-313) Merlin {Human (Homo sapiens)}
EMYGVNYFAIRNKKGTELLLGVDAALGLHIYDPENRLTPKISFPWNEIRNISYSDKEFTIKPLDKKIDVFKFNSSKLRV
NKLILQLCIGNHDLFMRRRK
>d1ytfc1 b.56.1.1 (C:) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
ENLMLCLYDKVTRTKARWKCSLKDGVVTINRNDYTFQKAQVEAEWV
>d1ytd2 b.56.1.1 (D:55-119) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
NTQSCLTVGNLDTYGFCDVWTFIVKNCQVTVEDSHRDASQNGSGDSQSVISVDKLRIVACNSK
>d1iega_b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}
QAVAPVYVGGFLARYDQSPDEAEELLPRDVVEHWLHAQGQQGQPSLSVALPLNINHDDTAVVGHVAAMQSVR
DGLFCLCVTSPrfleIVRRASEKSELVSRGPVSPLOPDVKVEFLSGSYAGLSLASRRCDDVEQATSLGSETPFK
AVALCSVGRRRGTLAVYGRDPEWVTQRFPDLTAADRDGLRAQWQRCGSTAVDASGDPFRSDSYGLGNSVDA
LYIRERLPKLRYDKQLGVTERESYVKA
>d1jq6a_b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}
VAPVYVGGFLARYDQSPDEAEELLPRDVVEHWLHAQGQQGQPSLSVALPLNINHDDTAVVGHVAAMQSVRDG
LFCLGCVTSPrfleIVRRASEKSELVSRGPVSPLOPDVKVEFLSGSYAGLSLSSRRCDDVEQATSLGSETPFKHV
ALCSVGRRRGTLAVYGRDPEWVTQRFPDLTAADRDGLRAQWQRCGSTAVDASGDPFRSDSYGLGNYVDALY
>d1at3a_b.57.1.1 (A:) HSV-2 protease {Herpes simplex virus type 2}
RAVPIYVAGFLALYDSDGDPGELALDPDTVRAALPPENPLPINVDHRARCEVGRVLAVVNDPRGPFFVGLIACVQ

LERVLETAASAAIFERRGPALSREERLLYLITNYLPSVSLSTKRRGDEVPPDRTLFAHVALCAIGRRLGTIVTYDTSLD
AAIAPFRHLDPATREGVRREAAEAEALAGRTWAPGVTEALTHTLSTAVNNMMLDRWSLVAERRRQAGIAG
HTYLQA
>d1f1a_ b.57.1.1 (A:) KSHV protease {Kaposi's sarcoma-associated herpes virus}
AQGLYVGGFVDVSCPKEQELYLDPDQVTDYLPVTEPLPITIEHLPETEVGWTGLFQVSHGIFCTGAITSPAFL
LASRLADTSHVARAPVKNLPKEPLLEILHTWLPGLSLSIHPRELSQTSGPVFQHVSLCALGRRRGTVAVYGH
AEWVVSFSSVSKSERAHILQHVSSCRLEDLSTPNFVSPLETMAKAIDAGFIRDRLLKTDRGVASILSPVYLKA
>d1vzv__ b.57.1.1 (-) VZV protease {Varicella-Zoster virus}
EALYVAGYLALYSKDEGEELNITPEIVRSALPPTSKIPINIDHRKDCVVGIVIAIIEDIRGPFFLGIVRCPQLHAVLFEAA
HSNFFGNRDSVLSPLERALYLVNTYLPVSLSKRLFTHVALCVVGRRVGTVVNYDCTPESSIEPFRVLSMESKAR
LLSLVKDYAGLNKVWKVSEDKLAKVLLSTAVNNMLLRDRWDVVAKRRREAGIMGH
>d1a49a1 b.58.1.1 (A:116-217) Pyruvate kinase (PK) {Rabbit (*Oryctolagus cuniculus*)}
PEIRTGLIKSGTAEVELKKGATLKITLDNAYMEKCDENILWLDYKNICKVVDVGSKVVDDGLISLQVKQKGPDF
LTVEVENGGFLGSKKGVNLPGAAVDL
>d1pkm_1 b.58.1.1 (116-217) Pyruvate kinase (PK) {Cat (*Felis domestica*)}
PEIRTGLIKSGTAEVELKKGATLKITLDNAYMEKCDENVLWLDYKNICKVVEVGSKVVDDGLISLLVKEKGADFL
VTEVENGGSLGSKKGVNLPGAAVDL
>d1pkla1 b.58.1.1 (A:88-186) Pyruvate kinase (PK) {Leishmania mexicana}
EIRTGQFVGDAVMERGATCYVTTDPAFADKGTKDKFYIDYQNLSKVVRPGNYIYIDDGILILQVQSHEDEQTLE
CTVTSNSHTISDRRGVNLPGCDVLD
>d1a3wa1 b.58.1.1 (A:88-188) Pyruvate kinase (PK) {Baker's yeast (*Saccharomyces cerevisiae*)}
PEIRTGTTNDVDYPPIPPNHEMIFTDDKYAKACDDKIMYVDYKNITKVISAGRIIYVDDGVLSFQVLEVDDKTL
KVKALNAGKICSHKGVNLPGTDVDL
>d1e0ta1 b.58.1.1 (A:70-167) Pyruvate kinase (PK) {Escherichia coli}
PEIRTMKLEGGNDVSLKAGQTFITDKSVIGNSEMVAVTYEGFTTDLSVGNTVLVDDGLIGMEVTAIEGNKVI
CKVLNNNGDLGENKGVNLPGVSI
>d1g8fa1 b.58.1.2 (A:2-168) ATP sulfurylase N-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}
PAPHGGILQDLIARDALKNELLSEAQSSDILVWNLTQRLCDIELILNGGSPLTGFLNENDYSSVVTDSRLADGT
LWTIPITLDVDEAFANQIKPDTRIALFQDDEIPIAILTQDVYKPNKTIEAERVFRGDPEHPAIRSYLFNVAGDYYVG
GSLEAIQLPQHYD
>d1i2da1 b.58.1.2 (A:2-170) ATP sulfurylase N-terminal domain {Fungus (*Penicillium chrysogenum*)}
ANAPHGGVLKDLLARDAPRQELAAEAESLPAVTTERQLCDLELIMNGGSPLEGFMNQADYDRVCEDNRA
DGNVFSMPITLDASQEVIDEKKLQAGSRITLRDFRDRRNLAILTDDIYRPDKTKEAKLVFGGDPEHPAIRYLNNT
VKEFYIGGGKIEAVNKLHYD
>d1jhda1 b.58.1.2 (A:1-173) ATP sulfurylase N-terminal domain {unnamed symbiont of *Riftia pachyptila*}
MIKPVGSDELKPLFVYDPEEHHKLSHEAESLPSVVISSQAAGNAVMMGAGYFSPLQGFMNVADAMGAAEKM
TLSRDGSFFPVPVLCLLENDAIGDAKRIALRDPNVEGNPVLAVMDIEAIEEVSDQMAVMTDKVYRTTDMDF
GVKTFNSQGRVAVSGPIQVLNFSYFQADF
>d1ik9a1 b.59.1.1 (A:1-117) XRCC4, N-terminal domain {Human (*Homo sapiens*)}
MERKISRIHLVSEPSITHFLQSVWEKTLESGFVITLTDGHSAWTGTVSESEISQEADDMAMEKGKYVGELRKALL
SGAGPADVYTFNFSKESAYFFFKEKNLKDVSFRLGSFNLEKVE

>d1hbq_ b.60.1.1 (-) Retinol binding protein {Cow (Bos taurus)}

ERDCRVSSFRVKENFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGQMSATAKGRVRLNNWDVCA
DMVGTFTDTEPAFKMKYWGVASFLQKGNDHWIIDTDYETFAVQYSCRLLNLDGTCADSYSFVFARDPSGF
SPEVQKIVRQRQEELCLARQYRLIPHNGYCNGK

>d1aqb_ b.60.1.1 (-) Retinol binding protein {Pig (Sus scrofa domestica)}

ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDENGHMSATAKGRVRLNNWDVCA
DMVGTFTDTEPAFKMKYWGVASFLQKGNDHWIIDTDYDTAVQYSCRLLNLDGTCADSYSFVFARDPH
GFSPEVQKIVRQRQEELCLARQYRIITHNGYCD

>d1rbp_ b.60.1.1 (-) Retinol binding protein {Human (Homo sapiens)}

ERDCRVSSFRVKENFDKARFSGTWYAMAKKDPEGLFLQDNIVAEFSVDETGQMSATAKGRVRLNNWDVCA
DMVGTFTDTEPAFKMKYWGVASFLQKGNDHWIVDTDYDTAVQYSCRLLNLDGTCADSYSFVFSRDPN
GLPPEAQKIVRQRQEELCLARQYRLIVHNGYCD

>d1iiua_ b.60.1.1 (A:) Retinol binding protein {Chicken (Gallus gallus), plasma isoform}

MDCRVSSFKVKENFDKNRYSGTWYAMAKKDPEGLFLQDNVVAQFTVDENGQMSATAKGRVRLFNNWDVC
ADMIGSFTDTEPAFKMKYWGVASFLQKGNDHWVVDTDYDTYALHYSCRELNEDGTCADSYSFVFSRDPK
GLPPEAQKIVRQRQEELCLARQYRLIVHNGFCS

>d1hn2a_ b.60.1.1 (A:) Odorant-binding protein {Cow (Bos taurus)}

AQEEEAEQNLSSELGPWRTVYIGSTNPEKIQENGPFRTYFRELVFDEKGTVDFYFSVKRDGKWKNVHVAKATK
QDDGTYVADYEGQNVFKIVSLSRTHLVAHNINVDKHGQTTELTELFVKLNVEDEDLEKFWKLTEDKGIDKKNVV
NFLENENHPHPE

>d1dzka_ b.60.1.1 (A:) Odorant-binding protein {Pig (Sus scrofa)}

FELSGKWITSYIGSSDLEKIGENAPFQVFMRSIEFDDKESKVYLNFFSKENGICEEFSLIGTKQEGNTYDVNYAGN
NKFVVSYASSETALIISNINVDEEGDKTIMTGLGKGTDIEDQDLEKFKEVTRENGIPEENIVNIIERDDCPA

>d1bj7_ b.60.1.1 (-) Lipocalin allergen {Cow (Bos taurus), bos d 2}

IDPSKIPGEWRIIYAAADNKDKIVEGGPLRNYYRRIECINDCESLSITFYLKDGQGTCLLTEVAKRQEGYVYVLEFYG
TNTLEVIHSENMLVTYVENYDGERITKMTEGLAKGTSFTPSEELEYQQLNSERGVPNENIENLIKTDNCPP

>d1ew3a_ b.60.1.1 (A:) Lipocalin allergen {Horse (Equus caballus), equ c 1}

VAIRNFDISKISGEWYSIFLASDVKEKIEENGSMRVFVDVIRALDNSSLYAEYQTKVNGETEFPMVFDKTEEDGV
YSLNYDGYNVFRISEFENDEHIILYLVNFDKDRPFQLFEFYAREPDVSPEIKEEFVKIVQKRGIVKENIIDLTKIDRCF
QLRG

>d1e5pa_ b.60.1.1 (A:) Aphrodisin, a sex pheromone {Golden hamster (Mesocricetus auratus)}

FAELQGKWYTIVIAADNLKIEEGGPLRFYFRHIDCYKNCSEMEITFYVITNNQCSKTTVIGYLKGNGTYETQFEG
NNIFQPLYITSKIFFTNKNMDRAGQETNMIVVAGKGNALTPEENEILVQFAHEKKIPVENILNILATDTCPE

>d1beba_ b.60.1.1 (A:) beta-Lactoglobulin {Cow (Bos taurus)}

QTMKGLDIQKVAGTWYSLAMAASDISLLDAQSAPLRVYVEELKPTPEGDLEILLQKWENGECAQKKIIAEKTIP
AVFKIDALNENKVLVLDTDYKKYLLFCMENSAEPEQSLVCQCLVRTPEVDEALEKFDKALKALPMHIRLSFNPT
QLEEQC

>d1exsa_ b.60.1.1 (A:) beta-Lactoglobulin {Pig (Sus scrofa)}

VEVTPIIMTELDTQKVAGTWHTVAMAVSDVSLLDAKSSPLKAYVEGLKPTPEGDLEILLQKRENDKCAQEVLAK
KTDIPAVFKINALDENQLFLLDTDYDSHLLCMENSASPEHSVCQSLARTLEVDDQIREKFEDALKTLSVPMRILP
AQLEEQCVR

>d1epba_ b.60.1.1 (A:) Retinoic acid-binding protein {Rat (Rattus norvegicus), albino}

VKDFDISKFLGFWYEIAFASKMGTPLAHKEEKGAMVVELKENLLALTYYSEDHCVLEKVTATEGDGPASF
QVTRLSGKKEVVVEATDLYAIIDITSLVAGAVHRTMKLYSRSLDDNGEALYNFRKITSDHGFSETDLYILKHDLTC

VKVLQSAA

>d1jv4a_b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Mouse (Mus musculus)}
EEASSTGRNFNVEKINGEWTIILASDKREKIEDNGNFRLFLEQIHVLEKSLVLKFHTVRDEECSELSMVADKTEK
AGEYSVTYDGFNTFTIPKTDYDNFLMAHLINKEKGDFQLMGLYGREPDLSIDIKERFAQLCEEHGIILRENIIDL
NANRC

>d2a2ua_b.60.1.1 (A:) Major urinary protein/alpha-2u-globulin {Rat (Rattus norvegicus)}
EEASSTRGNLDVAKLNGDWFSIVVASNKREKIEENGSMRVFMQHIDVLENSLGFKFRIKENGECRELYLVAYKTP
EDGEYFVEYDGGNTFTILKTDYDRYVMFHЛИNKNGETFQLMVLYGRTKDLSSDIKEKFAKLCEAHGITRDNIIDL
TKTDRCL

>d1qqsa_b.60.1.1 (A:) Neutrophil gelatinase-associated lipocalin (NGAL) {Human (Homo sapiens)}
TSIDLIPAPPLSKVPLQQNFQDNQFQGKWYVVGLAGNAILREDKDPQKMYATIYEKEDASYNVTSVLFKKCD
YAIRTFVPGCQPGEFTLGNIKSYPGLTSYLVRVVSTYNQHAMVFFKKVSQNREYFKITLYGRTKELTSELKNNFIR
FSKSLGLPENHIVFPVPIDQCID

>d1bbpa_b.60.1.1 (A:) Bilin-binding protein {Cabbage butterfly (Pieris brassicae)}
NVYHDGACPEVKPVDFDWSNYHGKWWEVAKYPNSVEKYGCGWAETYPEGKSVKVSNSYHVIHGKEYFIEG
TAYPVGDSDKIGKIYHKLYGGVTKENVFNVLSTDNKNYIIGYYCKYDEDKKGHQDFWVLSRSKVLGEAKTAVE
NYLIGSPVVDSQKLVYSDFSEAACKVN

>d1i4ua_b.60.1.1 (A:) Alpha-crustacyanin {European lobster (Homarus gammarus)}
DKIPDFVPGKCASVDRNKLWAEQTPNRNSYAGVWYQFALTNNPYQLIEKCVRNEYSFDGKQFVIESTGIAYDG
NLLKRNGKLYPNPFGEPHLSIDYENSFAAPLVIETDYSNYACLYSCIDYNFGYHSDFSFIKSRSANLADQYVKKCEA
AFKNINVDTTRFVKTVQGSSCPYDTQKTL

>d1qfta_b.60.1.1 (A:) Histamine binding protein {Brown ear tick (Rhipicephalus appendiculatus)}
NQPDWADEAANGAHQDAWKSIAKDVENVYYMVKATYKNDPVWGNDFTCVGVMANDVNEDEKSIQAEFL
FMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAYSDDNCVIYVPGTDGNEEGYELWTT
DYDNIPANCLNKFNEYAVGRETRDVFTSACLEIAAA

>d1np1a_b.60.1.1 (A:) Nitrophorin 1 {Rhodnius prolixus}
KCTKNALAQTGFNPKDKYFNGDVWYVTDYLDLEPDDVPKRYCAALAAAGTASGKLKEALYHYDPKTQDTFYDVSE
LQEESPGKYTANFKVEKNGNVKVDVTSGNYYTFTVMYADDSSALIHTCLHKGNKDLGDLYAVLNRNKDTNAG
DKVKGAVTAASLKFSDFISTKDNKCEYDNVSLKSLTK

>d1euoa_b.60.1.1 (A:) Nitrophorin 2 (prolixin-s) {Rhodnius prolixus}
MDCSTNISPQKQLDKAKYFSGKWVTHFLDKDPQVTDQYCSSFTPRESDGTVKEALYHYNANKTSFYNIGEG
KLESSGLQYTAKYKTVDDKKAVLKEADEKNSYTLTVLEADDSSALVHICLREGSKDLGDLYTVLHQKDAEPSAKV
KSAVTQAGLQLSQFVGTKDLGCQYDDQFTSL

>d1koia_b.60.1.1 (A:) Nitrophorin 4 {Rhodnius prolixus}
ACTKNAIAQTGFNPKDKYFNGDVWYVTDYLDLEPDDVPKRYCAALAAAGTASGKLKEALYHYDPKTQDTFYDVSE
LQVESLGKYTANFKVKDKNGNVKVAVTAGNYYTFTVMYADDSSALIHTCLHKGNKDLGDLYAVLNRNKDAAG
DKVKSAVSAATLEFSKFISTKENNCAYDNDLSLKSLLTK

>d1hms_b.60.1.2 (-) Muscle fatty acid binding protein (m-fabp) {Human (Homo sapiens)}
VDAFLGTWKLVDSKNFDDYMKSLGVGFATRQVASMTKPTTIIEKNGDILTLKTHSTFKNTEISFKLGVEFDETTAD
DRKVKSIVTLDGGKLVHLQKWDGQETTLVRELIIDGKLILTHTGTAVCRTTYEKE

>d1bwya_b.60.1.2 (A:) Muscle fatty acid binding protein (m-fabp) {Cow (Bos taurus)}
VDAFGVTWKLVDSKNFDDYMKSLGVGFATRQVGNTKPTTIIEVNGDTVIKTQSTFKNTEISFKLGVEFDETTA
DDRKVKSIVTLDGGKLHVQKWNGQETSLVREMVDGKLILTHTGTAVCRTTYEKQA

>d1a57 __ b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}
AFDGTWKVDRNENYSGAHDNLKLTITQEGNKFTVKESSNFRNIDVVFELGVDFAYSLADGTELGTWTMEGNK
LVGKFKRVNDNGKELIAVREISGNELIQTYTYEGVEAKRIFKKE

>d1ifc__ b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}
AFDGTWKVDRNENYEKFMEKGINVVKRKLGHDNLKLTITQEGNKFTVKESSNFRNIDVVFELGVDFAYSLA
DGTELGTWTMEGNKLVGKFKRVNDNGKELIAVREISGNELIQTYTYEGVEAKRIFKKE

>d3ifba_ b.60.1.2 (A:) Intestinal fatty acid binding protein {Human (Homo sapiens)}
AFDSTWKVDRSENYDKFMEKGVNIVRKLAHDNLKLTITQEGNKFTVKESSAFRNIEVVFELGVTFNLYNA
DGTELRTWSLEGNKLIGKFKRTDNGNELNTVREIIGDELVQTYYEGVEAKRIFKDD

>d1fdqa_ b.60.1.2 (A:) Brain fatty acid binding protein {Human (Homo sapiens)}
VEAFCATWKLTNSQNFDEYMKALGVGFATRQVGNVTKPTVIISQEGDKVVIRTLSTFKNTEISFQLGEFFETTA
DDRNCSSVSLDGDKLVHIQKWDGKETNFVREIKDGKVMVMTLFGDVAVRHYEKA

>d1b56__ b.60.1.2 (-) Epidermal fatty acid binding protein {Human (Homo sapiens)}
TVQQLEGRWRLVDSKGFD EYMKELGVGIALRKMGMAMAKPDCIITCDGKNLTIKTESTLKTTSQFSCTLGEKFEETT
ADGRKTQTCNFDTGALVQHQEWGDGKESTITRKLKDGLVVECMNNVTCTRIYEKA

>d1lid__ b.60.1.2 (-) Adipocyte lipid-binding protein, ALBP {Mouse (Mus musculus)}
CDAFVGTVKLVSENFD DYMKEVGVGFATRKVAGMAKPNMIIISVNGDLVTIRSESTFKNTEISFKLGVEFDEITA
DDRKVKSITLDGGALVQVQKWDGKSTTIKRKRDGDKLVVECMNKVTRVYERA

>d1mdc__ b.60.1.2 (-) Fatty acid-binding protein {Tobacco hornworm (Manduca sexta)}
SYLGKVYSLVKQENFDGFLKSAGLSDDKIQALVSDKPTQKMEANGDSNTSTGGGAKTVSFKSGVEFDDVIG
AGDSVKSMYTVDGNVVTHVVKGDAGVATFKKEYNGDDLVTITSSNWGVARRYKA

>d1ftpa_ b.60.1.2 (A:) Fatty acid-binding protein {Desert locust (Schistocerca gregaria)}
VKEFAGIKYKLDSQTNFEEYMAIGVGAIERKAGLALSPVIELEILDGDKFKLTSKTAIKNTEFTFKLGEEFDEETLD
GRKVKSITQDGPNKLVHEQKGDHPTIIREFSKEQCVITKLGDLVATRIYKAQ

>d1cbs__ b.60.1.2 (-) Cellular retinoic-acid-binding protein (CRABP) {Human (Homo sapiens), CRABP-II}
PNFSGNWKIIRSENFEELLKVLGVNVMLRKIAAAASKPAVEIKQEGDTFYIKTSTTVRTTEINFVGEEFEEQTV
GRPKCSLVWESENK MVCEQKLLKGE GP KTSW TREL N DGE LIL MT ADD VV CTR VY RE

>d1cbia_ b.60.1.2 (A:) Cellular retinoic-acid-binding protein (CRABP) {Cow and mouse (Bos taurus) and (Mus musculus), CRABP-I, identical sequences}
PNFAGTWKMRSENFD ELLKALGVNAMLRKVA AAASKPHVEIRQDG DQFYIKTSTTVRTTEINFVGEGFEE
TVDGRKCRSLPTWENENKIHCQTLLLEGDPKTYWTR EL DEL I LTFGADDV V CTR IY VRE

>d1crb__ b.60.1.2 (-) Cellular retinol-binding protein II (CRBP) {Rat (Rattus norvegicus)}
PVDFNGYW KMLS NENFEEYL RAL DVNVAL R KIAN LLKPD KEIV QDG DHMI RTL STFR NYIM DFQ VGKE FEEDL
TGID DRK CMTT VSW DG DKLQ CVQ KG EKE GRG WTQ WIE GDE LHLEM RAEG VTCK QV FK KV
>d1opaa_ b.60.1.2 (A:) Cellular retinol-binding protein II (CRBP) {Rat (Rattus norvegicus)}
TKDQNGTWEMESNENFEGYMKA LDIDFATRKIAVRLTQTKIIVQDGDNFKTKTNSTFR NYIM DFQ VGKE FEEDL
TKGLDGRNVKTLVTWEGNTLVCVQKG EKENRGWQVWEGDKLYELTCGDQVCRQVFKKK

>d1gbla_ b.60.1.2 (A:) Cellular retinol-binding protein III {Human (Homo sapiens)}
PPNL TGYYRFV SQKN MEDYLQ ALNISL A VRKIA LLLKPD KEI H QGNH MVT RL STFR NYTV QFD VG VE FEEDL
SVDGRKC QTIV TWEEEHLVCVQ KG E VP NRG WRH WLEG EML YEL TARD AVCE QV FR KV
>d1lfo__ b.60.1.2 (-) Liver fatty acid binding protein {Rat (Rattus norvegicus)}
MNFS GK YQVQS QENFEP FMKAM GLP EDL IQKG KDI KG VSEI VHEG KK VKL TITY GS KVI HNE FT LGEE CE LETM
TGEKVKAVV KM EG DN K MVT TF KG I KS VTE FNG DT IT NT M TLG DIV YK RV SK RI

>d1pmpa_b.60.1.2 (A:) P2 myelin protein {Cow (Bos taurus), caudal spinal root myelin}
SNKFLGTWKLVSENFDPEYMKALGVGLTRKLGNLAKPRVIISKKDIITIRTESPFKNTEISFKLGQEFETTADN
RKTGSTVTLARGSLNQVKWNGNETTIKRKLVDGKMWCKMKDVFCTRIYEKV

>d1eal_b.60.1.2 (-) Ileal lipid binding protein {Pig (Sus scrofa)}
AFTGKYIESEKNYDEFMKRLALPSDAIDKARNLKIISVEVKQDGQNFTWSQQYPGGHSITNTFTIGKECDIETIGG
KKFKATVQMEGGKVVVNSPNYHHTAEIVDGKLVEVSTVGGVSYERVSKKLA

>d1avgi_b.60.1.3 (I:) Thrombin inhibitor {Triatomine bug (Triatoma pallidipennis)}
AEGDDCSIEKAMGDFKPEEFFNGTWYLAHGPGBTAVCQKFTTSGSKFTQIVEIGYNKFESNVKFQCNQVD
NKNGEQYSFKCKSSDNTEFEADFTFISVSYDNFALVCRSITFTSQPKEDRYLVFERTKSQDTPDAKEIC

>d1swga_b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}
SRYVLTGRYDSAPATDGSgtALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWLTSgtTEANAWKS
TLVGHDTFTKVKPsaASGGSAEAGITGTWYNQLGSTFIVTAGADGALTGTYESA

>d1swua_b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}
GITGTWYNQLGSTFIVTAGADGALTGTfESAVGNAESRYVLTGRYDSAPATDGSgtALGWTVAWKNNYRNAHS
ATTWSGQYVGGAEARINTQWLTSgtTEANAWKSTLVGHDTFTKVKP

>d1ij8a_b.61.1.1 (A:) Avidin {Chicken (Gallus gallus)}
KCSLTGKWTNDLGSNMTIGAVNSRGEFTGYTTAVTATSNEIKESPLHGTTINKRTQPTFGFTVNWKFSETT
VFTGQCFIDRNGKEVLKTMWLLRSSVNDIGDDWKAtrvginiFTRL

>d1smpi_b.61.2.1 (I:) Metalloprotease inhibitor {Erwinia chrysanthemi}
SSLRLPSAAELSGQWVLSGAEQHCDIRLNTDVLDGTTWKLADTACLQKLLPEAPVGWRPTPDGLTQADGS
AVAFFSRNRDRYEHKLVDGSVRTLKKK

>d1jiwi_b.61.2.1 (I:) Metalloprotease inhibitor {Pseudomonas aeruginosa, aprin}
SSLILSASDLAGQWTLQQDEAPAICHLELRDSEVAEASGYDLGGDTACLTRWLPEPRPAGIALLERGG
LTLMILLGRQGEGDYRVQKGDGQQVLRRAT

>d1ei5a1 b.61.3.1 (A:336-417) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum anthropi}
EVSRVEADSAWFGSWLDDETGLVLSLEDAGHGRMKARFGTSPEMMDVVSANEARSAVTTIRRDGETIELVRA
SENLRLSMKR

>d1ei5a2 b.61.3.1 (A:418-520) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum anthropi}
VKGEAKHDIIGRYHSDELADLLLSEGGAIYGAFEGFLGKSDMYPLYSVGSDVWLLPVQRSMdapspGEWKLV
FRRDDKGEITGLSGCWLARGVEYRRVQP

>d1jjua5 b.61.4.1 (A:166-273) Quinohemoprotein amine dehydrogenase A chain, domain 3
{Paracoccus denitrificans}
PDAYADDASGAYVLAGRQPGRGDYTGRIVLKAGEDYEVTMTLDFADGSRSFSGTGRILGAGEWRATSDGT
TIRQIFALQDGRFSGRWHDADSDVIGGRLLAAVKAD

>d1jmxa5 b.61.4.1 (A:163-281) Quinohemoprotein amine dehydrogenase A chain, domain 3
{Pseudomonas putida}
ESAAWAEWQKARPkadALPGQWAFSGHMLAKGDVRGVMsvTPDQGDTFKVEVKGAYADGTPFNGSGSAIL
YNGYEWRGNVKVGDNLRQVFAALDGEKMGRMFEAEHDERGLDFTAVKE

>d2cpl_b.62.1.1 (-) Cyclophilin (eukaryotic) {Human (Homo sapiens), variant A}
VNPTVFFDIAVDGEPLGRVSFELFADKVPKTAENFRALSTGEKGFGYKGSCFHRIIPGFMCQGGDFTRHNGTGG
KSIYGEKFEDENFILKHTGPGILSMANAGPNTNGSQFFICTAKTEWLDGKHVVFGKVKEGMNIVEAMERFGSR
NGKTSKKITIADCGQLE

>d1cyna_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens), variant B}
GPKVTVKVYFDLRIGDEDVGRVIFGLFGKTVPKTVDNFVALATGEKGFGYKNSKFHRVIKDFMIQGGDFTRGDGTGGKSIYGERFPDENFKLKHYPGPWVSMANAGKDTNGSQFFITVKTAWLDGKHVVFGKLEGMEVRKVESTKTDSDKPLKDVIAACGKIEVEKPFIAKE

>d1qoia_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Human (Homo sapiens), U4/U6 snRNP-specific cyclophilin snucyp-20}
NSSPVNPVFFDVSIGGQEGRMKIELFADVVPKTAENFRQFCGEFRKDGVPIGYKGSTFHRVIKDFMIQGGDFVNGDGTGVASIYRGPFADENFKLHSAPGLSMANSGPSTNGCQFFITCSKCDWLDGKHVVFGKIIDGLLVMRKIENVPTGPNNKPKLPVVISQCGEM

>d2rmca_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Mouse (Mus musculus), variant C}
KRGPSVTDKVFFDVRIGDKDVGRIVIGLFGNVVPKTENFVALATGEKGFGYKGSIFHRVIKDFMIQGGDFTARDGTGGMSIYGETFPDENFKLKHYPGIGWVSMANAGPDTNGSQFFITLKPTWLDGKHVVFGKVLGDMTVVHSIELQATDGHDRLTDCTIVNSGKIDVKTPFVVEVPDW

>d1a33__b.62.1.1 (-) Cyclophilin (eukaryotic) {Nematode (Brugia malayi)}
KDERRRVFLDTIDGNLAGRIVMELYNDIAPRTCNNFLMLCTGMAGTGKISGKPLHYKGSTFHRVIKNFMIQGGDFTKDGDTGGESIYGGMFDEEFVMKHDEPFVVS MANAKGPNTNGSQFFITTPAPHLNNIHVVFGKVVSGQEVVTKIEYLKTN SKNRPLADV VILNCGELV

>d1dywa_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Caenorhabditis elegans, isoform 3}
MSRSKVFFDITIGGKASGRIVMELYDDVVPKTAGNFRA LCTGENGIGKSGKPLHF KGSKFHRIIPNFMIQGGDFT RGNGTGGESIYGEKFPDENFKEKHTGPVLSMANAGPNTNGSQFFLCTVKT EWL DGKHVVFGRVVEGLD VVKA VESNGSQSGKPVKDCMIACGQLK

>d1qnga_b.62.1.1 (A:) Cyclophilin (eukaryotic) {Plasmodium falciparum}
SKRSKVFFDISIDNSNAGRIIFELFS DITPRT CENFRA LCTGEKIGSRGKNLHYKNSIFHRIIPQFMCQGGDITNGNGSGGESIYGRSFTDENFN MKHDQPG LLSMANAGPNTNGSQFFITLVPCPWLDGKHVVFGK VIEGMNVVREM EKEGA KSGYVKRSV VITDCGEL

>d1ihga2 b.62.1.1 (A:2-196) Cyclophilin 40 isomerase domain {Cow (Bos taurus)}
SHPS PQA KPS NPS N P RVFF DV DIGGER VGRIVLELFADIVPKTAENFRA LCTGEKIGPTTGKPLHFKGCPFHRIIKKFMIQGGDFSNQNGTGGESIYGEK FEDENFHYKHDKEGLLSMANAGSNTNGSQFFITVPTPHLDGKHVVFG QVIKG MGVA KILENVEVKGEKPAKLCVIAECGELKEGDDWGIFPKD

>d1clh_b.62.1.1 (-) Bacterial cyclophilin {Escherichia coli}
AKGDPHVLLTSAGNIEELDKQKAPVSVQNFVDYVNSGFYNNTFHRVIPGMFIQGGGFTEQMQQKKPNPPIKNEADNGLRNTRGTIAMARTADKDSATSQFFINVADNAFLDHGQRDFGYAVFGKVVKGMDVADKISQVPTHDVGPYQNVPSKPVVILSAKVL P

>d1lopa_b.62.1.1 (A:) Bacterial cyclophilin {Escherichia coli}
MVTFH TNHG DIVIKTFDDKAPETVKNFLDYCREGFYNNTIFHRVINGFM IQGGGFEPGMKQKATKEPIKNEAN NGLKNTRGTLAMARTQAPHSATAQFFINVVNDFLNFGESLQGWG YCVFAEVVDGMDEVDKIKGVATGRSGMHQDV PKEDVIIESTVSE

>d1jsg_b.63.1.1 (-) p14-TCL1 {Human (Homo sapiens)}
CPTLG EA VTDHPD RLWAWEKFVYLDEKQHAWLPLTIEIKDRLQLRVLL REDVVL GRPMPTQIGPSLLPIMW QLYPDGRYRSSDSSFWRLVYHIKIDGV EDMI LLELPDD

>d1jnpa_b.63.1.1 (A:) p14-TCL1 {Mouse (Mus musculus)}
RAETPAHPNRLWIWEK H VYLDEFRRSWLPVVIKSNEKFQVILRQEDVTLGEAMSPSQLV PYELPLMWQLYPKDRYRSADSMYWQILYHIKFRDVEDM LLE

>d1a1x_b.63.1.1 (-) p13-MTCP1 {Human (Homo sapiens)}

AGEDVGAPPDHLWVHQEGIYRDEYQRTWVAVVEEETSLRARVQQIQVPLGDAARPSHLLTSQLPLMWQLYP
EERYMDNNNSRLWQIQHHLMVRGVQELLKLLPDD

>d1ijaa_ b.100.1.1 (A:) Sortase {Staphylococcus aureus}

MQAKPQIPKDKSKVAGYIEIPDADIKEPVYPGPATPEQLNRGVFAEENESDDQNISIAGHTFIDRPNYQFTNLK
AAKKGSVMVFVGNETRKYKMTSIRDVKPTDVGLDEQKGKDKQLTLITCDDYNEKTGVWEKRKIFVATEVK

>d1c39a_ b.64.1.1 (A:) Cation-dependent mannose 6-phosphate receptor, extracytoplasmic domain {Cow (Bos taurus)}

EKTCDLVGEKGKESEKELALLKRLTPLFQKSFESTVGQSPDMYSYVFRVCREAGQHSSGAGLVQIQKSNGKETVV
GRFNETQIFQGSNWIMLIYKGGDEYDNHCGREQRAVMISCRHTLADNFNPVSEERGKVQDCFYLFEMD
SSLACS

>d1e6fa_ b.64.1.1 (A:) Cation-independent mannose-6-phosphate receptor (MIR-receptor) {Human (Homo sapiens)}

DDCQVTNPSTGHFLDLSLSGRAGFTAAYSEKGLVYMSICGENENCPPGVGACFGQTRISVGKANKRLRYVDQ
VLQLVYKDGSPCPSKSGLSYKSVISFVCRPEAGPTNRPMLISLDKQTCTLFFSWHTPLACE

>d1f3ua_ b.65.1.1 (A:) TFIIF beta subunit, Rap30 {Human (Homo sapiens)}

AERGELDLTGAKQNTGVWLKVPKYLSQQWAKASGRGEVGKLRIAKTQGRTEVSFTLNEDLANIHIGGKPAS
VSAPREHPFVLQSVGGQTLTVFTESSSDKLSLEGIVVQRAECRPA

>d1f3ub_ b.65.1.1 (B:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}

GPSSQNVTEYVVRVPKNTTKYNIMAFNAADKVNFAWNQARLERDLSNKKIYQEEEMPESGAGSEFNRLKR
EEARRKKYGYIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQCPDGAFAFPVHNWYNFTPLA
RHR

>d1f3ud_ b.65.1.1 (D:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}

SSQNVTEYVVRVPKNTTKYNIMAFNAADKVNFAWNQARLERDLSNKKIYQEEEMPESGAGSEFNRLKREE
ARRKKYGYIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTQCPDGAFAFPVHNWYNFTPLARH
RTLTAEEAEWWERRN

>d1hxn_ b.66.1.1 (-) Hemopexin {Rabbit (Oryctolagus cuniculus)}

ESTRCDPDLVLSAMVSDNHGATYVFSGS HYWRLDTNRDGWH SWPIAHQWPQGPSTVDAAFSWEDKLYLIQ
DTKVVFLTKGGYTLVNGYPKRLEKELGSPPVISLEAVDAAFVCPGSSRLHIMAGRRLWWLDLKSGAQATWTEL
PWPHEKVDGALCMEKPLGPNSCSTSGPNLYIHGPNLYCYRHVDKLNAKNLPQPQRVSRLLGCTH

>d1qhua1 b.66.1.1 (A:24-215) Hemopexin {Rabbit (Oryctolagus cuniculus)}

IEQCSGDGWSFDATTLDNGTMLFFKDEFVWKSHRGIRELISERWKNFIGPVDAFRHGHTSVYLIKGDKVWVY
TSEKNEKVPKSLQDFPGIPFPLDAAVECHRGEQCQDEGILFFQGNRKWFWDLTGKERSWPAGVNCTSAL
RWLGRRYYCFQGNQFLRFNPVS GEVPPGYPLDVRDYFLSCPGRGHRS

>d1gen_ b.66.1.1 (-) Gelatinase A (MMP-2), C-terminal domain {Human (Homo sapiens)}

LGPVTPEICKQDIVFDGIAQIRGEIFFFKDRFIWRTVTPRDKPMGPLLVATFWPELPEKIDAVYEAPQEEKAVFFA
GNEYWIYASTLERGYPKPLTLSLGLPPDVQRVDAAFNWSKNKKTYIFAGDKFWRYNEVKKMDPGFPKLIADA
WNAIPDNLDAVVDLQGGGHSYFFKGAYYLKLENQLSKSVKFGSIKSDWLGC

>d1fb1_1 b.66.1.1 (272-466) Collagenase, C-terminal domain {Pig (Sus scrofa)}

PQTPQVCDSKLTFAITLRLGELMFFKDRFYMRNTSFYPEVELNFISVFWPQVNGLOAAYEIADRDEVRFKG
NKYWAVRGQDVLYGYPKDIHRSFGFPSTVKNIDA AVFEEDTGKTYFFVAHECWRYDEYKQSMDTGYPKMIAEE
FPGIGNKDAVFQKDGFLYFFHGTRQYQFDFKTKRILTLQKANSWFNC

>d1pex_ b.66.1.1 (-) Collagenase-3 (MMP-13), C-terminal domain {Human (Homo sapiens)}

TPDKCDPSLSDAITSRGETMIFKDRFFWRLHPQQVDAELFLTKSFWPELPNRIDAAYEHPSHDLIFRGRKF
WALNGYDILEGYPKKISELGLPKEVKKISA AVHFEDTGKTLFSGNQVWRYDDTNHIMDKDYPRLIEEDFPGIGDK

VDAVYEKNGYIYFFNGPIQFEYSIWSNRIVRVMMPANSILWC

>d1tl2a_ b.67.1.1 (A:) Tachylectin-2 {Japanese horseshoe crab (*Tachylepus tridentatus*)}
GGESMLRGVYQDKFYQGTPQNKNLARATLIGKGGWSNFKFLSPGGELYGVLNDKIYKGTPPTHDND
NWMGRAKKIGNGGWNQFQLFPNGYLYAVSKDKLYKASPPQSNTDNWIARATEVGSGGWSGFKFLLFH
NGYLYAVHGQQFYKALPPVSNQDNWLARATKIGQGGWDTFKFLFSSVGTFLGVQGGKFYEDYPPSYAYDNW
LARA KLIGNGGWDDFRFLFF

>d3sil_ b.68.1.1 (-) Salmonella sialidase {*Salmonella typhimurium*, strain lt2}
EKSVVFKAEGEHFTDQKGNTIVSGSGGTTKYFRI PAMCTTSKGTVFADARHNTASDQSFDAA RSTDGG
KTWNKKIAIYNDRVNSKLSRVMDPTCIVANIQGRETILVMVGKWNNNDKTWGAYRDKAPDTDWDLVLYKST
DDGVTFSKVETNIHDIVTKNGTISAMLGGVGSGLQLNDGKLVFPVQMVRTKNITVLNTSFIYSTDGITWSLPS
GYCEFGSENNIIIFNAVLVNNIRNSGLRRSFETKDFGKTWTEFPMDKKVDNRN HGVQGSTITPSGNKLVA
HSSAQNKNNNDYTRSDISLYAHNLYSGEVKLIDDFYPKVGNA SGAGYSCLSYRKNV DKE TLYVVYEANGSIEFQDL
SRHLPVIKSYN

>d1f8ea_ b.68.1.1 (A:) Influenza neuraminidase {Influenza A virus, different strains}
RDFNNLTGLCTINSWHYGKD NAVRIGEDSDVLTREPVVSCDPDEC RFYALSQGTTIRGKHSNGTIHDRSQYR
ALISWPLSSPPTVYNSRVECIGWSSTSCHDGKTRMSICISGPNNNASAVIWYNRRPTEINTWARNILRTQESEC
VCHNGVCPVVFTDGSAT GPAETRIYYFKEGKILKWEPLAGTAKHIEECSCYGERAEITCTCRDNWQGSNRPVIRI
DPVAMTHTSQYICPVLTDNPRPNDPTVGKNDPYPGNNNNVGKFSYLDGVNTWL GRTSIASRSGYEMLK
VPNALTDDKS KPTQGQTIVLNTDWSGYSGSFMDYWAEGECYRACFYVELIRGRPKEDKVWWTSNSIVSMCSS
TEFLGQWDWPDGAKIEYFL

>d2bat_ b.68.1.1 (-) Influenza neuraminidase {Influenza A virus, different strains}
VEYRNWSKPQCQITGFAPFSKDNSIRLSAGGDIWVTREPVVSCDPVKCYQFALGQGTTLDNKHSNDTVHDRIP
HRTLLMNELGVPFH GTRQVCI AWSSS CHDGKA WLHV C ITGDDKNATASFIYDGRLVDSIGSW SQNILRTQES
ECVCINGTCTVMTDGSASGRADTRILFIEEGKIVHISPLAGSAQHVEECSCYPRYPGVRCICRDNWKG SNRPV
VDINMEDYSIDSSYVCSGLVGDT PRNDRSSNSNCNPNNERGTQGVKG WAFDNGNDLWMGRTISKDLRSG
YETFKVIGGWSTPN SKSQINRQVIVDSDNRSGYSGIFSVEGKSCINRCFYVELIRGRKQETRVWW TSNSIVFCG
TSGTYGTGSWP DGANINF MPI

>d1inv_ b.68.1.1 (-) Influenza neuraminidase {Influenza B virus, different strains}
EPEWTYPR LSCQGSTFQKALLISPHRFGEIKGNSAPLI REP VACGPKECRHF ALTHYAAQPGGYY NGTRKDRN
KLRHLVSKLGKIPTVENSIFHMAAWSGSACHD GREWTYIGV DGPNDALV KIKYGEAYTDTYHSYAHN ILRTQ
ESACNCIGGDCYLMITDGSASGISKCRFLKIREGRIIKEILPTGRV EHTEECTCGFASNK TIECAC RDNSYTA KRPFV
KLN VETD TAEIRLMCTYLDTPR PDDG SIAGPCESNGDKWLGGIKGGF VHQR MASKIG RWYSRTMSK TNR
GMELYVRYDGD PWTD SALTSG VMVSIE PGWY SFGEIKDKKCDV PCIGI EMVHDGGK DTW HSAATAI YCL
MGSGQLLWDTV TVGDMAL

>d1nsca_ b.68.1.1 (A:) Influenza neuraminidase {Influenza B virus, different strains}
EPEWTYPR LSCQGSTFQKALLISPHRFGEARGNSAPLI REP FIACGPKECKH FAL THYAAQPGGYY NGTREDRN
KLRHLVSKLGKIPTVENSIFHMAAWSGSACHD GREWTYIGV DGPDSN ALIKIKYGEAYTDTYHSYANN ILRTQ
SACNCIGGDCYLMITDGSASGISKCRFLKIREGRIIKEIFPTGRV EHTEECTCGFASNK TIECAC RDNSYTA KRPFV
LN VETD TAEIRLMCTYLDTPR PDDG SIAGPCESNGDKGRGGIKGGF VHQR MASKIG RWYSRTMSK TERN
MELYVRYDGD PWTD SALTSG VMVSIE PGWY SFGEIKDKKCDV PCIGI EMVHDGGK DTW HSAATAI YCL
LMGSGQLLWDTV TVGDMAL

>d1e8ua_ b.68.1.1 (A:) Paramyxovirus hemagglutinin-neuraminidase head domain {Newcastle disease virus}

GAPIHDPDFIGGIGKELIVDNASDVTSF YPSAFQEH LNFIPAP TTGSGCTRIPSFDMSATHCYTHNVILSGCRDH

SHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSVSATPLGCDMLCSKVTETEEEDYNSAVPTLMAHGRL
GFDGQYHEKLDVTLFEDWVANYPGVGGGSIDGRVWFVYGLKPNSPSDTVQEGKYVIYKRYNDTCPDE
QDYQIRMAKSSYKPGRGKGRIQQAILSIVSTLGEDPVLTVPPNTVLMGAEGRILTVTSHFLYQRGSSYFSP
ALLYPMVTNSNKTATLHSPYTNAFRPGSIPCQASARCPNSCTGVYTDYPLIFYRNHTLRGVFGTMLDSEQAR
LNPASAVFDSTSRSRITRVSSSTAAYTTSTCFKVVTKNTKTYCLSLAISNTLGEFRIVPLLVEILKND

>d1eur_ b.68.1.1 (-) Micromonospora sialidase, N-terminal domain {Micromonospora viridifaciens}

GEPLYTEQDLAVNGREGFPNYRIPALTVPDG DLLASYDGRPTGIDAPGPNSILQRRSTDGGRTWGEQQVVSA
GQT TAPIKGFS DPSYLV DRETGTIFNFHVYSQRQGFAGSRPGTDPADPNVLHANVATSTDGGLTWSHRTITADIT
PD PGWRSRFAASGEIGIQLRYGPHAGRLIQQYTIINAAGAFQAVSVY SDDHGR TWAGEAVGVGMIDENKTVE
LSDGRVLLNSRDSARSGYRKAVSTDGGHSYGPVTIDRDLDPPTNNASIIRAFPDAPAGSARAKVLLFSNAASQT
SRSQGTIRMSCDDGQTWPVSKVFQPGSMSYSTLTALPDGYGLLYEPGTGIRYANFNLAWLGGICAP

>d2sli_2 b.68.1.1 (277-759) Leech intramolecular trans-sialidase, C-terminal domain {North american leech (*Macrobdella decora*)}

GENIFYAGDVTESYFRIPSLLTSTGTVISAADARYGGTHDSKSKINIAFAKSTDGGNTWSEPTLPLKFDDYIAKN
IDWPRDSVGKVNQIQGSASYIDPVLEDKLTKRIFLFA DLMPAGIGSSNASVGSGFKEVNGKKYLKLWRHKDAG
RAYDYTIREKGVIYN DATNQPTEF RVDGEY NLYQHDTNLTCQYDYNFSGNNLIESKTDVDVN MNIFYKNSVFK
AFPTNYLAMRYS DDE GASWS D DIVSSFKPEVSKFLVVGPGIGKQISTGENA GRLLVPLYSKSSAELGF MYSDDH
GDNWTYVEADNL TGGATAEAQIVEMP D GSLKTYL RTGSNCIAEVTSIDGGETWSDRVPLQGISTTSYGTQLSVI
NYSQPIDGKPAII LSSPNATN GRKNGKI WIGLVNDTGNTGIDKYSVEWKYSYAVDTPQM GY SYSCLAE LPDGQV
GLYEKYDSWSRNEHLKDILKFEKYSISELTGQA

>d1kit_3 b.68.1.1 (217-346,544-781) Vibrio cholerae sialidase {Vibrio cholerae}

VIFRGPD RI PSIVASSVTPGVVT AFAEKRVGGGD PGALSNTNDIITRTSRDGGITWDTELNLTEQINVSDEFDFSD
PRPIYDPSSNTVLVSYARWPTDAAQNGDRIKPWMPNGIFYSVYDVASGNWQAPIXVNPGPGHGI TLTRQQNI
SGSQNGLRIYPAIVLDRFFLN VMSIYSD DGGSNWQ TGSTLPI F RWKSSILETLEPSEADMVELQNGD LLLTARL
DFNQIVNGVNYS PRQQFLSKDGGITWSL LE ANNANVFSNISTGTV DASITRF E QSDGSHFLLFTNPQGNPAGT
NGRQNGLWFSFDEGVTWKGPIQLVNGASAYS DIYQLDSENAIVIVETDNSNM RILR MPITLLKQ KLTLSQN

>d1crua_ b.68.2.1 (A:) Soluble quinoprotein glucose dehydrogenase {Acinetobacter calcoaceticus}
DVPLTPSQFAKSENFDKKVILS NLNKPH ALLWGP DNQIWLTERATGKIL RVNP EGSV KTVFQVPEIVNDAD
GQNGLLGFAHPDFKNNPYIYISGTFKNPKSTDKE LPN QTII RRYT YNKSTD TLEK PVDLLA GLPSSKDHQS GRLVI
GPDQK IYYTIGDQGRNQLAYLFLPNQAQHTPTQ QELNGKD YHTYMGKV RLNL DGSI PKDN P SFNGVV SHIYT
LGHRNPQGLAFTPNGKLLQSEQGPNSD DE INLIVKG GNGWPNVAGYKDDSGYAYAN YSAA ANKS IKDLAQN
GVKVAAGVPVT KESEWTGKNFV PPLK TLYTVQ DTYN YNDPTCGEM TYICWPTVAPSSAYVYKGGKA ITGWE
NTLLVPSLKRGVIFRIKLDPTY STTYDDA VPMFKSNN RYRD VIASPDGNVLYVLT DAGNVQKDDGS VTNTLEN P
GSLIKFT

>d1h6la_ b.68.3.1 (A:) Thermostable phytase (3-phytase) {Bacillus amyloliquefaciens}

KLSDPYHFTVAAAETEPVDTAGDAADDPAIWLPKNPQNSKLIT TNKKG LAVY SLEGKMLHSYHTGKLNNV
DIRYDFPLNGKKV DIAASNRSEGKNTIEIYAI DGKNGTLQSITDPNRPI ASAI DEVYGFSLYHSQKTGKYYAMVT
GKEGEFEQYELNADKNGYISGKKVRAFKMNSQTEGMAADDEYGS LYIAEEDEAIWKFSAEPDGG SNGT VIDRA
DGRHLTPDIEGLI YYA ADGKG YLLASSQGN SSYAIYERQGQNK YVADFQITDGPETDGTSDTDGIDVLGFGLGP
EYPFGLFVAQNGENIDHGQKANQNFKM VPWERIADKIGFHPQVN KQV DPKMTDRS

>d1crza1 b.68.4.1 (A:141-409) TolB, C-terminal domain {Escherichia coli}

AFRTRIAYV VQTNGGQFPYELRVSDYDGYNQFVVRSPQPLMSPAWSPDGSKLAYVT FESGRS ALVIQTLANG
AVRQVASFPRHNGAPAFSPDGSKLA FSKTGS LNLYVMDLASGQIRQVTDGRSNNT EPTWFPDSQNL AFTSD

QAGRPQVYKVNINGGAPQRITWEGSQNQDADVSSDGKFMVMVSSNGQQHIAKQDLATGGVQVLSSTFLD
ETPSLAPNGTMVIYSSSQGMGSVLNLVSTDGRFKARLPATDGQVKFPAWSYL

>d1ijqa1 b.68.5.1 (A:377-642) Low density lipoprotein (LDL) reseptor YWTD domain {Human (Homo sapiens)}

IAYLFFTRHEVRKMTLDRSEYTSIPNLNVVALDTEVASNRIYWSDLSQLMICSTQLDRAHGVSYDTVISRDI
QAPDGLAVDWIHSNIYWTDSLTVSVADTKGVKRKTLFRENGSKPRAIVVDPVHGFMYWTDWGTPAKIKK
GGLNGVDIYSLVTENIQWPNGITLDLSGRLYWVDSLHSISIDVNGGNRK TILEDEKRLAHPFLAVFEDKVF
WTDIINEAIFSANRLTGSVDVNLLAENLLSPEDMVLFHNLQTQPRG

>d1e1aa_ b.68.6.1 (A:) Diisopropylfluorophosphatase (phosphotriesterase, DFP) {Squid (Loligo vulgaris)}

IPVIEPLFTKVTEDIPGAEGPVFDKNGDFYIVAPEVEVNGKPAGEIELRIDLKTGKKTICKPEVNGYGGIPAGCQCD
RDANQLFADMRLGLVVQTDGTFEIACKDSEGRRMCGCNDCAF DYEGNLWITAPAGEVAPADYTRSMQE
KFGSIYCFTTDGQMIQVDTAFQFPNGIAVRHMNDGRPYQLIVAETPTKKLWSYDIKGPAK IENKKVWGHIPGTH
EGGADGMDFDEDNNLLVANWGSSHIEVFGPDGGQP KMRIRCPFEKPSNLHFKPQTKTIFVTEHENNAVWKF
EWQRNGKKQYCETLKFGIF

>d1k32a2 b.68.7.1 (A:39-319) Tricorn protease N-terminal domain {Archaeon Thermoplasma acidophilum}

MPNLLNPDIHGDRIFI VCCDDLWEHDLKSGSTRKIVSNLGVINNARFFPDGRKIAIRVMRGSSLNTADLYFYNG
ENGEIKRITYFSGKSTGRRMFTDVAGFDPDGNIISTDAMQPFSMTCLYRVENDGINFVPLNLGPATHILFADG
RRVIGRNTFELPHWKGYRGGRGKIWIEVNSGAFKKIVDMSTHVSSPVIVGHRIFYFITDIDGFGQIYSTLDGKD
LRKHTSFTDYYPRHLNTDGRRILFSKGGSIYIFNPDTEKIEKIEIGDLESPEDRII

>d1k3ia3 b.69.1.1 (A:151-537) Galactose oxidase, central domain {Fungi (Fusarium spp)}

YTAPQPGGLRWGPTIDLPIVAAAAIEPTSGRVLMWSSYRNDAFGGSPGGITLTSSWDPSTGIVSDRTVTVKH
DMFCPGISMDDNGQIVVTGGNDAKKTSLYDSSSDSWIPGPDMQVARGYQSSATMSDGRVFTIGGSWSGGV
FEKNGEVYSPSSKTWTSPLNAKVNPMLTADKQGLYRSDNHAWLFGWKKGSVFQAGPSTAMNWYYTSGSGD
VKSAGKRQSNRGVAPDAMCGNAV MYDAVKGKILT FGGSPDYQDSDATTNAHIITLGE PGTPNTVFA SNGLYF
ARTFHTSVVLPDGSTFITGGQRRGIPFEDSTPVFTPEIYVPEQDTFYKQNPNSIVRVYHSISLLPDGRVFNGGGG
LCGDCTTNHFDAQIFTPNLYNSN

>d1mdah_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}

EKS VAGSAAAASAAAASDGSSCDHGPAGAISRRSHITLPAYFAGTTENWVSCAGCGVTLHSLGAFLSLAVAGH
SGSDFALASTSFARS A KGKRTDYVEVFDPTFLPIADI ELPDAPRFSVGPRVHIGNCASSACLLFLGSSAAAGLS
VPGASDDQLTKSASC FH IHPGAAATHYL GSCPASLAASD LAAAPAAAGIVGAQCTGAQNCSQAAQANYPGM
LVWA VASSILQGDIPAAGATMKAIDGNESGRKADNFRSAGFQMVAKLKNTDGIMILTVEHSRSCLAAENTS
SVTASVGQTSGPISNGHDSIAIAAQDGASDNYANSAGTEVLDIYDAASDQDQSSVELKG PESLSVQNEA

>d2bbkh_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Paracoccus denitrificans}

DEPRILEAPAPDARRVYVNDPAHFAAVTQQFVIDGEAGR VIGMIDGGFLPNPVADDGSFIAHASTVFSRIARG
ERTDYVEVFDPTLLPTADI LPDAPRFLVG TYPWMTSLPDGKTLF YQFSPAPAVGVVDLEGKAFKRM LDV PD
CYHIFPTAPDTFFMHCRDGS LAKVAFGTEGTPEIHTHEVFP EDEF LINHPAYS QKAGR LVWPT YTG KIH QIDL SS
GDAKFLPAVEALTEAERADGW RP GG WQQVAYH RALD RIY LLV DQR DEW RHKT ASRF VV VLD AKTGER LAK FE
MGHEIDSINVSQDEKPLL YALSTGDKT LYIH DAESGEELRSV NQLGHGPQVITTAD MG

>d2madh_ b.69.2.1 (H:) Methylamine dehydrogenase, H-chain {Gram negative methylotrophic bacteria (Thiobacillus versutus)}

SSASAAAAAAAALAAGAADGPTNDEAPGADGRRSYINLPAHH SAI QQWVLDAGSGSILGHVNGGFLPNPV
AAHSGSEFALASTSF SRIAKGKRTDYVEVFDPTFLPIADI LPDAPRFDVGPYSWMNANTPNNADLLFFQFAA

GPAVGLVVQGGSSDDQLSSPTCYHIHPGAPSTFYLLCAQGGI AKTDHAGGAAGAGLVGAML TAAQNL TQPA
QANKSGRIVWPVYSGKILQADISAAGATNKAPIDALSGGRKADTWRPGGWQQVAYLKSSDGIYLLSEQS AWK
LHAAAKEVTSVTGLVGQTSSQISLGHDVDAISVAQDGDPDLYALSAGTEVLHIYDAGAGDQDQSTVELGSGPQ
VLSVMNEA

>d1jjub_b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Paracoccus denitrificans}
RDYILAPARPDKLVIDTEKMAVDKVITIADAGPTPMVPMVAPGGRIAYATVNKSESLVKIDLVTGETLGRIDLST
PEERVKSLFGAALSPDGKTLAIYESPVRLELTHFEVQPTRVALYDAETLSRRKAFAEPRQITMLAWARDGSKLYGL
GRDLHVMDPEAGTLVEDKPIQSWEAETYAQPDVLA VWNQHESSGVMATPFYTARKDIDPADPTAYRTGLLT M
DLETGEMAMREVIRIMDVYFYSTAVNPAKTRAFGAYNVLESFDLEKNASIKRVPPLPHSYYSVNVSTDGSTVWL G
GALGDLAAYDAETLEKKGQV DLPGNASMSLASVRLFTRDE

>d1jmx b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Pseudomonas putida}
GPALKAGHEYMIVTNYPNNLHVVDVASDTVYKSCVMPDKFGPGTAMMAPDNR TAYV LNNHYGDIYGIDLDT
CKNTFHANLSSVPGEVGRSMYSFAISPDGKEVYATVNPTQRLNDHYVVKPPRLEV FSTADGLEAKPVRTFPMP R
QVYLMRAADDGSLYVAGPDIYKMDVKTGKYTV ALPLRNWNRKGYSAPDVLYFWPHQSPRHEFSML YTIARFK
DDKQDPATADLLYGYLSVDLKTGKTHTQEFADLTEL YFTGLRSPKDNPQIYGVNLAKYDLKQRKLIKAANLDHT
YYCVAFDKKGD KLYLG GTFNDLAVFNPDTLEKVKNIKLPGGDMSTTPQVFIR

>d1qnia2 b.69.3.1 (A:10-450) Nitrous oxide reductase, N-terminal domain {Pseudomonas nautica}
AHVAPGELDEYYGFWSGGHQGEVRLGVPSMRELMRIPVFNVDSATGWGITNESKEI LGGDQQYNGDCHH
PHISMTDGRYDGKYLFI NDKANTRVARIRLDIMKTDKITHIPNVQAIHGLRLQKVPKTNYFCNAEFVIPQPND
GTDFSLNSYTMFTAIDAETMDVAWQVIVDGNLDNTDADYTGKYATSTCYN SERAVDLAGTMRND RDWVV V
FNVERIAAAVKA GNFKTIGDSKVPVVDGRGESEFTRYIPVPKNPHGLNTSPDGKYFIANGKLSPTVS VIAIDKL DD
LFEDKIELRDTIVAEPELGLGPLHTTFDGRGNAYTTLIDSQVCKWNIADA IKHYNGDRVNYIRQKLDVQYQPGH
N HASLTERDADGKWL VVLSKFSKDRFLPVGPLHPENDQLIDISGEEMKLVHDGPTYAE PHDCILVRRDQIKTK
>d1fwxa2 b.69.3.1 (A:8-451) Nitrous oxide reductase, N-terminal domain {Paracoccus denitrificans}
ADGSVAPGQLDDYYGFWSGGQSGEMRILGIPSMRELMRVPVFNRCSATGWGQTNESVRIHERTMSERTKKFL
AANGKRIHDNGDLHHVHMSFTEGKYDGRFLFMNDKANTRVARVRC DV MKCDAILEIPNAKG IHLRPQKWP
RSNYVFCNGEDETPLVNDGTN MEDVANYNVFTA VDADKWEVA WQVLVSGNLDNCADYEGKWA FSTS YN
SEKGMTLPEM TAAEMDHIVVFNIAIEIEKAIAAGDYQELNGVKVVDGRKEASSLTRYIPIANPHGCNMAPDK
KHLCVAGKLSPTVTVLDVTRFDAV FYENADPRSAVVAEPELGLGPLHTAFDGRGNAYTSLFLDSQVVKWNIEDAI
RAYAGEKVDPIKDKLDVH YQPGH LKTVM GETLDATNDWL VCLSKFSKDRFLNVGPLP ENDQLIDISGDKMVL
VHDGPTFAEPHDAIAVHPSILSDIK

>d1tbga_b.69.4.1 (A:) beta1-subunit of the signal-transducing G protein heterotrimer {Cow (Bos taurus)}

MSELDQLRQEAEQLKNQIRDARKACADATLSQITNNIDPVGRIQMTRR TLRGH LAKIYAMHWG TD SRLV SA
SQDGKLIWDSYTTNKVHAIPRSSWVMT CAYAPSGNYVACGGLDNICSIYNLKTREGNVR VSREL AHTGYLS
CCRF LDDNQIVTSSGDTT CALW DIETGQQTTFTGHTGDVMSL SLAPDTRLFVSGACDASAKLWDVREGMC R
QTFTGHE SDINAICFPNGNAFATGSDDATCRLF DLRADQELMTYSHDNIICGITSFSKSGRLLAGYDDFNC N
VWDALKADRGVLAGHDNRVSLCGVTDDGM AVATGSWDSFLKIWN

>d1erja_b.69.4.1 (A:) Tup1, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

HYLVPYNQRANHSKPIPPFLLDLSQSVPDALKKQTNDYYILNPALPREIDVELHKSLDHTSVVCCVKFSNDGEY
LATGCN TTQVYRVSDGSLVARLSDDSAANKDPENLNTSSPSSDLYI RSVCFS PDGKFLATGAEDRLIRI WDIEN
RKIVMIQGHEQDIYSLDYFPGD KLVSGSGDRTV RIWDLRTGQCSL TSIEDGVTTV AVSPGDGKYIAAGSLDR
AVRVWDSETGFLVERLDSENE SGTHKDSV SVFTRDGQSVVSGSLDRSVKLWNLQNANNKSDSKTPNSGT

CEVTYIGHKDFVLSVATTQNDEYILSGSKDRGVLFWDKSGNPLLMLQGHRNSVISAVANGSSLGPEYNVFAT
GSGDCKARIWKYKKI

>d1k8kc_b.69.4.1 (C:) Arp2/3 complex 41 kDa subunit ARPC1 {Cow (Bos taurus)}
AYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKSGNKWVQVHELKEHNGQVTGVWDWAPDSNRIVTCGTD
RNAYVWTLKGRTWKPTLVLRINRAARCVRWPNEKKFAVGSGSRVISICYFEQENDWWVCKHKKPIRSTVLS
LDWHPNSVLLAAGSCDFKCRIFSAVIKEVEERPAPTPWGSKMPFGELMFESSSSCGWVHGVCFSANGSRVAW
VSHDSTVCLADADKKMAVATLASETPLLAVTFITESSLVAAGHDCFPVLFTYDSAAGKLSFGGRLDVPKQSSQR
GLTARERFQNLDKKASSEGSAAGAGLDSLHKNSVSQISVLSGGAKCSQFCTGMDGGMSIWDRSLESALK
DLKIV

>d1a12a_b.69.5.1 (A:) Regulator of chromosome condensation RCC1 {Human (Homo sapiens)}
KKVKVSHRSHTEPGLVLTGQGDVGQLGLGENVMERKKPALVSIPEDVVQAEAGGMHTVCLSKSGQVYSFGC
NDEGALGRDTSEVGSEMVPKGVELQEKKVQVSAGDSHTAAALTDDGRVFLWGSFRDNNNGVIGLLEPMKKS
PVQVQLDPVVVKVASGNDHLVMLTADGDLTYLGCSEQGQLGRVPELFANRGGRQGLERLLVPKCVMLKSRGS
RGHVRFQDAFCGAYFTFAISHEGHVYGFGLSNYHQLGTPGTESCFIPQNLTSFKNSTKSWVGSGQQHHTVCM
DSEGKAYSLGRAEYGRGLGEGAEEKSIPTLISRLPAVSSVACGASVGYAVTKDGRVFAWMGNTYQLGTGQDE
DAWSPVEMMGKQLENRVVLSVSSGGQHTVLLVKDKEQS

>d1jtdb_b.69.5.2 (B:) of beta-lactamase inhibitor protein-II, BLIP-II {Streptomyces exfoliatus}

VAATSVVAWGNNNDWGEATVPAEAQSGVDAIAGGYFHGLALKGGKVLGWGANLNGQLTMPAATQSGVD
AAGNYHSLALKDGEVIAWGGNEDGQTTVPAEARSGVDAIAAGAWASYALKDGKVIAWGDDSDGQTTVPAEA
QSGVTALDGGVYTALAVKNGGVIAWGDNYFGQTTVPAEAQSGVDDVAGGIFHSLALKDGKVIAWGDNRYKQ
TTVPTEALSGVSAIASGEWYSLALKNGKVIAWGSSRTAPSSVQSGVSSIEAGPNAAYALKG

>d1c9la2 b.69.6.1 (A:3-330) Clathrin heavy-chain terminal domain {Rat (Rattus norvegicus)}
QILPIRFQEHLQLQNLGINPANIGFSTLTMESDKFICIREKVGEQAQVVIIDMNDPSNPIRRPISADS
IAALKAGKTLQIFNIEMKSFMKAHTMTDDTFWKWISLNTVALVTDNAVYHWSMEGESQPVKMFDRHSSLAG
CQIINYRTDAKQKWLLTGISAQQNRVVGAMQLYSVDRKVSQPIEGHAASFAQFKMEGNAEESTLFCFAVRGQ
AGGKLHIIEVGTPPTGNQPFPKKAVDVFFPPEAQNDFPVAMQISEKHDVVFLITKYGYIHLYDLETGTCIYMNRIS
GETIFVTAPHEATAGIIGVNRKGQVLSVCVE

>d1jv2a4 b.69.8.1 (A:1-438) Integrin alpha N-terminal domain {Human (Homo sapiens)}
FNLDVDSPEYSGPEGSYFGFAVDFFVPSASSRMFLVGAPKANTTQPGIVEGGQVLKCDWSSTRRCQPIEFDA
TGNRDYAKDDPLEFKSHQWFGASVRSKQDKILACAPLYHWRTEMKQEREPPVGTCFLQDGKTV
EYAPCRSQDI
DADGQGFCQGGFSIDFTKADRVLGGPGSFYWQGQLISDQVAEIVSKYDPNVYSIKYNNQLATR
TAQAFDDSY
LGYSVAVGDFNGDGIDDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGEQMAAYFG
FSVAATDINGDDYADV
FIGAPLFMDRGSQDGKLQEVGQVSVSLQRASGDFQTTKNGFEV
FARFGSIAIPLGDLQDG
FNDIAIAAPYGG
EDKKGIVYIFNGRSTGLNAVPSQILEGQWAARS
MPPSGYSMKGAT
DIDKNGYP
DLIVGA
FGVD
RAILYRAR

>d1qfma1 b.69.7.1 (A:1-430) Prolyl oligopeptidase, N-terminal domain {Pig (Sus scrofa)}
MLSFQYPDVRDETAIQDYHGHKVC
DPYAWLED
PDSEQTKAF
VEAQNK
ITV
PFLEQC
PIRGLY
KERM
TELYD
YD
P
KYSCHFKKGKRYFYFYNTGLQNQRVLYVQDSLEG
EARVFLDPN
ILSDDGT
VALRGYAF
SEDGEY
FAYGL
SAS
GSD
WVTIKFM
KVDGA
KE
LPDV
LERV
KFSC
MAW
THDG
KGMF
NAY
PQQDG
KSDG
TET
STNL
HQK
LYY
HVL
GTDQ
SE
D
IL
CA
EF
P
DE
PK
WM
GGA
E
LS
DD
G
RY
V
LL
S
IRE
G
CDP
V
N
RL
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>d1k32a3 b.69.9.1 (A:320-679) Tricorn protease N-terminal domain {Archaeon Thermoplasma acidophilum}

SIPSKFAEDFSPLDGDLIAFVSRGQAFIQDVSGTYVLKVEPLRIRYVRRGGDTKVAFIHGTRREGDFLGIYDYRTGK
AEKFEENLGNVFAMGVDRNGKFAVVANDRFEIMTVDLETGKPTVIERSREAMITDFTISDNSRFIAYGFPLKHGE
TDGYVMQAIHVYDMEGRKIFAATTENSHDYAPAFDADSKNLYYLSYRSLDPSDPRVVLNFSFEVSKPFVPLIPG
SPNPTKLVPRTSMTSEAGEYDLNDMYKRSSPINVDPGDYRMIIPLESSILIYSVPVHGEFAAYYQGAPEKGVLLKYD
VKTRKVTEVKNNLTLRLSADRKTVMVRKDDGKIYTFPLEKPEDERTVETDKRPLV

>d1g72a_ b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylophilus methylotrophus, w3a1}

DADLDKQVNAGAWPIATGGYYSQHNSPLAQINKSNVKNVKAAWSFSTGV LNGHEGAPLVIGDMIMYVHSAF
PNNTYALNLNDPGKIVWQHKPKQDASTKAVMCCDVDRGLAYGAGQIVKKQANGHLLADAKTGKINWEVE
VCDPKVGSTLTQAPFVAKDTVLMGCSAELGVRGAVNAFDLKTGELKWRAFATGSDDSVRLAKDFNSANPHY
GQFGLGTKTWEGDAWKIGGGTNWGWWAYDPKLNLFYYGSGNPAPWNEMRPGDNKWTMTIWGRDLDTG
MAKWGYQKTPHDEWD FAGVNQMVLTDQPVNGKMTPLLSHIDRNGILYTLNRENGNLIVAEKVDPAVNFKK
VDLKTGTPVRDPEFATRMDHKGTNICPSAMGFHNQGVDSYDPESRTLYAGLNHICMDWEPMILPYRAGQFF
VGATLAMYPGPNGPTKKEMGQIRAFDLTGKAKWTKWEKFAAWGGTLYKGLVWYATLDGYLKALDNKDG
KELWNFKMPGIGSPMTYSFKGKQYIGSMYVGWPGVGLVFDLTDPSAGLGAVGAFRELQNHTQMGGG
LMVFSL

>d1h4ia_ b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylobacterium extorquens}

NDKLVELSKSDDNWVMPGKNYDSNNFSDLKQINKGNVKQLRPAWTFSTGLLN HEGAPLVVDGKMYIHTSFP
NNTFALGLDDPGTILWQDKPKQNPAAVACCDLVNRGLAYWPGDGKTPALIKTQLDGNVAALNAETGETV
WKVENSDIKVGSTLTIAPIVVKDKVIIGSSGAELGVRGYLTAYDVKTGEQVWRAYATGPDKDLLLASDFNIKNPH
YGQKGLGTGTWEGDAWKIGGGTNWGWWAYDPGTNLIYFGTGNPAPWNEMRPGDNKWTMTIFGRDADT
GEAKFGYQKTPHDEWDYAGVNMMMLSEQKDKDGKARKLLTHPDRNGIVYTLRTDGALVSANKLDDTVNVF
KSVDLKTGQPVRDPEYGRMDHLAKDICPSAMGYHNQGHDSYDPKRELFFMGINHICMDWEPMILPYRAG
QFFVGATLNMYPGPKGDRQNYEGLGQIKAYNAITGDYKWEKMERFAVWGGTMATAGDLVFYGTLDGYLKAR
DSDTGDLLWKFKIPSGAIGYPMTYTHKGTQYVAIYYVGWPGVGLVFDLADPTAGLGAVGAFKKLANYTQM
GGGVVVFSLDGKGPyDDPNVGEWK

>d1flga_ b.70.1.1 (A:) Ethanol dehydrogenase {Pseudomonas aeruginosa}

KDVTWEDIANDDKTTGDVLQYGMGTHAQRWSPLKQVNADNVFKLPAWSYSFGDEKQRGQESQAIVSDGVI
YVTASYSRLFALDAKTGKRLWTYNHRLPDIRPCCDVNRGAIIYGDVKVFFTLDAVASVALNKNTKVVWKKK
FADHGAGYTMTGAPTIVKDGKTGKVLLIHSSGDEFGVVGRLFARDPDTGEEIWMRPFVEGHMGRNGKDS
TVTGDVKAPSWPDDRNSPTGKVESWSHGGAPWQSASFDAETNTIIVGAGNPGPWNTWARTAKGGNPHD
YDSLYTSGQVGVDPSSGEVKWFYQHTPNDAWDFSGNNELVFDYKAKDGKIVKATAHADRNGFFYVVDRSNG
KLQNAFFPVDNITWASHIDLKTGRPVEREGQRPLPEPGQKHGKAVEVSPFLGGKNWNPMAYSQDTGLFYV
PANHWKEDYWTEEVSYTKGSAYLGMGFRRIKRYDDHVGSLRAMDPVSGKVVWEHKEHPLWAGVLATAGN
LVFTGTGDGYFKAFDAKSGKELWKFQTGSGIVSPPITWEQDGEQYLGTVGYGGAVPLWGGMADLTRPVAQ
GGSFWVFKLPSW

>d1kb0a2 b.70.1.1 (A:1-573) Quinoprotein alcohol dehydrogenase, N-terminal domain {Comamonas testosteroni}

TGPAQQAAA VQRVDGDFIRANAARTPDWPTIGV DYAE TRYSL RDQINAANVKDLGLAWSYNLESTRGVEAT
PVVVDGIMYVSASWSVVHAIDTRTGNIW TYDPQIDRSTGF KGCCDVNRGVALWKGKVYVGAWDGR LIAL
DAATGKEVWHQNTFEGQKGSLTITGAPRVFKGKVIINGGA EYGV RGYITAYDAETGERKWRWF SVP GDPSK P
FEDESMKRAARTWDPGKWW EAGGGGTMWDSMTFDAELNTMYVGTGNGSPWSHKVRSPKG DNL YLA
SIVALDPDTGKYKWHYQETPGDNWDTSTQPMILADI KAGKPRKVLHAPKNGFFFVLDRTNGKFISAKNFV P

VNWASGYDKHGKPIGIAAARDGSKPQDAVPGPYGAHNWHPMSFPQTGLVYLPAQNVPVNLMDDKKWEF
NQAGPGKPQSGTGWNATAKFFNAEPPSKPFGRLAWDPVAQKAAWSVEHSPWNGGTLTTAGNVVFQGTA
DGRLVAYHAATGEKLWEAPTGTGVVAAPSTYMDGRQYVSAVGGVYGLAARATERQGPGBTYTFVVGG
KARMPE

>d1nira2 b.70.2.1 (A:118-543) C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase {*Pseudomonas aeruginosa*}

EWGMPEMRESWKVLVKPEDRPKKQLNDLDPNLFSVTLRDAGQIALVDGDSKKIVKVIDTGYAVHISRMSASG
RYLLVIGRNDARIDMIDLWAKEPTKVAEIKIGIEARSVESSFKGYEDRYTIAGAYWPPQFAIMDGETLEPKQIVSTR
GMTVDTQTYHPEPRVAIIASHEHPEFIVNVKETGKVLLVNYKDIDNLTVTSIGAAPFLHDGGWDSSHRYFMTA
ANNSNKVAVIDSKDRRLSALDVGKTPHPGRGANFVHPKYGPVWSTSHLDGSISLIGTDPKNHPQYAWKKV
AELQGQGGGSLFIKTHPKSSHLYVDTTFNPNDARISQSVAVFDLKNLDAKYQVLPPIAEWADLGEAKRQQPEYN
KRGDEVVFSVWNGKNDSSALVVVDDKTLKLKAVVKDPRILPTGKFNVYNTQHDVY

>d1qksa2 b.70.2.1 (A:136-567) C-terminal (heme d1) domain of cytochrome cd1-nitrite reductase {*Paracoccus denitrificans*}

EFGMKEMRESWKVHVAPEDRPTQQMNDWDLENLFSVTLRDAGQIALIDGSTYEIKTVLDTGYAVHISRLSASG
RYLFVIGRDKVNMDLWMKEPTTVAEIKIGSEARSIETSKMEGWEDKYAIAGAYWPPQYVIMDGETLEPKKIQ
STRGMYDEQEYHPEPRVAAILASHYRPEFIVNVKETGKILLVDYTDLNNLKTTEISAERFLHDGGLDGSHRYFIT
AANARNKLVIDTKEGKLVIAEDTGGQTTPHPGRGANFVHPTGPVWATSHMGDDSVALIGTDPEGHPDNAW
KILDSPALGGGSLFIKTHPNSQYLYVDATLNPEAEISGSVAVFDIKAMTGDGSDPEFKTLPIAEWAGITEGQPRV
VQGEFNKDGEVWFSVWNGKDQESALVVVDDKTLKLKAVVKDPRILPTGKFNVYNTMTDTY

>d1e43a1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {*Bacillus licheniformis*}

YAYGAQHDYFDHHDIVGWTREGDSSVANSGLAALITDGGAKRMYVGRQNAGETWHDIRNRSEPVVINS
EGWGEFHVNGGSVSIYVQR

>d1g94a1 b.71.1.1 (A:355-448) Bacterial alpha-Amylase {*Pseudoalteromonas haloplancis* (*Alteromonas haloplancis*)}

NWAVTNWWNDNTNNQISFGRGSSGHMAINKEKEDSTLTATVQTDMASGQYCNVLKGELSADAKSCSGEVITVNS
DGTINLNIGAWDAMAIHKNAKLN

>d1bag_1 b.71.1.1 (348-425) Bacterial alpha-Amylase {*Bacillus subtilis*}

QPEELSNPNGNNQIFMNQRGSHGVVLANAGSSSVINTATKLPDGRYDNKAGAGSFQVNDGKLTGTINARSA
AVLYPD

>d1hvxa1 b.71.1.1 (A:394-483) Bacterial alpha-Amylase {*Bacillus stearothermophilus*}

YAYGTQHDYLDHSIIGWTREGVTEKPGSGLAALITDGGSKWMYVGKQHAGKVFYDLTGNRSDTVINS
GWGEFKVNGGSVSVWVPR

>d1gjwa1 b.71.1.1 (A:573-636) Maltosyltransferase {*Thermotoga maritima*}

GKFENLTTKDLVMSYEKNGQKIVIAANVGKEPKEITGGRVWNGKWSDEEKVVLKPLEFALVVQ

>d1cgt_3 b.71.1.1 (407-494) Cyclodextrin glycosyltransferase {*Bacillus circulans*, different strains}

GSTQQRWINNDVYVYERKFGKSVAVVAVNRNLSTSASITGLSTSLPTGSYTDVLGGVLNGNNITSTNGSINNFTL
AAGATAVWQYTTA

>d1kcla3 b.71.1.1 (A:407-495) Cyclodextrin glycosyltransferase {*Bacillus circulans*, different strains}

GSTQERWINNDVLIYERKFGSNVAVVAVNRNLNAPASISGLVTSPLPQGSYNDVLGGLLNGNTLSVGSGGAASN
FTLAAGGTAVWQYTA

>d1cgy_3 b.71.1.1 (403-491) Cyclodextrin glycosyltransferase {*Bacillus stearothermophilus*}

GDTEQRWINGDVYVYERQFGKDVVLAVNRSSSNYSITGLFTALPAGTYTDQLGGLLDGNTIQVGGSNGSVNA
FDLGPGEVGVWAYSAT

>d1qhoa3 b.71.1.1 (A:408-495) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}

GTQQQRWINNDVYIYERKFFNDVVLVAINRNTQSSYSISGLQTALPNGSYADYLSGLGGNGISVSNGVASFTLA
PGAVSVWQYSTS

>d1pama3 b.71.1.1 (A:407-496) Cyclodextrin glycosyltransferase {Bacillus sp., strain 1011} GSTHERWINNDVIIYERKFGNNVAVVAINRNMTPASITGLVTSLPRGSYNDVLGGILNGNTLVGAGGAASNF
TLAPGGTAVWQYTTDA

>d1ciu_3 b.71.1.1 (407-495) Cyclodextrin glycosyltransferase {Thermoanaerobacterium thermosulfurigenes, EM1}

GTQQQRWINNDVYIYERKFGNNVALVAINRNLSTSNTGLYTALPAGTYTDVLGGLLNGNSISVSDGSVTPFTL
SAGEVAVWQYVSS

>d1hx0a1 b.71.1.1 (A:404-496) Animal alpha-amylase {Pig (Sus scrofa)}

QPFTNWDNGSNQVAFGRGNRGFIVFNNDDWQLSSTLQTGLPGGYCDVISGDKVGNCTGIKVYVSSDGT
AQFSISNSAEDPFIAIHAESKL

>d1smd_1 b.71.1.1 (404-496) Animal alpha-amylase {Human (Homo sapiens)}

QPFTNWDNGSNQVAFGRGNRGFIVFNNDDWTFSLTLQTGLPAGTYCDVISGDKINGNCTGIKIYVSSDGKA
HFSISNSAEDPFIAIHAESKL

>d1jae_1 b.71.1.1 (379-471) Animal alpha-amylase {Yellow mealworm (Tenebrio molitor), larva}

GTQVENWWSNDDNQIAFSRGSQGFVAFTNGGDLNQNLNTGLPAGTYCDVISGELSGGSCTGKSVTVGDNGS
ADISLGSAEDDGVLAIHVNAKL

>d2aaa_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus niger, acid amylase}

YANDAFYTDNTIAMAKTGSQVITVLSNKSGSSYTLTSGSGYTAGTKLIEAYTCTSVDSSGDIPVPMAS
GLPRVLLPASVVDSSLCG

>d2taaa1 b.71.1.1 (A:382-478) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}

YKNPYIKDDTTIAMRKGTDSQIVTILSNKGASGDSYTLSGAGYTAGQQLTEVIGCTTVGSDGNVPVPMA
GGLPRVLYPTEKLAGSKICSDSS

>d7taa_1 b.71.1.1 (382-476) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}

YKNWPIYKDDTTIAMRKGTDSQIVTILSNKGASGDSYTLSGAGYTAGQQLTEVIGCTTVGSDGNVPVP
MAGGLPRVLYPTEKLAGSKICS

>d1smaa2 b.71.1.1 (A:506-588) Maltogenic amylase {Thermus sp.}

GDVAFLTADDEVNHLVYAKTDGNETVMIIINRSNEAAEIPMPIDARGKWLNVLLTGERFAAEATLCVSLPPYGF
VLYAVESW

>d1bvza2 b.71.1.1 (A:503-585) Maltogenic amylase {Thermoactinomyces vulgaris, TVAII}

GNVRSWHADKQANLYAFVRTVQDQHGVVVLNNRGEKQTVLLQVPESGGKTWLDCLTGEEVHGKQGQLKLT
RPYQGMILWNGR

>d1eh9a2 b.71.1.1 (A:491-557) Glycosyltrehalose trehalohydrolase {Archaeon Sulfolobus solfataricus, km1}

CDRRVNVNGENWLIKGREYFSLYVFSKSSIEVKYSGTLLSSNNFPQHIEEGKYEFDKGFALYK

>d1bf2_2 b.71.1.1 (638-750) Isoamylase {Pseudomonas amylofera}

YSGSQLTWYQPSGAVADSNYWNNTSNYAIAYAINGPSLGDNSIYVAYNGWSSVTFTLPAPPSTQWYRVTD
TCDWNDGASTFVAPGSETLIGGAGTTYGQCGQSLLLISK

>d1gcya1 b.71.1.1 (A:358-418) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase)

{Pseudomonas stutzeri}

RADSAISFHSGYGLVATVSGSQQLVVALNSDLGNPGQVASGSFSEAVNASNGQVRVWRS

>d1avaa1 b.71.1.1 (A:347-403) Plant alpha-amylase {Barley (*Hordeum vulgare*), seeds, AMY2 isozyme}

HNESKLQIIEADADLYLAEIDGKVIVKLGPRYDVGNLIPGGFKVAAHGNDYAVWEKI

>d1uok_1 b.71.1.1 (480-558) Oligo-1,6-glucosidase {Bacillus cereus}

GSYDLILENNPSIFAYVRTYGVEKLLVIANFTAEECIFELPEDISYSEVELLIHNYDENGPIENITLRPYEAMVFKLK

>d1g5aa1 b.71.1.1 (A:555-628) Amylosucrase {Neisseria polysaccharea}

RLVTFTNNKHIIGYIRNNALLAFGNFSEYPQTVAHTLQAMPFKAHDLLIGGKTVSLNQDLTLQPYQVMWLEIA

>d1f8ab1 b.72.1.1 (B:1-42) Mitotic rotamase PIN1 {Human (Homo sapiens)}

GSHGMADEEKLPPGWEKRMSRSSGRVYYFNHITNASQWERPS

>d1i8hb_ b.72.1.1 (B:) Mitotic rotamase PIN1 {Human (Homo sapiens)}

KLPPGWEKRMSRSSGRVYYFNHITNASQWERPSGNSSG

>d1pina1 b.72.1.1 (A:6-39) Mitotic rotamase PIN1 {Human (Homo sapiens)}

KLPPGWEKRMSRSSGRVYYFNHITNASQWERPSG

>d1e0la_ b.72.1.1 (A:) Formin binding protein FBP28 domain {Domestic mouse (*Mus musculus*)}

GATAVSEWTEYKTADGKTYYNNRTLESTWEKPQELK

>d1eg3a3 b.72.1.1 (A:47-84) Dystrophin {Human (Homo sapiens)}

PASQHFLSTSVQGPWERAISPINKVPYYINHETQTCWD

>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*)}

PGWEIIHENGRPLYNAEQKTKLHYPP

>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}

MGDCANANVYPNWVSKDWAGGQPTHNEAGQSIVYKGNLYTANWYTASVPGSDSSWTQVGSCN

>d1ed7a_ b.72.2.1 (A:) Chitin-binding domain of chitinase A1 {Bacillus circulans}

AWQVNTAYTAGQLTYNGKTYKCLQPHTSLAGWEPSNVPALWQLQ

>d1goia1 b.72.2.1 (A:447-498) Chitinase B, C-terminal domain {Serratia marcescens}

NLPIMTAPAYVPGTTYAQGALVSYQGYVWQTKWGYITSAPGSDSAWLKVGRV

>d1dkga1 b.73.1.1 (A:139-197) Head domain of nucleotide exchange factor GrpE {Escherichia coli}

VEVIAETNVPLDPNVHQAIAMIVESDDVAPGNVLGIMQKGYTLNGRTIRAAAMVTAKAKA

>d1e44b_ b.101.1.1 (B:) Ribonuclease domain of colicin E3 {Escherichia coli}

GFKDYGHDYHPAPKTENIKGLDLKPGIPKTPKQNGGGKRKRWTGDKGRKIYEWDSQHGELEGYRASDGQHL
GSFDPKTGNQLKGPDPKRNICKYL

>d1hcb__ b.74.1.1 (-) Carbonic anhydrase {Human (Homo sapiens), erythrocytes, isozyme I}

PDWGYDDKNGPEQWSKLYPIANGNNQSPVDIKTSETKHDTSLKPIVSYNPATAKEIINVGHSFHVNFDNDN

RSVLGGPFSDSYRLFQFHFWGSTNEHGSEHTVDGVVKYSAELHVAHWNSAKYSSLAEAASKADGLAVIGVL

MKVGEANPKLQKVLDALQAIKTKGKRAPFTNFDPLPSSLDFWTYPGSLTHPPLYESVTWIICKESISVSSEQ

AQFRSLLSNVEGDNAVPMQHNNRPTQPLKGRTVRASF

>d2cba__ b.74.1.1 (-) Carbonic anhydrase {Human (Homo sapiens), erythrocytes, isozyme II}

HHWGYGKHNGPEHWKDFPIAKGERQSPVDIDHTAKYDPSLKPLSVSYDQATSLRILNNGHAFNVEFDDSQ
DKAVLKGGLDGTYRLIQFHFHWGSLDGQGSEHTVDKKYAAELHLVHWNTKYGDFGKAVQQPDGLAVLGIF
LKVGSAKPGLQKVVDVLDSIKTKGSADFTNFDPRGLLPESLDYWTPGSLTPPLECVTWIVLKEPISVSSEQV
LKFRKLNFNGEGEPEELMVNDWRPAQPLKNRQIKASF

>d1flja_b.74.1.1 (A:) Carbonic anhydrase {Rat (*Rattus norvegicus*), isozyme III}
AKEWGYASHNGPEHWHELYPIAKGDNQSIELHTKDIRHDPSLQPWSVSYDPGSAKTILNNNGKTCRVVFDDTF
DRSMLRGGPLSGPYRLRQFHLHWGSSDDHGSEHTDGVKYAAELHLVHWNPKYNTFGEALKQPDGIAVVGIF
LKIGREKGEFQILLDALDKIKTGKEAPFNHFDPSCLPACRDYWTYHGSFTPPCEECIVWLLKEPMTVSSDQ
MAKLRSLFASAENEPPVPLVGNWRPPQPKGRVVRASFK

>d1znca_b.74.1.1 (A:) Carbonic anhydrase {Human (*Homo sapiens*), isozyme IV}
WCYEVQAESSNYPCLPVWKGGNCQKDRQSPINIVTTAKVDKKLRFFFSGYDKKQTWTVQNNGHSVMM
LLENKASISGGGLPAPYQAKQLHLHWSDLPYKGSEHSDLGEHFAMEMHIVHEKEKGTSRNVKEAQDPEDEIAV
LAFLVEAGTQVNNEGFPQLVEALSNIPKPEMSTTMAESSLLDLPKEEKLRHYFRYLGSLTPTCDEKVVWTVFREP
IQLHREQILAFSQKLYDKEQTVSMKDNRPLQQLGQRTVIKS

>d2znc_b.74.1.1 (-) Carbonic anhydrase {Mouse (*Mus musculus*), isozyme IV}
WCYEIQTEDPRSSCLGPEKWPGACKENQQSPINIVTARTKVNPRLTFFILVGYDQKQQWPIKNNQHTVEMTLG
GGACIIGGDLPARYEAVQLHLHWSNGNDNGSEHSIDGRHFAMEMHIVHKKLSSKEDSKDKFAVLAFMIEVGD
KVNKGFPQLVEALPSISKPHSTTVRESSLQDMLPPSTKMYTYFRYNGSLTPNCDETVIWTVYKQPKIHKNQFL
EFSKNLYYDEDQKLNMKDNVRPLQPLGKRQVFKSHA

>d1dmxa_b.74.1.1 (A:) Carbonic anhydrase {Mouse (*Mus musculus*), liver, isozyme V}
GTRQSPINIWKDSVYDPQLAPLRVSYDAASCYRLWNTGYFFQEFDDSCEDSGISGGPLGNHYRLKQFH
WGATDEWGSEHAVDGHYPAAELHLVHNSTKYENYKKASVGENGALVIGVFLKGAAHQALQKLVDFLPEVR
HKDTQVAMGPFDPSCLMPACRDYWTYPSLTPPLAESVTWIVQKTPVEVSPSQLSMFRLLFSGRGEEEDV
MVNNYRPLQPLRDRKLRRSSFR

>d1jd0a_b.74.1.1 (A:) Carbonic anhydrase {Human (*Homo sapiens*), isozyme XII}
KWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLTNNGHSVKLNLP
HIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHAAELHIVHYNSDLYPDASTASNKSEGLAVLAVLI
SFNPSYDKIFSHLQHVKYKGQEAFVPGFNIELLPERTAEYYRYRGSLLTPCPTVLT
VFRNPVQJSQEQLLA
ETALYCTHMDDPSPREMINNFRQVQKFDERLVYTSFS

>d1kopa_b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}
HTHWGYTGHDSPEWGNLSEEFRLCSTGKNQSPVNITETVSGKLP
AIKVNYKPSMV
DVENNGHTIQVNYPEG
GNTLT
VNGRTYTLQFH
FHVPS
ENQIKGRT
FPMEAHFV
HLDEN
KQPLV
LAVLY
EAGKT
NGRLSS
IWNV
MPMT
AGKV
KLNQ
PFD
AST
LLPK
RLK
YYRF
AGSL
TTPC
TEGV
SWL
KTYD
HIDQA
QAEK
FTRAV
GSENN
RPV
QPLN
ARVV
IE

>d1koqa_b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}
THWGYTGHDSPEWGNLSEEFRLCSTGKNQSPVNITETVSGKLP
AIKVNYKPSMV
DVENNGHTIQVNYPEG
NTLT
VNGRTYTLQFH
FHV
VPS
ENQIKGRT
FPMEAHFV
HLDEN
KQPLV
LAVLY
EAGKT
NGRLSS
IWNV
MPMT
RSL
LAVLY
EAGKT
NGRLSS
IWNV
MPMT
AGKV
KLNQ
PFD
AST
LLPK
RLK
YYRF
AGSL
TTPC
TEGV
SWL
KTYD
HIDQA
QAEK
FTRAV
GSENN
RPV
QPLN
ARVV
IE

>d4bcl_b.75.1.1 (-) Bacteriochlorophyll A protein {Prosthecochloris aestuarii, strain 2k}
TTAHSDYEIILEGSSSWGQVKGRAKVNVPAAIPLLPTDCNIRIDAKPLDAQKG
VVRFTKIESVV
DSVK
NTLN
EV
DI
AN
ET
K
DR
RI
AV
GE
GS
LS
VG
DF
SH
SF
EG
SV
NM
YY
RS
DA
RR
NIP
NPI
YMQ
GR
QF
HD
IL
MK
V
PL
DN
NL
DV
DT
WE
GF
QQ
SI
GG
GA
NG
FD
WI
RF
WF
IG
PA
FA
AIN
EG
GQ
RIS
PI
V
N
SS
V
EG
GE
KG
GP
VG
TR
WF
SH
A
G
SV
V
DS
IS
RW
TE
LF
PV
EQL
N
KP
AS
IE
GG
FR
SD
SQ
GIE
V
KD
GN
L
PG
V
SR
D
AG
GG
GL
RR
IL
NH
PL
V
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GM
VG

KFNDFTVDTQLKIVLPKGYKIRYAAPQFRSQNLEEYRWSGGAYARWVEHVCKGGTGQFEVLYAQ
>d1ksaa_ b.75.1.1 (A:) Bacteriochlorophyll A protein {Green sulfur bacterium (Chlorobium tepidum)}
TTAHSDYEIVLEGGSSWGKVKARAKVNAPPASPLPADCDVKLNVKPLDPAKGFVRISAVFESIVDSTKNKLIE
ADIANETKERRISVGEGMVSVGDFSFHTSFEGSVVNLFYRSDAVRRNVPNPIMQGRQFHDILMKVPLDNND
LIDTWEGTVKAIGSTGAFNDWIRDFWFIGPAFTALNEGGQRISRIEVNGLNTESGPKGPGVSRWRFSHGGSG
MVDSISRWAELFPSDKLNRPQAQEAGFRSDSQGIEVKDGEFPGVSDAGGGLRRILNHPLIPLVHHGMVGKF
NNFNVDAAQLKVVLPKGYKIRYAAPQYRSQNLEEYRWSGGAYARWVEHVCKGGVGQFEILYAQ
>d1ospo_ b.76.1.1 (O:) Outer surface protein A {Lyme disease spirochete (Borrelia burgdorferi)}
SLDEKNSVSVDLPGEMKVLVSKEKNKDGYDLATVDKLELKTSKNNNGSGVLEGVKADKCKVKTISDDLQQT
TLEVFKEDGKTLVSKKVTSKDSSTEKFNEKGEVSEKIITRADGTRLEYTGIKSDGSGKAKEVLKGYVLEGTLTAEK
TTLVVKEGTVTLSKNISKSGEVSVLNDTSSAATKKTAAWNNSGTSTLTITVNSKKTDLVFTKENTITVQQYDSN
GTKLEGSAVEITKLDEIKNALK
>d1vmoa_ b.77.1.1 (A:) Vitelline membrane outer protein-I (VMO-I) {Hen (Gallus gallus)}
RTREYTSVITVPNGGHWGKWIRQFCHSYANGFALKVEPSQFRDDTALNGIRLRCLDGSVIESLVGKWT
WTSFLVCPTGYLVSFSLRSEKSQGGDDTAANNIQFRCSDEAVLVDGLSWGRFGPWSRKCKICGLQTKVES
QGLRDDTALNNVRFFCCK
>d1dlc_2 b.77.2.1 (290-499) delta-Endotoxin (insecticide), middle domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}
LYPKEVKTELTRDVLTDPIVGVNNLRGYGTTSNIENYIRKPHLFYDYLHRIQFHTRFQPGYYGNDSFNYWSGNVY
STRPSIGSNDIITSFPYGNKSSEPVQNLEFNGEKVYRAVANTNLAVWPSAVYSGVTKVEFSQYNDQTDEASTQTY
DSKRNVGAVSWSDSIDQLPPETTDEPLEKGYSQHQLNYVMCFLMQGSRGRTIPVLTWTHKSVD
>d1ji6a2 b.77.2.1 (A:291-502) delta-Endotoxin (insecticide), middle domain {Bacillus thuringiensis, CRY3bb1}
LYSKGVKTELTRDIFTDPISLNTLQEYGPFLSIENSIRKPHLFYDYLQGIEFHTRLQPGYFGKDSFNYWSGNVYETR
PSIGSSKTITSPFYGDKSTEPVQKLSFDGQKVYRTIANTDVAAPNGKVYLGVTKVDFSQYDDQNETSTQTYD
SKRNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAECLMQDRRGRTIPFFTWTHRSD
>d1ciy_2 b.77.2.1 (256-461) delta-Endotoxin (insecticide), middle domain {Bacillus thuringiensis, CRYIA (A)}
PIRTVSQLTREIYTNPVLENFDGSFRGMAQRIEQNIRQPHLMDILNSITIYTDVHRGFNYWSGHQITASPVGFSG
PEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTNLPSTIYRQRGTV
DSLDPPIPQDNSVPPRAGFSHRLSHVTMLSQAAGAVYTLRAPTFSWQHRSAEF
>d1i5pa2 b.77.2.1 (A:264-472) delta-Endotoxin (insecticide), middle domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}
YQSLMVSSGANLYASGSGPQQTQSFTAQNWPFLYSLFQVNSNYILSGISGTRLSITFPNIGGLPGSTTHSLNSAR
VNYSGGVSSGLIGATNLNHNFCSTVLPLSTPFVRSWLDGTDRAVATSTNWQTESFQTTSLRCGAFSARG
NSNYFPDYFIRNISGVPLVIRNEDLTRLHYNQIRNIESPSGTPGGARAYLVSVHNRKN
>g1jac.5 b.77.3.1 (B;A:) Jacalin {Jackfruit (Artocarpus integrifolia)}
SGKSQTVIVGSWGAKGKAFDDGAFTGIREINLSYNKETAIGDFQVYDNGSPYVGQNHKSFITGFTPVKISLD
FPSEYIMEVSGYTGNGVSGYVVRSLTFKTNKTYGPYGVTSGTPNLPIENG丽VGFKG SIGYWLDYFSMYLSL
>g1jot.2 b.77.3.1 (B;A:) Lectin MPA {Osage orange (Maclura pomifera)}
RNGKSQSIIVGPWGDRXGVTFDDGAYTGIREINFEYNSETAIGGLRVTYDLNGMPFVAEDHKSFITGFKPVKISLE
FPSEYIVEVSGYVGKVEGYTVIRSLTFKTNKTYGPYGVTSGTPNLPIENG丽VGFKG SIGYWLDYFSIYLSL
>d1c3ma_ b.77.3.1 (A:) Heltuba lectin {Jerusalem artishoke (Helianthus tuberosus)}

ASDIAVQAGPWGGNGGKRWLQTAHGGKITSIIKGTCIFSICFVYKDKDNIEYHSGKFGVLGDKAETITFAEDE
DITAISGTGFAYYHMTVVTSLFQTNKVKYGPFGTVASSFSLPLTKKFAGFFGNSGDVLDIGGVVVP
>d1jpc_ b.78.1.1 (-) Lectin (agglutinin) {Snowdrop (Galanthus nivalis)}
DNILYSGETLSTGEFLNYGSFVFIMQEDCNLVLYDVDKPIWATNTGLSRSCFLSMQTDGNLVNVNPSNKPIWAS
NTGGQNGNYVCILQKDRNVVIYGTDRWATGTHT
>d1bwua_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (Allium sativum)}
RNILRNDEGLYGGQSLDVNPYHFIMQEDCNLVLYDHSTS WASNTGILGKKCRAVLQSDGNFVVYDAEGRSL
WASHSVRGNGNYVVLQEDGNVVIYRSDIWSTN
>d1bwud_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (Allium sativum)}
RNILTNEGLYGGQSLDVNPYHLIMQEDCNLVLYDHSTS WASNTGILGKKCRAVLQSDGNFVVYDAEGRSL
WASHSVRGNGNYVVLQEDGNVVIYRSDIWSTNTYR
>d1kj1a_ b.78.1.1 (A:) Lectin (agglutinin) {Garlic (Allium sativum)}
RNLLTNDEGLYAGQSLDVEPYHFIMQEDCNLVLYDHSTS WASNTGILGKKCRAVLQSDGNFVVYDAEGRSL
WASHSVRGNGNYVVLQEDGNVVIYRSDIWSTNTYR
>d1kj1d_ b.78.1.1 (D:) Lectin (agglutinin) {Garlic (Allium sativum)}
RNILMNDEGLYAGQSLDVEPYHLIMQEDCNLVLYDHSTS AVWTNTDIPGKKCRAVLQSDGNFVVYDAEGRSL
WASHSVRGNGNYVVLQEDGNVVIYRSDIWSTNTYK
>d1npla_ b.78.1.1 (A:) Lectin (agglutinin) {Daffodil (Narcissus pseudonarcissus)}
DNILYSGETLSPGEFLNNGRYVFIMQEDCNLVLYDV DKPIWATNTGLDRCHLSMQSDGNLVVYSPRNNPIW
ASNTGGENGNYVCVLQKDRNVVIYGTARWATGTNIH
>d1b2pa_ b.78.1.1 (A:) Lectin (agglutinin) {Bluebell (Scilla campanulata)}
NNIIFSKQPDDNHPQLHATESLEILFGTHVYRFIMQEDCNLVLYDNNNPIWATNTGLGNGCRAVLQPDGVLV
VITNENVTVWQSPVAGKAGHYVLVLPDRNVVIYGDALWATQTVR
>d1dipa1 b.78.1.1 (A:1-115) Fetuin-binding protein Scafet precursor {Bluebell (Scilla campanulata)}
NNILFGLSHEGSHPQLHAAQSLELSSFRFTMQSDCNLVLFSDVRVWASNTAGATGCR AVLQSDGLLVILTAQ
NTIRWSSGTKGSGNYVVLQPDRTVTIYGPGLWDGTSNK
>d1dipa2 b.78.1.1 (A:116-235) Fetuin-binding protein Scafet precursor {Bluebell (Scilla campanulata)}
GSVVVANNGNSILYSTQGNDNHPQLHATQSLQLSPYRLSMETDCNLVLFDRDRVWSTNTAGKGTGCR AVL
QPNGRMDVLTNQNIAVWTSGNSRSAGRYVFVLQPDRLN LAIYGGALWTT
>d1kapp1 b.79.1.1 (P:247-470) Metalloprotease, C-terminal domain {Pseudomonas aeruginosa, alkaline protease}
GANLTTRTGDTVYGFNSNTERDFYSATSSSKLVFSVWDAGGNDTDFSGFSQNQKINLNEKALSDVGGLKGN
VSIAAGVTVENAIGGSGSDLIGNDVANVLKGGAGNDILYGLGADQLWGGAGADTFVYGDIAESSAAPDTL
RDFVSGQDKIDLSGLDAFVNGGLVLQYVDAFAGKAGQAILS YDAASKAGSLAIDSGDAHADFAINLIGQATQA
DIVV
>d1sat_1 b.79.1.1 (247-471) Metalloprotease, C-terminal domain {Serratia marcescens}
GANLSTRGDTVYGFNSNTGRDFLSTSNSQKVIFA WDGAGNDTDFSGTANQRINLNEKSFDVGGLKGN
VSIAAGVTEN AIGGSGNDVIVGNAANNVLKGGAGNDVLFGGGGADELWGGAGKDIFVFS AASDSAPGASD
WIRDFQKGIDKIDLSFFDKEANSSFIHFVDHFSGTAGEALLSYNASSNVTLSVNIGGHAAPDFLVKIVGQVDV
ATDFIV
>d1air_ b.80.1.1 (-) Pectate lyase {Erwinia chrysanthemi, type C}
ATDTGGYAATAGGNVTGAVSKTATSMQDIVNIIDAARLDANGKKVKGAYPLVITYTG NEDSLINA AAAANICGQ
WSKDPRGVEIKEFTKGITIIGANGSSANFGIWIKKSSDV VVQNM RIGYLP GGAKDGMIRVDDSPNVWVDH

ELFAANHECDGTPNDTTFESAVDIKGASNTVTSYNYIHGVKKVGLDGSSSDTGRNITYHHNYYNDVNARLP
LQRGGLVHAYNNLYTNITGSGLNVRQNGQALIENNWFKAIPVTSRYDGKNFGTWVLKGNNITKPADFSTYSI
TWTADTKPYVNADSWTSTGTFPTVAYNYSVSAQCVKDLPYAGVGKNLATLTSTAC

>d1pcl__ b.80.1.1 (-) Pectate lyase {Erwinia chrysanthemi, type E}

AVETDAATTGWATQNGGTTGGAKAAKAVEVKNSDFKKALNGTDSSAKIUKVTGPIDISGGKAYTSFDDQKARS
QISIPSNTTIIGVGSNGKFTNGSLVIKGVKNVILRNLYIETPVDAPHYESGDGWNAEWDAVIDNSTNVWVDH
VTISDGSFTDDKYTTDGEKYVQHDGALDIKKGSDDYTISYSRFELHDKTILIGHSDSNGSQDSGKLRTFHNNV
FDRVTERAPRVRFGSIHAYNNVYLGDVKHSVYPYLYSFGLGTSGSILSESNSFTLSNLKSIDGKNPECSIVKQFNSK
VFSDKGSVLNGSTTKLDTCLAYKPTLPYKYSQAQTMTSSLATSINNNAGYGKL

>d1bn8a_ b.80.1.1 (A:) Pectate lyase {Bacillus subtilis}

ADLGHQTLGSNDGWGAYSTGTTGGSKASSNVYTVSNRNLVSALGKETNTTPKIIYIKGTIDMNVDDNLKPLG
LNDYKDPEYDLDKYLKAYDPSTWGKKEPSGTQEEARARSQKNQKARVMVDIPANTTIVSGTNAKVVGGNFQ
IKSDNVIIRNIEFQDAYDYFPQWDPTDGSSGNWNSQYDNITNGTHIWIDHCTFNDGSRPDSTSPKYYGRKY
QHHDGQTDASNGANYITMSYNYHDHDKSSIFGSSDSKTSDDGKLKITLHHNRYKNIVQRAPRVRFGQVHVY
NNYYEGSTSSSSYPSYAWGIGKSSKIYAQNNVIDVPGLSAAKTISVSGGTALYDSGTLNGTQINASAANGLSS
VGWTPSLHGSIDASANVKSNNVQAGAGKLN

>d1ee6a_ b.80.1.1 (A:) Pectate lyase {Bacillus sp., strain ksmp15}

APTVVHETIRVPAGQTFDGKGQTYVANPNTLGDGSQAENQPKIFRLEAGASLKNVVIGAPAADGVHCYGDCTI
TNVIWEDVGEDALTLKSSGTVNISGGAAYKAYDKVFQINAAGTINIRNFRADDIGKLVRQNGGTTKVVMNVE
NCNISRVKDAILRTDSSTGRIVNTRYSNVPTLFKGFKSGNTTASGNTQY

>d1idk__ b.80.1.2 (-) Pectin lyase {Aspergillus niger, type A}

VGVSGSAEGFAKGVTGGGSATPVYPDTIDELVSYLGDEARVIVLTKTFDSEGTGTCAPWGTASACQV
AIDQDDWCENYEPDAPSVEYYNAGTLGITVTSNKSЛИGEГSSGAIKGKGLRIVSGAENIIIQNIAVTDINPKYV
WGGDAITLDDCDLVWIDHVT TARIGRQHYVLGT SADNRVSLNNYIDGVSDY SATCDGYHYWAIYLDGDADLV
TMKGNYIYHTSGRSPKVQDNLLHAVNNYWYDISGHAFEIGEGGYV LAEGNVFQNVDTVLETYEGEAFTPSS
TAGEVCSTYLRDCVINGFGSSGTFSEDSTSFLDFEGKNIASASAYTSVASRVVANAGQGNL

>d1qcx_ b.80.1.2 (A:) Pectin lyase {Aspergillus niger, type B}

AGVVGAAEGFAHGVTGGGSASPVYPTTDELVSYLGDEPRVIILDQTFDTGTEGTETTGCAFWGTASQCQ
VAINLHSWCDNYQASAPKSVTYDKAGILPITVNSNKSIVGQGTGVKGKGLRVSGAKNVIQNIAVTDINPK
YVWGGDAITVDDSDLVWIDHVT TARIGRQHYVLGT SADNRVLTISYSLIDGRSDY SATCNGHHYWG VYLDGSND
MVTLKGNYFYNLSGRMPKVQGNTLLHAVNNLFHNFDGHAFEIGTGGYV LAEGNVFQDVNVVETPISGQLFS
SPDANTNQQCASVFGRSCQLNAFGNSGMSGSDTSIISKFAGKTIAAHPPGAIAQWTMKNAGQGK

>d1rmg__ b.80.1.3 (-) Rhamnogalacturonase A {Aspergillus aculeatus}

QLSGVGPLTSASTKGATKTCNILSYGAVADNSTDVGPATSAWAACKSGGLVYIPSGNYALNTWVLTGGSATAI
QLDGIYRTGTASGNMIAVTDTDFELFSSTSKGAVQGFYVYHAEGTYGARILRLTDVTHFSVHDIIILVDAPAFH
FTMDTCSDGEVYNMAIRGGNEGGLDGIDVWGSNIWVHDVEVTNKDECVTVKSPANNILVESIYCNWSGGCA
MGSLGADTDVTDIVRNVTWSSNQMYMIKSNGGSGTVSNVLENFIGHGNAYS LDIDGYWSSMTAVAGDG
VQLNNITVKNWKGTEANGATRPIRVVCSDTAPCTDLTLEDIAWTESGSSELYLCRSAYGSGYCLKDSSHTSYT
TTSTVTAAPSGYSATTMAADLATAFGLTASIPIPTSFYPGLTPYALAG

>d1bhe__ b.80.1.3 (-) Polygalacturonase {Erwinia carotovora, subsp. carotovora}

SDSRTVSEPKTPSSCTTLKADSSTATSTIQKALNNCDQGKAVRLSAGSTSFLGPLSLPSGVSLIDKGVTLRAVN
NAKSFENAPSSCGVVDKNGKGCAFITAVSTTNSGIYGP GTIDGQGGVKLQDKKVSWELAADAKVKKLQN
TPRLIQINKSKNFTLYNVLINSNPFHVV FSDGDGFTAWKTTIKTPSTARNTD GIDPMSSKNITIAYSNIATGDDN
VAIKAYKGRAETRNISILHNDFTGTHGMSIGSETMGVYNVTVDDLKMNGTTNGLRIKSDKSAAGVVNGVRY

NVVMKNVAKPIVIDTVYEKKEGSNVPDWSGITFKDVTSETKGVVVLNGENAKKPIEVTMKNVKLTSDSTWQIK
NVNVKK

>d1ia5a_ b.80.1.3 (A:) Polygalacturonase {Fungus (*Aspergillus aculeatus*)}
ATTCTFSGSNGASSASKSKTSCSTIVLSNAVPSGTTLDLKNDGTHVIFSGETTFGYKEWSGPLISVGSIDLITG
ASGHISINGDGSRWDGEGGNGGKTPKFFAAHSLTSVISGLKIVNSPQVFSAGSDYTLKDITIDNSDGD
DNGGHNTDAFDIGTSTYVTISGATVYNQDDCVAVNSGENIYFSGGYCSGGHGLSIGSVGRSDNTVKNVTFVD
STIINSDNGVRKIKNIDTTGSVSDVTYKDITLTSIAKYGIVVQQNYGDTSTTGPITDFVLDNVHGSVVSSGTN
ILISCGSGSCSDWTWTDVSVSGGKTSSKCTNVPSGASC

>d1czfa_ b.80.1.3 (A:) Polygalacturonase {Fungus (*Aspergillus niger*), endo-polygalacturonase II}
DSCTFTAAAAGKAKCSTILNNIEVPAGTTLDLGLTSGTKVIFEGTTFQYEEWAGPLISMGEHITVTGAS
GHLINCDGARWWDGKGTSGKKPKFFYAHGLDSSSITGLNIKNTPLMAFSVQANDITFTDVTINNADGDTQG
GHNTDAFDVGNSVGVNIIKPWVHNQDDCLAVNSGENIWFTGGTCIGGHGLSIGSVGDRSNNVVKNVTIEHST
VSNSENAVRKITISGATGSVSEITYSNIVMSGISDYGVVIQQDYEDGKPTGKPTNGVTIQDVKLESVTGSVDSGAT
EIYLLCGSGSCSDWTWDDVKVTGGKKSTACKNFPSVASC

>d1hg8a_ b.80.1.3 (A:) Polygalacturonase {*Fusarium moniliforme*}
DPCSVTEYGLATAVSSCKNIVLNGFQVPTGKQLDLSSLQNDSTVTFKGTTFATTADNDFNPVISGSNITITGAS
GHVIDGNGQAYWDGKGSNSNSNQPDHFIVVQKTTGNSKITNLNIQNWPVHCFDITGSQLTISGLILDNRAG
DKPNAKSGSLPAAHNTDGFDISSSDHVTLNNHVYNQDDCVAVTSGTNIVVSNMYCSGGHGLSIGSVGGKSD
NVVDGVQFLSSQVVSQNGCRIKSNSGATGTINNVTYQNIALTNISTYGVDVQQDYLNGGPTGKPTNGVKISNI
KFIKVGTVAASSAQDWFILCGDGSCSGFTSGNAITGGGKTSSCNYPTNTCP

>d1dbga_ b.80.1.4 (A:) Chondroitinase B {*Flavobacterium heparinum*}
QVVASNETLYQVVKEVKPGGLQIADGTYKDVQLIVNSGKGLPITIKALNPGVKFFTGDAKVELRGEHLILEGI
WFKDGNRAIQAWKSHGPGLVAIYGSYNRITACVFDCFDEANSAYITSLTEDGKVPQHCRIDHCSFTDKITFDQV
INLNNTARAIDGSVGGPGMYHRVDHCFFSNPQKPGNAGGGIRIGYYRNDIGRCLVDSNLFMQRQDSEAEIITSK
SQENVYYGNTYLNCQGTMNFRHGDHQVAINNFYIGNDQRFGYGGMFVWSRHHVACNYFELSETIKSRGNA
ALYLNPGAMASEHALAFDMLIANNAFINVNGYAIHFNPPLERRKEYCAANRLKFETPHQLMLKGNLFFKDQPV
VYPFFKDDYFIAGKNSWTGNVALGVEKGIPVNISANRSAYKPVKIKDIQPIEGIALDLNALISKGITGKPLSWDEVR
PYWLKEMPGTYALTARLSADRAAKFKAVIKRNKEH

>d1h80a_ b.80.1.8 (A:) iota-carrageenase {*Alteromonas* sp., atcc 43554}
VSPKTYKDADFYVAPTQQDNYDLVDDFGANGNTDSDSLQRAINAIISRKPNGGTLIPNGTYHFLGIQMK
SNVHIRVESDVIKPTWNGDGKNHRLFEVGVNNIVRNFSFQGLGNGFLVDFKDSRDKNLAVFKLGDRVNYKISN
FTIDDNKTIFASILVDTERNGRLHWSRNGIIERIKQNNALFGYGLIQTGADNILFRNLHSEGGIALRMETDNL
MKNYKQGGIRNIFADNIRCSKGAAVMFGPHFMKNGDVQVTNVSSVSCGSAVRSDSGFVELFSPTDEVHTRQ
SWKQAVESKLGRGCAQTPYARGNGGTRWAARVTQKDACLDAKLEYGIEPGSFGTVKVFDTARFGYNADLK
QDQLDYFSTSNCMCKRVCLPTKEQWSKQGQIYIGPSLAVIDTTPETSKYDYDVKTFNVKRINFVNSHKTIDTN
TESSRVCNYYGMSECSSSRWER

>d1qjva_ b.80.1.5 (A:) Pectin methylesterase PemA {*Erwinia chrysanthemi*}
ATTYNAVVKSSSDGKTFKTIADAIASAPAGSTPFVILKNGVYNERLTIRNNLHLKGESRNGAVIAAATAAGTLK
SDGSKWGTAGSSTITISAKDFSAQSLTIRNDFDPANQAKSDSSKIKDTQAVALYVTKSGDRAYFKDVSLVGYQ
DTLYVSGGRSFFSDCRISGTVDFIFGDTALFNNCDLVSRYRADVKSGNVSGYLATPSTNINQKYGLVITNSRVIRE
SDSVPAKSYGLGRPWHPTTFSDFGRYADPNAIGQTVFLNTSMDNHIYGWDKMSGKDNGNTIWFNPEDSRF
FEYKSYGAGAAVSKDRRQLTDAQAAEYTQSKVLGDWTPTLP

>d1qq1a_ b.80.1.6 (A:) P22 tailspike protein {*Salmonella* phage P22}
YSIEADKKFKYSVKLDYPTLQDAASAAVDGLLIDRDYNFYGETVDFGGKVLTIECKAKFIGDGNLIFTKLGKGSR

IAGVFMESTTPWVIKPWTDDNQWLTDAAAVVATLKQSCTDGYQPTVSDYVKFPGIETLLPPNAKGQNITSTL
EIRECIGVEVRASGLMAGFLFRGCHFCKMVDANNPSGGKDGIIIFENLSGDWGKGNYVIGGRTSYGSVSSAQ
FLRNNGGERDGGVIGFTSYRAGSGVKTWQGTVGTTSRNLYNQFRDSVVIYPVWDGFDLGADTMNPEL
DRPGDYPITQYPLHQLPLNHLDNLLVRGALGVFGMDKGKGMVVSNTVEDCAGSGAYLLTHESVFTNIAIDTN
TKDFQANQIYISGACRVNGLRLIGIRSTDGQSLTIDAPNSTVSGITGMVDPISRINVANLAEGLGNIRANSFGYDS
AAIKLRIHKLSKLDGALSHINGGAGSGSAYQLTAISGSTPAVSLKVNHKDCRGAEIFPVVDIASDDFIKDSSC
FLPYWENNSTSLKALVKKPNGLVELVRLTLATL

>d1daba_b.80.1.7 (A:) Virulence factor P.69 pertactin {Bordetella pertussis}

DWNNQSVKTGERQHGIHQGSDPGGVRTASGTTIKVSGRQAQGILLENPAAELQFRNGSVTSSGQLSDDGIR
RFLGTVVKAGKLVADHATLANVGDTWDDGIALYVAGEQAQASIADSTLQGAGGVQIERGANVTVQRSAIV
DGGLHIGALQSLQPEDLPPSRVVLRTDNTAVPASGAPAAVSLGASELTLDGGHITGGRAAGVAAMQGAVVH
LQRATIRRGDALAGGAAPGGAVPGGAVPGGAVPGGFPGGGFPVLGWWYGVDSGSSVLAQSIVEAPELGAAIRVG
RGARVTVPGGSLSAPHGNVIETGGARRFAPQAAPLSITLQAGAHQAQGKALLYRVLPEPVKLTGTGGADAQGDIV
ATELPSIPGTSIGPLDVALASQARWTGATRAVDSLISDNATWVMTDNSNVGALRLASDGSVDFQQPAEAGRFK
VLTVNTLAGSGLFRMNVFADLGLSDKLVVMQDASGQHRLWVRNSGSEPASANTLLVQTPLGSAATFTLANKD
GKVDIGTYRYRLAANGNGQWSLVGAKAPP

>d1ezga_b.80.2.1 (A:) Insect cysteine-rich antifreeze protein {Yellow mealworm (Tenebrio molitor)}

QCTGGADCTSCTGACTGCGNCPNAVTCTNSQHCVKANTCTGSTDCNTAQCTCTNSKDCFEANTCTDSTNCYKA
TACTNSSGCP

>d1hf2a1_b.80.3.1 (A:100-206) Cell-division inhibitor MinC, C-terminal domain {Thermotoga maritima}

TGKVIRNIRSGQTVVHSGDVIVFGNVNKGAELAGGSVVVFGKAQGNIRAGLNEGGQAVVAALDLQTSLIQIA
GFITHSKGEENVPSIAHVKGNRIVIEPFDKVSF

>d1ea0a1_b.80.4.1 (A:1203-1472) Alpha subunit of glutamate synthase, C-terminal domain {Azospirillum brasilense}

GRNEVPDTLDARIVADARPLFEEGEKMQLAYNARNTQRAIGTRLSSMVTRKFGMFLQPGHITIRLRGTAGQS
LGAFAVQGIKLEVMDANDYVGKGLSGGTIVVRPTTSSPLETNKNTIIGNTVLYGATAGKLFAAGQAGERFAVR
NSGATVVVEGCGSNGCEYMTGGTAVILGRVGDNFAGMTGGMAYVYDLDDSLPLYINDESVIFQRIEVGHYES
QLKHLIEEHVTETQSRFAAEILNDWAREVTKFWQVVPKEMLNRLEVPVHL

>d1kq5a_b.80.5.1 (A:) C-terminal domain of adenylylcyclase associated protein {Baker's yeast (Saccharomyces cerevisiae)}

MPPRKELVGNKWFIENTESLVIDANKDESIFIGKCSQVLQIKGVNAISLSETESCSVVLDSISGMDVIKS
NKFGIQVNHSLPQISIDKSDGGNIYLSKESLNTEIYTSCSTAINVNLPIGEDDDYVEFPISEQMKHSFADGKFKSAV
FE

>d1lxa_b.81.1.1 (-) UDP N-acetylglucosamine acyltransferase {Escherichia coli, gene lpxA}

MIDKSAFVHTAIVEEGASIGANAHGPFICVGPHEIGEGTVLKSHVVVNGHTKIGRDNEIYQFASIGEVNQDL
KYAGEPTRVEIGDRNRIRESVTIHRGTVQGGGLTKVGSNDNLLMINAHIAHDCTVGNRCILANNATLAGHVSVDD
FAIIGGMTAVHQFCIIGAHVMMVGGCSGVAQDVPPVIAQGNHATPFGVNIEGLKRRGSREAITAIRNAYKLIYR
SGKTLDEVKPEIAELAETYPEVKAFTDFFARSTRGLIR

>d3tdt_b.81.1.2 (-) Tetrahydrodipicolinate-N-succinyltransferase, THDP-succinyltransferase, DapD {Mycobacterium bovis}

MQQLQNVIESAFERRADITPANVDTVTREAVNQVIGLLSGALRVAEKIDGQWVTHQWLKAVLLSFRINDNK

VMDGAETRYYDKVPMKFADYDEARFQKEGFRVPPATVRQGAFIARNTVLMPSYVNIGAYVDEGTMVDTWA
TVGSCAQIGKNVHLSGGVGIGGVLEPLQANPTIIEDNCFIGARSEVVEGVIVEEGSVISMGVYLQSTRIYDRET
GEIHYGRVPAGSVVVSGNLP SKDG SYSLYCAVIVKKVDAKTRGKVGINELLRTID
>d1xat_ b.81.1.3 (-) Xenobiotic acetyltransferase {Pseudomonas aeruginosa}
NYFESPRFGKLLSEQVSNP NIRGVGRYSYYGHHSFDDCARYLMPDRDDVKLVGSFC SIGGAAFIMAGN
QGHRAEWASTFPFHFMHEEP AFAGAVNGYQPAGDTLIGHEVWIGTEAMFMPGV RVGHGAIIGSRALVTGDV
EPYAI VGGNPARTIRKRFSDGDIQN LLEM AWWDWPLADIEAAMPLLCTGDIPAL YQHWKQRQA
>d1kk6a_ b.81.1.3 (A:) Xenobiotic acetyltransferase {Enterococcus faecium, VAT(D)}
MGPNPMKMYPIEGNKS VQF KPILEKLENVEVGEY SYYDSKNGETFDKQILYHYPILNDKLKIGKFC SIGPGV TII
MNGANHRMDG STYPFNLFGNGWEKHMPKLDQLPIKGDTIIGNDVWIGKDV VIMP GV KIGDGAIVAANSVV
VKDIAPYMLAGGNPANEIKQRFDQDTINQLDIKW NWPN PIDIINENIDKILDNSIIREVIW
>d1fxja1 b.81.1.4 (A:252-329) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
C-terminal domain {Escherichia coli}
VMLRDPARFDL RGTL THGRDVEIDTNVII EGNV TLGHRV KIGT GCVIKNSV IGDCEIS PYTVVEDAN LAACTIG
PF
>d1hv9a1 b.81.1.4 (A:252-452) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
C-terminal domain {Escherichia coli}
VMLRDPARFDL RGTL THGRDVEIDTNVII EGNV TLGHRV KIGT GCVIKNSV IGDCEIS PYTVVEDAN LAACTIG
PFARLRPGAE LLEGAHVGNF VEMKKARLGKGS KAGHLTYLGDAEIGDNVNIGAGTITC NYDGANKFTIIGDDV
FVGSDTQLVAPVTVKGATIAAGTTVTRNVGENAL AISRV PQTQKEGW RRP
>d1hm9a1 b.81.1.4 (A:252-459) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
C-terminal domain {Streptococcus pneumoniae}
VS FVNPE ATYID IDV EIAPEV QIE ANVIL KGQT KIGAET VL NGT YV D STIGAG AVIT NSMIEESS VADG VTVGPY
AH IRP NSSL GAQV HIGNF VEV KGSSIGENT KAGHL TYI GNCE VGS NVN FGAGT ITV NYDG KNKY KT VIGDN VF
GSNST IIAPV ELDNS LV GAGS TIKD VPA DAIAI GRGR QINK DEY ATRL PHHP KNQ
>d1qrea_ b.81.1.5 (A:) Carbonic anhydrase {Archaeon Methanosa rca thermophila}
TVDEF SNIRENP VTPWNPEPSAPVIDPTAYIDPQASVIGEV TIGAN VMVSPM ASIRSDE GMPI FVGDRSNVQD
GVVL HALET INEE GEPI EDN IVEVDGKEY AYV I GNNV SLA HQSQV HGPAV GDDT FIGM QA FV FKSKVGN NC
LE PRSA AI GVTIPD GRYI PAGM VV TSQ AEAD KLPEV TDDY ASHT NEAVV YV NVH LAEGY KETS
>d1ewwa_ b.81.2.1 (A:) An insect antifreeze protein {Spruce budworm (Choristoneura fumiferana)}
DG SCT NTN SQL SAN SK CEK ST LTNC YVDK SEV YGTT CT GS RDG VT IT ST GS RIS GPG C KIST CI TGG VPAPS
AAC KIS GCT FSAN
>d1dzra_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC {Salmonella typhimurium}
MMIVIKTAIPDVLILEPKVFGDERGFFFESYNQQT FEELIGRKVTFVQDNHSKSKNVLRLHFQREGNAQGKLV
RCAVGEVFDVAVDIRKESPTFGQWVG NVNLSAENKRQLWIPEGFAHGFVTLSEYA EFLYKATNYYSPSSEG SILWN
DEAIGIEWPFSQ LP ELSAKDAAAPLLDQALLTE
>d1ep0a_ b.82.1.1 (A:) dTDP-4-dehydrorhamnose 3,5-epimerase RmlC {Archaeon
Methanobacterium thermoautotrophicum}
EFRFIKTS LDGAI III EPEV YT DERGY FMETFNEA IFQENG LEVRFVQDNE MSVR GVLRLHFQREKPQGKL VRVI
RGEIFDV AVDLRKN SDT YGEWTGV RLSD ENR REFFIPEGFAHGF LALSDECIV NYKCTELYHPEY DSGIPWDDPD
IGIDWPLEMVDDLI SEKDRNWKPLREN PVY
>d1fi2a_ b.82.1.2 (A:) Germin {Barley (Hordeum vulgare)}
TDPDPLQDFCVADLDGKA VSNGH TCKPMSEAGDDFLFSSKLT KAGNT STPNGSAVTEL DVAE WPGTNT LGV
SMNRVDFAPGGTNPPHIHPRATEIGMVMKGELLVGILGSLDSGNKLYSRVVRAGETFVIPRGLMHFQFNVGKT

EAYMVVSFNSQNPGIVFVPLTLFGSDPPIPTPVLTAKALRVEAGVVELLKSKFAGGS
>d2phla1 b.82.1.2 (A:11-210) Seed storage 7S protein {French bean (Phaseolus vulgaris), phaseolin}
DNPFYFNDSNWSNTLFKNQYGHIRVLQRFDQQSKRLQNLEDYRLVEFRSKPETLLPQQADAELLLVVRSGSAIL
VLVKPDDRREYFFLTSNDNPIFSDHQKIPAGTIFYLVNPDPKEDLRIQLAMPVNPNPQIHEFFLSSTEAQQSYLQEFS
KHILEASFNSKFEETNRVLFEEEGQQEGVIVNIDSEQIKELSKHAKSS
>d2phla2 b.82.1.2 (A:220-381) Seed storage 7S protein {French bean (Phaseolus vulgaris), phaseolin}
NTIGNEFGNLERTDNSLNVLISIEMEEGALFVPHYYSKAIVILVNEGEAHVELVGPKGNKETLEYESYRAELSK
DDVFVIPAAPVAIKATSNVNFTFGINANNNRNLLAGKTDNVISSIGRALDGKDVLGLTFSGSGDEVMKLINK
QSGSYFVDAH
>d1dgwa_ b.82.1.2 (A:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}
NNPYLFRSNKFLTLFKNQHGSLRLLQRFNEDTEKLENLRDYRVLEYCSKPNTLLPHHSDSLVLVLEGQAILVLV
NPDGRDTYKLDQGDAIKIQAGTPFYLINPDNNQNLRLKFAITFRRPGTVEDFFLSSTKRLPSYLSAFSKNFLEASY
DSPYDEIEQTLQEEQEGVIVKMP
>g1dgr.3 b.82.1.2 (M;N:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}
QLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQVSDLTFPGSGEEVE
ELLENQKESYFVDGQPXDKPFNLRSRDPIYSNNYGKLYEITPEKNSQLRDLDILLNCLQMNEGALFVPHNSRAT
VILVANEGRAEVELVGLE
>g1dgw.1 b.82.1.2 (X;Y:) Seed storage 7S protein {Jack bean (Canavalia ensiformis), canavalin/vinculin}
DKPFNLRSRDPIYSNNYGKLYEITPEKNSQLRDLDILLNCLQMNEGALFVPHNSRATVILVANEGRAEVELVGLE
XQLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQVSDLTFPGSGEEV
EELLENQKESYFVDGQP
>d1fxza1 b.82.1.2 (A:10-248) Seed storage 7S protein {Soybean (Glycine max), proglycinin}
NECQIQKLNALKPDNRIESEGGLIETWNPNPKPQCAGVALSRTCLRNALRRPSYTNGPQEYIQQGKGIFGM
IYPGCPSTFEEPQQPQQRGQSSRPQDRHQKIYNFREGDLIAVPTGVAWWMYNNEDTPVVAWSIIDTSLENQL
DQMPRRFYLAGNQEFLKYQQEQGGHQSQKGKHQQEEENEGGSILSGFTLEHAFSDKQIAKNLQGEN
EGEDKGAIKVKGGLSVIKP
>d1fxza2 b.82.1.2 (A:297-470) Seed storage 7S protein {Soybean (Glycine max), proglycinin}
ICTMRLRHNIQGTSSPDYINPQAGSVTTATSLDFPALSWLRLSAEFGSLRKNAMEVPHYNLNANSIIYALNGRALI
QVVNCNGERVFDELQEGRVLIVPQNFVVAARSQSDNFYVSFKTNTPMIGTLAGANSLLNALPEEVIQHTF
NLKSQQARQIKNNNPFKFLVPPQES
>d1pmi_ b.82.1.3 (-) Phosphomannose isomerase {Yeast (Candida albicans)}
SSEKLFRIQCGYQNYDWGKIGSSAVAQFVHNDSPTSITDETCKPYAELWMGTHPSVPSKAIDLNNQTLRDLVTAK
PQEYLGESIITKFGSSKELPFLFKVLSIEKVLSIQAHPDKKLGAQLHAADPKNYPDDNHKPEMAIAVTDFEGFCGF
KPLDQLAKTLATVPELNEIIGQELVDEFISGIKLPAAEVGSQDDVNNRKLQKVFGKLMNTDDVIKQQTAKLLERT
DREPQVFKDIDSRLPELIQRLNKQFPNDIGLFCGCLLNHVGLNKGEAMFLQAKDPHAYISGDIIECMAASDNV
VRAGFTPDKDVNLVEMLTYSYESVEKQKMPQEFPRSKGDAVKSVLYDPPIAEFSVLQTIIFDKSKGGKQVIEGL
NGPSIVIATNGKTIQITGDDSTKQKIDTGYVFFVAPGSSIELTADSANQDQDFTYRAFVEA
>d1eyba_ b.82.1.4 (A:) Homogentisate dioxygenase {Human (Homo sapiens)}

AELKYISGFGNECSSEDPRCPGLPEGQNNPQVCPYNLYAEQLSGSAFTCPRSTNKRSWLYRILPSVSHKPFESID
EGHVTHNWDEVDPDPNQLRWKPFEIPKASQKKVDFVSGLHTLCGAGDIKSNNGLAIHIFLCNTSMENRCFYN
SDGDFLIVPKGNLLIYTEFGKMLVQPNEICVIQRGMFRSIDVFEETRGYILEVYGVHFELPDLPPIGANGLANPR
DFLIPIAWYEDRQVPGGYTVINKYQGKLFAAKQDVSPFNVAWHGNYTPYKYNLKNFMVINSVAFDHADPSIF
TVLAKSVRPGVIAADFVIFPPRWGVADKTFRPPYYHRNCMSEFMGLIRGHYEAKQGGFLPGGGSLHSTMTPH
GPDADCFCASKVKLAPERIADGTMAFMFESSLSAVTKWGLKASRCLDENYHKCWEPLKSHFTPNSRN
>d1qjea_ b.82.2.1 (A:) Isopenicillin N synthase {*Emericella nidulans*}

SKANVPKIDVSPLFGDDQAAMRVAQQIDAASRTGFFYAVNHGINVQRLSQKTKEHMSITPEEKWDLAIRA
YNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNTPDHPRIQAKTPTHEVNVPDETCKHPGFQDFAEQYYWDV
FGLSSALLKGYALALGKEENFFARHFKPDDTLASVVLIRYPYLDPPPEAAIKTAADGTKLSFEWHEDVSLITVLYQS
NVQNLQVETAAGYQDIEADDTGYLINC SYMAHLTNYYKAPIRVKVVNAERQLPFFVNLGYDSVIDPFDP
REPNGKSDREPLSYGDYLQNGLVSLINKNGQT

>d1dcs_ b.82.2.1 (-) Deacetoxycephalosporin C synthase {*Streptomyces clavuligerus*}

MDTTVPTFSLAELQQGLHQDEFRRCLRDKGFLYLTDCGLTDTELKSAKDLVIDFFEHGSEAEKRAVTSPVPTMRR
GFTGLESESTAQITNTGSYSYDMCYSMTGADNLFPSGDFERIWTQYFDRQYTASRAVAREVLRATGTEPDGGV
EAFLDCEPLLFRYFPQVPEHRSAAEQPLRMAPHYDLSMVTLIQQTPCANGFVSLQAEVGAFTDLPYRPDAVL
VFCGAIATLVTGGQVKAPRHHVAPRRDQIAGSSRTSSVFLRPNADFTSVPLARECGFDVSLDGETATFQDWI
GGNYVNIRRTSKA

>d1gp6a_ b.82.2.1 (A:) Anthocyanidin synthase {Mouse-ear cress (*Arabidopsis thaliana*)}
VAVERVESLAKSGIISIPKEYIRPKEELESINDVFLEEKEDGPQVPTIDLKNIESDDEKIRENCEELKKASLDWGV
MHLINHGIPADLMERVKKAGEEFFSLSVEEKEYANDQATGKIQGYGSKLANNASGQLEWEDYFFHLAYPEEK
DLSIWPKTPSDYIEATSEYAKCLRLLATKVFKALSVGLGLEPDRLEKEVGGLEELLQMKINYYPKCPQPEALGVE
AHTDVSALTFLHNMVPGQLFYEGKWVTAKCVPDSIVMHIGDTLEILSNGKYKSILHRLVNEKVRISWAVFC
EPPKDKIVLKPLPEMVSVESPAKFPPRTFAQHIEHKLFGKEQEEL

>d1ds1a_ b.82.2.2 (A:) Clavaminate synthase {*Streptomyces clavuligerus*}

TSVDCTAYGPELRALAARLPRTPRADLYAFLDAAHAAASLPGALATALDTFNAEGSEDGHLLRGLPVEADADL
PTTPSSTPAPEDRSLLTMEAMLGLVGRRGLHTGYRELRSGTVYHDVYPSGAHHLSSETSETLLEFHTEMAYHR
LQPNYVMLACSRADHERAATLVASVRKALPLIDERTRARLLDRRMPCCVDVAFRGGVDDPGAIAQVKPLYGD
ADDPFLGYDRELLAPEDPADKEAVAALKALDEVTEAVYLEPGDLLIVDNFRTTHARTPFSPRWDGKDRWLHRV
YIRTRNGQLSGGERAGDVVAFTPRG

>d1jr7a_ b.82.2.3 (A:) Gab protein (hypothetical protein YgaT) {*Escherichia coli*}

GQDYSGFTLTPSAQSPRLLELTFTEQTTKQFLEQVAEWPVQALEYKSFLRFRVAKILDDL CANQLQPLLLKTLLNR
AEGALLINAVGVDDVKQADEMVKLATAVAHLIGRSNFDAMMSGQYYARFVVKNVNDNSDYLQPHRVMELHN
DGTYVEITDYVLMMKIDEQNMQGGNSLLLHLDWEHLDNYFRHPLARRPMRFAAPPSKNVSKDVFHPVFD
VDQQGRPVMRYIDQFVQPKDFEEGVWLSELSDAIETSKGILSVPVPGKFLLINNLFWLHGRDRFTP HDPLRRE
LMRQRGYFAYASNHYQTHQ

>d1e5sa_ b.82.2.4 (A:) Type II Proline 3-hydroxylase (proline oxidase) {*Streptomyces* sp.}

MRS HILGKIELDQTRLAPDLAYLAAVPTVEEYDEFSNGFWKHVPLWNASGDSEDRLYRDLKAAAQPTAHVE
HVPYLKEIVTTVFDGTHLQMARSRNKLNAIVIPH RDFVELDREVDRYFRTFMVLED SPLAFHSNEDTVIHM RPG
EIWF LDAATVHS AVNFSEISRQSLCVDFAFDGPDEKEIFADATLYAPG STPDLPERRPFTA EHRRRILSLGQVIERE
NFRDILFL SKVHYKYDVHPSETYDWLIEISKQAGDEKM VVKA EQI RDFA VEAR ALSERF SLTSW

>d1ft9a2 b.82.3.1 (A:2-133) CO-sensing protein CooA, N-terminal domain {*Rhodospirillum rubrum*}

PPRFNIANVLLSPDGETFFRGFRSKIHAKGSLVCTGEGDENGVFVVDGRLRVYLVGEEREISLFYLTSGDMFCM

HSGCLVEATERTEVRFADIRTFEQKLQTCPSMAWGLIALGRALTSCMRTIEDLMFH
>d1hw5a2 b.82.3.2 (A:1-137) Catabolite gene activator protein, N-terminal domain {Escherichia coli}
VLGKPQTDPTLEWFLSHCHIKYPSKSTLIHQGEKAETLYYIVKGSAVLIKDEEGKEMILSYLNQGDFIGELGLFE
EGQERSAWVRAKTACEVAEISYKKFRQLIQVNPDILMRLSAQMARRLQVLAEKVGNLAFL
>d1rgs_1 b.82.3.2 (113-244) Regulatory subunit of Protein kinase A {Cow (Bos taurus)}
RKVIPKDYKTMALAKAIEKNVLFSHLDNERSIDFAMFPVSFIAGETVIQQGDEGDNFYVIDQGEMDVYVN
NEWATSVGEGGSFGELALIYGTPRAATVKAKTNVKLGIDRDSYRRILMGSTLRKRKMY
>d1rgs_2 b.82.3.2 (245-376) Regulatory subunit of Protein kinase A {Cow (Bos taurus)}
EEFLSKVSIKESLDKWERLTVDAALEPVQFEDGQKIVVQGEPGDEFFIILEGSAAVLQRRSENEEFVEVGRGLGPSD
YFGEIALLMNRPRAATVVARGPLKCVKLDRPRFERVLGPCSDILRKNIQQYNSFV
>d1cx4a1 b.82.3.2 (A:130-265) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}
RIIHPKTDDQRNRQLQEACKDILLFKNLDP EQMSQVLDAMFEKLVKEGEHVIDQGDDGDNFYVIDRGTDFIYVKC
DGVGRCVGNYDNRGSFGELALMYNTPRAATITATSPGALWGLDRVTFRIIVKNNAKKRKMY
>d1cx4a2 b.82.3.2 (A:266-412) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}
ESFIESLPFLKSLEVSRERLKVV DVIGTKVYN DGEQIIAQGDSADSFFIVESGEVRITMKRGKSDIEENGAVEIARCL
RGQYFGELALVTNKPRAASAHAIGTVKCLAMD VQA FERLLGPCMEIMKRNIATYEEQLVALFGTNMDIV
>d2arca_b.82.4.1 (A:) Regulatory protein AraC {Escherichia coli}
DPLLPGYSFNAHLVAGLPIEANGYLDFFIDRPLGMKG YILNL TIRGQGVVKNQGREFVCRPGDILLFPPGEIH
GRHPEAREWYHQWVYFRPRAYWHELNWPSIFANTGFFRPDEAHQPHFSDLFGQIINAGQGEGRYSELLAI
NLLEQLLLRRMEAI
>d1ig3a1 b.82.6.1 (A:179-263) Thiamin pyrophosphokinase, substrate-binding
domain {Mouse (Mus musculus)}
DSLIYLLQPGKHLHVDTGMEGSWCGLIPVGQPCNQVTTGLKWNLNDVLGFTLVTSNTYDGSGLVTVET
DHPLLWTMAIKS
>d1ig0a1 b.82.6.1 (A:224-319) Thiamin pyrophosphokinase, substrate-binding
domain {Baker's yeast (Saccharomyces cerevisiae)}
TDLIFLIKNGTLIEYDPQFRNTCIGNCGLLPIGEATLVKETRGLKWDVKNWPTS VVTGRVSSSNRFVGDNC
TKDDIIILNVEIFVDKLIDFL
>d1wapa_b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP) {Bacillus subtilis}
DFVVIKAVEDGVNVIGLTRGLDTKFHHSEKLDKGEVIIAQFTEHTSAIKVRGEALIQTAYGEMKSEKK
>d1c9sa_b.82.5.1 (A:) Trp RNA-binding attenuation protein (TRAP) {Bacillus stearothermophilus}
SDFVVIKALEDGVNVIGLTRGADTRFHSEKLDKGEVIIAQFTEHTSAIKVRGKAYIQT RGVIESEGK
>g1h6w.1 b.108.1.1 (A:,B:) Heat- and protease-stable fragment of the short fibre {Bacteriophage T4}
TGATLNGRGSTTSMRGVVKLTTAGSQSGGDASSALAWNADVIHQRGQTINGTLRINNTLTIASGGANITGT
VNMTGGYIQGKRVVTQNEIDRTIPVGAIMMWADSLPSDAWRFC HGGTVSASDCPLYASRIGTRYGGSSNP
GLPDMRXSLNYIIKVKE
>d1k28a2 b.108.1.2 (A:362-584) Tail-associated lysozyme gp5, C-terminal domain
{Bacteriophage T4}
DPADPPIPNDSRILFKEPVSSYKGEYPVHTMETESGHIQEFDDTPGQERYRLVHPTGTYEVSPSGRRTRKTV
NLYDITNADGNFLVAGDKKTNVGGSEIYYMDNRLHQIDGSNTIFVRGDET KVEGNGTILVKGNVTIIVEGNA
DITVKGDATTLVEGNQNTVNGNLSWKVAGTVWDVGGDWTEKMASMSSI SSGQYTIDGSRIDIGSVDHHH
HHH

>d1qiu2 b.83.1.1 (A:319-395) Adenovirus {Human adenovirus type 2}
VSIKKSSGLNFDNTAIAINAGKGLEDTNTSESPDINPIKTIGSGIDYNENGAMITKLGAGLSFDNSGAITIGNKN
>d1kke2 b.83.1.2 (A:313-455) Reovirus attachment protein sigma 1 {Reovirus}
YRFRQSMWIGIVSYSGSLNWRVQVNNSDIFIVDDYIHICLPAFDGFSIADGGDLSLNFTGLPPLTGDTEPAFH
NDVVVTYGAQTVAILLSSGGAPQYMSKNLWVEQWQDGVLRLRVEGGGSITHSNSKPAMTVSYPRSFT
>d1h8ga_b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}
TDGNWYWFDNSGEMATGWKKIADKWWYFNEEGAMKTGWWKYKDTWYYLDAKEGAMVSNAFIQSADGTG
WYYLKPDGTLADRPEFTVEPDGLITVK
>d1hcxa_b.109.1.1 (A:) Choline binding domain of autolysin C-LytA {Streptococcus pneumoniae}
GSYPKDKFEKINGTWYYFDSSGYMLADRWRKHTDGNWYWFDNSGEMATGWKKIADKWWYFNEEGAMKT
GWVVKYKDTWYYLDAKEGAMVSNAFIQSADGTGWWYLKDGTIADRPEFTVEPDGLITVK
>d1bdo_b.84.1.1 (-) Biotinyl domain of acetyl-CoA carboxylase {Escherichia coli}
EISGHIVRSPMVGTFYRTPSDAAKAFIEVGQKVNVGDTLCIVEAMKMMNQIEADKSGTVKAILVESGQPVEFDE
PLVVIE
>d1dd2a_b.84.1.1 (A:) Biotin carboxyl carrier domain of transcarboxylase (TC 1.3S)
{Propionibacterium freudenreichii, subsp. shermanii}
AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKVLVKERDAVQGGQGL
IKIG
>d1htp_b.84.1.1 (-) Protein H of glycine cleavage system {Pea (Pisum sativum)}
SNVLDGLKYAPSHEWKHEGSVATIGITDHAQDHGEGVVFVELPEPGVSVKGKGFGAVESVKATSVDVNPISG
EVIEVNTGLTGKPGLINSSPYEDGWMIKIKPTSPDELESLLGAKETYTKFCEEEDAAH
>d1lac_b.84.1.1 (-) Ipyol domain of dihydrolipoamide acetyltransferase
{Bacillus stearothermophilus}
AFEFKLPDIGEGIHEGEIVKWFVKPGDEVNEDDVLCLEVQNDKAVVEIPSPVKGKVLIELVPEGTVATVGQLTLD
APGY
>d1iyu_b.84.1.1 (-) Ipyol domain of dihydrolipoamide acetyltransferase
{Azotobacter vinelandii}
SEIIRVPDIGGDGEVIELVKTGDLIEVEQGLVVLESAKASMEVPSPKAGVVKSVSVKLGDKLKEGDAAIELEPAAG
AR
>d1qjoa_b.84.1.1 (A:) Ipyol domain of dihydrolipoamide acetyltransferase
{Escherichia coli}
MVKEVNVPDIGGDEVETVMVKVGDKVAEQSLITVEGDKASMEVPFAGVVKELVNVGDKVKTGSLIM
IFEVEGAA
>d1gjxa_b.84.1.1 (A:) Ipyol domain of dihydrolipoamide acetyltransferase
{Neisseria meningitidis}
ALVELKVPDIGGHENVDIIAVEVNNGDTIAVDDTLITLETDKATMDVPAEVAGVVKEVKVKVGDKISEGGVV
EAEGTA
>d1fyc_b.84.1.1 (-) Ipyol domain of dihydrolipoamide acetyltransferase
{Human (Homo sapiens)}
GSNMSYPPHMQVLLPALSPTMTMGTVQRWEKKVGEKLSEGDLLAEIETDKATIGFEVQEEGYLAKILVPEGTR
DVPLGTPLCIIVEKEADISAFADYRPTEVTDLK
>d1ghk_b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex
{Azotobacter vinelandii}
AIDIKAFTFPESIADGTVATWHKKPGEAVKRDELIVDIETDKVVMEVLAEGDGVIAEIVKNEGDTVLSGELLGKLT

EGG

>d1pmr_ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Escherichia coli}

SSVDILVPDLPEVADATVATWHKKPGDAVRDEVLVEIETDKVVLEVPASADGILDAVLEDEGTTVSRQILGR
REGN

>d1k8ma_ b.84.1.1 (A:) Lipoyl domain of the mitochondrial branched-chain alpha-ketoacid dehydrogenase {Human (Homo sapiens)}

MGQVVQFKLSDIGEGIREVTKEWYVKEGDTVSQFDSICEVQSDKASVTITSRYDGVIKKLYYNLDDIAYVGKPL
VDIETEALKDLE

>d1dv1a1 b.84.2.1 (A:331-446) Biotin carboxylase subunit of acetyl-CoA carboxylase, C-terminal domain {Escherichia coli}

RGHAVECRINAEDPNTFLPSPGKTRFHAPGGFGVRWESHIYAGYTVPYYDSMIGKLICYGENRDVAIARMKN
ALQELIIDGIKTNVDLQIRIMNDENFQHGGTNIHYLEKKLGL

>d1gsoa1 b.84.2.1 (A:328-426) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}

ERASLGVVMAAGGYPGDYRTGDIHGLPLEEVAGGKVFHAGTKLADDEQVVTNGGRVLCVTALGHTVAEAQK
RAYALMTDIHWDDCFCRKDIGHRAIER

>d1b6ra1 b.84.2.1 (A:277-355) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

NNPSVMINLIGSDVNYDWLKLPLVHLHWYDKEVRPGRKVGHNLTDSTSRLTATLEALIPLLPPEYASGVIWAQ
SKFG

>d1eyza1 b.84.2.1 (A:319-392) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

GPAASAVILPQLTSQNVTFDNVQNAVGAQADLQIRLFKPEIDGSRRLGVALATAESVDAIERAKHAAGQVKVQG

>d1hc2_2 b.84.2.2 (168-230) Cytochrome f, small domain {Turnip (Brassica rapa)}
NTVYNATAGGIISKILRKEKGGYEITIVDASNERQVIDIIPRGLELLVSEGESIKLDQPLTSN

>d1e2wa2 b.84.2.2 (A:169-232) Cytochrome f, small domain {Chlamydomonas reinhardtii}

TIYNASAAGKIVAITALSEKKGGFEVSIEKANGEVVVDKIPAGPDLIVKEGQTVQADQPLTNNP

>d1ci3m2 b.84.2.2 (M:170-231) Cytochrome f, small domain {Phormidium laminosum}

AVYNASAAGVITAIKADDGSAEVKIRTEDGTTIVDKIPAGPELIVSEGEEVAAGAALTNNP

>d1gpr_ b.84.3.1 (-) Glucose permease Ila domain, Ila-glc {Bacillus subtilis}

EPLQNEIGEEVFVSPITGEIHPITDVPDQVFSGKMMGDGFAILPSEGIVVSPVRGKILNVFPTKHAIGLQSDGGRE
ILIHFGIDTVSLKGEGFTSFVSEGDRVEPGQKLLEVLDKVNPSLMTPIVFTNLAEGETVSIKASGSVNREQE
DIVKIE

>d2gpr_ b.84.3.1 (-) Glucose permease Ila domain, Ila-glc {Mycoplasma capricolum}

MWFFNKNLKVLAPCDGTIITLDEVEDEVFKERMLGDDGFAINPKSNDHFAPVSGKLVTAFPTKHAFGIQTSGVE
ILLHIGLDTVSLDGNGFESFVTQDQE VNAGDKLTVDLKSVAKKVPISKPIIFTNNGGKTLIEVKMGEVKQGDV
VAILK

>d1glaf_ b.84.3.1 (F:) Glucose-specific factor III (glsIII) {Escherichia coli}

GLFDKLKSLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEKIVGDGIAIKPTGNKMVAPV DGTIGKIFETNHAFS
IESDSGVELFVHFGIDTVELKGEGFKRIAEEGQRVKVGDTVIEFDPLLEEKAKSTLTPVISNMDEIKELIKLSGSV
TVGETPVIRIKK

>d2f3ga_ b.84.3.1 (A:) Glucose-specific factor III (glsIII) {Escherichia coli}

TIEIIAPLSGEIVNIEDVPDVVF AEKIVGDGIAKPTGNKMVAPVDGTIGKIFETNHAFSIESDSGVELFVHFGIDTV
ELKGEGFKRIAEEGQRVKVGDTVIEFDLPLLEEKAKSTLTPVVISNMDEIKELIKLSGSVTVGEPVIRIKK
>d1hg7a_ b.85.1.1 (A:) Type III antifreeze protein {Ocean pout (Macrozoarces americanus), different isoforms}
MNQASVVANQLIPINTALTLVMMRSEVVTPVGIPAEDIPRLVSMIQVNRAVPLGTTLMPDMVKGYAA
>d1ops_ b.85.1.1 (-) Type III antifreeze protein {Ocean pout (Macrozoarces americanus), different isoforms}
SQSVVATQLIPMNTALTPAMMEGKVTPNPIGIPFAEMSQLVKGQVNTPVAKGQTLMPNMVKTYAA
>d1c8aa2 b.85.1.1 (A:69-134) Type III antifreeze protein {Antarctic eel pout (Austrolycichthys brachycephalus) and (Lycodichthys dearborni)}
SPGLKSVVANQLIPINTALTLVMMKAEEVSPKGIPSEEISKLVGMQVNRAVYLDQTLMPDMVKNYE
>d3rdn_ b.85.1.1 (-) Type III antifreeze protein {Antarctic eel pout (Austrolycichthys brachycephalus) and (Lycodichthys dearborni)}
NKASVVANQLIPINTALTLIMMIKAEVVTPMGIPAAEIPNLVGMQVNRAVPLGTTLMPDMVKNYEDGTTSPGLK
>d1c5ea_ b.85.2.1 (A:) Head decoration protein D (gpD, major capsid protein D) {Bacteriophage lambda}
SDPAHTATAPGGLSAKAPAMTPLMLDTSSRKLVADGTTDGA AVGILAVAADQTSTLTIFYKSGTFRYEDVLWP
EAASDETKKRTAFAGTAISIV
>d1ejrb_ b.85.3.1 (B:) Urease, beta-subunit {Klebsiella aerogenes}
MIPGEYHVKGQIALNTGRATCRV VENHGDRPIQVGSHYHFAEVNPALKFDRQQAAGYRLNIPAGTAVRFEP
GQKREVELVAFAGHRAVFGFRGEVMGPL
>d4ubpb_ b.85.3.1 (B:) Urease, beta-subunit {Bacillus pasteurii}
NYIVPGEYRVAEGEIEINAGREKTTIRVSNTGDRPIQVGSHIHFVEVNKE LLFDRAEGIGRRLNIPSGTAARFEP
GEMEVELTELGGNREVFGISDLTNGSVDNKELILQRAKE LGYKGVE
>d1e9ya1 b.85.3.1 (A:106-238) Urease, beta-subunit {Helicobacter pylori}
LVPGELFLKNEDITINEGKKAVSVKVKNVGDRPVQIGSHFFEVNRCLDFDREKTFGKRLDIAAGTAVRFEP
EKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGFHGAKSDDNYVKTIKE
>d1g8la1 b.85.6.1 (A:327-409) Molybdenum cofactor biosynthesis protein MoeA, C-terminal domain {Escherichia coli}
LPARQRVRTASRLKKTPGRLDFQRGV LQRNADGELEVTTGHQGSHIFSSFSLGNCFIVLERDRGNVEVGEW
VEPFNALFG
>d1euwa_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate
nucleotidohydrolase (dUTPase) {Escherichia coli}
MMKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGD TTVPTGLAIHIADPSLAAMMLPRSGLG
HKHGIVLGNL VGLIDSDYQGQLMISVWNRGQDSFTI QPGERIAQMIFVPVVQA EFNLV EDF
>d1f7da_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase
(dUTPase) {Feline immunodeficiency virus}
MIIEGDGILDKRSEDAGYDLLAAKEIHLLPGEVKVIPTGVKLM LPKG YWGLIIGKSSIGSKGLDVLGGVIDEGYR
IGVIMINVSRKSITLMERQKIAQLIILPCKHEVLEQGKV VM
>d1f7ra_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase
(dUTPase) {Feline immunodeficiency virus}
MIIEGDGILDKRSEDAGYDLLAAKEIHLLPGEVKVIPTGVKLM LPKG YWGLIIGKSSIGSKGLDVLGGVIDEGYR
IGVIMINVSRKSITLMERQKIAQLIILPCKHEVLEQGKV VMDSERGDNGYGSTGV
>d1dun_ b.85.4.1 (-) Deoxyuridine 5'-triphosphate nucleotidohydrolase

(dUTPase) {Equine infectious anemia virus}

MLAYQGTQIKEKRDEDAGFDLCVPYDIMIPVSDTKIPTDVKIQVPPNSFGWVTGKSSMAKQGLLINGGIIDEGY
TGEIQVICTNIGKSNIKLIQGKQFAQLIILQHHSNSRQPWDENKI

>d1tul__ b.85.5.1 (-) ACMNPV telokin-like protein {Baculovirus (Autographa californica), nuclear polyhedrosis virus}

GTPDIIVNAQINSEDENVLDFIIEDEYYLKKRGVGAHIKVASSPQLRLYKNAYSTVSCGNYGVLCLNVQNGEYDL
NAIMFNCAEIKLNKGQMLFQTICKWR

>d1at0__ b.86.1.1 (-) Hedgehog {Fruit fly (Drosophila melanogaster)}

CFTPESTALLESGVRKPLGELSIGDRVLSMTANGQAVSEVILFMDRNLEQMQNMFVQLHTDGGAVLTTPAHLV
SVWQPESQKLTFFVADRIEKNQVLVRDVETGELRPQRVVKGSRSGVVAPLTREGTIVNSVAASCYA

>d1dfa1 b.86.1.2 (A:1-180,A:416-454) PI-Scei intein {Baker's yeast (Saccharomyces cerevisiae)}

CFAKGTNVLMADGSIECIENIEVGKVMGKDGRPREVIKLPGRRETMYSVVQKSQHRAHKSDSSREVPELLKFT
CNATHELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELKEVSKSYPISEGPERANELVESYRKASN
KAYFEWTIEARDLSSLGSHVRKATYQTYAXCRGFYFELQELKEDDYYGITLSDDSDHQFLANQVVHN

>d1dq3a1 b.86.1.2 (A:1-128,A:415-454) PI-Pfui intein {Archaeon Pyrococcus furiosus}

CIDGKAKIIFENECEEHHLTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPESKRVVKGVNVIWKYE
LGKDVTKYEIITNKGTKILTSPWHPFFVLPDFKIVEKRADELKEGDIIGGMXGLEVVRHITTNEPRTFYDLTVE
NYQNYLAGENGMIKVHN

>d1am2__ b.86.1.2 (-) GyrA intein {Mycobacterium xenopi}

ASITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDHGPNVLADRLFHSGEHPVYAVRTVEGLRVGTAN
HPLLCLVDVAGVPTLLWKLIDEIKPGDYAVIQRSAFSVDCAGFARGKPEFAPTTYTVGVPGLVRFLEAHHRDPDA
KAIADELTDGRFYAKVASVTDAGVQPVYSLRVDADHAFITNGFVSHN

>d1umua_ b.87.1.1 (A:) UmuD' {Escherichia coli}

DYVEQRIDLNLQQLIQHPSATYFKASGDSMIDGGISDGDLLIVDSAITHGDIVIAAVDGEFTVKKLQLRPTVQLI
PMNSAYSPTISSEDLDVFGVVIHVVK

>d1jhfa2 b.87.1.1 (A:73-198) LexA C-terminal domain {Escherichia coli}

EEGLPLVGRVAADEPLLAQQHIEGHYQVDPSLFKPNAFDLLRVSGMSMKDIGIMGDLLAVHKTQDVRNGQV
VVARIDDEVTVKRLKKQGNKVELLPENSEFKPIVVDLRQQSFTIEGLAVGVIRN

>d1f39a_ b.87.1.1 (A:) lambda repressor C-terminal domain {Bacteriophage lambda virus}

ASASAFWLEVEGNSMTAPTGSKPSFPDGMLILVDPEQAVEPGDFCIARLGGDEFTFKLIRDGQVFLQPLNPQ
YPMIPCNECSVVGKVIASQWPEETFG

>d1b12a_ b.87.1.2 (A:) Type 1 signal peptidase {Escherichia coli}

RSFIYEPFQIPSGSMMPPTLLIGDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDK
VTYDPVSKELTIQPGCSSGQACENALPVTSNVEPSDFVQTFSRRNGGEATSGFFEVPKNETKENGIRLSERKETL
GDVTHRILTVPIAQDQVGMYQQPGQQLATWIVPPGQYFMMGDNRDNSADSRYWGFPEANLVGRATAI
WMSFDKQEWEPTGLRLSRIGGIH

>d1jcha2 b.110.1.1 (A:84-315) Colicin E3 translocation domain {Escherichia coli}

VAAPVAFGFPALSTPGAGGLAVSISAGALSAAIADIMAALKGPFKGLWGVALYGVLPQIAKDDPNMMSKIVT
SLPADDITESPVSSLPLDKATVNVRVDDVKDERQNISVSGVPMSPVVDAKPTERPGVFTASIPGAPVLNI
SVNNSTPAVQTLSPGVTNNTDKDVRAFGTQGGNTRDAIRFPKDSGHNAVYVSVDLSPDQVKQRQDEEN
RRQQEWDATHP

>d1hxra_ b.88.1.1 (A:) RabGEF Ms4 {Rat (Rattus norvegicus)}

ELVSAEGRNRKAVLCQRCGSRVLQPGTALFSRRQLFLPSMRKKPDLVGDGSNPDVDLEEHWLNDMFIFENVG

FTKDVG NVKFLV CADCEIGPIGWHCLDDKNSFYVALERSHE
>d1fwqa_ b.88.1.1 (A:) RabGEF Ms4 {Human (Homo sapiens)}
ELVSAEGRNRKAVLCQRCGSRVLQPGTALFSRRQLFLPSMRKKPALSDGSNPDG DLLQEHWLVEDMFIFENVG
FTKDVG NIKFLV CADCEIGPIGWHCLDDKNSFYVALERSHE
>d1h6qa_ b.88.1.2 (A:) Translationally controlled tumor-associated protein tctp, p23fyp {Fission yeast (Schizosaccharomyces pombe)}
MLLYKDVISGDELVSDAYDLKEVDDIVYEADCQMVTVKQGGDVDIGANPSAEDAEENAEGTETVNNLVYSFR
LSPTSF DKKSYMSYIKGYMKAIKARLQESNPERVPVFEKNAIGFVKKILANFKDYDFYIGESMDPDAMVVL MNY
REDGITPYMIFFKDGLVSEKF
>d3ezma_ b.89.1.1 (A:) Cyanovirin-N {Cyanobacterium (Nostoc ellipsosporum)}
LGKFSQT CYNSAIQGSVLTSTCERTNGGYNTSSIDLNSVIENV DGS LKWQPSNFIETCRNTQLAGSSELAAECKTR
AQQFVSTKINLDDHIANIDGTLKYE
>d1fjra_ b.102.1.1 (A:) Methuselah ectodomain {Fruit fly (Drosophila melanogaster)}
DILECDYFD TVDISAAQKLQNGSYLFEGLLVPAILTGEYDFRILPDDSKQKV ARHIRGC VCKLPCVR FCCPHDHIM
DNGVCYDNMSDEELAELDPFLNVTLDDGSVSR HFKNELIVQWDLPMPCDMFYLDNREEQDKYTLFENG
FFRHFD RVTLKREYCLQH LT FADGNATSIRIAPHNCLIV
>d1lkta_ b.90.1.1 (A:) Head-binding domain of phage P22 tailspike protein {Salmonella bacteriophage P22}
ANVVVSNPRPIFTE RSFKAVANGKIYIGQIDTPVNPANQIPVYIENEDGSHVQITQPLIINAAGKIVYNGQLVKI
VTVGHSMAIYDANGSQVDYIANV LKY
>d1qqha_ b.91.1.1 (A:) E2 regulatory, transactivation domain {Human papillomavirus type 18}
KSKAHKAIE LQMALQGLAQSAYKTEDWTLQDTCEELWNTPE THCFKKGGQTVQVYFDGNKDNCMTYVAWD
SVYYMTDAGTW DKTATCVSHRG LYVKEGYNTFYIEFKSECEKYGNTGTWEVFGNNVDCNDSCMCSTSDDT
VS
>d1dtoa_ b.91.1.1 (A:) E2 regulatory, transactivation domain {Human papillomavirus type 16}
HMETLCQR LNVCQDKILTHYENDSTDLRDHIDYWKHMRLECAI YYKAREMGFKHINHQV VPTLA VSKN KALQ
AIELQLTLETIYNSQYSNEKWT LQDV SLEV YLTAPTGC IKKH GYTVEVQFDG DICNTM HYTNW THIYICEEASVTV
VEGQV DYY GLYY VHEGIR TYFVQFK DDAEKYSKN KVWEV HAGG QVIL CPTS VFS
>d1g8la2 b.103.1.1 (A:7-177) Molybdenum cofactor biosynthesis protein MoeA, N-terminal and linker domains {Escherichia coli}
LMSLD TALNEMLS RVTPLTAQETLPLVQCFG RILASDV SPLDVP GF DNSAMDGYAVRLADIASGQPLPVAGKS
FAGQPYHGEWPAGTCIRIMTGAPVPEGCEAVVMQEQT EQMDNGVRFTA EVRSGQNI RRG EDISAGAVVFP
AGTRLTTAELPVIASLGIAEV PVIRK
>d1k6wa1 b.92.1.2 (A:4-55,A:376-426) Cytosine deaminase {Escherichia coli}
ALQT IINARLPGE EGLWQIHLQDGKISAIDAQSGVMPITENS LDAEQGLVIPXLIILPAENGFDALRRQVPVRY SV
RGGKVI ASTQPAQTTVYLEQPEAIDYKR
>d1ejrc1 b.92.1.1 (C:1002-1129,C:1423-1475) alpha-Subunit of urease {Klebsiella aerogenes}
SNISRQAYADMFGPTVGDKVRLADTELWIEV EDDLT GEEVKG GGVIRDGMGQGQMLAAC CVDLVLTNA
LIVDHWGIVKADIGVKDGRIFAIGKAGNPDIQPNVTIPIGAATEVIAAEGKIVTAGXSIEVGKLADLVW SPAFFG
VKPATVIKGGMIAIAPMGDINASIPTPQPVHYRP
>d4ubpc1 b.92.1.1 (C:1-131,C:435-483) alpha-Subunit of urease {Bacillus pasteurii}
MKINRQQAESYGP TVGDEV RLAD TLWIEV EKDYTTYGDEVNF GGGKVREG MGENG TYTRTEN VL DLLT
NALILDYTG IYKADIGVKDGYIVGIGKGGNP DIMDG VTPNMIV GTATEVIAAEGKIVTAXLVLWEPKFFGVKADR
VIKGGIIAYAQIGDPSASIPTPQPV MGRR MYGTV

>d1e9yb1 b.92.1.1 (B:1-131,B:432-480) alpha-Subunit of urease {Helicobacter pylori}
MKKISRKEYVSMYGPPTGDKVRLGDTDLIAEVEHDYIYGEELKFGGGKTLREGMSQSNNPSKEELDLIITNALIV
DYTGIKYADIGIKDGKIAGIGKGGNKDMQDGVKNNLSVGPATEALAGEGLIVTAGXADLVLWSPAFFGVKPNMI
IKGGFIALSQMGDANASIPTPQPVYYREMFA

>d1aqt_2 b.93.1.1 (2-86) Epsilon subunit of F1F0-ATP synthase N-terminal domain {Escherichia coli}
STYHLDVVSAEQQMFSGLVEKIQVTGSEGELGIYPGHAPLLTAIKPGMIRIVQHGHEEFIYLSGGILEVQPGNVT
VLADTAIRG

>d1e79h2 b.93.1.1 (H:15-100) Epsilon subunit of F1F0-ATP synthase N-terminal domain {Cow (Bos taurus)}
QMSFTFASPTQVFNSANVRQDVPTQTGAFGILAAHVPTLQVLRPGLVVHAEDGTTSKYFVSSGSVTVNAD
SSVQLLAEAVTL

>d1hhna_ b.104.1.1 (A:) Calreticulin {Rat (Rattus norvegicus)}
SKKIKDPDAAKPEDWDERAKIDDPTDSKPEDWDKPEHIPDPDAKKPEDWDEEMDGEWEPPVIQNPEYKGE
WKPRQIDNPDYKGTVIHPEDIQNPEYSPDANI

>d1jhna3 b.104.1.1 (A:270-411) Calnexin {Dog (Canis familiaris)}
PVNPSREIEDPEDQKPEDWDERPKIPDPDAVKPDDWNEDAPAKIPDEEATKPDGWLDDEPEYVPDPDAEKPE
DWDEDMDGEWEAPQIANPKCESAPGCGVWQRPMIDNPNEYKGKWKPPMIDNPNEYQGIWKPRKIPNPDFFE
D

>d1tph1_ c.1.1.1 (1:) Triosephosphate isomerase {Chicken (Gallus gallus)}
RKFFVGGNWKMNGDKSLGELIHTLNGAKLSADTEVVCAGPSIYLDFAHQKLDKIGVAACQNCYKVPKGAF TG
EISPAMIKDIGAAWVILGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKLDEREAGITEKVVFEQT KAIAD
NVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKTHVSDAVAQSTRIYGGSVTGGNC KELASQH
DVDGFLVGGASLKPEFVDIINAKH

>d1htia_ c.1.1.1 (A:) Triosephosphate isomerase {Human (Homo sapiens)}
APSRKFFVGGNWKMNGRKQSLGELIGTLNAAKVPADTEVVCAPPTAYIDFARQKLDKIAVAAQNCYKVTNGA
FTGEISPGMIKDCGATWVVLGHSERRHVFGESDELIGQKVAHALAEGLGVIACIGEKLDEREAGITEKVVFEQT K
VIADNVKDWSKVVLAYEPVWAIGTGKTATPQQAQEVHEKLRGWLKSNVSDAVAQSTRIYGGSVT GATCKELA
SQPDVDGFLVGGASLKPEFVDIINAKQ

>d1i45a_ c.1.1.1 (A:) Triosephosphate isomerase {Baker's yeast (Saccharomyces cerevisiae)}
ARTFFVGGNFNLNGSKQSIKEIVERLNTASIPENVEVICPPATYLDYSVSLVKKPQVTVGAQNAYLKASGAFTGE
NSVDQIKDVGAKYVILGHSERRSYFHEDDKFIADKTFALGQGVGVILCIGETLEEKKAGKTL DVVERQLNAVLEE
VKDFTNVV VAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSKIGADVAGELRILYGGSVNGKNARTLYQQRDVN
GFLVGGASLKPEFVDIINSRN

>d1ttj_ c.1.1.1 (-) Triosephosphate isomerase {Trypanosoma brucei}
SKPQPIAAANWKCNGSQSLSELIDL FNSTSINHDVQCVVASTSSH LAMTKERLSHPKFVIAAQNAGNADALA
SLKDFGVNIVLGH SERRYYGETNEIVADK VAAVASGF MVIA CIGETLQERESGR TAVVLTQIAAIAKKLKA
DWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSKIGADVAGELRILYGGSVNGKNARTLYQQRDVN
GFLVGGASLKPEFVDI IKATQ

>d5tima_ c.1.1.1 (A:) Triosephosphate isomerase {Trypanosoma brucei}
SKPQPIAAANWKCNGSQSLSELIDL FNSTSINHDVQCVVASTF VH LAMTKERLSHPKFVIAAQN AIAKSGAFT
GEVSLPILKDFGVNIVLGH SERRYYGETNEIVADK VAAVASGF MVIA CIGETLQERESGR TAVVLTQIAAI
KKLKKADWAKVVIAYEPVWAIGTGKVATPQQAQEAHALIRSWVSSKIGADVAGELRILYGGSVNGKNARTLYQ

QRDVNGFLVGGASLKPEFVDIHKATQ

>d1tcda_ c.1.1.1 (A:) Triosephosphate isomerase {Trypanosoma cruzi}

KPQPIAAANWKCNGSESLLVPLIETLNAATFDHDVQCVVAPTFLHIPMTKARLTNPKFQIAAQNAITRSGAFTGE
VSLQILKDYGISWVLGHSERLYYGETNEIVAEKVAQACAAGFHIVCVGETNEEREAGRATAVLTQLAAVAQ
KLSKEAWSRVVIAYEPVWAIGTKVATPQQAQEVHELLRRWVRSKLGTDIAAQLRILYGGSVTAKNARTLYQMR
DINGFLVGGASLKPEFVEIIEATK

>d1ydfa_ c.1.1.1 (A:) Triosephosphate isomerase {Plasmodium falciparum}

RKYFVAANWKCNGTLESIKSLTSFNNLDPSKLDVVVFPPSVHYDHTRKLLQSKFSTGIQNVSKFGNGSYTGE
VSAEIAKDLNIEYVIIGHFERRKYFRETDEDVREKLQASLKNNLKAVVCFGESLEQREQNKTIEVITKQVKAFVDLI
DNFDNVILVYEPVWAIGTKTATPEQAQLVHKEIRKIVKDTCEKQANQIRILYGGSVNTENCSSLIQQEDIDGFL
VGNASLKESFVDIHKSAM

>d1amk_ c.1.1.1 (-) Triosephosphate isomerase {Leishmania mexicana}

SAKPQPIAAANWKCNGTTASIEKLVQVFNEHTISHDVCVAPTFVHIPLVQAKLRLNPKVISAENAIAKSGAFT
GEVSMPILKDIGVHWVILGHSERRTYYGETDEIVAQKVSEACKQGFMVIACIGETLQQREANQTAKVVLSQLTSAI
AAKLTDAWNQVVLAYEPVWAIGTKVATPQQAQEVHLLRKWVSENIGTDVAAKLRILYGGSVNAANAATLY
AKPDINGFLVGGASLKPEFRDIIDATR

>d1trea_ c.1.1.1 (A:) Triosephosphate isomerase {Escherichia coli}

MRHPLVMGNWKLNNSRHMVHELVSRLKELAGVAGCAVIAIPPEMYIDMAKREAEGSHIMLGAQNVNLNL
SGAFTGETSAAMLKDIGAQYIIGHSERRTYHKSDELIAKKFAVLKEQGLTPVLCIGETEAENEAGKTEEVCARQI
DAVLKTQGAAAFEGAVIAYEPVWAIGTKSATPAQAAQAVHKFIRDHIAKVDANIAEQVIIQYGGSVNASNAEL
FAQPDIDGALVGGASLKADAFAVIVKAAEAAKQA

>d2btma_ c.1.1.1 (A:) Triosephosphate isomerase {Bacillus stearothermophilus}

RKPIIAGNWKMNGTLAEAVQFVEDVKGHVPPADEVISVVCAPFLDRLVQAADGTDLKIGAQTMHFADQGA
YTGEVSPVMLKDLGVTVYLGHSERRQMAETDETVNKKVLAATRGLIPIICCGESLEEREAGQTNAVVASQVE
KALAGLTPEQVKQAVIAYEPIWAIGTKSSTPEDANSVCGHIRSVSRLFGPEAAEAIRIQYGGSVKPDNIRDFA
QQQIDGALVGGASLEPASFQLQLVEAGRH

>d1aw1a_ c.1.1.1 (A:) Triosephosphate isomerase {Vibrio marinus}

RHPVVMGNWKLNNSKEMVVDDLLNGLNAELEGVTGVDVAVAPPALFDLAERTLTEAGSAIILGAQNTDLNN
GAFTGDMSPAMLKEFGATHIIGHSERREYHAESDEFVAKKFAFLKENGTPVLCIGESDAQNEAGETMAVCAR
QLDAVINTQGVEALEGAIAYEPIWAIGTKAATAEDAQRIHAQIRAHIAEKSEAVAKNVVIQYGGSVKPNAAA
YFAQPDIDGALVGGAAALDAKSFAAIAKAAAEEAKA

>d1b9ba_ c.1.1.1 (A:) Triosephosphate isomerase {Thermotoga maritima}

TRKLILAGNWKMHTISEAKKFVSLVNELHDVKEFEIVVCPPFTALSEVGEILSGRNKLGQAQNVFYEDQGAFTG
EISPLMLQEIGVEYVIVGHSERRRIFKEDDEFINRKVKAVLEKGMTPILCVGTELEEREGLTCVVEKQVREGFYG
LDKEEKRVVIAYEPVWAIGTRVATPQQAQEVHAFIRKLSEMYDEETAGSIRILYGGSIKPDNFLGLIVQKDID
GGLVGGASLKESFIELARIMRGV

>d1hg3a_ c.1.1.1 (A:) Triosephosphate isomerase {Archaeon Pyrococcus woesei}

AKLKEPIIAINFKTYIEATGKRALEIAKAAEKVYKETGTVIVVAPQLVDRMIAESVEIPVFAQHIDPIKPGSHTGHVL
PEAVKEAGAVGTLLNHSENRMILADLEAIRRAEEVGLMTVCNNPAVSAAVAALNPDYVAVEPPELIGTGIP
VSKAKPEVITNTVELVKKVNPEVKVLCGAGISTGEDVKKIAELGTVGVLLASGVTAKDPEKAIWDLVSGI

>d1qo2a_ c.1.2.1 (A:) Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
isomerase HisA {Thermotoga maritima}

MLVVAIDLFRGKVARMIKGRKENTIFYEKDPVELVEKLIEEGFTLIHVVDLSNAIENSGENLPVLEKLSEFAEHIQI
GGGIRSLDYAEKLRKLGYRRQIVSSKVLEDPSFLKSLREIDVEPVFSLDTRGGRAFKGWLAEEEIDPVSLKRLKEY

GLEEIVHTEIEKDGTIQLQEHDFSLTKKIAIEAEVKVLAAGGISSENSLKTAKVHTETNLLGVIVGRAFLEGILTVE
VMKRYAR

>d1thfd_ c.1.2.1 (D:) Cyclase subunit (or domain) of
imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}

MLAKRIACLDVKDGRVVKGNSNFENLRDSDGPVELGKFYSEIGIDELVFLDITASVEKRKTMLELVEKVAEQIDIPF
TVGGGIHDFETASELILRGADKVSINTAAVENPSLITQIAQTFGSQAVVVAIDAKRVDGEFMVFVFTYSGKKNTGILL
RDWVVEVEKRGAGEILLTSIDRGTKSGYDTEMIRFVRPLTLPIIASGGAGKMEHFLEAFLAGADAALAASFH
FREIDVRELKEYLKKHGVNVRLEGL

>d1jvna1 c.1.2.1 (A:230-552) Cyclase subunit (or domain) of
imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}

DYSNYGLTRRIIACLDVRTNDQGDLVVTKGDQYDVREKSDGKGVRLNLKPVQLAQKYYQQGADEVTFLNITSFR
DCPLKDTPMLEVLKQAAKTVFVPLTVGGGIKDIVDVGDKIPALEVASLYFRSGADKVSIGTDAVYAAEKYYELGN
RGDGTSPIETISKAYGAQAVVISVDPKRVVNSQADTKNKVFETEYPGPNGEKYCWCYQCTIKGGRESRDLGVW
ELTRACEALGAGEILLNCIDKDGNSNGYDLELIEHVKDAVKIPVIASSGAGVPEHFEAFLKTRADACLGAGMFHR
GEFTVNDVKEYLLEHGLKVRMDEE

>d1h5ya_ c.1.2.1 (A:) Cyclase subunit (or domain) of
imidazoleglycerolphosphate synthase HisF {Archaeon Pyrobaculum aerophilum}
HMALRIIPCLIDGGAKVVVKGVNFQGIREVGDPVEMAVRYEEGADEIAILDITAAPEGRATFIDSVKRVAEAV
SIPVLVGGGVRSLEDATTLFragADKVSNTAAVRNPQLVALLAREFGSQSTVVAIDAKWNGEYYEVVKGGRE
ATGLDAVKWAKEVEELGAGEILLTSIDRGDTGLGYDVELIRRVADSVRIPVIASGGAGRVEHFYEAAGADAVL
AASLFHFRVLSIAQVKRYLKERGVREVRI

>d1rpxa_ c.1.2.2 (A:) D-ribulose-5-phosphate 3-epimerase {Potato (Solanum tuberosum)}
SRVDKFSKSDIIVSPSILSANFSKLGSEQVKAIEQAGCDWIHDVMDGRFVPNITIGPLVVDLRLPITDPLDVHLM
IVEPDQRVPDFIKAGADIVSVHCEQSSTIHLHRTINQIKSLGAKAGVVLNPGLTAIEYVLDAVDLVIMSVNPGF
GGQSFIESQVKKISDLRKICAERGLNPWIEVDGGVGPKNAYKVIEAGANALVAGSAVFGAPDYAEAIKGKITSKR
PE

>d1dbta_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Bacillus subtilis}

MKNNLPIIALDFASAETLAFLAPFQQEPLFKVGMELFYQEGPSIVKQLKERNCELFLDLKLHDIPPTVNKAMK
RLASLGVDLVNVHAAGGKKMMQAALEGLEEGTPAGKKRPSLIAVTQLTSEQIMKDELLIEKSLIDTVVHYSKQ
AEEGLDGVVCSVHEAKAIYQAVSPSFLTVPGIRMSEDAANDQVRVATPAIREKGSSAIVVGRSITKAEDPVK
AYKAVRLEWEGL

>d1eixa_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Escherichia coli}

VTNSPVVVALDYHNRDDALAFVDKIDPRDCRLKVGKEMFTLFGPQFVRELQQRGFDIFFLDKFHDIPNTAAHA
VAAAADLGWVMVNVHASGGARMMTAAREALVPGKDAPLLIAVTVLTSMEASDLVDMTLSPADYAERLA
ALTQKCGLDGVVCSAQEAVERFKQVFGQEFKLVTGIRPQGSEAGDQRIMTPEQALSAGVDYMVIGRPVTQSV
DPAQTLKAINASLQ

>d1dvja_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Archaeon Methanobacterium thermoautotrophicum}

MDVMNRLILAMDLMNRDDALRVTGEVREYIDTVKIGYPLVSEGMDIIAEFRKRGCRRIADFKVADIPETNEKI
CRATFKAGADAIIVHGFPGADSVRACLNAEEMGREVFLLTEMSPGAEMFIQGAADEIARMGVDLGVKNVY
GPSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSIYLADNPAAAAGIIESIKDLLIPEDPAA

NKARKEAELAAATA

>d1dvjb_c.1.2.3 (B:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Archaeon Methanobacterium thermoautotrophicum}

RLILAMDLMNRDDALRTGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRGCRRIADFKVADIPETNEKICRATFKA
GADAIIVHGFPGADSVRACLNVAEEMGREVFLTEMISHPGAEMFIQGAADEIARMGVDLGVKNYVGSTRPE
RLSRLREIIGQDSFLISPGVGAQGGDPGETLRFADAIIVGRSIYLADNPAAAAGIIESIKD

>d1dqwa_c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Baker's yeast (*Saccharomyces cerevisiae*)}

MHKATYKERAATHPSPVAAKLFNIMHEKQTNLCASLDVRTTKELLELVEALGPKICLLKTHVDILDFSMEGTVKP
LKALSAKYNFLLFEDRKFADIGNTVKLQYSAGVYRIAEWADITNAHGVVGPGIVSGLKQAAEEVTKEPRGLLMLA
ELSCKGSLSTGEYTKGTVDIAKSDKDFVIGFIAQRDMGGRDEGYDWLIMTPGVGLDDKGDALGQQYRTVDDV
VSTGSDIIIVGRGLFAKGRDAKVEGERYRKAGWEAYLRCGQQD

>d1pii_2 c.1.2.4 (255-452) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Escherichia coli}
GENKVCGLTRGQDAKAAYDAGAIYGGLIFVATSPRCVNVEQAQEVMAAAPLQYVGVRNHDIADVVDKAKVL
SЛАAVQLHGNEEQLYIDLREALPAHVAIWKALSVGETLPAREFQHVVKYVLDNGQGGSGQRFDWSLLNGQSL
GNVLLAGGLGADNCVEAAQTGCAGLDFNSAVESQPGIKDARLLASVFQTLRAY

>d1nsj_c.1.2.4 (-) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Thermotoga maritima}
MVRVKICGITNLEDALFSVESGADAVGFVFYPKSKRYISPEDARRISVELPPFVFRGVVFVNEEPEKILDVASYVQL
NAVQLHGEPIELCRKIAERILVIKAVGVSNERDMERALNYREFPILLDTKTPYGGSGKTFDWSLILPYRDRFRYL
VLSGGLNPNENVRSAIDVVRPFADVVSSGVEAFPGKKDHDSIKMFNIKNAKGL

>d1pii_1 c.1.2.4 (1-254) Indole-3-glycerophosphate synthase, IPGS {Escherichia coli}
MQTVLAKIVADKAIWVEARKQQQPLASFQNEVQPSTRHFYDALQGARTAFILECKKASPSKGVIRDDFDPARIA
AIYKHYASAISVLTDEKFQGSFNFLPIVSQIAPQPILCDFIIDPYQIYLARYYQADACLLMLSVLDDDQYRQLAAV
AHSLEMGVLTEVSNEEQERAIALGAKVVGINNRDLRDLSIDLNRTRELAPKLGHNVTVISESGINTYAQVRELS
HFANGFLIGSALMAHDDLHAAVRRVLL

>d1a53_c.1.2.4 (-) Indole-3-glycerophosphate synthase, IPGS {Archaeon *Sulfolobus solfataricus*}
PRYLGWLKDVVQLSLRPSFRASRQRPIISLNERILEFNKRNTAIIAEYKRKSPLSGLDVERDPIEYSKFMERYAVG
LSILTEEKYFNGSYETLRKIASSVSIPILMKDFIVKESQIDDAYNLGADTVLLIVKILTERELESLEYARSYGMEPLIEIN
DENDLDIALRIGARFIGINSRDLETLEINKENQRKLISMIPSNVVKVAESGISERNEIEELRKLGVNAFLIGSSLMRN
PEKIKEFIL

>d1qopa_c.1.2.4 (A:) Trp synthase alpha-subunit {Salmonella typhimurium}
MERYENLFAQLNDRREGAFVPFVTLGDPGIEQSLKIIDLADAGADALELGVPFSDPLADGPTIQNANLRAFAAG
VTPAQCFEMLAIIREKHPTIPIGLLMYANLVNNNGIDAFYARCEQVGVDSDLVADVPVEESAPFRQAALRHNIAPI
FICPPNADDLLRQVASYGRGYTYLLSRSGVTGAENRGALPLHHIEKLKEYHAAPALQGFGISSPEQVSAAVRA
GAAGAISGSAIVKIIKNLASPKQMLAELRSFVSAMKAASR

>d1geqa_c.1.2.4 (A:) Trp synthase alpha-subunit {Archaeon *Pyrococcus furiosus*}
MFKDGSILPYLTAGDPDKQSTLNFLALDEYAGAIELGIPFSUPIADGKTIQESHYRALNGFKLREAFWIVKEFRR
HSSTPIVLMTYYNPIYRAGVRNFLAEAKASGVDGILVVDLPVFHAKEFTIAREEGIKTVFLAAPNTPDERLKVID
DMTTGFVYLVSLYGGTGTGAREEIPKTAYDLLRRAKRICRNCVAVGFGVSKREHVVSLKEGANGVVVGSAVLKIIGE
KGCREATEFLKKKVEELLGI

>d2tpsa_c.1.3.1 (A:) Thiamin phosphate synthase {Bacillus subtilis}
HGIRMTRISREMMKELLSVYFIMGSNNTKADPVTVVQKALKGGATLYQFREKGGDALTGEARIKFAEKAQAAC
REAGVPIVNDVELALNLKADGIHIGQEDANAKEVRAAIGDMILGVSAHTMSEVKQAEEDGADYVGLGPIYP

TETKKDTRAVQGVSLIEAVRRQGISIPIVGIGGITIDNAAPVIQAGADGVSMISAISQAEDPESAARKFREEIQTYK
TGR

>d1ho1a_ c.1.24.1 (A:) Pyridoxine 5'-phosphate synthase {Escherichia coli}

AELLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHTDRDVRILRQTLDRMNLEMAV
TEEMLAIAVETKPHFCCLVPEKRQEVTEGGLDVAGQRDKMRDACKRLADAGIQVSLFIDAEEQIKAAAEGV
APFIEIHTGCYADAKTDAEQAQELARIAKAATFAASLGLKVAGHGLTYHNVKAIAAIPMHELNIGHAIGRAV
MTGLKDAVAEMKRLMLEARG

>d2dora_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme A}

MNNTTFANAKFANPFMNASGVHCMTIEDLEELKASQAGAYITKSSTLEKREGNPLPRYVDLELGSINSMGLPNL
GFDYYLDYVLKNQKENAQEGPIFFSIAGMSAAENIAMKKIQESDFSGITENLSCPVPKGPKQLAYDFEATEKLL
KEVFTFTKPLGVKLPPYFDLVHDIMAEILNQFPLTYVNSVNSIGNGLFIDPEAESVVKPKDGFGGIGGAYIKPT
ALANVRAFYTRLKPEIQIIGTGGIETGQDAFEHLLCGATMLQIGTALHKEGPAIFDRIIKELEEIMNQKGYQSIADF
HGKLKSL

>d1ep3a_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme B}

MTENNRLSVKLPGLDLKNPIIPASGCFGGEYYAKYDNLKGSIMVKATTLHPRFGNPTPRVAETASGMLNAIG
LQNPGLEVIMTEKLPWLNNENFPELPIIANVAGSEEADYVAVCAKIGDAANVKAIELNISCNVKHGGQAFGTDP
EVAAALVKACKAVSKVPLYVKLSPNVTDIVPIAKAVEAAGADGLTMINTLMGVRFDLKTRQPILANITGGLSGPAI
KPVALKLIHQVAQDVDIPIIGMGGVANAQDVLEMAGASAVAVGTANFADPFVCPKIIDLKPELMDQYRIESL
ESLIQEVEKGKK

>d1d3ga_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Human (Homo sapiens)}

MATGDERFYAEHLMPTLQGLDPESAHRЛАVРFTSLGLLPRARFQDSDMLEVРVLGHKFRNPVGIAAGFDKHG
EAVDGLYKMGFGFVEIGSVTPKPQEGNPRPRVFRLPEDQAVINRYGFNSHGLSVEHRLRARQQKQAKLTEDG
LPLGVNLGKNKTSVDAE DYAEGVRLGPLADYLVVNVSSPNTAGLRSLQGKAELRRLITKVLQERDGLRRVHR
PAVLVKIAPDLTSQDKEDIASVVKELGIDGLIVTTVSRPAGLQGALRSETGGLSGKPLRDLSTQTIREMYALTQG
RVPIIGVGGVSSGQDALEKIRAGASLVQLYTALTFWGPPVVGKVKRELEALLKEQGF GGVTDAIGADHRR

>d1oyb_ c.1.4.1 (-) Old yellow enzyme (OYE) {Brewer's yeast (Saccharomyces carlsbergensis)}

SFVKDFKPQALGDTNLFKPIKIGNNELLHRAV ррLTMRAЛHPGNIPNRDWAVEYYTQRAQRPGTMITEGAIFI
SPQAGGYDNAPGVWSEEQMVEWTKIFNAIHEKSFVWVQLWVLGWAAPDNLARDGLRYDSASDNVFMD
AEQEAKAKKANNPQHSLTKDEIKQYIKEYVQAAKNSIAAGADGVEIHSANGYLLNQFLDPHSNTRTDEYGGSIE
NRARFTLEVVDALVEAIGHEKVLRLSPYGVFNSMSGGAETGIVAQYAYVAGELEKRAKAGKRLAFVHLVEPRVT
NPFLTEGEYEYEGGSNDVFVSIWKGПVIRAGNFALHPEVREEVKDKRTLIGYGRFFISNPDLVDRLEKGLPLNKY
DRDTFYQMSAHGYIDYPTYEEALKLGWDKK

>d1icpa_ c.1.4.1 (A:) 12-oxophytodienoate reductase 1 (OYE homolog) {Tomato (Lycopersicon esculentum)}

QVDKIPLMSPCKMGKFELCHRVLAPLTRQRSYGYIPQPHAILHYSQRSTNGLLIGEATVISETGIGYKDVPGIW
TKEQVEAWKPIVDAVHAKGGIFFCQIWHVGRVSNKDFQPNGEDPISCTDRGLTPQIMSGNIDIAHFRPRRLTT
DEIPQIVNEFRVAARNAIEAGFDGVEIHGAHGYLIDQFMKDQVNDRSDKYGGSLENRCFALEIVEAVANEIGS
DRVGIRISPFAHYNEAGDTNPTALGLYMVESLNKYDLAYCHVVEPRMKTAWEKICTESLPMRKAYKGTIVAG
GYDREDGNRALIEDRADLVAYGRLFISNPDLPKRFELNAPLNKYNRDTFYTSDPIVGYTDYPFLE

>d1gox_ c.1.4.1 (-) Glycolate oxidase {Spinach (Spinacia oleracea)}

MEITNVNEYAIAKQKLPKMVYDYYASGAEDQWTLAENRNAFSRILFRPRILIDVTNIDMTTILGFKISMPIMIA
PTAMQKMAHPEGEYATARAASAAGTIMTLSWATSSVEEASTGPGIRFFQLYVYKDRNVVAQLVRAERAGF
KAIALTVDTPLGRREADIKNRFVLPPFLTKNFEGIDLGKMDKANDSGLSSYVAGQIDRSLSWKDVWLQITSL

PILVKGVITAEDARLAVQHGAAGIIVSNH GARQLDYVPATIMALEEVVKAAQGRIPVFLDGGVRRGTDVF KALAL
GAAGVFIGRPVVFS LAAEGEAGVKVLQMMRDEFELTMALSGCRSLKEISRSHIAADWD

>d1huva_ c.1.4.1 (A:) Membrane-associated (S)-mandelate dehydrogenase
{*Pseudomonas putida*}

NLFNVEDYRKLAQKRLPKMVYDYLEGGADEYEYGVKHNRDVFQQWRFKP KRLVDVSRRSLQAEVLGKRQSMP
LLIGPTGLNGALWPKGDLALARATKAGIPFVLSTASNMSIEDLARQCDGDLWFQLYVIHREIAQGMVLKALHT
GYTTLVTTDVAVNGYRERDLHNRFKIPPFTLKNFEGIDL GKM DKA NLEMQA ALMSR QMDASFNWEALRWL
RDLWPHKLLVKGLLSAEDADRCIAEGADGVILSNHGRQLDC AISPMEV LAQSVAKTGKPV LIDSGFRRGSDIV
KALALGAEAVLGRATL GLAARG ETV D E V L T L K A D I D R T L A Q I G C P D I T S L S P D Y L Q N E

>d1h61a_ c.1.4.1 (A:) Pentaerythritol tetranirate reductase {Enterobacter cloacae}
SAEKLFTPLKVGAVTAPNRVFMAPLRLSIEPGDIPTPLMGEYYRQRASAGLI SEATQISAQAKGYAGAPGLHS
PEQIAAWKKITAGVHAEDGRIA VQLWHTGRISHSSIQPGGQAPVSASALNANTRTSLRDENGNAIRVDTTTPR
ALELDEIPGIVNDFRQAVANAREAGFDLVELHSAHGYLLHQFLSPSSNQRTDQYGGSVENRARLVLEVDAVCN
EWSADRIGIRVSPIGTFQNVDNGPNEEADALYLIEELAKRGIA YLHMSETDLAGGKP YSEAFRQKV RERFHGVII
GAGAYTAEKAEDLIGKGLIDAVA FGRDYIANPDLVARLQKKAELNPQRPESFYGGGAEGYTDYPSL

>d1djna1 c.1.4.1 (A:1-340) Trimethylamine dehydrogenase, N-terminal domain {Methylophilus methylotrophus, w3a1}

ARDPKHDILFEPIQIGPKTLRNRFYQVPHCIGAGSDKPGFQSAHRSVKAEGGWAA NLTEYCSINPESDDTHR LS
ARIWDEGDVRNLKAMTDEVHKY GALAGVELWYGGAHAPNMESRATPRG PSQYASEFETLSYCKEMDLS DIA
QVQQFYVDAAKRSRDAGFDIVVYGAHSYLPQLNPYNNKRTDKYGG SLENRARFWLETLEKVKHAVGSDCA
IATRGVDTVYGPQIEAEVDGQKFVEMADSLVDMWDITIGDIAEWGEDAGPSRFYQQGHTIPWVKLVKQVS
KKPVLGVGRYTDPEK MIEVT KGYADIIGCARPSIADPFLPKVEQGRYD

>d1ltda1 c.1.4.1 (A:98-511) Flavocytochrome b2, C-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}

APGETKEDIARKEQLSLLPPLDNIIINLYDFEYLASQTLTKQAWAYSSGANDEVTHRENHNAYHRIFFKPKILVDV
RKVDISTDMLGSHVDVPFYVSATALCKLGNPLEGEKD VARGCGQGVTKVPQMISTLASC SPEEEIAAPSDKQIQ
WYQLYVNSDRKITDDL VKNVEKLGVKALFVTVDAPS LGQREKDMKLKSNTKAGPKAMKKTNVEESQGASRA
LSKFIDPSLTWKDIEELKKKTLP I VIKGVQ RTEDV KAAEIGVSGVVL SNHGRQLDFSRAPIEVLAETMPILEQR
NLKDKLEVFDGGVRRGTDVLKALCLGAKGVGLGRPFLYANSCYGRNGVEKAIEILRDEIEMSMRLLGVT SIAEL
KPDLLLSTLKARTVGVPNDVLYNEVYEGPTLTFEDA

>d1h7wa2 c.1.4.1 (A:533-844) Dihydropyrimidine dehydrogenase, domain 4 {Pig (*Sus scrofa*)}
ISVEMAGLKFINPFGLASAAPTSSSMIRRAFEAGWGFA LKTFSLDKDIVNVSPRIVRGTTSGPMYGPQ QSSF
LNIELISEKTAAYWCQSVTELKADFPDNIVIASIMCSYNKNDWMELSRKAEASGADALENLSCP HGMGERGM
GLACGQDP E LVRNICRW VRQAVQIPFFAKLTPNVT DIVSIARA AKEGGADGV TATNTV SGLMGLKADGTPWPA
VGAGKRTTYGGVSGTAIRPIALRAVTTIARALPGFPILATGGIDSAESGLQFLHSGASVLQVCSAVQNQDFTVI QD
YCTGLKALLYLKSIE

>d1ea0a2 c.1.4.1 (A:423-1193) Alpha subunit of glutamate synthase, central and FMN domains
{*Azospirillum brasilense*}

TTHLDELVKTASLKGEPSMDKAELRRQQAFGLTMEDMELILHPMVEDGKEIGSMGDDSPIAVLSDKYRGL
HHFFRQNFSQVTNPPIDS LRERRVMSLKTRLGNLGNILDEDETQTRLLQLES PVLTAEFRAMRDYMGDTAAEI
DATFPVDGGPEALRRI RQETEDAVRGGATHVILTDEAMGPARA AIPAILTGAVH THLIRS NLRTFTSLNVR
TAEGLDTHYFAVLIGV GATTVNAYLAQEAI AERHRRGLFGSMPLEKG MANYKKAIDDGLLKIMSKMGISVISSYR
GGGNFEAIGLSRALVAEHFPAMVSRISGIGLNGI QKKVLEQHATAYNEEVVALPVGGFYRFRKSGDRHGWE GG
VIHTLQQAVTNDSYTFKKYSEQVNKRPPMQLDLLELRSTKAPVPVDEVESITAIRKRFITPGMSMGALSPEAH

GTLNVAMNRIGAKSDSGEGGEDPARFRPDKNGDNWNSAIKVASGRFGVTAEYLNQCRELEIKVAQGAKPGE
GGQLPGFKVTEMIARLRHSTPGVMLISPPPHDIYSIEDLAQLIYDLQINPDAKTVKLVSRSIGTIAAGVAKA
NADIILISGNSGGTGASPQTTSIKFAGLPWEMGLSEVHQVLTLRHRVRLRTDGLKTGRDIVIAAMLGAEFF
GIGTASLIAMGCIMVRQCHSNTCPVGCVQDDKLQRKFVGTPEKVNLFVLAEEVREILAGLFRSLNEVIGRT
DLLHQVSRGAEHLDLDPRLAQVDPG

>d1eepa_c.1.5.1 (A:) Inosine monophosphate dehydrogenase (IMPDH) {Lyme disease spirochete (Borrelia burgdorferi)}

NKITKEALTFDDVSLIPRKSSVLPSEVSLKTQLTKNISLNIPFLSSAMDTVTESQMAIAIAKEGGIGIIHKNMSIEAQ
RKEIEKVKTYKFQKTINTNGDTNEQKPEIFTAKQHLEKSDAYKNAEHKEDFPNACKDLNNKLRVGAAVSIDITIE
RVEELVKAHV DILVIDSAHG HSTRIIELIKKIKTYPNLDL IAGNIVTKEAALDLISVGADCLKV GIGPGSIC TTRIVAG
VGVPQITAICDVYEACNNTN CIIADGGIRFS GDVVKAIAAGADSV MIGNLFAGT KESPSEEI YNGKKFKSYVGM
GSISAMKRGSKSRYFQLENNEPKKLVPEGIEGMVPSGKLKDILTQLKGGLMSGMGYLGAATISDLKINSKFVKIS
HS

>d1zfja1 c.1.5.1 (A:2-94,A:221-492) Inosine monophosphate dehydrogenase (IMPDH) {Streptococcus pyogenes}

SNWDTKFLKKGYTFDDVLLIPAESHVLPNEVDLTKLADNLTLNIPITTAAMDTVTGSKMAIAIA RAGGLGVIHKN
MSITEQAEEVRKVKRSEXGRLLVAAAVGVTSDTFERAEALFEAGADAVIDTAHGH SAGVLRKIAEIRAHFPNRTL
IAGNIATAEGARALYDAGDVVKVGIGPGSICTRVVAGVGPQVTAIYDAAAVAREYGTIIADGGIKYSGDIVK
ALAAGGNAVMGSMFAGTDEAPGETEIYQGRKYKTYRGMGSIAAMKKGSSDRYFQGSVNEANKLVPEGIEGR
VAYKGAASDIVFQMLGGIRSGMGYVGAGDIQELHENAQFVEMSGAGLIESHPHDVQJTNEAPNYSV

>d1ak5_1 c.1.5.1 (2-101,222-483) Inosine monophosphate dehydrogenase (IMPDH) {Tritrichomonas foetus}

AKYYNEPCHTFNEYLLIPGLSTVDCIPS NVNLSTPLVKFQKGQQSEINLKIPVSAIMQS VSGEKMAIALAREGGIS
FIFGSQSIESQAAMVHAVKNFKAXHNELVDSQKRYLVGAGINTRDFRERVPALVEAGADVLCIDSSDGFSEWQK
ITIGWIREKYGDVKVGAGNIVDGEGFRYLAGADAFIKIGIGGGSICITREQKGIGRGQATAVIDVVAERNKYFE
ETGIYIPVCS DGGIVYDYHMTLALAMGADFI MLGRYFARFEESPTRKVTING SVMKEYW GEGSSRARNWQRY
DLGGKQKLSFEEGVDSYV PYAGKLKD NVEASLNKVKSTM CNGALTIPQLQSKAKITLVSSVI

>d1jr1a1 c.1.5.1 (A:17-112,A:233-514) Inosine monophosphate dehydrogenase (IMPDH) {Chinese hamster (Cricetulus griseus)}

GLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALT KITLKTPLVSSPM DTVTEAGMAIA MALTGGIGFIH
HNCTPEFQANEVRKVKKYEQXYPLASKDAKKQLLCGAAIGTHEDDKYRL DLLLAGV D VVLDSSQGNSIFQIN
MIKYMKEKPNLQVIGGNVVTAAQAKNLIDAGVDALRVGMGCGSICITQEVLACGRPQATAVYKVSEYARRFG
VPVIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLK KYRGMGSLAMD KHLSSQNRYF
SEADKIKVAQGVSGAVQDKGSIHKFV PYLIAGIQHSCQD IGA KS LTQVRAMMYS GELKF EKRTSSAQVEGGVHS
LHSYEKRLF

>d1bd0a2 c.1.6.1 (A:12-244) Alanine racemase {Bacillus stearothermophilus}

VLDLAIYDNVENLRRLLPDDTHIMAVV KANAYGHGDVQVARTALEAGASRLAV AFLDE ALREKGIEAPIVLG
ASRPADAALAAQQR ALTVFRSDWLEEASALYSGPFPIHFHLKMDTGMGR LVKDEETKRIVALIERRPHFVLE
GLYTHFATADEVNTDYFSYQYTRFLHM LEWLPSRPLVHCANS AASLRFPDRTFNMVRFG IAMYGLAPSPGIKP
LLPYPLK EA

>d1d7ka2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Human (Homo sapiens)}

DLGDILKKHRLWLKALPRVTPFYAVKCND SKAIVKTLAATGTGFDCASKTEIQLVQSLGVPPERIYANPCKQVSQI
KYAANNGVQM MTFDSEVELMKVARAHPKAKLVLRIATDDSKAVCR LSVKFGATLRTS RLLE RAKELNIDVVGV

SFHVGSGCTDPETFVQAISDARCVFDMGAEVGFSMYLLDIGGFPGSEDVKLKFEITGVINPALDKYFPSDSGVRIIAEPGRYYVASA

>d7odca2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Mouse (Mus musculus)}
DLGDILKKHLRWLKALPRVTFFAVKCNSRAIVSTLAAIGTGFDCASKTEIQLVQGLGVPAERVIYANPCKQVSQIKYAASNGVQMMLDFSEIELMKVARAHPKAKLVLRIATDDSKAVCRLSVKFGATLTSRLLERAKELNIDVIGVSFHVGSGCTDPDTFVQAVSDARCVFDMATEVGFSMHLDIGGFPGSEDTKLKFEITSVINPALDKYFPSDSGVRIIAEPGRYYVASA

>d2toda2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Trypanosoma brucei}
DLGDIVRKHETWKCLPRVTFFAVACNDDWRVLGTLAALGTGFDCASNTEIQRVRGIGVPPEKIIYANPCKQISHIRYARDSGVDVMTFDCVDELEKVAKTHPKAKMVLRISTDDSLARCRLSVKFGAKVEDCRFILEQAKKLNIDVTGVSFHVGSGSTDASTFAQAISDSRFVFDMGTELGFNMHILDIGGFPGTRDAPLKFEIAGVINNALEKHFPDLKLTIVAEPGRYYVASA

>d1ct5a_c.1.6.2 (A:) "Hypothetical" protein ybl036c {Baker's yeast (Saccharomyces cerevisiae)}
TGITYDEDRKTLQIAQYESVREVVNAEAKNVHVNENASKILLVVSKLPASDIQILYDHGVREFGENYVQELIEKA
KLLPDDIKWHFIGGLQTNKCKDLAKVPNLYSvetDSLKKAKKLNESRAKFQPDNCNPILCNVQINTSHEDQKSGLNNEAEIFEVIDFFLSEECKYIKLNLGLMTIGSWNVSHEDSKENRDFATLVEWKKIDAKFGTSLKLSMGMSADFRE
AIRQGTAEVRIGHTDIFG

>d1frb_c.1.7.1 (-) FR-1 (fibroblast growth factor-induced) protein {Mouse (Mus musculus)}
ATFVELSTKAKMPIVGLGTWKSPPNQVKEAVKAAIDAGYRHIDCAYACNEEVGEAIQEKIKEKAVQREDLFIV
SKLWPTCFEKLLLKEAFQKTLTDLKLDYLQDLYLIHWPKQGLQPGKELFPKDDQGRILTSKTTFLEAWEGMEELVDQ
GLVKALGVSNFNHFQIERLLNKPLKHKPVTNQVECHPYLTQEKLQYCHSKGISVTAYSPLGSPDRPSAKPEDPS
LLEDPKIKEIAAKHEKTSQAQVLIRFHIQRNVVVIPKSVTSPSRIQENIQVFDFQLSDEEMATILSFNRNWRACLLPET
VNMEEYPYDAEY

>d1exba_c.1.7.1 (A:) Voltage-dependent K+ channel beta subunit {Rat (Rattus norvegicus)}
LQFYRNILGKSLRVSCGLGTWVTFGGQITDEMAEHLMTLAYDNGINLFDTAEVYAGKAEVVLGNIIKKKGW
RRSSLVITTKIFWGKGKAETERGLSRKHIEGLKASLERLQLLEYVDVVFANRPDPNTPMEETVRAMTHVINQGMA
MYWGTSRWSSMEIMEAYSVARQFNLIPIICEQAHEYMFQREKVEVQLPELFHKIGVGAMTWSPLAGIVSGK
YDSGIPPSRASLKGYQWLKDILSEEGRRQQAKLKELOQIAERLGCTLPQLIAWCLRNEGVSLLGASNAEQ
LMENIGAIQVLPKLSSIVHEIDSILGNKPYS

>d1ads_c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (Homo sapiens)}
ASRLLLNNAGKMPILGLGTWKSPPGQVTEAVKVAIDVGYRHIDCAHVYQNENEVGVAIQEKLREQVKREELFI
VSKLWCTYHEGLVKGACQKTLSDLKLDYLQDLYLIHWPTGFKPGKEFFPLDEGNVPSDTNILDWTAAAMEELV
DEGLVKAIGISNFNHLQVEMILNKPLKYKPAVNQIECHPYLTQEKLQYCSKGIVVTAYSPLGSPDRPWAKPED
PSLLEDPRIKAIAAKHNKTTAQVLIRFPMQRNLVVIPSVTPERIAENFKVFDLSSQDMTLLSYNRNWRVCA
LLSCTSHKDYPFHEEF

>d2alr_c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (Homo sapiens)}
AACSVLLHTGQKMPILGLGTWKSPPGQVKAALKYALSGYRHIDCAAIYGNEPEIGEALKEDVGPBKAVPREEL
FVTSLWNTKHHPEDVEPALRKTADLQLEYLDLYLMHWPYAVERGDNPFPKNADGTICDSTHYKETWKALE
ALVAKGLVQALGLSNFNSRQIDDILSVASVRPAVLQVECHPYLAQNEELIAHCQARGLEVTAISPLGSSDRAWRDP
DEPVILLEPVLALAEKYGRSPAQILLRWQVQRKVICPKSITPSRILQNIKVFDFTFSPEEMKQLNALKNWRYIV
PMLTVDGKRVPRDAGHPLYPFNDPY

>d1ah4_c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Pig (Sus scrofa)}
ASHLVLYTGAKMPILGLGTWKSPPGQVTEAVKVAIDLGYRHIDCAHVYQNENEVGGLQEKLQGQVVKREDLFIV
VSKLWCTDHEKNLVKGACQTLRDLKLDYLQDLYLIHWPTGFKPGKDPFPLGDGNVVPDESDFVETWEAMEEL

VDEGLVKAIGVSNFNHLQVEKILNKPGALKYKPAVNQIEVHPYLQEKLIEYCKSKGIVVTAYSPLGSPDRPWAKPE
DPSLLEDPRIKAIAAKYNKTTAQVLIRPMQRNLIVPKSVT PERIAENFQVFDFELSPEDMNTLLSYNRNWRVC
ALMSCASHKDYPFHEEY

>d1hqta_c.1.7.1 (A:) Aldose reductase (aldehyde reductase) {Pig (Sus scrofa)}

AASCVLLHTGQKMPLIGLTWKSEPGQVKAAIKYALTGYRHIDCAAIFGNELEIGEALQETVPGPKAVPREELF
VTSKLWNTKHHPEDVEPALRKTADLQLEYLDLYMHWPYAFERGDNPFPKNADGTIRYDATHYKDTWKALEA
LVAKGLVRALGLSNFSSRQIDDVLSVASRPAVLQVECHPYLAQNELIAHCQARGLEV TAYSPLGSSDRAWRDPN
EPVLLEPPVVQALAEKYNRSPAQILLRWQVQRKVICIPKS VTPS RIPQNIQVF DFTFSPEEMKQLDALNKNLRFIV
PMLTVDGKRVPRDAGHPLYPFNDPY

>d1afsa_c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Rat (Rattus norvegicus)}
MDSISLRVALNDGNFIPVLF GFTTVPEKVA KDEV IKATKIAIDNGFRHFD SAYLYEV EEEVGQA IRSKIEDGTVKRE
DIFYTSKLWSTFH RPELVRTCLE TLKST QLDYVD LYIIHFPMALQPGD IFFPRDEHGKLLFETV DICDTWEAMEK
CKDAGLAKSIGVSNFNCRQLERILNKPGLK YKPVCNQVECHLYLNQS KMLDYCKSKD II LSYCTLGSSRDKTWV
DQKSPVLLDDPVLCIAKKYKQTPALVALRYQLQRGVVPLRSFNAKRIKELTQVFEFQLASEDMKALDGLNRNF
RYNNAKYFDDHPNHPF

>d1ihia_c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Human (Homo sapiens), type III}
SKYQCVKLNDGHFMPVLF GFTYAPAEVP SKALEAVK LAIEAGFHHIDS AHVYNNEEQV GLAIRSKIADGSVKRE
DIFYTSKLWSNSHRPELVRPA LERSLKNLQ LDYVD LYI HF PVS VP GEEVIP KDEN GKLF DTVDLCATWEAMEK
CKDAGLAKSIGVSNFNRHLLEMILNKPGLK YKPVCNQVECHPYFNQRKLLDFCKSKD IV LVAYS ALGSHREEPW
VDPNSPVLLDDPVLCIAKKH KRTPAL ALR YQLQ RGVV VLAKSY NEQR IRQNVQ VFE FQLTSEEMKAIDGLNR
NVRYLTLDIFAGPPNYPFSDE

>d1c9wa_c.1.7.1 (A:) CHO reductase {Chinese hampster (Cricetus griseus)}

STFVELSTKAKMPIVGLTWQSPPGQVKEAVKVAIDAGYRHIDCAYAYNEHEVGEAIQEKIKEKAVRREDLFIVS
KLWPTCFERKLLKEAFQKTLTDLKLDYLDLYLIHW P QGLQ PGKELFPKDDQGNV LSKITFLDAWEVMEELVDEG
LVKALGVSNFNFHQIERILNKPGLKHKPV TNQVECHPYLTQEKLIEYCHSKGITV TAYSPLGSPNRPWAKPEDPSL
LEDPKIKEIAAKHKKTSAQVLIRFHIQRNVV VPKSVTPARIHENFQVFDQLSDQEMATILGFNRNWRACLLPET
VN MEEYPYDAEY

>d1hw6a_c.1.7.1 (A:) 2,5-diketo-D-gluconic acid reductase A {Corynebacterium sp.}
TVPSIVLNDGNSIPQLGYGVFKVPPADTQRAVEEALEVGYRHIDTAIYGNEEGVGAAIAASGIARDDL FITTKLW
NDRHDGDEPAAAIAESLAKLALDQVDLYLVHWP TPAADNYVHAWEKMIELRAAGLRSIGVSNHLP HLERIVA
ATGVVP AVNQIELHPAYQQREITDWAAAH DVKIESWG PLQGKYDLFGAEPVTAAAAAHGKTPAQAVLRWHL
QKG FVVF PKS VRER RLEEN LDVFD FDLTDTEIAAIDAMDP

>d1bli_2_c.1.8.1 (3-393) Bacterial alpha-amylase {Bacillus licheniformis}

LNGTLMQYFEWYMPNDGQHWKRLQND SAYLAEH GITAVWIP PAYK GT SQADVGYGAYDLYDLGEF HQKG TV
RTKYGT KGE LQSAIKSLHS RDIN VYGDV VNH KGGA DATE DVT AV EVD PADRN RVIS GEH LIKA WTH FHF PGRG
STY SDFKWHWYHFD GTD WDES RKL NRYK FQG KAWD WEV SNE FG NYD LYMYAD IDYD HPD VAA EIK RWG T
WYAN ELQLDGFR LDAV KH KFSFL RDW VN HV REKT G KEM FTVA EYW SYDL GALE NYLN KTN FN H SVFDVPLH
YQFHAA STQGGYDMRKLLN GTV VSKHPLS VTFVDN HDTQ PGQS LESTV QTWF KPLAYA FILTRES GYPQ VF
YGD MYG TKG DSQ REIP AL KH KIEP IL KARK Q

>d1e43a2_c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus amyloliquefaciens/Bacillus licheniformis chimera}

VNGTLMQYFEWYPTNDGQHWKRLQND AEH LSDI GITA VWIP PAYK GLS QSD NGYGP YDLYDLGEF QQKG TV
RTKYGT KSELQDAIGSLHS RNVQVYGDV VLNH KAGA DATE DVT AV EVN PAN RNQ ETSE EYQIK AW TD FRP GR
GNTY SDFKWHWYHFDGADWDES RKISRIFKFRG EGKA WDWEV SSEN GNYD LYMYADV DYDHP DVVAET KK

WGIWYANELSLDGFRIDAAKHIKFSFLRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVD
VPLHFNLQAASSQGGGYDMRKLLNGTVSKHPLKSFTFDNHDTPQGQSLESTVQTWFKPLAYAFILTRESGY
PQVFYGDMDYGTGDSQREIPALKHIEPILKARKQ

>d1g94a2 c.1.8.1 (A:1-354) Bacterial alpha-amylase {Pseudoalteromonas haloplancis (Alteromonas haloplancis)}

TPTTFVHLFEWNWQDVAQECEQYLGPKGYAAVQVSPPNEHTGSQWWTRYQPVSYELQSRGGNRQFIDM
VNRCSAAGVDIYVDTLINHMAAGSGTGAGNSFGNKSFPISPQDFHESCTINNSDYGNDRYRVQNCELVGLA
DLDTASNYVQNTIAAYINDLQAIKGFRFDASKHVAASDIQSLMAKVNGSPVFQEVIDQGGEAVGASEYLST
GLVTEFKYSTELGNTFRNGSLAWLSNFEGEGWGFMPSSAVVFDNHDNQRGHGGAGNVITFEDGRLYDLAN
VFMLAYPYGYPKVMSSYDFHGDTDAGGPNVPHNNGNLECFASNWKCEHRWSYIAGGVDFRNNTAD

>d1bag_2 c.1.8.1 (1-347) Bacterial alpha-amylase {Bacillus subtilis}

LTAPSIGSTILHAWNWSFNTLKHNMKDIHDAGYTAITSPINQVKEGNQGDKMSMSNWYWLQPTSYQIGNR
YLGTEQEFKEMCAAAEYGIKIVDAVINHTFDYAAISNEVKSIPNWTHGNTQIKNWSDRWDVTQNSLLGY
DWNTQNTQVQSYLKRFLERALNDGADGFRFDAAKHIELPDDGSYGSQFWPNITNTSAEFQYQGQILQDSASRD
AAVANYMDVTASNYGHSIRSALKNRNLGVSNISHYASDVSAKLVTVESHTDYANDDEESTWMSDDDIRLG
WAVIASRGSTPLFFSRPEGGGNGVRFPGKSQIGDRGSALFEDQAITAVNRFHNV MAG

>d1hvxa2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus stearothermophilus}

AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWPPAYKGTTSRSDVGYGVYDLYDLGEFNQKG
AVRTKYGTKAQYLQAIQAAHAAGMQVYADVFDHKGGADGTEWVDAEVNPSDRNQEISGTYQIQAWTKF
DFPGRGNTYSSFKWRWYHFDGVWDERSKLSRIYKFRGIGKAWDWEVDTENGNYDLYMYADLMDHPEV
VTELKSWGKWYVNTTNIDGFRDAVKHIKFSFFPDWLSYVRSQTGKPLFTVGEYWSYDINKLHNYIMKTNGTM
SLFDAPLHNKFYTASKSGGTDMRTLMTNTLMKDQPTLAFTFDNHDTEPGQALQSWVDPWFKPLAYAFILT
RQEGLYPCVFYGDYYGIPQYNIPSLKSKIDPILLIARRD

>d1gjwa2 c.1.8.1 (A:1-572) Maltosyltransferase {Thermotoga maritima}

MLLREINRYCKEKATGKRIYAVPKLWIPGFFKKFDEKSGRCFVDPYELGAEITDWILNQSREWDSQPLSFLKGEK
TPDWIKRSVYVGSLPRTTAAYNHKGSYYEENDVLGFREAGTFFKMMLLLPGVSKLGADAIYLLPVSRSMSDLFKK
GDAPSPYSVKNPMELDERYHDPLEPFVDEEFKAFVEACHILGIRVILDIFPRTAARDSDLIREHPDWFYWIKE
ELADYTPPRAELPFKVPDEDELEIYNIKENVRHLKKFTLPPNLIDPQKWEKIKREEGNILELIVKEFGIITPPGFSD
LINDPQPTWDDVTFLRLYLDHPEASKRFLDPNQPPVLYDVIKASKFPGKEPNRELWEYLAGVIPHYQKKYGDG
ARLDMGHALPKELLDIKNVKEYDPAFVMIAEELDMEKDKASKEAGYDVLGSSWYFAGRVEEIGKLKDIAEEL
VLPFLASVETPDTPRIATRKYASKMKKLAFFVTLNPKVNTGQEIGEKQPMNLGLDTPNLRKVLSPTDEFF
GKLAFFDHVVLHWSDPDRGVLFNFIKKLIKVRHEFLDFVNL

>d1cgt_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

DPDTAVTNQSFSTDVIYQVFTDRFLDGNNPSNNPTGAAYDATCSNLKLYCGGDWQGLINKINDNYFSDLGVTA
WISQPVENIFATINYSGVTNTAYHGYWARDFKKTNPYFGTMADFQNLITTAHAKGKIVIDFAPNHTSPAMETD
TSFAENGRLYDNGTLVGGYTNDTNGYFHHNGGSDFSSLLENGIYKNLYDLADFNHNNTIDKYFKDAIKLWLD
GVDGIRVDAVKHMPLGWQKSWMSSIYAHKPVFTFGEWFLGSAASDADNTDFANKSGMSLLDFRFNSAVRN
VFRDNTSNMYALDSMINSTATDYNQVNDQVTFIDNHMDRFKTSAVNNRLEQALAFTLTSRGVPAIYYGTEQ
YLTGNGDPDNRAKMPFSKSTTAFNVISKLAFLRKSNPAY

>d1kcla4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Bacillus circulans, different strains}

APDTSVNKQNFSTDVIYQIFTDRFSDGNPANNPTGAAFDGTCNLRLYCGGDWQGIINKINDGYLTGMGVTA
WISQPVENIYSIINYSGVNNTAYHGYWARDFKKTNPAYGTIAFDQNLIAAHAKNIVIIDFAPNHTSPASSDQPS
FAENGRLYDNGTLLGGYTNDTQNLFHHLGTDFTTENGYKNLYDLADLNHNNTVDVYLKDAIKMWLDLGI

DGIRMDAVKHMPFGWQKSMAAVNNYKPVFTGEWFLGVNEVSPENHKFANESGMSLLDFRFAQKVRQVF
RDNTDNMYGLKAMLEGSAADYAQVDDQVTFIDNHDMERFHASNANRRKLEQALAFTLTSRGVPAIYYGTEQY
MSGGTDPDNRARIPSFTSTTAYQVIQKLAPLRKNPAIAY

>d1cyg_4 c.1.8.1 (1-402) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus}
AGNLNKVNFTSDVYQIVVDRFDGNTSNNPSGALFSSGCTNLRKYCDDWQGIINKINDGYLTDMGVTAIW
ISQPVENVFSVMNDASGSASYHGYWARDFKPNPFFGTLSDFQRLVDAAHAKGIKVIIDFAPNHTSPASETNPS
YMENGRLYDNGTLLGGYTNDANMYFHHNGGTFSSLEDGIYRNLFDLADLNHQNPVIDRYLKDAVKMWIDM
GIDGIRMDAVKHMPFGWQKSLMDEIDNYRPVFTGEWFLSENEVDANNHYFANESGMSLLDFRGQKLRQV
LRNNNSDNWYGFNQMIQDTASAYDEVLDQVTFIDNHDMDRFMIDGGDPRKVDMALAVLLTSRGVPNIYYGTE
QYMTGNGDPNNRKMMSSFNKNTRAYQVIQKLSSLRRNNPALAY

>d1qhoa4 c.1.8.1 (A:1-407) Cyclodextrin glycosyltransferase {Bacillus stearothermophilus, maltogenic alpha-amylase}

SSSASVKGDVIYQIIIFRDYDGTNNNPAKSYGLYDPTKSWKMYWGGDLEGVRQKLPYLQQLGVTTIWLSPV
LDNLDTLAGTDNTGYHGYWTRDFKQIEEHFGNWTTFDTLVNDAHQNGIKVIVDFVPNHSTPFKANDSTFAEG
GALYNNNGTYMGNYFDDATKGYFHHNGDISWDDRYEAQWKNFTDPAGFLSADLSQENGTLAQYLTDAAVQL
VAHGADGLRIDAVKHFNSGSFSKLADKLYQKKDIFLVGEWYGDDPGTANHLEKVRVYANNSGVNVLDLNTVI
RNVFGTFTQTMYDLNNMVNQGTNEYKYKENLITFIDNHDMSRFLSVNSNKANLHQALAFILTSRGTPSIYYGTE
QY MAGGNDPYNRGMMMPAFDTTTAFKEVSTLAGLRRNNAAIQY

>d1pama4 c.1.8.1 (A:1-406) Cyclodextrin glycosyltransferase {Alkalophilic bacillus sp., strain 1011}

APDTSVSKQNFSSTDVIYQIFTDRFSDGNPANNPTGAAFDGSCNLRLYCGGDWQGIINKINDGYLTGMGITAI
WISQPVENIYSVINSGVNNTAYHGYWARDFKKTNPAYGTMQDFKNLIDTAHANNIKVIIDFAPNHTSPASSDD
PSFAENGRLYDNGNLLGGYTNDTQNLFHGGTDFSTIENGYKNLYDLADLNHNNSVDVYLKDAIKMWLDL
GVDGIRDAVKHMPFGWQKSFMATINNYKPVFTGEWFLGVNEISPEYHQFANESGMSLLDFRFAQKARQV
FRDNTDNMYGLKAMLEGSEVDYAQVNDQVTFIDNHDMERFHTSNGDRRKLEQALAFTLTSRGVPAIYYGSEQ
YMSGGNDPDNRARLPSFTTTAYQVIQKLAPLRKSNAIAY

>d1ciu_4 c.1.8.1 (1-406) Cyclodextrin glycosyltransferase {Thermoanaerobacterium thermosulfurigenes, EM1}

ASDTAVSVNVNYSTDVIYQIVTDRFDGNTSNNPTGDLYDPTHTSLKKYFGGDWQGIINKINDGYLTGMGVTAI
WISQPVENIYAVLPDSTFGGSTSYHGYWARDFKRTNPYFGSFTDFQNLINTAHANNIKVIIDFAPNHTSPASETD
PTYAENGRLYDNGTLLGGYTNDTNGYFHHGGTDFSSYEDGIYRNLFDLADLNQQNSTIDSYLSAIKVWLDL
GIDGIRDAVKHMPFGWQKNFMDISILSYRPVFTGEWFLGTNEIDVNNTYFANESGMSLLDFRSQKVRQVF
RDNTDTMYGLDSMIQSTASDYNFINDMVTFIDNHDMDRFYNGGSTRPVEQALAFTLTSRGVPAIYYGTEQYM
TGNGDPYNRAMMITSFTNTTAYNVVIKKLAPLRKSNAIAY

>d1hx0a2 c.1.8.1 (A:1-403) Animal alpha-amylase {Pig (Sus scrofa)}

EYAPQTQSGRTSIVHLFEWRWVDIALECERYLGPKGFGGVQVSPPNENIVVTNPSRPWWERYQPVSYKLCTRS
GNENEFRDMVTRCNNVGVRIVDAVINHMC GSGAAAGTGTGCSYCNPGNREFPAVPYSAWDFNDGKCKTA
SGGIESYNDPYQRDCQLVGLLDALEKDYVRSMIADYLNKLIDIGVAGFRIDASKHMWPGDIKAVLDKLHNLN
TNWFPAGSRPFIFOEVIDLGGAEAIKSEYFGNGRVTEFKYGA KLT VVRKWSEKMSYLNWGEWGWFMPSD
RALVFVDNHDNQRGHGAGGSSILTFWDARLYKIAVGFMLAHPYGFTRVMSSYRWARNFNGEDVNDWIGPP
NNNGVIKEVTINADTCGNDWVCEHRWREIRNMVVFRNVVDG

>d1smd_2 c.1.8.1 (1-403) Animal alpha-amylase {Human (Homo sapiens)}

EYSSNTQQGRTSIVHLFEWRWVDIALECERYLAPKGFGGVQVSPPNENVIAHNPFRPW WERYQPVSYKLCTRS
GNEDEFRNMVTRCNNVGVRIVDAVINHMC GNAVSAGTSSTCGSYFNPGSRDFPAVPYSGWDFNDGKCKTG

SGDIENYNDATQVRDCRLSGLLDLALGKDYVRSKIAEYMNHLIDIGVAGFRIDASKHMPGDIKAILDKLHNLN
SNWFPEGSKPFIYQEVIDLGGEPIKSSDYFGNGRVTEFKYGAKLGTIRKWNGEKMSYLNWGEWGFMPSD
RALVFVDNHDNQRHGAGGASILTFWDARLYKMAVGFLAHPYGFTRVMSSYRWPRTFENGKDVNWDVG
PPNDNGVTKEVTINPDTCGNWDVCEHRWRQIRNMVNFRNVVVG

>d1jae_2 c.1.8.1 (1-378) Animal alpha-amylase {Yellow mealworm (*Tenebrio molitor*), larva}

EKDANFASGRNSIVHLFEWKWNDIADECERFLQPQGFGGVQISPPNEYLVADGRPWWERYQPVSYIINTRSG
DESAFTDMTRRCNDAGVRIYDAVINHMTGMNGVGTSGSSADHDGMNYPAVPYGSGDFHSPCEVNYYQD
ADNVRNCELVGLRDLNQGSODYVRGLIDYMNHMIDLGVAGFRVDAAKHMSPGDLSVIFSGLKNLNTDYGFA
GARPFYIYQEVIDLGGEAIKNEYTGFCVLEFQFGVSLGNAFQGGNQLKNLANWGPEWGLLEGDAVVFDN
HDNQRTGGSQILTYKNPKPYKMAIAFMLAHPYGTTRIMSSFDFTNDQGPPQDGSGNLISPGINDDNTCSNG
YVCEHRWRQVYGMVGMVGRNAVE

>d2aaa_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus niger, acid amylase}

LSAASWRTQSIYFLLTDRFGRTDNSTTACNTGNEIYCGGSWQGIIDHLDYIEGMGFTAIWISPITEQLPQDTAD
GEAYHGWWQQKIYDVNSNFTGADNLKLSDALHARGMYLMVDVVDHMGYAGNGNDVDYSVFPFDSSY
FHPYCLTDWDNLTMVEDCWEGDTIVSLPDLTTETAVRTIWYDWVADLVSNSVDGLRIDSVLEVQPDFFPG
YNKASGVYCVGEIDNGNPASDCPYQKVLDGVLYPIYWQLYAFESSGSISNLYNMIKSVASDCSDPTLLGNFIE
NHDNPRFAKYTSQAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWSGYDTSAELYTWIATTNAIR
KLAIAADSAYIT

>d7taa_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus oryzae, Taka-amylase}

ATPADWRSQSIYFLLTDRFARTDGTTACNTADQKYCGGTWQGIIDKLDYIQGMGFTAIWITPVTAQLPQTTAY
GDAYHGWWQQDIYSLNENYGTADDLKALSSALHERGMYLMVDVANHMGYDGAGSSVDYSVFKPFSSQDYF
HPFCFIQNYEDQTQVEDCWLDNTVSLPDLTTKDVVKNEWYDWVGSLVSNSIDGLRIDTVKHVQKDFWP
GYNKAAGVYCIQEVLGDGPAYTCPYQNVMMDGVLNYPYIYPLLNNAFKSTSGSMDDLYNMINTVKSDCPDSTLLG
TFVENHDNPRFASYTNIALAKNVAIFIILNDGIPIIYAGQEQQHYAGGNDPANREATWSGYPTDSELYKLIASAN
AIRNYAISKDTGFVT

>d1smaa3 c.1.8.1 (A:124-505) Maltogenic amylase, central domain {Thermus sp.}

DLFQAPDWVKDTVWYQIFPERFANGNPAISPKGARPWGSEDPTPTSFGGDLQGIIDHLDYLADLGITGIYLTP
FRAPSNIKYDTADYFEIDPHFGDKETLKTIVKRCKEKGIRVMLDAVFNHCGYEAPFQDVLKNGAASRYKDWF
HIREFPLQTEPRPNYDTFAFVPHMPKLNTAHPEVKRYLLDVATYWIREFDIDGWRLDVANEIDHQFWREFRQA
VKALKPDVYILGEIWHDAMPWLRGDQFDAVMNYPLADAALRFFAKEDMSASEFADRLMHVLHSYPKQVNEA
AFNLLGSHDTPRLLVCGGDVRKVKLLFLQLTGSPCIYYGDEIGMTGGNDPECRKCMVWDPEKQNKELEYEH
VKQLIALRKQYRALRR

>d1bvza3 c.1.8.1 (A:121-502) Maltogenic amylase, central domain {Thermoactinomyces vulgaris, TVAII}

VFTTPEWAKEAVIYQIFPERFANGDPSNDPPGTEQWAKDARPRHDSFYGGDLKGVIDRLPYLEELGVTALYFTPI
FASPSHHKYDTADYLAIDPQFGDLPTFRLVDEAHRGIKIILDAVFNHAGDQFFAFRDVLQKGEQSRYKDWF
EDFPVSKTSRTNYETFAVQVPAMPKLRLENPEVKEYLFDFVARFWMEQGIDGWRLDVANEVDHAFWREFRRLV
KSLNPDALIVGEIWHDASGWLMGDQFDVMNYLFRESVIRFFATGEIHAERFDAELTRARMLYPEQAAQGLW
NLLDSHDERFLTSCGGNEAKFRLAVLFQMTRYLGTLIYYGDEIGMAGATDPDCRRPMIWEKEQNRLFEFYK
ELIRLRHRLASLTR

>d1eh9a3 c.1.8.1 (A:91-490) Glycosyltrehalose trehalohydrolase, central domain
{Archaeon *Sulfolobus solfataricus*, km1}

FNNETFLKKEDLIYIEHVGTFTPEGFVIRKLDYLKDLGITAEIMPIAQFPKGKRDWGYDGVLYAVQNSYGGP

EGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKYKTPWGLTFNFDDAESDEVRKFILENVEYW
IKEYNDGFRLDAVHAIIDTSPKHILEEIADVHKYNRIVIAESDLNDPRVNPKECGYNIDAQWVDDFHHSIH
AYLTGERQGYTDGFNLDDIVKSYKDVFVYDGKYSNFRRKTHGEPVGELDCNFVVIQNHQDQVGNRGKGERII
KLVDRESYKIAAALYLLSPYIPMIFMGEEYGEENPFYFFSDFSDSKLIQGVREGRKKENGQDTPQDESTFNASKL
SWKIDEEIFSFYKILIKMRKELSIA

>d1bf2_3 c.1.8.1 (163-637) Isoamylase, central domain {Pseudomonas amylofera}

PSTQSTGTPKTRAQKDDVIYEVHVRGFTEQDTSIPAQYRGTYAGLKASLASGVTAVEFLPVQETQNDAND
VVPNSDANQNYWGYMTENYFSPDRRYAYNKAAGGPTAEFQAMVQAFHNAGIKVYMDVVYNHTAEGGTWT
SSDPTTATIYSWRGLDNATYYELTSQNYFYDNTGIGANFNTYNTVAQNLIVDSLWANTMGVDGFRFDLAS
VLGNSCNGAYTASAPNCPNGGYNFDAADSNVAINRILREFTVRPAAGGSGLDLFAEPWAIGGNSYQLGGFPQ
GWSEWNGLFRDSLRAQNELGSMTIYVTQDANDFSGSSNLQSSGRSPWNSINFIDVHDGMTLKDVYSCNG
ANNSQAWPYGPSDGGTSTNYSWDQGMSAGTGAAVDQRRAARTGMAFEMLSAGTPLMQGGDEYLRTLQC
NNNAYNLDSSANWLTSWTTDQSNTYTAQRLIAFRKAHPALRPSSW

>d1gcy2 c.1.8.1 (A:1-357) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase)
{Pseudomonas stutzeri}

DQAGKSPNAVRYHGGDEIILQGFHWNVVREAPNDWYNILRQQATIAADGFSAIWMPVPWRDFSSWSDGS
KSGGGEGYFWHDFNKNGRYGSDAQLRQAASALGGAGVKVLYDVPNHNMRGYPDKEINLPAGQGFWRND
CADPGNYPNDCCDGDRFIGGDADLNTGHPQVYGMFRDEFTNLSQYGAGGFRDFVRGYAPERVNSWMTD
SADNSFCVGEWKGPSEYPNWDRNTASWQQIIDWSRAKCPVFDFALKERMQNGSIADWKHGLNGNP
DPRWREVAVTVDNHDTGYSPGQNGQHHWALQDGLIRQAYAYILTSPGTPVYWDHMYDWGYGDFIRQL
IQVRRAAGV

>d1avaa2 c.1.8.1 (A:1-346) Plant alpha-amylase {Barley (Hordeum vulgare), seeds, AMY2 isozyme}
QLFQGFNWESWKHNGGWYNFLMGKVDDIAAGITHVWLPPASQVAEQGYMPGRLYDLDASKYGNKAQ
LKSLIGALHGKGVKAIADIVINHRTAEHKDGRGIYCIFEGGTPDARLDWGPHEMICRDRPYADGTGNPDTGADF
GAAPDIDHLNLRVQKELVEWLNLKADIGFDGWRDFAKGYSADVAKIYIDRSEPSFAVAEIWTSLAYGGDGKP
NLNQDQHRQELVNWVDKVGKGPPATTFDFTTKGILNVAVEGELWRLRGTDGKAPGMIGWWPAKAVTFVDN
HDTGSTQHMWPFPNSDRVVMQGYAYILTHPGTPCIFYDHFFDWGLKEEIDRLSVRTRHGI

>d1uok_2 c.1.8.1 (1-479) Oligo-1,6, glucosidase {Bacillus cereus}

MEKQWWKESVYQIYPRSFMDNSNGDGGDLRGIIKLDYLKELGIDVIWLSHVESPVYESPNDDNGYDISDYCKIMNE
FGTMEDWDELLHEMHERNMKLMMDLVNHTSDEHNWFIESRKSKDNYRDYYIWRPGKEGKEPNNWGA
AFSGSAWQYDEMTDEYYLHLFSKKQPDLNWDNEKVRQDVYEMMKFWLEKGIDGFRMDVINFISKEEGLPTV
ETEEEGYVSGHKHFMNGPNIHKLHEMNEEVLSHYDIMTVGEMPGVTTEEAKLYTGEERKELQMVFQFEHM
DLDSGEGGKWDVKPCSLTLKENLTWKQALEHTGWNNSLYWNNHDQPRVVSFGNDGMYRIESAKMLATVL
HMMKGTPYIYQGEEIGMTNVRFESIDEYRDIETLNMYKEKVMERGEDIEKVMQSIYIKGRDNARTPMQWDD
QNHAGFTTGEPWITVNPNEYKEINVKQAIQNKSIFYYYKKLIELRKNNEIVYY

>d1g5aa2 c.1.8.1 (A:1-554) Amylosucrase {Neisseria polysaccharea}

SPNSQYLKTRILDIYTPEQRAGIEKSEDWRQFSRRMDTHFPKLMNELDHSVGNNEALLPMLEMLAQAWQSYS
QRNSSLKDIDIARENNDPWILSNKQVGGVCYVDFIFNHTSNEHEWAQRCAAGDPLFDNFYYIFPDRRMPDQYD
RTLREIFFPDQHPGGFSQLEDGRWVWTTFNSFQWDLNNSNPWVFRAMAGEMLFLANLGVDILRMDAVAFIW
KQMGTCENLPQAHALIRAFNAVMRIAAPAVERFKSEAIVHPDQVVQYIGQDECQIGYNPLQMALLWNTLATRE
VNLLHQALTYRHNLPEHTAWVNYVRSHDDIGWTFADAAYLGISGYDHRQFLNRFFVNRFDGSFARGVPFQ
YNPSTGDCRVSGTAAALVGLAQDDPHAVDRIKLLSIALSTGGLPLIYLGDEVGTLNDDDSQDSNKSDDSRWA
HRPRYNEALYAQRNDPSTAAGQIYQDLRHMIAVRQSNPRFDGG

>d1eswa_c.1.8.1 (A:) Amylomaltase MalQ {Thermus aquaticus}
MELPRAFGLLLHPTSLPGPYGVGVLGREARDFLRLKEAGGRYWQVLPLGPTGYGDSPYQSFSAFAGNPYLIDL
RPLAERGYVRLEDPGFPQGRVDYGLLYAWKWPALKEAFRGFKEASPEEREAAFREREAWWLEDYALFMAL
KGAHGLLPWNRWPLPLRKREEKALREAKSALAEVAFAHTQWLFFRQWGALKAEAEALGIRIIGDMPIFVAE
DSAEVWAHPEWFHLDEEGRPTVVAGVPPDYFSETGQRWGNPLYRWDVLEREGFSWIRRLEKALELFHLVRID
HFRGFEAYWEIPASCPTAVEGRWVKAPGEKLFQKIQEVFGEVPVLAEDLGVTPEVEALDRFGLPGMKVLQFA
FDDGMENPFLPHNYPAHGRVVYTGTHDNDTTLGWYRTATPHEKAFMARYLADWGIFTFREEEEVPWALMH
LGMKSVARLAVYPVQDVLA LGSEARMNYPGRPSGNWAWRLLPGELSPEH GARL RAMAEATERL
>d1byb_c.1.8.2 (-) beta-Amylase {Soybean (Glycine max)}
SNMILLNYVPVYVMLPLGVVNVDNVFEDPDGLKEQLLQLRAAGVDGVMVDVWWGIIELKGPKQYDWRAYRS
LFQLVQECGLTLQAIMSFHQCGGNVGDIVNIPIPQWLDIGESNHIFYTNRSGTRNKEYLTGVDNEPIFHGR
TAIEIYSDYMKSFRENMSDFLESGLIIDIEVGLGPAGELRYPSPQSQGWEFPRIGEFQCYDKYLKADFKAAVARA
GHPEWELPDDAGKYNDVPESTGFFKSNGTYVTEKGFFLTWYSNKLLNHGDQILDEANKAFLGCKVKLAIKVS
GIHWYKVENHAAELTAGYYNLNDRDGYRPIARMLSRHHAILNFTCLEMRDSEQPSDAKSGPQELVQQVLSG
GWREDIRVAGENALPRYDATAYNQIILNAKPQGVNNNGPPKLSMFGVTYRLSDDLLQSKSNFNIFKKFVLKMH
ADQDYCANPQKYNHAITPLKPSAKIPIEVILLEATKPTLPFWLPETDMKVDG
>d1b1ya_c.1.8.2 (A:) beta-Amylase {Barley (Hordeum vulgare)}
MKGNYVQVYVMLPLDAVSVNNRFEKGDELRAQLRKLV EAGVDGVMVDVWWGLVEKGPKAYDWSAYKQL
FELVQKAGLKLQAIMSFHQCGGNVGDAVNIPQWVRDVGTRDPDIFYTDHGTRNIEYLTGVDNQPLFHGR
SAVQMYADYMTSFRENMKDFLDAGVIVDIEVGLGPAGELRYPSPQSHGWSFPGIGEFICYDKYLQADFAAA
AAVGHPEWEFPNDAGQYNDTPERTQFFRDNGTYLSEKGRFFLAWYSNNLIKHGDRILDEANKVFLGYKVQLAI
KIAGVHWWYKVPSHAAELTAGYYNLHDRDGYRTIARMLKRHRASINFCAEMRDSEQPPDAMSAPEELVQQ
VLSAGWREGLNVSCENALPRYDPTAYNTILRNARPHGINQSGPPEHKLFGFTYRLSNQLVEGQNYVNFKTFVD
RMHANLPRDPYVDPMAPLPRSGPEISIEMILQAAQPKIQPFQFQEHTDLPVGPTGGMGGQAEGPTCG
>d1fa2a_c.1.8.2 (A:) beta-Amylase {Sweet potato (Ipomoea batatas)}
APIPGVMPIGNYVSLYVMLPLGVVNADNVFPDKEKVEDELKQVKAGGCDGVMVDVWWGIIEAKGPKQYDW
SAYRELFLVKKCGLKIQAIMSFHQCGGNVGDAVFIPQWILQIGDKNPDIFYTNRAGNRNQEYLSLGVDNQR
LFQGRTALEMRYRDFMESFRDNMADFLKAGDIVDIEVCGAAGELRYPSPETQGWVFPGIGEFQCYDKYMVA
DWKEAVKQAGNADWEMPGKGAGTYNDTPDKTEFFRPNGTYKTDMGKFFLTWYSNKLIHGQVLEEANKV
FVGLRVNIAAKVSGIHWWYHVSHAAELTAGFYNVAGRDGYRPIARMLARHHATLNFTCLEMRDSEQPAEAK
SAPQELVQQVLSSGWKEYIDVAGENALPRYDATAYNQMLLKRPNGVNLNGPPKLMSGTLYRLSDDLLQTD
NFELFKKFVKKMHADLDPSPNAISPAVLERNSAITIDELMEATKGSRFPWYDVTDMPPVDGSNPFD
>d1b9za2_c.1.8.2 (A:1-417) Bacterial beta-amylase, catalytic domain {Bacillus cereus}
AVNGKGMNPDYKAYLAMPLKKIPEVTNWETFENDLRWAKQNGFYAITVDFWWGDMEKNGDQQFDFSYAQ
RFAQSVKNAGM KMIPIISTHQC GGNGDDCNVPI SWVWNQKSDDSLYFKSETGTVNKETLNPLASD VIRKEY
GELYTAFAAAMKPYKDVI AKIYLSGGPAGELRYPSPYTTSDGTGYP SRGKFQAYTEFAKS KFRLWVLNKY GSLNEV
NKA WGTKLISELAI LPPSDGEQFLMNGYLSMYGKDYLEWYQGILENHTKLIGELAHNAFD TTFQVPIGAKIAGV
HWQYNNPTIPHGAEK PAGYNDYSHLLDAFKSAKLDVTFTCLEMDKG SYPEY SMPKTLVQNIATLANEKGIVLN
GENALSIGNEEEYKRAE MAFN YNFAGFTLLRYQDV MYNN SLMGKF K DLLGV
>d1xyza_c.1.8.3 (A:) Xylanase {Clostridium thermocellum, XynZ}
NALRDYAEARGIKIGTCVNYPFNNSDPTYNSILQREFSMVV CENEMKFDALQPRQNVDFSKGDQ LLAFAER
NGMQMRGHTLIWHNQNPSWLTNGNWN RDSLLAVMKNHIT TVMTHYKGKIVEWDVANE CMDDSGNGLR
SSIWRNIVGQDYLDYAFRYAREADPD ALLFYNDY NIEDLGPKSNAV FMNIKSMK ERGV PIDGVGFQCHFINGM
SPEYLASIDQNIKRYAEIGVIVSFTEIDIRIPQSEN PATAFQVQANNYKELMKICL ANPNCNTFVMWGFTDKY TWI

PGTFPGYGNPLIYDSNYNPKPAYNAIKEALM

>d1hiza_c.1.8.3 (A:) Xylanase {Bacillus stearothermophilus, Xt6}

SYAKKPHISALNAPQLDQRYKNEFTIGAAVEPYQLQNEKDVQMLKRHFNSIVAENVMKPISIQPEEGKFNFQAD
DRIVKFAKANGMDIRFHTLVWHSQVPQWFLLKEGKPMVNETDPVKREQNKQLLKRLETHIKTIVERYKDDI
KYWDVVNEVGDDGKLRLNNSPWYQIAGIDYIKVAFQAARKYGGDNIKLYMNDYNTVEPKRTALYNLVQLKEE
GVPIDGIGHQSHIQIGWPSEAEIEKTINMFAALGLDNQITELDVSMSYGWPPRAYPTYDAIPKQKFLDQAARYDR
LFKLYEKLSDKISNVTFWGIADNHTWLDSRADVYYDANGNVVVDPNAPYAKVEKGKGKDAPFVFGPDYKVKA
YWAIIDHK

>d1bg4_c.1.8.3 (-) Xylanase {Penicillium simplicissimum}

EASVSIDAKFAHGKKYLGTIGDQYTLTKNTKNPAAIKADFGQLTPENSMKWDATEPNRGQFTSGSDYLVNFA
QSNGKLIRGHTLVWSQLPGWVSSITDKNTLISVLKNHITVMTRYKGKLYAWDVLNEIFNEDGSLRNSVFYNVI
GEDYVRIAFETARSVDPNAKLYINDYNLDSAGYSKVNGMVSHVKKWLAAGIPIDGIGSQTHLGAGAGSAVAGA
LNALASAGTKEIAITELDIAGASSTDYVNVVNACLNQAKCVGITVWGVA
DPDSWRSSSPLLFDGNYNPKAAYN
ANAL

>d1edg_c.1.8.3 (-) Endoglucanase CelA {Clostridium cellulolyticum}

MYDASLIPNLQIPQKNIPNNDGMNFVKGLRLGWNLGNTFADFNGTNITNEODYETWSGIKTTKQMIDAIIKQK
GFNTVRIPVSWHPHVGSDYKISDVWMNRVQEVVNYCIDNKMYVILNTHHDVDVKGYFPSSQYMASSKKYI
TSVWAQIAARFANYDEHLIFEGMNEPRLVGHANEWWPELTNSDVDSINCINQLNQDFVNTVRATGGKNAS
RYLMCPGYVASPDGATNDYFRMPNDISGNNNKIIVSVHAYCPWNFAGLAMADGGTNAWNINDSKDQSEVT
WFMDNIYNKYTSRGIPVIIGECGAVDKNNLKTRVEYMSYYAQAKARGILCILWDNNNFSGTGELGFFDRRSC
QFKFPEIIDGMVKYAFGLIN

>d1ceo_c.1.8.3 (-) Endoglucanase CelC {Clostridium thermocellum}

MVSFKAGINLGGWISQYQVFSKEHFDTITEKDIETIAEAGFDHVRLPFDYPPIIESDDNVGEYKEDGLSYIDRCLE
WCKKYNGLVLDMHHAAPGYRFQDFKTSTLFEDPNQQKRFVDIWRFLAKRYINEREHIAFELLNQVVEPDSTRW
NKLMLECIKAIREIDSTMWLYIGGNINYNSPDELKNLADIDDDYIVYNFHYNPFFFTHQKAHWS
SESAMAYNRT
VKYPGQYEGIEEFVKNNPKYSFMMELNNLKLNLKELLRKDLKPAIEFREKKCKLYCGEFGVIAIADLESRIKHED
YISLLEEYDIGGAVWNYKKMDFEIYNEDRKPVSQELVNILAR

>d1cz1a_c.1.8.3 (A:) Exo-beta-(1,3)-glucanase {Yeast (Candida albicans)}

AWDYDNNVIRGVNLGGWFVLEPYMTPSLFEPEFQNGNDQSGVPVDEYHWTQTLGKEAALRILQKHWSTWIT
EQDFKQISNLGLNFVRIPIGYWAFQQLDNDPYVQGQVQYLEKALGWAR
KNNIRVWIDLHGAPGSQNGFDNSGLR
LRSYNFQNGDNTQVTLNVLNTIFKKYGGNEYSDV
VIGIELLNEPLGPVLNMDKLQFFLDGYNSLRQTGSVTP
VIIHDAFQVFGYWNFLTV
AEGQWNVV
DHHHYQVFSGGELSRNINDHISVACNWGD
DAK
KESHWNVAG
EWSAALT
DCAKWLNGVNRGARYEGAYDN
APYIGSCQPL
LDISQWS
DEHKT
DTRRY
IAQLDAF
EYTGGW
VFW
WSWK
TENA
PEWS
FQTL
TYNGL
FPQP
VTDRQ
FPN
QCGF
H

>d1ece_a_c.1.8.3 (A:) Endocellulase E1 {Acidothermus cellulolyticus}

AGGGYWHTSGREILDANNPV
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IAGINW
FGF
ETCN
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VHGL
WSRD
YRSM
LDQ
IKSL
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YNT
IRLP
YS
DD
ILK
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TMP
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YQMN
QDL
QGL
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>d7a3ha_c.1.8.3 (A:) Endoglucanase Cel5a {Bacillus agaradhaerens}

SVVEEHGQLSISNGELV
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GAAIFVSEWGTSAATGDGGVFLDEAQVWIDFMDERNLSWANWSLHKDESSAALMPGANPTGGWTEAELS
PSGTFVREKIRES

>d1egza_c.1.8.3 (A:) Endoglucanase Cel5a {Erwinia chrysanthemi}

SVEPLSVNGNKIYAGEKAKSFAGNSLFWSNNGWGGEKFYTADTVASLKKDWKSSIVRAAMGVQESGGYLQDP
AGNKAKVERVVDAAIANDMYAIIGWHSHSAENNREAIRFFQEMARKYGNKPNVIYEIYNEPLQVSWSNTIKP
YAEAVISAIRAIIDPDNLIIVGTPSWSQNVDEASRDPINAKNIAYTLHFYAGTHGESLRNKARQALNNGIALFVTE
WGTVNADNGGGVNQTETDAWVTFRDNNISNANWALNDKNEGASTYPDSKNLTESGKKVKSIIQSWPYK
A

>d1g0ca_c.1.8.3 (A:) Alkaline cellulase K catalytic domain {Bacillus sp.}

PAGMQAVKSPSEAGALQLVELNGQLTLAGEDGTPVQLRGMSTHGLQWFGEIVNENAFVALSNDWGSNMIRL
AMYIGENGYATNPEVKDLVYEGIELAFEHDMDYVIVDWHVHAPGDPRADVSGAYDFFEEIADHYKDHPKNHYI
IWELANEPPNNNGGPGLTNDEKGWEAVKEYAEPIVEMLREKGDNMILVGNPNWSQRPDLSADNPIDAENI
MYSVHFYTGSHGASHIGYPEGTPSSERSNVMANVRYALDNGVAVFATEWGTQANGDGGPYFDEADVWLNF
LNKHNIISWANWSLTNKNEISGAFTPFLGRTDATLDPGANQVVAPEELSLSGEYVRARIKIEYTPIDRTK

>d1bqca_c.1.8.3 (A:) Beta-mannanase {Thermomonospora fusca}

ATGLHVKNGRLEYANGQEFIGVSHPHNWYPQHTQAFADIKGANTVRVVLNGVRWSKNGPSDVANVIS
LCKQNRLICMLEVHDTTGGEQSGASTLDQAVDYWIELKSVLQGEEDYVLINIGNEPYGNDSATVAAWATDTSA
AIQLRRAAGFEHTLVVDAPNWQDWTNTMRNNADQVYASDPTGNTVFSIHMYGVYQASTITSYLEHFVNA
GLPLIIGEFGHDHSDGNPDEDTIMAEAERLKLGYIGWSWSGNNGGVEYLMVYNFDGDNLSPWGERIFYGPN
GIASTAKEAVIFG

>d1qnra_c.1.8.3 (A:) Beta-mannanase {Trichoderma reesei}

ASSFTISGTQFNIDGKVGYFAGTCYWCFLTNHADVDSTFSHISSGLKVRRVWGFNDVNTQPSPGQIWFO
KLSATGSTINTGADGLQTLDYVVQSAEQHNLKLIIPFVNNWSDYGGINAYVNAFGGNATTWYTNTAAQTQYRK
YVQAVVSRVANSTAIFAWELGNEPRCNCGCDTIVQWATSVSQVKSLSNHLVTLGDEGLGSTGDGAYPYTY
GEGTDFAKNVQIKSLDFGTFHLYPDGTNYTWGNGWIQTHAAACLAAGKPCVFEYGAQQNPCTNEAPW
QTTSLTRGMGGDMFWQWGDTFANGAQNSDPYTVWYNSSNWQCLVKNHVDAIN

>d1j9ya_c.1.8.3 (A:) Mannanase 26A {Pseudomonas fluorescens, subsp. cellulosa}

PTVTKLVDQSQATMETRSLFAFMQEQRHSIMFGHQHETTQGLTITRDGTQSDTFNAVGDFAAVYGWDTLSIV
APKAEGDIVAQVKKAYARGGIITVSSHFDNPKTDTQKGWVPGTSWDQTPAVVDSLPGGAYNPVLNGYLDQV
AEWANNLKDEQGRILPIVIFRLYHENTGSFWWGDQKSTPEQYKQLFRYSVEYL RDVKGVRNFLYAYSPNNFW
DVTEANYLERPGDEWVDVLGDTYGPVADNADWFRNVVANAALVARMAEARLGIPVISEIGRAPDIEAGLY
DNQWYRKLIKADPDAREIAFLLVWRNAPQGVPGPNTQVPHWVPANRPENINNGTLEDQAFYADEF
TAFNRDIEQVYQRPT

>d1ghsa_c.1.8.3 (A:) Plant beta-glucanases {Barley (Hordeum vulgare), 1,3-beta-glucanase}

IGVCYGVIGNNLPSRSDDVVQLYRSKGINGMRIYFADGQALSALRNNSIGLILDIGNDQLANIAASTSNAASWVQ
NNVRPYPAVNIKYIAAGNEVQGGATQSILPAMRNLNAAALSAAGLGAIVKSTSIRFDEVANSFPPSAGVFKNAY
MTDVARLLASTGAPLLANVYPYFAYRDNPGLSISLYATFQPGTTVRDQNNGLTYTSLFDAMVDAVYAALEKAGA
PAVKVVSEGWPSAGGFAASAGNARTYNQGLINHVGGGTPKKREALETYIFAMFNENQKTGDATE SFGLF
NPDKSPAYNIQF

>d1aq0a_c.1.8.3 (A:) Plant beta-glucanases {Barley (Hordeum vulgare), 1,3-1,4-beta-glucanase}

IGVCYGMSANNLPAASTVSMFKSNGIKSMRLYAPNQAALQAVGGTGINVVVGAPNDVLSNLAASPAAAAS
WVKSNIQAYPKVSFRYVCVGNEVAGGATRNLVPAMKNVHGALVAAGLGHIKVTTSVSQAILGVFSPPSAGSFT
GEAAAFMGPVVQFLARTNAPLMANIYPYLAWAYNPSAMDGYALFNASGTVVRDGAYGYQNLFDTTVDAF
YTAMGKHGGSSVKLVSEGWPSGGTAATPANARFYQHHLINHVGRTPRHPGAIETYIFAMFNENQKDSG

VEQNWLFPNMQHVYPINF

>d1jz8a5 c.1.8.3 (A:334-625) beta-Galactosidase, domain 3 {Escherichia coli}
EVRIENGLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRCSHYPNHPLWYTLCDRY
GLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRMVQRDRNHPsviIwSLGNESGHGANHDALYRWI
KSVDPSRPVQYEGGGADTTATDIICPMYARVDEDQPFPAVPKWSIKKWLSPGETRPLILCQYAHAMGNSLGGF
AKYWQAQRQYPRLQGGFVWDWVDQSLIKYDENGNPWSAYGGDFGDTNDRQFCMNGLVFADRTPHPALT
EAKHQQQ

>d1bhga3 c.1.8.3 (A:329-632) beta-Glucuronidase, domain 3 {Human (Homo sapiens)}
VAVTKSQQFLINGKPFYFHGVNKHEDADIRGKGFDWPLLVKDFNLLRWLGANAFRTHYPYAEVMQMCDRYG
IVVIDECPGVGLALPQFFNNVSLHHHMQVMEEVRRDKNHPAVVMWSVANEPAHLESAGYYLKMVIAHTK
SLDPSRPVTFSNSNYAADKGAPYVDVICLNSYYSWYHDYGHLEIQLQLATQFENWYKKYQKPIIQSEYGAETI
AGFHQDPPLMFTEEYQKSLEQYHLGLDQKRRKYVVGELIWNFADFMTEQSPTRVLGNKKGIFTQRQPKSAA
FLLRERYWKIANE

>d1e0wa_ c.1.8.3 (A:) Xylanase A, catalytic core {Streptomyces lividans}
AESTLGAAAQSGRYFGTAIASGRLSDSTYTSIAGREFNMVTAELEMKIDATEPQRQFNFSADR VYNWAVQ
NGKQVRGHTLAWHSQQPGWMQSLSGSALRQAMIDHINGVMAHYKGKIVQWDVVNEAFADGSSGARRDS
NLQRSGNDWIEVAFR TARAADPSAKLCYNDVNENWTWAKTQAMYNMRDFKQRGVPI DCVGFQSHFNS
GSPYNSNFRTTLQNFAALGV DVAITELDIQGAPASTYANVTNDCLAVSRCLGITVWGV RDSDSWRSEQTPLFN
NDGSKKAAYTAVLDALNG

>d1clxa_ c.1.8.3 (A:) Xylanase A, catalytic core {Pseudomonas fluorescens}
GLASLADFP IGVAVAASGGNADIFTSSARQNIVRAEFNQITAENIMKMSYMGSNSFTNSDRLVWA AQNG
QT VHGH ALVWHPSY QLPN WASDS NANFRQDFAR HIDTVAAHFAGQVK SWDV VNEALF DSADD PDGRGSA
NGYRQSVFYRQFGGPEYIDEA FRRARAADPTAELY NDFNT EENGAKT TALV NLVQ RLLN NGV P IDGV GFQ MH
VMNDYPSIANIRQAMQKIVALSP TLKIKITE LDV RLNNPYD GNSS NDY TNR NDCAVSCA GLDR QKARY KEIV QA
YLEV VPPG RRG GITV WGIADPDSW LYTHQ NLP DWPLL FN DLQ PKPAY QGV VEALS

>d1fxma_ c.1.8.3 (A:) Xylanase A, catalytic core {Thermoascus aurantiacus}
QAAQSV DQLIKARGK VYFGVATDQNRLTTGKNAIIQADFGQVTPENS MKWDATEPSQGNF NFAGADYL VN
WAQQNGKL IRGHTLWHSQ LPSW VSSITDKNTLT NVMK NHITTLMTRYKGKIR AWDV VNEAFN EDGSLR QT
VFLNVIG EYIPIAF QTARAADPNAKLYINDY NLD SAS YPKT QAI VNRV KQW RAAGV P IDGIGSQ THLS AGQ GA
GVLQALPLL ASAGTPEV AITEL DVAGASPT DYV NVV NA CLNV QSCV GITV WGV ADPDS WRAS TTPLL FDGN FN
PKPAYNAIVQDLQ

>d1tux_ c.1.8.3 (-) Xylanase A, catalytic core {Thermoascus aurantiacus}
AAAQSV DQLIDARGK VYFGVATDQNRLTTGKNAIIQADFGQVTPENS MKWDATEPSQGNF NFAGADYL VN
WAQQNGKL IRGHTLWHSQ LPSW VVSITDKNTLT NVMK NHITTLMTRYIGKIR AWDV VNEAFN EDGSLR QT
FNNVIG EYIPIAF QTARAADPNAKLYINDY NLD SAS KPK TS AIVK RVKK WRAAGV P IDGIGSQ THLS AGQ GASI
DAALPNL ASAGTPEV AITEL DIAGATSTDY DVV NA CLD VDSCIG ITV WGV ADPDS WRAS TTPLL FDGN FNPK P
AYNAIVQLL

>d1xyfa2 c.1.8.3 (A:1-303) Xylanase A, catalytic core {Streptomyces olivaceoviridis}
AESTLGAAAQSGRYFGTAIASGKLGDSAYTTIASREFNMVTAELEMKIDATEPQRQFNFSAGDR VYNWAVQ
NGKQVRGHTLAWHSQQPGWMQSLSGSSTLRQAMIDHINGVMGH YKGKIAQW DV VNEAFS DDGSGG RRDS
NLQRTGNDWIEVAFR TARAADPAAKLCYNDVNENWTWAKTQGV YNMVRDFKQRGVPI DCVGFQSHFNSG
SPYNSNFRTTLQNFAALGV DVAITELDIQGASS STYAA VTNDCLAVSRCLGITVWGV RDSDSWRSGD TPLLFNG
DGSKKAAYTAVLNALNGG

>d1fh9a_ c.1.8.3 (A:) Xylanase A, catalytic core {Cellulomonas fimi}

ATTLKEAADGAGRDFGFALDPNRLSEAQYKAIADSEFNLVVAENAMKWDATEPSQNSFSFGAGDRVASYAADT
GKELYGHTLVWSQLPDWAKNLNGSAFESAMVNHTKVADHFEGKVASWDVVNEAFADGGGRQDSAFQ
QKLNGNYIETAFRAARAADPTAKLCINDYNVEGINAKSNSLYDLVKDFKARGVPLDCVGQSHLIVGQVPGDFR
QNLQRFADLGVDVRITELDIRMRTPSDATKLATQAADYKKVVOACMQVTRCQGVTVWGITDKYSWVPDVFP
GEAALWDASYAKKPAYAAVMEAF

>d1e4mm_ c.1.8.4 (M:) Plant beta-glucosidase (myrosinase) {White mustard (*Sinapis alba*)}
EITCQENLPFTCGNTDALNSSSFSDFIFGVASSAYQIEGTIGRGLIWDFTHRYPNKSGPDHGNGDTCDSFS
YWQKDIDVLDELNATGYRSIAWSRIIPRGKRSRGVNEKGIDYYHGLISGLIKKIGTPVTLFWDLQTLQDEYE
GFLDPQIIDDFKDYADLCFEFGDSVKYWLTIQLYSVPTRGYGSALDAPGRCSPTVDPSCYAGNSSTEPIVAHH
QLLAHAKVVDLYRKNYTHQGGKIGPTMITRWFLPYNDTRHSIAATERMKEFFLGWMGPLTNGTYPQIMID
TVGERLPSFSPEESNLVKGSYDFGLNYYFTQYAQPSPNPVNSTNHTAMMDAGAKLTYINASGHYIGPLFEKDK
ADSTDNIYYYPKGIYSVMDYFKNKYYNPLIYTENGISTPGDENRNQSMILDYTRIDYLCSHLCFLNKVIKEKDVN
VKGYLAWALGDNYEFNKGFTVRFLSYIDWNNVTDRDLKKSGQWYQSFISP

>d1cbg__ c.1.8.4 (-) Plant beta-glucosidase (myrosinase) {Creeping white clover (*Trifolium repens*)}
FKPLPISDDFSDLNRSCFAPGFVFGTASSAFQYEGAFAEDGKGPSIWTFTHKYPEKIKDRTNGDVAIDEYHRYK
EDIGIMKDMNLDAYRFSISWPRVLPKGKLSGGVNREGINYYNNLINEVLANGMQPVTLFHWDPVPALEDEY
RGFLGRNIVDDFRDYAELCFKEFGDRVKHWITLNEPWGVSMNAYAYGTFAPGRCSDWLKLNCCTGGDGREPY
LAAHYQLLAHAAAARLYTKYQASQNGIIGITLVSHWFEPASKEKADVDAAKRGLDFMLGWFHMPLTKGRYPE
SMRYLVRKRLPKFSTEESKELTGSFDLGLNYYSSYYAAKAPRIPNARPAIQTDSSLINATFEHNGKPLGPMAASSW
LCIYPQGIRKLILYVKNHYNNPVIYITENGNEFNDPTSLQESLLDTPRIDYYRHLYYVITAIGDGVNVKGYFAW
SLFDNMEWDGTYVRFLVFDFKNNLRHPKLSAHWFKSFLKK

>d1e55a_ c.1.8.4 (A:) Plant beta-glucosidase (myrosinase) {Maize (*Zea mays*), zmglu1}
VQMLSPSEIPQRDWFPSDFTFGAATSAQIEGAWNEDGKGESNWDHFCHNPERILDGSNSDIGANSYHMY
KTDVRLKEMGMADYRFSISWPRILPKGKTKEGGINPDGIKYRNLLINLLLENGIEPYVTIFHWDPVPALEEKYGG
FLDKSHKSIVEDTYFAKVCDFNFGDKVKNWLTNFNDPQTTSFSYGTGVFAPGRCSPLDCAYPTGNSLVEPYTA
GHNILLAHEAVDLYNKHYKRDDTRIGLAFDVMGRVPYGTFSFLDKQAEERSWDINLGWFLEPVVRGDYPSM
RSLARERLPFFKDEQKEKLAGSYNMLGLNYYTSRFSKNIDISPNSPVLTDDAYASQEVENGPDGKPIGPPMGN
PWIYMPPEGLKDLMIMKKNKYGNPPIYITENGIDVDTKETPLPMEAALNDYKRLDYIQRHIATLKESIDLGSNV
QGYFAWSLLDNFEWFAGFTERYGIVYVDRNNNCTRYMKESAKWLKEFNTA

>d1pbga_ c.1.8.4 (A:) 6-phospho-beta-D-galactosidase, PGAL {*Lactococcus lactis*}
MTKTPKDFIFGGATAAYQAEQATHDGKGPVAWDKYLEDNYWYTAEPASDFYHKYPVDLELAEEYGVNGIRIS
IAWSRIFTGYGEVNEKGVEFYHKLFAECHKRHVEPFVTLHHFDTPEALHSNGDFLNRENIEHFIDYAAFCFEFP
EVNYWTTFNEIGPIGDGQYLVGFPPGIKYDLAKVFQSHHNMMVSHARAVKLYDKGYKGEIGVVHALPTKYP
YDPENPADVRAAELEDIIHNKFILDATYLGHYSDKTMEGVNHLAENGGEELRDEDFAQALDAAKDLNDFLGIN
YYMSDWMQAFDGETEIIHNGKGEKGSSKYQIKGVGRRVAPDYPRTDWIYPEGLYDQIMRVKNDYPNYK
KIYITENGLGYKDEFVDNTVYDDGRIDYVKQHLEVLSDAIADGANVKGYFIWLSMDVFSWSNGYEKRYGLFYVD
FDTQERYPKKSAHWYKKLAETQVIE

>d1e4ia_ c.1.8.4 (A:) Beta-glucosidase A {*Bacillus polymyxa*}
TIFQFPQDFMWGTATAAYQIEGAYQEDGRGLSIWDTFAHTPGKVNGDNGNVACDSYHRYEEDIRLMKELGIR
TYRFSVSWPRIFPNGDGEVNQKGLDYYHRVVDLLNDNGIEPFCTLYHWDLQALQDAGGWGNRTIQAFVQ
FAETMFREFHGKIQHWLTFNEPWCIALSNMLGVHAPGLTNLQTAIDVGHHLVAHGLSVRRFELGTSGQIGI
APNVSWAJVYDGGTSEEDKAACARTISLHSDWFLQPIYQGSYPQFLDWFAEQGATVPIQDGDMIIGEPIDMIGI
NYYSMSVNRFNPEAGFLQSEEINMGLPTDIGWPVESRGLYEVHLQKYGNIIDYITENGACINDEVVNGKVQ
DDRRISYMQQHLVQVHRTIHDGLHVKGYMAWSLLDNFEWAEGYNMRFGMIHVDFRTQVRTPKQSYYWYR

NVVSNNWLETTR

>d1qoxa_ c.1.8.4 (A:) Beta-glucosidase A {Bacillus circulans, subsp. alkalophilus}

SIHMFPSDFKVGVATAAYQIEGAYNEDGRGMSIWDTFAHTPGKVNGDNGNVACDSYHRVEEDVQLLKDGLGVKVYRFISWPRVLPQGTGEVNRAGLDYYHRLVDELLANGIEPFTLYHWDLQALQDQGGWGSRITIDAFAYAELMFKEKGKIKQWITFNEPWCMALSNYLGVHAPGNKDLQALDVSHLLVAHGRAVTLFRELGISGEIGIAPNTSWAVPYRRTKEDMEACLRVNGWSGDWYLDPIYFGEYPKFMLDWYENLGYKPPIVDGDMELIHQPIDFIGINYYTSSMNRYNPGEAGGMLSSEAISMGAPKTDIGWEIYAEGLYDLLRTADKYGNPTLYITENGACYNDGLSLDGRHDQRRIDYLAMHLIQASRAIEDGINLKGYMEWSLMDNFEWAEGYGMRFGLVHVVDYDTLVRTPKDSFYWYKGVISRGWLDL

>d1gowa_ c.1.8.4 (A:) beta-Glycosidase {Archaeon Sulfolobus solfataricus}

MYSPNSFRFGWSQAGFQSEMGTPGSEDPNTDWYKWVHDPEMAAGLVSGDLPENGPGYWGNYKTFHDNAQKMGLKIARLNSEWSRQFPNPLPRPQNFDESKQDVTEVEINENELKRLDEYANKDALNHYREIFKDLKSRLGYFIQNMYHWPLPLWLHDPIRVRRGDFTPSGWLSTRTVYE FARFSAYTAWKFDDLVDEYSTMNEPNVVGGLGYVGVKSGFPPGylSFELSRRAMYNIIQAHARAYDGIVSKKPVGIIYANSSFQPLTDKDMEA VEMAENDNRWWFFDAIRGEITRGNEKIVRDDLKGRDWIGVNYYTRTVKRTEKGYVSLGGYGHGCERNSVSLAGLPTSDFGWEFFPEGLYDVLTKYWNRYHLYMYVTENGIADDADYQRPYYLVSHVYQVHRAINSGADVRGYLHWSLADNYEWASGFSMRFGLKVDYNTKRLYWRPSALVYREIATNGAITDEIEHLNSVPPVKPLRH

>d1qvba_ c.1.8.4 (A:) beta-Glycosidase {Archaeon Thermosphaera aggregans}

MKFPKDFMIGYSSPFQFEAGIPGSEDPNSDWWVVWVHDPENTAAGLVSGDFPENGPGYWNLNQNDHDLAEKLGVNTRGVGEWSRIFPKPTFNVKVPVERDENGSIVHVDVDDKAVERLDELANKEAVNHYVEMYKDWERGRKLILNLYHWPLPLWLHNPIMVRRMGPDRAPSGWLNEESVVEFAKYAAVIAWMGELPVMWSTMNEPNVYVEQGYMFVKGGFPPGylSLEAADKARRNMIIQAHARAYDNIKRFSKKPVGLIYAFQWFELLEGPAEVFDKFKSSKLYYFTDIVSKGSSIINVEYRRDLANRLDWLGVNYSRLVYKIVDDKPIILHGYGFLCTPGGISPAENPCSDFGWEVYPEGLYLLLKELYNRGYVDLIVTENGVSDSRDALRPAYLVSHVYVWKAANE GIPVKGYLHWSLTDNYEWAQGFRQKFGLVMDKTFKRYLRPSALVFREIATHNGIPDELQHLTIQ

>d2hvm_ c.1.8.5 (-) Hevamine A (chitinase/lysozyme) {Para rubber tree (Hevea brasiliensis)}

GGIAIWGQNGNEGTLTQTCSTRKSYVNIAFLNKFGNGQTPQINLAGHCNPAA GGCTIVSNGIRSCQIQGIKVMLSLGGGIGSYTLASQADAKNVADYLWNNFLGGKSSRPLGDAVLGIDF DIEHGSTLYWDDLARYLSAYSKQGKKVYLTAAQCPFPDRYLGTLNTGLFDYVVQFYNNPPCQYSSGNINNIINSWNRWTT SINAGKIFGLPAAPEAAGSGYVPPDV LISRILP EIKKSPKYGGVMLWSKFYDDKNGYSSILDSV

>d1nar_ c.1.8.5 (-) Seed storage protein {Vicia narbonensis, Narbonin}

PKPIFREYIGVKPNSTLHDFPTEIINTETLEFHILGFAIESYYESGKGTGTFEESWDVELFGPEVKVNLKRRHPEVKVISIGGRGVNTPFDAEENVVVSNAKESLKLIIQKYSDDSGNLIDGIDIHYEHIRSDEPFATLMGQLITEKKDDDLNINVVIAPSEN NSSHYQKLYNAKKDYINWVDYQFSNQQKPVSTDADFVEIFKSLEKDYHPHKVLPGFSTDPLDTKHNKITRDIFIGGCTRLVQTSLPGVFFWNANDSVIPKRDGDKFIVE LTLQQLAA

>d1cnv_ c.1.8.5 (-) Seed storage protein {Jack bean (Canavalia ensiformis), Concanavalin B}

DISSTEIAVYWGQREDGLLRTCKTN NYKIVFISFLDKFGCEIRKPELELEGVCGPSGNPCSFLESQIKECQRMGVKVFLALGGPKGTYACSADYAKD LAEYLHTYFLSERREGPLGKVALDGIHF DIQKPVDELNW DNLL EELYQIKD YQSTFLLSAAPGCLSPDEYLDNAIQTRHF DIFYVRFYNDRSCQYSTGNIQ RIRNAWLSWTKS VYPRDKNLFELPA SQATAPGGYIPPSALIGQVLPYLPDLQTRYAGIALWNRQADKETGYSTNIIRY

>d2ebn_ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {Flavobacterium meningosepticum, endoglycosidase F1}

TTKANIKLFSFTEVNDTNPLNNLNFTLNSKGKPLVDMVVLFSANINYDAANDKVFVSNNPNVQHLLTNRAKYLKPLQDKGIVKVLISILGNHDRSGIANLSTARAKAFAQELKNTCDLYNLDGVFFDEYSAYQT PPPSGFVTPSNAAAAR

LAYETKQAMPNKLTVVYYSRTSSPTAVDGVNAGSYVDYAIHDYGGSYDLATNYPGLAKSGMVMSSQEFNQ
GRYATAQALRNIVTKGYGGHMIFAMDPNRSNFTSGQLPALIKIAKELYGDELVYSNTPYSKDW

>d1eoka_ c.1.8.5 (A:) Endo-beta-N-acetylglucosaminidase {*Flavobacterium meningosepticum*, endoglycosidase F3}

NGCIAYYITDGRNPTFKLKDIPDKVDMVILFGLKYWSLQDTTKLPGGTGMMGSFKSYKDLDTQIRSLQSRGIK
VLQNIDDDVSWQSSKPGGFASAAAYGDAIKSIVIDKWKLDGISLDIEHSGAKPNPIPTFGYAATGYNGWYSGS
MAATPAFLNVISELTKYFGTTAPNNKQLQIASGIDVYAWNKIMENFRNNFNYIQLQSYGANVSRTQLMMNYAT
GTNKIPASKMVFGAYAEGGTNQANDVEVAKWPTQGAKGGMIMIYTYSNSVSYANAVRDAVK

>d1edt_ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {*Streptomyces plicatus*, endoglycosidase H}

KQGPTSVAYVEVNNNSMLNVKYTLADGGNAFDVAVIFAANINYDTGKTAYLFNENVQRVLDNAVTQIRP
LQQQGIKVLLSVLGHNHQGAGFANFPSQQAASAFAKQLSDAVAKYGLGVDFDDEYAEGNNNTAQPNDSFFV
HLVTALRANMPDKIISLYNIGPAASRLSYGGVDVSDKFDYAWNPPYGTWQVPGIALPKAQLSPAVERGRTSRST
VADLARRTVDEGYGVYLTYNLGGDRTADVSAFTRELYGSEAVRT

>d1edqa2 c.1.8.5 (A:133-443,A:517-563) Chitinase A, catalytic domain {*Serratia marcescens*}

TDGSHLAPLKEPLLEKNKPYKQNSGKVGSYFVEWGVBGRNFTVDKIPAQNLTLLYGFIFICGGNGINDSLKEIE
GSFQALQRSCQGREDFKVSIHDPFAALQKAQKGVTAWDDPYKGNFGQLMALQAHPPDLKILPSIGGWTLSDP
FFFMGDKVKRDRFVGSKFELQTWKFFDGVDIDWEFPGGKGANPNLGSPQDGETYVLLMKELRAMLDQLSV
ETGRKYELTS AISAGKDKIDKVAYNVAQNSMDHIFLMSYDFYGAFLDKNLGHQTALNAPAWKPDATYTTVNGV
NALLAQGVKPGKIVVGTAMXDARSVQAKGKYVLDKQLGLFSWEIDADNGDILNSMNASLGNSAGVQ

>d1goia2 c.1.8.5 (A:3-291,A:380-446) Chitinase B, catalytic domain {*Serratia marcescens*}

TRKAVIGYYFIPTQNINNYTETDTSVVPFPVSNTPAKAKQLTHINFSFLDINSLECAWDPATNDAKARDVVNRL
TALKAHNPSLRIMFSIGGWYYNDLGVSHANYVNAVTPASRAKFAQSCVRIMKDYGFDGVNIDWEYPQAAE
VDGFIAlAQEIRTLNNQQTITDGRQALPYQLTIAGAGGAFFLSRYSKLAQIVAPLDYINLMTYDLAGPWEKVTN
HQAAALFGDAAGPTFYNALREANLGWSWEELTRAFPSFSLTVDAAVQQHLMMEGVPSAKIVMGVPFXDDAE
SKFYKAKYIKQQQLGGVMFWHLGQDNRNGDLAALDRYFNAAADYDDSQLDMGTGLRYTGVGPG

>d1d2ka1 c.1.8.5 (A:36-292,A:355-427) Chitinase 1 {Fungus (Coccidioides immitis)}

GGFRSVVYFVNWAIYGRGHNPQDLKADQFTHILYAFANIRPSGEVYLSDTWADTDKHYPGDKWDEPGNNVY
GCIKQMYLLKKNNRNLKTLISIGGWTYSPNFKTPASTEEGRKKFADTSLKLMKDLGFDGIDIDWEYPEDEKQAN
DFVLLLKACREALDAYSAKHPNGKKFLTIASPAGPQNYNKLKLAEMDKYLDFWNL MAYDFSGSWDKVSGHM
SNVFPSTTKPESTPFSSDKAVKDYIKAGVPANKIVLGMPLEXDTVIAGKKAEYITKNGMGGMWESSSDKTG
NESLVTVVNGLGGTGKLEQRENELSYPESVYDNLKNGMPS

>d1e9la1 c.1.8.5 (A:22-266,A:337-393) Chitinase-like lectin ym1, saccharide binding domain {Mouse (*Mus musculus*)}

YQLMCYYTSWAKDRPIEGSFKPGNIIDPCCLCTHILYAFAGMQNNEITYTHEQDLRDYEALNGLKDKNTELKTLAI
GGWKFGPAPFSAMVSTPQNRQIFIQS VIRFLRQYNFGLNLDWQYPGSRGSPPKDKHLFSVLVKEMRKAFEEE
SVEKDIPRLLLSTGAGIIDVIKSGYKIP ELSQSLDYIQVMTYDLHDPKDGYTGENSPLYKSPYDIGKSADLNVDIIS
YWKDHGAASEKLVGFPA XDNVRSFKLKAQWLKDNNLGGAVVVPLDMDDSGSFCHQRHFPLSTLKGDLNI
HSAS

>d1jfxa_ c.1.8.8 (A:) Streptomyces lysozyme {*Streptomyces coelicolor*, "mueller" dsm3030}

DTSGVQGIDVSHWQGSINWSSVKSAGMISFAYIKATEGTNYKDDRF SANYTNA NAGI RGAYHFARPNASSGT
AQADYFASNGGGWSRDNR LPGVLDIEHNP SGAMCYGLSTTQMRTWINDFHARYKARTTRDVVIYTTASW
WNTCTGSWNGMAAKSPFWVAHWGVSA PTVPSGFPTWTFWQYSATGRVGGVSGDVRNKFNGSAARLLA

LANNTA

>d1qba_3 c.1.8.6 (338-780) Bacterial chitobiase (beta-N-acetylhexosaminidase) {*Serratia marcescens*}

FPYRGIFLDVARNFHKKDAVLRLLDQMAAYKLKNFHFHLSDEGWRIEIPGLPELTEVGGQRCHDLSETTCLLPQ
YQGQPDVYGGFFSRQDYIDIICKYQAQARQIEVIPEIDMPAHAARA AVVSMEARYKKLHAAGKEQEANEFRLVDPD
TSNTTSVQFFNRQS YLNPCLDSSQRFDVKVIGEIAQMHEAGQPIKTWHFGGDEAKNIRLGAGYTDKAKPEPG
KGII DQGNEDKPWAKSQVCQTMIKEGVADMEHLPYFGQEVSKLVKAHGIDRMQAWQDGLKDAESSKAFA
TSR VGVNFWD TLYWGGFD SVNDWANKGYEV VVSNPDVYMDFPYEVNPDERGYYWGTRFSDERKVFSFAP
DNMPQNAETSVDRDGNHFN A KSDKPWPGAYGLSAQLWSETQRTDPQMEYMFPRALSVAERSWH RAGWE
QDYRAGREYKG

>d1jaka1 c.1.8.6 (A:151-506) beta-N-acetylhexosaminidase {*Streptomyces plicatus*}

YAWRSAMLDVSRHFFGVDEVKRYIDRVARYKYNKLHLHLSDDQGWRIAIDSWPRLATYGGSTEVG GPGGYY
TKAEYKEIVRYAASRHLEV VPEIDMPGHTNAALASYAELNCGVAPPLYTGKVGSSL CVDKDVTYDFVDDVIG
ELAALTPGRYLHIGGDEAHSTPKADFVAFMKRVQPIVAKYGKTVVGWHQLAGAEPVE GALVQYWG LDRTGDA
EKAEVAEAARNGTGLLSPADRTYLDMKYTKDTPLGLSWAGYVEVQRSYDWDPAGYLP GAPADA VRGVEAPL
WTETLSDPDQLDYMAFPRLPGVAELGWSPASTHDWDTYKVRLAAQAPYWEAAGIDFYRSPQVPWT

>d1iexa1 c.1.8.7 (A:1-388) Beta-D-glucan exohydrolase, N-terminal domain {*Barley (Hordeum vulgare)*}

DYVLYKDATKPVEDRVADLLGRMTLAEKIGQMTQIERLVATPDVL RDNFIGSLLSGGGSVPRKGATA KEWQDM
VDGFQKACMSTRLGIPMIYGIDAVHGQNNVYGATIFPHNVGLGATRD PYLVKRIGEATA LEVRATGIQYAFAPCI
AVCRDPRWGRCYESYSEDRRIVQSMTELIPGLQGDVPKDFTSGMPFVAGKNKVAACAKHFVGDGGTVDGINE
NNTIINREGLMNIHMPAYKNAMDGVSTVMISYSSWNGVKMHANQDLVTG YLKDTLKFGFVISDWE GIDRI
TT PAGSDYSYSVKASILAGLDMIMVPNKYQQFISLTGHVNGGVIPMSRIDD ATRILRVKFTMGLFENPYADPA
MAEQLGKQEHRDLAREAARKS

>d1fcqa_ c.1.8.9 (A:) Bee venom hyaluronidase {*Honeybee (Apis mellifera)*}

EFNVYWNVPTFMCHKYGLRFEVSEKYGILQNWM DKFRGEEI AILYDPGMFP ALLKDPNGNVVARNGGPQL
GNLTKHLQVFRDH LINQIPDKSF PGVGVIDFESWRPIFRQN WASLQPYKKL SVEV VRREHPFWDDQR VE QEA
RRFEKYGQLFMEETLKA AKRMRPAANW GYYA PYCYNLTPNQPSAQCEATTMQENDKMSWL FESEDVLLPS
VYLRWNLTSGERV GLVGG RVKE ALRIARQMTTSRK KVLP YYW KYQD RR DTL SRA DLEAT LRKIT DLGADG FII
WGSSDDINTKAKCLQFREYLNNE LGPAVKR

>d1a4ma_ c.1.9.1 (A:) Adenosine deaminase (ADA) {*Mouse (Mus musculus)*}

TPAFNPKVELHVHLDGAIK PETILYFGKKRGIALPADTVEELRN II GMDKPLSLPGFLAKFDY YMPVIAGCREAIK
RIAYEFVEMKAKEGVVYVEVRYSPHLLANSKVDPMPWNQTEG DVT PDDVV D LVNQGLQEGEQAFGIK VRSIL
CCMRHQPSWSLEVLELCKKYNQKTVVAM DLAGDETIEGSSLFPGHVEA YEGAVKNGI HRTV HAGEV GSPEVV
REAVDILKTERV GHGYHTIEDEALYNRLLKENMH FEVCPWSSYLTGA WDPKTT HAVVRFKNDKAN YSLNTDDP
LIFKSTLTDYQMTKDMGFTEE FKRLNINA AKSSFLPEEEKKELLERLYREYQ

>d1j79a_ c.1.9.4 (A:) Dihydroorotase {*Escherichia coli*}

SQVLKIRRPDDWHLHLDGDM LKTVV PYTSEIYGRAIVMPNLAPPVTT VEA VAVYRQR ILDA VPAP HDFTPLM
TCYLTDSLDPNE LERGFNEG VFTA AKLYP ANATTNSH GVT SVDA IMPVLERMEK IGM PLLV HGEV THAD IDIFD
REAR FIESVMEPLRQRLTALKV VFEH ITT KDA ADYVRDG NERLA ATITPQHLMF NRNHMLVGGVRPH LYCL PILK
RNIHQ QALREL VAS GFQ RVFL GTDSAP H RKE SS CGCAG CFN APTAL GSYATV FEEM NALQH FEA FC SVNG
PQFYGLPVNDT FIELV REEQ QVA ESI ALT DDTL VPFLAG ET VRWSVK

>d1k6wa2 c.1.9.5 (A:56-375) Cytosine deaminase catalytic domain {*Escherichia coli*}

PFVEPHIHLDTTQAGQPNWNQSGTLFEGIERWAERKALLHDDVKQRAWQTLKWQIANGIQHVRTHVDVS
DATLTALKAMLEVQEVAPWIDLQIVAFPQEGILSYPNGEALLEALRLGADVGAIPHFEFTREYGVESLHKTF
LAQKYDRLIDVHCDEIDDEQSFRVETVAALAHHEGMGARVTASHATTAMHSYNGATSRLFLLKMSGINFVAN
PLVNIHLQGRFDTPKRRGITRVKEMLESGINVCFGHDDVFPWYPLGTANMLQLVLMGLHVCQLMGYGQI
NDGLNLITHHSARTNLQDYGIAAGNSAN

>d1ejrc2 c.1.9.2 (C:1130-1422,C:1476-1567) alpha-subunit of urease, catalytic domain {Klebsiella aerogenes}

GIDTHIHWCQQAAEALVSGVTTMVGGGTGPAAAGTHATTCTPGPWYISRMLQAADSLPVNIGLLGKGNVSQ
PDALREQVAAGVIGLKIHEAWGATPAAIDCALTVADEMDIQLVALHSDTLNESGFVEDTAAIGGRTIHTFHTEGA
GGGHAPDIITACAHPNILPSSTNPTLPYTNTIDEHLDMLMVCHHLDPIAEDVAFAESRIRRETIAAEDVLHDLG
AFSLTSSDSQAMGRVGEVILRTWQVAHRMKVQRGALAETGDNDNFRVKRYIAKYTINPALTHGIAHEVGXM
FGALGSARHHCRLTFLSQAAAANGVAERLNLSAIAVVKGCRTVQKADMVHNSLQPNITVDAQTYEVRDGEL
ITSEPADVLPMAQRYFLF

>d4ubpc2 c.1.9.2 (C:132-434,C:484-570) alpha-subunit of urease, catalytic domain {Bacillus pasteurii}

GGIDTHVHFNPQDVVALANGITLFGGGTGPAAEGSKATTVTPGPWNIKMLKSTEGLPINVGILGKGHGSSI
APIMEQIDAGAAGLKIHEDWGATPASIDRSLTVADEADVQVAIHSDTLNEAGFLEDTLRAINGRVIHSFHEVAG
GGHAPDIMAMAGHPNVLPSSNPTRFVTNTIDEHLDMLMVCHHLDKQNIPEVAFADSIRPETIAAEDILHD
LGIISMMSTDALAMGRAGEMLVRTWQTADMKKQRGPLAEEKNGSDNFRLKRYVSKYTINPAIAQGIAHEVG
SIEEGKFADXGDLIHDTNITFMSKSSIQQGVPAKGLKRRIGTVKNCRNIGKKDMKWNDVTTDIDINPETYEVKV
DGEVLTCEPVKELPMAQRYFLF

>d1e9yb2 c.1.9.2 (B:132-431,B:481-569) alpha-subunit of urease, catalytic domain {Helicobacter pylori}

GIDTHIFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRRNLKWMLRAAEYSMNLGFLAKGNASND
ASLADQIEAGAIGFKIHEDWGTPSAINHALDVADKYDVQVAIHTDTLNEAGCVEDTMAAIAGRTMHTFHTEG
AGGGHAPDIIKVAGEHNILPASTNPTIPFTVNTEAEHMDMLMVCHHLDKSIKEDVQFADSIRPQTIAAEDTLH
DMGAFSITSSDSQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEYVGS
VEVGKVXHHGKAKYDANITFVSQAAYDKGIKEELGLERQVLPVKNCRNVTKKDMQFNNTTAIEVNPETYHVF
VDGKEVTSKPANKVSLAQLFSIF

>d1i0da_c.1.9.3 (A:) Phosphotriesterase {Pseudomonas diminuta}

DRINTVRGPITISEAGFTLTHEHICSSAGFLRAWPEFFGSRKALAEKAVRGLRARAAGVRTIVDVSTFDIGRDV
SLLAEVSRaadVHIVAATGLWDFPPLSMRLSVEELTQFFLREIQYGIEDTGIRAGIIKVATTGKATPFQELVLKAAA
RASLATGVPVTTHTAASQRDGEQQAAIFESEGLSPSRVCIGHSDTDDLSYLTAARGYLIGLDHIPHSAGLED
NASASALLGIRSWQTRALLIKALIDQGYMKQILVSNDWLFGFSSYVTNIMDVMDRVNPDGMAFIPLRVIPFLRE
KGVPQETLAGITVTNPARFLSPTLRAS

>d1bf6a_c.1.9.3 (A:) Phosphotriesterase homology protein {Escherichia coli}
SFDPTGYTLAHEHLHIDLSGFKNVDCRLDQYAFICQEMNDLMTGVRNVIEMTNRYMGRNAQFMLDVMR
ETGINVVACTGYYQDAFFPEHVATRSVQELAQEMVDEIEQGIDGTELKAGIIAEIGTSEGKITPLEEKVFIAAALAH
NQTGRPISTHTSFSTMGLEQLALLQAHGVDSLRTVGHCDLKDNLDNLMKIDLGAYVQFDTIGKNSYPDEKR
IAMLHALRDRGLLNRVMILSMDITRRSHLKANGGYGYDYLTTFIPQLRQSGFSQADVDVMLRENPSQFFQ

>d1jcla_c.1.10.1 (A:) Deoxyribose-phosphate aldolase DeoC {Escherichia coli}
HMTDLKASSLRAKLMDDTLNDDDTDEKVLCHQAKTPVGNTAACIYPRFIPIARKTLKEQGTPEIRIATVTNF
PHGNDDIDIALAETRAAIAYGADEVVFPYRALMAGNEQVGFDLVKACKEACAAANVLLVIIETGELKDEALI
RKASEISIKAGADFIKTSTGKAVVNATPESARIMMEVIRDMGVEKTVGFKPAGGVRTAEDAQKYLAIADELFGAD

WADARHYRGASSLLASLLKALGHG

>d1nal1_c.1.10.1 (1:) N-acetylneuraminate lyase {Escherichia coli}

NLRGVMAALLTPFDQQQALDKASLRLVQFNQQGIDGLYVGGSTGEAFVQLSEREQVLEIVAEKGKIKLIA
HVGCVTTAESQQLAASAKRYGFDAVSAVTPFYYPFSFEEHCDHYRAIDSADGLPMVVNIPALSGVKLTLDQIN
TLVTLPGVGALKQTSGDLYQMEQIRREHPDLVLYNGYDEIFASGLLAGADGGIGSTYNIMGWRYQGIVKALKEG
DIQTAQKLQTECNKVIDLLIKTVFRLKTVLHYMDVVSPLCRKPFGPVDEKYQPELKALAQQLMQ

>d1f74a_c.1.10.1 (A:) N-acetylneuraminate lyase {Haemophilus influenzae}

MRDLKGIFSALLVSFNEDGTINEKGLRQIIRHNIDKMVKDGLYVGGSTGENFMLSTEKKEIFRIAKDEAKDQIALI
AQVGSVNLKEAVELGYATELGCLSAVTPFYKFSPEIKHYYDTIIAETGSNMIVSIPFLTGVNMIGIEQFGELY
KNPKVLGVKFTAGDFYLLERLKKAYPNHLIWAGFDEMMLPAASLGVDGAIGSTFNVNGVRARQIFELTKAGKLK
EALEIQHVTNDLIELGILANGLYLTIKELLKLEGVDAGYCREEPMTSKATAEQVAKAKDLKAKFLS

>d1dhp_a_c.1.10.1 (A:) Dihydrodipicolinate synthase {Escherichia coli}

MFTGSIVAIITPMDEKGNVCRASLKKLIDYHVASGTSIAIVSGTTGESATLNHDEHADVMMTLDLADGRIPVI
AGTGANATAEAIISLTQRFDNSGIVGCLTVTPYYNRPSQEGLYQHFKIAEHTDLPQILYNVPSRTGCDLLPETVGR
LAKVKNIIIGIKEATGNLTRVNQIKELVSDDFVLLSGDDASALDFMQLGGHGVISVTANVAARDMAQMCKLAAE
GHFAEARVINQRLMPLHNKLVEPNPIPVKWACKELGLVATDTLRLPMTITDSGRETVAALKHAGLL
>d1qo5b_c.1.10.1 (B:) Fructose-1,6-bisphosphate aldolase {Human (Homo sapiens), liver isozyme}

AHRFPALTQEQQKELSEIAQSIVANGKGILAADESVGTMGNRLQRIKVENTEENRRQFREILFSVDSSINQSIGGV

ILFHETLYQKDSQGKLFRNILEKGIVVGKIKLDQGGAPLAGTNKETTIQGLDGLSERCAQYKKDGVDGFKWRAVL
RIADQCPSSLAIQENANALARYASICQQNGLVPIVEPEVIPDGDHDLEHCQYVTEKVLAavyKALNDHHVYLEGT
LLKPNMVTAGHACTKKYTPEQVAMATVTALHRTVPAAVPGICFLSGGMSEEDATLNNAINLCPLPKPWKLSFS
YGRALQASALAAWGGKAANKEATQEAFMKRAMANCQAAGQYVHTGSS

>d1adoa_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus), muscle isozyme}

PHSHPALTPHQKKELESDIAHRIVAPGKGILAADESTGSIKRLQSIGTENTEEENRRFQRQLLTADDRVNPCIGGVIL
FHETLYQKADDGRFPQVIKSQKGGVVGIVDKGVVPLAGTNGETTQGLDGLSERCAQYKKDGADFAKWRCVL
KIGEHTPSALAIMENANVLARYASICQQNGLVPIVEPEVIPDGDHDLEHCQYVTEKVLAavyKALSDHHIYLEGTL
LKPNMVTAGHACTKKYTPEQVAMATVTALHRTVPAAVPGICFLSGGMSEEDATLNNAINLCPLPKPWKLSFS
RALQASALKAWGGKKENLKAAQEEYVKRALANSACQGKYTSSGQAGAAASESLFISNHAY

>d1fdja_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus), liver isozyme}

AHRFPALTPEQKKELESDIAQRIVANGKGILAADESVGTMGNRLQRIKVENSEENRRQFREILFTVDNSINQSIGG
VILFHETLYQKDSQGKLFRNILEKGIVVGKIKLDQGGAPLAGTNKETTIQGLDGLSERCAQYKKDGVDGFKWRA
VLRIADQCPSSLAIQENANTLARYASICQQNGLVPIVEPEVIPDGDHDLEHCQYVTEKVLAavyKALNDHHVYLE
GTLLKPNMVTAGHACTKKYTPEQVAMATVTALHRTVPAAVPGICFLSGGMSEEDATLNNAINLCPLPKPWKLS
FSYGRALQASALAAWGGKAENKKATQEAFMKRAVNVNCQAAGQYVHTGSSGAASTQLFTASYTY

>d1fbba_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Drosophila melanogaster}

TTYFNYPSELQDELREIAQKIVAPGKGILAADESGPTMGKRLQDIGHVENTEDNRRAYRQLLSTDPKLAENISG
VILFHETLYQKADDGTPFAEILKKKGIIILGIVDKGVVPLFGSEDEVTTQGLDDLAARCAQYKKDGCDFAKWRCVL
KIGKNTPSYQSILENANVLARYASICQSQRIVPIVEPEVLPDGDHDLDRAQKVTEVLAavyKALSDHHVYLEGTL
LKPNMVTAGQSAKNTPEEIALATVQLRRTVPAAVGTVTFLSGGQSEEATVNLNAINNVPLRPWALTFSYGR
ALQASVLRRAWAGKKENIAAGQNEELLKRAKANGDAAQGKYVAGSAGAGSGSLFVANHAY

>d1a5ca_c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Plasmodium falciparum}

LPADVAEELATTAQKLVQAGKGILAADESTQTICKRFDNIKLENTIENRASYRDLLFGTKGLGFISGAILFEETLFQ
KNEAGVPMVNLLHNENIIPGIKVDKGLVNIPCTDEEKSTQGLDGLAERCKEYYKAGARFAKWRVLVIDTAKGKP
TDLSIHETAWGLARYASICQQNRLVPIVEPEILADGPHSIEVCAVVTQKVLCVFKAHQENGVLLEGALLKPNMV
TAGYECTAKTTQDVGLTVRTLRTVPPALPGVVFLSGQSEEEASVNLNSINALGPHPWALTFSYGRALQASV
LNTWQGKKENVAKAREVLLQRAEANSLATYGKYKGGAGG

>d1epxa_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (Leishmania mexicana)}

MSRTVQLSQLPAYNRLKTPYESELIAVKKLTPGKGLLAADESIGSCTKRFQPIGLSNTEHRRQYRALMLEAE
GFEQYISGVILHDETGVQKASNGQTFPEYLTARGVPGIKTDMGLCPLEGAEGEQMT EGLGYVKRASAYKK
GCRFCKWRNVYKIQNQTVSEAVRFNAETLARYAILSQMSGLVPIVEPEVMIDGKHDIDTCQRVSEHVWREVV
AALQRHGVWEGLCKPNMVVPGAESGKTAAPQVAHYTVMLARTMPAMLPGVMFSLGGLSEVQASEYLN
AINNSPLPRPYFLFSYARALQSSALKAWGGKESGLAAGRRAFLHRARMNSMAQLGKYKRSDD

>d1f2ja_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Trypanosome (Trypanosoma brucei)}

SKRVEVLLTQLPAYNRLKTPYEAEELIETAKKMTAPGKGLLAADESTGSCSKRFAIGLSNTAEHRRQYRALMLECE
GFEQYISGVILHDETIVYQKAKTGETFPQYLRRRGVPGIKTDCGLEPLVEGAKGEQMTAGLDGYIKRACKYYAM
GCRFCKWRNVYKIQNQTVSEAVVRFNAETLARYAILSQLCGLVPIVEPEVMIDGTHDIETCQRVSQHVWSEVVS
ALHRHGVVWEGLCKPNMVVPGAESGLKGHAEQVAEYTVKTLARVIPPALPGVTFLSGGLSEVMASEYLNAM
NNCPLPRPWKLTSYARALQSSAIKWGGKESGVAGRRAFMHRAKMNSLAQLGKYNRADD

>d1euaa_ c.1.10.1 (A:) KDPG aldolase {Escherichia coli}

MKNWKTSAESILTTGPVVPVIVVKLEHAVPMAKALVAGGVRVLEVTLTECAVDAIRAIKEVPEAIVGAGTVL
NPQQLAEVTEAGAQFAISPGLTEPLLKAATEGTIPLPGISTVSEMLGMDYGLKEFKFFPAEANGGVKALQAIAG
PFSQVRCPTGGISPANYRDYLALKSVLCIGGSWLVPADEAGDYDRITKLAREAVEGAKL

>d1qfea_ c.1.10.1 (A:) Type I 3-dehydroquinate dehydratase {Salmonella typhi}

MKTVTVKNLIIIGEGMPKIIVSLMGRDINSVKAELAYREATFDILEWRVDHFMDIASTQSVLTAARVIRDAMPDI
PLLFTFRSAKEGGEQTITQHYTLNRAIDSGLVDMIDLELFTGDADVATVDYAHAHNVYVMSNHDFHQT
SAEEMVSRLRKMQALGADIPKIAVMPQSKHDVLTLLTATLEMQQHYADRPVITMSMAKEGVISRLAGEVFGSA
ATFGAVKQASAPGQIAVNDLRSVLMILHN

>d1i2oa_ c.1.10.1 (A:) Transaldolase {Escherichia coli}

TDKLTSLRQYTTVVADTGIAAMKLYQPQDATTNPSLILNAAQIPEYRKLIIDDAWAKQQSNDRQQIVDATD
KLAVNIGLEILKLVPGRISTAVDARLSYDTEASIAKAKRLLKLYNDAGISNDRILIKLASTWQGIRAAEQLKEGINCN
LTLLFSFAQARACAEAGVFLSPFVGRILDWYKANTDKKEYAPAEDPGVVSVEIYQYYKEHGYETVVMGASFRN
IGEILELAGCDRLTIAPALLKELAESEGAIERKLSYTGEVKARPARITESEFLWQHNQDPMAVDKLAEGIRKFAIDQ
EKLEKMIGDLL

>d1f05a_ c.1.10.1 (A:) Transaldolase {Human (Homo sapiens)}

MESALDQLKQFTVVADTGDFHAIDEYKPQDATTNPSLILNAAQIPEYRKLIIDDAWAKQQSNDRQQIVDATD
DKLFVLFGAEILKKIPGRVSTEVDARLSFDKDAMVARARRLIELYKEAGISKDRILIKLSSTWEGIQAGKELEEQHGI
HCNMTLLFSFAQAVACAEGVTLSPFVGRILDWYKANTDKKEYAPAEDPGVVSVEIYQYYKEHGYETVVMGAS
FRNTGEIKALAGCDFLTISPKLLGELLQDNAKLVPVLSAKAAQASDLEKIHLDKEKSFRWLHNEDQMAVEKLSDG
RKFAADAVKLERMLTERMNF

>d1dosa_ c.1.10.2 (A:) Fructose-bisphosphate aldolase {Escherichia coli}

SKIFDFVKPGVITGDDVQKVFQVAKENNFAFPNVNCVGTDSINAVLETAAKVKAPVIVQFSNGGASFIAGKGVKS
DVPQGAIALGAISGAHHVHQMAEHYGVPLHTDHCAKKLLPWIDGLLAGEKHFAATGKPLFSSHMDLSEES
LQENIEICSKYLERMSKIGMTLEIELGCTGGEEDGVDNSHMDASALYTQPEDVDYAYTELSKISPRFTIAASFGNV

HGVYKAGNVVLPTILRDSQEYVSKKHNLPHNSLNFVFHGGSGSTAQEIKDSVSYGVVKMNIIDTDTQWATWE
GVLNYYKANEAYLQGQLGNPKGEDQPNKKYYDPRVWLRAQQTSMIARLEKAQELNAIDVL

>d1h7na_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Baker's yeast (*Saccharomyces cerevisiae*)}

MHTAEFLETEPEISSLVAGGYNHPLLRQWQSERQLTKNMLIFPLFISDNPPDFTEIDSLPNINRIGVNRLKDYLK
PLVAKGLRSVILFGVPLIPGTDPVGAADDPAGPVIQGIKFIREYFPELYIICDVCLEYTSHGHCGLYDDGTINR
ERSVSRLAAAVAVNYAKAGAHCVAPSMDGRIRDIKRGLINANLAHKTFVLSYAAKFSGNLYGPFRDAACSA
GDRKCYQLPPAGRGLARRALERDMSEGADGIIVKPSTFYLDIMRDASEICKDLPICAYHVSGEYAMLHAAAEGK
VVDLKTIATFESHQGFLRAGARLIITYLAPEFLDWLDE

>d1e51a_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Human (*Homo sapiens*)}

MQPQSVLHSGYFHPLLRAWQTATTLNASNLIYPITVTDVPDDIQPITSPLGVARYGVKRLEEMLRPLVEEGLRC
VLIFGVPSRVPKDERGSAADSEESPAIEAIHLLRKTFPNLLACDVCLCPYTSHGHCGLLSENGAFRAEESRQRLAE
VALAYAKAGCQVVAPSMDGRVEAIKEALMAHGLGNRVSMSYSAKFASCFYGPFRDAAKSSPAFGDRRCY
QLPPGARGLALRAVDRDVREGADMLMVKGMPYLDIVREVKDKHPLPLAVYHVSGEFAMILWHGAQAGAF
DLKAAVLEAMTAFRRA GADI II YYTPQLLQWLK

>d1b4ka_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Pseudomonas aeruginosa}

YPYTRLRRNRRDDFSRRLVRENVLTVDLILPVFVLGVNQRESIPSMPGVERLSIDQLLIAEEWVALGIPALALF
PVTPVEKKSLAAEAYNPEGIAQRATRALRERFPELGIITDVALDPFTTHGQDGILDDGYVLNDVSDVLRQAL
SHAEAGAQVVAAPSMDGRIGAIRALESAHNTVRIMAYSAKYASAYYGPFRDAVGASNLGKGNKATYQM
DPANSDEALHEVAADLAEGADMVMVKPGMPYLDIVRRVKEFRAPTFVYQVSGEYAMHMGAIQNGWLAES
VILESLTAFKragadgilTYFAKQAAEQLRR

>d1b4ea_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Escherichia coli}

TDLSQRPRRLRKSPALRAMFEETTLSNLDLVLPIFVEEEIDDYKAVEAMPGVMRIPEKHLAREIERIANAGIR SVM
TFGISHHTDETGSDAWREDGLVARMSRICKQTVPEMIVMSDCFCEYTSHGHCGLKEHGVDNDATLENLGK
QAVVAAAAGADFIAPSAMDGQVQAIRQALDAAGFKDTAIMSYSTKFASSFYGPFRREAAGSALKGDRKS YQM
NPMNRREAIRESLLDEAQGADCLMVKPAGAYLDIVRELERTELPIGAYQVSGEYAMIKAALAGAIDEEKVVLE
SLGSIKRAGADLIFS YFALDLAEKKILR

>d1gg1a_ c.1.10.4 (A:) 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (DAHP synthase, AroG) {Escherichia coli}

DLRIKEIKELLPPVALLEKFPATENAANTVAHARKAIHKILKGNDRLLVVGPCSIHDPVAAKEYATRLLALREELK
DELEIVMRVYFEKPTTVGWKGLINDPHMDNSQINDGLRIARKLLLIDNSGLPAAGEFLDMITPQYLA
WGAIGARTTESQVHRELASGLCPVGFKNQTDGTIVKAIDAINAAGAPHCFLSVTKWGHSAIVNTSGNGDCHII
LRRGGKEPNYSAKHVAEVKEGLNKAGLPAQVMIDFSHANSSQFKQMDVCADVCQQIAGGEKAIIGVMVES
LVEGNQSLESGEPLAYGKSITDACIGWEDTDALLRQLNAV KARR

>d1d9ea_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P synthase) {Escherichia coli}

MKQKVVSIGDINVANDLPVLFGGMNVLESRDLAMRICEHYVTQKLGIYVFKASF DKA NRSSIH SYRGPGL
EEGMKIFQELKQTFGVKIITDVHEPSQAQPVADVVDIQLPAFLARQTDLVEAMAKTGAVINVKKPQFVSPGQ
MGNIVDKFKEGGNEK VILCDRGANFGYDNLV DMLGFSIMKKVSGNSP VIFDV THALQCRDPFGAASGGRR
QVAELARAGMAVGLAGLFIEAHPDPEHAKCDGPSALPLAKLEPFLKQMKAIDDL VKGFEELDTSK

>d1jcxa_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P

synthase) {Aquifex aeolicus}

EKFLVIAGPCAI ESELLLKVGE EIKRLSEKFKEVEFVKSSFDKANRSSIHSFRGH GLEYGVKALRKVKEEGLKITT
DIHESWQAEPVAEVADIQIPAFCLCRQTDLLA AAKTGRAVN VKKQFLAPWDTKNVVEKLKGGAKEIYLTERG
TTFGYNNLVVDFRSLPIMKQWAKVIYDATHSVQLPGGLGDKSGGMREFIFPLIRAAAVAVGCDGVFMETHPEPE
KALSDASTQLPLSQLEGIIEAILEIREVASKYYETI

>d1onea1 c.1.11.1 (A:142-436) Enolase {Baker's yeast (*Saccharomyces cerevisiae*)}

SPYLPVPFLNVNLNGGSHAG GALALQE FMIAPTGA KTA E ALRIGSEV YHNLKSLTKRY GASAGN VGD EGGVA
PNI QTAE E ALDLIVDA IKAAGHDGKV KIGLDCASSEFFKDGY DLFKNPNSDKSKWLTGPQLADLYHSLMKRY
PIVSIE DPFA EDDWEA WSHFFTAGIQIVADDLTVNP KRIATAIEKKAAD ALLKVNQIGTLSESIAAQDSFAAG
WGVMVSHRSGETEDTFIADLVVGLRTGQIKTGAPARSERLAKLNQLLRIEEELGDNAVFAGENFHGDKL

>d1pdz_1 c.1.11.1 (140-433) Enolase {Lobster (*Homarus vulgaris*)}

DEVILPVPA FN VINGGSHAG NKLAM QEFM I LP TGAT SFTEAM R MGTEVY HHLKAVI KARF GLD AT AVG D EGGF
APN ILNNK DALD LQEA IKKAG YT G KIEIGMDV AASEFY KQNNIY D LDFKTAN NDGSQK ISGDQL RD M YMEFCK
DFPI VSIE DPFD QDDW ETWSKMTSGTTI QIVG DDLTVNP KRITTA VEKKACKC LLLKVNQIGS VTESIDA HLLAK
KNGW GTMVSHRSGETEDCFIADLVVGLCTGQIKTGAPCRSERLAKYNQILRIEEELGSGAKFAGKNFRAPS

>d1e9ia1 c.1.11.1 (A:140-430) Enolase {Escherichia coli}

PGKYSMPVPM MN IINGGE HADNNV D I QEFM IQPV GAKTVK EAIR MGSEV FH LAKV LAK GMNT AVG D EG
GYAPN LGSNAE ALAVIA EAVKAAGY ELG KDTI LAM DC AASEF YKDG KYVLAGE G NKAFT SEE FTHF LEEL T KQYPI
VSIEDGLDES DW DGFAYQT KVLG DKIQLVG DDLF VNT KILKE GIANSI LIKFN QIGSLT ET LAAI KMAK DAG
YTAVI SHRS GETE DATI ADL AVG TAAG QIKT GS MSRS DRV A KYN QL RI EAL GEKA PYN GRK EIKG Q

>d1bqg_1 c.1.11.2 (144-422) D-glucarate dehydratase {Pseudomonas putida}

EGQQQR DAVEMLGYLFYVGDRNKTDLGYRSEHEAD NEWFRLRNKEALTPESVVALAE AAYDRYGF KDFKLKG V
LRGEDEIAAVT ALSERFPDARITLD PNGA WSLKEAVAL CRDQHHVLAYAEDPCGAENG YSGREVMAE FRRSTGL
RTATNMIATDWRQM GHAIQLQ SVDIPLADPHFW TMQGSVRVAQMCNEWGLTWGSHSNHF DISLAM FT
HVAAA APGNITAID THWIWQDGQRLTKEPLQIKGGLVEVPKKPGLGV ELDWD ALMKAHEVY KSM

>d1ec7a1 c.1.11.2 (A:138-446) D-glucarate dehydratase {Escherichia coli}

DGQQQR SEV EMLGYLFVGNR KATPLPYQS QPDDSCD WYRLRHEEAMTPDAV VRLA E AAYE KYG FND FK LKG
V LAGEEEA SIVALA QRFPQ ARITLD PNGA WSLNEA IKIG KYLKG SLAYAEDPCGA E QGF SGRE VMAE FRR STGL
PTATNMIATDWRQM GH TLSQL SVDIPLADPHFW TMQGSVRVAQMCHEF GLTWGSHSNHF DISLAM FT HV
AAA APG KITAID THWIWQEGNQRLTKEPFEIKGGLVQVPEKPGLG V EIDMDQ VMKAHELYQKHGLGARDDA
MG MQYLI PGWTFDNKR PCMV R

>d1fhua1 c.1.11.2 (A:100-320) O-succinylbenzoate synthase {Escherichia coli}

QA ANYRAAPLCNGDP DDLI LKLAD MPGEK VAKV KV GLYE AVR DGMVV NLL EAPDLH RL DAN RAW TPLKG
QQFAKYVNP DYRDRIA FLEEP CKTR DDSRAFA RETGIAIAWDES LREP DFAV AE EG VR AVV I KPTL GS LEK VRE
QVQAAHALGLT AVISSI ESSL GLTQLARIA AWL PDTIP GLD TL DMQA QQV RR WP G STLP VVEV DALER LL

>d1muca1 c.1.11.2 (A:131-372) Muconate-lactonizing enzyme {Pseudomonas putida}

RVRDSLEV AWT LASG DTARDIAEARH MLEIRRHRVFKLKIGANPVEQDLKHVVTIKREL GDSASRV DVNQYW
DESQAIRACQV LGDNG IDLIEQ PISR INRG GQVRLN QRT PAPIMADESIESVEDAFSLA ADGA ASI FALKIA KNGG
PRAVLRTAQIAEAAGIGLYGGTMLEG SIGT LASAH AF LRL QLT WGTEL FGPLL TEEIVNEPPQYRDFQLH I PRTP
GLGLTL DEQRLAR FAR

>d2mnr_1 c.1.11.2 (133-359) Mandelate racemase {Pseudomonas putida}

PVQAYD SHSL DGV K LATERA VTAELG FRAV KTKIGYP ALDQ DLAV VRSIR QAVG DDFG IMV DYN QSL DV PAI
KRSQ ALQQ EGV TWIEE PTLQHDYEGH QRIQS KLN VPV QM GEN WL GPEEM F KAL SIGACR LAMP DAM KIGG

VTGWIRASALAQQFGIPMSSHLFQEISAHLLAATPTAHWLERLDSLGSVIEPTLTATEGNAVIPDLPVGIIWRE
KEIGKYLV

>d2chr_1 c.1.11.2 (127-370) Chlormuconate cycloisomerase {Alcaligenes eutrophus}

PLRSAPIAWTLASGDTKRDLSAVEMIERRHNRFKVKGFRSPQDDLIHMEALNSLGSKAYLRVDVNQAW
DEQVASVYIPELEALGVELIEQPVGRENTQALRRLSDNNRAIMADESLSTLASAFDLARDRSVDVSLKLCNMG
GVSATQKIAAAEASGIASYGGTMLDSTITGTSVALQLYSTVPSLPGCELGPFLADTLSHEPLEIRDYELQVPTGV
GHGMTLDEDKVQRQYARVS

>d1jpdx1 c.1.11.2 (X:114-321) L-Ala-D/L-Glu epimerase {Escherichia coli}
TLPETVITAQTVIGTPDQMANSASTLWQAGAKLLVKLDNHLISERMAIRTAVPDATLIVDANESWRAEGLA
ARCQLLADLGVAMLEQPLPAQDDAALENFHPLPICADESCHTRSNLKALKGRYEMVNICKLDTGGTEALALAT
EARAQGFSMLGCMCLCTSRAISAALPLVPQVSFADLDGPTWLAVDVEPALQFTTGEHLH

>d1jpma1 c.1.11.2 (A:126-359) L-Ala-D/L-Glu epimerase {Bacillus subtilis}
YRDTLETDYTVSNSPEEMAADAENYLKQGFQLKIKVGKDDIATDIARIQEIRKRVGSAVKRLDANQGWRPK
EAVTAIRKMEDAGLIELVEQPVHKDDLALKKVTDATDTPIMADEFVTPRQAFEVLQTRSADLINIKLMKAG
GISGAEKINAMAECAGVEMVGSMIETKLGITAAAHFAASKRNITRFDFDAPLMLKTDVFNGGITYSGSTISMP
GKPGLGIIGAAL

>d1kcza1 c.1.11.2 (A:161-413) beta-Methylaspartase {Clostridium tetanomorphum}
GAEINAVPVFAQSGDDRYDNVDKMIKEADVLPHALINNVEEKLGLKGEKLLEYVKWLRDRIIKLRVREDYAPIFH
IDVYGTIGAAFVDIKAMADYIQTLAEEAKPFHLRIEGPMVDERDQKQMEAMRDLRAELDGRGVDAELVADE
WCNTVEDVKFFTNDKAGHMVQIKTPDLGGVNNIADAIMYCKANGMGAYCGGTCNETNRSAEVTTNIGMAC
GARQVLAKPGMGVDEGMMIVKNEMNRVLALVGRK

>d1kkoal c.1.11.2 (A:161-411) beta-Methylaspartase {Citrobacter amalonaticus}
PCVPEAPIPLFGQSGDDRYIAVDKMILKGVDLPHALINNVEEKLGLKGEKLREYVRWLSDRILSLRSSPRYHPTLHI
DVYGTIGLIFDMDPVRCAEYIASLEKEAQGLPLYIEGPVDAGNKPDQIRMLTAITKELTRLGSGVKIVADEWCNTY
QDIVDFTDAGSCHMVQIKTPDLGGIHNIIDAVLYCNKHGMEAYQGGTCNETEISARTCVHVALAARPMRMLIK
PGMGFDEGLNIVFNEMNRHTALLQT

>d1a49a2 c.1.12.1 (A:12-115,A:218-395) Pyruvate kinase, N-terminal domain {Rabbit (Oryctolagus cuniculus)}

IQTQQLHAAMADTFLEHMCRDIDSAPITARNTGIICTIGPASRSVETLKEMIKSGMNVARMNFSHGTHEYHAE
TIKNVRTATESFASDPILYRPVALDTKGXPVSEKDIQDLKFGVEQDVDMVFASFIRKAADVHEVRKILGEKGK
NIKIISKIENHEGVRRFDEILEASDGIMVARGDLGIEIPAEKVFLAQKMIIGRCNRAGKPVICATQMLESMIKKPRP
TRAEGSDVANAVLDGADCIMLSGETAKGDYPLEAVRMQHЛИREAЕАAMFHRKLFE

>d1pkla2 c.1.12.1 (A:1-87,A:187-357) Pyruvate kinase, N-terminal domain {Leishmania mexicana}
SQLAHNLTLSIFDPVANYRAARIICTGPSTSVEALKGLIQSGMSVARMNFSHGSHEYHQTINVRQAAAELG
VNIAIALDTKGXPXPAVSAKDRVLDLQFGVEQGVDMIFASFIRSAEQVGDVRKALGPKGRDIMIICKIENHQGVQNI
DSIIIESDGIMVARGDLGVEIPAEKVVVAQKILISKCNVAGKPVICATQMLESMTYNPRPTRAEVSDVANAVFNG
ADCVMLSGETAKGKYPNEVVQYMARICLEAQASAL

>d1a3wa2 c.1.12.1 (A:2-87,A:189-366) Pyruvate kinase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

SRLERLTSNVAGSDLRRTSIIGTIGPKTNNPETLVALRKAGLNIVRMNFHSYEHKSVIDNARKSEELYPGGRP
LAIALDTKGXPALSEKDKELRGVKNGVHMVFASFIRTANDVLTIREVLGEQGKDVKIIVKIENQQGVNNFDEIL
KVTDGVMVARGDLGIEIPAEPVLAQKKLIAKSNLAGKPVICATQMLESMTYNPRPTRAEVSDVGNAILDGADC
VMLSGETAKGNYPINAVTTMAETAVIAEQAIAYLPNYD

>d1e0ta2 c.1.12.1 (A:1-69,A:168-344) Pyruvate kinase, N-terminal domain {Escherichia coli}
MKKTKIVCTIGPKTESEEMI AKML DAGMNVMR LNF SHGDYAEHGQRIQNLRNVMSKTGKTA ILLDTKGXPA
LA EKD QDLIFGCEQGVDFVAAS FIRSDVIEIREHLKA HGENIHIISKIENQEGLNNFDEILEASDGM VARG
DLGVEIPVEEVIFAQKMMIEKCIRARKVVITATMMLDSMIKNPRPTDAEAGDVANAILDGTDAVMLS GESAKG
KYPLEAVSIMATICERTDRVMNSRLE

>d1kbla1 c.1.12.2 (A:510-873) Pyruvate phosphate dikinase, C-terminal domain {Clostridium symbiosum}

IETQEASVGSFERIMWADKFRTLKVRTNADTPEDTLNAVKLGAEGIGLCRTEHMFFEADRMKIRKMILSDSV
EAR EALNE LIPFQKGDFKAMYKALEGRPM TVRYLDPLHEFVPHTEEQ AELAKNMGLTAEVKAKVDELHEF
NPMMGHRGCRLAVTYPEIAKM QTRAVMEA AIEVKEETGIDIVPEIMIPLVGEKKELKFV KDV VVEVAEQVKKEK
GSDM QYHIGTMIEPRAALTADAIAEEA EFFSGTNDLTQMTFGS RDDAGKFLDSYYKAKIYESDPFAR LDQTG
VGQLVEMAVKKGRQTRPGLKCGICGEHGGDPSSVEFCHKVLNYVSCSPFRVPIARLAAQAALNN

>d1fiy_ c.1.12.3 (-) Phosphoenolpyruvate carboxylase {Escherichia coli}

QYSALRSNVSMILGKVLGETIKDALGEHILER VETIRKLSSRAGNDANRQELLTLQNLSDELLPVARAFSQL
NLANTAEQYHSISPKGEAASNPEVIATLRKLKNQPEL SEDTIKAVESLSLEVLTAHPTEIRRTLIHKMVEVNAC
LKQLDNKDIADYEHNQLMRRRLRQLIAQS WHTDEIRKL RPSPVDEAKWGFAV VENSLWQGVPN YLRELNEQLE
ENLG YKLPVEFV PVRF TSWMGGDRDG NPNTADITRVH VLLSRWKATDLFLKDIQVLVSELSMVEATPELLALV
GEEGAEPYR YLMK NLRSRLMATQ AWLEARLKGEELPKPEG LLTQNEELWEPL YACYQSLQACGMIIANGDL
DTLRRV KCFGVPLV RIDIRQESTRTEALGELTRYLGIGDYEWSEADKQ AFLRE LNSKRPLL PRNWQPSAETRE
VLDTCQVIAEAPQGSIAAYVISM A KTPSDV LAHV HLLKEAGIGFAMPVAPLFETLDDLN N ANDVMTQ LNI DWY
RGLIQGKQMVMIGYSDSAK DAGVMA ASWAQYQA QD ALIKTCEKAGIELTLFHGRGGSIGRGGA PAHA ALLSQ
PPGSLKGGLRVTEQGEMIRFKYGLPEITVSSLSLYTGAILEANLLPPEPKESWRRIMDELSVISCDVYRGYVRENK
DFVPYFRSATPEQELGKLPLGSRPAKRRPTGGVESLRAIPWIFAWTQNRLMLPAWL GAGTALQKVVEDGKQSEL
EAMCRDW PFFSTRLGMLEMVFAKADLWLA EYYDQRLVDKALWPLGKELRN LQEE DIKV VLA IANDSHL M ADL
PWIAESIQLRNIYTDPLNVLQ AELLHRSRQAEKEGQEPDPRV EQALMVTIAGIAAGMRNTG

>d1pyma_ c.1.12.4 (A:) Phosphoenolpyruvate mutase {Blue mussel (Mytilus edulis)}

VKKTTQLKQMLNSK DLFIMEAHNGLSARI VQEAGFKGIWGS GLSVAQLGVRDSNEASWTQVVEVLE FMSD
ASDVPILLADTG YGNF NNARRL VRKLED RG VAGAC LEDKLFPKTN SLHDG RAQPLADIEEFALKI KACK DSQ TD
PDFCIVARVEAFIAGW GLDEALKRAEAYRNAGADAILMHSKKADPSDIEAFMKAWNNQGPV VIVPTKYYKPT
DHFRDMGVSMVIWANHNL RASVSAIQQTTKQIYDDQSLVNVEDKIVSVKEIFRLQR DDELVQAEDKYL PKN

>d1dxe a_ c.1.12.5 (A:) 2-dehydro-3-deoxy-galactarate aldolase {Escherichia coli}

DVFPNKFK AALAAKQVQIGCWSALS NPISTEVLGLAGFDWL VLGEHAPN DISTFIPQLMALK GSASAPVVR VP
TNEPVIIKRLLDIGFYNFLIPF VETKEE AELA VASTY PPEGIRGV SVSHRANMFGTVADYFAQSNKNITILVQIESQ
QGV DNVA DAIAATEGV DGIFVG PSDLAA ALGH LGNASH PDVQKAIQHIFNRASA HGKPSG ILAPV EA DARRY LE
WGATFVAVGSDLGVFRSATQKLADTFKK

>d1dqua_ c.1.12.6 (A:) Isocitrate lyase {Aspergillus nidulans}

SYIEEDQRYWDEVA AVKNWWKDSR WRYTKR PFTA EQIVAKRGNL KIEYPSNVQAKKLW GILER NFKN KEAS F
TYGCLDPTMVTQMA KYL DT VYVSGW QSS STAS STDEPSPD LADY PMNTV PNKVN H LWMA QL FH DRK QREE
RMTTPKDQRHKVANVDYL RPIIADADTGH GGLT AVM KLT KLFVERGAAGIHIEDQAPG T KKCGH MAGK VLP I
SEHINRLVAIR AQADIM GT DLLAI ARTDSEA ATLT STIDH RDHPFIIGSTNPDIQPLNDL MVMA EQAGKNGA EL
QAI EDEWLAKAGLKL FND AVV DAIN NSPLPNK KAAIE KYLTQSKG KSNLE ARAIAKEIAGT D IYFDWEAPRT REG
YYRYQGGTQC AIN RAVAYAPFADL IWMESKLPDYKQAKEFADGVH A伟WPEQKLAYNLSPSF NWKKAMP RDE
QETYIKRLGALGYAWQFITLAGLHTT ALISDTFAKAYAKQGM RAYGELVQEPEMANGV DVVTHQK WSGANYV
DNMLKMITGG

>d1f8ma_c.1.12.6 (A:) Isocitrate lyase {Mycobacterium tuberculosis}

ASVGTPKSAEQIQQEWTNPRWKDVTRTYSaedVVALQGSVVEEHTLARRGAEVLWEQLHDLEVNALG
ALTGNMAVQQVRAGLKAIYLSGWQVAGDANLSGHTYPDQSlyPANSVPQVVRRINNALQRADQIAKIEGDT
VENWLAPIVADGEAGFGGALNVYELQKALIAAGVAGSHWEDQLASEKKCGHLGGVLPTQQHIRTLSARLA
ADVADVPTVIARTDAEAATLTSVDERDQPFTGERTREGFYRTKNGIEPCIARAKAYAPFADIWMETGTPDL
EAARQFSEAVKAEYPDQMLAYNCSPSFNWKKHLDATIACKFQKELAAMGFKFQFITLAGFHANYSMFDLAYG
YAQNQMSAYVELQEREFAAEERGYTATKHQREVGAGYFDRIATTVDPNSTALTGSTEEGQF

>d1igwa_c.1.12.6 (A:) Isocitrate lyase {Escherichia coli}

KTRTQQIEELQKEWTQPRWEGITRPSaedVVKLRGSVNPECTLAQLGAAKMWRLLHGESKKGYINSLGALTG
GQALQQAKAGIEAVYLSGWQVAADANLAASMPDQSlyPANSVPAVVERINNTFRRADQIQWSAGIEPGDP
RYVDYFLPIVADAEGFGGVNAFELMKAMIEAGAAAVHFEDQLASVKKCGHMGKGVLVPTQEAIQLVAARL
CADVTGVPTLLVARTDADAADLITSDCPDSEFITGERTSEGFFRTHAGIEQAISRLAYAPYADLVWCETSTPD
LELARRFAQAIHAKYPGKLLAYNCSPSFNWQKNLDDKTIASFQQQLSDMGYKFQFITLAGIHSMWFNMFDLA
NAYAQGEGMKHYVEKVQQPEFAAKDGYTFVSHQQEVGTGYFDKVTTIIGQ

>d1d8ca_c.1.13.1 (A:) Malate synthase G {Escherichia coli}

QTITQSRLRIDANFKRFVDEEVLPGLDAAAFWRNFDEIVHDLAPENRQLLAERDRIQAALDEWHRSNPGPV
KDKAAYKSFLRELGYLVPQPERVTVETTGIDSEITSQAGPQLVVPAMNARYALNAANARWGSYDALYGSIDIIPQ
EGAMVSGYDPQRGEQVIAWVRRFLDESLPLENSYQDVFKVVKQLRQLKNGKETTLRTPAQFVGYRGD
AAAPTCILLKNNGLHIELQIDANGRIGKDDPAHINDVIVEAAISTILDCEDSVAAVDAEDKILLYRNLLGMLMQGTLQ
EKMEKNGRQIVRKLNDDRHYTAADGSEISLHGRSLLFIRNVGHLMTIPVIWDSEGNEIPEGILDGVMTGAIAYL
DLKVQKNSRTGSVYIVPKPMHGPQEVAFANKLFTRIETMLGMAPNTLKMGIIMDEERRTSNLRSCIAQARNR
VAFINTGFLDRTGDEMHSVMEAGPMLRKNQMKTSPWIKAYERNNVLSGLFCGLRGKAQIGKGMWAMPDL
MADMYSQKGDQLRAGANTAWPSPTAATLHALHYHQTNVQSVQANIAQTEFNAEFPLDDLLTIPVAENAN
WSAQEIQQELDNNVQGILGYVWRVEQGIGCSKVPDIHNVALMEDRATLRISSQHIANWLRHGILTKEQVQA
SLENMAKVVDQQNAGDPAYRPMAGNFANSCAFKAASDLIFLGVKQPNGYTEPLLHAWRLREKES

>d3rubl1 c.1.14.1 (L:148-467) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}

FQGPPHGIQVERDKLNKYGRPLLGCТИPKLGLSAKNYGRAVYECLRGGLDFKDDENVNSQPFMRWRDRFLF
CAEALYKAQAETGEIKGHYNATAGTCEEMIKRAVFARELGVPIVMHDYLGGFTANTSLAHYCRDNGLLLHIHR
AMHAVIDRQKNHGIHFRVLAKALRMSGGDHIIHSGTVVGKLEGERDITLGFV DLLRDDFVEQDRSRGIYFTQD
WVSLPGVLPVASGGIHVWHMPALTEIFGDDSVLQFGGMLGHPWGNAPGAVANRVALEACVKARNEGRLD
AQEGNEIIREACKWSPELAAACEVWKEIVF

>d1bura1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}

FQGPPHGIQVERDKLNKYGRPLLGCТИPKLGLSAKNYGRAVYECLRGGLDFKDDENVNSQPFMRWRDRFLF
CAEALYKAQAETGEIKGHYNATAGTCEDMMKRAVFARELGVPIVMHDYLGGFTANTTLSHYCRDNGLLLHIH
RAMHAVIDRQKNHGMHFRVLAKALRMSGGDHIIHSGTVVGKLEGERDITLGFV DLLRDDYTEKDRSRGIYFTQS
WVSTPGVLPVASGGIHVWHMPALTEIFGDDSVLQFGGMLGHPWGNAPGAVANRVALEACVKARNEGRLD
AREGNTIIREATKWSPELAAACEVWKEIKFEFPAMDV

>d1bwva1 c.1.14.1 (A:150-478) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

GPATGVILERERLDKFGPLLCTTKPKLGLSGKNYGRVVEALKGGDFVKDDENINSQPFMRWRERYLFTME
AVNKASAATGEVKGHYNVTAAATMEEMYARANFAKELGSIIMIDLVIGYTAIQTMAKWARDNDMILHLHRAG
NSTYSRQKNHGMNFRVICKWMRMAGVDHIHAGTVVGKLEGDPITRGFYKTLLPKLERNLQEGLFFDMEWA

SLRKVMPVASGGIHAGQMHQLIHYLGEDVVLQFGGGTIGHPDGIQAGATANRVALEAMILARNENRDYLTEG
PEILREAAKTCGALRTALDLWKDITFNYTSTDTSDFV

>d1gk8a1 c.1.14.1 (A:150-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Chlamydomonas reinhardtii}

GPPHGIQVERDKLNKYGRGLLCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENVNSQPFMRWRDRFLFVA
EAIYKAQAETGEVKGHYLNATAGTCEEMMKRAVCACHELGVPIIMHDYLGGFTANTSIAICRDNGLLHIHRA
MHAVIDRQRNHGIHFRLAKALRMSGGDHLHSGTVVGKLEGEREVTGFVDMRDDYVEKDRSRGIYFTQD
WCSMPGVMPVASGGIHVVWHMPALVEIFGDDACLQFGGTLGHPWGNAPGAAANRVALEACTQARNEGR
DLAREGGDVIRSACKWSPELAAACEWKEIKFEFDTIDKL

>d1bxna1 c.1.14.1 (A:151-467) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Alcaligenes eutrophus}

FAGPSTGIIVERERLDKFGRPLLGATTKPCKLGLSGRNYGRVVYEGLKGGDFMKDDENINSQPFMHWWRDRFLFV
MDAVNKASAATGEVKGSYLNVTAGTMEEMYRRAEFAKSLGSVIIMVDLIVWTCIQSMSNWCRQNDMILHL
HRAGHGTYTRQKNHGVSVRIAKWLRLAGVDHMHTGTAVGKLEGDPPLTVQGYYNCRDAYTQTDLTRGLFFD
QDWASLRKVMPVASGGIHAGQMHQLIHLFGDDVVLQFGGGTIGHPQGIQAGATANRVALEAMVLARNEGR
DILNEGPEILRDAARWCGPLRAALDTWGDI

>d1rbla1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Synechococcus sp., strain pcc 6301}

FQGPPHGIQVERDLLNKYGRPMILGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENINSQPFQRWRDRFLF
VADAIHKSAATGEIKGHYLNVTAPTCEEMMKRAEFAKELGMPPIIMHDFLTAGFTANTTLAKWCRDNGVLLHI
HRAVHADRIDRQRNHGIHFRLAKCLRLSGGDHLHSGTVVGKLEGDKASTLGFVDMREDHIEADRSRGVFFT
QDWASMPVLPVASGGIHVVWHMPALVEIFGDDSVLQFGGTLGHPWGNAPGATANRVALEACVQARNEG
RDLYREGGDILREAGKWSPELAAALDLWKEIKFEFETMDKL

>d5ruba1 c.1.14.1 (A:138-457) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Rhodospirillum rubrum}

GPSVNISALWKVLRPEVDGGLVVGTIICKPKLGLRPKFAEACHAFWLGGDFIKNDEPQGNQPFAPLRTDTIALVA
DAMRRAQDETGEAKLFSANITADDPEIIARGEYVLETFGENASHVALLVDGYVAGAAAITTARRRFPDNFLHYH
RAGHGAVTSPQSQRGYTAFVHCKMARLQGASGIHTGTMGFKMEGESSDRAIAYMLTQDEAQGPFYRQSW
GGMKACTPIISGGMNALRMPGFFENLGNANVILTAGGGAFGHIDGPVAGARSLRQAWQAWRDGVPVLDYA
REHKEKELARAFESFPGDADQIYPGWRKALGV

>d1geha1 c.1.14.1 (A:137-443) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Archaeon Thermococcus kodakaraensis}

DGPAFGIEGVRKMILEIKDRPIYGVPKPKVGYSPPEEFKLAYDLLSNGADYMKDDENLTSPWYNRFEERAЕIMA
KIIDKVENETGEKKTWFANITADLLEMEQRLEVADLGLKHAMVDVVTGWGALRYIRDLAADYGLAIHGHRA
MHAAFTRNPYHGISMFVLAKLYRLIGIDQLHVGTAGAGKLEGGKWDVIQNARILRESHYKPDEDNFHLEQKF
YSIKAAFPSSGGLHPGNIQPVIEALGTDIVLQLGGTLGHPDGAAGARAVRQAIDAIMQGIPLDEYAKTHKE
ARA LEKWGHVTP

>d1qtwa_c.1.15.1 (A:) Endonuclease IV {Escherichia coli}

MKYIGAHVSAAGGLANAAIRAAEIDATAFALFTKNQRQWRAAPLTQTIDEFKAACEKYHYTSAQILPHDSYLN
LGHPVTEALEKSRAFIDEMQRCEQLGLSLLNHPGSHLMQISEEDCLARIAESINIALDKTQGVTAVIENTAGQ
GSNLGFKEHLAAIIDGVEDKSRVGVCIDTCHAFAAGYDLRTPAECEKTFADFARTVGFKYLRGMHLNDAKSTFG
SRVDRHSLGEGNIGHDAFRWIMQDDRFDGIPLILETINPDIWAEEIAWLKAQQTEKAVA

>d1d8wa_c.1.15.2 (A:) L-rhamnose isomerase {Escherichia coli}

TQLEQAWELAKQRFAAVGIDVEEARQLDRLPVSMHCWQGDDVSGFENPEGSLTGGIQTGNYPGKARNASE

LRADLEQAMRLIPGPKRLNLHAIYLESDTPVSRDQIKPEHFKNWVEWAKANQLGLDFNPSCFSHPLSADGFTLS
HADDSIRQFWIDHCKASRRVSAYFGEQLGTPSVMNIWIPDMKDITDRLAPRQRLLAALDEVISEKLNPAHHI
DAVESKLFIGAESAFTVGSNEFYMGYATSRQTALCDAGHFHTPEVISDKISAAMLYVPQLLHVSRPVRWDSD
HVVLDDETQAIASEIVRHDLFDRVHIGLDFFDASINRIAAWVIGTRNMKKALLRALLEPTAELRKLEAPGDYTAR
LALLEEQKSLPWQAVWEMYCQRHDTPAGSEWLESVRAYEKEILSRR

>d1dxia_c.1.15.3 (A:) D-xylose isomerase {Streptomyces murinus}

MSFQPTPEDRFTFGLWTGVWQGRDPFGDATRPALDPVETVQRLAELGAYGVTFHDDDLIPFGSSDTERESHIK
RFRQALDATGMTVMATTNLFTPVFKDGGFTANDRDVRRYALRKTIGNIDLAAELGAKTYVAWGREGAES
GGAKDVRDALDRMKEAFDLLGEYVTAQGYDLRFAIEPKPNEPRGDILLPTVGHALAFIERLERPELYGVNPEVGH
EQMAGLNFPHGIAQALWAGKLHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLETAGYEGPRHDFKPPR
TEDFDGVWASAAGCMRNYLILKDRAAFRADEPVQEALRAARLDQLAQPTAADGLDALLADRAAFEDFDVD
AAAARGMAFEHLDQLAMDHLLGARG

>d2gyia_c.1.15.3 (A:) D-xylose isomerase {Streptomyces olivochromogenes}
YQPTPEDRFTFGLWTGVWQGRDPFGDATRPALDPVETVQRLAELGAHGVTFHDDDLIPFGSSDTERESHIKRF
RQALDATGMTVMATTNLFTPVFKDGGFTANDRDVRRYALRKTIKNIDLAVELGAKTYVAWGREGAESGA
AKDVRVALDRMKEAFDLLGEYVTSQGYDTRFAIEPKPNEPRGDILLPTVGHALAFIERLERPELYGVNPEVGHEQ
MAGLNFPHGIAQALWAGKLHIDLNGQSGIKYDQDLRFGAGDLRAAFWLVDLLESAGYEGPRHDFKPPRTE
DIDGVWASAAGCMRNYLILKERAFAFRADPEVQEALRASRLDELAQPTAADGVQELLADRTAFEDFDVDAAA
ARGMAFERLDQLAMDHLLGAR

>d1xis_c.1.15.3 (-) D-xylose isomerase {Streptomyces rubiginosus}

NYQPTPEDRFTFGLWTGVWQGRDPFGDATRRALDPVESVRLAELGAHGVTFHDDDLIPFGSSDSEREEHVK
RFRQALDDTMKVMATTNLFTPVFKDGGFTANDRDVRRYALRKTIKNIDLAVELGAETYVAWGREGAES
GGAKDVRDALDRMKEAFDLLGEYVTSQGYDIRFAIEPKPNEPRGDILLPTVGHALAFIERLERPELYGVNPEVGH
EQMAGLNFPHGIAQALWAGKLHIDLNGQNGIKYDQDLRFGAGDLRAAFWLVDLLESAGYEGSGPRHDFKPPR
TEDFDGVWASAAGCMRNYLILKERAFAFRADPEVQEALRASRLDELARPTAADGLQALLDRSAFEEFDVDAA
AARGMAFERLDQLAMDHLLGARG

>d1qt1a_c.1.15.3 (A:) D-xylose isomerase {Streptomyces diastaticus, M1033}

SYQPTPEDKFTFGLWTGVWQGRDPFGDATRGALDPAESVRLAELGAHGVTFHDDDLIPFGATDSERAEHIKR
FRQGLDETGMKVMATTNLFTPVFKDGGFTANDRDVRRYALRKTIKNIDLAVELGAQTYVAWGREGAESG
AAKDVRVALDRMKEAFDLLGEYVTSQGYDTPFAIEPKPNEPRGDILLPTIGHALAFIDGLERPELYGVNPEVGHE
QMAGLNFPHGIAQALWAGKLHIDLNGQSGIKYDQDLRFGPGDLRAAFWLVDLLESAGYEGPRHDFKPPRTE
EDFDGVWASAAGCMRNYLILKERAFAFRADPEVQEALRAARLDELAQPTAGDGLQALLPDRSAFEDFDPDAA
AARGMAFERLDQLAMDHLLGARG

>d4xiao_c.1.15.3 (A:) D-xylose isomerase {Arthrobacter, strain b3728}

VQPTPADHFTFGLWTGVWTGADPFGVATRANLDPVEAVHKLAELGAYGITFHNDLIPFDATAAEREKILGDFN
QALADTGLKVMVTTLNLFSHPVFKDGGFTSNDRSIRRFALAKVLHNIDLAAEMGAETFVMWGGREGSEYDGS
KDLAAALDRMREGVDTAAGYIKDKGYNLRIALEPKPNEPRGDIFLPTVGHGLAFIEQLEHGDIVGLNPETGHEQ
MAGLNFTHGIAQALWAELHIDLNGQRGIKYDQDLVFGHGLTSAAFTVLLENGFPNGGPKYTGPRHFDYK
PSRTDGYDGVWDSAKANMSMYLLKERALAFAFRADPEVQEAMKTSGVFELGETTLAGESADLMNDSASFA
GFDAEAAAERNFAIRLNQLAIEHLLGSR

>d1xima_c.1.15.3 (A:) D-xylose isomerase {Actinoplanes missouriensis}

VQATREDKFSFGLWTGVWQARDAFGDATRTALDPVEAVHKLAEIGAYGITFHDDDLIPFGSDAQTRDGIIAGFK
KALDETGLIVPMVTTNLFTPVFKDGGFTSNDRSIRRFALAKVLHNIDLAAEMGAETFVMWGGREGSEYDGS
DVSAALDRYREALNLLAQYSEDRGYGLRFAIEPKPNEPRGDILLPTAGHIAFVQELERPELFGINPETGHEQMS

NLNFTQGIAQALWHKKLFHIDLNGQHGPKFDQDLVFGHGDLNAFSLVDLLENGPDGAPAYDGPRHF DYKPS
RTEDYDGVWESAKANIRMYLLLKERAKAFRADPEVQEALAASKVAELKPTLNPGEGYAELLADRS AFEDYDAD
AVGAKGFGFVKLNQLAIEHLLGAR

>d1a0ca_ c.1.15.3 (A:) D-xylose isomerase {Clostridium thermosulfurogenes,
also known as Thermoanaerobacter thermosulfurigenes}

NKYFENVSKIKYEGPKSNNPYSFKFYNPSEEVIDGKTMEELRFSIAYWHTFTADGTDQFGKATMQR PWNH YTD
PMEDIAKARVEAAFFFDKINAPYFCFH DRDIAPEGDTLRETNKNLDTIVAMIKDYLKTSKTVLWGTANLFSNPR
F VH GASTSCNADV FAYSAAQVKALEITKELGGENYFWGGREGYETLLNTDMEFELDN FARFLHMAVDYAKE
IGFEGQFLIEPKPKEPTKHQYDFDVANVLAFLRKYDLDKYFKVNIEANHATLAFDFQHELYARINGVLGSIDAN
TGDMILLGWDTDQFPTDIRMTT AMYEVIKMGFDKGGLNFDAKVRRASFEPE DLFLGHIAGMDAFAKGFKV
AYKLVKDRVFDKFIEERYASYKD GIGADIVSGKADFRSLEYALERSQIVNKSGRQELLESILNQYLFA

>d1a0da_ c.1.15.3 (A:) D-xylose isomerase {Bacillus stearothermophilus}
PYFDNISTIAYEGPASKNPLAFKFYNPSEEVKGDKTMEELRFSVAYWHTFTGDGSDPGAGNMIRPWNK YSG
MDLA KARVEAAFFFEKLNIPFFCFHDV DIAPEGETLKETYKNLDIIVDMIEEYMKTSKTL WNTANLFTHPRF V
HGAATSCNADV FAYAAAKVKKGLEIAKRLGAENYFWGGREGYETLLNTDMKLEDLNARFLHMAVDYAKEIG
FDGQFLIEPKPKEPTKHQYDFDVATALAFLQTYGLKD YFKFNIEANHATLAGHTFEHELRVARIHGMILGSVDAN
QGDMLLGWDTDEFPTDLYSTT AMYEILKNGGLRGGLNFDAKVRRGSFEPE DLFYAHAGMDSF AVGLKVA
HRLIEDRVFDEFIEERYKS YTEGIGREIVEG TADFHKLEAHALQLGEIQNQSGRQERLKTL NQYLLEVC

>d1a0ea_ c.1.15.3 (A:) D-xylose isomerase {Thermotoga neapolitana}

AEFFPEIPKVQFEGKESTNPLAFKFYDP EIIDGKPLKDH LKFSVAFWHTFVN EGRDPFGDPTADRPW NR YTDP
MDKA FARVDALF ECEKLNIEYFCFH DRDIAPEGKTLRET NKILD KVVERIKERM KDSNVKLLWGTANLF SHPRY
MHGAATTCSADV FAYAAQVKALEITKELGGEGYV FWGGREGYETLLNTDLF ELENLARFLR MAVA DYAKRIG
FTGQFLIEPKPKEPTKHQYDFDVATA Y AFLKSHGLDEYFKFNIEANHATLAGHTF QHELRMARI LGKLSIDAN Q
GDLLLGWDTDQFPTNVYDTT AMYEVIKAGGFTKGGLNFDAKVRRAS YKVEDLFIGHIAGMDTF ALGF KVAYK
LVKDGVL DKFIEEKYRSF REGIGRDIVEG KVDFE KLEYIIDKETIELPSG KQEY LESLINSYIVKTILER

>d1bxca_ c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp. Caldophilus}

MYEPKPEH RFTF GLWTGVGNVGRDPFGDAVRERLDPVYVGHKLAELGVHGVNLHDEDLIPRGTPPQERDQIVR
RFKRALDETGLKVPMTVGNLFSDPGFKDGGFTSRDPWVRAYAFRKSLETMDLGAELGAEIYVVWPGREGAEV
EATGKARKVWDWVREPLNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFATVGSM LALIHTLERPERFGLNPEF
AHETMAGLNFVHAVAQAL DAGKLLHIDLNGQRMNRFDQDLRGFSEN LKAFAFLVL DLESSGYQGPRHF DAHA
L RTEDEEGVWAFARGCMRTYLILKERA EA FREDPEV KELLA AYYQEDPA ALPLMDPYSHEKAEALKRAELPLEAK
R RGYALERLDQLAVEYLLGVRG

>d1bxba_ c.1.15.3 (A:) D-xylose isomerase {Thermus aquaticus, subsp. Thermophilus}

MYEPKPEH RFTF GLWTGVGNVGRDPFGDAVRERLDPVYVHKLAELGAYGVNLHDEDLIPRGTPPQERDQIVR
RFKKALDETGLKVPMTANLFSDPAFKDGAFTSPDPWVRAYALRKSLETMDLGAELGAEIYVVWPGREGAEVE
ATGKARKVWDWVREALNFMAAYAEDQGYGYRFALEPKPNEPRGDIYFATVGSM LAFIHLDRPERFGLNPEF
HETMAGLNFVHAVAQAL DAGKLFHIDLNDQ RMSRFDQDLRGFSEN LKAFAFLVL DLESSGYQGPRHF DAHAL
R TEDEEGVWAFARGCMRTYLILKERA EA FREDPEV KELLA AYYQEDPA ALLLGPYSREKAEALKRAELPLEAK
R RGYALERLDQLAVEYLLGVRG

>d1luca_ c.1.16.1 (A:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}

MKFGNLLTYQPPELSQT EVMKRLVNLGKASECGCGFDTVWLLEHHFT EFGLLGNPYAAHLLGATE TNVGT
AAIVLPTAHPVRQAEDVNLLDQMSKGRFRFGICRGLYDKDFRVFGTDM DNSRALMDC WYDLMKEGFNEG YI
AADNEHIKFPKIQLNPSAYTQGGAPVYVVAESASTTEWAERGLPMILSWIINTHEKKAQLDLYNEVATEHGYD
VT KIDHCLSYITSVDHDSNRAK DICRNFLGH WYDSYV NATKIFDDSDQTKGYDFNKGQWRDFVLKGHKDTNRR

IDYSYEINPVGTPEECIAIIQQDIDATGIDNICCGFEANGSEEEIASMKLFQSDVMPYLKEKQ

>d1lucb_c.1.16.1 (B:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}

MKFGLFFLNFMNSKRSSDQVIEEMLDTAHYDQLKFDTLAVYENHFSNNGVVGAPLTAGFLLGMTKNAKVA
SLNHVITTHHPVRVAEEACLLDQMSEGRCFGSDCEKSADMRRFNPTDSQFQLFSECHKIINDAFTTGCHP
NNDFYSFPKISVNPHAFTEGGPAQFNATSKEVVEWAALKGLPLVFRWDDDNAQRKEYAGLYHEVAQAHGVD
VSQVRHKLTLLVNQNVDGEAARAEARVYLEEVRESYSNTDFEQKMGESELLSENAIGTYEESTQAARVAIECCGA
ADLLMSFESMEDKAQQRAVIDVVNANIV

>d1nfp_c.1.16.2 (-) Non-fluorescent flavoprotein (luxF, FP390) {Photobacterium leiognathi}

MTKWNYGVFFLNFYHVGQQEPSTMSNALETLRIIDEDTSIYDVAFSEHHIDKSYNDETKLAPFVSLGKQIHVL
ATSPETVVKAAKYGMPLLFKWDDSQKRIELLNHYQAAAACKNVDIANVRHRLMLFVNNDNPTQAKAELSI
YLEDYLSYTQAETSIDEIINSNAAGNFDTCLHHVAEMAQGLNNKVDLFCFESMKDQENKKSLMINFDKRVINY
RKEHNLN

>d1fvpa_c.1.16.2 (A:) Non-fluorescent flavoprotein (luxF, FP390) {Photobacterium phosphoreum}

MNKWNYGVFFVNFYNKGQQEPSTMMNALETLRIIDEDTSIYDVINIDDHYLVKKDSEDKKLAPFITLGEKLYVL
ATSENTVDIAAKYALPLVKWDDINEERLKLLSFYNASASKYNKNIDLVRHQLMLHVNVNEATVAKEELKLYIEN
YVACTQPSNFNGSIDSIQSNTGSYKDCLSYVANLAGKFDNTVDFLLCFESMQDQNKKKSVMDLNNQVIKFR
QDNNLI

>d1ezwa_c.1.16.3 (A:) Coenzyme F420 dependent tetrahydromethanopterin reductase {Archaeon Methanopyrus kandleri}

AEVSFGIELLPDDKPTKIAHLIKVAEDNGFEYAWICDHYNNSYMGVLAAVITSKIKLPGGITNPYTRHPLITAS
NIATLDWISGGRAIIGMGPDKATFDKMGGLPFPCPKIPIWNPEAEDEVGPATAIREVKEVIYQYLEGGPVEYEGKY
VKTGTADVKARSIQGSDIPFYMGAAQGPIMLKTAGIEIANGVLVNASNPKDFEVAVPKIEEGAKEAGRSLDEIDVA
AYTCFSIDKDEDKAIEATKIVVAFIVMGSPDVVLERHGIDTEKAEQIAEAIGKGDFGTAIGLVDEDMIEAFSIAGDP
DTVVDKIEELLKAGVTQVVVGSPIGPDKEKAIELVGQEVIPHFK

>d1f07a_c.1.16.3 (A:) Coenzyme F420 dependent tetrahydromethanopterin reductase {Archaeon Methanobacterium thermoautotrophicum}

MKFGIEFVPNEPIEKIVKLVKLAEDVGFEYAWITDHYNKNVYETLALIAEGTETIKLPGVTNPYVRSPAITASAI
ATLDELSNGRATLGIGPGDKATFDALGIEWVKPVSTIRDAIAMMRTLLAGEKTESGAQLMGVKAVQEKIPIYMG
AQGPMMLKTAGEISDGALINASNPKDFEAAPLIKEGAEEAGKSIADIDVAAYTCCSIEDAAAAANAAKIVVAF
IAAGSPPPVERHGLPADTGKKFELLKGDFGGAIGAVDDALMEAFSVVGTPDEFIPKIEALGEMGVTVQYVAG
SPIGPDKESIKLLGEVIASF

>d1qapa1_c.1.17.1 (A:130-296) Quinolinic acid phosphoribosyltransferase, C-terminal domain {Salmonella typhimurium}

VASEVRRYVGLLAGTQTQLLDRTRKTLPLGLRTALKYAVLCGGGANHRLGLTDAFLIKENHIIASGSVRQAVEKAFW
LHPDPVVEVENLDELDALKAGADIIMLDNFNTDQMREAVKRVNGQARLEVSGNVTAEFLREFAETGVDFI
SVGALTGHVRALDLSMRFC

>d1qpoa1_c.1.17.1 (A:117-285) Quinolinic acid phosphoribosyltransferase, C-terminal domain {Mycobacterium tuberculosis}

IATATAAWVDAVRGTTAKIRDTRKTLPLGLRALQKYAVRTGGGVNHRGLGDAALIKDNHVAAGSVVDALRAV
RNAAPDLPCVEVDSLEQLDAVLPEKPELILLDNFAVWQTQTAVQRRDSRAPTVMLESSGLSLQTAATYAETG
VDYLVGALTHSVRVDIGLDM

>d1qasa3_c.1.18.1 (A:299-625) Phospholipase C isozyome D1 (PLC-D1) {Rat (Rattus norvegicus)}

DQPLSHYLVSSSHNTYLLEDQLTGPSSTEAYIRALCKGCRCLELDCWDGPNQEPIYHGYFTSKILFCDVLRPAIRD

YAFKASPYPVILSLENHCSLEQQRVMARHLRAILGPILLDQPLDGVTTSPLSPPEQLKGKILLKGKKLGGLLPAGGEN
GSEATDVSDEVEAAEMEDEAVRSQVQHKPKEDKLKLVPESDMIIYCKSVHFGFSSPGTSGQAFYEMASFSES
RALRLLQESGNGFVRHNVSCLSRIYPAGWRTDSSNYSPEMWNGGCQIVALNFQTPGPEMDVYLGFQDNG
GCGYVLKPAFLRDPNTTFNSRALTQGPW

>d2ptd__ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Bacillus cereus}

ASSVNELENWSKWMQPIPDSIPLARISIPGTHDSGTFKLQNPIKVWGMTQEYDFRYQMDH GARIFDIRGRLT
DDNTIVLHHGPLYLYVTLHEFINEAKQFLKDNPSETIIMSLKKEYEDMKGAE DSFSSTFEKKYFVDPIFLKTEGNIKL
GDARGKIVLLKRYSGSNEPGYNNFYWPDNETFTTVNQNANVTQEKYKVSYDEKVKSIKDTMDETMNNS
EDLNHLYINFTSLSSGGTAWNSPYYASYINPEIANYIKQKNPARVGWVVIQDYINEKWSPLLYQE VIRANKSLI
>d2plc__ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Listeria monocytogenes}

VTTKQWMSALPDTTNLAALSI PGTHD TMSYNGDITWTLTKPLAQTQTM SLYQQLEAGIRYIDIRAKDNL NIYHG
PIFLNASLGVLETITQFLKKNP KETI MRLKDEQNSNDSFDYR I QPLINIYKDYFYTTPRT DTSNKIPTLK DV RGK IL
LLSENHTKKPLVINSRKFGM QFGAPNQV IQDDYNGPSVKTFKEIVQTAYQASKADNKLFLNHISATSLTFTPRQ
YAAA LNNKVEQFVLNL TSEKVRGLGILIMDFPEKQT IKNII KNNKF

>d7reqa1 c.1.19.1 (A:4-560) Methylmalonyl-CoA mutase, alpha and beta subunits
{Propionibacterium freudenreichii, subsp. shermanii}

LPRFDSV DGNAPVPADAARRFEELAKAGTGEAWETA EQIPVG TL NEDV YK DMDW LD TYAGIPPFV HGP YA
TMYA FRPW TIRQYAG FSTAKESNAF YRRN LAAGQKG LSV AF DL PTHRG YD SDN P R VAGD VG MAGVA ID SIYD
MRELFAGIPLDQMSVSMTMNGAVLPIL ALYVVTAEEQGVKPEQLAGTIQNDILKE FMVR NTYIYPPQPSM RIIS
EIFAYTSANMPKW NSISISGYHM QEAG ATADI EMAYTLADGV DYIRAGESV GLNVDQFAPRLSFFWGIG MNFF
MEVAKLRAARMLWAKLVHQFGPKNP KSM SLR THS QTSGWSL TAQDV YNNV RCTIEAMAATQGHTQSL HT
NSLDE AIALPTDFSARIARNTQLFLQQESGTT RVIDP WSGSAYVEELTWDLARKAWGH IQEV EKVGGMA KAI EK
GIPKM RIEAAARTQARIDS GRQPLIGVN KYR LEHEPPLD VLKV DN STV LAEQKAKL V KLA ERDPEK V KA ALDK
ITWAAGNPDDKDPDRNLLKLCIDAGRAMATV GEMSDALEKVFGR YT

>d7reqb1 c.1.19.1 (B:16-475) Methylmalonyl-CoA mutase, alpha and beta subunits
{Propionibacterium freudenreichii, subsp. shermanii}

LTPTTLSLAGDFPKATEEQWEREVEKVLNR GRPPEKQLTFAE CLKRLTVHTV DGI DIVPMYRPKDAPKKLGYPGV
APFTRGTTVRNGDMDA DWV RALHEDPDEKFTRKAILEGLERGVTSLLL RVDPDAI APEH LDEVLS DVLLEM T K
VEVFSRYDQGAAA EALV SYERSDKPAKDLA NLGLD PIGFA ALQG TEPDLTV LGDWV RRLAKFSPD SRA VTIDA
NIYHNAGAGDVAELAWALATGA EYV RALV E QGFTATEAFDTINFRVTATHDQFLTIARL RAL REA WARI GEVFGV
DEDKRGARQNAITSW RELTREDPYVNILRGSIATFSASVGAESITL PFTQALGLP EDDFPLRIARNTGIVLAEEV
NIGRVNDPAGGSYYVESL RSLADA AWKEF QVEK LGGMSKAVMTEHVT KVLDACNAERA KRLANRK QP ITAV
SEFPMIGARSIE

>d1ccwb_ c.1.19.2 (B:) Glutamate mutase, large subunit {Clostridium cochlearium}

MELKNKKWTDEEFHKQREEVLQQWPTGKEV D LQEA DVY LKKI PAE KNFAE KLVL AKK GITMA QP RAGVAL LD
EHIELLRYLQDEGGADFLP STIDAYTRQ NRYDECENG I KESEKAGR SLL NGFPGV NFGV KGCR KV LEAV NLPLQA
RHGTPDSRLLAEIIHAGGWTSNEGGG ISYNVPYAKNVTIEKSLL DWQYCD RL VGFYEEQGVH INREPFGPLTGT L
VPPSMSNAVGITE ALLA E QGV K NITV GY GEC GNMI QDIA ALRC LE EQT NEYL KAYG YNDV FVTTV FHQ WMG
GFPQDES KAFGV VITATTIA ALAGATK VIKTPHEA I GPTKEA NAAGI KATK M ALNM LEGQR MPMSKELETEM
AVIKAETK CILD KM FELG KGD LAIG TVKA FETGV MDI PFGPSK YAGK MM PVRD NLGCV RYLEFG NV PFT E EK
NYNRERLQERAKFEG RDV SFQM VIDDI FAVG KGR LIGR PE

>d1eexa_ c.1.19.3 (A:) Diol dehydratase, alpha subunit {Klebsiella oxytoca}

MRSKRFEALAKRPVNQDG FVKE WIEEGFIAMESPNDPKPSIKIVNGAVTEL DGKP VSDFD LIDH FIA RYGINL NR
AEEVMAMDSVKLANMLCDPNV KRSEI VP LT AMTPAK IVEV VSHM NVV EMM MAMQKMRARRTPSQQAH

VTNVKDNPVQIAADAAEGAWRGFDEQETTVAVARYAPFNAILVGSQVGRPGVLTQCSLEEATELKLGMIGH
TCYAETISVGTEPVFTGDDTPWSKGFLASSYASRGLKMRFTSGSGEVQMGYAEGKSMLYLEARCIYITKAAG
VQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSSLDECASSNDQFTHSDMRRSTARLLMQFLPGTDFISSGYA
VPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREEDVIAIRNKAARALQAVFAGMGLPPITDEEVEA
ATYAHGSKDMPERNIVEDIKFAQEIIKNRNGLEVVKALAQGGFTDVAQDMLNIQKAKLTGDYLHTSAIIVGDG
QVLSAVNDVNDYAGPATGYRLQGERWEEIKNIPGALDPN

>d1f3ea_ c.1.20.1 (A:) tRNA-guanine transglycosylase {Zymomonas mobilis}

RPRFSFSIAAREGKARTGTIEMKRGVIRTPAFMPVGTATVKALKPETVRATGADIILGNTYHMLRPGAEARIAKL
GGLHSFMGWDRPILTDGGYQVMSLSSLTQSEEGVTFKSHLDGRHMLSPERSIEIQHLLGSDIVMAFDCTP
YPATPSRAASSMERSMRWAKRSDRDAFDSRKEQAENAALFGIQQGSVFENLRQQSADALAEIGFDGYAVGGLA
VGEQQDEMFRVLDFSVPMPLDDKPHYLMGVGPDDIVGAVERGIDMFDCVLPTRSGRNGQAFTWDGPINIR
NARFSEDLKPLDSECHCAVCQKWSRAYIHHLIRAGEILGAMLTEHNIAFYQQLMQKIRDSISEGRFSQFAQDF
RARYF

>d1aj2__ c.1.21.1 (-) Dihydropteroate synthetase {Escherichia coli}

MKLFAQTSLDLSPHVMGILNVTPDSFSDDGGTHNSLIDAVKHANLMINAGATIIDVGGESTRPGAAEVSVEEE
LQRVIPVVEAIAQRFEVVISVDTSKPEVIRESAKVGAIINDIRSLSEPGALEAAAETGLPVCLMHMQGNPKTM
QEAPKYDDVFAEVNRYFIEQIARCEQAGIAKEKLLDPGFQFGKNLSHNYSLLARLAEFHHFNLPOLLVGMSRKSM
IGQLLNVPSERLSGSLACAVIAAMQGAHIIRVHDVKETVEAMRVVETLSAKENKRYE

>d1ad1a_ c.1.21.1 (A:) Dihydropteroate synthetase {Staphylococcus aureus}

TKTKIMGILNVTPDSFSDDGGFNNVESAVTRVKAMMDEGADIIDVGGVSTRPGHEMITVEEELNRVLPVVEAI
VGFDVKISVDTFRSEVAEACLKGVDIINDQWAGLYDHMFQVVAKYDAEIVLMHNGNGNRDEPVVEEMLTS
LLAQAHQAKIAGIPSNIKIWLDPGIGFAKTRNEEAEMARLDELVATEYPVLLATSRKRTKEMMGYDTTPVERD
EVTAATTAYGIMKGVRRAVRVHNVELNAKLAKGIDFLKENENARHN

>d1eyea_ c.1.21.1 (A:) Dihydropteroate synthetase {Mycobacterium tuberculosis}

PVQVMGVNVNTDDSFSDGGCYLDLDDAVKHGLAMAAAGAGIVDVGGESSRPGATRVDPAVETSRVIPVVKEL
AAQGITVSIDTMRADVARAALQNGAQMVNDVSGGRADPAMGPLLAEADVPWVLMHWRAVSADTPHPV
RYGNVVAEVRADLLASVADAAGVDPARLVLDPLGLGFAKTAQHNWAILHALPELVATGIPVLVGASRKRFGLA
LLAGPDGVMRPTDGRDTATAVISALAALHGAWGVRVHDVRASVDAIKVVEAWMGAE

>d1f6ya_ c.1.21.2 (A:) Methyltetrahydrofolate: corrinoid/iron-sulfur protein methyltransferase
MetR {Moorella thermoacетica}

MLIIGERINGMFGDIKRAIQERDPAPVQEWRARRQEEGGARALDLNVGPVQDKVSAMEWLVEVTQEVSNLTL
CLDSTNIKAIAGLKCKNRAMINSTNAEREKVEKLFPLAVEHGAALIGLTMNKTPKIPKDSDTRLAFAMELVAAA
DEFGLPMEDLYIDPLILPANVAQDHAPEVLKTLQQIKMLADPAPKTVGLSNVSQNCQNPLINRTFLAMAMA
CGLMSAIADACDEALIETAATAEILLNQTVCYCDSFVKMFKTR

>d1uroa_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Human (Homo sapiens)}

GFPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAQQDFFSTCRSPEACCELTQPLRRFLDAAIIF
SDILVVPQALGMEVTMVPKGPSFPEPLREEQDLERLRDPEVVASELGYVFQAITLTRQRLAGRVPPLIGFAGAP
WTLMTYMVEGGGSTMAQAKRWYQRQPASHQLLIRLTALPVYLVGQVAGAQALQLFESHAGHLGPQLF
NKFALPYIRDVAKQVKARLREAGLAPVPMIIAKDGHFALEELAQAGYEVVGLDWTVAPKKARECVGKTVTLQG
NLDPICALYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYPMDPEHVGAFVDAVHKHSRLLRQ

>d1j93a_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Tobacco (Nicotiana tabacum),
UROD-III}

TQPLLLDAVRGKEVERPPVWLMRQAGRYMKSYQLLCEKYPLFRDRSENVDLVVEISLQPWKVFRPDGVILFSDI
LTPLSGMNIPFDIIGKGKGPVIFDPLRTAADVEKVREFIPEKSVPYVGEALTILRKEVNNQAAVLGFVGAPFTLASYV

VEGGSSKNFTKIKRLAFAEPKVLHALLQKFATSMAKYIRYQADSGAQAVQIFDSWATELSPVDFFEEFLPYLKQIV
DSVKLTHPNLPLILYASGSGGLLERLPLTVGDVVSLSLDWTVDMADGRRRLGPNAIQGNVDPGVLFGSKEFITNRI
NDTVKKAGKGKHILNLGHGIVGTPEENFAHFEIAKGLRY
>d1b5ta_ c.1.23.1 (A:) Methylenetetrahydrofolate reductase {Escherichia coli}
GQINVSEFFPPRTSEMEQLWNSIDRLSSLKPVSVTYGANSGERDRTHSIIGKIKDRTGLEAAPHLTCIDATPD
ELRTIARDYWNNGIRHIVALRGDLPPGSGKPEMYASDLVTLLKEVADFDISVAAYPEVHPEAKSAQADLLNLKRK
VDAGANRAITQFFFVESYLFRDRCVSAGIDVEIIPGILPVSNFKQAKKFADMTNVRIPAWMAQMFDGLDDD
AETRKLVGANIAMDMVKILSREGVKDFHFYTLNRAEMSIAICHTLGVRPA
>d1heta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Horse (Equus caballus)}
GFSTGYGSAVKVAKVTQGSTCAVFGLGGVGLSIMGCKAAGAAARIIGVDINKDKFAKAKEVGATECVNPQDYK
KPIQEVLTEMSNGGVDFSFEVIGRLDTMVTALSCCQEAYGVSVIVGVPPDSQNLSMNPMLLSGRTWKGAIFG
GFKS
>d1d1ta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}
GFSTGYGAAVKTGKVPGSTCVFGLGGVGLSIMGCKSAGASRIIGIDLNKDKFEKAMAVGATECISPKDSTKP
ISEVLSEMTGNNGYTVEIGHLETMIDALASCHMNYGTSVVGVPPDSQNLSINPMILLTGRWKGCVF
GK
LKS
>d1ht0a2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}
GFSTGYGSAVKVAKVTPGSTCAVFGLGGVGLSVMGCKAAGAAARIAVDINKDKFAKAKELGATECINPQDYKK
PIQEVLKEMTDGGVDFSFEVIGQLDTMMASLLCCEACGTSVIVGVPPDSQNLSINPMILLTGRWKGAIFG
FKS
>d1teha2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Human (Homo sapiens), different isozymes}
GISTGYGAAVNATAKLEPGSVCASFGLGGVGLAVIMGCKVAGASRIIGVDINKDKFARA
KEFGATECINPQDFSKPI
QEVLIEDGVDYSFECIGNVKVMRAALEACHKGWGVSVVGVAASGEIATRFQLVTGRTWK
GTAFGG
WKS
>d1e3ia2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Mouse (Mus musculus), class II}
LIGCGFSSGYGAAINTAKVTPGSTCAVFGLGCVGLSAIIGCKIAGASRIIAIDINGE
KFPKAKALGATDCLNPRELDK
PVQDVITELTAGGVVDYSLDCAGTAQTLKAAVDCTVLWG
SCTVVGAKVDEM
TIPTVDVILGRSINGTFFGGW
>d1cdoa2 c.2.1.1 (A:176-324) Alcohol dehydrogenase {Cod (Gadus callarias)}
GVSTGFGAAVNATAKVEPGSTCAVFGLGA
VLA
VMGCHSAGAKRIIAVDLN
PDKFEKAKVFGATDFV
NPNDH
SEPISQVLSKMTNGGVDFSLECVGNVGVMRNALESCLKGWGV
SVLVGWTDLHDVATRPIQLIAGRTWK
GSM
FGGFKG
>d1keva2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase
{Clostridium beijerinckii}
MMTTGFHGAELADIQMGS
VVVIGIGAVGL
MIAGAKLRGAGRIIGVG
SRPIC
VEAAKF
YGATDIL
NYKNGHIV
DQVMKLTNGKG
VDRVIMAGGG
SETLSQAV
SMVKPG
IIISNINYHG
SGDALL
IPRVEWG
CGMAHK
TIKGG
LCP
GGRLRAEMLRD
MVVYN
RV
>d1ykfa2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase
{Thermoanaerobacter brockii}
MMTTGFHGAELADI
ELGATV
AVLG
IGPV
GLMA
VAGAK
LRGAG
RIIAV
GSRP
VC
DA
AK
YYG
ATD
IV
NY
KD
GPIE
SQIMNL
TEGKG
VDA
IIAG
GNAD
IMATA
VKIV
KPG
GTIAN
VNY
FGE
GEV
LPV
PRLE
WG
CGMA
HK
TI
KGG
LCP
GRL
RMER
LIDL
VFY
KRV
>d1e3ja2 c.2.1.1 (A:151-313) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (Bemisia argentifolii)}
LEPLSVGVHACRRAGVQLGTTVLV
IGAG
PIGLV
SVA
AKAY
GAF
VV
CTAR
SPRR
LEV
AKNC
GAD
VT
LV
VD
PAKEE

ESSIIERIRSAIGDLPNTIDCSGNEKCITIGINTRGGTMLVGMGSQMVPLVNACAREIDIKSVFRCNDYPI
ALEMVASGRCA

>d1qora2 c.2.1.1 (A:136-265) Quinone oxidoreductase {Escherichia coli}

YEIKPDEQFLFHAAAGVGGLIACQWAKALGAKLIGTVGTAQKAQSALKAGAWQVINYREEDLVERLKEITGGKK
VRVYDSVGRDTWERSLDCLQRGLMVSFGNSSGAVTVNLGILNQKGSLYVTRPS

>d1udc_ c.2.1.2 (-) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase) {Escherichia coli}

MRVLVTGGSGYIGSHTCVQLLQNGHVDIILDNLCKNSKRSVLPVIERLGGKHPTFVEGDIRNEALMTEILHDHAID
TVIHAGLKVAGESVQKPLEYYDDNNVNGTLRLISAMRAANVKNFIFSSSATVYGDQPKIPYVESFPTGTPQSPYGV
KSKLMVEQILDLQKAQPDWSIALLRYFNPGAHPSGDMGEDPQGIPNNLMPYIAQVAVGRRDSLAIFGNDY
PTEDGTGVRDYIHVMDLADGHVAMEKLANKPGVHIYNLGAGVGNSVLDVVNAFSKACGKPVNYHFAPRRE
GDLPAYWADASKADRELNWRTVRTLDEMAQDTWHWQSRHPQGYPD

>d1ek6a_ c.2.1.2 (A:) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-epimerase) {Human (Homo sapiens)}

MAEKVLVTGGAGYIGSHTVLEAGYLPVIDNFHNAFRGGSLPESLRRVQELTGRSVEFEEMDILDQGALQ
RLFKKYSFMAVIHAGLKVAGESVQKPLDYYRVNLGTIQLLEIMKAHGKVNLVFFSSATVYGNPQYLPDEAHP
TGGCTNPYGKSKFFIEEMIRDLCQADKTWNNAVLLRFNPTGAHASGCIGEDPQGIPNNLMPYVSQVAIGRREA
LNVFGNDYDTEDGTGVRDYIHVVDLAKGHIAALRKLEQCGCRIYNLTGTGYSVLQMVQAMEKASGKKIPYK
VVARREGDVAACYANPSLAQEELGWTAAALGLDRMCEDLWRWQKQNPSGFGT

>d1bxka_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Escherichia coli}

MRKILITGGAGFIGSALVRYIINETS DAVVVVDKLTYAGNLMSLAPVAQSERFAFEKVDICDRAELARVFTEHQPD
CVMHLAAESHVDRSIDGPAAFIETNIVGTYTLLEAARAYWNALTEDKKSAFRFHISTDEVYGDLHSTDDFTET
TPYAPSSPYASKASSDHVRAWLRTYGLPTLITNCNNYGPYHFPEKLIPLMILNALAGKSLPVYNGQQIRDW
LYVEDHARALYCVATTGKVGGETYNIGGHNERKNLDVVTICELLEELAPNKPHGVAHYRDLITFADRGHDLRY
AIDASKIARELGCVPQETFESGMRKTVQWYLANESWWKQVQDGSYQGER

>d1kepa_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Streptococcus suis, serotype 2}

QFKNIITGGAGFIGSNFVHYVYNNHPDVHVTVLKLYAGN KANLEAILGDRVELVGGDIADAELVDKLAAKA
DAIVHYAAESHNDNSLNDPSPFIHTNFIGTYTLLEAARKYDIRFHHSTDEVYGDLPLREDLPGHGE GPGEKFTA
ETNYNPSSPYASKASSDHVRAWRRTYGLPTLITNCNNYGPYHQHIEKFIPRQITNLAGIKPKLYGEGKNVRDWI
HTNDHSTGVWAILTKGRMGETYLIGADGEKNNKEVLELILEKMGQPKDAYDHVTDRAGHDLRYAIDASKLRDE
LGWTPQFTDFSEGLEETIQWYTDNQDWKAEKEAVEANYAKTQEVIK

>d1kewa_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {Streptococcus suis, serotype 2}

MKILITGGAGFIGSAVRHIIKNTQDTVNVIDLKLYAGNLESLSIDESNRNFEHADICDSAEITRIFEQYQPAV
MHLAAESHVDRSITGPAAFIETNIVGTYALLEVARKYWSALGEDKKNNFRFHISTDEVYGDLPHPDEVENSVTL
PLFTETTAYAPSSPYASKASSDHVRAWRRTYGLPTLITNCNNYGPYHFPEKLIPLVILNALEGKPLPIYGKGDQI
RDWLYVEDHARALHMVTEKGAGETYNIGGHNEKKNLDVFTICDLLDEIVPKATSYREQITYVADRGHDLRR
YAIDAGKISRELWKPLETFESGIRKTVEWLANTQWVNNVKSGAYQSWIEQNYEGRQ

>d1e6ua_ c.2.1.2 (A:) GDP-4-keto-6-deoxy-d-mannose epimerase/reductase (GDP-fucose synthetase) {Escherichia coli}

AKQRVFIAGHRGMVGSIRRQLEQRGDVELRTRDELNLDSRAVHDFFASERIDQVYAAKVGIVANNTY
PADFIYQNMIMIESNIIHAAHQNDVNKLLFLGSSCIYPKLAQQPMAESELLQGTLEPTNEPYAIKIAIGIKLCESY
RQYGRDYRSVMPNLYGPHDNFHPNSHVIPALLRFHEATAQKAPDVVVWGSGTPMREFLHVDDMAASI

HVMELAHEVWLENTQPMMLSHINVGTGVDCIRELAQTIAKVVGKGRVVFDASKPDGTPRKLLDVTRLHQLGWYHEISLEAGLASTYQWFLENQ

>d1db3a_ c.2.1.2 (A:) GDP-mannose 4,6-dehydratase {Escherichia coli}

SKVALITGVTGQDGSYLAEFLLEKGYEVHGIKRRASSFNTERVDHLYQDPHTCNPKFHLHYGDLSDTSNLTRILREVQPDEVYNLGAMSHAVSFESPEYTADVDAMGTLRLLEAIRFLGLEKKTRFYQASTSELYGLVQEIPQKETTPFYPRSPYAVAKLYAYWITVNYRESYGMYACNGILFNHESPRRGETFVTRKITRAIANIAQGLESCLYLGNMDSLRDWGHAKDYVKMQWMMLQQEQPEDFVIATGVQYSVRQFVEMAAAQLGIKLRFEGTGVEEKGIVVSVTGHADPGVKPGDVIIVDPRYFRPAEVETLLGDPTKAHEKLGWKPEITLREMVSEMVANDLEAAKKHS

>d1eq2a_ c.2.1.2 (A:) ADP-L-glycero-D-mannoheptose 6-epimerase {Escherichia coli}MIIVTGGAGFIGSNIVKALNDKGITDILVVDNLKDGTKFVNLDLNIADYMDKEDFLIQIMAGEEFGDVEAIFHEGACSSTEWDGKYMMDDNNYQYSKELLHYCLEREIPIFLYASSAATYGGRTSDFIESREYEKPLNVYGYSKFLFDEYVRQILPEANSQIVGFRYFNVYGPREGHKGSMASVAFHNLTNNGESPKLFESENFKRDFVYVGDVADVNLWFLENGVSGIFNLGTGRAESFQAVADATLAYHKKQIEYIPFPDKLKGRYQAFTQADLTNLRAAGYDKPFKTVAEVTTEYMAWLN

>d1qrra_ c.2.1.2 (A:) Sulfolipid biosynthesis protein SQD1 {Thale cress (*Arabidopsis thaliana*)}KRVMVIGGDGYCGWATALHLSKKNYEVICVDNLVRRFLDHQLGLESLTPIASIHDRISRWKALTGKSIELYVGDICDFEFLAESFKSFEPDSVVFGEQRSAPESMIDRSRAVYTQHNNVIGTLNVLFIAIKEFGEECHLVKLGTMGEGYGTPNIDIEEGYITITHNGRTDTLPYPKQASSFYHLSKVHDHSNIAFTCAWGIRATDNLQGVVYGVKTDETEMHEELRNRLDYDAVFGTALNRFCVQAAVGHPLTVYGKGGQTRGYLDIRDVQCVIAIANPAKAGEFRVFNQFTEQFSVNELASLVTKAGSKLGLDVKKMTVPNPRVEAEHHYNAKHTKLMELGLEPHYLSDSLDSLNFNFAVQFKDRVDTKQIMPSVSWKKIGVKTKS

>d1k6xa_ c.2.1.2 (A:) Negative transcriptional regulator NmrA {Aspergillus nidulans}QQKKTIAVVNATGRQAASLIRVAAAVGHHVRAQVHSLKGLIAEELQAIPNVTLFQGPNNVPLMDTLFEGAHLAFINTTSQAGDEIAIGKDLADAALKRAGTIQHYIYSSMPDHSLYGPWPAPVMWAPKFTVENYVRQLGLPSTFVYAGIYNNNNFTSLPYPLFQMELMPDGTFEWHAPFDPIPLPWLDAEHDVGPALLQIFKDGPQKWNGHRIALTFTLSPVQVCAAFSRALNRRVTYVQVPKEIKVNIPVGYREQLEIAEVVFGEHKAPYFPLPEFSRPAAGSPKGGLGPANGKGAGAGMMQGPGGVISQRVTDEARKLWSGRDMEEYAREVFPIEEEANGLDWML

>d1cyda_ c.2.1.2 (A:) Carbonyl reductase {Mouse (*Mus musculus*)}LNFSGLRALVTGAGKGIGRDTVKALHASGAKVVAVRTNSDLVSLAKECPGIEPVCVDLGDWDATEKALGGIGP

VDLLVNNAALVIMQPFLFVTKAEDRSFSVLRSVFQVSQMVARDMINRGVPGSIVNVSSMVAHVTFPNLITYSSTKGAMTMLTKAMAMELGPHKIRVNSVNPTVVLTDMGKKVSADPEFARKLKERHPLRKFAEVEDVVNSILFLSDRSASTSGGGILVDAGYLAS

>d1oaa_ c.2.1.2 (-) Sepiapterin reductase {Mouse (*Mus musculus*)}ADGLGCAVCVLTGASRGFGRALAPQLARLLSPGSVMLVSARSESMRLQLKEELGAQQPDLKVVLAADLGTEA

GVQRLLSAVRELPRPEGLQRLLLINNAATLGDVSKGFLNVNDLAEVNNYWALNLTSMCLSTGTLNAFQDSPGLSKTVVNISSLCALQPKWGWGLYCAKGKAARDMLYQVLAEEPSVRVLSYAPGPLDNDMQQLARETSKDPELRSKQLKLSDGALVDCGTSAQKLLQLQKDTFQSGAHVDFYD

>d1hdr_ c.2.1.2 (-) Dihydropteridin reductase (pteridine reductase) {Human (*Homo sapiens*)}EARRVLVYGGRGALGSRCVQAFRARNWWVASVDVVENEEASASIIVKMTDSFTEQADQVTAEVGKLLGEEKVDAILCVAGGWAGGNAKSLSFKNCALMWKQSIWTSTISHLATKHLKEGGLTLAGAKAALDGTPGMIGYGMAGKAVHQLCQSLAGKNSGMPPGAAIAVLPVTLTPMRKSMPEADFSSWTPLEFLVETFHDWITGKNRPSSGSLIQVVTTEGRTELTPAYF

>d1e7wa_ c.2.1.2 (A:) Dihydropteridin reductase (pteridine reductase) {Leishmania major}TVPVALVTGAAKRLGRSIAEGLHAEGYAVCLHYHRSAEANALSATLNARRPNSAITVQADLSNVATAPVSGAD

GSAPVTLFTRCAELVAACYTHWGRCDVLVNNASSFYPTPLRNDEDGHEPCVGDRREAMETADLFGSNAIAP
YFLIKAFahrVAGTPAKHRGTNYSIINMVDAMTNQPLLGYTIYMAKGAEGLTRSAALELAPLQIRVNGVGPG
SVLVDMDPPAVWEGRSKVPLYQRDSSAAEVSDVIFLCSSKAKYITGTCVKVDDGGYSLTRA
>d1fds_ c.2.1.2 (-) Human estrogenic 17beta-hydroxysteroid dehydrogenase {Human
(Homo sapiens)}
ARTVVLITGCSSGIGLHLAVRLASDPSQSFKVYATRLDLKTQGRLWEAARALACPPGSLTQLDVRDSKSAAA
RERVTEGRDVLCVNCAGLGLLGPALGEDAVASVLDVNVTGTVRMLQAFLPDMKRRGSGRVLTVGGLM
GLPFNDVYCASKFALEGLCESLAVLLPFGVHLSLIECGPVHTAFMEKVLGSPEEVLDRTDIHTFHRFYQYLAHSK
QVFREAAQNPEEVAEVFLTALRAPKPTLRYFTTERFLPLRMRLDDPSGSNYVTAMHREVFGDV
>d1fmca_ c.2.1.2 (A:) 7-alpha-hydroxysteroid dehydrogenase {Escherichia coli}
MFNSDNLRDGKCAITGAGAGIGKEIAITFATAGASVVSDINADAANHVDEIQQLGGQAFACRCDTSEQEL
SALADFAISKLGKVDILVNNAGGGGPKFDMPMADFRRAYELNVFSFFHLSQLVAPEMEKNGGGVILTTSMA
AENKNINMTSYASSKAAASHLVRNMAFDLGEKNIRVNGIAPGAILTDALKSVITPEIEQKMLQHTPIRRLGQPQ
DIANAALFLCSPAASWVSGQILTVSGGGVQELN
>d1hdca_ c.2.1.2 (A:) 3-alpha,20-beta-hydroxysteroid dehydrogenase {Streptomyces hydrogenans}
NDLSGKTVIITGGARGLGAEARQAVAAGARVVLADVLDEEGAATARELGDAARYQHLDVTIEEDWQRVVAYA
REEFGSVDGLVNNAGISTGMFLETESVERFRKVVEINLTGVFIGMKTIPAMKDAGGGSIVNISSAAGLMGLALT
SSYGASKWGVVRGLSKLAAVELGTDRIRVNSVHPGMTYTPMTAETGIRQEGGNYPNTPMGRVGEPEIAGAVV
KLLSDTSSYVTGAELAVDGGWTTGPTVKYVMGQ
>d1fjha_ c.2.1.2 (A:) 3-alpha-hydroxysteroid dehydrogenase {Comamonas
testosteroni}
MSIIVISGCATGIGAATRKVLEAAGHQIVGIDIRDAEVIADLSTAEGRKQAIADVLAKCSKGMDGLVLCAGLPQT
KVLGNVSVNYFGATELMDAFLPALKKGHQPAAVVISSVASAHLAFDKNPLALALEAGEEAKARAIVEHAGEQG
GNLAYAGSKNALTVAVRKRAAAWGEAGVRLNTIAPGATEPLLQAGLQDPRYGESIAKFVPPMGRRAEPSEMA
SVIAFLMSPAASYVHGAQIVIDGGIDAVMRPTQF
>d1bdb_ c.2.1.2 (-) Cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase {Pseudomonas sp., lb400}
MKLKGEAVLITGGASGLGRALVDRFVAEGAKAVLDKSAERLAELETDHGDNVLGIVGDVRSLEDQKQAAASC
VARFGKIDTLPNAGIWDYSTALVDLPEESLAAFDEVFHINVKGYIHAVKACLPALVASRGNVIFTISAGFYPNG
GGPLYTAAKHAIVGLVRELAFELAPYVRVNGVSGGINSDLRGPSLGMGSKAISTVPLADMLKSVLPIGRMPE
VEEYTGAYVFFATRGDAAPATGALLNYDGGLGVRGFFSGAGGNDLLEQLNIH
>d1b16a_ c.2.1.2 (A:) Drosophila alcohol dehydrogenase {Fruit fly (Drosophila lebanonensis)}
MDLTNKVIFVAALGGIGLDTRELVKRNLKNFVILDRVENPTALAEKAINPKVNITFHTYDVTVPVAESKKLLKK
IFDQLKTVIDLINGAGILDDHQIERTIAINFGLVNTTTAILDFWDKRKGPGGIIANICSVTFNAIHQVPVYSAS
KAAVVSFTNSLAKLAPITGVTAYSINPGITRPLVHTFNSWLDVEPRVAELLSHPTQTSEQCGQNFVKAIEANKN
GAIWKLDLGTLEAIEWTKHWDSHI
>d1gcoa_ c.2.1.2 (A:) Glucose dehydrogenase {Bacillus megaterium}
MYKDLEGKVVVITGSSTGLKSMAIRFATEKAKVVVYRSKEDEANSVLEEIKVGGEIAVKGDTVESDVINL
VQSAIKEFGKLDVMINNAGLENPVSSHESLSDWNKVIDTNTLGAFLGSREAIFYVENDIKGTVINMSSVHEKI
PWPLFVHYAASKGGMCLMTETLALEYAPKGIRVNNIIGPAINTPINAEKFADPEQRADVESMIPMGYIGEPEE
AAVAAWLASSEASYVTGITLFADGGMTQYPSFQAGRG
>d1gega_ c.2.1.2 (A:) meso-2,3-butanediol dehydrogenase {Klebsiella pneumoniae}
KKVALVTGAGQGIGKAIARLKVKGFAVADYNDATAKAVASEINQAGGHAVAVKVDVSDRDQVFAAVEQAR
KTLGGFDVIVNNAGVAPSTPIESITPEIVDKVYNINVKGVIWGIQAAVEAFKKEGHGGKIINACSQAGHGNPEL
AVYSSSKFAVRGLTQTAARDLAPLGITVNGYCPGIVKTPMWAEIDRQVSEAGKPLGYGTAEFAKRITLGRSLPE

DVAACSYLASPDSDYMTGQSLLIDGGMVFN

>d1h5qa_ c.2.1.2 (A:) Mannitol dehydrogenase {Mushroom (*Agaricus bisporus*)}

PGFTISFVNKTIIVTGGNRIGLAFTRAVAAGANVAVIYRSAADAVEVTEKGKEFGVKTKAYQCDVSNTDIVT
KTIQQIDADLGPISGLIANAGSVVKPATELTHEDFAFVYDVNVFGVFNTCRAVALWLQKQQKGSIVTSSMSS
QIINQSSLNGSLTQVFYNSSKAACSNLVKGAAWEASAGIRVNALSPGYVNTDQTAHMDKKIRDHQASNIPLNR
FAQPEEMTGQAILLSDHATYMTGGEYFIDGGQLIW

>d1edoa_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Oil seed rape (*Brassica napus*)}
SPVVVVTGASRGIGKAIASLGKAGCKVLVNYARSAAEEVSKQIEAYGGQAITFGGDVSKEADVEAMMKTAI
DAWGTIDVVNNAGITRDTLLIRMKKSQWDEVIDLNLTVFLCTQAATKIMMKRKGRRIINIASVVGLIGNIQQ
ANYAAAKAGVIGFSKTAAREGASRNINVNVCPGFIASDMTAKLGEDMEKKILGTIPLGRTGQPENVAGLVEFL
ALSPAASYITGQAFTIDGGIAI

>d1i01a_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {Escherichia coli}
MNFEKGKIALVTGASRGIGRAIAETLAARGAKVIGTATSENGAQAAISDYLGANGKGLMLNVTDPASIESVLEKIRAE
FGEVDILVNNAGITRDNLLMRMKDEEWNDIETNLSSVFRLSKAVMRAMMKKRHGRIITIGSVVGTMGNGQQ
ANYAAAKAGLIGFSKSLAREVASRGITVNVVAPGFIETDMTRALSDDQRAGILAQVPAGRLGGAQEIANAVAFL
ASDEAAYITGETLHVNGGM

>d1eno_ c.2.1.2 (-) Enoyl-ACP reductase {Oil seed rape (*Brassica napus*)}

LPIDLRGKRAFIAGIADDNGYGWAVAKSLAAAGAEILVGTWVPALNIFETSLRRGKFDQSRVLPD GSLMEIKKVY
PLDAVFDNPEDVPEDVKANKRYAGSSNWTQEEAACVRQDFGSIDILVHS LANGPEVSKPLLETSRKGYLAIS
ASSYSFVSLSSHFLPIMNP GGASISLTYIASERIIPGYGGGMSSAKAALES DTRVL AFEAGR KQNIRVNTISAGPLG
SRAAKAIGFIDTMIEYSNNAPIQKTLTADEVGNAAAFLVPLASAITGATIYVDNGLNSMGVALDSPVFK

>d1eny_ c.2.1.2 (-) Enoyl-ACP reductase {Mycobacterium tuberculosis, TB, gene InhA}

AGLLDGKRILVSGIIDSSIAFHIA RVVAQE QGAQLVLTGFDRRLIQRITDRLPAKAPLLELDVQNEEH LASLAGRV
EAIGAGNKLDGVVHSIGFMPQTGMGINPFFDAPYADVSKGIHISAYSYASMAKALLPIMNP GGSIVGMDFDPS
RAMPAYNWMTVAKSALESVNRFVAREAGKYGVRSNLVAAGPIRTLAMSAIVGGALGE EAGAQIQLLEEGWD
QR APIGW NMKD ATPVAKTV CALLSDWLPATTGDIYADGGAHTQLL

>d1qg6a_ c.2.1.2 (A:) Enoyl-ACP reductase {Escherichia coli}

GFLSGKRILVTGVASKLSIAYGIAQAMHREGAELFTYQNDKLGRVEEFAAQLGSDIVLQCDVAEDASIDTMFA
ELGVWPKFDGFVHSIGFAPGDQLGDYVNAVTREGFKIAHD ISSY SFVAMAKACRSMLNPGSALLTLSYLGAE
RAIPN NVVMGLAKASLEANVRYMANAMGPEG V RVNAISAGPIRTL AASG IKDFRKMLAHCEAVTPIRRTVIE
DVGN SAAFLCS DLSAGISGEV VHVDGGF SIAAMNE

>d1ae1a_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (*Datura stramonium*), I}

RWSLK GTT ALVTGGSKGIGYAI VEELAGL GARV YTCRNE KELDEC LEI WREK GLN VEGS VCDL SS RTER DKL M Q
TV AHVFDG KLN ILV NNAGV VIKE AKD FTEK DYN I MGT NFE AY H L S QI AY PLL KAS QNG N VIF L S IAG F S AL P
SV SLY S AS KGAIN QM T KSL ACE WAKDN IRV NSV APG VIL TPL VET AI KNP HQ KEE IDNF IVKTPM GRAG K P QEV
SALIAFLCFPAASYITGQIIWADGGFTANGGF

>d2ae2a_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (*Datura stramonium*), II}

AGRWNLEGCTALVTGGSRGIGYGI VEELASLGASV YTCSR NQKELNDCLTQWR SKGF KVEASV CDL SS RSER QE
LMNTVANHFHG KLN ILV NNAGV VIKE AKD FTEK DYN I MGT NFE AY H L S QI AY PLL KAS QNG N VIF L S IAG F S AL P
AVPYEAVY GATKG AMD DQL TRCL AF EWAKDN IRV NGVG PGVI ATSL VEM T IQD PEQ KEN LNKL IDRC AL RR M GE
PKELAAMVAFLCFPAASYVTGQIIYVDGGLMANC GF

>d1g0oa_ c.2.1.2 (A:) 1,3,8-trihydroxynaphthalene reductase (THNR, naphtol reductase) {Rice blast fungus (*Magnaporthe grisea*)}

KYDAIPGPLGPQSASLEGKVALVTGAGRGIGREMAMELGRRGCKVIVNYANSTESAEEVVAI KKNGSDAACVK

ANVGVVEDIVRMFEEAVKIFGKLDIVCSNSGVVSFGHVKDVTPEEFDRVFTINTRGQFFVAREAYKHLEIGGRIL
MGSITGQAQAKAVPKHAVYSGSKGAIETFARCMAIDMADKKITNVVAPGGIKTDMYHAVCREYIPNGENLSNEE
VDEYAAVQWSPLRRVGLPIDIARVVCFLASNDGGWVTKVIGIDGGACM
>d1ja9a_ c.2.1.2 (A:) 1,3,6,8-tetrahydroxynaphthalene reductase {Rice blast fungus (Magnaporthe grisea)}
SKPLAGKVALTTGAGRIGRGIAIELGRRGASVVNYGSSSKAAEEVVAELKKLGAQGVAIQADISKPSEVVALFD
KAWSHFGGLDFVMSNSGMEEWCDELEVTQELFDKVFNLTTRGQFFVAQQGLKHCRGGRIILTSSIAAVMTGI
PNHALYAGSKAAVEGFCRAFVDCGAKGTVNCIAPGGVKTDMFDENSWHYAPGGYKGMPQEKEGLAN
MNPLKRIGYPADIGRAVSALCQESEWINGQVILGGGI
>d1hdoa_ c.2.1.2 (A:) Biliverdin IX beta reductase {Human (Homo sapiens)}
MAVKKIAIFGATGQTGLTTLAQAVQAGYEVTVLVRDSSRLPSEGPRPAHVVGDLQAAVDKTVAGQDAIV
LLGTRNDSLPTTVMSEGARNIVAAMKAHGVDKVVACTSAFLWDPTKVPPLQAVTDHIRMHKVLRESGLK
YVAVMPPHIGDQPLTGAYTVTLDRGRGPSRVISKHDLGHFMRLCLTDEYDGHSTYPSHQY
>d1e6wa_ c.2.1.2 (A:) 3-hydroxyacyl-CoA dehydrogenase {Rat (Rattus norvegicus)}
SVKGLVAVITGGASGLSTAQLVQGQATAVLLDPNSEGEGTEAKKLGGNCIFAPANVTSEKEVQAALTAKF
GRIDVAVNCAGIAVAIKTYHEKKNQVHTLEDFQRVINVNLTGTFNIRLVAGVMQNEPDQGGQRGVINTASV
AAFEGQVGQAAYSASKGGIVGMTLPIARDLAPIRGIRVVTIAPGLFATPLTLPDKVRNFLASQVPFPSRLGDPAE
YAHLVQMVIENPFLNGEVIRLDGAIRMQP
>d1hu4a_ c.2.1.2 (A:) Carbonyl reductase/20beta-hydroxysteroid dehydrogenase {Pig (Sus scrofa)}
SSNTRVALVTGANKGIGFAIVRDLRQFAGDVVLTARDVARGQAAVKQLQAEGLSPRFHQLDIIDLQSIRALCDF
LRKEYGGGLDVNNAAIAFQLDNPTFHIQAEALTMKTNFMGTRNVCTELLPLIKPQGRVVNVSSTEGVRALNEC
SPELQQKFSETITEELVGLMNKFVEDTKNGVHRKEGWSYSTYGVTKIGVSVLSRIYARKLREQRAGDKILLNA
CCPGWVRTDMGGPKAPKSPEVGAETPVYALLPSDAEGPHGQFVTDKKVVEWGVPPESYPWVNA
>d1gado1 c.2.1.3 (O:0-148,O:313-330) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Escherichia coli}
TIKVGINGFGRIGRIVFRAAQKRS DIEIAVINDLLADYMAYMLKYDSTHGRFDGTVEVKDGHLIVNGKKIRVTA
ERDPANLKWDEVGVDVVAEATGLFLTDETARKHITAGAKKVVMTGPSKDNTPMFVKGANFDKYAGQDIVSNA
SXNETGYSNKVLDLIAHISK
>d1gd1o1 c.2.1.3 (O:0-148,O:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Bacillus stearothermophilus, nca 1503}
AVKVGINGFGRIGRNVFRAALKNP DIEVVAVNLDANTLAHLLKYDSVHGRDAEVSVNGNNLVNGKEIIVK
AERDPENLAWGEIGVDIVVESTGRFTKREDAAKHLEAGAKKVIISAPAKNEDITIVMGVNQDKYDPKAHHVISN
ASXNETGYSHRVVDLAAYIASKGL
>d1cero1 c.2.1.3 (O:1-148,O:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermus aquaticus}
MKVGINGFGRIGRQVFRLHSRGVEVALINDTDNKT LAHLLKYDSIYHRFPGEVAYDDQLYVDGKAIRATAVK
DPKEIPWAEAGVGVVIESTGVFTDADKAKAHLEGGAKKVIITAPAKGEDITIVMGVNHEAYDPSRHHIISNASXN
EWGYANRVADLVELVLRKGV
>d1hdgo1 c.2.1.3 (O:1-148,O:313-331) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermotoga maritima}
ARVAINGFGRIGRLVYRIIYERKNP DIEVVAINDLTDKTLAHLKYDSVHKFPKGVEYTENSIVDGKEIKVFAEP
DPSKLPWKDLGVDFVIESTGVFRNREKAELHLQAGAKKVIITAPAKGEDITVIGCNEDQLKPEHTIISCASXNEY
GYSNRVVDTLELLKM

>d1b7go1 c.2.1.3 (O:1-138,O:301-340) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon *Sulfolobus solfataricus*}
MNVAVANGYGTIGKRVADAIKQPMKLVGVAKTSPNYEAFIAHRRGIRIYVPQQSIKKFEESGIPVAGTVEDLIK
TSDIVDTPNGVGAQYKPIYLQLQRNAIFQGGEKAEVADISFALCNYNEALGKKYIRVVSXESIVVOPENIDAIRA
SMKLMSAEDSMRITNESLGLKGYLI

>d1cf2o1 c.2.1.3 (O:1-138,O:304-336) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon *Methanothermus fervidus*}
MKAVAINGYGTVGKRVADAIQQDDMKVIGVSKTRPDFEARMALKGYDLYVAIPERVKLFKEKAGIEVAGTV
DMLDEADIVIDCTPEGIGAKNLKMYKEGIKAIFQGGEKHEDIGLSFNSLSNYEESYGKDYTRVXIVPENVDAV
RAILEMEEDKYKSINKTNKAMNIL

>d1gaa1 c.2.1.3 (A:1-164,A:334-358) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Trypanosoma brucei brucei, glyosome}
TIKVGINGFGRIGRMVFQALCDDGLLGNEIDVVAVVDMNTDARYFAYQMKYDSVHGKFHKHSVSTTKSKPSVAK
DDTLVVNGHRILCVKAQRNPADLPWGKLGVEYVIESTGLFTVKSAAEGLRGARKVVISAPASGGAKTFVMG
VNHNHNNPREQHVVSNASXNEWGYSHRVVDLVRHMAARDRAAKL

>d1i32a1 c.2.1.3 (A:1-165,A:335-358) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Leishmania mexicana}
APIKVGINGFGRIGRMVFQACDQGLIGTEIDVVAVVDMSTNAEFAYQMKHDTVHGRPKYTVEAVKSSPSVE
TADVLVNGHRIKCVKAQRNPADLPWGKLGVDYVIESTGLFTDKLKAEGHIKGGAKKVVISAPASGGAKTIVMG
VNQHEYSPASHHVVSNASXNEWWAYSHRVVDLVRYMAAKDAASS

>d1dssg1 c.2.1.3 (G:1-148,G:313-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Lobster (*Palinurus versicolor*)}
SKIGINGFGRIGRLVRAALEMGAQVVAVNDPFIALEYMVYMFKYDSTHGMFKGEVKAEDGALVVDGKKITVF
NEMKPENIPWSKAGAEYIVESTGVFTTIEKASAHFKGGAKKVIISAPSADAPMFVCVGVLKYSKDMKVVSNAS
XNEFGYSQRVIDLIKHMQKVDSA

>d3gpdg1 c.2.1.3 (G:1-150,G:315-334) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Human (*Homo sapiens*)}
GKVKVGVDGFGRIGRLVRAAFNSGKVDIVAINDPFIDLHYMVFQYDSTHGKFHGTVAEDGKLVIDGKAI
TIFQERDPENIKWGDAGTAYVVESTGVFTTMEKAGAHKGAKRIVISAPSADAPMFVMGVNHFKYANSLKIIS
NASXNEFGYSERVVVDLMAHMASKE

>d1jn0a1 c.2.1.3 (A:0-148,A:313-333) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Spinach (*Spinacia oleracea*)}
KLKVAINGFGRIGRNFLRCWHGKDSPLDVVINDTGGVKQASHLLKYDSILGTFADVKTAGDSAISVGKVIKVV
SDRNPVNLPWGDMGIDLVIEGTGVFVDRDGAGKHLQAGAKVLITAPGKGDPTYVVGVNEEGYTHADTIISN
ASXNEWGYSQRVVDLADIVANKWQ

>d1gl3a1 c.2.1.3 (A:1-133,A:355-367) Aspartate beta-semialdehyde dehydrogenase {Escherichia coli}
MKNVFIGWRGMVGSVLMQRMVEERDFDAIRPVFFSQLGQAAPSFGTTGTLQDAFDLEALKALDIIVTC
QGGDYTNEIYPKLRESGWQGYWIDAASSLRMKDDAIILDPVNQDVITDGLNNNGIRTFGGXAAEPLRRMLRQ
LA

>d1ebfa1 c.2.1.3 (A:2-150,A:341-359) Homoserine dehydrogenase {Baker's yeast (*Saccharomyces cerevisiae*)}
STKVVNVAVIGAGVVGSAFLDQLLAMKSTITYNLVLLAEAERSLISKDFSPLNVGSDWKAALAASTTKTPLDDLI
AHLKTSPKPVLVDNTSSAYIAGFYTKFENGISIATPNKAFSSDLATWKALFSNKPTNGFVYHEATVGAGLXAA

VTAAGVLGDKVIAQRL

>d1e5qa1 c.2.1.3 (A:2-124,A:392-450) Saccharopine reductase {Rice blast fungus (Magnaporthe grisea)}

ATKSVLMLSGFVTRPTLDVLTSGIKVTVACRTLESAKKLSAGVQHSTPISLDVNDDAALDAEVAKHDLVISLIPY
TFHATVIKSIRQKKHVVTSYSPAMMELDQAQDAGITVMNEIGXYSAMAKLGVPCA AVKFVLDGTISD
RGVLAPMNSKINDPLMKELKEKYGIECKEKVVA

>d1f06a1 c.2.1.3 (A:1-118,A:269-320) Diaminopimelic acid dehydrogenase
(DAPDH) {Corynebacterium glutamicum}

MTNIRVAIVGYGNLGRSVEKLIAKQPDMDLVGIFSRRATLDTKTPFDVADVDKHADDVDVLFLCMGSATDIPE
QAPKFAQFACTVDTYDNHRDIPRHRQVMNEATAAGNVALVSTGXRNPDFTASSQIAFGRAAHRMKQQGQS
GAFTVLEVAPYLLSPENLDDLIARDV

>d1dih_1 c.2.1.3 (2-130,241-273) Dihydrodipicolinate reductase {Escherichia coli}
HDANIRVAIAGAGGRMGRQLIQAALALEGVQLGAALEREGSSLLGSDAGELAGAGKTGTVQSSLDAVKDDFD
VFIDFTRPEGTLNHLAFCRQHGKGGMVIGTTGFDEAGKQAIRDAAADIAIVFAANFSXMTFANGAVRSALWLSG
KESGLFMDRVDLNLNLL

>d1k5ha2 c.2.1.3 (A:1-125,A:275-300) 1-deoxy-D-xylulose-5-phosphate reductoisomerase
{Escherichia coli}

MKQLTILGSTSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLESPRYAVMDDEASAKLLKTMLQQQG
SRTEVLSGQQACDMAALEDVDQVMAAI VGAAGLLPTLAIRAGKTILLANKXDMRTPIAHTMAWPNRVNS
GVKPLDFC

>d1gcua1 c.2.1.3 (A:1-128,A:247-292) Biliverdin reductase {Rat (Rattus norvegicus)}
MDAEPKRKFGVVVVGVRAGSVRLRDLKDPRSAFLNLIGFVSRRELGSDEVRQISLEALRSQEIDVAYICSES
SSHEDYIRQFLQAGKHLVVEYPMTLSFAAAQELWELAAQKGRVLHEEHVELLXKNIFLKQDIFVQKLLDQVSA
EDLAAEKKRIMHCLGLASDIQKLCH

>d1evja1 c.2.1.3 (A:30-160,A:323-381) Glucose-fructose oxidoreductase, N-terminal domain {Zymomonas mobilis}

RRFGYAIVGLKYALNQILPGFAGCQHSRIEALVDGNAEKAKIVAAEYGVDPRKIYDYSNFDKIAKDPKIDAVYIIL
PNSLHAEFAIRAFKAGKHMCEKPMATSVADCQRMIDA AKAANKKLMIGYRCHYXNQFSAQLDH LAEAVINN
KPVRSPGEEMQDVRLIQAIYEARTGRPVNTDWGYVRQGGY

>d1h6da1 c.2.1.3 (A:51-212,A:375-433) Glucose-fructose oxidoreductase, N-terminal domain {Zymomonas mobilis}

QAATLPAGASQVPTTPAGRMPYAIRPMPEDRRFGYAIVGLKYALNQILPGFAGCQHSRIEALVSGNAEKAKIV
AAEYGVDPRKIYDYSNFDKIAKDPKIDAVYIILPSLHAEFAIRAFKAGKHMCEKPMATSVADCQRMIDA AKA
NNKLMIGYRCHYXNQFSAQLDH LAEAVINNKPVRSPGEEMQDVRLIQAIYEARTGRPVNTDWGYVRQGG
Y

>d1dpga1 c.2.1.3 (A:1-181,A:413-426) Glucose 6-phosphate dehydrogenase, N-terminal domain {Leuconostoc mesenteroides}

VSEIKTLVTFFGGTGDLAKRKLYPSVFNL YKKGYLQKHF AIVGTARQALNDDEFKQLVRDCIKDFTDDQAQAEAFI
EHFSYRAHDVTDAASYAVLKEAIEEAADKFDIDGNRIFYMSVAPRFFGTIAKYLKSEGLLADTGYNRLMIEKPFGT
SYDTAAELQNDLEN AFDDNQLFRIDHYLGXE PYERMIHDTMNGD

>d1qkia1 c.2.1.3 (A:12-199,A:435-449) Glucose 6-phosphate dehydrogenase, N-terminal domain {Human (Homo sapiens)}

VCGILREELFQGD AFHQSDTHIFIIMGASGDLAKK IYPTIWWLFRDGLLPENTFIVGYARSRLTVADIRKQSEPFF
KATPEEKLKLEDFFFARN SYVAGQYDDAASYQRLN SHMN ALHLGSQANRLFYALPPTVYEAVTKNIHES CMSQI

GWNRIIVEKPFGRDLQSSDRLSNHISSLFREDQIYRIXDAYERLILDVFCGSQ

>d2naca1 c.2.1.4 (A:148-335) Formate dehydrogenase {Pseudomonas sp., strain 101}

ISVAEHVVMAMILSLVRNYLPSHEWARKGGWNIACVSHAYDLEAMHVGTVAAAGRIGLAVLRRRAPFDVHLHY
TDRHRLPESVEKELNLTHATREDMYPVCDVTLNCPLHPETEHMINDETLKLFKGAYIVNTARGKLCRDAV
ARALESGRLAGYAGDVWFPQPAPKDHPWRTMPYNGMTPHISG

>d1qp8a1 c.2.1.4 (A:83-263) Putative formate dehydrogenase {Archaeon Pyrobaculum aerophilum}
ADAVAEFALALLLAPYKRIIQYGEKMGRGDYGRDVEIPLIQGEKVALGLGEIGTRVGKILAALGAQVRGFSRTPK
EGPWRFTNSLEEALREARAACALPLNKHTRGLVKYQHLALMAEDAVFVNVRGAEVLDRGVLRLKERPQFIF
ASDVWWGRNDFAKDAEFFSLPNVVATPWVAG

>d1dxy_1 c.2.1.4 (101-299) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}
SPAAIAEFALTDTLYLLRNMGKVQAQLQAGDYEKAGTFIGKELGQQTVGVMGTGHIGQVAIKLFKGFAKVIAY
DPYPMKGDHPDFDYVSLEDLFQSDVIDLHVPGIEQNTHIINEAAFNLMKPGAIINTARPNLIDTQAMLSNLK
SGKLAGVGIDTYEYETEDLLNLAHKGSFKDPLWDELLGMPNVVLSPIAYY

>d1gdha1 c.2.1.4 (A:101-291) D-glycerate dehydrogenase {Hyphomicrobium methylovorum}

VTVATAEIAMLLLGSARRAGEGEKMRTRSWPGWEPLEVGEKLDNKTGIGFGSIGQALAKRAQGFDMID
YFDTHRASSSDEASYQATFHDSDLSSVSQFFSLNAPSTPETRYFFNKATIKSLPQGAIVVNTARGDLVDNELVV
AALEAGRLLAYAGFDVFAGEPNINEGYYDLPNTFLPHIGSA

>d1psda1 c.2.1.4 (A:108-295) Phosphoglycerate dehydrogenase {Escherichia coli}
NTRVAELVIGELLLLRLGVPEANAKAHRGVWNKLAAGSFEARGKKLGIIGYGHIGTQLGILAESLGMVYFYDIE
NKLPLGNATQVQHLSDLLNMSDVSLHVPENPSTKNMMGAKEISLMKPGSLLINASRGTVVDIPALCDALASK
HLAGAAIDVFPTEPATNSDPFTSPLCEFDNVLLTPHIGG

>d2dlda1 c.2.1.4 (A:104-300) D-lactate dehydrogenase {Lactobacillus helveticus}

PNAIAEHAAIQAARVLRQDKRMDEKMAKRDLRWAPTIGREVRDQVVGVTGHIGQVFMRIMEFGAKVI
AYDIFKNPELEKKGYYVDSLDDLYKQADVISLHVPDVPANVHMINDKSIAEMKDGVVIVNCSRGRLVDTAVIR
GLDSGKIFGFMDTYEDEVGVFNKDWEGKEFPDKRLADLIDRPNVLVTPHTAF

>d1pjca1 c.2.1.4 (A:136-303) L-alanine dehydrogenase {Phormidium lapideum}

AGRLSVQFGARFLERQQGGGRGVLLGGVPGVKPGKVVILGGGVVGTEAAKMAVGLGAQVQIFDINVERLSLET
LFGSRVELLYNSAEIETAVAEDLLIGAVLPGRRAPILPASLVEQMRTGSVIVDVAVDQGGCVETLHPTSHTQ
PTYEVFGVVHYGVNPMPGA

>d1f8ga1 c.2.1.4 (A:144-326) Nicotinamide nucleotide transhydrogenase di component {Rhodospirillum rubrum}

AGYRAVIDGAYEFARAFPMMMTAAGTVPPARVLVFGVGVAGLQAIATAKRLGAVVMATDVRAATKEQVESLG
GKFITVDDEAMKTAETAGGYAKEMGEEFRKKQAEAVLKELVKTDIAITTALIPGKPAPVLITEEMVTKMKGPSVII
DLAVEAGGNCPLEPGKIVVKHGVKIVGHTNVPSR

>d1b3ra1 c.2.1.4 (A:190-352) S-adenosylhomocysteine hydrolase {Rat (Rattus norvegicus)}

NLYGCRESLIDGIKRATDVMIAKGKAVVAGYGDVGKGCAQALRGFGARVIITEIDPINALQAAMEGYEVTTMDE
ACKEGNIFVTTTGCVDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWLNEAVEKVNICKPQVDRYLLKNGHRIILL
AEGRLVNLGCAMGH

>d1gpja2 c.2.1.10 (A:144-302) Glutamyl tRNA-reductase middle domain {Archaeon Methanopyrus kandleri}

SEGAVSIGSAAVELAEREELGSLHDKTVLVGAGEMGKTVAKSLVDRGVRAVLVANRTYERAVELARDLGGEAVR
FDELVDHLARSDDVVVSATAAPHVIHVDDVREALRKDRRSPILIIDIANPRDVEEGVENIEDVEVRTIDDLRVIAR
ENLERRK

>d1mlda1 c.2.1.5 (A:1-144) Malate dehydrogenase {Pig (Sus scrofa)}

AKVALGASGGIGQPLSLLLKNSPVSRFLTLYDIAHTPGVAADLSHETRATVKGYLGPQLPDCLKGCDDVVIPAG
VPRKPGMTRDDLFTNTATVLTAAACAQHCPDAMICIIISNPVNSTIPITAEVFKKHGKVYNPNKIFG

>d5mdha1 c.2.1.5 (A:1-154) Malate dehydrogenase {Pig (Sus scrofa)}

SEPIRVLVTGAAGQIAYSLYSIGNGSVFGKDQPIILVLLDITPMGVLDGVLMEQLDCALPLKDVIAKKEEIAF
KDLDVAILVGSMPPRDGMERKDLLKANVKIFKCQGAALDKYAKKSVKIVVGNPANTNCLTASKSAPSIPKENFS
CL

>d7mdha1 c.2.1.5 (A:23-197) Malate dehydrogenase {Sorghum (Sorghum vulgare), chloroplast}

DCFGVFCTTYDLKAEDKTWSKKLVNIAVSGAAGMISNHLLFKLASGEVFGQDQPIALKLLGSERSFQALEGVA
MELEDLSYPLLREVSIGIDPYEVFEDVDWALLIGAKPRPGPMERAALLDINGQIFADQGKALNAVASKNVKLV
VGNPCNTNALICLNAPDIPAKNFHAL

>d1civa1 c.2.1.5 (A:12-193) Malate dehydrogenase {Flaveria bidentis, chloroplast}

LPAKQKPECFGVFCITYDLKAEEETKSWKKIINVAVSGAAGMISNHLLFKLASGEVFGPDQPISLKLLGSERSFAAL
EGVAMELEDLSYPLLQVSIGIDPYEIFQDAEWALLIGAKPRPGPMERADLLINGQIFAEQGKALNAVASPNVK
VMVVGNCNTNALICLNAPNIPPKNFHAL

>d2cmd_1 c.2.1.5 (1-145) Malate dehydrogenase {Escherichia coli}

MKVAVLGAAGGIGQALALLKTQLPSGSELSLYDIAPVTPGAVADLSHIPTAVKIKGFSGEDATPALEGADVVLISA
GVRRKPGMDRSDFNVNAGIVKNLVQQVAKTCPKACIGIITNPVNTTVAIAAEVLKKAGVYDKNKLF

>d1bdma1 c.2.1.5 (A:0-154) Malate dehydrogenase {Thermus flavus}

MKAPVRVAVTGAAGQIGYSLLFRIAAGEMLGKDQPVILQLLEIPQAMKALEGVVMELEDCAFPLLAGLEATDD
PDVAFKDADYALLVGAAPRKAGMERRDLLQVNGKIFTEQGRALAEVAKDVKVLVGNPANTNALIAYKNAPG
LNPRRNFTAM

>d2hlp1 c.2.1.5 (A:22-162) Malate dehydrogenase {Archaeon Haloarcula marismortui}

TKVSVVGAAGTVGAAAGYNIALRDIADDEVVFVDIPDKEDDTVGQAADTNHGIAYDSNTRVRQGGYEDTAGSD
VVVITAGIPRQPGQTRIDLADGNAPIIMEDIQSSLDEHNDYISLTTSNPVDLNRHLYEAGDRSREQVIG

>d1b8pa1 c.2.1.5 (A:3-158) Malate dehydrogenase {Aquaspirillum arcticum}

KTPMRVAVTGAAGQICYSLLFRIANGDMLGKDQPVILQLLEIPNEKAQKALQGVMMIEIDDCAFPLLAGMTAH
ADPMFTAfkDADVALLVGARPRPGPMERKDLLEANAQIFTVQGKAIDAVASRNIKVLVGNPANTNAYIAMKSA
PSLPAKNFTAM

>d1guya1 c.2.1.5 (A:1-143) Malate dehydrogenase {Chloroflexus aurantiacus}

MRKKISIIGAGFVGSTTAHWLAAKELGDIVLLDIVEGPQKGKALDMYEESGPVGLFDTKVTGSNDYADTANS DIVV
VTSGAPRKPGMSREDLIKVNADITRACISQAAPLSPNAVIIMVNNPLDAMTYLAAEVSGFPKERVIGQ

>d1gv0a1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium tepidum}

MKITVIGAGNVGATTAFRLAEKQLARELVLLDVEGIPQKGKALDMYEESGPVGLFDTKVTGSNDYADTANS DIVV
TAGLPRKPGMTREDLLSMNAGIVREVTGRIMEHSKNPIIVVSNPLDIMTHVAWQKSLPKERVIGM

>d1guza1 c.2.1.5 (A:1-142) Malate dehydrogenase {Chlorobium vibrioforme}

MKITVIGAGNVGATTAFRLAEKQLARELVLLDVEGIPQKGKALDMYEESGPVGLFDTKVTGSNDYADTANS DIVV
TAGLPRKPGMTREDLLMKNAGIVKEVTDNIMKHSKNPIIVVSNPLDIMTHVAWVRSGLPKERVIGM

>d1hyha1 c.2.1.5 (A:21-166) L-2-hydroxyisocapronate dehydrogenase, L-HICDH {Lactobacillus confusus}

ARKIGIIGLNVGAAVAHLIAQGVADDYVFIDANEAKVKADQIDFQDAMANLEAHGNIVINDWAALADADV
VISTLGNIKLQQDNPTGDRFAELKFTSSMVQSVGTNLKESGFHGVLVVISNPVDVITALFQHVTGFPAHKVIGT

>d5ldh_1 c.2.1.5 (1-162) Lactate dehydrogenase {Pig (Sus scrofa)}

ATLKEKLIAPVAQQETTIPDNKITVVGVGQVGMACAISILGKSLTDELALVDVLEDKLKGEMMDLQHGSFLQTP

KIVANKDYSVTANSKIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSYNCIIIVSNPVDILTYVAWKLSG
LPKHRVIG

>d9ldta1 c.2.1.5 (A:1-162) Lactate dehydrogenase {Pig (Sus scrofa)}

ATLKDKQLIHNLKEEHVPHNKITVVGVGAVGMACAIISLMKELADEIALVDVMEDKLKGEMMDLQHGSFLRTP
PKIVSGKDYNVTANSRLVITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSYNCCKLLVSNPVDILTYVAWKIS
GFPKNRVIG

>d1i0za1 c.2.1.5 (A:1-160) Lactate dehydrogenase {Human (Homo sapiens), heart isoform (H chain)}

ATLKEKLIAPVAEEEATVPNNKITVVGVGQVGMACAISILGKSLADELALVDVLEDKLKGEMMDLQHGSFLQTP
KIVADKDYSVTANSKIVVVTAGVRQQEGESRLNLVQRNVNVFKFIIPQIVKYSPDCIIIVSNPVDILTYVTWKLSG
LPKHRVIG

>d1i10a1 c.2.1.5 (A:1-159) Lactate dehydrogenase {Human (Homo sapiens), muscle isoform (M chain)}

ATLKDKQLIYNLLKEEQTPQNKITVVGVGAVGMACAIISLMKDLADELALVDVIEDKLKGEMMDLQHGSFLRTP
KIVSGKDYNVTANSKLVITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKYSYNCCKLLVSNPVDILTYVAWKISGF
PKNRVIG

>d2lIdx_1 c.2.1.5 (1-159) Lactate dehydrogenase {Mouse (Mus musculus)}

STVKEQLIQNLVPEDKLSRCKITVVGVGDVGMACAISILLKGLADELALVDADTDKLGEALDLQHGSFLSTPKI
VFGKDYNVSANSKLVITAGARMVSGQTRLDLLQRNVAIMKAIVPGVIQNSPDCKIIVVTPVDILTYVWKISG
FPVGRVIG

>d1ldm_1 c.2.1.5 (1-160) Lactate dehydrogenase {Dogfish (Squalus acanthias)}

ATLKDKLIGHLATSQEPRSYNKITVVGVGAVGMACAIISLMKDLADEVALVDVMEDKLKGEMMDLQHGSFLFH
TAKIVSGKDYSVSAGSKLVITAGARQQEGESRLNLVQRNVNIFKFIIPNIVKHSPDCIILVSNPVDVLTYVAWKLS
GLPMHRIIG

>d1ceqa1 c.2.1.5 (A:19-163) Lactate dehydrogenase {Malaria parasite (Plasmodium falciparum)}

PKAKIVLVGSGMIGGVMATLIVQKNLGDVLFDIVKNMPHGKALDTSHTNVMAYSNCKVSGSYDDLAGSD
VVIVTAGFTKAPGKSDKEWNRDDLLPLNNKIMIEIGGHIKKNCPNAFIIVVTPVDVMVQLHQHSGVPKNII
GL

>d1ldna1 c.2.1.5 (A:15-162) Lactate dehydrogenase {Bacillus stearothermophilus}

MKNNGGARVVVIGAGFVGASYVFALMNQGIADEIVLIDANESKAIGDAMDFNHGKVAPKPVDIWHGDYDD
CRDADLVVICAGANQKPGETRLDLVDKNIAIFRSIVESVMASGFQGLFLVATNPVDILTYATWKFSGLPHERVIGS
G

>d1llc_1 c.2.1.5 (13-164) Lactate dehydrogenase {Lactobacillus casei}

ASITDKDHQKVLVGDGAVGSSYAFAMAQQGIAEEFVIVDVVKDRTKGDALDLEDAQAFTAPKKIYSGEYSDCKDA
DLVVITAGAPKQPGETRLDLVNKNLKLKSLIVDPIDSGFNLFVAANPVDILTYATWKLSGFPKNRVVGSG

>d1ez4a1 c.2.1.5 (A:16-162) Lactate dehydrogenase {Lactobacillus pentosus}

SMPNHQKVVLVGDGAVGSSYAFAMAQQGIAEEFVIVDVVKDRTKGDALDLEDAQAFTAPKKIYSGEYSDCKDA
DLVVITAGAPQKPGESRLDLVNKNLNILSSIVKPVVDSGFQGLFLVAAANPVDILTYATWKFSGFPKERVGSG

>d1llda1 c.2.1.5 (A:7-149) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}

PTKLAVIGAGAVGSTLAFAAAQRGIAREIVLEEDIAKERVEAEVLDMQHGSSFYPTVSIDGSDDPEICRDADMVVI
TAGPRQKPGQSRELGVATVNILKAIMPNLVKVAPNAIYMLITNPVDIATHVAQKLTGLPENQIFGSG

>d1a5z_1 c.2.1.5 (22-163) Lactate dehydrogenase {Thermotoga maritima}

MKIGIVGLGRVGSSTAFALLMKGFAREMVVIDVDKKRAEGDALDLIHGTPFTRRANIYAGDYADLKGSDDVVIVAA
GVPQKPGETRLQLLGRNARVMKEIARNVSKYAPDSIVVVTNPVDVLTYFFLKESEGM DPRKVFGS

>d1hyea1 c.2.1.5 (A:1-145) MJ0490, lactate/malate dehydrogenase {Archaeon Methanococcus jannaschii}
MKVTIIGASGRVGSATALLAKEPMKDLVLIGREHSINKLEGLREDIYDALAGTRSDANIYVESDENLRIIDESDV
VIITSGVPRKEGMSRMDLAKTNAKIVGKYAKKIAEICDTKIFVITNPVDVMTYKALVDSKFERNQVFG

>d1qmga2 c.2.1.6 (A:82-307) Acetohydroxy acid isomeroreductase, ketoacid reductoisomerase (KARI) {Spinach (*Spinacia oleracea*)}
SATTFDFDSSVFKKEKVTLGHDEYIVRGGRNLFPLLPDAFKGIQIGVIGWGSQAPAQAQNLKDSLTEAKSDVV
VKIGLRKGSNSFAEARAAGFSEENGLGDMWETISGSDLVLLISDAQADNYEKVFSHMKPNSILGLSHGFLLG
HLQSLGQDFPKNISVIAVCPKGMPGPSVRLYVQGKEVNGAGINSSFAVHQDVDGRATDVALGWSIALGSPFTF
ATT

>d2pgd_2 c.2.1.6 (1-176) 6-phosphogluconate dehydrogenase {Sheep (*Ovis orientalis aries*)}
AQADIALIGLAVMGQNLLNMMNDHGFVVCAFNRVSKVDDFLANEAKGTVLGAHSLEEMVSKLKKPRRIILLV
KAGQAVDNFIEKLVPLLDIGDIIDGGNSEYRDTMRCRDLKDKGILFVGSGVSGGEDGARYGPSLMPGGNKEA
WPHIKAIQFGIAAKVGTGEPCCDWVGDD

>d1pgja2 c.2.1.6 (A:1-178) 6-phosphogluconate dehydrogenase {Trypanosoma brucei}
SMDVGVVGLVMGANLALNIAEKGFKVAVFNRTYSKSEEFMKANASAPFAGNLKAFETMEAFAASLKKPRKA
LILVQAGAATDSTIEQLKKVFEKGDILVDTGNAHKDQGRRAQQLEAGLRFMGISGGEEGARKGPAFFPGG
TLSVWEIRPIVEAAAACKADDGRPCVTMNGSG

>d1f0ya2 c.2.1.6 (A:12-203) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (*Homo sapiens*)}
KIIVKHVTVIGGGLMAGIAQVAAATGHTVVLVDQTEDILAKSKKGIEESLRKVAKKKFAENPKAGDEFVEKTLST
IATSTDAAASVHVSTDLVVEAIVENLKVKNELFKRLDKFAAEHTIFASNTSSLQITSIANATTRQDRFAGLHFFNPVP
VMKLVEVIKTPMTSQKTFESLDFSKALGKHPVSKDTP

>d1dlja2 c.2.1.6 (A:1-196) UDP-glucose dehydrogenase (UDPGDH) {Streptococcus pyogenes}
MKIAVAGSGYVGLSLGVLLSLQNEVTIVDILPSKVDKINNGLSPIQDEYIEYYLKSQLSIKATLDSKAAYKEAELVII
ATPTNYNSRINYFDTQHVETVIKEVLSVNSHATLIIKSTIPIGFITEMRQKFQTDRIIFSPEFLRESKALYDNLYPSRIIV
SCEENDSPKVKADAEEKFALLKSAAKKNVPVLIMG

>d1bg6_2 c.2.1.6 (4-187) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}
SKTYAVLGLGNGGHAFAYLALKGQSVLAWDIDAQRKEIQDRGAIIAEGPGLAGTAHPDLLSDIGLAVKDADI
LIVVPAIHHASIAANIASYSEGQLIILNPGATGGALEFRKILRENGAPEVTIGETSSMLFTCRSERPGQVTVNAIKG
AMDFACLPAAKAGWALEQIGSVLPQYVAVE

>d1evya2 c.2.1.6 (A:9-188) Glycerol-3-phosphate dehydrogenase {Trypanosome (*Leishmania mexicana*)}
KDELLYLNKAVVFGSGAFGTALAMVLSKKCREVCVWHMNEEVRLVNEKRENVFLKGVLQASNITFTSDVEKA
YNGAEIILFVIPTQFLRGFFEKGNNLIAYAKEKQVPVLVCTKGIERSTLKFPAEIIGEFLPSPLSVLAGPSFAIEVATG
VFTCVSIASADINVARRLQRIMSTG

>d1ks9a2 c.2.1.6 (A:1-167) Ketopantoate reductase PanE {Escherichia coli}
MKITVLGCGALGQLWLTAQKQGHEVQGWLVPQPYCSVNLVETDGSIFNESLTANDPDFLATSDLLLVTLKAW
QVSDAVKSLASTLPVTPILLIHNGMGTIEELQNIQQPLLMGTTHAARRDGNVIIHVANGITHIGPARQQDGD
YSYLADILQTVLPDVAWHN

>d1jaya_c.2.1.6 (A:) Coenzyme F420H₂:NADP⁺ oxidoreductase (FNO) {Archaeon *Archaeoglobus fulgidus*}

MRVALLGGTGNLGKGLALRLATLGHEIVVGSRREEKAEEAKAAEYRIAGDASITGMKNEDAAEACDIAVLTIW
EHAIIDTARDLKNILREKIVSPLVPVSRGAKGFTYSSERSAAEIVAEVLESEKVVSALHTIPAARFANLDEKFWDV
PVCGDDDESKKVVMSLISEIDGLRPLDAGPLSNSRLVESLTPILNIMRFNGMGEGLIKFL
>d1bgva1 c.2.1.7 (A:195-449) Glutamate dehydrogenase {Clostridium symbiosum}
KARSFGGSLVRPEATGYGSVYYVEAVMKHENDTLGKTVLAGFGNVAWGAACKLAEGLAKAVTLSGPDGYIY
DPEGITTEEKINYMLEMRASGRNKVQDYADKFGVQFFGEKPWGQKVDIIMPCATQNDVDLEQAKKIVANN
KYYIEVANMPTTNEALRFLMQQPNNMVAPSCKAVNAGGVLVSGFEMSQNRSWTAAEVDSKLHQVMTDIH
DGSAAAERYGLGYNLVAGANIVGFQKIAADAMMAQGIAW
>d1gtma1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}
GGSLGRIEATARGASYTIREAAKVLGWDTLKGKTIAIQGYGNAGYYLAKIMSEDGMKVVAVSDSKGGIYNPDG
LNADDEVLKWKNEHGSVKDFPGATNITNEELLELEVDTVAPAAIEEVITKKNADNIKAKIVAEVANGPVTPEADEIL
FEKILQIPDFLCNAGGVTVSYFEWVQNITGYYWTIEEVRRERLDKKMTKAFYDVYNIKEKNIHMRAAYVVA
QRVYQAMLDRGWVKK
>d1euza1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Thermococcus profundus}
IGGSLGRGTATAQGAIFTIREAAKALGIDLKGKKIAVGYGNAGYYTAKLAKEQLGMTVVAVSDSRGGIYNPDGL
DPDEVLKWKREHGSVKDFPGATNITNEELLELEVDTVAPAAIEEVITEKNADNIKAKIVAEVANGPVTPEADDILR
EKGILQIPDFLCNAGGVTVSYFEWVQNITGYYWTIEEVREKLDKKMTKAFWDVYNTHKDKNIHMRAAYVVA
VSRVYQAMKDRGWVKK
>d1bvua1 c.2.1.7 (A:181-418) Glutamate dehydrogenase {Archaeon Thermococcus litoralis}
GGIVARM DATARGASYTVREA AKALGMDLKGKTIAIQGYGNAGYYMAKIMSEYGMKVVAVSDTKGGIYNPD
GLNADEVLA WKKKTGSVKDFPGATNITNEELLELEVDTVAPAAIEEVITEKNADNIKAKIVAELANGPTTPEADEI
LYEKGILIIPDFLCNAGGVTVSYFEWVQNITGDYWTVEETRAKLDKKMTKAFWDVYNTHKEKNINMRDAAYVVA
AVSRVYQAMKDRGWIKK
>d1b26a1 c.2.1.7 (A:179-412) Glutamate dehydrogenase {Thermotoga maritima}
GGSKGREEATGRGVKVCAGLAMDVLGIDPKATVAVQGFGNVGQFAALLISQELGSKVVAVSDSRGGIYNPEG
FDVEELIRYKKEHGTVVTPKGGERITNEELLELDVILVPAALEGAIHAGNAERIKAKAVVEGAN GPTTPEADEILS
RRGILVVPDILANAGGVTVSYFEWVQDLQSFFWLDQVRNALEKMMKGAFNDVMKVKEKYNVDMRTAAYIL
AIDRVAYATKKRG
>d1hwxa1 c.2.1.7 (A:209-501) Glutamate dehydrogenase {Cow (Bos taurus)}
HGRISATGRGVFHGIENFIENASYMSILG MTPGFDKTFAVQGFGNVGLHS MRYLH RFGAKC VAG ESDG SIW
NP DGDIPKELEDFKLQHGTILGFPKAKIYEGSILEVDCDILIPAASEKQLTKSNAPRVKAKIIAEGANGPTT P QADKI
FLERNIMVIPDLYLNAGGVTVSYFQILKLNHVS YGRLTFKYERDSNYHLLMSVQESLERKFGKHGGTIPIVPTAE
FQDRISGASEKD IVHSGLAYTMERSARQIMRTAMKYNLGLDLRTAAYVNAIEKVFRVYNEAGVTFT
>d1leha1 c.2.1.7 (A:135-364) Leucine dehydrogenase {Bacillus sphaericus}
GISPAFGSSGNPSPVTAYGVYRGMKAAAKEAFGSDSLEGLAVSVQGLGNVAKALCKKLNT EGAKLVVTDV NKA
AVSAAVAEEGADAVAPNAIYGVTCDFAPCALGAVLNDFTIPQLKAKVIAGSADNQLKDP RGKYLHEL GIVYAP
DYVINAGGVINVADELYGYNRTRAMKRV DGIYDSIEKIFAI SKRDGVPSYVAADRMAEERIAK VAKAR SQFLQD
QRN I L N GR
>d1c1da1 c.2.1.7 (A:149-349) Phenylalanine dehydrogenase {Rhodococcus sp., M4}
SAFTTAVGVFEAMKATVAH RGLGSLDG ITVLVQGLGAVGGSLASLAAEAGAQLVADTD TERVAHAVALGHTA
VALEDVLSTPCDV FAPCAMGGVITTEVARTLDCS VVAGA ANN VIADEAASDILH ARG ILYAPDFVANAGGAIHLV

GREVLGWSESVVHERAVAIGDTLNQVFEISDNDGVTPEAARTLAGRRAREAS

>d1a4ia1 c.2.1.7 (A:127-296) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Human (Homo sapiens)}

LTSINAGRLARGDLNDCFIPCTPKGCLELIKETGVPIAGRHAVVVGRSKIVGAPMHDLWWNNATVTTCHSKTAH
LDEEVNKGDILVVATGQPEMVKGEWIKPGAIVIDCGINYVPDDKKPNRKVVGDVAYDEAKERASFITPVPGGV
GPMTVAMLMQSTVESAKRFLE

>d1b0aa1 c.2.1.7 (A:123-288) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Escherichia coli}

FHPYNVGRLCQRAPRLLPCTPRGIVTLLERYNIDTFGLNAVIGASNIVGRPMMSMELLAGCTTVTHRFTKNLR
HHVENADLLIVAVGKPGFIPGDWIKEGAIVIDVGINRLENGKVVGDVVFEDAARKASYITPVPGVGPMTVATL
IENTLQACVEYHDPQDE

>d1edza1 c.2.1.7 (A:149-319) Methylenetetrahydrofolate dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}

PCTPLAIVKILEFLKIYNNLLPEGNRLYGKKCIVINRSEIVRPLAALLANDGATVYSVDVNNIQKFTRGESLKNKH
HVEDLGEYSEDLLKKSLSDDVVITGPSENKFPTYEIKEGAVCINFACTKNFSDDVKEKASLYVPMTGKVTIAM
LLRNMLRLVRNVELSKE

>d1do8a1 c.2.1.7 (A:280-573) Mitochondrial NAD(P)-dependent malic enzyme {Human (Homo sapiens)}

IQGTAVALAGLLAAQKVISKPISEHKILFLGAGEAALGIANLIVMSMSMVENGLSEQEAQKKIWMFDKYGLVKGR
KAKIDSYQEPFTHSAPESIPDTFEDAVNLKPSTIIGVAGAGRLFTPDVIRAMASINERPVI~~F~~NSPTAQAE~~C~~TAEFF
AYTLTEGRCLFASGSPFGPVKLTDRVFTPGQGNVYIFPGVALAVILCNTRHISDSVFLEAAKALTSQLTDEELAQ
GR~~LY~~PPLANIQEVSINIAIKVTELYANKMAFRYPEPEDKAKYVKERTWRSEYDSLLPDVYEW~~P~~

>d1id1a_ c.2.1.9 (A:) Rck domain from putative potassium channel Kch {Escherichia coli}

HRKDHFIVCGHSILAINILQLNQRGQNVTVISNLPEDDIKQLEQRLGDNADVPGDSNDSSVLKKAGIDRCRAIL
ALSDNDADNAFVVL~~S~~AKDMSSDVKT~~V~~LA~~S~~DSKLN~~K~~IKMVHPDIILSPQLFGSEILARVLNGEEINNDMLVSM
LLN

>d1jkja1 c.2.1.8 (A:1-121) Succinyl-CoA synthetase, alpha-chain, N-terminal (CoA-binding) domain {Escherichia coli}

SILIDKNTKVICQGFTGSQGTFHSEQAIAYGTMVGGVTPGKG~~G~~TT~~H~~GLPVFNTVREAVAATGATASVIYVPAP
FCKDSILEAIDAGIKLIIT~~I~~TEGIPTLDMLTVKVKLDEAGVRMIGP

>d1euca1 c.2.1.8 (A:1-130) Succinyl-CoA synthetase, alpha-chain, N-terminal (CoA-binding) domain {Pig (Sus scrofa)}

CSYTASRKHLYVDKNTKVICQGFTGKQGTFHSQQALEYGTNLVGGTPGKG~~G~~KTHLGLPVFNTVKEAKEQTGAT
ASVIYVPPPFAAAINEAIDAEVPLVVCITEGIPQQDMVRVKHRLRQGKTRLIGP

>d1djna2 c.3.1.1 (A:490-645) Trimethylamine dehydrogenase, C-terminal domain {Methylophilus methylotrophus, w3a1}

RWNTDGTNCLHDPIPGADASLPQLTPEQVMDGKKKIGKRVVILNADTYFMAPSLAEKLATAGHEVTIVSGV
HLANYMHFTLEYPNMMRRLHELHVEELGDHFC~~S~~RIE~~P~~GRMEIYNIWGDGSKRTYRGPGVSPRDANTSHRWIE
FDSLVLVTGRH

>d1cjca1 c.3.1.1 (A:107-331) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos taurus)}

HQALDIPGEELPGVFSARAFVGWYNGLPENRELAPDSCDTAVILGQGNVALDVARILLTPPDHLEKTDITEAAL
GALRQSRVKTWIVGRRGPLQVAFTIKELREMIQLPGTRPM~~L~~DPA~~F~~GLQDRIKEAARPRKRLMELLRTATEK
PGVEEAARRASASRAWGLRFFSPQQVLPSPDGRRAGIRLAVTRLEGIGEATRAVPTGDVEDLPCGLVLSSIGY

>d1h7wa3 c.3.1.1 (A:288-440) Dihydropyrimidine dehydrogenase, domain 3 {Pig (*Sus scrofa*)}
PKTDDIFQGLTQDQGFYTSKDFLPLVAKSSKAGMCACHSPLPSIRGAVIVLGAGDTAFDCATSALRCGARRVFLV
FRKGFVNIRAVPEEVELAKEEKCEFLPFLSPRKVIVKGGRIVAVQFVRTEQDETGKWNEDEDQIVHLKADVVISAF
GS

>d1coy_1 c.3.1.2 (4-318,451-506) Cholesterol oxidase {Brevibacterium sterolicum}
RTLADGDRVPALVIGSGYGGAVAALRLTQAGIPTQIVEMGRSWDTPGSDGKIFCGMLNPDKRSMWLADKTDQ
PVSNFMIGFGINKSIDRYVGVLDSERFSGIKVYQGRGVGGSLVNGGMAVTPKRNYFEELPSVDSNEMYNKYF
PRANTGLGVNNIDQAWFESTEWYKFARTGRKTAQRSGFTTAFPNVYDFEYMKKEAGQVTKSLGGVEIYG
NNAGKKSLDKTYLAQAAATGKLTTLHRVTKVAPATGSGYSVTMEQIDEQGNVVATKVVTADRVFFAAGSVGT
SKLLVSMKAQGHLPNLSSQVGEGWXGVLLNKATDNFGLPEYPGLYVVDGSLVPGNVGVNPFTITALAERN
MDKIISDI

>d1ijha1 c.3.1.2 (A:9-318,A:451-506) Cholesterol oxidase {Streptomyces sp.}
GYVPAVWIGTYGAAVSALRLGEAVGVTLMLEMQLWNQPGPDGNIFCGMLNPDKRSSWFKNRTEAPLGSF
LWLDVVNRNIDPYAGVLRVNYDQMSVYVGRGVGGSLVNGGMAVEPKRSYFEELPRVDSSEMYDRYFPR
ANSMLRVNHIDTKWFEDTEWYKFARVSREQAGKAGLTVFVNPVYDFGYMQREAAGEVPKSALATEVIYGN
NHGKQSLDKTYAAALGTGKVTIQLHQVKTIROTKDGGYALTVEQKDTDGKLLATKEISCRYLFLGAGSLGSTE
LVRARDTGLPNLNSEVGAGWXGCVLGKATDDYGRVAGYKNLYVTDSLIPGSVGVLPFVTITALAERNVERIIK
QDV

>d1k0ia1 c.3.1.2 (A:1-173,A:276-394) p-Hydroxybenzoate hydroxylase, PHBH {Pseudomonas aeruginosa}
MKTQVAIIAGPSGLLLQQLHKAGIDNVILERQTPDYVLGRIRAGVLEQGMVDLLREAGVDRRMARDGLVHE
GVEIAFAGQRRRIDLKRLSGGKTVTVGQTEVTRDLMEAREACGATTVYQAAEVRHDLQGERPYVTFERDGE
RLRLDCDYIAGCDGFHGISRQSIPAERXMQHGRFLAGDAAHIVPPTGAKGLNLAASDVSTLYRLLLKAYREGRG
ELLERYSAICLRRIWKAERFSWWMTSVLHRFPTDAFSQRQQTELEYLGSEAGLATIAENYVGLPYEEIE

>d1el8a1 c.3.1.2 (A:1-217,A:322-385) Sarcosine oxidase {Bacillus sp., strain b0618}
STHFDVIVVGAGSMGMAAGYQLAKQGVKLLVDAFDPPHTNGSHGDTRIIRHAYGEGREYVPLALRSQELW
YELEKETHHKIFTKTGVLVFGPKGESAFVAETMEAACEHSLTVDLLEGDEINKRWPGITVPENYNAIFEPNSGVLF
SENCIRAYRELAEARGAKVLTHTRVEDFDISPSVKIETANGSYTADKLIVSMGAWNNSKLLSKLNLDIPXDEHFIID
LHPEHSNVIAAGFSGHGFKFSSGVGEVLSQLALTGKTEHDISIFSINRPALKESLQ

>d1foha5 c.3.1.2 (A:1-240,A:342-461) Phenol hydroxylase {Soil-living yeast (Trichosporon cutaneum)}

TKYESYCDVLIVGAGPAGLMAARVLSEYVRQKPDLKVRIIDKRSTKVYNGQADGLQCRTLESKLNGLADKILSE
ANDMSTIALNPDENGHIRRDRIPDTLPGISRYHQVVLHQGRIERHILDSIAEISDTRIKVERPLIPEKMEIDSSKA
EDPEAYPVMTLRYMSDHESTPLQFGHKTENSLFHSNLQTQEEDANYRLPEGKEAGEIETVHCKYVIGCDGG
HSWVRRTLGFEMIXVTEKFSKDERVFIAGDACHTHSPKAGQGMNTSMMDTYNLGWKLGLVTGRAKRDILKT
YEEERHAFAQALIDFDHQFSRLSGRPAKDVADEMGVSMDFVKEAFVKGNEFASGTAINYDE

>d1cf3a1 c.3.1.2 (A:3-324,A:521-583) Glucose oxidase {Aspergillus niger}
GIEASLLTDPKDVSGRTVDYIAGGGLTGLTTAARLTENPNISVLVIESGSYESDRGPIIEDLNAYGdifGSSVDHAYE
TVELATNNQTALIRSGNGLGGSTLVNGGTWTRPHKAQVDSWETVFGNEGWNWDNVAAYSLQAERARAPNA
KQIAAGHYFNASCHGVNGTVHAGPRDTGDDYSPIVKALMSAVEDRGVPTKKDFGCGDPHGVSMPNLTCHED
QVRSDAAREWLLPNYQRPNLQVLTGQYVGKVLLSQNGTTPRAVGVEFGTHKGNTHNVYAKHEVLLAAGSAVS
PTILEYSGIGMKSILEPLGIDTVVDPVGLXCSMMPKEMGGVVVDNAARVYGVQGLRVIDGSIPPTQMSSHVMT
VFYAMALKISDAILEDYASMQ

>d1gpea1 c.3.1.2 (A:1-328,A:525-587) Glucose oxidase {Penicillium amagasakiense}

YLPAQQIDVQSSLLSDPSKVAGKTYDYIIAGGLTGLTVAAKLTEPKIKVLVIEKGFYESNDGAIIEDPNAYGQIFGTTVDQNYLTVPINNRTNNIKAGKGLGGSTLINGDSWTRPDKVQIDSWEVKFGMEGNWDNMFEYMKKAE

AARTPTAAQLAAGHSFNATCHGTNGTVQSGARDNGQPWSPIMKALMNTVSALGPVQQDFLCGHPRGVSMIMNNLDENQRVDAARAWLLPNYQRSNLEITGQMVGKVLFKQTASGPQAVGVNFGTNKAVNFDVFAKH

EVLLAAGSAISPLILEYSIGLKSVDQANVTQLLDLPGIXCSMMSRELGGVVDATAKVYGTQGLRIDGSIPPT

QVSSHVMTIFYGMALKVADAILDDYAKSA

>d1b5qa1 c.3.1.2 (A:5-293,A:406-463) Polyamine oxidase {Maize (*Zea mays*)}

PRVIVVGAGMSGISAALKRLSEAGITDLILEATDHIGGRMHKTNFAGINVELGANWVEGVNGGKMNPWPIVN
STLKLRNFRSDFDYLAQNRYKEDGGVYDEDYVQKRIELADSVEEMGEKLSATLHASGRDDMSILAMQLRNEHQ
PNGPATPVDMVVYKFDYFAEPPRVTSLQNTVPLATFSDFGDDVYFVADQRGYEAVVYLAGQYLKTDDKS
GKIVDPRQLQNKVREIKYSPGGVTVKTEDNSVSYADYVMVSASLGVLQSDLIQFKPKLPTWKVRAIYQFXWPV
GVNRYEYDQLRAPVGRVYFTGEHTSEHYNGVHGAYLSGIDSÆILINCAQKKMC

>d1f8ra1 c.3.1.2 (A:4-319,A:433-486) L-amino acid oxidase {Malayan pit viper (*Calloselasma rhodostoma*)}

RNPLAECFQENDYEELIARNGLKATSNPKHVVIVGAGMAGLSAAYVLAGAGHQVTYLEASERPGGRVRTYR
NEEAGWYANLGPMRLPEKHRIVREYIRKFDLRLNEFSQENDNAWYFIKNIRKKVGEVKKDPLKYPVKPSEAG
KSAGQLYEESLGKVVEELKRTNCYILNKYDTYSTKEYLIKEGDLSPGAVIDMIGDLLNEDSGYYVSIESLKHDIFAYEKRFDEIVDGMDKLPTAMYRDIQDKVHFNAQVIQKIQNDQKVTVVYETLSKETPSVTADYVIVCTTSRAVRLIK
FNPPLLPKKAHALRSVXFTPYQFQHFSPLTASQGRIFYAGEYTAQAHGWIDSTIKSGLRAARDVNASEN

>d1gosa1 c.3.1.2 (A:4-289,A:402-500) Monoamine oxidase B {Human (*Homo sapiens*)}

KCDVVVVGGSIGMAAKLLHDGLNVVLEARDRVGGRTYTLRNQKVYV рDLGGSYVGPTQNRILRALKEL
GLETYKVNEVERLIHHVKGKSYFPFRGPFPVWNPITYLDHNNFWRTMDDMGRREIPSDAPWKAPLAEEWDN
MTMKELLDKLCWTESAKQLATLFVNLCVTAETHEVSALWFLWYVKQCGGTTRIISTTNGGQERKFVGGSGQVS
ERIMDLLGDRVKLERPVIYDQTRENVLVETLNHEMYEAKYVISAPIPTLMKIHFNPPLMMRNQMITRVXFPP
PGILTQYGRVLRQPVDRIYFAGTETATHWSGYMEGAVEAGERAAREILHAMGKIPEDEIWQSEPESVDVPAQPI
TTTFLERHLPSVPGLRLIGLTT

>d1d5ta1 c.3.1.3 (A:-2-291,A:389-431) Guanine nucleotide dissoiation inhibitor, GDI {Cow (*Bos taurus*)}

HHMDEEYDVIVLGTGLTECILSGIMSVNGKKVLHMDRNPYYGGESSSITPLEELYKRFQLLEGPPETMGRGRDW
NVLDLIPKFLMANGQLVKMLLYTEVTRYLDFKVEGSFVYKGGKIYKVPSTETEALASNLMGMFKEKRRFRKFLVF
ANFDENDPKTFEGVDPQNTSMRDVYRKFDLGQDVIDFTGHALALYRTDDYLDQPCLETINRIKLYSESLARYGKS
PYLYPLYGLGELPQGFARLSAIYGGTYMLNKPVDIIMENGKVVGVKSEGEVARCKQLICDPSYVPDRVXPIDDG
SESQVFCSCSYDATTHFETTCNDIKDIYKRMAGSAFDF

>d1chua2 c.3.1.4 (A:2-237,A:354-422) L-aspartate oxidase {Escherichia coli}

NTLP EHSCDVLIIGSGAAGLSSLALRLADQHQVIVLSKGPVTEGSTFYAQGGIAAVFDETDSIDSHVEDTLIAGAGI
CDRH AVEFVASN ARSCVQWLIDQGVLF DTHIOPNGEESYH LTREGGHSHRRILHAADATGREVETTLVSKALN
HPNIRVLERTNAV DLI VSDKIGLPTRRVVG AWV WNRN KETV ETC HAKAVV LATGG ASK VY QY TTNP DISSGD
GIAMA WRAGCRVAN XCGGVMV DDH GRTD VEG LYAIGEV SYT GLHG ANRM ASN SLL ECL VY GW SAA EDIT RR
MPYAH DIST LPPW

>d1fuma2 c.3.1.4 (A:1-225,A:358-442) Fumarate reductase flavoprotein subunit {Escherichia coli}

QTFQADLAIVGAGGAGLRAIAAAQANPNAKIALISKVYPMRSHTVAE EGSAAVAQDHDSFEYHFHD TVAG
GDWLCEQDVVDYFVHHCPTEM TQLE LWGCPWSRRPDGSVNRRFGGMKIERTWFAADKTGFHMLHTLFQ
TSLQFPQIQRDFEHFVLDILVDDGHVRGLVAMNMMEGTLVQIRANA VVMATGGAGR VY RY NTNGGIVTGDG
MG M ALSHGVPL RD XMG GIETD NCET RI KGL FAV GEC SSV GL HG AN RL GS NS LA EL VV FG RL AGE QATERA AT

AGNGNEAAIEAQAAAGVEQRLKDLVNZ

>d1qlaa2 c.3.1.4 (A:1-250,A:372-457) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}

MKVQYCDSLVIIGGLAGLRAAVATQQKGLSTIVSLIPVKRSHSAAAQGGMQASLGNSKMSDGDNEDLFMD
TVKGSDWGCDQKVARMFVNTPAKIRELAAWGVPWTRIHKGDRMAIINAQKTTITEEDFRHGLIHSRDFGGT
KKWRTCYTADATGHTMLFAVANECLKLGVSIQDRKEAIALIHQDGKCYGAVVRDLVTGDIAYVAKGTLIATGGY
GRIYKNTTNAVVCEGTGTALETGIAQLGNXMGGIRTDYRGEAKLKGLFSAGEAACWDMHGFNRLGGNSVS
EAVVAGMIVGEYFAEHCANTQVDLETKTLEKFVKGQEAYMKSLES

>d1e39a2 c.3.1.4 (A:103-359,A:506-568) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

PTIAELAKDKSERQAALASAPHDTVDVVVVGSGGAGFSAAISATDSGAKVILIEKEPVIGGNAKLAAGGMNA
WTDQQKAKKITDSEPLMFEDTMKGQNINDPALVKVLSSHSKDSVDWMTAMGADLTDVGMMGGASVNR
AHRPTGGAGVGAHVQVLYDNAVRKNIDLRMNTRGIEVLKDDKGTVKGILVKGMYKGYYWVKADAVILATGG
FAKNNERVAKLDPSLKGFIStNQPGAVGDGLDVAENAGGALKDMXTMGGVMIDTKAEVMNAKKQVIPGLY
AGEVTGGVHGANRLGGNAISDIITFGRLAGEEAKYS

>d1qo8a2 c.3.1.4 (A:103-359,A:506-565) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

DGWDQDKIQKAIAAGPSETTQVLVVGAGSAGFNASLAALKAGANVILVDKAPFSGGNSMISAGGMNAVGTK
QQTAGVEDKVEWFIEDAMKGGRQQNDIKLVTILAEQSADGVQWLESLGANLDDLKRSGGARVDRTHRPHG
GKSSGPPIIDTLRKAKEQGIDTRLNSRVVKLVVNDHSVVGAVVHKGHTGYYMIGAKSVVLATGGYGMNKE
MIAYYRPTMKDMTSSNNITATGDGVLMKEIGASMTIDWVQAXAINTTASVLDLQSKPIDGLFAAGEVTGG
VHGYNRLGGNAIADTVVFGRIAGDNAAKHALD

>d1d4ca2 c.3.1.4 (A:103-359,A:506-570) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella putrefaciens}

KFVPVDADKAQDKAIAAGVKETTDVVIIGSGGAGLAAVSARDAGAKVILLEKEPIPGGNTKLAAGGMNA
TKPQAKLGIEDKKQIMDDTMKGGRNINDPELVKVLANNSSDSIDWLTSMGADM TDVGRMGGASVNRSHRP
TGGAGVGAHVAQVLWDNAVKGTDIRLNSRVVRILEDASGKVTGVLVKGEYTGYYVIKADAVVIAAGGFAKNN
ERVSKYDPKLKGFKATNHPGATGDGLDVALQAGAATRDLEXMGGVIDTKAEVKSEKTGKPITGLYAAGEVTGG
VHGANRLGGNAISDIVTYGRIAGASA AKFAKD

>d1jnra2 c.3.1.4 (A:2-256,A:402-502) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

VYYPKKYELYKADEVPTEVVETDILIGGGFSGCGAAYEAAYWAKLGGLKVTLVEKAVERSGAVAQGLSAINTYI
DLTGRSERQNTLEDYVRYVTLDMMGLAREDLVADYARHVDGTVHLFEKWGLPIWKPDGKYVREGQWQIMI
HGESYKPIIAEAKMAVGEENIYERVFIFELLKDNNDPNAVAGAVGFSVREPKFYVFKA KAVILATGGATLLFRPR
STGEAAGRWTWAIFDTGSGYYMGLKAGAMLTQXAGFWVCGPEDLMPEEYAKLFPLKYNRMTTVKGLFAIGDC
AGANPHKFSSGSFTEGRIA KAAVRFLEQKPNPEIDDAVVEELKKKAYAPMERFMQYKDLS

>d3grs_1 c.3.1.5 (18-165,291-363) Glutathione reductase {Human (Homo sapiens)}

VASYDYLVIGGGSGGLASARRAELGARA AVVESHKLGGTCVNVCVPKVMWNTAVHSEFMHDHADYGFP
SCEGKFNWRVIKEKRDAYSRLNAIQNNLTKSHIEIIRGHAAFTSDPKPTIEVSGKKYTAPHILIATGGMPSTPHE
XRVPNTKDLSLNKLGIQTDDKGHIIVDEFQNTNVKGIVAVGDVCGKALLTPVIAAGRKLAHRLFEYKEDSKLD

>d3grs_2 c.3.1.5 (166-290) Glutathione reductase {Human (Homo sapiens)}

SQIPGASLGITS DGFQLEELPGRSIVGAGYIA VEMAGILS ALGSK TSLMIRHD KV LRSF DSMIST NCTEELENA
GVEVLKFSQVKEVKTL SGLEVSMVTAVPGRLPVMTMIPDVDC LLWAIG

>d1gera2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}

DIPGVEYGIDSDGFFALPALPERVAVVGAGYIAVELAGVINGLAKTHLFVRKHAAPRSFDPMISETLVEVMNAE
GPQLHTNAIPKAVVKNTDGSLTLELEDGRSETVDCLIWAIG
>d1gesa1 c.3.1.5 (A:3-146,A:263-335) Glutathione reductase {Escherichia coli}
KHYDYIAIGGGSGGIASINRAAMYGQKCALIEAKELGGTCVNVCVPKKVMWHAQIREAIHMYGPDYGFDT
TINKFNWETLIASRTAYIDRHTSYENVLGKNNVDVIKG FARFVDAKTLEVNGETITADHILATGGRPSHPXREPA
NDNINLEAAGVKTNEKGYIVVDKYQNTNIEGYAVGDNTGAELTPAVAAGRRLSERLFNNKPDEHLD
>d1gesa2 c.3.1.5 (A:147-262) Glutathione reductase {Escherichia coli}
DIPGVEYGIDSDGFFALPALPERVAVVGAGYIGVELGGVINGLAKTHLFEMFDAPLPSFDPMISETLVEVMNAE
GPQLHTNAIPKAVVKNTDGSLTLELEDGRSETVDCLIWAIG
>d1feca1 c.3.1.5 (A:1-169,A:287-357) Trypanothione reductase {Crithidia fasciculata}
SRAYDLVVIGAGSGGLEAGWNAASLHKKRVAVIDLQKHGGPHYAALGGTCVNVCVPKKLMVTGANYMDSI
RESAGFGWELDRESVRPNWKALIAAKNAVSGINDSYEGMFADTEGLTFHQGFGALQDNHTVLVRESADPNS
AVLETLDTEYILLATGSWPQHLGIEXVPRSQTQLKEKAGVEAKNGAIKVDAYSKTNVDNIYAIGDVTDRVMLTP
VAINEGAAVFVDTVFANKPRATD
>d1feca2 c.3.1.5 (A:170-286) Trypanothione reductase {Crithidia fasciculata}
GDDLCITSNEAFYLDEAPKRALCVGGGYISIEFAGIFNAYKARGGQVDLAYRGDMILRGFDSELRKQLTEQLRAN
GINVRTHENPAKVTKNADGTRHVVFESGAEADYDVVMLAIGR
>d1aoga1 c.3.1.5 (A:3-169,A:287-357) Trypanothione reductase {Trypanosoma cruzi}
SKIFDLVVIGAGSGGLEAAWNAATLYKKRVAVIDVQMVGPPFFSALGGTCVNVCVPKKLMVTGAQYMEHL
RESAGFGWEFDRTTLRAEWKNLIAVKDEAVLNINKSYDEMFRDTEGLEFFLGWGSLESKNVVNVRESADPASA
VKERLETEHILLASGSWPMPNXGRSPRTKDLQLQNAGVMIKNGGVQVDEYSRTNVSNIYAIGDVTNRVMLT
PVAINEAAAALVDTVFGTTPRKT
>d1aoga2 c.3.1.5 (A:170-286) Trypanothione reductase {Trypanosoma cruzi}
IPGIEHCISSENEAFYLPEPPRRVLTGGGFISVEFAGIFNAYKPKDGQVTLCYRGEMILRGFDHTLREELTKQLTAN
GIQILTKENPAKVELNADGSKSVTFESGKKMDFDLVMMAI
>d1h6va1 c.3.1.5 (A:10-170,A:293-366) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}
SYDFDLIIIGGGSGGLAAAKEAAKFDKKVMVLDFVTPTPLGTNWGLGGTCVNVCIPKKLMHQALLGQALKD
SRNYGW/KLEDTVKHDWEKMTESVQNHIGSLNWGYRVALREKKVYENAYGKFIGPHKIMATNNKGKEKVYS
AERFLIATGERPRYLGIXRDSCTRTIGLETGVVKINEKTGKIPVTDEEQTNVPIYAIGDILEGKLELTPVAIQAGRLL
AQRLYGGSTVKCD
>d1h6va2 c.3.1.5 (A:171-292) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}
PGDKEYCISSDDLFLSLPYCPGKTLVVGASYVALECAGFLAGIGLDVTVMVRSILLRGFDQDMANKIGEHMEEHGI
KFIRQFVPTKIEQIEAGTPGRLKVTAKSTNSEETIEDFNTVLLAVG
>d1trb_1 c.3.1.5 (1-118,245-316) Thioredoxin reductase {Escherichia coli}
GTTKHSKLLILGSGPAGYTAAYAARANLQPVLITGMEKGGQLTTTEVENWPGDPNDLTGPLLTERMHEHAT
KFETEIIFDHINKVDLQNRPFRLNGDNGEYTCALIIATGASARYXHSPNTAIFEGQLELENGYIKVQSGIHGNAT
QTSIPGVFAAGDVMMDHIYRQAITSAGTGCMALDAERYLDGL
>d1trb_2 c.3.1.5 (119-244) Thioredoxin reductase {Escherichia coli}
LGLPSEEAFKGRGV SACATSDGFFYRNQKVAVIGGGNTAVEEALYLSNIASEVH LIHRRDG FRAEK KILKRLMDKV
ENGNIILHTNRTLEEVTGDQMVGTVVRLRTQNSDNIESLDVAGLFVAIG
>d1vdc_1 c.3.1.5 (1-117,244-316) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}
LETHNTRLICVGSGPAAHATAIYAARAELKPLLFE GWMANDIAPGGQLTTTDVENFPGFPEGILGV ELTDKFRK
QSERFGTTIFTETVTKVDFSSKPKLFTDSKAILADAVILAIGAVAKXGHEPATKFLDGGVELSDG YVVT KPGTTQ

TSVPGVFAAGDVQDKKRYRQAITAAGTGCMAALDAEHYLQE
>d1vdc_2 c.3.1.5 (118-243) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}
RLSFVGSGEVGGFWNRGISACAVCDGAAPIFRNKPLAVIGGGDSAMEEANFLTKYGSKVYIIRRDAFRASKI
MQQRALSNPKIDVIWNSSVVEAYGDGERDVLGLKVKNVVTGVDSDLKVSGLFFAI
>d1hyua1 c.3.1.5 (A:199-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Salmonella typhimurium}
AEKRAAEALNKRDAYDVLIVGSGPAGAAAAYSARKGIRTGLMGERFGGQVLDVDIENYISVPKTEGQKL
LKAHVSDYDVEDVIDSQSASKLVPAAATEGGLHQIETASGAVLKARSIIATGAKXLPNTHWLEGALERNRMGEIID
AKCETSVKGVFAAGDCTTVPYKQIIATGEGAKASLSAFDYLIRTKIA
>d1fl2a1 c.3.1.5 (A:212-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Escherichia coli}
AYDVLIVGSGPAGAAAAYSARKGIRTGLMGERFGGQILDTVDIENYISVPKTEGQKL
AGALKVHVDEYDVEDVID
SQSASKLIPAAVEGGLHQIETASGAVLKARSIIATGAKXLPNTNWLEGAVERNRMGEIIDAKCETNVKGVFAAG
DCTTVPYKQIIATGEGAKASLSAFDYLIRTKA
>d1fl2a2 c.3.1.5 (A:326-451) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains {Escherichia coli}
WRNMNVPGEDQYRTKGVTVYCPHCDGPLFKGKRVAVIGGGNSGVEAAIDL
AGIVEHVTLEFAPEMKADQVLQ
DKLRSLSKNDIILNAQTTEVKGDGSKVVGLEYRDRVSGDIHNIELAGIFVQIGL
>d1nhp_1 c.3.1.5 (1-119,243-321) NADH peroxidase {Enterococcus faecalis}
MKVIVLGSSHGGYEAVEELLNLHPDAEIQWYEKGDFISFLSAGMQLYLEGKV
KDVSNSVRYMTGEKMESRGVN
VFSNTEITAIQPKEHQVTVKDLVSGEERVENYDKLIISPGAVPFELDXGVRPNTAWLKGT
LEHPNGLIKTEYMR
TSEPDVFVAGDATLIKYNPADTEVNIALATNARKQGRFAVKNLEEPVKPFP
>d1nhp_2 c.3.1.5 (120-242) NADH peroxidase {Enterococcus faecalis}
IPGKLDNIYLMRGRQWAIKLKQKTV
DPEVNNVVIGSGYIGIEAAEAFAKAGKKV
TVIDILDPLGVYLDKEFT
DVLTEEMEANNITIATGETVERYEGDGRVQKV
VTDKNAYDADLVVVAV
>d1d7ya1 c.3.1.5 (A:5-115,A:237-308) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}
ALKAPVVVLGAGLASVS
FVAELRQAGYQGLITV
VGDEAERP
YDRPPLSKDFMAHGDAE
KIRLDCKRAPEVEWL
LGVTAQS
FDPQAHTVALSDGRTLPY
GTLV
LATGAAPRAXV
LANDALARAGLAC
DDGIFV
DAYGRTTCPDV
YAL
GDVTRQRNPLSGRF
ERIETWS
NAQNQGIAVARHLVDP
>d1d7ya2 c.3.1.5 (A:116-236) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}
LPTLQGATMPV
HTLRTLEDARR
IQAGLRP
QSRLIV
GGGVIGLE
LAATARTAG
VHVS
LVTQPR
LMSRAA
PATLA
DFVARYHAAQGV
DVLRF
ERSVTG
SVDGV
VLLDDG
GTRIAADM
VVVGIG
>d1lvl_1 c.3.1.5 (1-150,266-335) Dihydrolipoamide dehydrogenase {Pseudomonas putida}
QQTIQTTLII
IIGGGPGGY
VAAIRAG
QLGIPTV
LVEQ
QALGGT
CLNIGC
IPS
PSK
KALI
HVA
EQFH
QASRF
TEP
SPLG
ISV
ASPRLD
IGQSV
AWKDG
IVDRL
TTGVA
ALLKK
HGV
VVG
WAK
VLDG
KQVE
VDG
QRI
QCE
HLLL
ATG
SSV
ELP
XRRP
RTKGF
NLECL
DLKM
NGAAIA
IDER
CQTS
MHN
VWAIG
DVA
GEPM
LAH
RAMA
AQG
EMVA
EIIAG
KARR
FE
>d1lvl_2 c.3.1.5 (151-265) Dihydrolipoamide dehydrogenase {Pseudomonas putida}
MLPLGGPV
ISSTEAL
APKALP
QHLVV
GGGYIG
LELGI
YRK
LGA
QVS
VEAR
ERI
LPT
YDSEL
TAP
VAES
LKKL
GI
ALHLGH
SVE
GYENG
CLL
AND
GKGG
QLR
LEAD
RVL
VAVG
>d1lpfa1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}

SQKFDVVVIGAGPGGYVAAIRAAQLGLKTACIEKYIGKEGKVALGGTCLNVGCIPS KALLDSSYKYHEAKEAFKVH
GIEAKGVTIDVPAMVARKANIVKNLTGGIATLFKANGVTSFEGHGKLLANKQVEVTGLDGKTQVLEAENVIIASG
SRPVEIPXRRPVTTDLAADSGVTLDERGFYVDDHCKTSVPGVFAIGDVVRGAMLAHKASEEGVMVAERIAGH
KAQMN

>d1lpfa2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}

PAPLSDDIIVDSTGALEFQAVPKKLGVIGAGVIGLELGSVWARLGAEVTVLEALDKFLPAADEQIAKEALKVLTQ
GLNIRLGARVTASEVKKKQVTFTDANGEQKETFDKLIVAVG

>d3lada1 c.3.1.5 (A:1-158,A:278-348) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}

SQKFDVIVIGAGPGGYVAAIKSAQLGLKTALIEKYKGKEGKTALGGTCLNVGCIPS KALLDSSYKFHEAHESFKLHG
ISTGEVAIDVPTMIARKDQIVRNLTGGVASLIKANGVTLFEHGKLLAGKKVEVTAADGSSQVLDENVILASGSK
PVEIPXRRPVTTDLAADSGVTLDERGFYVDDYCATS VPGVYAI GDVVRGAMLAHKASEEGVVVAERIAGHKA
QMN

>d3lada2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}

PAPVDQDVIVDSTGALDFQNVPKGKLVIGAGVIGLELGSVWARLGAEVTVLEAMDKFLPAVDEQVAKEAQKILT
KQGLKILLGARVTGTTEVKNKQVTVKFVDAE GEKSQAFDKLIVAVG

>d1ebda1 c.3.1.5 (A:7-154,A:272-346) Dihydrolipoamide dehydrogenase {Bacillus stearothermophilus}

AIETETLVVGAGPGGYVAAIRAAQLGQKVIVEKGNGLGGVCLNVGCIPS KALISASHRYEQAKHSEEMGIKAENV
TIDFAKVQE WKASVVKKLTGGVEGLLKGNKVEIVKGEAYFVDANTRVVVNGDSAQTYTFKNAIITGSRPIELXV
GRRPNTDELGLEQIGIKMTNRGLIEVDQQCRTSVPNIFAIGDIVPGPALAHKASYEGKVA AEAIAGHPSAVDYV

>d1ebda2 c.3.1.5 (A:155-271) Dihydrolipoamide dehydrogenase {Bacillus stearothermophilus}

PNFKFSNRILDSTGALNLGEVPKSLVVIGGGYIGIELGTAYANFGTKVTILEGAGEILSGFEKQMAIIKKRLKKKG
EVVTNALAKGAEEREDGVTVYEANGETKTIDADYVLVT

>d1ojt_1 c.3.1.5 (117-275,401-470) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

GSADA EYDVVVLGGGPGGYSAAFAAAD EGLKVAI VERYKTLGGVCLNVGCIPS KALLHNAAVIDEVRHLAANGI
KYPEPELDIDMLRAYKDGVV SRLTGGLAGMAKS RKV DVIQGDGQFLDPH HLEVSLTAGDAYEQAAPTGEKKIVA
FKNCIIAAGSRXAPNGKLISA EKAGVAVTDRGFIEVDKQMRTNVPHIYAIGDIVGQPMLAHKAVHEGHVAAEN
CAGHKAYFD

>d1ojt_2 c.3.1.5 (276-400) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}

VTKLPFI PEDPRIIDSS GALALKEVPGKLLI IGGGIIGLEMGTVYSTLGSRLDVEMMDGLMQGADRLV KVWQ
KQNEYRFDNIMVN TKTVAVEPKEDGVYVTFEGANAPKEPQR YDAVLVAAGR

>d1jeha1 c.3.1.5 (A:1-160,A:283-355) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

TINKSHDVVIIGGGPAGYVAAIKAAQLGFNTACVEKRGKLG GTCLNVGCIPS KALLNN SHLFHQ MHTEAQKRG
DVNGDIKINVANFQKAKDDAVKQLTGGI ELLFKKNV TYYKGNGSFEDETKIRVTPVDGLEGTVKEDHILDVKNII
VATGSEVTPFXVGRPYIAGLGA EKIGLEVDKRGRLVIDDQFNSKFPHIKVVGDTVFGPMLAHKAEEEGIAAVE
MLKTGHGHVN

>d1jeha2 c.3.1.5 (A:161-282) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

PGIEIDEEKIVSSTGALSLKEIPKRLTIIGGGIIGLEMGSVSRLGSKVTVVFQPQIGASMDGEVAKATQKFLKKQG
LDFKLSTKVISAKRNDDKNVVEIVVEDT KTNQENLEAEVLLVA

>d1dxla1 c.3.1.5 (A:4-152,A:276-347) Dihydrolipoamide dehydrogenase {Garden pea (*Pisum sativum*)}
SDENDVVIIGGGPGGYVAAIKAAQLGFKTTIEKRGALGGTCLNVGCIPS KALLHSSHMYHEAKHSFANHGVKV
SNVEIDLAMMKGQKDKAVSNLTRGIEGLFKKNKVTYVKGYGKFSPSEISVDTIEGENTVVKGKHIITGSDVKX
GRTPFTGLNLKDYGKETDKLGRILVNERFSTNVSGVYAI GDVIPGPMLAHKAEEGVACVEYLAGKVGHD
>d1dxla2 c.3.1.5 (A:153-275) Dihydrolipoamide dehydrogenase {Garden pea (*Pisum sativum*)}
SLPGVTIDEKKIVSSTGALALSEPKKLVVGAGYIGLEMGSVWGRIGSEVTVEFASEIVPTMDAEIRKQFQRSLE
KQGMKFKLTKVVGVDTSAGVKTVEPSAGGEQTIIEADVVLSA
>d1fcda1 c.3.1.5 (A:1-114,A:256-327) Flavocytochrome c sulfide dehydrogenase, FCSD,
flavin-binding subunit {Purple phototrophic bacterium (*Chromatium vinosum*)}
AGRKVVVVGGSATAAKYIKLADPSIEVTLIEPNTDYYTCYLSNEVIGGDRKLESIKHGVDGLRAHGIQVVHD
SATGIDPDKKLVKTAGGAEGFYDRCVVAPGIELIYDKIEXQRAGKIAQIAGLTNDAGWCPVDIKTFESSIHKGIVI
GDASIANPMPKSGYSANSQGVAAA AVVLLKGEE
>d1fcda2 c.3.1.5 (A:115-255) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding
subunit {Purple phototrophic bacterium (*Chromatium vinosum*)}
GYSEEAAAKLPHAWKAGEQTAILRKQLED MADGGTVVIAPP AAPFRCPPGYERASQVAYYLKAHKPM SKVII
DSSQTFSKQSQFSKGWERLYFGTENAMIEWHPGPDSAVVKV DGGEMMVETAFGDEFKADVINLIPP
>d1djna3 c.4.1.1 (A:341-489,A:646-729) Trimethylamine dehydrogenase, middle domain
{*Methylophilus methylotrophus*, w3a1}
DIRVCIGCNVCISRWEIGGPPMICTQNATAGEEYRRGWHPEKFRQTKNKS VLVAGAGPSGSEAARVLMESGY
TVHL TDAEKIGGHLNQVAALPGLGEWSYHRDYRETQITKLLKKNKESQLAQKPMTADDVLQYGADKVIIAT
GAXSECTLWNE LKARESEWAENDIKGIYLIGDAEAPR LIADATFTGHRVAREIEEANPQIAIPYKRETI AWGTPH
MPGGNFKIEYKV
>d1cjca2 c.4.1.1 (A:6-106,A:332-460) Adrenodoxin reductase of mitochondrial p450
systems {Cow (*Bos taurus*)}
TPQICVVGSGPAGFYTAQHLLKHH SRAHVDIYEKQLVPFGLVRFGVAPDHPEVKNVINTFTQTARSDRC AFYGN
VEVGRDTVQELQDAYHAVVLSYGAEDXSRPIDPSVPFDPKLG VVPNMEGRVVDVPGYCSGWV/KRGPTGV
ITTTMTDSL TGQILLQDLKAGHLPSGPRPGSAFIK ALLDSRGVWPVS FSDWEKLD AEEVSRGQAS GKP REKLL
PQEMLRL GH
>d1h7wa4 c.4.1.1 (A:184-287,A:441-532) Dihydropyrimidine dehydrogenase,
domain 2 {Pig (*Sus scrofa*)}
EAYSAKIALLGAGPASISCASFLARLG YSDITIFEKQ EYVGG LSTSEIPQFRLPYDV VNFEIELMKDLGVKIICGKSLSE
NEITLNTLKEEGYKAFIGIGLPEXVL RD PKVKEAL SPIK FN RWD LPEV DPET M QTSEP WVFAGG DIVGMANTT
VESVNDGKQASWYIHKYIQAQY GASVSAKPELPLFYTPV DLD
>d1an9a1 c.4.1.2 (A:1-194,A:288-340) D-amino acid oxidase, N-terminal domain {Pig (*Sus scrofa*)}
MRVVVIGAGVIGL STALCIHERYHSVLQPLDV KVYADRFTPFTTDVAAGLWQPYTSEPSNPQ EANWNQQTFN
YLLSHIGSPNAANM GLTPVSGYNLFREAVPDPYWKDMVLGFRKL P RE LD MF PDYRYGWFNTS LILEGRKYLQ
WLTERLTERGVKFFLRKVESFEEVARGGADVIIN CTGVWAGVLQPDPLXQV RLEREQLRGSSNTEVIHNYGHG
GYGLTIHWGCALEVAKLFGKVLEERNLL
>d1c0pa1 c.4.1.2 (A:999-1193,A:1289-1361) D-amino acid oxidase, N-terminal domain
{Yeast (*Rhodotorula gracilis*)}
LMMHSQKRVVVLGSGVIGLSSALILARKGYSVHILARDLPEDVSSQT FASP WAGANWTPM LTDGPRQAKW
EESTFKKWV L VPTGHAMWLKGTRRFAQNEDG LLGHWYK DITPNYRPLPSSEC PG AIGV TYDTLSVHAPK YC
QYLARELQKLGATFERRTVTSLEQAFDGADLV NATGLGAKSIAGIDDQAXRGGPRVEAERIVLPLDRTKSPLSLG

RGSARAACEKEVTLVHAYGFSSAGYQQSWGAAEDVAQLVDEAFQRYHG

>d1i8ta1 c.4.1.3 (A:1-244,A:314-367) UDP-galactopyranose mutase, N-terminal domain {Escherichia coli}

MYDYIIVGSGLFGAVCANELKKLNKKVLVIEKRNHIGGNAYTEDCEGIQIHKYGAHIFHTNDKYIWDVNDLVF
NRFTNSPLAIYKDKLFNLPFNMMNTFHQMVGVKDPQEAQNIINAQKKKGDKVPENLEEQAISLVGEDLYQALI
KGYTEKQWGRSAKELPAFIKRIPVRFDFDNNYFSDRYQGIPVGGYTKLIEKMILEGVVDVKLGIDFLKDSDLASKA
HRIIYTGPIDQYFDYRFGALXNDNKNMELFKKYRELASREDKVIFGGRLAEYKYYDMHQVISAALYQVKNIMSTD

>d2uaga1 c.5.1.1 (A:1-93) UDP-N-

acetyl muramoyl-L-alanine:D-glutamate ligase MurD, N-terminal domain {Escherichia coli}

ADYQGKVNVIIGLGLTGLSCVDFFLARGVTPRVMMDTRMTPPGLKLPEAVERHT GSLNDEWLMAADLIVASPG
IALAHPSLSAAADAGIEIVG

>d1tml_ c.6.1.1 (-) Cellulase E2 {Thermomonospora fusca, strain yx}

NDSPFYVNPNMSSAEVRNNPNDPRTPVIRDRIASVPQGTWFAHHNPGQTGQVDALMSAAQAAGKIPILV
VYNAPGRDCGNHSSGGAPSHSAYRSWIDEFAAGLKNRPAYIIVEPDLSLMSSCMQHVQQEVLETMAYAGKAL
KAGSSQARIYFDAGHSAWHSPAQM ASWLQQADISNSAHGIATNTSNRWT ADEVAYAKAVLSAIGNPSLRAVI
DTSRNGNGPAGNEWCDPSGRAIGTPSTTNTGDPMIDAFLWIKLPGEADGCIAGAGQFVPAAYEMAIAA

>d1qjwa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Trichoderma reesei, Cel6a}

ATYSGNPFGVGT PWANAYYASEVSSLAIPLTGAMATAAAAVAKVPSFMWLDTLDKTPLMEQTLADIRTANKN
GGNYAGQFVVFDL PDRDCAALASNGEYIADGGVAKYKNYIDTIRQIVVEYSDIRTLVIEPDSL ANLVTNLGTPK
CANAQSAYLECINYAVTQLNLPNVAMYLDAGHAGWLGPANQDPA AQLFANVYKNASSP RALRGLATNVAN
YNGWNITSPPSYTQGNavyNEKLYIHAIGPLL ANHGWSNAFFITDQGRSGKQPTGQQWGDWCNVIGTGFG
IRPSANTGDSLLSFVWVKPGGECDGTS DSSAPRFDSH CALPD ALQPAPQAGAWFQAYFVQLLT NANPSFL

>d2bvwa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6a}

NGNP FEGVQLWANN YRSEVHTLAIPQITDPAL RAAASAVA EVPSFQWL DRNVTDT LLV QTL SEIREANQAG
ANPQYAAQIVVYDLPDRD CAAA ASNGEWAIA NGVNNYKAYINR IREI LSF DVRT ILVIEPDSL ANMV TNMN
VPKCSGA ASTYRELT IYALKQL DLP HVAM YM DAG HAG WL GPAN IQPA E LFA KI YED AGK PRA VR GLAT NV
NYNAWSVSSPP PYTSPN PNYDEKHYIEA FRPL LEARGF PAQFIVDQGRSGKQPTGQ KEW GHW CNA IGT GFG
MRPTANTGHQYVDAFVWVKPGGECDGTS DTTA ARYDYHCG L EALKP APEAGQWF NEYFIQ L RNAN PPF

>d1dysa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6b}

GNP FSGRTLLVNSD SS KLDQ TRQ AFLS RGD QTNA AKV KYV QEK VGT FWIS NI FLL RDID VAI QNARA AKARG
ENPIVGLVLYNLPDRDCSAGE SSGELK LSQN GLNRYKNEYVNPFAQKLKAASD VQFAVILEPDAIGNMVTG TS AF
CRNARGPQ QEAIGYAI SQLQASHI HLYLDVANGW LGWAD KLEPTA QEVATILQKAGNNAK IRGF SS NVSN YN
PYSTS NPPP YTSGSP SPDES RYAT NIAN AMR QRG LPTQ FII DQS RVAL SGAR SEW GQ WC NVN PAG FG QPFT TN
TNNPNVDAI VVWVKPGG ESDG QCG MGGAPA AGMW FDAYA QML TQNAH DEIA

>d1cm5a_ c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}

SELNEKLATAWEGFTKGDWQNEVNRDFIQK NYTPYEGDESFLAGATEATT LWDKVM EGVKLENR THAPVD
FDTAVASTITSHDAGYINKQ LEKIVGLQTEAPLKRALIPFGGIKMI EG SCKAYNRE LDPMIKKIF TEYRKTHNQGVF
DVYTPDILRCRKSGVLTGLP DAYGRGRIIGDYRRVALY GIDYLMKD KLAQFTSLQADLENGVNLEQ TIRL REEIA EQ
HRALGQMKE MA KYGY DISGPATNA QEA IQW TYFGYLA AVKS QNGAAM SF GRT STFL DVYI ERDL KAG KITE
QEAQEMV DHL VMK LRMV RFL RTPEY DELF SGD P I WATES IGGM GLD GRT L VT KNSFR FLNT LYTM GPS PE PN
MTILWSEK LPLNF KKFAAKV S IDT S LQY ENDDLMR PDFNN DDYIA AAA VSPM IV GKQMQFF GARAN LAK TM
LYAING GVDE KLMQ VGP KSE PI KG DV LN YDEV MER MDH FMDW LAK QY ITAL NII HYM HDK YSE ASL MAL H
DRD VIRT MAC GIAGL SVAAD SL SA IKYAKV KPI RDE DGLA IDF EIE GEY P QFG NN D PRV DDLA VDL VER FM KI Q
KLHTYR DA IPT QSV LIT S NVV YG KKT GNT PDG RRAGA PFG PG A NP MH GRD QKG AVA S LT SVAK LPF AYAK DGI

SYTFSIVPNALGKDDEVRTNLAGLMDGYFHEASIEGGQHNVNVMNREMILDALENPEKYPQLTIRVSGY
AVRFNSLTKEQQQDVITRTFTQSM

>d1qhma_ c.7.1.1 (A:) Pyruvate formate-lyase, PFL {Escherichia coli}

NEKLATAWEGFTKGDWQNEVNVRDFIQKNYTPYEGDESFLAGATEATTLWDKVMEGVKLENRTHAPVDFDT
AVASTITSHDAGYINKQLEKIVGLQTEAPLKRALIPFGGIKMIEGSCKAYNRELDPMIKKIFTEYRKTHNQGVFDVV
TPDILRCRKSGVLTGLPDAYGRGRIIGDYRRVALYIDYLMKDKLAQFTSLQADLENGVNLEQTIRLREEIAEQHR
ALGQMKEAKYGYDISGPATNAQEAIQWTYFGYLAAVKSQNGAAMSGFRSTFLDVYIERDLKAGKITEQEQA
QEMVDHLMVKLRMVRFLRTPEYDELFSGDPIWATESIGGMGLGRTLTKNSFRFLNTLYTMGPSPEPNMTIL
WSEKLPNFKFAAKVSIITSSLQYENDDLMRPDFNNDDYAIACCVSPMIVGKQMQFFGARANLAKTMLYAIN
GGVDEKLKMQVGPKSEPIKGDVLNYDEVMERMDHFMDWLAKQYITALNIIHYMHDKYSYEASLMALHDRDV
IRTMACCIAGLSVAADSLSAIKYAKVKPIRDEDGLAIDFEIEGEYPQFGNNPDRVDDLAVDLVERFMKKIQLHTY
RDAIPTQSVLTITSNVVYGKK

>d1rlr_2 c.7.1.2 (222-748) R1 subunit of ribonucleotide reductase, C-terminal domain {Escherichia coli}

FSSCVLIECGDSLDSINATSSAIVKYVSQRAGIGINAGRIRALGSPIRGGEAFHTGCIPFYKHFQTAVKSCSQGGVR
GGAATLFPMPWHLEVESLLVLKNNRGVEGNVRVRHMDYGVQINKLMYTRLLKGEDITLFSPSDVPGLYDAFFAD
QEEFERLYTKYEKDDSRKQRVKAVEFLSMMQERASTGRIYIQNVDHCNTHSPFDPAIAPVRQSNLCLEIALPTK
PLNDVNDENGEIALCTLSAFNLGAINNLDELDELAILAVRALDALLDYQDYPPIAAKRGAMGRRTLGIGVINFAYY
LAKHGKRYSDGSANNLTHKTFEAIQYYLLKASNELAKEQGACPWFNETTYAKGILPIDTYKKDLDTIANEPLHYD
WEALRESIKTHGLRNSTLSALMPSETSSQISNATNGIEPPRGYVSIKASKDGIIRQVVPDYEHLHDAYELLWEMP
GNDGYLQLVGIMQKFIDQSIANTNYDPSRFPSGKVMQQLLKDLLTAYKFGVKTLYYQNTRDDIDDSNFQL

>d1b8ba_ c.7.1.3 (A:) Class III anaerobic ribonucleotide triphosphate reductase NRDD subunit {Bacteriophage T4}

SRVFPTQRDLMAGIVSKHIAKNMVPSFIMKAHESGIIHVHDIDYSPALPFTNCCLVDLKGMLENGFKLGNAQIET
PKSIGVATAIMAQITAQVASHQYGGTTFANVDKVLSFYVKRTYAKHIEDAEKWQIADALNYAQSKTEKDVTYDAF
QAYEYEVNTLFSSNGQTPFVTLFGTGTDWTERMIQKAILKNRIKGLGRDGITPIFPKLVMFVEEGVNLYKDDPN
YDIKQLALECASKRMYPDIISAKNNKAITGSSVPVSPMGRCSFLSVKDSTGNEILDGRNNLGVVTLNLPRIALD
SYIGTQFNEQKFVELFNERMDLCFEALMCRISLKGVKATVAPILYQEGAFCVRLKPDDDIELFKNGRSSVSLGYI
GIHELNILVGRDIGREILTKMNAHLKQWTERTGFAFSLYSTPAENLCYRFCKLDTEKYGSVKDVTDKGWYTNFH
VSVEENITPFEKISREAPYHFIATGGHISYVELPDMKNNLKGLEAVWDYAAQHLDYFGVNMPVDKCFCTCGSTHE
MTPTENGFVCSICGETDPKKMNTIRRTCAVLGNPNERG

>d1kbla2 c.8.1.1 (A:377-509) Pyruvate phosphate dikinase, central domain {Clostridium symbiosum}

LHPTFNPAALKAGEVIGSALPASPGAAAGKVYFTADEAKAAHEKGERVILVLETSPEDIEGMHAAEGILTVRGG
MTSHAAVVARGMGTCVSGCGEIKINEEAKTFELGGHTFAEGDYISLDGSTGKIYKGD

>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}

SGILASPGIAFGKALLKEXKIIDSAIQDEVLVAADLTPSETAQLNLKKVLGFITDAGGRTSHTSIMARSLELPAIVG
TGSVTSQVKNDDYLILDAVNNQVYVNPTNEVIDKMRAVQEQQVASE

>d1aco_1 c.8.2.1 (529-754) Aconitase, C-terminal domain {Cow (Bos taurus)}

VDVSPTSQRLQLLEPFDKWDGKDLEDLQILIKVKGKCTTDHISAAGPWLKFRGHLDNISNNLLIGAINSENKRKAN
SVRNAVTQEFGPV PDTARYYKQHGRWVVGDENYGE GSSREHSALEPRFLGGRAIITKSFARIHETNLKKQGLL
PLTFADPADYNKIHPVDKLTIQGLKDFAPGKPLTCIHKPNTQETILLNHTNETQIEWFRAGSALNRMKELQQK

>d1a9xb1 c.8.3.1 (B:1502-1652) Carbamoyl phosphate synthetase, small subunit N-terminal

domain {Escherichia coli}

IKSALLVLEDGTQFHGRAIGATGSAVGEVVNTSMTGYQEILTDPSYSRQIVTLYPHIGNVTNDADEESSQVH
AQGLVIRDLPLIASNFRNTEDLSSYLKRHNIVAIADIDTRKLTRLLREKGAQNGCIAGDNPDAALALEKARAFPG
>d1de4c2 c.8.4.1 (C:190-382) Transferrin receptor ectodomain, apical domain {Human (Homo sapiens)}

IQVKDSAQNNSVIVDKNGLRVYLVENPGGVAYSKAATVGKLVHANFGTKKDFEDLYTPVNGSIVIVRAGKITFA
EKVANAESLNAIGVLIYMDQTKFPIVNAELSSFFGH AHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPVQTISRAA
AEKLFGNMEGDCPSDWKTDS CRMVTSESKNVKLT VSNVLK

>d1dk7a_ c.8.5.1 (A:) GroEL {Escherichia coli}

EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNI REMLPVLEAVAKAGKPLLIIAEDVEGEALATLVNTM
RGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVVINKDTTIIDGV

>d1kid_ c.8.5.1 (-) GroEL {Escherichia coli}

GLVPRGSEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNI REMLPVLEAVAKAGKPLLIIAEDVEGEALA
TLVVNTMRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVVINKDTTIIDG
VGEEAAIQGRVAQRQQIEEATSDYDREKLQERVAKLAGGV

>d1oela2 c.8.5.1 (A:191-366) GroEL {Escherichia coli}

EGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNI REMLPVLEAVAKAGKPLLIIAEDVEGEALATAVVNTIR
GIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVVINKDTTIIDGVGEEAAIQ
GRVAQRQQIEEATSDYDREKLQ

>d1ioka2 c.8.5.1 (A:191-366) GroEL {Paracoccus denitrificans}

EGMQFDRGYLSPYFVTNADKMIAELEDAYILLHEKKLSSLQPMVPLLESVIQSQKPLLIVAEDVEGEALATLVVNK
LRGGLKIAAVKAPGFGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVVINKDTTIIDGVGEEAAIQ
EIEARVSQIRQQIEETTS DYDREKLQ

>d1srva_ c.8.5.1 (A:) GroEL {Thermus thermophilus}

GYQFDKGYISPYFVTNPETMEA VLEDAFILIVEKKVSNVRELLPILEQVAQTGKPLLIIAEDVEGEALATLVNKLRG
TLSVAAVKAPGFGDRRKEMLKDIAAVTGGTVISEELGFKLENATLSMLGRAERVRITKDETTIVGGK

>d1a6db2 c.8.5.2 (B:216-367) Thermosome {Archaeon Thermoplasma acidophilum}
GIIVDKEVKHPGMPDVVKDAKIALLDAPLEIKKPEFDTNLRIEDPSMIQKFLAQUEENMLREMVDKIKSGANVVI
TQKGIDDMAQHYLSRAGIYAVRRVKKSDMDKLAKATGASIVSTIDEISSSDLGTAERVEQVKVGEDYMTFVTGC
KNP

>d1ass_ c.8.5.2 (-) Thermosome {Archaeon Thermoplasma acidophilum}

MSGIVIDKEVKHSKMPDVVKNAKIALIDS AL EIKKTEIEAKVQISDPSKIQDFLNQETNTFKQMVEKIKSGANVV
LCQKGIDDVAQHYLAKEGIYAVRRVKKSDMEKLAKATGAKIVTLDL DTPSVLGEAETVEERKIGDDRMTFVMG
CK

>d1ay7b_ c.9.1.1 (B:) Barstar (barnase inhibitor) {Bacillus amyloliquefaciens}

KKAVINGEQIRSISDLHQLKKE LALPEYYGENLDALWDCLTGWVEYPLVLEWRQFEQSKQLTENGAESVLQVFR
EAKAEGCDITIILS

>d1jj2x_ c.9.2.1 (X:) Ribosomal protein L32e {Archaeon Haloarcula marismortui}

TELQARGL TEKTPDLSDEDARLLTQRHRVGKPQFN RQDHKKK RVSTS WRKPRGQLSKQRRGIKGKD TVEAG
FRSPTAVRGKH PSGFEE VRVHN VDDLEG VDG DTEAVRIASKVGARKRERIEEEAEDAGIRVLNPTYVEV

>d1e8ca1 c.98.1.1 (A:3-87) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}

RNL RDLLAPWVPDAPSRALREMTLDSR VAAAGDLF VAVVGHQADGRRYIPQ AIAQGVAA IIIAEAKDEATDGEI
REM HGVPVI YLS

>d1gg4a3

c.98.1.1

(A:1-81)

UDP-murNac-tripeptide D-alanyl-D-

alanine-adding enzyme MurF {Escherichia coli}

MISVTLSQLTDILNGELQGADITLDAVTTDTRKLTPGLFVALKGERFDAHDFADQAKAGGAGALLVRPLDIDL
PQLIVK

>d2bnh__ c.10.1.1 (-) Ribonuclease inhibitor {Pig (Sus scrofa)}

MNLDIHCEQLSDARWTELLPLQQYEVVRLLDDCGLTEEHCKDIGSALRANPSLTELCLRTNELDAGVHLVLQG
LQSPTCKIQKLSLQNCSLTEAGCGVLPSTLRLPTRLRELHLSDNPLGDAGLRLCEGLLDPQCHLEKLQLEYCRLTA
ASCEPLASVLRATRALKELETVSNNDIGEAGARVLGQGLADSACQLETLRLENCGLTPANCKDLCGIVASQASLREL
DLGSNGLGDAGIAELCPGLLSPASRLKTLWLWECDITASGCRDLCRVLQAKETLKELSLAGNKLGDEGARLLCESL
LQPGCQLESLVVKSCSLTAACCQHVSLMILTQNKHLLQLSSNKGDSGIQELCQALSQPGTTLRVLCLGDC
NSGCSSLASLLLNRSLRELDLSNNCVGDPGVQLLLGSLEQPGCALEQLVLYDTYWTEEEVEDRLQALEGSKPGLR
VIS

>d1a4ya_ c.10.1.1 (A:) Ribonuclease inhibitor {Human (Homo sapiens)}

SLDIQSLDIQCEELSDARWAELLPLLQQCQVVRLLDDCGLTEARCKDISSALRVNPALAELNRSNELGDVGVHCV
LQGLQTSPCKIQKLSLQNCCLTGAGCGVLSSTLRTLQELHLSDNLLGDAGLQLLCEGLLDPQCRLEKLQLEYCS
LSAASCEPLASVLRAPDFKELTSNNNDINEAGVRVLCQGLKDSPCQLEALKESCGVTSDNCRDLCGIVASKASL
RELALGSNKLGDVGMAELCPGLLHPSSRLRTLWIWECGITAKCGDLCRVLRAKESLKELSLAGNELGDEGARLL
CETLLEPGCQLESVVKSCSFATACCSHFSSVLAQNRFLLQISNNRLEDAGVRELCQGLQPGSVLRVLWAD
CDVSDSSCSSLAATLLANHSLRELDLSNNCLGDAGILQLVESVRQPGCLLEQLVLYDIYWSEEMEDRLQALEKDK
PSLRVIS

>d1yrga_ c.10.1.2 (A:) Rna1p (RanGAP1), N-terminal domain {Fission yeast (Schizosaccharomyces pombe)}

ARFSIEGKSLKLDAITTEDEKSVFAVLLEDDSVKEIVLSGNTIGTEARWLSENIASKDLEIAEFSIFTGRVKDEIP
EALRLLLQALLKCPKLHTVRLSDNAFGPTAQEPLIDFLSKHTPLEHYLHNNGLPQAGAKIARALQELAVNKKAK
NAPPLRSIIICGRNRENGSMKEWAKTFQSHRLHTVKMVQNGIRPEGIEHLLLEGAYCQELKVQLDQDNTFTH
LGSSALAIALKSWPNLRELGLNDCLLSARGAAAVVDAFSKLENIGLQTLRLQYNEIELDAVRTLKTVIDEKMPDLL
FLELNGNRFSEEDDVVDEIREVFSTRGRGEDELDDME

>d1fqva2 c.10.1.3 (A:146-431) Cyclin A/CDK2-associated p19, Skp2 {Human (Homo sapiens)}

ESLWQTLDLTGKNLHDPVTGRLLSQGVIAFRCPRSFMDQPLAEHFSPFRVQHMDLSNSIEVSTLHGILSQCSKLN
QNLSEGLRLSDPIVNTLAKNSNLVRLNLSGCSGFSEFALQTLSSCSRDELNLSCFDFTEKHVQVAHVSET
ITQLNLSGYRKNLQKSDLSTVRRCPNLVHLDLSDSVMKNDCFQEFLQNLQHLSLSRCYDIIPETLLEGEIPTL
KTLQVFGIVPDGTQLLKEALPHLQINCSHFTTIARP TIGNKKNQEIWGIKCRLTLQ

>d1fs2a2 c.10.1.3 (A:146-401) Cyclin A/CDK2-associated p19, Skp2 {Human (Homo sapiens)}

ESLWQTLDLDEFRVQHMDLSNSIEVSTLHGILSQCSKLNQNLSEGLRLSDPIVNTLAKNSNLVRLNLSGCSGFSEFA
LQTLSSCSRDELNLSCFDFTEKHVQVAHVSETITQLNLSGYRKNLQKSDLSTVRRCPNLVHLDLSDSVM
LKNDCFQEFLQNLQHLSLSRCYDIIPETLLEGEIPTLQVFGIVPDGTQLLKEALPHLQIN

>d1h6ta2 c.10.2.1 (A:31-240) Internalin B {Listeria monocytogenes}

GPLGSETITVPTPIKQIFSDDAFAETIKDNLKKSVTDAVTQNELNSIDQIIANNSDIKSVQGIQYLPNVTKLFLNG
NKLTIDIKPLANLKNLGLWLFDENKVKVLDLSSKDLKKLKSLSLEHNGISDINGLHLPQLESLYLGNNKITDITVLSRL
TKLDTLSLEDNQISDIVPLAGLTKLQNLYLSKNHISDLRALAGLKNDVLELFSQ

>d1h6ua2 c.10.2.1 (A:36-262) Internalin H {Listeria monocytogenes}

GSITQPTAINVIFPDPA LANAIKIAAGKSNVTDTVQADLDGITTSAFGTGVTTIEGVQYLNLLIGLELKDNQITD
LAPLKNLTKITELELSGNPLKNVSAIAGLQSIKTLDTSTQITDVTPLAGLSNLQVLYLDLNQITNISPLAGLTNLQYL
SIGNAQVSDLTPLANLSKLTTLKADDNKISSDISPLASLPNIEVHLKNNQISDVPLANTSNLFIVTLTNQ

>d1jl5a_ c.10.2.6 (A:) Leucine rich effector protein YopM {Yersinia pestis}

KSKEYYNAWSEVERNAPPNGEQREMAVSRLRDLRQAHELELNNLGLSSLPELPPHESLVASCNSLTEP
ELPQSLKSLVDNNNLKALSDLPLLEYLGVSNNQLEKLPQLNSSLKIIDVDNNSLKKLPDLPPSLEFIAAGNNQ
LEELPELQNLPFLTAIYADNNSLKKLPDLPLSLESIVAGNNILEELPELQNLPFLTTIYADNNLLKTLPLPPSLEALNV
RDNYLTDLPELPQLTFLDVSENIFSGLSELPPNLYYLNASSNEIRSLCDLPPSLEELNVSNNKIELPALPPRLERLIA
SFNH LAEVPELPQNLKQLHVEYNPLREFPDIPESVEDLRMNS

>d1dcea3 c.10.2.2 (A:444-567) Rab geranylgeranyltransferase alpha-subunit, C-terminal domain {Rat (Rattus norvegicus)}

RVLHLAHKDLTVLCHLEQLLLVTHLDLSHNRLRALPPALAALRCLEVQASDNALENVDGVANLPRLQELLCNN
RLQQSAAIQPLVSCPRLVLLNLQGNSLCQEEGIQERLAEMLPSVSSILT

>d1koha1 c.10.2.3 (A:201-362) mRNA export factor tap {Human (Homo sapiens)}

LNEKPEQVEQLKLIMSKRYDGSSQQALDLKGLRSDPDLVAQNIDVVLNRRSSMAATLRIIEENIPELLSLSNLSNNR
LYRLDDMSSIVQKAPNLKILNLSGNELKSERELDKIKGLKLEELWLDGNSLSDTFRDQSTYISAIRERFPKLLRLDG
HELPPPIAF

>d1a9na_c.10.2.4 (A:) Splicesomal U2A' protein {Human (Homo sapiens)}

VKLTAELIEQAAQYTNAVRDRELDLRGYKIPVIENLGATLDQFDAIDFSNEIRKLDGFPLRRLKTLVNNNRCRI
GEGLDQALPDLTEILTNNSLVELGDLTPLASLKSITYLCLIRNPVTNKKHYRLVYIKVPQVRVLDFFQKVKLKERQ
EAEKMFK

>d1igra1 c.10.2.5 (A:1-149) L1 and L2 domains of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

EICPGPIDIRNDYQQQLKRLENCTVIEGYLHILLISKAEDYRSYRFPKLTVITEYLLLFRVAGLESLGDLFPNLTVIRGW
KLFNYALVIFEMTNLDIGLYNLRNITRGAIRIEKNADLCYLSTWDWSLILDAVSNNYIVGNKPPKECG

>d1igra2 c.10.2.5 (A:300-478) L1 and L2 domains of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}

KVCEEEKKTKTIDSVTSAQMLQGCTIFKGNNLLINIRRGNNIASELENFMGLIEVVTGYVKIRHSHALVSLFLKNLR
LILGEEQLEGNYSFYVLDNQNLQLWDWDHRNLTIKAGKMYFAFNPKLCVSEIYRMEEVTGTKGRQSKGDINT
RNNGERASCESDVDDDDKEQKLISEEDLN

>d1ds9a_c.11.1.1 (A:) Outer arm dynein light chain 1 {Green algae (Chlamydomonas reinhardtii)}

MAKATTIKDAIRIFEERKSVAATEAKVELHGMPIPIEKMADTLSTLKACKHLALSTNNIEKISSLSGMENLRILSLG
RNLIKKIENLDAVADTLEELWISYNQIASLGGIEKLVNLRVLYMSNNKITNWGEIDKLAALDKLEDLLAGNPLYND
YKENNATSEYRIEVV/KRLPNLKLDGMPVDEREQANVARGG

>d1jj2k_c.12.1.1 (K:) Ribosomal protein L15 (L15p) {Archaeon Haloarcula marismortui}

TSKKKRQRGSRTHGGGSHKNRRGAGHRRGRGDAGRDKHEFHNEPLGKSGFKRPQKVQEEAATIDVREIDE
NVTLLAADDVAEVEDGGFRVDVRDVVEEADDADYVKVLGAGQVRHELTIAADDSEGAREKVEGAGGSVELT
DLGEERQ

>d1jj2n_c.12.1.1 (N:) Ribosomal protein L18e {Archaeon Haloarcula marismortui}

SKTNPRLSSIADLKAARSSGGAVWDVAERLEKPRRTHAEVNLGRIERYAQEDETVVPGKVLGSGVLQKDVT
TVAAVDFSGTAETKIDQVGEAVSLEQAIENNPEGSHVRVIR

>d1aua_2 c.13.1.1 (97-299) C-terminal domain of phosphatidylinositol transfer protein sec14p {Baker's yeast (Saccharomyces cerevisiae)}

YDEKPLIAKFYPQYYHKTDKDRGPVYFEELGAVNLHEMNKTSEERMLKNLVWEYESVQYRLPACSRAAGHL
VETSCTIMDLKGISISSAYSVMYSVREASYISQNYYPERMGKFYIINAPFGFSTAFLFKPFLDPVTISKIFILGSSYQ
KELLKQIPAENLPVKFGGKSEVDESKGGYLSDIGPWRDPKYIGPEGEAPE

>d1h4xa_c.13.2.1 (A:) Anti-sigma factor antagonist Spollaa {Bacillus sphaericus}

AFQLEMVTRETIVIRLFGELDHHAVEQIRAKISTAIFQGAVTTIWNFERLSFMDSSGVGLVGRMRELEAVAGR
TILLNPSPTMRKVQFSGLGPWMMDATEEEAIDRVR

>d1auz_c.13.2.1 (-) Anti-sigma factor antagonist Spollaa {Bacillus subtilis}

SLGIDMNVKESVLCIRLTGELDHHTAETLKQKVTQSLEKDDIRHIVLNLEDLSFMDSSGLGVILGRYKQIKQIGGE
MVVCAISPAVKRLFDMSGLFKIIRFEQSEQQALLTGVAS

>d1tyfa_c.14.1.1 (A:) Clp protease, ClpP subunit {Escherichia coli}

SRGERSFDIYSRLLKERVIFLTGQVEDHMANLIVAQMFLFLEAENPEKDIYLYINSPGGVITAGMSIYDTMQFIKPD
VSTICMGQAASMGAFLTAGAKGKRFCLPNSRVMIHQPLGGYQGQATDIEIHAREILKVKGRCNEMLALHTG
QSLEQIERDTERDRFLSAPEAVEYGLVDSLTHRN

>d1fc6a4 c.14.1.2 (A:78-156,A:249-463) Photosystem II D1 C-terminal processing protease {Algae (Scenedesmus obliquus)}

VTSEQLLFLEAWRAVDRAYVDKSFNGQSWFKLRETYLKKEPMDRRAQTYDAIRKMLAVLDDPFTRFLEPSRLA
ALRRGTXKVTINPVFTTCSNAAAALPPGAAKQQLGYVRLATFNSNTAAQQAFTELSKQGVAGLVDIRNN
GGGLFPAGVNVARMLVDRGDLVLIADSQGIRDIYSADGNSIDSATPLVVLVNRGTASASEVLAGALKDSKRLIA
GERTFGKGLIQTVVLDGSGVAVTVARYQTPAGVDINKIGVSPDVQLDPEVLTDLEGCRVLGSDAAPRLF

>d1k32a4 c.14.1.2 (A:680-762,A:854-1061) Tricorn protease {Archaeon Thermoplasma acidophilum}

SSIHEEFLQMYDEAWKLARDNYWNEAVAKEISERIYEKYRNLVPLCKTRYDLSNVIVEMQGEYRTSHSYEMGGT
FTDKDPFRSXDDRFIRYRSWVEANRRYVHERSKGTIGYIHIPDMGMMGLNEFYRLFINESSYQGLIVDVRFNGG
GFVSQLIIEKLMNKIRGYDNPRRGTLSPYPTNSVRGKIIAITNEYAGSDGDFIFSFSFKKLGKLGKLGTRTWGGVVG
TPKRRLIDGTVLTQPEFAFWFRDAGFGVENYGVDPDVEIEYAPHDYLSGKDPQIDYAIDALIEELRN

>d1j7xa_c.14.1.2 (A:) Interphotoreceptor retinoid-binding protein IRBP {African clawed frog (Xenopus laevis)}

DPSVTHVLHQLCDILANNYAFSERIPTLLQHLPNLDYSTVISEEDIAKLNYESQLTEDPRLVLKSKTDTLVMPGD
SIQAENIPEDEAMLQALVNTVFVKSILPGNIGYLRFQFADSVIAKLAPEVNTVWEPIITENLIIDLRYNVGGS
STAVPLLLSYFLDPETKIHLFTLHNRRQQNSTDDEVYSHPKVLGKPYGSKKGVYVLTSQQTATAAEEFAYLMQSLSRAT
IIGEITSGNLMHSKVFPFGDTQLSVTVPIINFIDSNGDYWLGGGVVPDAIVLADEALDKAKEIIAFHPPLA

>d1nzya_c.14.1.3 (A:) 4-Chlorobenzoyl-CoA dehalogenase {Pseudomonas sp., strain CBS-3}

MYEAIGHRVEDGVAEITIKLPRHRNALSVKAMQEVTDALNRAEEDDSVGAVMITGAEDAFCAFGYLREIPLDK
GVAGVRDHFRIAALWWHQMIHKIIRVKRPVLAINGVAAGGGGLGISASDMAICADSAKFVCWAHTIGND
TATSYSLARIVGMRRAAMEMLTNRTLYPEAKDWGLVSERVYPKDEFREVAVKARELAAAPTHLQVMAKERF
HAGWMQPVEECTEFIEIQNVIASVTHPHFMPCLTRFLDGHRADRPQVELPAGV

>d1ey3a_c.14.1.3 (A:) Enoyl-CoA hydratase (crotonase) {Rat (Rattus norvegicus)}

FQYIITEKKGNSSVGLIQLNRPKALNALCNGLIEELNQALETFEEDPAVGAIVLTGGKEKAAGADIEMQNRTF
QDCYSGKFLSHWDHITRIKKPVIAAVNGYALGGGCEAMMCIDIYAGEKAQFGQPEILLGTIPGAGGTQRLTRA
VGKSLAMEMVLTGDRISAQDAKQAGLVSKIFPVETLVEEAIQCAEKIANNSKIVAMAKESVNAAFEMTLTEGNK
LEKKLFYSTFATDDRREGMSAFVEKRKANFKDH

>d1dcia_c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Rat (Rattus norvegicus)}

AYESIQVTSQAQKHVLHVQLNRPEKRNAMNRAFWRELVECFQKISKDSDCRAVVSGAGKMFSGIDLMDMA
SDILQPPGDDVARIAWYLRDLISRYQKTFTVIEKCPKPVIAAIHGGCIGGGVDLISACDIRYCTQDAFFQVKEVDV
GLAADVGTQLRPLKIGNRSLVNELTFTARKMMADEALSGLVSFVFPDKDVMLNAAFALAADISSKSPVAVQ
GSKINLIYRDHSVDELDYMATWNMSMLQTQDIIKSVQAAMEKKDSKSITFSKL

>d1hnua_c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-

enoyl-CoA isomerase) {Baker's yeast (*Saccharomyces cerevisiae*)}

NEKISYRIEGPFFIHLINPDNLNALEGEDYIYLGELLEADRNRDVYFTIIQSSGRFFSSGADFKGIAKAQGDDTNK
YPSETSKWVSNFVARNVYVTDAFIHKSKVLICCLNGPAIGLSAALVALCDIVYSINDKVYLLYPFANGLITEGGTTV
SLPLKFGTNTTYECLMFNPKFYDIMCENGFISKNFNMPSSNAEAFAKVLLELREKVKGLYLPSCLMKKLLKS
NHIDAFNKANSVEVNESLKWWVDGEPLKRFRQ

>d1hzda_c.14.1.3 (A:) AUH protein {Human (*Homo sapiens*)}

EDELRVRHLEEENRGIVVLGINRAYGKNSLSKNLIKMLSKAVDALKSDKKVRTIIIRSEVPGIFCAGADLKERAKMS
SSEVGPFVSKIRAVINDIANLPVPTIAIDGLALGGGLELALACDIRVAASSAKMGLVETKLAIIPGGGGTQLPRA
IGMSLAKELIFSARVLDGKEAKAVGLISHVLEQNQEGDAAYRKALDLAREFLPQGPVAMRVAKLAINQGMEVD
LVTGLAIEEACYAQTIPTKDRLEGLLAFKEKRPPRYKGE

>d1ef8a_c.14.1.3 (A:) Methylmalonyl CoA decarboxylase {Escherichia coli}

MSYQYVNVTINKAVIAFNYGRKLNALSKVFIIDLMQALSDLNRPEIRCIILRAPSGSKVFSAGHDIELPSGGR
DPLSYDDPLRQITRMIQKFPKPIISMVEGSVWGGAFEMIMSSDLIAASTSTFSMTPVNLGVVPYNLVGIHNLT
AGFHIVKELIFTASPIAQRALAVGILNHVVEEELEDFTLQMAHHISEKAPLAIAVIKEELRLGEAHTMNSDEF
RIQGMRRAVYDSEDYQEGMNAFLEKRKPNFVGH

>d1jnxx1 c.15.1.3 (X:1649-1757) Breast cancer associated protein, BRCA1 {Human (*Homo sapiens*)}

RMSMVSGLTPEEFMLVYKFARKHHITLTNLITEETTHVVMKTDAEFCERTLKYFLGIAGGKWVVSYFWVTQS
IKERKMLNEHDFEVRGDVVNGRNHQGPKRARESQD

>d1jnxx2 c.15.1.3 (X:1758-1859) Breast cancer associated protein, BRCA1 {Human (*Homo sapiens*)}
RKIFRGLEICCYGPFNTMPTDQLEWMVQLCGASVVKELSSFTLGTGVHPIVVVQPDAWTEDNGFHAIGQMCE
APVVTREWVLDSDLVALYQCQELDTYLIPQIP

>d1cdza_c.15.1.1 (A:) DNA-repair protein XRCC1 {Human (*Homo sapiens*)}

ELPDFFQGKHFFLYGEFGDERRKLIRYVTAFNGELEDYMSDRVQFVITAQEWDPSFEALMDNPSLAFVRPR
WIYSCNEKQKLLPHQLYGVVPQA

>d1in1a_c.15.1.2 (A:) DNA ligase III alpha {Human (*Homo sapiens*)}

GSADETLCQTKVLLDIFTGVRLYLPPSTPDFSRLRRYFVAFDGLVQEFDMTSATHVLGSRDKNPAAQQVSPEWI
WACIRKRRILVAPC

>d1dgtb3 c.15.1.2 (B:2582-2660) NAD+-dependent DNA ligase, domain 4 {Thermus filiformis}
EEVSDLLSGLTFLTGECSRPREEVKALLGRLGAKVTDSVSRKTSYLVGENPGSKLEKARALGAVLTEEFWRFL
KE

>d1rvv1_c.16.1.1 (1:) Lumazine synthase {Bacillus subtilis}

MNIIQGNLVTGLKIGIVVGRFNDIFTSKLLSGAEDALLRHGVDTNDIDVAWVPGAFEIPFAKKMAETKKYDAI
ITLGTIVGATTHYDYVCNEAAKGIAQAANTTGVPIFGIVTTENIEQAIERAGTKAGNKGVDCAVSAIEMANLN
RSFE

>d1di0a_c.16.1.1 (A:) Lumazine synthase {Brucella abortus}

TSFKIAFIQARWHADIVDEARKSFVAELAAKTGGSVEVEIFDVPGAYEIPLHAKTLARTGRYAAIVGAVIDGGIY
DHDFVATAVINGMMQVQLETEPVVLSPVSVLTPHHFESKEHHDFFAHFVKVGVEAAHALQIVSERSRIA

>d1hqka_c.16.1.1 (A:) Lumazine synthase {Aequifex aeolicus}

MQIYEGKLTAEGLRFGIVASRFNHALVDRIVEGAIDCIVRHGGREEDITLVRVPGSWEIPVAAGELARKEDIDAVI
AIGVLIRGATPHFDYIASEVSKGLANLSLELRKPITFGVITADTLEQAIERAGTKHGNKGWEAALSAIEMANLFKSL
R

>d1c41a_c.16.1.1 (A:) Lumazine synthase {Rice blast fungus (*Magnaporthe grisea*)}

GPTPQQHDGSALRIGIVHARWNTEIPLLAGTKAKLLACGVKESNIVVQSVPGSWELPIAVQRQLYSASQLQTPS
SGPSLSAGDLLGSSTDLTALPTTASSTGPFDALIAIGVLIKGETMHFEYIADSVSHGLMRVQLDTGVPVIFGVLT

VLTDDQAKARAGVIEGSHNHGEDWGLAAVEMGVRRRDWAAGKT

>d1c2ya_ c.16.1.1 (A:) Lumazine synthase {Spinach (Spinacia oleracea)}

MNELEGYVTKAQSFRFAIVVARFNEFVTRRLMEGALDTFKKYSVNEDIDVVVWPGAYELGVTAQALGKSGKYH
AIVCLGAVVKGDTSHYDAVVNSASSGVLISAGLNSGPCVFGVLCDNMDQAINRAGGKAGNKGAESALTAIE
MASLFEHHLK

>d1ejba_ c.16.1.1 (A:) Lumazine synthase {Baker's yeast (Saccharomyces cerevisiae)}

AVKGLGKPDQVYDGSKIRVGIIHARWNRIIDALVKGAIERMASLGVEENNIIITVPGSYELPWGTKRFVDRQA
KLKGKPLDVVIPIGVLIKGSTMHFEYISDSTTHALMNLQEKVDMPVIFGLTCMTEEQALARAGIDEAHSMHNHG
EDWGAAAVERMAVKFGKNAF

>d1cp3a_ c.17.1.1 (A:) Apopain (caspase-3, cpp32) {Human (Homo sapiens)}

NSYKMDYPEMGLCIIINNKNFKSTGMTSRSGTDVDAANLRETFRNLKYEVRNKNDLTREEIVELMRDVSKED
HSKRSSFCVLLSHGEIGIIFGTNGPVDLKKITNFFRGDRCRSLTGKPFLIIQACRGTELDGIETDSGVDDDMA
CHKIPVDADFLYAYSTAPGYYSWRNSKDGSWFIQLSCAMLQYADKLEFMHILTRVNRKVATEFESFSFDATFHA
KKQIPCVSMLTKELYFYH

>g1ibc.1 c.17.1.1 (A:,B:) Interleukin-1beta converting enzyme (a cysteine protease) {Human (Homo sapiens)}

GNVKLCSEEAQRWKQKSAEIYPIMDKSSRTRLALIICNEEFDISPRRTGAEVDTGMTMLLQNLGYSVDVKKNL
TASDMTTELEAFahrPEHKTSDFLVFMShGIREGICGKKHSEQVPDILQLNAIFNMLNTKNPSLKDPKVIII
QACRGDSPGVVWFKDXAIKKAHIEKDFIAFCSSPDNVSWRHTMGSVFIGRLIEHMQFYACSCDVEEIFRKVR
FSFEQPAGRAQMPTTERVTLRCFYLFPGH

>d1f1ja_ c.17.1.1 (A:) Caspase-7 {Human (Homo sapiens)}

YQYNMNFEKLGCIIINNKNFDKVGMGVRNGTDKDAEALFKCFRSLGFDVIVYNDCSAKMQDLKKASEED
HTNAACFACILLSHGEENVIYGKDGVTPIKDLTAHFRGDRSKTLLEPKLFFIQACRGTELDGIQADSGPINDTD
ANPRYKIPVEADFLFAYSTVPGYYSWRSPGRGSWFVQALCSILEEHGKDLEIMQILTRVNDRVARHFESQSDDP
HFHEKKQIPCVVSMLTKELYFS

>g1qtn.1 c.17.1.1 (A:,B:) Caspase-8 {Human (Homo sapiens)}

DKVYQMKSKPRGYCLIINNNHNFAKAREKVPKLHSIRDNGTHLDAGALTTFEELHFEIKPHDDCTVEQIYEILKIY
QLMDHSNMDCFICCIILSHGDKGIIYGTGQEAPIOELTSQFTGLKCPAGKPKVFFIQACQGDNYQKGIPVETD
XTRYIPDEADFLGMATVNNCVSYRNPAEGTWYIQSLCQLRERCPRGDDILTILTEVNYEVSNKDDKKNMGKQ
MPQPTFLRKKLVFPSD

>d1jxqa_ c.17.1.1 (A:) Caspase-9 {Human (Homo sapiens)}

MGALESLRGNADLAYILSMEPCGHCLIINNNFCRESGLRTGNSIDCEKLRRFSSLHFMVEVKGDLTAKKM
VLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGCPVSVEKIVNIFNGTSCPSLGGKPKLFFIQAC
GGEQKDHGFEVASTSPEDESPGSNPEPDATPFQEGLRTFDQLDAISSLPTPSDIFVSYSTFPGFVSWRDPKSGS
WYVETLDDIFEQWAHSEDLQSLLRVANAVSVKGIVKQMPGCFNLRKKLFFKTS

>d1cvra2 c.17.1.2 (A:1-350) Gingipain R (RgpB), N-terminal domain {Porphyromonas gingivalis}
YTPVEEKENGRMIVIVAKKYEGDIKDFWDWKNQRGLRTEVKVAEDIASPVTANAIQQFKQYEKEGNDLYVL
LVGDHKDIPAKITPGIKSDQVYQIVGNDHYNEFIGRFSCESKEDLKTQIDRTIHVERNITTEDKWLQALCIAS
AEGGPSADNGESDIQHENVIANLLTQYGYTKIICKYDGPVTPKNIIDAFNGGISLVNYTGHGSETAWGTSFGTT
HVKQLTNSNQLPFIFDVACVNGDFLSMPCFAEALMRAQKDGPPTGTVAIIASTIDQYWAPPMRGQDEMNEI
LCEKHPNNIKRTFGVTMNGMFAMVEKYKKDGENMLDTWTVFGDPSLLVRTLV

>d1akz_ c.18.1.1 (-) Uracil-DNA glycosylase {Human (Homo sapiens)}

MEFFGESWKKHLSGEFGKPYFIKLMGFVAEERKHYTVYPPPHQVFTWTQMCDIKDVKVVILGQDPYHGPNQ

AHGLCFSVQRPVPPPSLENIYKELSTDIEDFVHPGHGDLSGWAKQGVLLLNAVLTVRHQANSHKERGWEQFTDAVVSWNQNSNGLVLLWGSYAQKKGSAIDRKRRHHVLQTAHPPLSVYRGFFGCRHFSKTNELLQKSGKKPIDWKEL

>d1laue_c.18.1.1 (E:) Uracil-DNA glycosylase {Herpes simplex virus type 1}

LDWTTFRRVFLIDDAWRPLMEPELANPLTAHLLAEYNRRQCQTEEVLPREDVFSWTRYCTPDEVRVVIIGQDPYHHPGQAHGLAFSVRGLAFSVRANVPPPSLRNVLAALKNCYPEARMSGHGCLEKWARDGVLLNTTLTVKRGAAASHRIGWDRFVGGVIRRLAARRPGLVFMLWGTHAQNAIRPDPRVHCVLKFSHPSLSKVPFGTCQHFLVANRYLETRSISPIDWSV

>d3euga_c.18.1.1 (A:) Uracil-DNA glycosylase {Escherichia coli}

LTWHDVLAEEKQQPHFLNTLQTVASERQSGVTIYPPQKDVNAFRTELGDVKVVLGQDPYHGPQAHGLAFSVRPGIAIPPSLLNMYKELENTIPGFTRPNHGYLESWARQGVLLNTLTVRAGQAHSHASLGWETFTDKVISLNQHREGVVFLWGSHAQKKGAIIDKQRHHVLKAPHPSPLSAHRGFFGCNHFLANQWLEQHGETPIDWMPVLPAESE

>d1muga_c.18.1.2 (A:) G:T/U mismatch-specific DNA glycosylase {Escherichia coli}MVEDILAPGLRVVFCGINPGLOSSAGTGFPAHPANRFWKVIYQAGFTDRQLKPQEAQHLLDYRCGVTKLVDRPTVQANEVSKQELHAGGRKLIKIEDYQPQALAILGKQAYEQGFSQRGAQWGKQTLIGSTQIWVLPNPSGLSRVSLEKLVEAYRELDQALVV

>d1mla_1 c.19.1.1 (3-127,198-307) Catalytic domain of malonyl-CoA ACP transacylase {Escherichia coli}

QFAFVFPGQGSQTVGMLADMAASYPIVEETFAEASAALGYDLWALTQQGPAEELNKTWQTQPALLTASVALYRVWQQQGGKAPAMMAGHSLGEYSALVCAGVIDFADAVRLVEMRGKFMQEAVPEXVPSHCALMKPAADKLAVELAKITFNAPTPVNVNNVDVKCETNGDAIRDALVRQLYNPVQWTKSVEYMAAQGVHLYEVGPGKVLTGLTKRIVDTLTASALNEPSAMAAL

>d1g7sa3 c.20.1.1 (A:329-459) Initiation factor IF2/eIF5b, domain 3 {Archaeon Methanobacterium thermoautotrophicum}

DPEKVREEILSEIEDIKIDTDEAGVVVKADTLGSLEAVV/KILRD MYVPIKVADIGDVSRRDVVNAGIALQEDRVYGAIIFNVKVIPSAAQELKNSDIKLFQGNVIYRLMEEYEEWVRGIEEEKKKKWMEA

>d1jj2i_c.21.1.1 (I:) Ribosomal protein L13 {Archaeon Haloarcula marismortui}

AEFDADVIVDARDCIMGRVASQVAEQALDGETVAVVNAERA VITGREEQIVEKYEKRV DIGNDNGYFYPKRPDGIFKRTIRGMLPHKKQRGREA FESVRVYLGNPYDEDGEVLDGTSLDRLSNIKFVTLGEISETLGANKTW

>d1dmga_c.22.1.1 (A:) Ribosomal protein L4 {Thermotoga maritima}

AQVDLLNVKGEGVGTLEISDFVNIDPNYDVMWRYVDMQLSNRRAGTASTKTRGEVSGGGRKPWPQKHTGRARHGSIRSPIWRHGGVVHGPKPRDW SKKLNNKKMKKLALRSALSVKYRENKLLVDDLKLERPKTSKLEIQLNQLSDKKTLIVLPWKEEGYMNVKLSGRNL PDVKVIIADNPNNSKNGEKAVRIDGLNVFDMLKYDYLVLTRDMVKIEEVLG

>d1jj2c_c.22.1.1 (C:) Ribosomal protein L4 {Archaeon Haloarcula marismortui}

MQATIYDLDGNTDGEV DLPDV FETPVRSIDLIGKAVRAAQANRKQDYGSDEYAGLRTPAESFGSGRGQAHVPKLDGRARRVPQAVKG RSAHPPKTEKDRSLDNDKERQLA VRSALAATADALVADRGHEFDRDEV PVV SDDFEDLVKTQEVSLSLEALDVHADIDRADET KIKAGQGSAR GRKYRRPASILFV TSDEPSTAARNLAGADV ATASEVNT EDLAPGGAPGRLTVFTESALAEVAER

>d1hey_c.23.1.1 (-) CheY protein {Escherichia coli}

DKELKFLVVGNGGTGKSTVRNLLKELGFNNVEDAEGVDALNK LQAGGYGFV ISDW NMPNMDGLELLKTIRADGAMSALPVLMV TAEAKKENIIAAAQAGASGYVVKPFTAATLEEKLNKIFEKLG M

>d1jbea_c.23.1.1 (A:) CheY protein {Escherichia coli}

ADKELKFLVVDDFSTMRRIVRNLLKELGFFNNVEEAEDGVDALNKLQAGGYGFISDWNPMDGLELLKTIR
ADGAMSALPVLMVTAEAKKENIIAAQAGASGYVVKPFTAATLEEKLNKIFEKLG
>d1tmy_ c.23.1.1 (-) CheY protein {Thermotoga maritima}
GKRVLIVDDAAFMRMMKLDTIKAGYEVAGEATNGREAVEKYKELKPDIVTMDITMPMEMNGIDAIKEIMKIDP
NAKIVCSAMGQQAMVIEAIKAGAKDFIVKPFQPSRVVEALNKVS
>d1a04a2 c.23.1.1 (A:5-142) Nitrate/nitrite response regulator (NARL), receiver domain
{Escherichia coli}
EPATILLIDDHPMLRTGVKQLISMADITVGEASNGEQGIELAESLDPLILDLNMPGMNGLETLDKLREKSLS
GRIVVFSVNHEEDVTALKRGADGYLLKDMEPEDLLKALHQAAAGEMVLSEALTPVLAASL
>d1ntr_ c.23.1.1 (-) NTRC receiver domain {Salmonella typhimurium}
MQRGIVVVVDDDSIRWVLERALAGAGLTCTTFENGNEVLAALASKTPDVLLSDIRMPGMDGLALLKQIKQR
HPMLPVIMTAHSDDAASVAYQQGAFDYLKPFDIDEAVALVERAISHYQE
>d1dbwa_ c.23.1.1 (A:) Transcriptional regulatory protein FixJ, receiver domain {Rhizobium meliloti}
MQDYTVHIVDDEPVRKSLAFMLTMNGFAVKMHQSAAFLAFAPDVRNGVLVTDLRMPDMSGVELLRNLG
DLKINIPSIVTGHGDVPMAVEAMKAGAVDFIEKPFEDTVIIEAIERASEHLV
>d1qkka_ c.23.1.1 (A:) Transcriptional regulatory protein DctD, receiver domain {Sinorhizobium meliloti}
PSVFLIDDRDLRKAMQQTLEAGFTVSSFASATEALAGSADFAGIVISDIRMPGMDGLALFRKILALDPDPM
ILVTGHGDIPMAVQAIQDGAYDFIAKPFAADRLVQSARRAEKRLVMENRSLRRAAEAASEG
>d1dz3a_ c.23.1.1 (A:) Sporulation response regulator SpoOA {Bacillus stearothermophilus}
SIKVICIADDNRELVSLDEYISSQPDMEVIGTAYNGQDCLQMEEKRPDILLDIIMPHLDGLAVLERIRAGFEHQ
PNVIMLTAFGQEDVTKKAVELGASYFILKPFDMENLAHHIRQVYGKT
>d1nat_ c.23.1.1 (-) Sporulation response regulator SpoOF {Bacillus subtilis}
NEKILIVDDQYGIRILLNEVFNKEGYQTFQAANGLQALDIVTKERPDVLVLLDMKIPGMDGIEILKRMKVIDENIRVI
IMTAYGELDMIQESKELGALTHFAKPFDIDEIRDAVKKYLPL
>d1a2oa1 c.23.1.1 (A:1-140) Methyl esterase CheB, N-terminal domain {Salmonella typhimurium}
MSKIRVLSVDDSALMRQIMTEIINSHSDMEMVATAPDPLVARDLIKFNPDVLTLDVEMPRMDGLDFLEKLMR
LRPMPVVMVSSLTGKGSEVTLRAELGAIDFVTKPQLGIREGMLAYSEMIAEKVRTAARARIAAHKP
>d1kgsa2 c.23.1.1 (A:2-123) PhoB receiver domain {Thermotoga maritima}
NVRVLVVEDERDLADLITEALKKEMFTVDVCYDGEEGMYMALNEPFDVVILDIMLPVHDGWEILKSMRESGV
NTPVLMILTALSDVEYRVKGKLNMGADDYLPKPFDLRELIARVRALIRRKE
>d1b00a_ c.23.1.1 (A:) PhoB receiver domain {Escherichia coli}
ARRILVVEDEAPIREMVCVLEQNGFQPVEAEDYDSAVNQLNEPWPDLLLDWMLPGGSGIQFIKHLKRESMT
RDIPVVMLTARGEEEDRVRGLETGADDYITKPFSPKELVARIKAVMRRI
>d1dcfa_ c.23.1.2 (A:) Receiver domain of the ethylene receptor {Thale cress (Arabidopsis thaliana)}
HMSNFTGLKVLMDENGVSRMVTKGLLVHLGCETTVSSNEECLRVVSHEHKVVFMDVCMGVENYQIALRI
HEKFTKQRHQRPLLVALSGNTDKSTKEKCMSFGLDGVLLKPVSLDNIRDVSDLLEPRVLYE
>d1qo0d_ c.23.1.3 (D:) Negative regulator of the amidase operon AmiR {Pseudomonas aeruginosa}
SANSLLGSLRELOVVLNPPGEVSDALVLQLIRIGCSVRCWPPPEAFDVPDVVFTSIFQNRHHDEIAALLAAG
TPRTTLVALVEYESPAVLSQLIIECHGVITQPLDAHRVLPVLVSARRISEEMAULKQKTEQLQDRIAGQARINQAK
VLLMQRHGWDEREAHQHLSREAMKRREPILKIAQELL
>d1fyva_ c.23.2.1 (A:) Toll-like receptor 1, TLR1 {Human (Homo sapiens)}
NIPPLEELQRNLQFHAFISGHDSFWVKNELLPNLEKEGMQICLHERNFVPGKSIVENIITCIEKSYKSIFVSPNFV
QSEWCHYELYFAHHNLFHEGSNSLILILLEPIPQYSIPSSYHKLKSLMARRTYLEWPKEKSKRLFWANLRAAINIK

LTEQAK

>d1fywa_ c.23.2.1 (A:) Toll-like receptor 2, TLR2 {Human (Homo sapiens)}

SRNICYDAFVSYSERDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNIIDSIEKSHKTVFVLSENFVKSE
WCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCRLRKIMNTKTYLEWPMDEAQREGFWVNLRRAIKS

>d1eiwa_ c.23.3.1 (A:) Hypothetical protein MTH538 {Archaeon Methanobacterium thermoautotrophicum}

VTAEIRLYITEGEVEDYRVFLERLEQSGLEWRPATPEDADAVIVLAGLGTRRDEILGAVDLARKSSKPIITVRPYG
LENVPPELEAVSSEVVGWNPHCIRDALEDALDVI

>d1jkja2 c.23.4.1 (A:122-287) Succinyl-CoA synthetase, alpha-chain, C-terminal domain {Escherichia coli}

NCPGVITPGECKIGIQPGHIHKPGKVGIVSRSGTLTYEAVKQTTDYFGQSTCVGIGGDPIPGSNFIDILEMFEKD
PQTEAIVMIGEIGGSAEEEAAAYIKEHTKPVVGYIAGVTAPKGKRMGHAGAIAGGKGTADKEFAALEAAGVKT
VRSLADIGEALKTVL

>d1euca2 c.23.4.1 (A:131-306) Succinyl-CoA synthetase, alpha-chain, C-terminal domain {Pig (Sus scrofa)}

NCPGVINPGECKIGIMPGBIHKKGRIGIVSRSGTLTYEAVHQTTQVGLGQSLCVGIGGDPFNGTDFTDCLEIFLN
DPATEGIILIGEIGGNAEENAAEFLKQHNSGPKS PKVVSFIAGLTAPPGRMGHAGAIAGGKGGAKEKITALQSA
GVVVSMSPAQLGTTIYKEFEKRKML

>d1jkjb1 c.23.4.1 (B:239-388) Succinyl-CoA synthetase, beta-chain, C-terminal domain {Escherichia coli}

DPREAQAAQWELNYVALDGNIGCMVNNGAGLAMGTMDIVKLHGGE PANFLDVGGGATKERVTEAFKIIISDD
KVKA VLNVNIFGGIVRCCLIADGIIGAVAEVGVNVPVVRLLEGNN AELGAKKLADSGLNIIAKGLTAAQQVVA
VEGK

>d1eucb1 c.23.4.1 (B:246-393) Succinyl-CoA synthetase, beta-chain, C-terminal domain {Pig (Sus scrofa)}

EPIENEA AKYDLKYIGLDNIACFVNGAGLAMATCDIIFLNGGKPANFLDLGGGVKESQVYQAFKLLTADPKVEA
ILVNIFGGIVNCIIANGITKACRELELK VPLV RLEG TNVHEAQNILT NSGLPITS AVDLEDAKKAVASVT

>d2fcr_ c.23.5.1 (-) Flavodoxin {Chondrus crispus}

KIGIFFSTGNTTEVADFIGKTLGAKADAPI DVDDVTDPQALKDY DLLFLGAPT WNTGADTERSGTSWDEFLYD
KLPEVDMKDLPV AIFGLGDAEGYPDNFCDAIEEIHD CFAKQGAKPVGF SNPDDYDYEESKSVRDGKFGLPLDM
VNDQIPMEKRVAGWV EA VVSETGV

>d1f4pa_ c.23.5.1 (A:) Flavodoxin {Desulfovibrio vulgaris}

PKALIVYGSTTGNT EYTAETIARELADAGYEVDSRDAASVEAGGLFEGFDLVLLGCSTWGDDSIELQDDFIPLFDS
LEETGAQGRKVACFGCGDSSWEYFCGAVDAIEEKLKNL GAEIVQDGLRIDGDPRAARDDIVGWAHDVRGAI

>d1rcf_ c.23.5.1 (-) Flavodoxin {Anabaena, pcc 7119 and 7120}

SKKIGLFYGTQTGKTESVAEII RDEF GNDV VTLHDV SQA EVTD LNDY QYLIIGCPTWNIGELQSDWEGLYSELDD
VDFNGKLVAYFGTGDQIGYADNFQDAIGILEEKISQRGGKTVGYWSTDGYDFNDSKALRNGKFVGLALDEDNQ
SDLTDDRIKSWVAQLKSEFGL

>d1ag9a_ c.23.5.1 (A:) Flavodoxin {Escherichia coli}

AITGIFFGSDTGN TENIAKMIQKQLGKD VADVHDIAKSSKED LEAYDILLG IPTWYYGEAQCDWDDFFPTLEEID
FNGKLVALFGCGDQEDYAEYFC DALG TIRD II EPRGATIVGHWP TAGYHFEASKGLADDDHFVGLA IDEDRQPEL
TAER VEKWKV KQ!SEELHLDEILNA

>d1czna_ c.23.5.1 (A:) Flavodoxin {Anacystis nidulans and Synechococcus, pcc 7942}
AKIGLFYGTQTGVTQ TIAESI QQEF GGESIVDLNDIANADASDLNAYDYLII GCPTWNVGE LQSDWEGIYDDLDS

VNFQGKKVAYFGAGDQVGYSDFNQDAMGILEEKISSLGSQTGYWPIEGYDFNESKAVRNNQFVGLAIDEDN
QPDLTKNRIKTWVSQKLSEFGL
>d5nul_c.23.5.1 (-) Flavodoxin {Clostridium beijerinckii}
MKIVWWSGTGNTEKMAELIAGIIIESGKDVTINVSDVNIDELLNEDILILGCSAMTDEVLEESEFEPFIEEISTKIS
GKKVALFGSYWGWDGKWMRDFEERMNGYGCVVETPLIVQNEPDEAEQDCIEFGKKIANI
>d1fuea_c.23.5.1 (A:) Flavodoxin {Helicobacter pylori}
GKIGIFFTDSGNAEAIAEKSKAIGNAEVVVDVAKASKEQFNGFTKVILVAPTAGAGDLQTDWEDFLGTLEASDF
ANKTIGLVGLDQDTYSETFAEGIFHIYEKAKAGKVVGQTSTDGYHFAASKAVEGGKFVGLVIDEDNQDDLTDE
RIAKWVEQVRGSFA
>d1bvf_c.23.5.1 (F:) FMN-binding domain of the cytochrome P450bm-3 {Bacillus megaterium}
NTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLVTASYNGHPPDNAKQFVDWL
DQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAENIADRGEADASDDFEGTYEEWREHMWS
DVAAYFNL
>d1e5da1_c.23.5.1 (A:251-402) Rubredoxin oxygen:oxidoreductase (ROO), C-terminal domain
{Desulfovibrio gigas}
PTNKVVIFYDSMWHSSTEKMARVLAESFRDEGCTVKLMWCKACHHSQIMSEISDAGAVIVGSPTHNNGLPYV
AGTLQYIKGLRPQNKKIGGAFGSFGWSGESTKVLAEWLTGMGFDMPATPVKVNVPYHADYEQLKTMQAQTIA
ALKAKLAA
>d1ja1a2_c.23.5.2 (A:63-239) NADPH-cytochrome p450 reductase, N-terminal domain
{Rat (Rattus norvegicus)}
PVKESSFVEKMKKTGRNIIVFYGSQTGTAAEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDKSLVVFC
MATYGEDPTDNAQDFYDWLQETDVDLSGVKFAVFLGNKTYEHFNAMGKYVDQRLEQLGAQRIFELGLGD
DDGNLEEDFITWREQFWPAVCEFFGVEATGEE
>d1b1ca_c.23.5.2 (A:) NADPH-cytochrome p450 reductase, N-terminal domain {Human (Homo sapiens)}
SSFVEKMKKTGRNIIVFYGSQTGTAAEFANRLSKDAHRYGMRGMSADPEEYDLADLSSLPEIDNALVVFCMATY
GEGDPTDNAQDFYDWLQETDVDLSGVKFAVFLGNKTYEHFNAMGKYVDKRLEQLGAQRIFELGLGDDDG
LEEDFITWREQFWPAVCEHFGV
>d1dxqa_c.23.5.3 (A:) NAD(P)H:quinone reductase {Mouse (Mus musculus)}
AARRALIVLAHSEKTSFNYAMKEAAVEALKRGWEVLESIDLAMNFNPISRNNDITGELKDSKNFQYPSESSLAY
EGRLSPDIVAEHKKLEADLVIQFPLQWFGVPAILKGWFERVLVAGFAYTYAAMYDNGPFQNKTKLLSITTGG
GSMYSLQGVHGDMNVILWPIQSGILRCFGFQVLEPQLVYSIGHTPPDARMQILEGWKKRLETVWEETPLYFAP
SSLFDLNQAGFLMKEVQEEQKKNKFGLSVGHHLGKSIPADNQIKARK
>d1qrda_c.23.5.3 (A:) NAD(P)H:quinone reductase {Rat (Rattus rattus)}
AVRRALIVLAHAERTSFNYAMKEAAVEALKKGWEVVESDLYAMNFNPISRNNDITGEPKDSENFQYPVESSLAY
KEGRLSPDIVAEQKKLEADLVIQFPLQWFGVPAILKGWFERVLVAGFAYTYATMYDKGPQNKTKLLSITTGG
GSMYSLQGVHGDMNVILWPIQSGILRCFGFQVLEPQLVYSIGHTPPDARMQILEGWKKRLETVWEESPLYFAP
SSLFDLNQAGFLKKEVQEEQKKNKFGLSVGHHLGKSIPADNQIKARK
>d1d4aa_c.23.5.3 (A:) NAD(P)H:quinone reductase {Human (Homo sapiens)}
VGRRALIVLAHSERTSFNYAMKEAAAALKKGWEVVESDLYAMNFNPISRKDITGKLKDPMFQYPAESVLAY
KEGHLSPDIVAEQKKLEADLVIQFPLQWFGVPAILKGWFERVFIGEFAYTYAAMYDKGPFRSKKAVLSITTGG
GSMYSLQGIHGDMNVILWPIQSGILHFQCFQVLEPQLTYSIGHTPADARIQILEGWKKRLENIWDETPLYFAPSS
LFQDNQAGFLMKKEVQDEEKKFGLSVGHHLGKSIPADNQIKARK
>d1qr2a_c.23.5.3 (A:) Quinone reductase type 2 (menadione reductase) {Human (Homo sapiens)}

AGKKVLIVYAHQEPKSFNGSLKNVAVDELSRQGCTVTSDLYAMINFEPRATDKDITGTLNPEVFNYGVETHEA
YKQRSLASDITDEQQKVREADLVIQFPLYWFSVPAILKGWMDRVLQCGFAFDIPGFYDSGLQKLALLSVTTG
GTAEMYTKGVNGDSRYFLWPLQHGTLLHFCGFKVLAPQISFAPEIASSEERKGMVAAWSQRLQTIWKEEPIPCT
AHWHFGQ

>d1bmta2 c.23.6.1 (A:741-896) Methionine synthase, C-terminal domain {Escherichia coli}
EQGKTNGKMTATVKGDVHDIGKNIVGVVLQCNYYEVDLGVMVPAEKILRTAKEVNADLIGLSGLTPSLDEM
VNVAKEMERQGFTIPLLIGGATTSKAHTAVKIEQNYSGPTVYVQNASRTVGVAALLSDTQRDDFVARTRKEYE
TVRIQHGR

>d1fmfa_ c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium tetanomorphum}
MEKKTIVLGIVGSDCHAVGNKILDHSFTNAGFNVVNIGVLSSQEDFINAAIETKADLICVSSLYGQGEIDCKGLRE
KCDEAGLKGKLFVGGNIVVGKQNWPDVQEQRFKAMIFDRVYPPGTSPETTIADMKEVLGVE

>d1ccwa_ c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium cochlearium}
MEKKTIVLGIVGSDCHAVGNKILDHAFTNAGFNVVNIGVLSPQELFIKAAIETKADAILVSSLYGQGEIDCKGLRQ
KCDEAGLEGILLYVGGNIVVGKQHWPDVEKRFKDMGYDRVYAPGTPPEVGIADLKDLNIE

>d7reqa2 c.23.6.1 (A:561-728) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta
subunits {Propionibacterium freudenreichii, subsp. shermanii}
AQIRTISGVYSKEVKNTPEVEEARELVEEFEQAEGRRPRILLAKMGQDGHDHGQKVIATAYADLGFVDVGPLF
QTPEETARQAVEADVHVVGVSSLAGGHLTLPALRKELDKLGRPDILITVGGVPIEQDFDELKDGAIVEIYPTGT
IPESAISLVKKLRASLDA

>d7reqb2 c.23.6.1 (B:476-638) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta
subunits {Propionibacterium freudenreichii, subsp. shermanii}
TKPFPAAPARKGLAWHRDSEVFEQLMDRSTSVERPKVFLACLGTRRGREGFSSPVWHIAGIDTPQVEGG
TTAEIVEAFKKSGAQVADLCSSAKVYQQGLEVAKALKAAAGAKALYLSGAFKEFGDDAAEAEKLIDGRLFMGM
DVVDTLSSTLDILGVAK

>d1c4ka1 c.23.7.1 (A:1-107) Ornithine decarboxylase N-terminal "wing" domain {Lactobacillus sp.,
strain 30a}

SSSLKIASTQEQRQYFDTDRVVVDAVGSDFTDVGAVIAMDYETDVIDAADATKFGIPVFAVTKDAQAISADELKK
IFHIIDLENKFATVNAREIETAVNNYEDSIL

>d1qcza_ c.23.8.1 (A:) N5-carboxyaminoimidazole ribonucleotide (N5-CAIR) mutase
PurE {Escherichia coli}

PARVAIVMGSKSDWATMQFAAEIFEILNVPHHVEVSAH RTPDKLFSFAESAEE NGYQVIIAGAGGAH LPGMI
AAKTLVPLGVPVQSAALSGVDSL SIVQMPRGIPVGTLAIGKAGAANA ALLAAQILATHD KELHQ RLNDWRK
AQTDEVLENPDPRGAA

>d1cex_ c.23.9.1 (-) Cutinase {Fungus (Fusarium solani), subsp. pisi}
RTTRDDLINGNSASCADVIFIYARGSTETGNLGLGPSIASNLESAFGKDGVIQGVGGAYRATLDNALPRGTS
SAAIREMLGLFQQANTKCPDATLIAGGYSQGA ALAASIEDLDSAIRDKIAGTVLFGYT KNLQN RGRIPNPY PADR
TKVFCNTGDLVCTGSLIVAAPHLAYGP DARGPAPEFLIEKVRAVRGS

>d1g66a_ c.23.9.1 (A:) Acetylxyran esterase {Penicillium purpurogenum}
SCPAIHVFGARETTASPGYGSSTVVNGVLSAYPGSTA EA INYPACGGQSSCGGASYSSVAQGIAAVASAVNSF
NSQCPSTKIVLVGYSQGGEIMDVALCGGGDPNQGYTNTAVQLSSAVNMVKAIFMGDPMFRAGLSYEVGTC
AAGGF DQR PAGFSCPSAAKIKSYCDASDPYCCNGSNAATHQGYGSEYGSQALAFVKS LG

>d1qoza_ c.23.9.1 (A:) Acetylxyran esterase {Trichoderma reesei}
ECPAIHVFGARETTVSQGYGSATVVNLVIQAHPGT SE AIVYPACGGQASC GG ISYAN SVNGT NAAA AINN
FHN SCPDTQLVLGVYSQGAQIFDNALCGGGDPGEGITNTAVPLTAGAVSAVKA IFMGDP RNIHGLPY NVGTC

TTQGFDARPAGFVCPASKIKSYCDAADPYCCTGNDPNVHQGYGQEYQQALAFINSQLS
>d1esc_c.23.10.1 (-) Esterase {Streptomyces scabies}
DPVPTVFFGDSYTANFGIAPVTNQDSERGWCFQAKENYPAVATRSLADKGITLDVQADVSCGGALIHHFWEKQ
ELPFGAGELPPQQDALKQDTQLTVGSLGGNTLGFNRILKQCSDELRKPSLLPGDPVDGDEPAAKCGEFFGTGDG
KQWLDDQFERVGAEELELLDRIGYFAPDAKRVLVGYPRLPEDTTKCLTAAPGQTQLPFADIPQDALPVLDQIQK
RLNDAMKAAADGGADFVDLYAGTGANTACDGADRGIGGLLEDSQLELLGKIPWYAHPNDKGRDIQAKQVA
DKIEEILN
>d1flca2 c.23.10.2 (A:1-150,A:307-427) Esterase domain of haemagglutinin-esterase-fusion glycoprotein HEF1 {Influenza C virus}
EKIKICLQKVNSSFLHNGFGGNLYATEEKRMFELVKPKAGASVNLQSTWIGFGDSRTDKNSAFPRSADVSAK
TADKFRFLSGGSLMISMGPPGKVDYLYQGCGKHVKFYEGVNWSPHAAINCYRKNWTDIKLFQKNIYELAS
QSHXEKGPVTAQSIWGKGRESDYAVDQACLSTPGCMLIQKQKPYIGEADDHHGDQEMRELLSGLDYEARCIS
QSGWVNETSPFTEKYLLPPKFGRCPЛАKEESIPKIPDGLLIPTSGTDTTVT
>d1es9a_c.23.10.3 (A:) Platelet-activating factor acetylhydrolase {Cow (Bos taurus)}
ENPASKPTPVQDVQGDGKWMMSLHHRFVADSKDKPEVVFIGDSLVQLMHQCEIWRELFSPLHALNFGIGGDS
TQHVLWRLENGELEHIRPKIVVVVWGTNNHGHTAEQVTGGIKAIQLVNERQPQARVVVLGLLPRGQHPNPL
REKNRRVNELVRAALAGHPRAHFLADPGFVHSDGTISHHDMDYLHLSRLGYTPVCRALHSLLRLL
>d1fxwf_c.23.10.3 (F:) Platelet-activating factor acetylhydrolase {Cow (Bos taurus)}
SNPAAIPHAAEDIQGDDRWMSQHNRFVLDCKDKEPDVLFVGDSMVQLMQQYEIWRELFSPLHALNFGIGGD
TTRHVLWRLKNGELENIKPKVIVVVGTNNHENTAAEVAGGIEAIVQLINTRQPQAKIIVLGLLPRGKEKPPLRQ
KNAKVNLKVS LPKLANVQLLTDGGFVHSDGAISCHDMFDLHLTGGGYAKICKPLHEIMQLL
>d1k7ca_c.23.10.4 (A:) Rhamnogalacturonan acetylesterase {Fungus (Aspergillus aculeatus)}
TTVYLAGDSTMANKGGSGTNGWGEYLASYLSATVVNDAVAGRSARSYTREGRFENIADVVTAGDYVIVEFG
HNDGGSLSTDNGRTDCSGTGAEVCVSYDGVNETILTFPAYLENAAKLFTAKGAKVILSSQTPNNPWETGTFVN
SPTRFVEYAAEVAGVEYVDHWSYVDSIYETLGNAATVNSYFPIDHTHTSPAGAEVVAEFLKAVVCTGTSLK
VLTTTSFEGTCL
>d1iexa2 c.23.11.1 (A:389-603) Beta-D-glucan exohydrolase, C-terminal domain
{Barley (Hordeum vulgare)}
LVLLKNGKTSTDAPLLPLPKAKPILVAGSHADNLGYQCGGWTIEWQGDTGRTTVGTTILEAVKAADVDPSTVV
FAENPDAEFVKSGGFSYAIVAVGEHPYETKGDNLNLTIPEPGLSTVQAVCGVRCATVLISGRPVVVQPLLAAS
DALVAAWLPSEGQQVTDALFGDFGFTGRLPRTWFKSVDQLPMNVGDAHYDPLFRLGYGLTTNATK
>d2naca2 c.23.12.1 (A:1-147,A:336-374) Formate dehydrogenase {Pseudomonas sp., strain 101}
AKVLCVLYDDPVDGYPKTYARDDLPKIDHYPGGQTLPTKAIDFTPGQLLGSVSGELGLRKYLESNGHTLVT
KGDPDSVFERELVDADVVISQPFWPAYLPERIAKAKNLKLALTAGIGSDHVDLQSAIDRNVTVAEVTYCNSXTT
TAQARYAAGTREILECFEGRPIRDEYLIVQGGALA
>d1qp8a2 c.23.12.1 (A:1-82,A:264-302) Putative formate dehydrogenase {Archaeon Pyrobaculum aerophilum}
MELYVNFEPEAEEELRKYFKIVRGGLGNVEALSRITAELAKMPRLKFIQVVTAGLDHLPWESIPPHTVA
GNAGSNXGYGNERVWRQMVMMEA VRNLIYATGGRPRNIAKREDYIG
>d1dxy_2 c.23.12.1 (1-100,300-330) D-2-hydroxyisocaproate dehydrogenase
{Lactobacillus casei}
MKIIAYGARVDEIQYFKQWAKDTGNTLEYHTEFLDENTVEWAKGFDGINSLQTPYAAVGFEKMHAYGIKFLTIR
NVGTDNIDMTAMKQYGIRLSNPAYXTETAVHNMVYFSLQHLVDLTKGETSTEVTG

>d1gdha2 c.23.12.1 (A:2-100,A:292-321) D-glycerate dehydrogenase {*Hyphomicrobium methylovorum*}

KKKILITWPLPEAMARARESYDVIAGDDPKITIDEMIETAKSVDALLITNEKCRKEVIDRIPENIKCISTYSIGFD
HIDLDAACKARGIKVGNAPHGXATQAREDMAHQANDLIDALFGGADMYSALA

>d1psda2 c.23.12.1 (A:7-107,A:296-326) Phosphoglycerate dehydrogenase {*Escherichia coli*}

EKDKIKFLLVEGVHQKALESRLAAGYTNIEFHKGALDDEQLKESIRDAHFIGLRSRTHLTEDVINAEEKLVAIGCFI
GTNQVLDAAAKRGIPVFNAPFSXSTQEAQENIGLEVAGKLICKYSDNGSTLSAVN

>d2dlda2 c.23.12.1 (A:1-103,A:301-337) D-lactate dehydrogenase {*Lactobacillus helveticus*}

MTKVFAYAIRKDEEPFLNEWKEAHKDIDVDYTDKLLPETAKLAGADGVVVYQQLDYTADTLQALADAGVTK
MSLRNVGVVDNIDMDKAKELGFQITNPVVSXYTTHAVRNMVVKAFNNNLKLINGEKPDSPVALNKNKF

>d1pjca2 c.23.12.2 (A:1-135,A:304-361) L-alanine dehydrogenase {*Phormidium lapideum*}

MEIGVPKEIKNQEFRVGLPSSVRTLVEAGHTVFIETQAGIGAGFADQDYVQAGAQVVPSAKDAWSREMVVK
VKEPLPAEYDLMQKDQLLFTYLHAAARELTEQLMRVGLTIAYETVELPNRSLTPMSIIXPWTATQALNNS
TLPYVVKLANQGLKALETDDALAKGLNVQAHLRVHPAVQQVFPDLA

>d1f8ga2 c.23.12.2 (A:1-143,A:327-384) Nicotinamide nucleotide transhydrogenase dI component {*Rhodospirillum rubrum*}

MKIAIPKERRPGEDRVAISPEVVKLVGLGFEVIVEQGAGVGASITDDALTAAGATIASTAAQALSQADVWWKV
QRPMFTAEGTDEVALIKEGAVLMCHLGALTNRPVVEALTKRKITAYAMELMRPRISRAQSMDILSSQSNLXVAAD
ASPLFAKNLLNFLTPHVDKDTKTLVMKLEDETSGTCVTRDGAIVHPALTGQGA

>d1a7aa2 c.23.12.3 (A:2-189,A:353-432) S-adenosylhomocysteine hydrolase {Human (*Homo sapiens*)}

SDKLPYKVADIGLAAGRKALDIAENEMPGLMRMREMYASKPLKGARIAGCLHMTVETAVLIETLVLGAEVQ
WSSCNIFSTQNHAAAIAKAGIPVYAWKGETDEEYLWCIEQTLFKDGPLNMILDDGGDLTNLIHTKYPQLLPGI
RGISEETTGvhNLYKMMANGILKVPAINVNDSTVKSKFXHPSFVMSNSFTNQVMAQIELWTHPDKYPVGVH
FLPKKLDEAVAEAHLGKLNVKLTKEKQAQYLGMSCDGPFKPDPHYRY

>d1b3ra2 c.23.12.3 (A:4-189,A:353-431) S-adenosylhomocysteine hydrolase {Rat (*Rattus norvegicus*)}

LPYKVADIGLAAGRKALDIAENEMPGLMRMREMYASKPLKGARIAGCLHMTVETAVLIETLVALGAEVRWS
SCNIFSTQDHAAAIAKAGIPVFAWKGETDEEYLWCIEQTLHFKDGPLNMILDDGGDLTNLIHTKHPQLLSIRG
ISEETTGvhNLYKMMANGILKVPAINVNDSTVKSKFXHPSFVMSNSFTNQVMAQIELWTHPDKYPVGVHFLP
KKLDEAVAEAHLGKLNVKLTKEKQAQYLGMPINGPFKPDPHYRY

>d2dhqa_ c.23.13.1 (A:) Type II 3-dehydroquinate dehydratase {*Mycobacterium tuberculosis*}

LIVNVINGPNLGRLRREPavyggthDELVALIERAAELGLKAVVRQSDSEAQLLDWIHQAADAAEPVILNA
GGLTHTSVALRDACAELSAPLIEVHISNVHAREEFRRHSYLSPIATGVIVGLGIQGYLLALRYLAEH

>d1d0ia_ c.23.13.1 (A:) Type II 3-dehydroquinate dehydratase {*Streptomyces coelicolor*}

PRSLANAPIMLNGPNLNLLGQRQPEIYGSCTLADVEALCVAAAAHGGTVDFRQSNHEGELVDWIHEARLNH
CGIVINPAAYSHTSVAILDALNTCDGLPVVEVHISNIHQREPFRHHSYVSQRADGVVAGCGVQGYVFGVERIAAL
AG

>d1f8ya_ c.23.14.1 (A:) Nucleoside 2-deoxyribosyltransferase {*Lactobacillus leichmannii*}

PKKTIYFGAGWFTDRQNKAYPEALKENPTIDLENSYVPLDNQYKGIRVDEHPEYLHDKVWATATYNNDLN

GIKTNDIMLGVYIPDEEDVGLGMELGYALSQGKYVLLVIPDEDYGKPINLMSWGVSDNVIKMSQLKDFNFNKP
RFDFYEGAVY

>d1fjgb_c.23.15.1 (B:) Ribosomal protein S2 {Thermus thermophilus}

VKELLEAGVHFGHERKRWNPKFARYIYAERNGIHIIDLQKTMEEELERTFRFIEDLAMRGGTILFGTKKKQAAQDIV
RMEAERAGMPVNQRWLGGMLTNFKTISQRVHRLEELAFLAFASPEIEERPKEQVRLKHELERLQKLSGFRL
KRLPDAIFVVDPTEKAIAVREARKLFIPVIALADTDSDPDLDVYIIPGNDDAIRSIQLILSRAVDLIIQARGGVVEPSP
SYALVQEAE

>d1f2va_c.23.17.1 (A:) Precorrin-8x methylmutase {Pseudomonas denitrificans}

PEYDYIRDGNAYIERSFAIRAEADLSRFSEEADLAVERMVHACGSVEATRQVFSPDFVSSARAALKAGAPILCD
AEMVAHGVTRARLPAGNEVICTLRDPRTPALAAEIGNTRSAAALKLWSERLAGSVVAIGNAPTAFLLEMLRD
GAPKPAAILGMPVGFGVGAESKDALAENSYGVFAIVRGRLLGGSAMTAALNSLARPGL

>d1gpma2 c.23.16.1 (A:3-207) GMP synthetase {Escherichia coli}

ENIHKHRILILDGSQYTQLVARRVRELGVYCELWAADVTEAQIRDFNPSPGIILSGGPESTTEENSPRAPQYVFEA
GVPVFGVCYGMQTMAMQLGGHVEASNEREFGYAQVEVVNDALVRGIEDALTADGKPLLDVWMSHGDKVT
AIPSDFITVASTESCPFAIMANEKRFYGVQFHPEVTHRQGMRMLERFVRDICQCEAL

>d1a9xb2 c.23.16.1 (B:1653-1880) Carbamoyl phosphate synthetase, small subunit C-terminal
domain {Escherichia coli}

LNGMDLAKEVTTAEAYSWTQGSWLTGGLPQAKKEDELPHVVAWDFGAKRNILRMLVDRGCRLTIVPAQTSA
EDVLKMNPDGIFLSNGPGDPAPCDYAITAIQKFLTDIPVFGICLGHQLLALASGAKTVKMKFGHHGGNHPVKD
VEKNVVMITAQNHGFAVDEATLPANLRVTHKSLFDGTLQGIHRTDKPAFSFQGNPEASPGPHDAAPLFDHFIELI
EQYRKT

>d1qdlb_c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Archaeon Sulfolobus solfataricus}

MDLTIIDNYDSFVYNIAQIVGELGSYPVIRNDEISIKIERIDPDRLIISPGPGTPEKREDIGVSLDVICKYLGKRTPIL
GVCLGHQAIGYAFGAKIRRARKVFHGKISNIILVNNPLSLYYIAKEFKATRYHSLVVDEVHRPLIVDAISAEDNEI
MAIHHEEYPIYGVQFHPESVGTSGLYKILYNFLNRV

>d1i1qb_c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Salmonella typhimurium}

ADILLLDNIDSFTWNLADQLRTNGHNVVIYRNHIPAQLTLIDRLATMKNPVLMSPGPVSEAGCMPPELLTRLR
GKLPIIGICLGHQAIVEAYGGVGQAGEILHGKATSIEHDGQAMFAGLANPLPVARYHSLVGSNVPAGLTINAHF
NGMVMAVRHDADRVCQFQFHPESILTQGARLLEQTLAWAQKQ

>d1i7qb_c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Serratia marcescens}

ADILLLDNVDSFTYNLVQLRASGHQVVIYRNQIGAEVIIERLQHMEQPVLMLSPGPVSEAGCMPPELLQRLR
GQLPIIGICLGHQAIVEAYGGVGQAGEILHGKASAIAHDGEGMFAGMANPLPVARYHSLVGSNIPADLTNAR
FGEMVMAVRDDRRVCQFQFHPESILTTHGARLLEQTLAWALAK

>d1k9vf_c.23.16.1 (F:) GAT subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}

MRIGIISVGPGNIMNLYRGVKRASENFEDVSIELVESPRNDLYDLLFIPGVGHFEGMRRRENDLIDFVRKHVEDERYVVGVCLGMQLLFESEEAPGVKGSLIEGNVVKLRSSRLPHMGWNEIFKDTFPNGYYYFVHTYRAVCEE
EHVLGTTEYDGEIFPSAVRKGRILGFQFHPEKSSKIGRKLLKEVCSLSR

>d1jvna2_c.23.16.1 (A:-3-229) GAT subunit (or domain) of imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}

GSHMPVVHIDVESGNLQSLTNAIEHLGYEVQLVKSPKDFNISGTSRLILPGVGNYGHFDNLNRGFEKPIREYIESGKPIMGICVGLQALFAGSVESPCKSTGLNYIDFKLSRFDDSEKPVPEIGWNSCIPSENLFGLDPYKRYYFVHSFA
AILNSEKKKNLENDGWKIAKAKYGEFFIAAVNKNNIFATQFHPEKSGKAGLNVIENFLKQQSPPINPNSAAEELK

LMN

>d1g2ia_ c.23.16.2 (A:) Intracellular protease {Archaeon Pyrococcus horikoshii}

MKVLFLTANEFEDVELIYPYHRLKEEGHEVYIASFERGTTGKHGSVKVDLTFDKVNPEEFDALVLPGRAPERVR
RNNEKAVSIARKMFSEGKPVASICHGPQILISAGVLRGRKGTSYPIKDDMINAGVEWVDAEVVVDGNWVSSR
VPADLYAWMREFVKLLK

>d1cf9a1 c.23.16.3 (A:598-753) Catalase, C-terminal domain {Escherichia coli, HPII}
VKGRVVAILLNDEVRSADELLAILKALKAKGVHAKLLYSRMGEVTADDGTVLPIAATFAGAPSLTVDAIVPCGNIA
DIADNGDANYYLMEAYKHLKPIALAGDARKFKATIKIADQGEEGIVEADSADGSFMDELLTLMAAHRVWSRIPK
IDKIPA

>d1fyea_ c.23.16.4 (A:) Aspartyl dipeptidase PepE {Salmonella typhimurium}

MELLLLSNSTLPGKAWLEHALPLIANQLNGRRSAVFIPFAGVTQTWDEYTDKTAEVLA
PLGVNVNTGIHRVADPLAAIEKAIIIVGGGNTFQLLKESRERGLLAPMADRVKRGALYIGWSAGANLACPTIRTTNDMPIVDPNGFDALDL
FPLQINPHFTNALPEGHKGETREQRIRELLVVAPELTVIGLPEGNWIQVSNGQAVLGGPNTTWVFKAGEEaval
EAGHRF

>d1a9xa2 c.24.1.1 (A:936-1073) Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain {Escherichia coli}

NSTMKKHGRALLSVREGDKERVVDLAAKLLQGFELDATHGTAIVLGEAGINPRLVNKVHEGRPHIQDRIKN
GYTYIINTTSGRRAIEDSRVIRRSLAQYKVHYDTTLNGGFATAMALNADATEKVISVQEMHAQIK

>d1b93a_ c.24.1.2 (A:) Methylglyoxal synthase, MgsA {Escherichia coli}

MELTTRTPARKHIALVAHDHCKQMLMSWVERHQPLLEQHVLYATGTTGNLISRATGMNVNAMLSGPMGGD
QQVGALISEGKIDVLIFFWDPLNAVPHDPDVKALLRLATVWNIPVATNVATADFIIQSPHFNDAVDILIPDYQRYL
A

>d1g8ma1 c.24.1.3 (A:4-200) IMP cyclohydrolase domain of bifunctional purine biosynthesis enzyme ATIC {Chicken (Gallus gallus)}

RQQLALLSVSEKAGLVEFARSLNALGLGLIASGGTATALRDAGLPVRDVSDLTGFPEMLGGRVKTLHPAVHAGIL
ARNIPEDNADMNKQDFSLRVVVVCNLYPFVKTSSPGVTVP
EA
VEKIDIGG
V
ALLRAAKNHARVTVVCDPAD
YSSVAKEMAASKDKDTSVETRRHLALKAFTH
TAQYD
AAISDYFRKEYSK

>d1fnc_2 c.25.1.1 (155-314) Ferredoxin reductase (flavodoxin reductase) {Spinach (Spinacia oleracea)}

MLMPKD
PNATIIMLG
TGTGIA
PFRSFLW
KMFFEK
HDDYKF
NGLA
WLFLGV
PTSS
LLYKEEF
KMKE
KAPDN
F
LDFAV
SREQT
NEKGE
KMYIQ
TRMAQ
YAEEL
W
EMLKK
DNTV
YMCGL
KGME
KGIDD
IMV
SLAA
EGID
WIEY
RQLK
KAEQ
WN
VEVY

>d1qfza2 c.25.1.1 (A:154-308) Ferredoxin reductase (flavodoxin reductase) {Garden pea (Pisum sativum)}

DPNATVIMLG
TGTGIA
PFRSFLW
KMFFEK
HDDYKF
NGLA
WLFLGV
PTSS
LLYKEEF
KMKE
KAPEN
F
RLDFAV
REQV
NDK
GEK
KMYIQ
TRMAQ
YAEEL
WELL
KKDNTF
V
YMCGL
KGME
KGIDD
IMV
SLAA
KGID
WIEY
KRTL
KKA
EQWN
VEVS

>d1fb3a2 c.25.1.1 (A:208-362) Ferredoxin reductase (flavodoxin reductase) {Paprika (Capsicum annuum)}

DPNATVIMLG
TGTGIA
PFRSFLW
KMFFEK
HDDYKF
NGLA
WLFLGV
PTSS
LLYKEEF
KMKE
KAPEN
F
RLDFAV
REQT
NEK
GEK
KMYIQ
TRMAQ
YAEEL
WTLL
KKDNTF
V
YMCGL
KGME
KGIDD
IMV
SSLAA
KEGID
WADY
KKQL
KK
AEQWN
VEVY

>d1gawa2 c.25.1.1 (A:157-314) Ferredoxin reductase (flavodoxin reductase) {Maize (Zea mays), leaf isoform}

MPKDPNATIIMLATGTGIAPFRSFLWKMFFEKHDDYKFNGLGLGVPTSSLLYKEFGKMKERAPENFRVD
YAVSREQTNAAGERMYIQTRMAEYKEELWELLKKDNTYVYMCGLKGMEKGIDDIMVSLAEKDGDIDWFDFYKKQ
LKRGDQWNVEVY
>d1jb9a2 c.25.1.1 (A:163-316) Ferredoxin reductase (flavodoxin reductase) {Maize (*Zea mays*), root isoform}
DPNATHIMIATGTGVAPFRGYLRRMFMEDVPNYRFGGLAWLFLGVANSDSLDEEFTSYLKQYPDNFRYDKAL
SREQKNRSGGKMYVQDKIEEYSDEFKLLDGGAHIFYCGLKGMMPGIQDTLKKVAERRGESWDQKLAQLKKN
KQWHVEVY
>d1que_2 c.25.1.1 (142-303) Ferredoxin reductase (flavodoxin reductase)
{Cyanobacterium (*Anabaena* sp.), pcc 7119}
LPDDPEANVIMLATGTGIAPMRTYLWRMFKAERAANPEYQFKGFSWLFGVPTTPNILYKEELEEIQQKYPD
NFRLTYAISREQKNPQGGRMYIQDRVAEHADQLWQLIKNQKTHTYICGLRGMEEGIDAALSAAAEGVTWS
DYQKDLKKAGRWHVETY
>d1fdr_2 c.25.1.1 (101-248) Ferredoxin reductase (flavodoxin reductase) {Escherichia coli}
DEVPHCETLWMLATGTIAIGPYLSILRLGKDLRFKNLVLVHAARYAADLSYPLMQELEKRYEGKLRIQTVVSRRET
AAGSLTGRIPALIESGELESTIGLPMNKETSHVMLCGNPQMVRDTQQLKETRQMTKHLRRRPGHMTAEHYW
>d1a8p_2 c.25.1.1 (101-258) Ferredoxin reductase (flavodoxin reductase) {Azotobacter vinelandii}
TSDLLPGKHLYMLSTGTGLAPFMSLIQDPEVYERFEKVVLIHGVRQVNELAYQQFITEHLPQSEYFGEAVKEKLIY
YPTVTRESFHQNQGRLTLMRSGKLFEDIGLPPINPQDDRAMICGSPSMLDESCEVLDGFLKISPRMGEPGDYL
IERAFVEK
>d1qfja2 c.25.1.1 (A:98-232) NAD(P)H:flavin oxidoreductase {Escherichia coli}
RDDEERPMILIAGGTGFSYARSILLTALARNPNRDITIYWGGREEQHLYDLCEALEALSKHPGLQVVPVVEQPEAG
WRGRTGTVLAVLQDHGTAEHDIVIAGRFE MAKIARDLFCSERNAREDRLFDAFAFI
>d2cnd_2 c.25.1.1 (125-270) Nitrate reductase {Corn (*Zea mays*)}
GSFVINGKQRNARRLAMICGGSGITPMYQIIQAVLRDQPEDHTEMHLVYANRTEDDILLRDELRWAAEYPDR
LKVWYVIDQVKRPEEGWKYSVGFVTEAVLREHVPEGDDTLALACGPPPMIQFAISPNEKMKYDMANSFVV
F
>d1ndh_2 c.25.1.1 (126-272) cytochrome b5 reductase {Pig (*Sus scrofa*), liver}
GKFAIRPDKKSSPVIKTVKSVGMIAGGTGITPMQLQVIRAIMKDPDDHTVCHLLFANQTEKDILLRPELEELRNEHS
ARFKLWYTVDRAPEAWDYSQGFVNEEMIRDHLPPPSEEPLVMCGPPPMIQYACLPNLERVGHPKERCAF
>d1i7pa2 c.25.1.1 (A:154-300) cytochrome b5 reductase {Rat (*Rattus norvegicus*)}
GKFAIRADKKSNPVVRTVKSVGMIAGGTGITPMQLQVIRAVLKDPNDHTVCYLLFANQSEKDILLRPELEELRNEH
SSRFKLWYTVDKAPDAWDYSQGFVNEEMIRDHLPPPGEETLILMCGPPPMIQFACLPNLERVGHPKERCTF
>d2pia_2 c.25.1.2 (104-223) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}
EFPLDKRAKSFILVAGGIGITPMILSMARQLRAEGLRSFRLYYLTRDPEGTAFFDELTSDEWRSDVKIHHGDPTK
AFDFWSVFEKS KPAQHVYCCGPQALMDTVRDMTGHWPSGTVF
>d1ep3b2 c.25.1.3 (B:103-262) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}
PVAEVSTDKILIIGGGIGVPPYLEAKQLEKTGCQMTILLGFAENVKILENEFSNLKNVTLKIATDDGSYGTGHV
GMLMNEIDFEVDA LYTCGAPAMLKAVAKKYDQLERLYISMESRMACGIGACYACVEHDKEDESHALKVCEDGP
VFLGKQLSL

>d1ja1a3 c.25.1.4 (A:519-678) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}
RLPFKSTTPVIMVGPGTGIAPFMGFIQERAWLREQGKEVGETLLYYGCRRSDEDYLYREELARFHKGALTQLN
VAFSREQAHKVYVQHLLKRDRHEHLWKLIHEGGAHIYVAGDARNMAKDVTQNTFYDIVAEFGPMEHTQAVDYY
KKLMTKGRYSLNVWS

>d1ddga2 c.25.1.4 (A:447-599) Sulfite reductase flavoprotein {Escherichia coli}
LPANPETPVIMIGPGTGIAPFRAFMQQRAADEAPGKNWLFFGNPHFTEDFLYQEWQRYVKEGVLTRIDLAW
SRDQKEKVYVQDKLREQGAELWRWINDGAHIYVCGDANRMAKDVEQALLEVIAEFGGMDEAADEFLSEL
VERRYQRDVY

>d1f20a2 c.25.1.4 (A:1233-1397) Neuronal nitric-oxide synthase FAD/NADP+ domain
{Rat (Rattus norvegicus)}
SFHLPRNPQVPCILVGPGTGIAPFRSFWQQRQFDIQHKGMNPCMVLVFGCRQSKIDHIYREETLQAKNKGVF
RELYTAYSREPDRPKYVQDVLQEQLAESVYRALKEQGGHIYVCGDVTMAADVLKAIQRIMTQQGKLSEEDAG
VFISRLRDDNRHYHEDIFGV

>d1cqxa3 c.25.1.5 (A:262-403) Flavohemoglobin, C-terminal domain {Alcaligenes eutrophus}
DVDAKTPIVLISGGVGLTPMVSMLKVALQAPPRQVFVHGARNSAHAMRDRRLREAAKYENLDLFVFYDQP
LPEDVQGRDYDYPGLVDVKQIEKSILLPDADYYICGPIPFMRMQHDALKNLGIHEARIHYEVFGPDLFAE

>d4ts1a_c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Bacillus stearothermophilus, nca 1503}
MDLLAELQWGRGLVNQTTDEDGLRKLNEERVTLYCGFDPTADSLHIGHLATITMRRFQQAGHRPIALVGGATG
LIGDPSGKKSERTLNAKETVEAWSARIKEQLGRFLDFEADGNPAKKNNDWIGPLDVITFLRDVGKHFSVNYM
MAKESVQSRIETGISFTFSYMMIQLQAYDFRLYETEGCRLQIGGSDQWGNITAGLELIRKTGEARAFGLTIPLVT
KADGTKFGKTESGTIWLDKEKTSPYEFYQFWINTDDRDVIRYLKYFTFLSKEEEIALEQELREAPEKRAAQKTLAE
EVTKLVHGEEALRQAIRYA

>d1jila_c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Staphylococcus aureus}
TNVLIEDLKWRGLIYQQTDEQGIEDLLNEEQVTLYCGADPTADSLHIGHLLPFLTLRRFQEHHGRPIVLIGGGTG
MIGDPSGKSEERVLQTEEQVDKNIEGISKQMHNIFEFGTDHGAVLVNNRDWLQISLISFLRDYGKHVGVNYM
LGKDSIQSRLEHGISYTEFTYTILQAIDFGHLNRELNCIQVGGSDQWGNITSGIELMRRMYGQTDAYGLTIPLVT
KSDGKKFGKSESGAVWLDAEKTPYEFYQFWINQSDEDIKFLKYFTFLGKEEIDRLEQSNEAPHLREAQKTLAE
EEVTKFIHGEGDALNDAIRISQALF

>d1i6la_c.26.1.1 (A:) Tryptophanyl-tRNA synthetase (TrpRS) {Bacillus stearothermophilus}
MKTIFSGIQPSGVITIGNYIGALRQFVELQHEYNCYFCIVDQHAITVVWQDPHELQNIRRLLAALYLAvgIDPTQAT
LFIQSEVPAHAQAAWMLQCIYIGELERMQTQFKEKSAGKEAVSAGLLTYPPLMAADILLYNTDIVPGEDQKQHI
ELTRDLAERFNKRYGELFTIPEARIPKVGARIMSLDPTKKMSKSDPNPKAYITLDDAKTIEKKIKSAVTDSEGTIR
YDKEAKPGISNLLNIYSTLSGQSIEELERQYEGKGYGVFKADLAQVVIETRPIQERYHHWMESEELDRVLDGAE
KANRVASEMVRKMEQAMGLR

>d1gtra2 c.26.1.1 (A:8-338) Glutaminyl-tRNA synthetase (GlnRS) {Escherichia coli}
TNFIRQIIDEDLASGKHTTVHTRFPPEPNGYLHIGHAKSICLNFGIAQDYKGQCNLRDDTNPVKEDIEYVESIKN
DVEWLGFHWSGNVRYSSDYFDQLHAYAIELINKGLAYVDELTPEQIREYRGTLTQPGKNSPYRDRSVEENLALFE
KMRAGGFEEGKA CLR KID MAS PFI VM RD P V LY R I K F A E H H Q T G N K W C I Y P M Y D F T H C I S D A L E G I T H S L C T L E
F Q D N R R L Y D W V L D N I T I P V H P R Q Y E F S R L N L E Y T V M S K R K L N L L V T D K H V E G W D D P R M P T I S G L R R G Y T A A S I
R E F C K R I G V T K Q D N T I E M A S L E S C I R E D L N E N

>d1gln_2 c.26.1.1 (1-305) Glutamyl-tRNA synthetase (GlRS) {Thermus thermophilus}
MVVTRIAPSPTGDPHVGTYIALFNYAWARRNGGRFIVRIEDTDRARYVPGAEERILAALKWLGLSYDEGPDVA
APTGPYRQSERLPLYQKYAEELLKRGWAYRAFETPEELEQIRKEKGGYDGRARNIPPEEAERARRGEPHVIRLKV

PRPGTTEVKDELRGVVYDNQEIPDVVLLKSDGYPTYHLANVDDHLMGVTDVIRAEELVSTPIHVLLYRAFG
WEAPRFYHMPLLNPDKTKISKRKSHTSLDWYKAEGFLPEALRNYLCLMGFSMPDGREIFTLEEFIQAFTWERV
SLGGPVF

>d1a8h_2 c.26.1.1 (1-348) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}
MEKVFYVTPPIYYVNAEPLHLGHAYTTVADFLARWHRLDGYRTFFLTGTDEHGETVYRAAQAAGEDPKAFVDR
VSGRFKRAWDLLGIAYDDFIRTTEERHKVVQLVLKKVYEAGDIYYGEYEGLYCVSCERYTEKELVEGLCPIHGRP
VERRKEGNYFFRMEKYRPWLQEYIQENPDLIRPEGYRNEVLAELAEPIDLSISRPKSRVPWGIPLPWDENHV
TYVWFDAALLNYVSALDYPEGEAYRTFWPHAWHLIGKDILKPHAVFWPTMLKAAGIPMYRHLNVGGFLGPDG
RKMSKTLGNVVDPFALLEKYGRDALRYLLREIPIYGQDTPVSEEALRTRYEAD

>d1f4la2 c.26.1.1 (A:4-140,A:176-388) Methionyl-tRNA synthetase (MetRS) {Escherichia coli}

AKKILVTCALPYANGSIHLGHMLEHIQADVWVRYQRMRGHEVNFCADDAGTPIMLKAQQQLGITPEQMIGE
MSQEHQTDAGFNISYDNYHSTHSEENRQLSELIYSRLKENGFIKNRTISQLYDPEKGMLPDRFXVSGATPV
MRDSEHFFFDLPSFSEMLQAWTRSGALQEQQVANKMQEWFESGLQQWDISRDAPYFGFEIPNAPGKYFYVWL
DAPIGYMGSKNLCDKRGDSVFDEYWKKDSTAELYHFIGKDIVFHSFWPAMLEGNSFRKPSNLFVHGTVT
NGAKMSKSRGTFIKASTWLNFADSLRYYTAKLSSRIDDIDLNLEDVFQRVNADIVNK

>d1ile_3 c.26.1.1 (1-197,387-641) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}
MFKEVGEPNFPKLEEVLAFWKREKIFQKSVENRKGGPRYTVEGPPANTLPHVGHAQARSYKDLFPRYKTM
RGYYAPRRAGWDTHGLPVELEVEKKLGLSKREIEAYGIERFNQACRESVFTYEKEWEAFTERIAYWVDLEDAYA
TLEPTYIESIWWSLKNLFDRGLLYRDHKVVPYCPRCGTPSSHEVALGYXPHCWCSTPLMYYATESWFIKNTLF
KDELIRNNQEIHWPVPHIKEGRYGEWLKNLVDWALSRNRYWTPLPIWVCQACGKEEAIGSFQELKARATKPL
PEPFDPHRPYVDQVELACACGGTMRRVPYIDVWYDSGAMPFASLHYPFEHEEVFRESFPADFIAEGIDQTRG
WFNSLHQLGVMLFGSIAFKNVICHGLILDEKGQKMSKSGNVVDPWDIIRKFGADALRWYIYVSAPPEADRRF
GPNLVRETVD

>d1ffya3 c.26.1.1 (A:1-200,A:395-644) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

MDYEKTLLMPKTDFPMRGGLPNKEPQIQEKWDAEDQYHKALEKNKGNETFILHDGPPYANGNLHMGHALN
KILKDFIVRYKTMQGFYAPYVPGWDTHGLPIEQALTGGVDRKKMSTAEOFRECKCEFALEQIELQKKDFRRLGVR
GDFNDPYITLKPEYEAAQIRIFGEMADKGLIYKGKKPVWSPSSESSLAEAEIEYXPHDWRTKPVIFRATPQWF
ASISKVRQDILDAIENTNFKNVNGKTRIYNMVRDRGEWVISRQRVWGVPLPVFAENGEIIMTKETVNHVADL
FAEHGSNIWFEREAKDLLPEGFTHPGSPNGTFTKETDIMDVWFDSSHRGVLETRPELSFPADMYLEGSDQY
RGWFNSSITTSVATRVSPYKFLLSHGFVMDGEGKKMSKSLGNIVPDQVVQKGADIARLWVSVSTDYLADVR
ISDEILKQTSD

>d1gaxa3 c.26.1.1 (A:1-189,A:343-578) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}
MDLPKAYDPKSVEPKWAEKWAKNPVANPKSGKPPVIFMPPPNVTGSLHMGHALDNLQDALIRYKRMRG
FEAVWLPGTDHAGIATQVVERLLLKEGKTRHDLGREKFLERVWQWKEESGGTILKQLKRLGASADWSREAFT
MDEKRSRAVRYAFSRYYHEGLAYRAPRLVNWCPRCETTLSLEVEXTCSRGTPIEYAIFPQWWLRMRPLAEEV
LKGLRRGDIASFPERWKKVNMDWLENVKDWNISRQLWWGHQIPAWEYCEDCQAVNPRPERYLEDPTSCEA
CGSPRLKRDEDVFDTWFSSALWPLSTLGWPEETEDLKAFYPGDVLTGYDILFLWVSRMEVSGYHFMGERPFF
TVLLHGLVLDEKGQKMSKSGNVIDPLEMVERYGADALRFALIYLATGGQDIRLDLRWLEMARNF

>d1f7ua2 c.26.1.1 (A:136-483) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast (Saccharomyces cerevisiae)}

SCKLVENKKVIIEFSSPNIAKPFHAGHLRSTIIGGFLANLYEKLGVWVIRMNYLGDWKGQFGLLAVGFERYGNEEA
LVKDPIHHLFDVYVIRNKDIEEGDSIPLEQSTNGKAREYFKRMEDGDEEALKIWKRFREFSIEKYIDTYARLNKY

DVYSGESQVSKEMLKAIDLKEKGLTHEDKGAVLIDLTKFNKKLGKAIVQKSDGTTLYLTRDVGAAAMDREKYH
FDKMIYVIASQQDLHAAQFFEILKQMGFEWAKDLQHVNFQMVQGMSTRKGTVVFLDNILEETKEKMHEVM
KKNENKYAQIEHPEEVADLVGISAVMIQDMQGKRINNYEFKWERMLSFEG

>d1iq0a2 c.26.1.1 (A:97-466) Arginyl-tRNA synthetase (ArgRS) {Thermus thermophilus}
PFPRRPGVLVEHTSVNPNKELHVGHRLNIALGDAIRALAYAGREVLVLNYIDDTGRQAAETLFALRHGYGLTWD
GKEKYDHFAGRAYVRLHQDPEYERLQPAIEEVHLALERGELREEVRILLAQMATMHALNARYDLLWESDIVR
AGLLQKALALLEQSPHVFVFRPREGKYAGALVMDASPVIPGLEDPFFVLLRSNGTATYYAKDIAFQFWKMGILEGLR
FRPYENPPYPLRTSAPEGEAYTPKAEEETINVVDVRQSHPQALVRAALALAGYPALAEKAHHLAYETVLEGRQ
MSGRKGLAVSVDEVLEATRRARAIVEEKNPDPKEEAARMVALGAIRFSMVKTEPKQIDFRYQEALSFE

>d1coza_c.26.1.2 (A:) CTP:glycerol-3-phosphate cytidylyltransferase {Bacillus subtilis}
MKKVITYGTFDLLHWGHIKLLERAKQLGDYLVAISTDEFNLQKQKKAYHSYEHRLILETIRYVDEVIPEKNWEQ
KKQDIIDHNIDVFVFMGDDWEGKDFLKDQCEVVYLPRTATEGISTTKIKEEI

>d1qjca_c.26.1.3 (A:) Phosphopantetheine adenylyltransferase {Escherichia coli}
KRAIYPGTFDPITNGHIDIVTRATQMFDHVILAIAASPSKKPMFTLEERVALAQQATAHGNVEVVGFSDLMAN
FARNQHATVLIRGLRAVADFEYEMQLAHMNRLMPELESVFLMPSKEWSFISSLVKEVARHQGDVTHFLPEN
VHQALMAKLA

>d1f9aa_c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase
{Archaeon Methanococcus jannaschii}
LRGFIIGRFQPFHKGHLEVKKIAEEVDEIIIGIGSAQKSHTLENPFTAGERILMITQSLKDYLTYYPIPIKIEFNSI
WVSYVESLTPPDIVYSGNPLVRLFEERGYEVKRPEMFNRKEYSGTEIRRRMLNGEKWEHLVPKAVVDVIKEIK
GVERLRKLA

>d1ej2a_c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase
{Archaeon Methanobacterium thermoautotrophicum}
MRGLLVGRMQPFRHGHLQVIKSILEEVDELIICIGSAQLSHSIRDPTAGERVMMLTKALSENGIPASRYYIIPVQ
DIECNALWVGHIKMLTPFDRVYSGNPLVQRLFSEDGYEVTAAPLFYDRYSGTEVRRRMLDDGDWRSLLPES
VVEVIDEINGVERIKHLA

>d1ihoa_c.26.1.4 (A:) Pantothenate synthetase (Pantoate-beta-alanine ligase, PanC) {Escherichia coli}
MLIIETLPLRQQIRRLRMEGKRVVALVPTMGNLHDGHMKLVDEAKARADVVSIFVNPMQFDRPEDLARYP
RTLQEDCEKLNKRKVDLVFAPSVEIYPNGTETHTYVDVPGSTMLEGASRPGHFRGVSTIVSKLFNLVQPDIACF
GEKDFQQLALIRKMVADMGF DIEIVGVPIRMRAKDGALSSRNGYLAEQRKIAPGLYKVSSIADKLQAGERDLD
IIITIAGQELNEKGFRADDIQIRDADTLLEVSETSKRAVILVAAWLGDARLIDNKMVEL

>d1g8fa2 c.26.1.5 (A:169-389) ATP sulfurylase central domain {Baker's yeast (Saccharomyces cerevisiae)}

YPGLRKTPAQLRLEFQSRQWDRVVAFQTRNPMHRAHRELTVAAREANAKVLIHPVVLTKPGDIDHHTRVR
VYQEIIKRYPNIGIAFLSSLPLAMRMSGDREA VWHAI RKNY GASHFIVGRDHAGPGKNSKGVDYGPYDAQELV
ESYKHELDIEVVPFRMVTYLPDEDRYAPIDQIDTTKTRTLNISGTTELRRRLRGGEIPEWFSYPEVKILRESNP

>d1i2da2 c.26.1.5 (A:171-390) ATP sulfurylase central domain {Fungus (Penicillium chrysogenum)}

YVALRYTPAELRVHFDKLGWSRVVAFQTRNPMHRAHRELTVAARSRQANVLIHPVVLTKPGDIDHFTRVRA
YQALLPRYPNGMAVLGLGLAMRMGGPREAIWHAIIRKNHGATHFIVGRDHAGPGNSKGEDFYGPYDAQH
AVEKYKDELGIEVVEFQMVTYLPDTDEYRPVDQVPAGVKT LNISGTTELRRRLRSGAHIPEWFSYPEVKILRESNP
P

>d1jhda2 c.26.1.5 (A:174-396) ATP sulfurylase central domain {unnamed symbiont of Riftia}

pachyptila}

PDTFRTAVEIRNEIKEHGWSKVVAFQTRNPMHRAHEELCRMAMESLDADGVVHMLLGKLKGDIAPVRDA
AIRTMAGEVYFPPTNTVMVTGYGFDMLYAGPAREAVLHAYFRQNMGATHFIIGRDHAGVGDYYGAFDAQTIFDDE
VPEGAMEIEIFRADHTAYSKKLNKIVMMRDVPDHTKEDFVLLSGTKVREMLGQGIAPPPEFSRPEVAKILMDYY
QSINS

>d1gpm1 c.26.2.1 (A:208-404) GMP synthetase, central domain {Escherichia coli}
WTPAKIDDAVARIREQVGDDKVLGLSGGVDSVTAMLLHRAIGKNLTCVFVDNGLLRLNEAEQVLDMDFGDHF
GLNIVHVPAEDRFLSALAGENDPEAKRKIIGRVFVEVFDEEALKLEDVKWLAQGTIYPDVIESAASATGKAHVIKS
HHNVGGLPKEMKMGVEPLKELFKDEVRKIGLELGLPYDMLYRHPFP

>d1ih8a_ c.26.2.1 (A:) NH3-dependent NAD+-synthetase {Bacillus subtilis}
SMQEKIMRELHVVKPSIDPKQEIEDRVNFLKQYVKKTGAKGFVLGISGGQDSTLAGRLAQLAVESIREEGGDAQFI
AVRLPHGTQQDEDADAQLALKFIKPDKSWKFDIKSTVSAFSDQQYQQETGDQLTDFNKGNVKARTRMIAQYAI
QEGLLVLGTDHAAEAVTGFITKYGDGGADLLPLTGLTKRGRTLLKELGAPERLYLKEPTADLLDEKPQQSDETEL
GISYDEIDDYLEGKEVSAKVSEALEKRYSMTEHKRQVPASMFDWWK

>d1ct9a1 c.26.2.1 (A:193-516) Asparagine synthetase B, C-terminal domain {Escherichia coli}
RDWFODYDAVKDNVTDKNELRQALEDVKSHLMSDVPYGVLSSGGLDSSIISAITKKYAARRVEDQERSEAWWP
QLHSFAVGLPGSPDLKAAQEVAHLGTVHHEIHTVQEGLDAIRDVIYHIETYDVTTIRASTPMYLMRSRKIKAM
GIKMVLSGEGSDEVFGGYLYFKAPNAKELEHEETVRKLLAHMYDCARANKAMSAGVVEARVPFLDKKFLDV
AMRINPQDKMCNGKMEKHILRECFAYLPSAVWRQKEQFSDGVGYSWIDLKEVAAQQVSDQQLETARF
RFPYNTPTSKEAUYLYREIFEELFPLPSAACVPG

>d1jgta1 c.26.2.1 (A:210-508) beta-Lactam synthetase {Streptomyces clavuligerus}
PGLSRRILPEGEAVAAVRAALEKAVAQRVTPGDTPLVLSGGIDSSGVAACAHRAAGELTVSMGTDTSNEFRE
ARAVVDHLRTRHREITIPTTELLAQLPYAVWASESVDPDIYEYLLPLTALYRALDGPERILTGYGADIPLGGMHRE
DRLPALDTVLAHDMATFDGLNEMSPVLSLAGHWTHPYWDREVLDLLSLEAGLKRHHGRDKWVLRAAMA
DALPAETVNRPKLGVHEGSGTSSFSRLLLHGVAEDRVHEAKRQVVREFDLTVGGGRHPSEVDTDVVRSV
ADRT

>d1k92a1 c.26.2.1 (A:1-188) Argininosuccinate synthetase, N-terminal domain {Escherichia coli}
TTILKHPVGQRIGIAFSGGLDTSAALLWMRQKGAVPYAYTANLGQPDEEDYDAIPRRAMEYGAENARLIDCRK
QLVAEGIAAIQCGAFHNTTGGTYFNTTPLGRAVTGMLVAAMKEDGVNIWGDGSTYKNDIERFYRYGLTN
AELQIYKPWLTDIFDELGGRHEMSEFMIACGFDYKMSVEK

>d1sur__ c.26.2.2 (-) Phosphoadenylyl sulphate (PAPS) reductase {Escherichia coli}
SKLDLNALNELPKVDRILALAETNAELEKLDAGRAWAALDNLPGEYVLSSSGIQAASLHLVNQIRPDIPVILTD
TGYLFPETYRFIDELETDKLKLNLKVYRATESAAWQEARYGKLWEQGVIEKYNDINKVEPMNRALKELNAQTW
FAGLRREQSGSRANLPVLAIRQVFKVLPIDIWDNRTIYQYLQKHGLKYHPLWDEGYLSVGDT

>d1dlja3 c.26.3.1 (A:295-402) UDP-glucose dehydrogenase (UDPGDH), C-terminal (UDP-binding)
domain {Streptococcus pyogenes}

AKQIINVLKEQESPVKVVGVYRLIMKSNSDNFRESAIKDVIDILSKDKIYEPMLNKLESEDQSVLVNDLENFKK
QANIIVTNRYDNELQDVKNKVYSRDIIFGRD

>d2tpt_2 c.27.1.1 (71-335) Thymidine phosphorylase {Escherichia coli}
DWKSLHLNGPIVDKHSTGGVGDVTSMLGPMVAACGGYIPMISGRGLGHTGGTLKLESIPGFDIFPDDNRFR
EIIKDVGVAIIGQTSSLAPADKRFYATRDITATVDSIPLITASILAKKLAEGLDALVMDVKVGSGAFMPTYELSEALAE
AIVGVANGAGVRTTALLDMNQVLASSAGNAVREAVQFLTGEYRNPRLFVDVTMALCVELISGKLAKDDAE
ARAKLQAVLDNGKAAEVFGRMVAAQKGPTDFVENYAKYLP

>d1brwa2 c.27.1.1 (A:71-330) Pyrimidine nucleoside phosphorylase {Bacillus stearothermophilus}

LSSIRGVVKDKHSTGGVGDTTTLVLGPLVASGVVPVAKMSGRGLGHTGGTIDKLESVPGFHVIEISKDEFIRLVNE
NGIAIIGQTGDLTPADKKLYALRDTATVNSIPLIASSIMSKIAAGADAIVLDVKTGAGAFMKKLDEARRLARVM
VDIGKRVGRRTMAVISDMSQLGYAVGNALEVKEAIETLKGNPQHDLTELCLTGSVMVYLAEKAPSLEARRL
LEEAIRSGAAIAAFKTFLAAQGGDASVVDDLDKLP

>d1dnpa2 c.28.1.1 (A:1-200) N-terminal domain of DNA photolyase {Escherichia coli}
TTHLVWFRQDLRLHDNLALAAACRNSSARVLALYIATPRQWATHNMSPRQAEELINAQLNGLQIALAEKGIPLLF
REVDDFVASVEIVKQVCAENSVTHLFYNYQYEVNERARDVEVERALRNVVCEGFDDSVILPPGAVMTGNHEM
YKVFTPFKNAWLKRLREGMPECVAAPKVRSSGSIEPSPSITNYPRQSFDTAHF

>d1iqlra2 c.28.1.1 (A:2-171) N-terminal domain of DNA photolyase {Thermus thermophilus}
GPLLVWHRGDLRLHDHPALLEALARGPVVGLVLDPPNNLKTPRRRAWFLENVRALREAYRARGGALWVLEG
LPWEKVPEAARRLKAKAVYALTSHPYGRYRDGRVREALPVPLHLLPAPHLLPPDLPRAYRVYTPFSRLYRGAAPP
LPPPEALPKGPEEGEIPREDPG

>d1qnf_2 c.28.1.1 (1-204) N-terminal domain of DNA photolyase {Anacystis nidulans}
MAAPIFWHRRDLRLSDNIGLAAARAQSAQLIGLFCCLDPQILQSADMAPARVAYLQGCLQELQQRYQQAGSRL
LLLQGDQPQHLPQLAQQLQAEAVYWNQDIEPYGRDRDGQVAALKTAGIRAVQLWDQLLHSPDQILSGSGNP
YSVYGPFWKNWQAQPKPTPVATPTELVDSLPEQLTIAPIPLLSELPTLKQLGFDWDGGF

>d1efva1 c.29.1.1 (A:20-207) Electron transfer flavoprotein, ETPF {Human (Homo sapiens)}
QSTLVIAEHANDSLAPITLNTITAATRLGGEVSCLVAGTKCDKVAQDLCKVAGIAKVLVAQHDVYKGLPEELTPLIL
ATQKQFNYTHICAGASAFGKNLLPRVAAKLEVAPISDIIAIKSPDTFVRTIYAGNALCTVKCDEKVVFVSRGTSFD
AAATSGGSASSEKASSTSPVEISEWLDQKLTKS

>d1efvb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETPF {Human (Homo sapiens)}
LRLVAVKRVVIDYAVKIRVKPDRTGVTDGVKHSMPCEIAVEEAVRLKEKKLVKEVIAVSCGPAQCQETIRTAL
AMGADRGIHVEVPPAEAERLGPLQVARVLAKLAEKEKVDLVLGGKQAIDDCNQTGQMTAGFLDWQPGTFAS
QVTLEGDKLKVEREIDGGLETRLKLPAVVTADLRLNEPRYATLPNIMKAKKKIEVIKPGDLGVDLTSKLSVISVED
PPQRTAGVKVETTEDLVALKEIGRI

>d1efpa1 c.29.1.1 (A:2-184) Electron transfer flavoprotein, ETPF {Paracoccus denitrificans}
AVLLLGEVTNGALNRDATAKAVA AVKALGDVTVCAGASA KAAAEEAAKIAGVAKVLVAEDALYGHRLAEP TAA
LIVLAGDYSHIAAPATTDAKNVMPRVA ALLDMVLSDVAILDADTFERPIYAGNAIQVVKS KDAKKVFTIRTAS
FDAAGEGGTAPVTETAAADPGLSSWVADEVAE

>d1efpb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETPF {Paracoccus denitrificans}
MKVLVPVKRLIDYNVKARVKSDGSGVDLANVKMSMNPDEIAVEEAIRLKEKGQAEIIAVSIGVKQAAETLRTA
LAMGADRAILVVAADDVQQDIEPLAVAKILA AVARAEGTELIIAGKQAI DNDMNATGQMLA ILGWQA QATFAS
KVEIEGAKAKVTREVDGGLQTIAVSLPAVVTADLRLNEPRYASLPNIMKAKKKPLDEKTAADYGVDVAPLEVVS
VREPEGRKAGIKVGSVDELVGK L

>d1mjha_ c.29.1.2 (A:) "Hypothetical" protein MJ0577 {Archaeon Methanococcus jannaschii}
VMYKKI LYPTDFSETAEIALKHVKAFKTLKAEEVILLHVIDEREIKKR DIFSLLGVAGLNKSVEEFENELKNKLTEEA
KNKMENIKKELEDVGFVKVDIVVGIPHEEIVKIAEDEGV DIIIMGSHGKTNLKEI LGSVTENVVI KSNKPVLVVKR
KNS

>d1jmva_ c.29.1.2 (A:) Universal stress protein A, UspA {Haemophilus influenzae}
MYKHILVAVDLSEESPILLKKAVGIAKRHD AKLSIIHVDVNFS DLYTGLIDVN MSSMQDRISTETQK ALLD LAESVD
YPISEKLSGSGDLGQVLSDAIEQYDVL LVTGHHQDFWSKLM SSTRQVMNTIKIDMLVVPLRD

>d1dv1a2 c.30.1.1 (A:1-114) Biotin carboxylase (BC) subunit of acetyl-CoA carboxylase {Escherichia coli}

MLDKIVIANRGEIALRILRACKELGIKTVAVHSSADRDLKHVLLADETVCIGPAPSVKSYLNIPAIISAAEITGAVAIH
PGYGLSENANFAEQVERSGFIFIGPKAETIRLMG

>d1gsoa2 c.30.1.1 (A:-2-103) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}
EFMKVLVINGGREHALAWKAAQSPLVETVFVAPGNAGTALEPALQNVIAVGVTDIPALLDFAQNEKIDLTVGPE
APLVGVVDTFRAAGLKIFGPTAGAAQLEG

>d1b6ra2 c.30.1.1 (A:1-78) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK
{Escherichia coli}

MKQVCVLNGQLGRMLRQAGEPLGIAWPVGLDAEPAAVPFQQSVITAEIERWPETALTRQLARHPAFVNRD
VFPIIA

>d1eyza2 c.30.1.1 (A:2-112) Glycinamide ribonucleotide transformylase PurT
{Escherichia coli}

TLLGTALRPAATRVMLLGSGLGKEVAIECQRLGVEVIAVDRYADAPAMHVAHRSHVINMLGDALRRVVELEK
PHYIVPEIEAIATDMIQLLEEGLNVVPCARATKLTM

>d1a9xa3 c.30.1.1 (A:1-127) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}
MPKRTDIKSILGAGPIVIGQACEFDYSGAQACKALREEGYRVINVNSNPATIMTDPEMADATYIEPIHWEVVR
KIIKERPDALPTMGGQTALNCALELERQGVLEFGVTMIGATADAIDKAE

>d1a9xa4 c.30.1.1 (A:556-676) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

STDREKIMVLGGGPNRIGQGIEFDYCCVHASLALREDGYETIMVNCNPETVSTDYDTSRFLYFEPVTLEDVLEIV
RIEKPKGVIVQYGGQTPLKLARALEAAGVPVIGTSPDAIDRAEDRE

>d1iow_1 c.30.1.2 (1-96) D-Ala-D-Ala ligase {Escherichia coli, gene ddIB}

MTDKIAVLLGGTSAEREVSLNSGAAVLAGLREGGIDAYPVDPKEVDVQLKSMGFQKVFIALHGRGGEDGTLQ
GMLELMGLPYTGSGVMASALSMD

>d1ehia1 c.30.1.2 (A:3-134) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}

KKRVALIFGGNSSEHDVSKRSAQNFYNAIEATGKYEIIVFAIAQNGFFLDTESSKKILALEDEQPIVDAFMKTVDAS
DPLARIHALKSAGDFDIFFPVVHGQLGEDGTLQGLFKLLDKPYVGAPLRGHAVSF

>d1e4ea1 c.30.1.2 (A:2-131) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}
NRIKVAILFGGCSEEHDSVSKSAIEIAANINKEKYEPLYIGITKSGVWKMCEKPCAEWENENCYSAVLSPDKKMH
GLVKKNHEYEINHVDVAFSALHGKGSGEDGSIQGLFELSGIPFVGCDIQSSAICM

>d1gsa_1 c.30.1.3 (1-122) Prokaryotic glutathione synthetase, N-terminal domain {Escherichia coli}

MIKLGIVMDPIANINIKKDSSFAMILLEAQRRGYELHYMEMGDLYLINGEARAHTRLNVKQNYEEWFSFVGEQ
DLPLADLDVILMRKDPPFDTEFYATYILERAAEKGLIVNKPQLRDC

>d2hgsa1 c.30.1.4 (A:202-303) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

PNALVLLIAQEKENIFDQRAIENELLARNIHVISRTFEDISEKGSDLQDRRLFVDGQEIAVVYFRDGYMPRQYSL
QNWEARLLERSHAAKCPDIATQLAG

>d1auva1 c.30.1.5 (A:112-213) Synapsin Ia domain {Cow (Bos taurus)}

AARVLLVIDEPHTDWAKYFKGKKIHGEIDIKEQAEFSDLNLVAHANGFSVDMEVLRNGVKVVRSLKPDFVLIR
QHAFSMARNGDYRSLVIGLQYAGIPSI

>d1dhs_ c.31.1.1 (-) Deoxyhypusine synthase, DHS {Human (Homo sapiens)}

APAGALAAVLKHSSTLPPESTQVRGYDFNRGVNYRALLEAFGTTGFQATNFGRAVQQVNAMEKLEPLTSCTIF
LGYTSNLISSGIRETIRYLVQHNMVDVLVTAGGVEEDLIKCLAPTYLGEFSLRGKELRENGINRIGNLLVPNENYC

KFEDWLMPILDQMVMEQNTEGVKWTSPKMIARLGKEINNPESVYYWAQKNHIPVFSPALTDGSLGDMIFFHS
YKNPGLVLIVEDLRLINTQAIFAKCTGMIILGGGVKHIANANLMRNGADYAVYINTAQEFDGSDSGARPDE

AVSWGKIRVDAQPVKYADASLVFPLLVAETFAQKMDAFMHEKNED

>d1efva2 c.31.1.2 (A:208-331) C-terminal domain of the electron transfer flavoprotein alpha subunit {Human (Homo sapiens)}

DRPELTGAKVVSGGRGLKSGENFKLLYDLADQLHAAVGASRAAVDAGFVPNDMQVGQTGKIVAPELYIAGI
SGAIQHLAGMKDSKTIVAINKDEEAPIFQVADYGIVADLFKVVPLEMTEILK

>d1efpa2 c.31.1.2 (A:185-308) C-terminal domain of the electron transfer flavoprotein alpha subunit {Paracoccus denitrificans}

SDRPELTSARRVVSRRGLGSKESFAIEELADKLGAAGVGASRAAVDAGYAPNDWQVGQTGKVAPELYIAGI
SGAIQHLAGMKDSKVIVAINKDEEAPIFQVADYGIVADLFKVVPLEMTEILK

>d1poxa1 c.31.1.3 (A:183-365) Pyruvate oxidase {Lactobacillus plantarum}

YASANNYQTPLLPEPDVQAVTRLTQTLLAERPLIYYGIGARKAGKELEQLSKTLKIPLMSTYPAKGIVADRYPAYL
GSANRVAQKPANEALAQADVVLFGNNYPFAEVSKAFKNTRYFLQIDIDPAKLGKRHKTDIAVLADAQKTLAAIL
AQVSERESTPWWQANLANVKNWRAYLASLED

>d1pvda1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

QTPIDMSLKPNDAESEKEVIDTILALKDAKNPVLADACCSRHDVKAETKKLIDLTQFPFVTPMGKGSISEQHP
RYGGVYVGTLSKPEVKEAVESADLILSVGALLSDKTKNIVEFHDHMKIRNATFPGVQMKFVLQKLLTNIADAQK
GYKPVAVPARTPANAAPP

>d1qpba1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

QTPIDMSLKPNDAESEKEVIDTILVLIKDAKNPVLADACCSRHDVKAETKKLIDLTQFPFVTPMGKGSIDEQHP
RYGGVYVGTLSKPEVKEAVESADLILSVGALLSDFNTGSFSYSYKTKNIVEFHDHMKIRNATFPGVQMKFVLQK
LLTAIAAAKGYKPVAVPARTPANAAPP

>d1zpda1 c.31.1.3 (A:188-362) Pyruvate decarboxylase {Zymomonas mobilis}

EASDEASLNAAVDETLKFIANRDKAVLVGSKLRAAGAEAAVKFTDALGGAVATMAAAKSFFPEENALYIGTS
WGEVSYPGVEKTMKEADAVIALAPVNDYSTTGWTIDPDKKLVAEPRSVVNGIRFPSVHLKDYLTRLAQKV
SKKTGSLDFFKSLNAGELKKAAPADPS

>d1bfd_1 c.31.1.3 (182-341) Benzoylformate decarboxylase {Pseudomonas putida}

SVRLNDQDLDILVKALNSASNPAIVLGPDVDAANANADCVMILAERLKAPVVWAPSAPRCFPTRHPCFRGLM
PAGIAAISQLLEGHDVVLVIGAPVFRYHQYDPGQYLPGTRLISVCDPLEAARAPMGDAIVADIGAMASALAN
LVEESSRQLPTAAP

>d1jsca1 c.31.1.3 (A:280-460) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

AQDEFVMQSINKAADLINLAKKPVLVGAGILNHADGPRLLKELSDRAQIPVTTLQGLGSFDQEDPKSLDMLG
MHGCATANLAVQNADLIIAVGARFDDRTGNISKFAPEARAAAEGRGGIIFHEVSPKNINKVVTQIAVEGDA
TTNLGKMMMSKIFPVKERSEWFAQINKWKKEYPY

>d1d4oa_c.31.1.4 (A:) Transhydrogenase domain III (dIII) {Cow (Bos taurus)}

GTHTEINLDNAIDMIREANSIIITPGYGLCAAKAQYPIADLVKMLSEQGKKVRFGIHPVAGRMPGQLNVLLAEAG
VPYDIVLEMDEINHDFPDTDLVIGANDTVNSAAQEDPNSIIAGMPVLEVWWSKQVIVMKRSLGVGYAAVDN
PIFYKPNTAMLLGDAKKTCDALQAKVRES

>d1hzzc_c.31.1.4 (C:) Transhydrogenase domain III (dIII) {Rhodospirillum rubrum}

SVKAGSAEDAAFIMKNASKVIIVPGYGMAVAQAQHALREMADVLKEGVEVSYAIHPVAGRMPGHMNVL
EANVPYDEVFELEEINSSFQTADVAFVIGANDVTNPAAKTDPSSIYGMPILDVEKAGTVLFIKRSMASGYAGVE
NELFFRNNTMMLFGDAKKMTEQIVQAMN

>d1icia_c.31.1.5 (A:) AF1676 sir2 homolog {Archaeon Archaeoglobus fulgidus}

GSHHHHHHGSHMDEKLLKTIAESKYLVALTGAGVSAESGIPTFRGKDGLWNRYRPEELANPQAFAKDPEKVWK
WYAWRMEKVFNAQPNKAHQAFALERLGVLCLITQNVDDLHERAGSRNVIHLHGSRLVVRCTSCNSFEVE
SAPKIPPLPKCDKCGSLLRPGVVWFGEMLPPDVLDRAMREVERADVIIVAGTSAVVQPAASLPLIVKQRGGAIIEI
NPDETPLTPIADYSLRGKAGEVMDELVRHVRKALS

>d1j8fa_c.31.1.5 (A:) Sirt2 histone deacetylase {Human (Homo sapiens)}

GEADMDFLRNLFSQTLQLGSQKERLLDELTLLEGVARYMQSERCRRVICLVGAGISTSAGIPDFRSPSTGLYDNLEK
YHLPYPEAIFEISYFKKHPEPFFALAKELYPGQFKPTICHYFMRLLDKGLLLRCYTQNIDTLERIAGLEQEDLVEAH
GTFYTSHCVSASCRCHEYPLSWMKEKIFSEVTPKCEDCQSLVKPDIVFFGESLPARFFSCMQSDLKVDLLVMGT
SLQVQPFASLISKAPLSTPRLLINKEKAGQSDPFLGMIMGLGGMDFDSSKKAYRDVAWLGECDQGCLALAELLG
WKKELEDLVRREHASIDAQS

>d1fsz_1 c.32.1.1 (23-231) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}

SPEDKELLEYLQQTKAKITVVGGAGNNITRLKMEGIAKTVAINTDAAQQLIRTKADKKILGKLTGLGAG
GNPKIGEEAKESAAEIKAAIQSDMVFITCGLGGGTGTGSAPVVAEISKKIGALTVAVVTLPVMEGVRMKN
AMEGLERLKQHTDTLVVIPNEKLFEIVPNMPLKLAFLKVADEVLINAVKGLVELITKDGL

>d1tuba1 c.32.1.1 (A:1-245) Tubulin alpha-subunit {Pig (Sus scrofa)}

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGKHVPRAVFVDLEP
TVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRIRKLAQCTGLQGFSVFHSFGGGTGSG
FTSLLMERLSVDYGGKSKEFSIYPAPQVSTAVVEPYNSILTHTTLEHSDCAFMDNEAIYDICRRNLDIERPTYT
NLNRLIGQIVSSITASLRFD

>d1tubb1 c.32.1.1 (B:1-245) Tubulin beta-subunit {Pig (Sus scrofa)}

MREIVHIQAGQCGNQIGAKFWEVISDEHGIDPTGSYHGDSDLQLERINVYYNEAAGNKYVPRAILVDLEPGTM
DSVRSGPFGQIFRPDNFVFGQSGAGNNWAKGHYTEGAELVDSLDVVRKESES CDCLQGFQLTHSLGGGTGS
GMGTLISKIREEYPRDRIMNTFSVVPSPKVSDTVVEPYNATLSVHQLVENTDETYCIDNEALYDICFRTLKLTTPTY
GDLNHLVSATMSGVTTCLRFP

>d1nbaa_c.33.1.1 (A:) N-carbamoylsarcosine amidohydrolase {Arthrobacter sp.}

TFNDIEARLAVALLEAFEAGTSIYNERGFKRRIGYGNRPAVIHIDLNAWTQPGHPFSCPGMETIIPNVQRINEA
ARAKGVPVFYTTNVYRNRDASSGTNDMGLWYSKIPTETLPADSYWAQIDDRAPADGEVIEKNRASAFCPTN
LELFITSNRIDTLITVGATAAGCVRHTVEDAIKGFRPIIPRETIGDRVPGVQWNLYDIDNKFGDVESTDSVVQY
LDALPQFEDTVPKTLSDPQPEVEAPADPV

>d1im5a_c.33.1.2 (A:) Pyrazinamidase/nicotinamidase {Archaeon Pyrococcus horikoshii}

PEEALIVVDMQRDFMPGGALPVPEGDKIIPKVNEYIRKFKEKGALIVATRDWHPEHISFRERGGPWPRHCVQ
NTPGAEFVVDLPEDAVIISKATEPDKEAYSGFEGTDLAKILRGNGVKRVYICGVATEYCVRATALDALKHGF
RDAVKGIKPEDEERALEMKSRGKIVQF

>d1yaca_c.33.1.2 (A:) YcaC {Escherichia coli}

TKPYVRLDKNDAAVLLVDHQAGLLSLVRDIEPDKFKNVNLALGDLAKYFNLPTILTTAETGPNGPLVPELKAQFP
DAPYIARPGNINAWDNEDFVKAVKATGKKQLIAGVVTTEVCVAFPALSAIEEGFDVFVVTDASGTFNEITRHS
DRMSQAGAQLMTWFGVACELHRDWRNDIAGLATLFSNHIPDYRNLMTSYDTLT

>d1hi9a_c.99.1.1 (A:) Zn-dependent D-aminopeptidase DppA {Bacillus subtilis}

MKLYMSVDMEGISGLPDDTFDSGKRNYERGRLIMTEEANYCIAEAFNSGCTEVLVNDSHSKMNNLMVEKLH
PEADLISGDVKPFSMVEGLDDTFRGALFLGYHARASTPGVMSHSMIFGVRHFYINDRPVGEGLNAYVAGYYD

VPVLMVAGDDRAAKEAEELIPNTAAVKQTISRAVKCLSPAKRGRLLTEKTAFA
LQNKDKVKPLPPDRPVLSI
EFANYGQAewanlmpgteiktgtttvqfqakdmleayqamlvmtelamrtsfc
>d1e20a_ c.34.1.1 (A:) Halotolerance protein Hal3 {Mouse-ear cress (*Arabidopsis thaliana*)}
RKPRVLLAASGSVAIKFGNLCHCFTEWAEVRAVTKSSLHFLDKLSPQEVTLYTDEDEWSSWNKIGDPVLHIE
LRRWADVLVIAPSLANTLGKIAGGLCDNLLTCIIRAWDYTAKPLFVAPAMNTLMWNNPFTERHLLSDELGITLIPP
IKKRLACGDYNGNGAMAEPSEIYSTVRLFWESQAH
>d1g5qa_ c.34.1.1 (A:) Epidermin modifying enzyme (peptidyl-cysteine decarboxylase) EpiD
{*Staphylococcus epidermidis*}
MYGKLICATASINVININHYIVELKQHFDEVNILFSPSSKNFINTDVLKLFCDNLYDEIKDPLLNNINIVENHEYILV
PASANTINKIANGICDNLTTVCLTGYQKLFIFPNMNIRMWGNPFLQKNIDLLKNNDVKVYSPDMNKSFEISSG
RYKNNITMPNIENVLFVN
>d1k1ea_ c.108.1.5 (A:) Probable phosphatase YrbI {Haemophilus influenzae, HI1679}
KLENIKFVITDVGVLTDGQLHYDANGEAIKSFHVRDGLGIKMLMDADIQAVLSGRDSPILRRRIADLGIKLFFL
GKLEKETACFDLMKQAGVTAEQTAYIGDDSVDLPAFAACGTSFAVADAPIYVNAVDHVLSTHGGKGAFREMS
DMILQAQGKSSVFTAQGFLKSVKSMGQ
>d1zrn_ c.108.1.1 (-) L-2-Haloacid dehalogenase, HAD {Pseudomonas sp., strain YL}
YIKGIAFDLYGTLFDVHSVVGRCDEAFPGRGREISALWRQKQLEYTWRLSLMNRYVNQQATEDALRFTCRHLG
LDLDARTRSTLCDAYLRLAPFSEVPDSLRELKRRGLKLAISNGSPQSIDAVVSHAGLRGFDHLLSDPVQVYKP
DNRVYELAEQALGLDRSAILFVASNAWDATGARYFGFPTCWINRTGNVFEEMGQTPDWEVTSLRAVVELF
>d1qq5a_ c.108.1.1 (A:) L-2-Haloacid dehalogenase, HAD {Xanthobacter autotrophicus}
MIKAVVFDAYGTLFDVQSVDATERAYPGRGEYITQVWRQKQLEYSWLRALMGRYADFWSVTREALAYTLGTL
GLEPDESFLADMAQAYNRLTPYPDAAQCLAEPLKRAILSNGAPDMLQALVANAGLTDSDAVISVDAKRVFK
PHPDSYALVEEVLGVTPAEVLFVSSNGFDVGGAKNFGFSVARVARLSQEALARELVSGTIAPLTMFKALRMREET
YAEAPDFVVPAVGDLPLRVLVRGMA
>d1ek1a1 c.108.1.2 (A:4-225) Epoxide hydrolase, N-terminal domain {Mouse (*Mus musculus*)}
RVAAFDLDGVLALPSIAGAFRRSEEALALPRDFLLGAYQTEFPEGPTEQLMKGKITFSQWWVPLMDESYRKSSKAC
GANLPENFSISQIFSQAMAARSINRPMLQAAIALKKKGFTTCIVTNNWLDDGDKRDSLQMMCELSQHDFLI
ESCQVGMKPEPQIYNFLDTLAKPNEVVFLLDFGSNLKPARDGMVTLVHNTASALRELEKVTGTQFPEAP
>d1feza_ c.108.1.3 (A:) Phosphonoacetaldehyde hydrolase {Bacillus cereus}
KIEAVIFDWAGTTVDYGCFALEVFMEIFHKRGV рТАЕЕАRKPMGLLIDHVRLTEMPIASEWNRVFRQLPT
EADIQEMYEEFFEEILFAILPRYASPINAVKEVIASLRERGIKIGSTTGYTREMMDIVAKEAALQGYKPDFLVT
PAGRYPWMCYKNAMELGVYPMNHMIKVGTVSDMKEGRNAGMWTVGVILGSSELGLTEEEVENMDSVE
LREKIEVVRNRFVENGAHFTIETMQELESVMEHIE
>d1j97a_ c.108.1.4 (A:) Phosphoserine phosphatase {Archaeon *Methanococcus jannaschii*}
EKKKKLILFDFDSTLVNNETIDEIAREAGVVEEVKKITKEAMEGKLNFEQSLRKRVSSLKDLPIEKVEKAIRITPTEG
AEETIKELNRGYVVAVVSGGFDIAVNKIKEKLGLDYAFANRLIVKDGKLTGDVEGEVLKENAKGEILEKIAKIEGIN
LEDTVAVGDGANDISMFKKAGLKIAFCAKPILKEKADICIEKRLREILKYIK
>d1fs5a_ c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Escherichia coli}
MRLIPLTAEQVGKWAARHIVNRINAfkPTADRPVGLPTGGTPMTTYKALVEMHKAGQVSFKHVVTFNMD
EYVGLPKEHPESYYSMHRNFFDHVDIPAENINLLNGNAPDIDAECRQYEKIRSYGKIHFMGGVGNDGHIAF
NEPASSLASRTRIKTLHDTRVANSRFFDNDVNQVPKYALTGVGTLDAEEVMILVLSQKALALQAAVEGCV
NHMWTISCLQLHPKAIMVCDEPSTMELKVKTLYFNELEAENIKGL
>d1d9ta_ c.35.1.1 (A:) Glucosamine 6-phosphate deaminase/isomerase {Human (*Homo sapiens*)}

MKLIILEHYSQASEWAAKYIRNRIIQFNPGPEKYFTLGLPTGSTPLGCYKKLIEYYKNGDLSFKYVKTFMDEYVG
LPRDHPEYHSFMWNNFFKHIDIHENTHILDGNAVDLQAECDAFEKIKAAAGGIELFVGGIGPDGHIAFNEPG
SSLVSRTVKTLAMDTILANARFFGEELKVPTMALTGVGTVMDAREVMILITGAHKAFALYKAIEEGVNHM
WTVSAFQQHPRTVFVCDEDATLELKVKTVKYFKGLMLVHNKLVDPLYSIKEKETEKSQ

>d1ig3a2 c.100.1.1 (A:10-178) Thiamin pyrophosphokinase, catalytic domain {Mouse (Mus musculus)}

HSSGLVPRGSHMEHAFTPLEPLLPTGNLYCLVVLNQPLDARFRHLWKALLRACADGGANHLYDLTEGERESF
LPEFVSGDFDSIRPEVKEYYTKKCDLISTPDQDHTDKCLQLQRKIEEKELQVDVIVTLGGLGGRFDQIMASV
NTLFQATHITPVPIIIQK

>d1ig0a2 c.100.1.1 (A:3-223) Thiamin pyrophosphokinase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

EECIENPERIKIGTDLINIRNKMLNLKELIHPNEDENSTLLNQKIDIPRPLFYKIWLHDLKVCADGAANRLYDYLD
DDETLRIKYLPNYIIGDLSLSEKVKYKYYRKKNKVTIICKQTTQYSTDFTKCVNLISLHFNSPEFRSLISNKDNLQSNHGI
ELEKGIGHLYNTMTESLVFSKVTPISSLALGGIGGRFDQTVHSITQLYTLENASYFKLCYMTP

>d1f75a_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Micrococcus luteus}
NINAAQIPKHIAIMDGNGRWAKQKMPRIKGHYEGMQTVRKITRYASDLGVKYLTLYAFSTENWSRPKDEVN
YLMKLPGDFLNTFLPELIEKNVKETIGFIDLDHDKAVLEAKEKTKHNTGLTLVFAINYGGRKEIISAVQLAER
YKSGEISLDEISETHNFNEYLFTANMPDPPELLRTSGEERLSNFLIWQCSYSEFVFIDEFWPDFNEESLAQCISIYQNR

>d1jp3a_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {Escherichia coli}
LPAHGCRHVAIIMDGNGRWAKKQGKIRAFGHKAGAKSVRAVSFAANNGIEALTYAFSSENWNRPAQFVSAL
MELFVWALDSEVKSLHRHNVRLRIIGDTSRFNSRLQERIRKSEALTAGNTGLTNIAANYGGRWDIVQGVRQLA
EKVQQGNLQPDQIDEEMLNQHVCMHELAPVDLVIRTGGEHRISNFLLWQIAYAELYFTDVLWPDFDEQDFEG
ALNAFANRE

>d1pvda2 c.36.1.1 (A:2-181) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

SEITLGKYLFERLKQVNNTVFGPGDFNLSLLDKIYEVGMRWAGNANELNAAYAADGYARIKGMSIITTFGV
GELSALNGIAGSYAEHGVVLHVVGVPSISHTLNGDFTVFHRMSANISETTAMITDIATAPAEIDRCIRTTYVTQ
RPVYLG PANLVDLNVPACKL

>d1pvda3 c.36.1.1 (A:361-556) Pyruvate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}

ASTPLKQEWMWNQLGNFLQEGDVIAETGTSAGFINQTTFPNNTYGISQVLWGSIGFTTGATLGAFAAEEID
PKKRVILFIGDGLSQLTVQEISTMIRWGLKPYLFVLNDGYTIEKLIHGPKAQYNEIQGWDHLSLLPTFGAKDYET
HRVATTGEWDKLTQDKSFNDNSKIRMIEIMLPVFDAPQNLVKQAKLT

>d1zpda2 c.36.1.1 (A:2-187) Pyruvate decarboxylase {Zymomonas mobilis}

SYTVGTYLAERLVQIGLKHFAVAGDYNLVLLDNLLNKNMEQVYCCNELNCGFSAEGYARAKGAAAATVY
GALSAFDAIGGAYAENLPVILISGAPNNNDHAAGHVLHHALGKTDHYQLEMAKNITAAAEEAIYTPEEAPAKID
HVIKTALREKKPVYLEIACNIASMPCAAPGPASALFND

>d1zpda3 c.36.1.1 (A:363-566) Pyruvate decarboxylase {Zymomonas mobilis}

APLVNAEIARQVEALLTPNTVIAETGDSWFNAQRMIKLPNGARVEYEMQWGHIGWSVPAAFGYAVGAPERR
NILMVGDGSFQLTAQEVAQMVRKLKVIFLINNYGYTIEVMIHDPYNNIKNWWDYAGLMEVFNGNGGYDSG
AAKGLKAKTGGELAEAIKVALANTDGPTLIECFIGREDCTEELVKWGKRVAANSRKPVNK

>d1poxa2 c.36.1.1 (A:9-182) Pyruvate oxidase {Lactobacillus plantarum}

TNILAGAAVIKVLEAWGVDHLYGIPGGSINSIMDALSAERDRHYIQVRHEEVGAMAAAADAKLTGKIGVCFG
AGPGGTHLMNGLYDAREDHPVPLALIGQFGTTGMNMDFQEMNENPIYADVADYNVTAVNAATLPHVIDEA
IRRAYAHQGVAVVQIPVDPWPQQISAEDW

>d1poxa3 c.36.1.1 (A:366-593) Pyruvate oxidase {Lactobacillus plantarum}

KQEGPLQAYQVLRAVNKIAEPDAIYSIDVGDINLNANRHLKLTPSNRHITSNLATMGVGIPGAIAAKLNYPERQ
VFNLAGDGGASMTMQDLVTQVQYHLPINVVFNCQYGFIKDEQEDTNQNDFIGVEFNDIDFSKIADGVHM
QAFRVNKIEQLPDVFEQAKAIAQHEPVLIDAVITGDRPLPAEKLRLDSAMSSAADIEAFKQRYEAQDLQPLSTYLK
QFGLDD

>d1bfd_2 c.36.1.1 (2-181) Benzoylformate decarboxylase {Pseudomonas putida}

ASVHGTTYELLRRQGIDTVFGNPGSNEPFLKDFPEDFRYILALQEACVVGIAQASRKPAFINLHSAAGTG
NAMGALSNAWNNSHSPLIVTAGQQTRAMIGVEALLTNVDAANLPRPLVKWSYEPASAAEVPHAMSRAIHMAS
MAPQGPVYLSVPYDDWDKDADPQSHLFDRHVSS

>d1bfd_3 c.36.1.1 (342-524) Benzoylformate decarboxylase {Pseudomonas putida}

EPAKVDQDAGRHLHPETVFDTLNDMAPENAIYLNESTTTAQMWQRLNMRNPGSYYFCAAGGLGFALPAAIGV
QLAEPERQVIAVIGDG桑NYSISALWTAAQYNIPTIFVIMNNNTYGALRWFAVGLEAENVPGLDVPGIDFRALA
KGYGVQALKADNLEQLKGSLOEAKGPVIEVSTV

>d1jsca2 c.36.1.1 (A:83-270) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

PDMDTSVGLTGGQIFNEMMSRQNVDTFGYPGGAILPVYDAIHNSDKFNFKLPKHEQGAGHMAEGYARAS
GKPGVVVLVSGPGATNVVTPMADAFADGIPMVVFTGQVPTSAIGTDAFQEADVVGISRSCTKWNVMVKSVE
ELPLRINEAFEIATSGRPGPVLVLDLKDVTAAIRNPIPTKTTLPS

>d1jsca3 c.36.1.1 (A:461-648) Acetohydroxyacid synthase catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

AYMEETPGSKIKPQTIVKKLSKVANDTGRHVITVGVGQHQMWAAQHWTWRNPHTITSGGLGTMGYGLPA
AIGAQVAKPESLVIDIDGDASFNMTELSSAVQAGTPVKILILNNEEQGMVTQWQSLFYEHRYSHTHQLNPDFI
KLAEMGLKGLRVKKQEELDAKLEFVSTKGPVLLVEVDKK

>d1gpus1 c.36.1.2 (A:3-337) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}

QFTDIDKLAStIRILAVDTVSKANSGHPGAPLGMAPAHLWSQMNRNPTNPDWINRDRFVLSNGHAVAL
YSMLHLTYDLSIEDLKQFRQLGSRTPGHPEFELPGVEVTGPLGQGISNAVGMAMAQANLAATYNKPGFTLS
DNYTYVFLGDGCLQEGISSEASSLAGHLKLGNLIAIYDDNKITIDGATSIKFDEDVAKRYEAYGWEVLYVENGND
LAGIAKAIAQAKLSKDKPTLIKMTTIGY GSLHAGSHSVHGAPLKADDVQQLSKFGNPDKSFVVPQEVDHY
QKTIKPGVEANNKWNKLFSYQKKFPELGAELARRLSGQ

>d1gpus2 c.36.1.2 (A:338-534) Transketolase, TK {Baker's yeast (Saccharomyces cerevisiae)}

LPANWESKLPTYTAKDSAVATRKLSETVLEDVYNQLPELIGGSADLPSNLTRWKEALDFQPPSSGSGNYSRYIR
YGIREHAMGAIMNGISAFCGANYKPYGGTFLNFVSYAGAVRLSALSGHPVIWATHDSIGVGEDGPTHQPIETL
AHFRSLPNIQVWRPADGNEVSAAYKNSLESKHTPSIIALSRQNLQL

>d1dtwa1 c.36.1.3 (A:) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}

PQFPGASAEIFDKLEFIQPNVISGIPIYRVMDRQGQIINPSEDPHLPKEKVLKLYKSMTLLNTMDRILYESQRQGRI
SFYMTNYGEEGTHVGSAALDNTDLVFGQYREAGVLMYRDYPLELFMAQCYGNISDLGKGRQMPVHYGCKE
RHFVTISSLATQIPQAVGAAYAAKRANANRVCYFGEAASEGDAHAGFNFATLECPIIFFCRNNGYAISTPT
SEQYRGDGIAARGPGYGYGIMSIRVDGNDVFAVYNATKEARRRAVAENQPFLIEAMTYRIGHSTSDDSSAYRSVD
EVNYWDKQDHPISLRHYLLSQGWWDEEQEKAWRKQSRRKVMEAFEQAERKPKPNPNLLFSDVYQEMPAQ
LRKQQESLARHLQTYGEHYPLDHFDFK

>d1dtwb1 c.36.1.3 (B:17-204) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}

QTQKMNLFQSNTSALDNLSAKDPTAVIFGEDVAFGGVFRCTVGLRDKYGDRLVFNTPLCEQGIVGFGIGIAVTG
ATAIAEIQFADYIFPAFDQIVNEAAKYRYRSGDLFNCGLTIRSPWCGVGHGALYHSQSPEAFFAHCPGIKVVIPRS
PFQAKGLLSCIEDKNPCIFFEPKILYRAAAEVPIE

>d1qs0a1 c.36.1.3 (A:) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

NEYAPLRLHVPEPTGRPGCQTDFSYLRLNDAGQARKPPVDAAADTADLSYSLVRVLDEQGDAQGPWAEDID
PQILRQGMRAMLKTRIFDSRMVVAQRQKMSFYMQSLGEEAIGSGQALALNRTDMCFPTYRQQSILMARDV
SLVEMICQLLSNERDPLKGRQLPIMYSVREAGFFTISGNLATQFVQAVGWAMASAIKGDTKIASAWIGDGATAE
SDFHTALTFAHVVYRAPVILNVVNNQWAISTFQAIAGGESTTFAGRGGVGCGIASLRVDGNDVFVAVYASRWAAE
RARRGGLGPSLIEWVTYRAGPHSTSDDPSKYRPADDWSHFPLGDIARLKQHLIKIGHWSEEHQATTAEEFEEAAVI
AAQKEAEQYGTLANGHIPSAASMFEDVYKEMPDHLRRQRQEL

>d1qs0b1 c.36.1.3 (B:2-205) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

ATTMTMTMIQALRSAMDVMLERDDNVVYQDVGYFGGVFRCTEGLQTKYGDRLVFNTPLCEQGDAQGPWAEDID
GAYGLRPVVEIQFADYFYPASDQIVSEMARLRYRSAGEFIAPLRLMPCGGGIYGGQTHQSPEAMFTQVCGLR
TVMPNSPYDAKGLLIAIECDDPVIFLEPKRLYNGPDFGHHDRPVTPWSKHPHSAVPDG

>d1ik6a1 c.36.1.3 (A:1-191) E1-beta subunit of pyruvate dehydrogenase {Archaeon Pyrobaculum aerophilum}

VAGVVMMANMAKAINMALHEEMERDERVVVLGEDVGKKGGVFLVTEGLYERFGPERVIDTPLNEGGILGFA
MGMAAGLKPVAEIQFVDFIWLGADELLNHIAKLRYRSGGNYKAPLVVRTPVSGTRGGLYHSNSPEAFVHT
PGLVVVMPSTPYNAKGLLAAIRGDDPVVFLEPKILYRAPREEVPEG

>d1keka1 c.36.1.4 (A:2-258) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

GKKMMTTDGNTATAHVAYAMSEVAAIYPITPSSTMGEAADDWAAQGRKNIFGQTLIREMQSEAGAAGAVH
GALAAGALTTFTASQGLLMIPNMYKISGELLPGVFHVTARAIAAHALSIFGDHQDIYARQTGFAMLASSVQ
EAHDMALVAHAAIESNPVFMHFFDGFRTSHEIQKIEVLDYADMASLVNQKALAEFRAKSMNPEHPHVRGTA
QNPDIYFQGREAAANPYYLKPGIVAEYMQKVASLTGRSY

>d1keka2 c.36.1.4 (A:786-1232) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

VKSEVLPDRSLKGSQLFQEPLMEFGACSGCGETPYVRVITQLFGERMFIANATGCSSIWGASAPSMPYKTNRLG
QGPAWGNSLFEDAAEYFGFMNMSMFARRTHLADLAAKALESDASGDVKEARLGWLAGKNDPIKSKEYGDK
LKKLLAGQKDGLGQIAAMSDFLYTKKSVWIFGGDGWAYDIGYGGLDHVLAGSEDVNVFVMDTEVYSNTGGQS
SKATPTGAVAKFAAAGKRTGKDLARMVMTYGYVVATVSMGYSKQQFLKVLKEAESFPGPSLVIAYATCINQG
LRKGGMGKSQDVMTAVKSGYWPFLFRYDPRLAAQGKNPQLDSKAPDGSVEEFLMAQNRFAVLDRSFPEDAK
RLRAQVAHELDVRFKELEHMAATNIFSFAPAGGKADGSVDFGEGAEFCTRDDTPMMARPDSGEACDQNRA
GTSEQQQGDLSSKRTKK

>d1gky_ c.37.1.1 (-) Guanylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SRPIVISGPGSGTGKSTLLKKLFAEYPDSFGFSVSSTTRPRAGEVNGKDYNFVSDEFKSMIKNNEFIEWAQFSGN
YYGSTVASVKQVKSGKTCILDIMQGVKSVKAPELNARFLFIAPPVEDLKKLEGRGTETEESINKRLSAAQAE
LAYAETGAHDKVIVNDDLDKAYKELKDFIAEK

>d1kgda_ c.37.1.1 (A:) Guanylate kinase-like domain of Cask {Human (Homo sapiens)}

HMRKTLVLLGAHGVGRRHIKNTLITKHPDRFAYPIPHTTRPPKKDEENGKNYYFVSHDQMMQDISNNEYLEYG
SHEDAMYGTLETIRKIHEQGLIAILDVEPQALKVLRTAEFAPFVVIAAPTITPGLNEDESQRLQKESDILQRTYA
HYFDLTIINNEIDETIRHLEEAVELVC

>d1kjwa2 c.37.1.1 (A:526-724) Guanylate kinase-like domain of Psd-95 {Rat (Rattus norvegicus)}
VTQMEVHYARPIILGPTKDRANDLLSEFPDKFGSCVPHTTRPKREYEIDGRDYHFVSSREKMEKDIQAHKFIE
AGQYNSHLYGTSQSVREVAEQGKHCILDVSANAVRRLQAAHLHPIAFIRPRSLENVLEINKRITEEQARKAFDR
ATKLEQEFTECFSIAVEGDSFEEIYHKVKRVIEDLSGPYIWVPARERL

>d1ukz_ c.37.1.1 (-) Uridylate kinase {Baker's yeast (Saccharomyces cerevisiae)}
PAFSPDQSVIFVLGGPGAGKGTQCEKLVDYSFVHLSAGDLLRAEQGRAGSQYGELIKNCIKEGQIVPQEITLAL
LRNAISDNVKANKHKFLIDGFPKRMDQAISFERDIVESKFILFFDCPEDIMLERLLERGKTSGRSDDNIESIKKRFN
TFKETSMPVIEYFETKSJVVRVRCDRSVEDVYKDVQDAIRDSL

>d1deka_ c.37.1.1 (A:) Deoxynucleoside monophosphate kinase {Bacteriophage T4}
MKLIFLSGVKRSGKDTTADFIMSNYSAVKYQLAGPIKDALAYAWGVFAANTDYPCLTRKEFEGIDYDRETNLNLT
KLEVITIMEQAFCYLNGKSPIKGVFVFDDEGKESVNFAFNKITDVINNIEDQWSVRRLMQALGTDLIVNNFDR
MYWVVKLFALDYLDKFNSGYDYYIVPDTRQDHEDAARAMGATVIHVVPRGQKSNDTHITEAGLPIRGDLVIT
NDGSLEELFSKIKNTLKVL

>d1j90a_ c.37.1.1 (A:) Deoxyribonucleoside kinase {Fruit fly (Drosophila melanogaster)}
TQPFTVIEGNIGSGKTTYNHFEKYKNDICLLEPVEKWRNVNGVNLLEMYKDPKKWAMPFQSYYVTLMLQ
SHTAPTNKKLIMERSIFSARYCFVENMRRNGSLEQGMYNTLEEWYKFIIESIHVQADLIYLRTSPEVAYERIRQ
RARSEESCVPLKYLQELHELHEDWLIHQRRPQSCKVLVLDADLNLE

>d1jaga_ c.37.1.1 (A:) Deoxyguanosine kinase {Human (Homo sapiens)}
GPRRLSIEGNIAVGKSTFKLLTKTYPEWHVATEPVATWQNIQAAGNQKACTAQSLGNLLDMMYREPARWSY
TFQTFSFLSRLKVQLEPFPEKLLQARKPVQIFERSVYSDRYIFAKNLFENGSLSDIEWHIYQDWHSFLWEFASRIT
LHGFIYLQASPQVCLKRLYQRAREEKGIELAYLEQLHGQHEAWLIHKTTKLHFEALMNIPVLVLDVNDDFSEEVT
KQEDLMREVNTFKNL

>d1ckeа_ c.37.1.1 (A:) CMP kinase {Escherichia coli}
AIAPVITIDGPSGAGKGTLCAMAELQWHLLSGAIYRVLALAALHHHVDAVEDALVPLASHLDVRFVSTNG
NLEVILEGEDVSGEIRTQEVANAASQVAAPRVREALLRRQAFRELPGLIADGRDMGTVVFPDAPVKIFLDASS
EERAHRRMLQLQVKGFSVNFERLLAEIKERDDRDRNRAVAPLVAADALVLDSTTLSIEQVIEKALQYARQKLAL
A

>d1qf9a_ c.37.1.1 (A:) UMP/CMP kinase {Dictyostelium discoideum}
MEKSKPNVVFVLGGPGSGKGTQCANIVRDFGVWVHLSAGDLLRQEQQSGSKDGEIMATMIKNGEIVPSIVTVK
LLKNAIDANQGKNFLVDGFPRNEENNNSWEENMKDFVDTKFVLFDCPEEVMTQRLKRGESSGRSDDNIESI
KKRFNTFNVQTKLVIDHYNKFDVKIIPANRDVNEYNDVENLFKSMGF

>d1e2ka_ c.37.1.1 (A:) Thymidine kinase {Herpes simplex virus type 1, different strains}
MPTLLRVYIDGPHGMGKTTTQLLVALGSRDDIVVPEPMTYWRLGASETIANIYTQHRLDQGEISAGDAA
VVMTSAQITMGMPYAVDAVLAPHIGGEAGSSHAPPALTIFDRHPIAACLLCYPARYLMGSMTPQAVLAFV
ALIPPTLPGTNIVLGALPEDRHIDRLAKRQRPGERLDLAMLAIRRVYGLANTVRYLQCGGSWREDWGQLSGT
AVPPQGAEPQSAGPRPHIGDTLFLFRAPELLAPNGDLYNVFAWALDVLAKRRLRSMHVFILDYDQSPAGCRD
ALLQLTSGMVQTHVTPGSIPICDLARTFAREMGE

>d3adk_ c.37.1.1 (-) Adenylate kinase {Pig (Sus scrofa)}
MEEKLKKSKIIFVVGPGSGKGTQCEKIVQKYGYTHLSTGDLLRAEVSSGARGKMLSEIMEKGQLVPLETVLD
MLRDAMVAKVDTSKGFLIDGYPREVKQGEEFERKIGQPTLLYVDAGPETMTKRLKRGTEGRVDDNEETIKK
RLETYYKATEPVIAFYEKRGIVRKVNAEGSVDDVFSQVCTHLDTLK

>d1nksa_ c.37.1.1 (A:) Adenylate kinase {Archaeon Sulfolobus acidocaldarius}
MKIGIVTGIPGVGKSTVLAKVKEILDNQGINNKIINYGDFMLATALKLGYAKDRDEMRLKLSVEKQKKLQIDAAGGI

AEEARAGGEGLFIDTHAVIRTPSGYLPGLPSYVITEINPSVIFLLEADPKIILSRQKRDTRNRNDYSDESVILETIN
FARYAATASAVLAGSTVKIVNVEGDPSIAANEIIRSMK

>d2ak3a1 c.37.1.1 (A:0-124,A:162-225) Adenylate kinase {Cow (Bos taurus), mitochondrial izozyme-3}

GASARLLRAAIMGAPGSGKGTVSSRITKHFEKLHLSGDLLRDNMLRGTEIGVLAKTFIDQGKLIPDDVMTRLVL
HELKNTQYNWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEVIKQRLTXDRPETVVKRLKAYEAQTEPVLEYYR
KKGVLETSGTETNIKIWPHVAFQLQTKLPQRSQETSVT

>d1ak2_1 c.37.1.1 (14-146,177-233) Adenylate kinase {Cow (Bos taurus), mitochondrial izozyme-2}

PKGVRAVLLGPPGAGKGTQAPKLAKNFCVCHLATGDMRAMVASGSELGKKLAKMDAGKLVSDEMVLEIEK
NLETPPCKNGFLLDGFPRTRQAEMLDDLMERKEKLDVSIEFSIPDSLLIRRITGRLIHXSDDNNKKALKIRLEAYH
TQTTPLVEYYSKRGIHSADASQTPDVVFASILAAFSKATS

>d1aky_1 c.37.1.1 (3-130,169-220) Adenylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

ESIRMVLIGPPGAGKGTQAPNLQERFHAAHLATGDMRSQIAKGTQLGLEAKKIMDQGGLVSDDIMVNMIKD
ELTNNPACKNGFILDGFPRTIQPQAEKLDQMLKEQGTPLEKAIELKVDDELLVARITXNADALKRLAAYHAQTEPI
VDFYKKTGIWAGVDASQPPATWADILNKLGN

>d1e4ya1 c.37.1.1 (A:1-121,A:157-214) Adenylate kinase {Escherichia coli}

MRIILLGALVAGKGTQAQFIMEKYGIPQISTGDMRAAVKSGSELGKQAKDIDMAGKLVTDDELVIALKERIAQE
DCRNGFLLDGFPRTIPQADAMKEAGINVYVLEFDVPDELIVDRIVXKDDQEETVRKRLVEYHQMTAPLIGYYS
KEAEAGNTKYAKVDDGTPVAEVRADLEKILG

>d1zaka1 c.37.1.1 (A:3-127,A:159-222) Adenylate kinase {Maize (Zea mays)}

ADPLKVMISGAPASGKGTQCIELIKTYQLAHISAGDLLRAEIAAGSENGKRAKEFMEKGQLVPDEIVVNMVKER
LRQPDAQENGWLLDGYPRTSQAMALETLEIRPDTFILLDVPDELLVERVVFDDTEEKVCLRLETYYQNIESLLS
TYENIIVKVQGDATVDAVFAKIDELLGSILEKKNEMVSST

>d1zin_1 c.37.1.1 (1-125,161-217) Adenylate kinase {Bacillus stearothermophilus}

MNLVLMGLPGAGKGTQAECIVAAYGIPHISTGDMFRAAMKEGTPGLQAKQYMDRGDLVPDEVTIGIVRERLS
KDDCQNGFLLDGFPRTVAQAEALETMLADIGRKLDYVIHIDVRQDVLMERLTADDNEATVANLEVNMKQ
MKPLVDFYEQKGYLRNINGEQDMEKVFADIRELLGGLAR

>d1tmka_ c.37.1.1 (A:) Thymidylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

GRGKLILIEGLDRTGKTTQCNILYKKLQPNCKLLFPERSTRIGGLINEYLDDSFQLSDQAIHLLFSANRWEIVDKI
KKDLLEGKNIVMDRYVYSGVAYSAAKGTNGMDLDWCLQPDVGLLKPDLTFLSTQDVDDNAEKSGFGDERYE
TVKFQEVKQTFMKLLDEIRKGDESITIVDTNKGIQEVEALIWQIVEPVLSTHIDHDKFSFF

>d1e9ea_ c.37.1.1 (A:) Thymidylate kinase {Human (Homo sapiens)}

ARRGALIVLEGVDRAGKSTQSRKLVEALCAAGHRAELLRFPERSTEIGKLLSSYLQKKSVDVEDHSVHLLFSANRWE
QVPLIKEKLSQGVTLVVDRYAFSGVAYTGAKENFSLDWCKQPDVGLPKPDVLFLQLQLADAAKRGAFGHERYE
NGAFQERALRCFHQLMKDTTLNWKMDASKSIEAVHEDIRVLSEDIAITATEKPLKELWK

>d4tmka_ c.37.1.1 (A:) Thymidylate kinase {Escherichia coli}

RSKYIVIEGLEGAGKTTARNVVVETLEQLGIRDMVFTREPGGTQLAEKLRSLLLDIKSVGDEVITDKAEVLMFYAA
RVQLVETVICKPALANGTWIGDRHDLSTQAYQGGGRGIDQHMLATRDAVLGDFRPDLTLYLDVTPEVGLKRA
RARGELDRIEQESFDFNRTRARYLEAAQDKSIHTIDATQPLEAVMDAIRTTVTHWVKE

>d1g3ua_ c.37.1.1 (A:) Thymidylate kinase {Mycobacterium tuberculosis}

MLIAIEGVDGAGKRTLVEKLSGAFRAAGRSVATLAFPRYQGQSVAADIAAEALHGEHGDLASSVYAMATLFALDR
AGAVHTIQGLCRGYDVVILDYVASNAAYSARLHENAAAGKAAAWVQRIEFARLGLPKPDWQVLLAVSAELAG

ERSRGRAQRDPGRARDNYERDAELQQRTGAVYAEELAAQGWGGRWLVVGADVDPGRLAATLA

>d1e6ca_ c.37.1.2 (A:) Shikimate kinase {Erwinia chrysanthemi}

MTEPIFMVGARGCGMTTVGRELARALGYEFVTDIFMQHTSGMTVADVVAEGWPGFRRRESEALQAVATP
NRVVATGGGMVLLEQNQRQFMRAHGTVVYLFAPAAEELRLQASLQAHQRPTLTGRPIAEEMEAVLREREALYQ
DVAHYVVDATQPPAAIVCELMQTMRL

>d1qhxa_ c.37.1.3 (A:) Chloramphenicol phosphotransferase {Streptomyces venezuelae}

MTTRMIIILNGGSSAGKSGIVRCLQSVLPEPWLAFGVDSLIEAMPLKMQSAEGGIEFDADGGVSIGPEFRALEGA
WAEGVVAMARAGARIIDDVFLGGAAAQERWRSFVGDLDVDLVGVRCGAVAEGRETARGDRVAGMAAK
QAYVVHEGVEYDVEVDTTHKESIECAWAIAAHVVP

>d1d6ja_ c.37.1.4 (A:) Adenosine-5'phosphosulfate kinase (APS kinase) {Penicillium chrysogenum}

HASALTRSERTELRNQRGLTIWLTGLSASGKSTLAVEREHLQVDRRRVHAYRLDGDNIRFGLNKDLGFSEADRNE
NIRRIAEVAKLFADSNSIAITSFISPYRKDRDTARQLHEVATPGEETGLPFVEVYDVPVEVAEQRDPKGLYKKARE
GVIKEFTGISAPYEAPANPEVHVKNYELPVQDAVKQIIDYLDTKGYLPAKK

>d1g8fa3 c.37.1.15 (A:390-511) ATP sulfurylase C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

PRPKQGFSIVLGNSLTVSREQLSIALLSTFLQFGGGRRYYKIFEHNNKTELLSLIQDFIGSGSGLIIPDQWEDDKDSV
VGKQNVYLLDTSSSADIQLESADEPISHIVQKVVLFLEDNGFFVF

>d1i2da3 c.37.1.15 (A:391-573) ATP sulfurylase C-terminal domain {Fungus (Penicillium chrysogenum)}

PRATQGFTIFLTGYMNSGKDAIARALQVTLNQQGGRSVLLLGDTRHELSSELGFTREDRHTNIQRIAFVATELT
RAGAAVIAAPIAPYEESRKFARDAVSQAGSFFLVHVATPLEHCEQSDKRGIYAAARRGEIKGFTGVDDPYETPEKA
DLVVDFSKQSVRSIVHEIILVLESQGFLERQ

>d1aqua_ c.37.1.5 (A:) Estrogen sulfotransferase {Mouse (Mus musculus)}

EYYEVFGEFRGVLMKDRAFTKYWEDVEMFLARPDDLVIATYPKSGTTWISEVVYMIYKEGDVEKCKEDAIFNRIPY
LECRNEDLINGIKQLKEKESPRIVKTHLPPKLLPASFWEKNCKMIYLCRANKADVAVSYYFLIMITSYPNPKSFSEF
VEKFMQGQVPGWSYDHVKAWWEKSKNRVLFMFYEDMKEDIRREVVKLIEFLERKPSAELVDRIIQHTSFQE
MKNNPSTNYTMMPEEMMNQKVSPFMRKGIIGDWKNHFPEALRERFDEHYKQQMKDCTVKFRME

>d1efha_ c.37.1.5 (A:) Hydroxysteroid sulfotransferase {Human (Homo sapiens)}

DFLWFEGIAFPTMGFRSETLRKVRDEFVIRDEDVIIILYPKSGTNWLAELCLMHSGDAKWIQSVPIWERSPW
VESEIGYTALSETESPRLFSSHLPQLFPKSFFSKAKVIYLMRNPRDVLVSGYFFWKNMKFIKKPKSWEELYFEWFC
QGTVLYGSWFDHIGHWMMPMREEKNFLLLSYEELKQDTGRTIEKICQFLGKTLPEEELNLILKNSSFQSMKENKM
SNYSLLSVDYVVDKAQLLRKGVSGDWKNHFTVAQAEFDKLFQEKMAADLPRKLAAALE

>d1cjma_ c.37.1.5 (A:) Aryl sulfotransferase sult1a3 {Human (Homo sapiens)}

SRPPLLEYVKGVPLIKYFAEALGPLQSFQARPDDLLINTYPKSGTTWVSQLDMIYQGGDLEKCNRAPIYVRVPFLE
VNPDGEPSGLETLKDTPPPRLIKSHLPLALLPQTLDQKVKVYYVARNPKDVAVSYYHFHRMEKAHEPGTWDS
FLEKFMAGEVSYGSWYQHVQEWWELSRTHPVLYLFYEDMKENPKREIQKILEFVGRSLPEETMDFMVQHTSF
KEMKKNPMTNYTTPQELMDHSISPFMRKGAMGDWKTTFTVAQNERFDADYAEKMAGCSLSFRS

>d1insta_ c.37.1.5 (A:) Heparan sulfate N-deacetylase/N-sulfotransferase domain {Human (Homo sapiens)}

DPLWQDPCEDKRHKDIWSKEKTCRFPKLLIIGPQKTGTTALYLFGLMHPDLSSNYPSETFEEIQFFNGHNYHK
GIDWYMEFFPIPSNTTSDFYFEKSANYFDSEVAPRRAAALLPKAKVLTILINPADRAYSWYQHQRAHDDPVALKY
TFHEVITAGSDASSKLRALQNRCVPGWYATHIERWLSAYHANQILVLDGKLLRTEPAKVMMDMVQKFLGVTNTI
DYHKTLAFDPKKGFWCQLLEGGKTCLGKSKGRKYPEMDLDSRAFLKDYYRDHNIELSKLLYKMGQLPTWLRE

DLQ

>d1fmja_c.37.1.5 (A:) Retinol dehydratase {Fall armyworm (Spodoptera frugiperda)}

PPFYEFRELNPEEDKLVKANLGAFPTTVKLGPKGYMVRPYLKDAANIYNMPLRPTDVFVASYQRSGTTMTQE
LVWLIENDLNFEAAKYMSLRYIYLDGFMIDPEKQEEYNDILPNPENLDMERYLGLLEYSSRPGSSLAAVPPTE
KRFVKTHLPLSLMPPNMLDTVKMVYLARDPRDVAVSSFHHARLLYLLNKQSNFKDFWEMFHRLGLYTLTPYFEH
VKEAWAKRHDPNMLFLFYEDYLKDLPGCIARIADFLGKKLSEEQIQLCEHLNFEKFKNNGAVNMEDYREIGILA
DGEHFIRKGKAGCWRDYFDEEMTKQAEKWIKDNLKDTRLRPNM

>d1a7j_c.37.1.6 (-) Phosphoribulokinase {Rhodobacter sphaeroides}

SKKHPIISVTGSSGAGTSTVKHTFDQIFRREGVKAVSIEGDAFHRFNRADMAKAELDRRYAAGDATFSHFSYEANE
LKELERVFREYGETGQGRTRTYVHDDAEAARTGVAPGNFTDWRFDSHLLFYEGLHGAVVNSEVNIAGLAD
LKIGVVVPVINLEWIQKIHDRATRGYTTAEVTDLRHMAYVHCIVPQFSQTDINFQRVPVVTSNPFIARWIP
TADESVVVIRFRNPRGIDFPYLTSMIHGSWMSRANSIVVPGNKLQLAMQLILTPLIDRVVRESKV

>d1esma_c.37.1.6 (A:) Pantothenate kinase PanK {Escherichia coli}

QLLMTPYLQFDRNQWAALRDSVPMTLSEDEIARLGKINEDLSLEEVAEIYLPLSRLLNFYISSNLRRQAVLEQFLG
TNGQRIPYIISIAGSVAVGKSTTARVLQALLSRWPEHRRVELITTDGFLHPNQLKERGLMKKGFPESYDMHRL
VKFVSDLKSGVPNTAPVYSHIYDVIDPGDKTVVQPDILILEGLNVLQSGMDYPHDPHHVFSDFVDFSIYVDA
PEDLLQTWYINRFLKFREGAFTDPDSYFHNYAKLTKEEAKTAMTLWKEINWLNLQNLPLTRERASLILTKSANH
AVEEVRLRK

>d1bif_1 c.37.1.7 (37-249) 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain {Rat (Rattus norvegicus)}

CPTLIVMVGLPARGKTYISKKLTRYLNFIGVPTREFNVGQYRRDMVKTYKSFEFLPDNEEGLKIRKQCALAALND
VRKFLSEEGGHVAVFADATNTTRERRAMIFNFGEQNGYKTFFVESICVDPEVIAANIVQVKLGSPDYVNRDSDEA
TEDFMRRIECYENSYESLDEEQDRDLSYKIMDVGQSYVVNRVADHIQSRIVYLMNIHVTPR

>d1ctqa_c.37.1.8 (A:) cH-p21 Ras protein {Human (Homo sapiens)}

MTEYKLVVVGAGGVGKSALTQLIQNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAGQEEYSAMRDQYMRT
GEGFLCVFAINNTKSFEDIHQYREQIKRVKDSDDVPMVLVGNKCDLAARTVESRQAQDLARSYGIPYIETSAKTR
QGVEDAFYTLVREIRQH

>d1ds6a_c.37.1.8 (A:) Rac {Human (Homo sapiens)}

MQAICKVVVGDAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDSKPVNGLWDTAGQEDYDRLRPLSYP
QTDVFLICFSLVPSPASYENVRAKWFPEVRHHCPSTPIILVGTKLDRDDKDTIEKLKEKKLAPITYPQGLALAKEIDS
VKYLECSALTQRGLKTVDEAIRAVLCPPQ

>d1mh1_c.37.1.8 (-) Rac {Human (Homo sapiens)}

GSPQAICKVVVGDAVGKTCLLISYTTNAFPGEYIPTVFDNYSANVMVDGKPVNLGLWDTAGQEDYDRLRPLS
YPQTDVSLICFSLVPSPASFENVRAKWFPEVRHHCPNTPIILVGTKLDRDDKDTIEKLKEKKLAPITYPQGLAMAKE
IGAVKYLECSALTQRGLKTVDEAIRAVLCPPP

>d1c1ya_c.37.1.8 (A:) Rap1A {Human (Homo sapiens)}

MREYKLVLGSGGVGKSALTQFVQGIFVEKYDPTIEDSYRKQVEVDCQQCMLEILDTAGTEQFTAMRDLYMK
NGQGFALVYSISITAQSTFNDLQLDREQILRVKDTEDVPMILVGNKCDLEDERVVGKEQGQNLARQWCNCAFLES
SAKSKINVNEIFYDLVRQJNR

>d1kao_c.37.1.8 (-) Rap2a {Human (Homo sapiens)}

MREYKVVVLGSGGVGKSALTQFVQTFIEKYDPTIEDFYRKEIEVDSSPSVLEILDTAGTEQFASMRDLYIKNGQ
GFILVYSLVNQQSFQDIKPMRDQIIRVKRYEKVPVILVGNKVDLESEREVSSEGRALAEWGCPFMETSAKS
MVDELFAEIVRQMNYA

>d3raba_c.37.1.8 (A:) Rab3a {Rat (Rattus norvegicus)}

NFDYMFKILIIGNSSVGKTSFLFRYADDSFTPAGVSTVGIDFKVKTIRNDKRIKQLQIWDTAGQERYRTITTAYYRGA
MGFILMYDITNEESFNAVQDWSTQIKTYSWDNAQVLLVGNKCDMEDERVSSERGRQLADHLGFFEASAK
DNINVKQTFERLVDVICEK

>d1huqa_ c.37.1.8 (A:) Rab5c {Mouse (Mus musculus)}

ICQFKLVLLGESAVGKSSLVLRFKGQFHEYQESTIGAAFLTVCLDDTTVKFEIWTAGQERYHSLAPMYYRG
AQAAIVVYDITNTDTFARAKNWVKELRQRQASNIVIALAGNKADLASKRAVEFQEAQAYADDNSLLFMETSAK
TAMNVNEIFMAIAKKL

>d1d5ca_ c.37.1.8 (A:) Rab6 {Malaria parasite (Plasmodium falciparum)}

KYKLVLGEQAVGKTSIITRFMYDTFDNNYQSTIGIDFLSKTLYLDEGPVRLQLWDTAGQERFRSLIPSYIRDAAA
VYVYDITNRQSFENTTKWIQDILNERGKDVIIALVGNKTDGLRKVTYEEGMQKAQEYNTMFHETSAKHNI
KVLFKKTASKL

>d1g16a_ c.37.1.8 (A:) Rab-related protein Sec4 {Baker's yeast (Saccharomyces cerevisiae)}

SIMKILLIGDSGVGKSCLLVRFVEDKFNPSETTIGIDFKIKTVTINGKKVQLQIWDTAGQERFRTITTAYYRGAMGI
ILVYDITDERTFTNIKWFKTVNEHANDEAQLLVGNKSDMETRVVTADQGEALAKELGIPFISSAKNDDNVN
EIFFTLAKLIQEKI

>d1byua_ c.37.1.8 (A:) Ran {Dog (Canis familiaris)}

EPQVQFKLVLDGGTGKTTFVKRHLTGEFEKKYVPTLGVEHPLVFHTNRGPIKFNVWDTAGQEKFGLRDG
YYIQAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDISAKS
NYNFEKPFLWLARKLIGDPNLEFVAMPALAPPEVVMDPALAAQYEHDLEVAQTT

>d1i2ma_ c.37.1.8 (A:) Ran {Human (Homo sapiens)}

QVQFKLVLDGGTGKTTFVKRHLTGEFEKKYVATLGVEHPLVFHTNRGPIKFNVWDTAGQEKFGLRDGYYI
QAQCAIIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVDIKDRKVKAKSIVFHRKKNLQYYDISAKSNY
NFEKPFLWLARKLIGDPNLEFV

>d1tx4b_ c.37.1.8 (B:) RhoA {Human (Homo sapiens)}

AIRKKLVIVGDGACGKTCLLIVNSKDFPVEVYVPTVFENYVADIEVDAQVELALWDTAGQEDYDRLRPLSYPDT
DVILMCFSIDSPDSLENIPKEWTPEVKHFCPNVPIILVGNKKDLRNDEHTRRELAKMKQEPVKPEEGRDMANRI
GAFGYMECSAKTKDGVRREVFEMATRAAL

>d1hura_ c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF1}

GNIFANLFKGLFGKEMRILMVLDAAGKTTILYKLKLGEIVTTIPTIGFNVETVEYNISFTVWDVGGQDKIRPL
WRHYFQNTQGLIFVVDSNDRERVNEAREELMRMLAEDELRAVLLVFANKQDLPNAMNAAEITDKLGLHSLR
HRNWIYIQATCATSGDGLYEGLDWLSNQLRNQK

>d1e0sa_ c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF6}

GKVLISKIFGNKEMRILMLGLDAAGKTTILYKLKLGSVTTIPTVGFNVETVYKNVFKNVWDTGGQDKIRPLWR
HYYTGTQGLIFVVDCADRDRIDEARQELHRIINDREMRDAIIIFANKQDLPDAMKPHEIQEKLGLTRIRDRNWY
VQPSCATSGDGLYEGLTWLTNSYK

>d1fzqa_ c.37.1.8 (A:) ADP-ribosylation factor {Mouse (Mus musculus), ARL3}

GLLSILRKLKSAPDQEVRILLGLDNAGKTTLLKQLASEDISHITPTQGFNIKSVSQGFKLNWVDTGGQDKIRPY
WRSYFENTDILIVVIDSADRKRFEETGQELTELLEEKLSCVPVLIFANKQDLLAAPASEIAEGLNLHTIRDRVWQI
QSCSALTGEGVQDGMMNWVCKNV

>d1f6ba_ c.37.1.8 (A:) SAR1 {Chinese hamster (Cricetulus griseus)}

SSVLQFLGLYKKTGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPTLHPTSEELTIAGMTFTFDLGGHIQARRVW
KNYLPAINGIVFLVDCADHERLLESKEELDSLMTDETIANVPILILGNKIDRPEAISEERLREMFGLYGQTTGKGSVS
LKELNARPLEVFMCSVLRQGYGEGFRWMAQYID

>d2ngra_c.37.1.8 (A:) CDC42 {Human (Homo sapiens)}

MQTIKCVVVGDAVGKTCLLISYTTNKFSEYVPTVFDNYAVTMIGGEPYTLGLFDTAGQEDYDRLRPLSYPQT
DVFLVCFSSVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRDDSTIEKLAKNKQKPIPETAEKLARDLKAV
KYVECSALTQKGLKNVFDEAILAALEPPEPKKSRRCVLL

>d1ek0a_c.37.1.8 (A:) Ypt51 {Baker's yeast (Saccharomyces cerevisiae)}

VTSIKLVLLGEAAVGKSSIVLRFVSNDFAENKEPTIGAAFLTQRVTINEHTVKFEIWDTAGQERFASLAPMYYRNA
QAALVVYDVTKPQSFIKARHWVKELHEQASKDIIIALVGNKIDMLQEGGERKVAREEGEKLAEKGLLFFETSAK
TGENVNDFVLGIGEKIPLK

>d1h65a_c.37.1.8 (A:) Chloroplast protein translocon GTPase Toc34 {Garden pea (Pisum sativum)}

VREWSGINTFAPATQTKLLELLGNLKQEDVNSLTILVMGKGGVGKSSTVNSIIGERVVSISPFQSEGPRPVMSRS
RAGFTLNIIDTPGLIEGGYINDMALNIIKSFLDKTIDVLLYVDRLDAYRVNDLKLVAKAITDSFGKGWNAVAL
THAQFSPPDGLPYDEFFSKRSEALLQVVRSGASLKKDAQASDIPVVLIELNSGRCNKNDSDEKVLPNGIAWIPH
QTITEVALNKSESIFVVDKNLIDKLAAD

>d1azsc2 c.37.1.8 (C:36-66,C:202-393) Transducin (alpha subunit) {Cow (Bos taurus)}

VYRATHRLLLGGAGESGKSTIVKQMRILHVNXVLTSGIFETKFQVDVKNFMDVGGQRDERRKWIQCFNDVT
AIIFVVASSSYNMVIREDNQTNRLQEALNLFKSIWNNRWLRTISVILFLNKQDLLAEVKLAGSKIEDYFPEFARYT
TPEDATPEPGEDPRVTRAKYFIRDEFRLISTASGDGRHYCYPHFTCAVDTENIRRVFNDCRDIQRMHLRQYEL

>d1tada2 c.37.1.8 (A:27-56,A:178-342) Transducin (alpha subunit) {Cow (Bos taurus)}

ARTVKLLLLGGAGESGKSTIVKQMKIIHQDGXTGIETQFSFKDLNFRMFDVGGQRSERKKWIHCFCGVTCIIFIAA
LSAYDMVLVEDDEVNRMHESLHLFNSICNHRYFATTISIVLFLNKDDVFSEKIKKAHLSICFPDYNGPNTYEDAGN
YIKVQFLELNMRDVKEIYSHMTCATDTQNVKFVFDAVTDIIKE

>d1bof_2 c.37.1.8 (10-60,182-354) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

KAVERSkmIDRNLRDGEKAAREVKLLLLGGAGESGKSTIVKQMKIIHEAGXTGIVETHFTKDLHFKMFDVGG
QRSERKKWIHCFCGVTAIIFCVALSdydLVAEDEEMNRMHESMKLFDSICNNKWFTDTIILFLNKDDLFEEKIK
KSPLTICYPEYAGSNTYEEAAAYIQCQFEDLNKRKDTKEIYTHFTCATDTKNVQFVFDAVTDVIKNNLKDCGLF

>d1cipa2 c.37.1.8 (A:32-60,A:182-347) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

REVKLLLLGGAGESGKSTIVKQMKIIHEAGXTGIVETHFTKDLHFKMFDVGGQRSERKKWIHCFCGVTAIIFCVAL
SDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTIILFLNKDDLFEEKIKKSPLTICYPEYAGSNTYEEAAAYIQ
CQFEDLNKRKDTKEIYTHFTCATDTKNVQFVFDAVTDVIKNN

>d1fqja2 c.37.1.8 (A:28-60,A:182-344) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

RTVKLLLLGGAGESGKSTIVKQMKIIHQDGYSLEXETQFSFKDLNFRMFDVGGQRSERKKWIHCFCGVTAIIFCVAL
SDYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTIILFLNKDDLFEEKIKKSPLTICYPEYAGSNTYEEAGNYIK
VQFLELNMRDVKEIYSHMTCATDTQNVKFVFDAVTDIIKENL

>d1gota2 c.37.1.8 (A:6-60,A:182-343) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

SAEEKHSRELEKKLKEDAKDARTVKLLLLGGAGESGKSTIVKQMKIIHQDGYSLEXETQFSFKDLNFRMFDVGGQ
RSERKKWIHCFCGVTAIIFCVALSdydLVAEDEEMNRMHESMKLFDSICNNKWFTDTIILFLNKDDLFEEKIKK
SPLTICYPEYAGSNTYEEAGNYIKVQFLELNMRDVKEIYSHMTCATDTQNVKFVFDAVTDIIKEN

>d1efca3 c.37.1.8 (A:8-204) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}

TKPHVNVTIGHVHDHGKTTAAITVLAKEYGGAARAFDQIDNAPEEKARGITINTSHVEYDTPTRHYAHVDC
PGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVDEELLELMEMEV
RELLSQYDFPGDDTPIVRGSALKALEGDAEWEAKILEAGFLDSYIPEPER

>d1efm_1 c.37.1.8 (12-190) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli}

VNVGTIGHVHDHGKTTAAITVLAKEYGGAARXXXXXXXXXXXXGITINTSHVEYDTPTRHYAHVDCPGHA
DYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVDEELLELMEMEVRELLS

QYDFPGDDTPIVRGSALKALEGDAEWEAKILE

>d1etu_1 c.37.1.8 (5-200) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Escherichia coli} FERTKPHVNVTIGHVDHGKTTAAITVLAKEYGAAXXXXXXXXXXXXXGITINTSHVEYDTPTRHYAHV DCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDMVDEELLELLEM EVRELLSQYDFPGDDTPIVRGSALKALEGDAEWEAKILELAGFLDSYIP

>d1exma3 c.37.1.8 (A:3-212) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Thermus thermophilus}

GEFIRTKPHVNVTIGHVDHGKTTAAITFVTAAPNVEVKDYGDIDKAPEERARGITINTAHVEYETAKRHY SHVDCPGHADYIKNMITGAAQMDGAILVVAADGPMPQTREHILLARQVGVPYIIVFMNKVDMVDDPELLD LVEMEVRDLLNQYEFPGDEVPIVRGSALLALEQMHRNPKTRRGENEWVDKIWELLDAIDEYIPT

>d1d2ea3 c.37.1.8 (A:55-250) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Cow (Bos taurus), mitochondrial}

KPHVNVTIGHVDHGKTTAAITKILAEGGGAKFKYEEIDNAPEERARGITINAAHVEYSTAARHYAHTDCPG HADYVKNMITGTAPLDGCILVVAANDGPMPQTREHLLARQIGVEHVVVYVNKADAVQDSEMVELVELEIREL LTEFGYKGEETPIIVGSALCALEQRDPPELGLKSQVQLDAVDTYIPV

>d1f60a3 c.37.1.8 (A:2-240) Elongation factor eEF-1alpha, N-terminal (G) domain {Baker's yeast (Saccharomyces cerevisiae)}

GKEKSHINVVIGHVDGKSTTGHLYKCGGIDKRTIEKFKEKEAAELGKGSFYAWVLDKLKAERERGITALW KFETPKYQVTVIDAPGHRDFIKNMITGTSQADCALIIAGGVGEFEAGISKDGQTREHALLAFTLGVRLIVAVNK MDSVKWDERSFQEIVKETSNIKKVGYNPKTVFVPISGWNGDNMIEATTNAPWYKGWEKETKAGVVKGKTL LEAIDAIEQPSRPT

>d1jnya3 c.37.1.8 (A:4-227) Elongation factor eEF-1alpha, N-terminal (G) domain {Archaeon Sulfolobus solfataricus}

KPHLNLVIGHVDHGKSTLVGRLLMDRGFIDEKTVKEAEAAKLGKESEKFAFLDRLKEERERGVTINLTMR ETKKYFTIIDAPGHRDFVKNMITGASQADAAILVVSACKGEYEAGMSVEGQTREHIIILAKTMGLDQLIVAVNK MDLTEPPYDEKRYKEIVDQVSKFMRSYGFNTNKVRFPVVAPSGDNITHKSENMKWYNGPTLEEYLDQLELPP K

>d1dar_2 c.37.1.8 (1-282) Elongation factor G (EF-G), N-terminal (G) domain {Thermus thermophilus}

MAVKVEYDLKRLRNIGIAAHIDAGKTTTERILYYTGRHKIGEVHEGAATMDFMEQERERGITAATTCFWK DHRINIIDTPGHVDFTIEVERSMRVLGAIIVFDSSQGVEPQSETVWRQAEKYKVPRIAFANKMDKTGADLWL VIRTMQERLGARPVVMQLPIGREDTFSGIIDVLRMKAYTYGNDLTDIREIPIPEEYLDQAREYHEKLVEVAADF DENIMLKYLEEEPTEELVAAIRKGTIDLKITPVFLGSALKNVQLLDAVVVDYLPS

>d1g7sa4 c.37.1.8 (A:1-227) Initiation factor IF2/eIF5b, N-terminal (G) domain {Archaeon Methanobacterium thermoautotrophicum}

MKIRSPIVSLGHVDHGKTTLDHIRGSAVASREAGGITQHIGATEIPMDVIEGICGDFLKFSIRETPGLFFIDTP GHEAFTTLRKRGALADLAILIVDINEGFKPQTQEALNIRMYRTPFVVAANKIDRIHGWRVHEGRPMETFSK QDIQVQQKQLDTKVYELVGLKHEEGFESERFDRVTFASQVSIPIASITGEGIPELLTMLMGLAQQYLREQLKIE

>d1egaa1 c.37.1.8 (A:4-182) GTPase Era, N-terminal domain {Escherichia coli}

DKSYCGFIAIVGRPNVGKSTLNKLLGQKISITSRKAQTRHRIVGIHTEGAYQAIYVDTPLGLHMEEKRAINRLMN KAASSSIGDVELVIFVEGTRWTPDEMVLNLREGKAPVILAVNKVDNVQEKADELLPHLQFLASQMNFLDIVP ISAETGLNVDTIAIVRKHLPEATHHFPE

>d1f5na2 c.37.1.8 (A:7-283) Interferon-induced guanylate-binding protein 1 (GBP1), N-terminal domain {Human (Homo sapiens)}

MTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNLAGKKGFSLGSTVQSHTKGW
MWCVPHPKKPGHILVLLDEGLDVEKGDNQNDSWIFALAVLLSSTFVYNSIGTINQQAMDQLYYTELTHRIR
SKSSPDENENEVEDSADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLTYSLKLKGTSQKDETFLPRLCIRKF
FPKKKCFVFDRPVHRRKLAQLEKLQDEELDPEFVQQVADFCSYIFSNSKTTLS

>d1jwyb_c.37.1.8 (B:) Dynamin G domain {Slime mold (Dictyostelium discoideum)}

DQLIPVINKLQDVFTLGSDPLDLPQIVVVGSSGKSSVLENIVGRDFLPRGSGIVTRRPLILQLTHLPIADDGSQ
TQEWFGEFLHKPNDMFYDFSEIREEIIRDTDRMTGKNKGISAQPINLKIYSPHVVNLTLDLPGITKVPVGQDQPTDI
EQQIRRMVMAYIKKQNAIIVAVTPANTDLANSDALQLAKEVDPEGKRTIGVITKLDLMDKGTDAMEVLTGRVIP
LTLGFIGVINRSQEDIIAKKSIRESLKSEILYFKNHPIYKSIANRSGTAYLSKTLNKLLMFHIRDTLPDLKVVKVSKMLS
>d1br2a2 c.37.1.9 (A:80-789) Myosin S1, motor domain {Chicken (Gallus gallus), pectoral muscle}
PPKFSKVEDMAELTCNEASVLHNLRERYFSGLIYTSGLFCVVNPYKQLPIYESEKIIDMYKGKKRHEMPPHYIAIA
DTAYRSMLQDREDSILCTGESGAGKTENTKKVIQYLAVVASSHHKGKDDTSITQGPSFSYGELEKQLQANPILEA
FGNAKTVKNDNSSRGKFIRINFVTGYIVGANIETYILLEKSRAIRQAKDERTFHIFYLIAGASEQMRNDLLLEGF
NNYTFLSNGHVPPIAQQQDDEMFOETLEAMTIMGFTEEQTSILRVVSSVLQLGNIVFKKERNTDQASMPDNTA
AQKVCHLGMINVTDTRSILTPRIKVGRDVVQKAQTKEQADFAIEALAKAKFERLFRWILTRVNKALDKTKRQG
ASFLGILDIAFGEIFEINSFEQLCINYTNEKLQLQFNHTMFILEQEEYQREGIEWNFIDFGLDLQPCIELIERPTNPP
GVLALLDEECWFPAKDTSFVEKLIQEQQGHAKFQSKSQLKDKTEFCILHYAGKVTYNASAWLTKNMDPLNDN
VTSLLNQSSDKFVADLWKDVDRIVGLDQMAKMTESSLPSASKTKGMFRVGQLYKEQLTKLMTLRTNPNP
FVRCIIPNHEKRAGKLD AHLVLEQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILAANAIPKGMDGKQACIL
MIKALELDPNLYRIGQSKIFFRTGVLAHLEEIRD

>d2mysa2 c.37.1.9 (A:4-33,A:80-843) Myosin S1, motor domain {Chicken (Gallus gallus), pectoral muscle}

DAEMAAFGEAAPYLRKSEKERIEAQNKFDXMNPPKYDKIEDMAMMTHLHEPAVLYNLKERYAAWMITYSG
LFCVTNPYKWLKVNPVVLAYRGKKRQEAPPHIFSISDNAYQFM LTDRENQSILITGESGAGKTVNTRKVIQY
FATIAASGEKKKEEQSGKMQGTLEDQIISANPLLEAFGNAKTVRNDNSSRGKFIRIHFGATGKLASADIETYLEK
SRVTFLQPAERSYHIFYQIMSNKKPELIDMILLTTNPYDYHYVSEGEITVPSIDDQEELEMATDSAIDLGFSADEKTA
IYKLTGAVMHYGNLKFQKQREEQAEPDGTEVADKAAYLMGLNSAELLKALCYPRVGVGNEAVTKGETVSEVH
NSVGALAKAVYEKMFWMVIRINQQLDTQPRQYFIGVLDIAGFEIFDFNSFEQLCINFTNEKLQQFFNHHMF
VLEQEEYKKEGIEWEFIDFGMDLAACIELIEKPMGIFSILEEEMFPKATDTSFKNKLYDEHLGKSNNFQKPKPAK
GKAEAHFSLVHYAGTVDYNISGWLEKNKDPLNETVIGLYQKSSVTLALLFATYGGEAEGGGGKGGKKKGSSF
QTVALFRENLNKLMANLRSTPHFVRCIIPNETKTPGAMEHEVLHQLRCNGVLEGIRICRKGFPSRVLYADFK
QRYRVLNASAPEGQFMDSKKASEKLLGGGDVDHTQYAFGHTKVFVFKAGLGLLEEMRDDKLAEITATQARCR
GFLMRVEYRAMVERRESIFCIQYNVRSMNVKHWPWMKLFKIKPLLK

>d1b7ta4 c.37.1.9 (A:5-28,A:77-835) Myosin S1, motor domain {Bay scallop (Aequipecten irradians)}

FSDPDFQYLA VDRKKLMKEQTAAXMNPPKFEKLEDMANMTYLNEASVLYNLR SRTGSLIYTSGLFCIAVNP
YRRLPIYTDVIAKYRGKRKTEIPPHLFSVADNAYQNMVTDRENQSCLITGESGAGKTENTKKVIMYLAKVACAV
KKKDEEASDKKEGSLEDQI IQANPVLEAGYNAKTRNNNNSRGKFIRIHFGPTGKIAGADIETYLEKSRVTYQQ
SAERNYHIFYQICNSAIPELNDVMLVTPDSGLYSFINQGCLTVDNIDDVEEFKLCDEAFDILGFTKEEKQSMFKCT
ASILHMGE MKFKQR PREEQAESGTAEAEKVAFLCGINAGDLLKALLKPKVGVTEMVTKGQNMNQVVNSV
GALAKSLYDRMFNWLVRRVNKTLDKAKRNYYIGVLDIAGFEIFDFNSFEQLCINYTNERLQQFFNHHMFILEQ
EEYKKEGIAWEFIDFGMDLQMCIDLIEKPMGILSILEEEMFPKADDKSFQDKLYQNHMGKNRMFTKPGKPTR
PNQGPAHFELHHYAGNVPYSITGWLEKNKDPINENVALLGASKEPLVAELKAPEEPAGGGKKKGKSSAFQTI
SAVHRESLNKLMKNLYSTPHFVRCIIPNELKQPGLVDAELVLHQLQCNGVLEGIRICRKGFPSRLIYSEFKQRYSIL

APNAIPQGFVDGKTVSEKILAGLQLQMDPAEYRLGTTKVFFKAGVLGNLEEMRDERLSKIISMFQAHIRGYLIRKAY
KKLQDQRIGLSVIQRNIRKWLVLRNWQWWKLYSKVKP

>d1lvk_2 c.37.1.9 (2-33,80-759) Myosin S1, motor domain {Slime mold (Dictyostelium discoideum)}

NPIHDRTSDYHKYLKVQGDSDLFKLTSDKXRNPFIKFDGVEDMSELSYLNEPAVFHNLRVRYNQDLIYTSGL
FLAVAVNPFKRIPIYTQEMVDIFKGRRRNEVAPHIFAISDVAYRSMLDDRQNQSLITGESGAGKTENTKKVIQYLA
SVAGRNCANGSGVLEQQILQANPILEAFGNAKTRNNNSRGKIEIQFNNAGFISGASIQSYLLEKSRVVFQS
TSERNYHIFYQLLAGATAEEKKALHLAGPESFNYLNQSGCVDIKGVSDEDEFKITRQAMDIVGFSQEEQMSIFKII
AGILHLGNIKFEKGAGEGAVLKDKTALNAASTFGVNPSVLEKALMEPRILAGRDLVAQHVNVEKSSSRDALVK
ALYGRFLWLVKKINNVLCERKAYFIGVLDISGFEIFKVNSFEQLCINYTNEKLQQFFNHMFKEQEYKLEKIN
WTFIDFGLDSQATIDLGRQPPGILALLDEQSVFPNATDNTLITKLHSHFSKKNAKYEEPRFSKTEFGVTHYAGQ
VMYEIQDWLEKNKDPLQQDLELCFKDSSDNVVTLFNDPNIASRAKKGANFLTVAACQYKEQLASLMATLETTN
PHFVRCIIPNNKQLPAKLEDKVVLQLRCNGVLEGIRITRKGFPNRIYADFVKRYYDAPNVPRDAEDSQKATDA
VLKHLNIDPEQFRFGITKIFFRAGQLARIEEARE

>d1mnd_2 c.37.1.9 (2-33,80-690) Myosin S1, motor domain {Slime mold (Dictyostelium discoideum)}

NPIHDRTSDYHKYLKVQGDSDLFKLTSDKXRNPFIKFDGVEDMSELSYLNEPAVFHNLRVRYNQDLIYTSGL
FLAVAVNPFKRIPIYTQEMVDIFKGRRRNEVAPHIFAISDVAYRSMLDDRQNQSLITGESGAGKTENTKKVIQYLA
SVAGRNCANGSGVLEQQILQANPILEAFGNAKTRNNNSRGKIEIQFNNAGFISGASIQSYLLEKSRVVFQS
ETERNYHIFYQLLAGATAEEKKALHLAGPESFNYLNQSGCVDIKGVSDEDEFKITRQAMDIVGFSQEEQMSIFKII
AGILHLGNIKFEKGAGEGAVLKDKTALNAASTFGVNPSVLEKALMEPRILAGRDLVAQHVNVEKSSSRDALVK
ALYGRFLWLVKKINNVLCERAAYFIGVLDISGFEIFKVNSFEQLCINYTNEKLQQFFNHMFKEQEYKLEKIN
WTFIDFGLDSQATIDLGRQPPGILALLDEQSVFPNATDNTLITKLHSHFSKKNAKYEEPRFSKTEFGVTHYAGQ
VMYEIQDWLEKNKDPLQQDLELCFKDSSDNVVTLFNDPNIASRAKKGANFITVAACQYKEQLASLMATLETTN
PHFVRCIIPNNKQLPAKLEDKVVLQLRCNGVLEGIRITRK

>d1bg2__ c.37.1.9 (-) Kinesin {Human (Homo sapiens)}

DLAECNIKVMCRFRPLNESEVNRGDKYIAFKFQGEDTVVIASKPYAFDRVFSQSTSSEQVYNDCAKKIVKDVLEG
YNGTIFAYGQTSSGKHTMEGKLHDPEGMGIIPRIVQDIFNYIYSMDENLEFHVKSYFEIYLDKIRDLLVSKTNL
SVHEDKNRVPYVKGCTERFVCPDEVMDTIDEKGKSNRHVAVTNMNEHSSRHSIFLINVKQENTQTEQKLSKG
LYLVDLAGSEKVKSTGAEGAVLDEAKNINKSLSALGNVISALAEGSTYVPYRDSKMTRILQDSLGGNCRTTIVICCS
PSSYNESETKSTLLFGQRAKTI

>g2kin.1 c.37.1.9 (A;B:) Kinesin {Rat (Rattus norvegicus)}

ADPAECSIKVMCRFRPLNEAEILRGDKFIPFKFGEETVVGQGKPYVFDRVLPPTTQEQQVYNACAKQIVKDVLE
GYNGTIFAYGQTSSGKHTMEGKLHDPEGMGIIPRIVQDIFNYIYSMDENLEFHVKSYFEIYLDKIRDLLVSKTN
LAVHEDKNRVPYVKGCTERFVSSPEEVMDVIDEGKANRHVAVTNMNEHSSRHSIFLINIKQENVETEKKLSKG
LYLVDLAGSEKVKXAKNINKSLSALGNVISALAEGTKTHVPYRDSKMTRILQDSLGGNCRTTIVICCSPSVFNEAETK
STLMFGQRAKTIKNTVSVNLETAEEWKKYKEKEKE

>d1i6ia_c.37.1.9 (A:) Kinesin {Mouse (Mus musculus), kif1a}

GASVKVAVRVRFNSREMSRDKCIIQMSGTTTIVNPKQPKEPKSFSDYWSHTSPEDINYASQKQVYRDI
GEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLCEDLSRINDTTNDNMSYSVEVSYMEI
YCERVRDLLNPKNKGNLRVREHPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNI
IFTQKRHDAETNITTEKVKISLVDLAGSERADSTGAKGTRLKEGANINKSLTLGKVISALAEMDSGPKNKKKK
KTDFIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLSTLRYADRAKQIRNTVSNNHHHH

>d1ii6a_c.37.1.9 (A:) Kinesin {Human (Homo sapiens), mitotic kinesin eg5}

GKNIQVVVRCRPFLAERKASAHSIVECDPVRKEVSVRTGLADKSSRKTYTFDMVFGASTKQIDVYRSVVCPII

DEVIMGYNCTIFAYGQTGTGKFTMEGERSPNEEYTWEEDPLAGIIPRTLHQIFEKLTNGTEFSVKVSLLEIYNE
ELFDLLNPSSDVSERLQMFDPRNKRGVIKGLEEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVFSVT
IHMKETTIDGEELVKIGKLNVLADLAGSENIGRSGAVDKRAREAGNIQSLLGRVITALVERTPHVPYRESKLTRIL
QDSLGGRTTSIIATISPASLNLEETLSTLEYAHRAKNILNKPEV

>d1goja_c.37.1.9 (A:) Kinesin {*Neurospora crassa*}

SSANSIKVVARFRPQRVEIESGGQPIVTFQGPDTCTVDSKEAQGSFTFDRVFDMSCKQSDIFDFSIKPTVDDIL
NGYNGTVFAYGQTGAGKSYTMMGTSIDDPDGRGVIPRIVEQIFTSILSSAANIEYTVRVSYMELYMERIRDLLAP
QNDNLPVHEEKNRGVYVKGLLEIYVSSVQEYEVMRGGNARAVAATNMNQESSRSHSIFVITITQKNVETGS
AKSGQLFLVLAGSEKVGKTGASGQTLLEEAKKINKSLSALGMVINALTGDKSSHVPYRDSLKTRILQESLGGNSRT
TLIINCSPSSYNDAEYLSTLRFGMRAKSINKAKVNAELSPAELKQMLAKAKTQ

>d2ncda_c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional) {*Fruit fly (Drosophila melanogaster)*}

LRQRTEELLRCNEQQAAELETCKEQLFQSNMERKELHNTVMDLRGNIRVFIRPPLSEENRMCCWTYHDE
STVELQSIDAQAKSKMGQQIFSFDQVFHPLSSQSDIFEMVSPLIQSALDGYNICIFAYGQTGSGKTYTMDGVPE
VGVIPRTVDLFDISRGYRNLGWEYEIKATFLEIYNEVLYDLLSNEQKDMEIRMAKNNKNDIYVSNITEETVLDPN
HLRHLMIHTAKMNRTASTAGNERSSRSHAVTKLELIGRHAEKQEISVGSINLVLAGSESPKTSTRMTETKNINR
SLSELTNVIALLQKQDHIPYRNSKLTHLLMPSLGGNSKTLMFINVSPFQDCFQESVKSRLFAASVNSC

>d1f9va_c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional) {*Baker's yeast (Saccharomyces cerevisiae), Kar*}

GNIRVYCRIPALKNLENSDTSLINVNEFDDNSGVQSMEVTKIQNTAQVHEFKFDKIFDQQDTNVDFKEVGQL
VQSSLGYNVCIFAYGQTGSGKFTMLNPGDGIIPSTISHIFNWINKLKKGWDYKVNCIEIYNENIVDLLRSD
NNNKEDTSIGLKHEIRHDQETKTTITNVTSCKLESEEMVEIILKKANKLRSTASTASNEHSSASHSIFIHLSGSNA
KTGAHSYGTNLVLAGSERINVSVVGDRRETQNINKSCLGDVIHALGQPDSTKRHIPFRNSKITYLLQYSL
TGDSKTLMFVNISPSSSHINETLNSLRFASKVNSTRLV

>d1byi_c.37.1.10 (-) Dethiobiotin synthetase {*Escherichia coli*}

SKRYFVTGTDTEVGKTVASCALLQAAKAAGYRTAGYKPVASGSEKTPEGLRNSDALALQRNSSLQLDYATVNPYT
FAEPTSPHIISAQEGRPIESLVMSAGLRALEQQADWVLVEGAGGWFTPLSDTFTFADWVTQEQLPVILVVGVKL
GCINHAMLTQAQVIQHAGLTLAGWVANDVTPPGKRHAEYMTLTRMIPAPLLGEIPWLAENPENAATGKYINLA
LL

>d1qf5a_c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {*Escherichia coli*}

GNNVVVLGTQWGDEGKGKIVDLTERAKYVVRYQGGHNAHTLIVINGEKTVLHLIPSGILRENVTSIIGNGVVL
SPAALMKELEDRGIPVRERLLLSEACPLILDYHVALDNAREKARGAKAIGTTGRGIGPAYEDKVARRGLRVG
DLFDKETFAEKLKEVMEYHNFQLVNYYKAEAVDYQKVLDMAVADILSMVVDSLDQARQRGDFVMFE
GAQGTLIDHGTYPYVTSSNTTAGGVATGSGLGPYVDYVLGILKAYSTRVGAGPFPTELFDETGEFLCKQGNE
FGATTGRRRTGWLDTVAVRAVQLNSLGFCLTKLVDGLKEVKLCVAYRMPDGREVTTPLAADDWKGVE
PIYETMPGWSESTFGVKDRSGLPQAALNYIKRIEELTGPIDIISTGPDRTETMILRDPFDA

>d1dj2a_c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {*Mouse-ear cress (Arabidopsis thaliana)*}

IGSLSQVSGVLGCQWGDEGKGKLVLDILAQHFDIVARCQGGANAGHTIYNSEGKKFALHLVPSGILNEDTCVIG
NGVVVHLPLGLKEIDGLESNGVSKGRILVSDRAHLLFDHQEVDFLRESELAKSFIGTTKRGIGPAYSSKVRNGI
RVGDLRHMDLTPQKLDLSSDAARFQGFKYTPEMLREEVEAYKRYADRLEPYITDTVHFINDSISQKKVLVEG
GQATMLIDFGTYPFVTSSPSAGGICTGLGIAPSVVGDLIGVVKAYTRVSGPFPTENLGTGGDLRLAGQEF
GTTTGRPRRCGWL DIVALKFSCQINGFASLNLTLDVSDLNEIQLGVAYKRSRGTPVKSFPGLRLLEELHVEYE
VLPGWKSDISSVRNYSLPKAQQYVERIEELGVGVPIHYIGIGPGRDALIYK

>d1dj3a_c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Bread wheat (Triticum aestivum)}

ADRVSSLSNVSGVLGSQWGDEGKGKLVVLAPRFIDIVARCQGGANAGHTIYNSEGKKFALHLVPSGILHEGTL
VVNGAVIHVGFFGEIDGLQSNGVSCDGRILSDRAHLLFDLHQVTVDGLREAEELANSFIGTTKRGIGPCYSSKV
TRNGLRVCMDLHMTFGDKLDLFEDAARFEGFKYSKGMKKEEVERYKKFAERLEPFIADTVHVLNESIRQKK
KILVEGGQATMILDIDFGTYPFTSSSPSAGGICTGLGIAPRVIDLIGVVKAYTRVSGPFPTELLGEEGDVLRA
GMEFGTTGRPRRCGWLDIVALKYCCDINGFSSLNLTKLDVSLPEIKLGVSYNQMDGEKLQSFPGLDTLEQ
VQVNYEVLPWDSDISSVRSYSELPQAARRYVERIEELAGVPVHYIGVGPGRDALIYK

>d1j4ba_c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Mouse (Mus musculus)}

AAATGSRVTVVLGAQWGDEGKGKVVDDLLATDADIVSRCQGGNNAGHTVVVDGKEYDFHLLPSGIINTKAVSF
GNGVVIHPLGLFEEAKNEKKGLKDWEKRLIISDRAHLVDFHQAVDGLQEVRQQAQEGKNIGTTKGIGPTYS
SKAARTGLRICDLSDFDEFSARFKNLAHQHQSMPFTLEIDVEGQLKRLKGFAERIRPMVRDGVYFMYEALHGP
PKKVLVEGANALLDIDFGTYPFTSSNCTVGGVCTGLGIPQPNIQDVGVVKAYTRVIGAFPTEQINEIGDLL
QRNGHEWGVTTGRKRCGWLDMILRYAHMVNGFTALALTLDVLSEIKVGISYKLNKGKRIPYFPANQEIL
QKVEVEYETLPWKADTTGARKWEDLPPAQSYVRFVENHMGVAWKWVGVGKSRESMIQLF

>d1eg7a_c.37.1.10 (A:) Formyltetrahydrofolate synthetase {Moorella thermoacetica}

DIEIAQAAKMKPVMELARGLGQEQEDEVLYGKYKAKISLDVYRRLKDPGKLILVTAITPTPAGEGKTTSVGLTD
ALARLGKRMVCLREPSLGPSPGIKGGAAAGGGYAQVVPMEDINLHFTGDIHAVTYAHNLLAAMVDNHLQQG
NVNLNIDPRTITWRRVIDLNERALRNIVIGLLGKANGVPRETGFDISVASEVMACLCLASDLMDLKERFSRKVVGY
TYDGKPVTAGDLEAQGSMALLMKDAIKPNLVQTLENTPAFIHGGPFANIAHGCNSIIATKTALKLADYVVTEAGF
GADLGAEKFYDVKCRYAGFKPDATVIVATVRAKMHHGVPKSDLATENLEALREGFANLEKHIEIGNKFGVPAVV
AINAFPTDEAELNLLYELCAKAGAEVALSWAKGEGGLELARKVLQTLSRPSNFHVLYNLDLSIKDKIAKIATEIY
GADGVNYTAEADKAIQRYESLGYGNLPVMAKTQYSFSDDMTKLGRPRNFTITVREVRLSAGGRILVPITGAIM
TMPGLPKRPAACNIDIDADGVITG

>d1fp6a_c.37.1.10 (A:) Nitrogenase iron protein {Azotobacter vinelandii}

AMRQCAIYGKGGIGKSTTQNLAALAEAMGKKVMIVGCDPKADSTRLLHSKAQNTIMEMAAEAGTVEDLELE
DVLKAGYGGVKCVESGGPEPGVGCAGRGVITAINFOEEGAYEDDDFVFYDVLGDVVCAGFAMPIRENKAQE
YIVCSGEMMAMYAANNISKIGIVKYANSGSVRLGGLICNSRNTDREDELIALANKLTQMIHFVPRDNVVQRA
EIRRMTVIEYDPKAKQADEYRALARKVVDNKLLVIPNPITMDELEELLMEFGIMEVEDESIVGKTAEEV

>d1cp2a_c.37.1.10 (A:) Nitrogenase iron protein {Clostridium pasteurianum}

MRQVAIYGKGGIGKSTTQNLTSGLHAMGKTIIVGCDPKADSTRLLGLAQKSVLDTLREEGEDVELDSILK
EGYGGIRCVESGGPEPGVGCAGRGIIITSINMLEQLGAYTDDLDYVFYDVLGDVVCAGFAMPIREGKAQEYIIVAS
GEMMALYAANNISKIGIQKYAKSGGVRLGGIICNSRKVANEYELDAFAKELGSQLIHFPVPRSPMVTKAEINKQTV
IEYDPTCEQAEYRELARKVDAELFVIPKPMTQERLEEILMQYG

>d1hyqa_c.37.1.10 (A:) Cell division regulator MinD {Archaeon Archaeoglobus fulgidus}

VRTITVASGKGGTGKTTITANLGVALAQLGHDTVADITMANLELILGMELPVTLQNVLAGEARIDEAIYVG
PGGVKVVPGVSLEGLRKANPEKLEDVLTQIMESTDILLDApaglersaviaaaaqellvnpeissitDGLKTK
IVAERLGTKVLGVVVNRITTLGIEMAKNEIEAILEAKVIGLIPEDPEVRRAAAYGKPVVLSPNSPAARAIVELANYI
A

>d1g3qa_c.37.1.10 (A:) Cell division regulator MinD {Archaeon Pyrococcus furiosus}

MGRIISIVSGKGGTGKTTVTANLSVALGDRGRKVLAVDGDLTMANLSVLGVDDPDVTLHDVLAGEANVEDAIY
MTQFDNVYVLPGADEVHEVLIKADPRKLPEVIKSLKDKFDFILIDCPAGLQLDAMSAMLSGEEALLVTNPEISCLT
DTMKVGIVLKKAGLAILGFVLNRYGRSDRDIPPEAAEDVMEVPLLAVIPEDPAIREGTLEGIPAVKYKPEKGAKA
FVKLAEIEKLA

>d1iona_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon Pyrococcus horikoshii}
MTRIISIVSGKGGTGKTTVTANLSVALGEMGRKVLAvgdltmanlslvlgvddvnitlhvdvlagdakledaiy
MTQFENVYILPGAVDWEHVIKADPRKLPEVIKSLKGKYDFILIDCPAGLQLRAMSAMLSGEEAILVTNPEISCLTD
TMKVGMVLKKAGLAILGFILNRYGRSERDIPPEAAQDVMDVPLAVIPEDPVIREGTLEGIPAVKYKPESKGAQA
FIKLAEEVDKLAGIKAKI

>d1jpna2 c.37.1.10 (A:89-296) GTPase domain of the signal sequence recognition protein Ffh {Thermus aquaticus}
EARLPVLKDRNLWFLVGLQGSGTKTTAAKLALYYKGKGRRPLLVAADTQRPAAREQLRLLGEKVGVPVLEVMDG
ESPESIRRVEEKARLEARDLILVDTAGRLQIDEPLMGEALARKEVLPDEVLLVLDAMTGQEALSVARAFDEKVG
VTGLVLTKLDGDARGGAALSARHVTGKPIYFAGVSEKPEGLEPFYPERLAGRILGMGD

>d1j8mf2 c.37.1.10 (F:87-297) GTPase domain of the signal sequence recognition protein Ffh {Archaeon Acidianus ambivalens}
DKEPKVIPDKIPYVIMLVGVQGTGKTTAGKLAYFYKKKGFKVGLVGADVYRPAALEQLQQLGQQIGVPVYGEP
GEKDVGIAKRGVEKFLEKMEIIIVDTAGRHYGEEAALLEEMKNIYEAIKPDEVTLVIDASIGQKAYDLASKFN
QASKIGITIITKMDGTAKGGAALSABAATGATIKFIGTGEKIDELEVFNPRRFVARLHHHH

>d1fts_2 c.37.1.10 (285-495) GTPase domain of the signal recognition particle receptor FtsY {Escherichia coli}
PLNVEGKAPFVILMVGVNGVGKTTIGKLARQFEQQGKSVMLAAGDTFRAAAVEQLQVWGQRNNIPVIAQH
TGADSASVIFDAIQAAKARNIDVLIADTAGRLQNKSHELMEEKKIVRVMKKLDVEAPHEVMLTIDASTGQNAVS
QAKLFHEAVGLTGITLKDGTAKGGVIFSADQFGIPRYIGVGERIEDLRPFKAADDFIEALFAR

>d1ihua1 c.37.1.10 (A:1-296) Arsenite-translocating ATPase ArsA {Escherichia coli}
MQFLQNIPPYLFFTGKGGVGKTSISCATAIRLAEGQKRVLLSTDPA_NVQVFSQTIGNTIQAIASVPGLSALEID
PQAAAQQYRARIVDPIKGVLPDDVVSSINEQLSGACTTEIAAFDEFTGLTDASLLTRFDHIIFDTAPTGHТИRLLQL
PGAWSSFIDSNEPEGASCLGPMAGLEKQREQYAYAVEALSDPKRTRLVVARLQKSTLQEVARTHLELAIGLKNQ
YLVINGVLPKTEAANDTLAAAIWEREQEALANLPADLAGLPTDTLFLQPVNMGVSALSRLLSTQP

>d1ihua2 c.37.1.10 (A:308-586) Arsenite-translocating ATPase ArsA {Escherichia coli}
QRPDIPSLSALVDDIARNEHGLIMLMGKGGVGKTTMAAAIAVRЛАDMGFVHLTSDPAAHLSMTLNGSLNN
LQVSRIDPHEETERYRQHVLETKGKELDEAGKRLLEEDLRSPCTEEIAVFQAFSRVIREAGKRFVVMDTAPTGHTL
LLL DATGAYHREIAKKMGEKGHTTPMMLLQDPERTKVLLVTPLEAANLQADLERAGIHPWGWIINNS
LSIADTRSPLLRMRAQQELPQIESVKRQHASRVALPVLA SeptGIDKLKQLAGHHH

>d2reb_1 c.37.1.11 (3-268) RecA protein, ATPase-domain {Escherichia coli}
DENKQKALAAALGQIEKQFGKGSIMRLGEDRSMDVETISTGSLSLDIALGAGGLPMGRIVEIYGPESSGKTTLT
QVIAAAQREGKTCAFIDAEHALDPIYARKLGVDIDNLCSQPDGEQALEICDALARSGAVDVIVVDSVAALTPK
AEIEGEIGDSHMGLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTGGNALKFYASVRDI
RRIGAVKEGENVGSETRVKVVKNKIAAPFKQAEFQILYGEGI

>d1g19a1 c.37.1.11 (A:1-269) RecA protein, ATPase-domain {Mycobacterium tuberculosis}
MTQTPDREKALELAVAQIEKSYKGKSVMRGDEARQPISVIPTGSIALDVALGIGGLPRGRVIEIYGPESSGKTTV
ALHAVANAQAAGGVAAFIDAEHALDPDYAKKLGVDTSLLVSPQDTGEQALEICDALIRSGALDIVVIDSVAAL
VPRAELEGEMGDSVGLQARLMSQALRKMTGALNNNSGTTAIFINQLRDKIGVMFGSPETTGGKALKFYASVR
MDVRRVETLKDGTAvgNRTRVKVVKNKCLAPFKQAEFDILYKGKI

>d1cr1a_ c.37.1.11 (A:) Gene 4 protein (g4p, DNA primase), helicase domain {Bacteriophage T7}
MRERIREHLSSEESVGLLFSGCTGINDKTLGARGGEVIMVTSGSGMGKSTFVRQQALQWGTAMGKKVGLAM
LEESVEETAEDLIGLHNVRVRLQSDLKREIIENGKFDQWFDELFGNDTFHYDSFAEAETDRLLAKLAYMRSGLG

CDVIILDHISIVVSAGESDERKIMDNLMTKLGFAKSTGVVIVCHLKNPDKGKAHEEGRPVSIIDL RGSGALR
QLSDTIIALERNQQGDMPNLVLRILKCRFTGDTGIAGYMEYNKETGWLEPSSY

>d1g8ya_ c.37.1.11 (A:) Hexameric replicative helicase repA {Escherichia coli, plasmid rsf1010}

ATHKPINILEAFAAAAPPPLDYVLPNMVAGTVGALVSPGGAGKSMLALQLAAQIAGGPDLLEV GELPTGPVIYLP A
EDPPTAIHHRLHALGAHLSAERQAVADGLLIQPLIGSLPNIMAPEWFDSLKRAAEGRRLMVLDTLRRFHIEEE
NASGPMAQVIGRMEAIAADTGSIVFLHHASKGAAMMGAGDQQQASRGSSVLVDNIRWQSYLSSMTSAEA
EEWGVDDDQRRFFVRFGVSKANYGAPFADRWFRRHDGGVLKPA

>d1e9ra_ c.37.1.11 (A:) Bacterial conjugative coupling protein TrwB {Escherichia coli}

VGQGEFGGAPFKRFLRGTRIVSGGKLKRMTREKAKQVTAGVPMRDAEPRHLLVNGATGTGKVLLRELAYT
GLLRGDRMVIVDPNGDMILSKFGRDKDIIINPYDQRTKGWSFFNEIRNDYDWQRYALS VVPRGKTDEAEWAS
YGRLLLRETAKKLALIGTPSMRELFHWTTIATFDDLRFLEGTLAESLFLAGSNEASKALT SARFVLSKLPEHVTM
PDGDFSIRSWLEDPNGGNLFITWREDMGPALRPLISAWVDVVCTSILS LPEEPKRRWL FIDELASLEKLASLAD
ALTGRKAGLRVVA GLQSTS QLDDVYGVKEAQT RASFRSLVVLGGSRDPKT NEDMSL S LGEHEVERDRYSKN
TGKHGSTGRALER VRERVVMPAEIANLPDLTAYVGAGNRPIAKQFANRQPAFVEGT

>d1e79a3 c.37.1.11 (A:95-379) Central domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

VDVPVGELLGRVVDALGNAIDGKGPIGSKARRVGLKAPGIIPRISVREPMQTGIKAVDSLVP IGRGQRELIIGD
RQTGKTSIAIDTIINQKRFNDGTDEKKKLYCIYVAIGQKRSTVAQLVKRLTDADAMKYTIVS ATASDAAPLQYLA P
YSGCSMGEYFRDNGKHALIYDDLSKQAVAYRQMSLLRRPPGREAYPGDVFYLHSRLLERAAKMND AFGGG S
LTALPVIETQAGDV SAYIPTNVISITDGQIFLET ELYKGIRPAINVGLSVSRVGSAQ

>d1e79d3 c.37.1.11 (D:82-357) Central domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

IRIPVGPETLGRIMNVIGEPIDERGPIKTQFAAIHAEAPEFVEMSVEQEILVTGIKVV DLLAPYAKGGKIGLFGGA
GVGKTVLIMELINNVAKAHGGSVFAGVGERTREGNDLYHEMIESGVINLK DATSKVALV YGQMNEPPGARAR
VALTGLTVAEYFRDQEGQDVLLFIDNIFRFTQAGSEVSALLGRIPS AVGYQPTLATDMGT M QERITTTKGSITSV
QAIYVPADDLTD PAPATTFAHLDATT VLSRAIAELGIYPAVDPLDSTSRI

>d1skyb3 c.37.1.11 (B:96-371) Central domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

EVPGVGETLGRV VNPLGQP DGLGP VETTETRPIESRAPGVMDRRSVHEPLQTG IKAIDALVPIGRGQRELIIGDR
QTGKTSVAIDTIINQKDQNMIC YVAIGQKE STVATV VETLA KHGAPD YTI VTA SASQ PA PLLF APYAGVAM GE
YFMIMGKHVLV VIDDLSKQAAAYRQLSLLRRPPGREAYPGDIFYLHSRLLERAAKLSDAKGGSL TALPFVETQA
GDISAYIPTNVISITDGQIFLQSDLFFSGVRPA INAGLSV SRVGGA AQ

>d1skye3 c.37.1.11 (E:83-356) Central domain of alpha and beta subunits of F1 ATP synthase {Bacillus sp., strain ps3}

ISPVVGQVTLGRVF NVLGEPIDLEG DIPADARRDPIHRPAPKFEELATEVEILET GIKVV DLLAPYIKGGKIGLFGGA
GVGKTVL IQELIH NIAQEHGGISV FAGVGERTREGNDLYHEM KDSGVISK TAMVFGQMNEPPGARM RVALTG
LTMAEYFRD EQGQDG L FIDNIFRFTQAGSEVS ALLGRMPSAIGYQPTLATEM GQLQERITSTAKSITSIQAIYV
PADDYTD PAPATTFS HLDATT NLERKLAEMGIYPAVDPLVSTS RALAP

>d1fx0a3 c.37.1.11 (A:97-372) Central domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

QIPVSEAYLGRVINALAKPIDGRGEITASES RLIESPAPGIMSRRS VYEPLQTGLIAIDAMIPVGRGQRELIIGDRQT
GKTA VATDTILNQQGQN VIVYVAIGQKASSVAQVVTNFQERGAMEY TIVVAETADSPATLQYLAPYTGAALAE
YFMYRERHTLIIYDDLSKQAAQAYRQMSLLRRPPGREAYPGDV FYLHSRLLERAAKLSSLLGE GSMTALPIVETQA

GDVSAYIPTNVISITDGQIFLSADLFNAGIRPAINVGISVRVGSAAQ

>d1fx0b3 c.37.1.11 (B:98-377) Central domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

LSVPVGGPTLGRIFNVLGEPVDNLRPVDTRTSPIHRSAPAFTQLDTKLSIFETGIKVVNLLAPYRGGKIGLFGGA
GVGKTVLIMELINNIAKAHHGSVFGGVGERTREGNDLYMEMKESGVINEQNIAESKVALVYGQMNEPPGAR
MRVGLTALTMAEYFRDVNEQDVLLFIDNIFRFVQAGSEVSALLGRMPSAVGYQPTLSTEM GSLQERITSTKEGSI
TSIQAVYVPADDLTDPA PATTFAHLDATTVLSRGLAAKG IYPAVDPDLS TSTM LQP

>d1cbua_ c.37.1.11 (A:) Adenosylcobinamide kinase/adenosylcobinamide phosphate guanylyltransferase CobU {Salmonella typhimurium}

MILVTGGARSGKS RHA EALIGDAPQVLYIATS QILDDEMAARIQHHKDGRPAHW RTAE CWRHLD TLITADLAP
DDAILLECITTMVTNLLF ALGGENDPEQW DYAMERAIDDEI QILIAACQRCPAKV VLTNEV GMGIV PENRLA
RHF RDIA GRVNQ RLAAADEVWL VVSGIGVKIK

>d1g5ta_ c.37.1.11 (A:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}

ERGIIIVFTGNGKGKTTA AFGTAARAVGHGKNVGVVQFIKGTWPNGERNLLEPHGVEFQVMATGFTWETQNR
EADTAACMAVWQHGKRLADPLDMVVLDELTYMVAYDYLPLEEVISALN ARPGHQ TVIITGRGCHRDILDLA
DTVSEL RPVKHA

>d1g64b_ c.37.1.11 (B:) ATP:corrinoid adenosyltransferase CobA {Salmonella typhimurium}

QQRQQKV KDRV D DARVAQA QAE ERGIIIVFTGNGKGKTTA AFGTAARAVGHGKNVGVVQFIKGTWPNGERNLLE
PHGVEFQVMATGFTWETQNR EADTAACMAVWQHGKRLADPLDMVVLDELTYMVAYDYLPLEEVISALN
ARPGHQ TVIITGRGCHRDILDLA DTVSEL RPVKHA FDAGV KAQM GIDY

>d1b0ua_ c.37.1.12 (A:) ATP-binding subunit of the histidine permease {Salmonella typhimurium}
NKLHVIDLHKRYGGHEV LKG VSLQARAGDV ISI GSSG SKSTFLRCINF LEKPSEGAI IVNGQNI NLRD KDGQL
KVADKNQLRLRTRL TMVFQHFNLWSHMTVLEN VME APIQV LGLSKHD RERALKYLA KV GIDERA AQG KYPV
HLSGGQQQR VSIR ALA M EPDV LLFDE PTSAL DPEL VGEV L RIM QQLAEEG KTMVVVTHE MG FARHV S SHVI
FLHQ GKIEEGDPEQVFGNPQSPRLQQFLKGSLKKLEH

>d1g6ha_ c.37.1.12 (A:) MJ1267 {Archaeon Methanococcus jannaschii}

TMEILRTENIVKYFGEFKALDGVSISVNKGDTVLIIGPNGSGKSTLINVITGFLKADEGRVYFENKDITNKEPAELYH
YGIVRTFQTPQPLKEMTVLENLLIGEICPGESPLNSFYKKWIPKEEEMVEKA FK IFLKL SHLYDRKAGE LSGGQ
MKLVEIGRALMTNPKMIVMDEPIAGVAPGLAHDIFNHVLELKAKGITFLIEHRLDIVNYIDHLYVMFNGQIIAE
GRGEEEIKNVLSDPKV VEIYIGE

>d1f3oa_ c.37.1.12 (A:) MJ0796 {Archaeon Methanococcus jannaschii}

MIKLKNVTKTYKMGE EIIYALKNVNLNIKEGEFV SIMGPSGSKSTMLNIIGCLDKPTEGEVYIDNIKTNDL DDE
LTKIRR DKIGFV FQQFN LIPLLTALEN VELPLIF KYRGAMS GEERRKRALECLKMAELEERFANHKPNQLSGGQQ
QRVAIARALANNPPII LADEPTGALDSKTGEKIMQ LKKL NEEDGKTVVVTHDINVARFGERII YLK DG EVEREE
KLRGF

>d1jj7a_ c.37.1.12 (A:) Peptide transporter Tap1, C-terminal ABC domain {Human (Homo sapiens)}
GLLTPLHLEG LVQFQDVSFAYPNRPDV LV LQGLTFTLRPGEV TALVGPNGSGKSTVA ALLQNL YQPTGGQLL D
KPLPQYEHRYLHRQVA AVGQEPQVFG RSLQENIAYGLTQKPTMEE ITAAVKG SAHSF ISGLPQGYDTEVDEAG
SQLSGGQRQ AVALARALIRKPCV LID DATSAL DANSQ LQVEQ LLYE SPERYSRVLLITQHLSL VEQADHILFLEG
GAIREGGTHQQLMEKKGCY WAMVQA

>d1g2912 c.37.1.12 (1:1-240) Maltose transport protein MalK, N-terminal domain {Archaeon Thermococcus litoralis}

MAGVRLVDVWKVFGEVTAVERMSLEVKDGEFMILLGPSGCGKTTLRMIAGLEEPSRGQIYIGDKLVADPEKGIFVPPKDRDIAMVFQSYALYPHMTVYDNIAPLKLKVPRQEIDQRVREVAELGLTELNKPRELGGQRQRA
ALGRAIVRKPVFLMDEPLSNLDALKLQRQLGVTTIYVTHDQVEAMTMDRIAVMNRGVLQ
QVGSPDEVYDKPANTFVAGFI

>g1f2t.1 c.37.1.12 (A.;B;) Rad50 {Archaeon Pyrococcus furiosus}

MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFTKVGARDTYIDLIFEK
DGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTPESSKAISAFMEKLIPYNIFLNAYIRQQGQIDAILESXAREA
ALSKIGELASEIFAEFTEGKYSEVVRAEENKVRLFVWEGKERPLTFLSGGERIALGLAFRLAMSPLYLAGESISLLIL
DEPTPYLDEERRRKLTIMERYLKKIPQVILVSHDEELKDAADHVIRISLENGSSKVEVVS

>g1ii8.1 c.37.1.12 (A.;B;) Rad50 {Archaeon Pyrococcus furiosus}

MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFTKVGARDTYIDLIFEK
DGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTPESSKAISAFMEKLIPYNIFLNAYIRQQGQIDAILESDEARE
KVVREVLNLDKFETAYKKLSELKKTINNRIKEYRDILARTEXRERVKKEIKDLEKAKDFTEELIEKVKKYKALAREAAL
SKIGELASEIFAEFTEGKYSEVVRAEENKVRLFVWEGKERPLTFLSGGERIALGLAFRLAMSPLYLAGESISLLIL
PTPYLDEERRRKLTIMERYLKKIPQVILVSHDEELKDAADHVIRISLENGSSKVEVVS

>d1e69a_ c.37.1.12 (A;) Smc head domain {Thermotoga maritima}

MRLKKLYKGFKSFGPSLIGFSDRVTAIVPNGSGKSNIIDAICWWVFGEQSKKELRASEKFDMIFAGSENLPAG
SAYVELVFEENGEEITVARELKRTGENTYYLNGSPVRLKDIDRFAUTGLVDFYSIVGQQIDRIVNASPEERLE
SSKHPTSLVPRGSYQRVNESFNRFISLLFFGEGRLNIVSEAKSILDAGFEISIRKPGRRDQKLSLLSGGEKALVGLA
LLFALMEIKPSPFYVLDEVDSPLDDYNAERFKRLLKENSHTQFIVITHNKIVMEAADLLHGVTMVNGVSAIPV
EV

>d1qhla_ c.37.1.12 (A;) Cell division protein MukB {Escherichia coli}

RGKFRSLTLINWNNGFFARTFDLDELVTTLSGGNGAGKSTTMAAFVTALIPDLTLLHFRNTTEAGATGSRDKGLH
GKLKAGVCYSMLDTINSRHQRVVGVRLQQVAGRDRKVDIKPFAIQGLPMSVQPTQLVTETLNERQARVPLN
ELDKKLEAMEGVQFKQFNSITDYHSLMFDLGIIARRRSASDRSKFYRLIEASLYGGISSAIRSLRDYLLPEN

>d1ewqa2 c.37.1.12 (A:542-765) DNA repair protein MutS, the C-terminal domain {Thermus aquaticus}

YVRPRFGDRLQIRAGRHPVVERRTEFPNDLEMAHELVLTGPNMAGKSTFLRQTALIALLAQVGSFVPAEEAH
LPLFDGIYTRIGASDDLADGGKSTFMVEMEEVALILKEATENSLVLLDEVGRGTSSLGVIAATAEAHLERRYTL
FATHYFELTALGLPRLKNLHVAAREEAGGLVFYHQVLPGPASKSYGVEVAAMAGLPKEVVARARALLQAMAAR

>d1e3ma2 c.37.1.12 (A:567-800) DNA repair protein MutS, the C-terminal domain {Escherichia coli}
YTCPTFIDKPGIRITEGRHPVVEQVLNEPFIANPLNLSPQRRMLIITGPNMGGKSTYMRQTALIALMAYIGSYVPA
QKVEIGPIDRIFTRVGAADDLASGRSTFMVEMTETANILHNATEYSLVMDEIGRGTSTYDGLSLAWACAENLA
NNIKALTFLATHYFELTQLPEKMEGVANVHLDALEHGDTIAFMHSVQDGAASKSYGLAVAALAGVPKEVIKRAR
QKLRELESIS

>d1pj_1 c.37.1.13 (1-318) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}

MNFLSEQLLAHLNKEQQEAVRTTEGPLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFTNKAAREMR
ERVQSLLGAAEDVVWISTFHSMCVRILRRDIRGINRNFSILDPTDQLSVMKTILKEKNIDPKKFEPRTILGTISA
AKNELLPPPEQFAKRASTYYEKVSDVYQEYQQRLLRNHSDFDDLMTTIQLFDRVPDVLYHYYQYKFQYIHIDEY
QDTNRQAQYTLVKKLAERFQNICAvgDADQSIYRWGADIQNILSFERDYPNAKVILLEQNYRSTKRILQAANEVI
EHNVNRKPKRIWTENPEG

>d1pj_2 c.37.1.13 (319-651) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}

KPILYYEAMNEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKANIPYQIVGGLKFYDRKEIK
DILAYLRVIANPDDLSLLRIINVPKRGIGASTIDKLVRYAADHELSFEALGELEMIGLAKAAGALAAFRSQLEQ
WTQLQEYVSVELVEELDKSGYREMLKAERTIEAQSRLENLDEFLSVTKHFENVSDDKSLIAFLTDLALISLDDEL
DGTEQAAEGDAVMLMTLHAAKGLEFPVVFLIGMEEGIFPHNRSLEDDDEMEEERRLAYVGITRAEEELVLTSQ
MRTLFGNIQMPPSRFLNEIPAHLLETASR

>g1qhh.1 c.37.1.13 (A:,B:,C:,D:) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}
MNFLSEQQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNILAITFTNKAAREMR
ERVQSLLGGAAEDVVISTFHSMCVRILRRDIRGINRNFSILDPTDQLSVMKTLKEKNIDPKKFEPRTILGTISA
AKNELLPPEQFAKRXXYEKVSDVYQEYQQRLLRNHSLFDDLIMTTIQLFDRVDPVLHYYQYKFQYIHIDEYQD
TNRAQYTLVKKLAERFQNICAvgdADQSIYRWRGADIQNLSFERDYPNAKVILLEQNYRSTKRLQAANEVIEH
NVNRKPRIWTENPEGKILYYEAMNEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVMEEMLLKAN
IPYQIVGGLKFYDRKEIKDILAYLRVIANPDDLSLLRIINVPKRGIGASTIDXLFEALGELEMIGLAKAAGALAAFR
SQLEQWTQLQEYVSVELVEELDKSGYREMLKAERTIEAQSRLENLDEFLSVTKHFENVSDDKSLIAFLTDLALIS
XGDAVMLMTLHAAKGLEFPVVFLIGMEEGIFPHNRSLEDDDEMEEERRLAYVGITRAEEELVLTSQAMRTLFGN
IQMDPPSRFLNEIPAHLLETASR

>d1uaaa1 c.37.1.13 (A:2-307) DEXX box DNA helicase {Escherichia coli, RepD}
RLNPGQQQAVEVTGPCLVLAGAGSGKTRVITNKIAHLIRGCGYQARHIAAVTFTNKAAREMKERVGQTLGRK
EARGLMISTFHTLGLDIKREYAALGMKANFSLFDDTDQLALLKELTEGLIEDDKVLLQQLISTISNWKNDLKTPSQ
AAASAIGERDRIFAHCYGLYDAHLKACNVLDFFDLILLPTLLLQANEEVRKRWQNKIRYLLDEYQDTNTSQYELV
KLVGSRARFTVVGDDDSIYSWRGARPQNLVLLSQDFPALVKVILEQNYRSSGRILKAANILIANNPHVFEKRLF
SELG

>d1uaaa2 c.37.1.13 (A:308-640) DEXX box DNA helicase {Escherichia coli, RepD}
YGAELKVLSANNEEHEAERTVGELIAHHFVNKTQYKDYLGYRGNHQSRVFEKFLMQNRPYKISGGTSFFSRPEI
KDLLAYLRLVLTNPDDDSNFLRIVNTPKREIGPATLKKLGEWAMTRNKSMTASFDMGLSQLSGRGYEALTRFTH
WLAEIQRLAEREPIAAVRDLIHGMDYESWLYETSPSPKAAEMRMKVNQLFSWMTEMLEGSELDEPMTLTQ
VVTRFTLRRMMERGESEEELDQVQLMTLHASKGLEFPYVYMVGMEGFLPHQSSIDEVDNIDEERRLAYVGITR
AQKELTFTLCKERRQYGELVRPEPSRFLLPEPQDDLIW

>d1hv8a1 c.37.1.13 (A:3-210) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}

VEYNMFNELNLSNDNILNAIRNKGFEKPTDIQMVKVPLFLNDEYNIVAQARTGSGKTASFAIPLIELVNENNGIEAI
LTPTRELAIQVADEIESLKGKGNKNLKIAKIYGGKAIYPQIKALKNANIVVGTGPRILDHINRGTNLKNVKYFILDEAD
EMLNMGFIKDVEKILNACNKDKRILLFSATMPREILNLAKKYMGDYSFIKAKI

>d1hv8a2 c.37.1.13 (A:211-365) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}

NANIEQSYVEVNENERFEALCRLLNKEFYGLVFCCKTRDTKELASMLRDIGFKAGAIHGDSLQSREKVIRLFKQ
KKIRILIATDMSRGIDVNDLNCVINYLQPQNPESYMHRIGHTGRAGKKGKAIISIINRREYKKLRYIERAMKLKIK
LK

>d1gm5a3 c.37.1.13 (A:286-549) RecG helicase domain {Thermotoga maritima}
ETLPERILEKRKLLGVKDAYYGMHFPKTFYHLEKARERLAYELFVLQLAFQKIRKEREKHGGIPKKIEGKLAEEFI
SLPFKLTNAQKRAHQEIRNDMISEKPMNRLQGDVGSGKTVVAQLAILDNYEAGFQTAFMVPTSILAIQHYRRT
VESFSKFNIHVALLIGATTPESEKEKIKSGLRNGQIDVVIGTHALIQEDVHFKNLGLVIIDEQHRGVKQREALMNK
GKMDTLVMSATPIPRSMALAFYGDLDVTVIDEMPP

>d1gm5a4 c.37.1.13 (A:550-755) RecG helicase domain {Thermotoga maritima}
GRKEVQTMLVPMDRVNEVYEFVRQEVMRGGQAFIVYPLIEESDKLNVKSAEMYEYLSKEVFPEFKLGLMHG

RLSQEEKDRVMLEFAEGRYDILVSTTVIEVGIDVPRANVMVIENPERGLAQLHQLRGRVGRGGQEAYCFLVVG
DVGEEAMERLRFITLNTDGKIAEYDLKTRGPGEFFGVVKQHGLSGFKVADLYRDLKLLEW
>d1fuka_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}
IKQFYVNVEEEYKYECLTDLYDSISVTQAVIFCNTRRKVEELTTKLRNDKFTVSAIYSDLPQQERDTIMKEFRSGSS
RILISTDLLARGIDVQQVSLVINYDLPANKENYIHRIGRRGRKGVAINFVTNEDVGAMRELEKFYSTQIELPS
DIATLLN
>d1qdea_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}
IQTNYDKVYKFDDMELDENLLRGVFGYGFEEPSAIQQRAIMPIEGHDVLAQAQSGTGKTGTFSSIAALQRIDTS
VKAPQALMLAPTRELALQIQKVVMALAFHMDIKVHACIGGTSFVEDAEGLRDAQIVVTPGRVFDNIQRRRFR
TDKIKMFILDEADEMLSSGFKEQIYQIFTLLPPTTVVLLSATMPNDVLEVTTKFMNRNPVRILV
>d1c4oa1 c.37.1.13 (A:2-409) Nucleotide excision repair enzyme UvrB {Thermus thermophilus}
TFRYRGPSPKGDQPKAIAGLVEALRDGERFVTLLGATGTGKTVTMAKVIEALGRPALVLAPNKILAAQLAELREL
FPENAVEYFISYYDYYQPEAYVPKDLYIEKDASINPEIERLHSTTRSLRRDVIVVASVSAIYGLGDPREYRARNL
VVERGKPYPREVLLERLLELGYQRNDIDLSPGRFRAKGEVLEIFPAYETEPIRVELFGDEVERISQVHPVTGERLREL
PGFVLFPATHYLSPEGLEEILKEIEKLWERVRYFEERGEVLYAQRLKERTLYDLEMLRVMGTCPGVENYARYFTGK
APGEPPYTLLDYFPEDFLVFLDESHVTVPQLQGMYRGDYARKKTLVDYGFRLPSALDNRPLRFEELERVSVQVF
VSATPGPFELAHSGRVVEQIIP
>d1c4oa2 c.37.1.13 (A:410-583) Nucleotide excision repair enzyme UvrB {Thermus thermophilus}
TGLLDPPLRVVKPTENQILDLMEGIRERAARGERTLTVLTVRMAEELTSFLVEHGIRARYLHHELDALKRQALIRD
LRLGHYDCLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRAARNARGEVWLYADRVSSEMQRAIEE
TNRRRALQEAYNLEHGIPETV
>d1d9xa1 c.37.1.13 (A:2-414) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}
EGRFQLVAPYEPQGDQPQAIKLVGDLRGVKHQTLGATGTGKFTISNVIAQVNKPTLVIHNKTLAGQLYSE
LKEFFPHNAVEYFVSYDYYQPEAYVPQTDYIEKDAKINDEIDKLRHSATSALFERRDVIIVASVSCIYGLGSPEEY
RELVVSLRVGMEIERNALLRRLVDIQYDRNDIDFRGTFRVRGVDVVEIFPASRDEHCIRVEFFGDEIERIRAEVDALT
GKVLGEREHVAIFPASHFTREEKMRLAIQNIEQELEERLAEQRAQGKLEAQRLEQRTTRYDLEMMREMGCFCG
IENYSRHLALRPPGSPYTLIDYFPDDFLIIVDESHVTLPQLRGMYNGDRARKQVLVDHGFRRLPSALDNRPLTFEE
FEQKINQIYVSATPGPYELEHSPGVVEQIIP
>d1d9xa2 c.37.1.13 (A:415-595) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}
TGLLDPTIDVRPTKGQIDDLIGEIRERVERNERLTVTTLKKMAEDLTDYLKEAGIKVAYLHSEIKTLERIEIIRDLRLG
KYDVLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRAARNANGHVIMYADTITKSMEIAIQETKRRR
AIQEEYNRKHGIVPRTVKKEIRDV
>d1jr3a2 c.37.1.13 (A:3-242) gamma subunit of DNA polymerase III, N-domain {Escherichia coli}
YQLVARKWRPQTADFVVGQEHVLTALANGLSQLGRHHAYLFSGTRGVGKTSIARLLAKGLNCETGITATPCGVCD
NCREIEQGRFVDLIEIDAASRTKVEDTRDLDNVQYAPARGRFKVYLIDEVHMLSRHSFNALLKLEPPEHVKF
LATTDPKLPVTLSRCLQFHAKLDVEQIRHQUEHILNEEHIAHEPRALQLLARAEGSLRDALS LTDQAIASGD
GQVSTQAVSAMLG
>d1a5t_2 c.37.1.13 (1-207) delta prime subunit of DNA polymerase III, N-domain {Escherichia coli}
MRWYPWLWLPDFEKVASYQAGRHHALLIQALPGMGDDALIYALSRYLLCQQPQGHKSCGHCRGCQLMQA
GTHPDYTYLAPEKGKNTLGDAREVTEKLNEHARLGGAKVVWVTDAAALLKLEPPEAETWFFL
ATREPERLLATLSRCSRCLHYLAPPPEQYAVTWLSREVTMSQDALAALRLSAGSPGAALALFQG
>d1jqlb_ c.37.1.13 (B:) delta subunit of DNA polymerase III, N-domain {Escherichia coli}

MIRLYPEQLRQLNEGLRAAYLLLGNPDLLQESQDAVRQVAAAQGFEEHHTFSIDPNTDWNAIFSLCQAMSLF
ASRQTLLLLPENGPNAAINEQLLTGLLHDDLLIVRGNKLSQAQENAAWFTALANRSVQVTCQ
>d1jr3d2 c.37.1.13 (D:1-211) delta subunit of DNA polymerase III, N-domain {Escherichia coli}
MIRLYPEQLRQLNEGLRAAYLLLGNPDLLQESQDAVRQVAAAQGFEEHHTFSIDPNTDWNAIFSLCQAMSLF
ASRQTLLLLPENGPNAAINEQLLTGLLHDDLLIVRGNKLSQAQENAAWFTALANRSVQVTCQTPEQAQQLPR
WVAARAKQLNLELDDAANQVLCYEGNLLALAQALERLSLWPDGKLTLPRTVEQAVNDAAH
>d1iqpa2 c.37.1.13 (A:2-232) Replication factor C {Archaeon Pyrococcus furiosus}
SEEIREVKVLEKPWVEKYRPQRLLDIVGQEHIVKRLKHYVKTGSMPHLLFAGPPGVGKTTAALALARELFGENW
RHNFLENASDERGINVIREKVKEARTKPIGGASFIIFLDEADALTQDAQQALRRTMEMFSSNVRFILSCNYSS
KIIEPIQSRCAlFRFRPLRDEDIAKRLRYIAENEGLTEGLQAILYIAEGDMRAINILQAAAALDKITDENVM
VAS
>d1hqca2 c.37.1.13 (A:5-242) Holliday junction helicase RuvB {Thermus thermophilus}
ALRPKTLDEYIGQERLKQKLRVYLEAAKARKEPLEHLLLFGPPGLGKTTLAHVIAHELGVNLRVTSGPAIEKPGDLA
AILANSLEEGDILFIDEIHRLSRQAEELYPAMEDFVMDIVIGQGPAARTIRLELPRFTLIGATTRPGLITAPLLSRFG
IVEHLEYYTPEELAQGVMRDARLLGVRITEAALEIGRRSRGTMRVAKRLFRRVRDFAQVAGEEVITRERALEAL
AALGLDE
>d1in4a2 c.37.1.13 (A:17-254) Holliday junction helicase RuvB {Thermotoga maritima}
QFLRPKSLSDEFIQQENVKKLSALEAKMRGEVLDHVLLAGPPGLGKTTLAHIIASELQTNIVTSGPVLVKQG
DMAAILTSLERGDVLFIDEIHRLNKAVEELLYSAIEDFQIDIMIGKGPSAKSIRIDIQPFTLVGATTRSGLSSPLRSRF
GIILELDFYTVKELKEIIKRAASLMVEIEDAAAEMIAKRSRGTPRIAIRLTKVRDMLTVVKADRINTDIVLKTME
VLNIDD
>d1fnna2 c.37.1.13 (A:1-276) CDC6, N-domain {Archaeon Pyrobaculum aerophilum}
AIVVDDSVFSPSYVPKRLPHREQQLQQLDILLGNWLNPNGHHYPRATLLGRPGTGKTVTLRKLWELYKDKTAR
FVYINGFIYRNFTAIIGEIARSLNIPFPRRGLRDEFALLVEHLRERDLYMFVLDDAFNLAPDILSTFIRLGQEADK
LGAFRIALVIGHNDAVLNNLDPSTRGIMGKYVIRFSPYTKDQIFDILLDRAKAGLAEGSYSEDILOQMIADITGAQ
TPLDTNRGDRALARIDLILYRSAYAAQQQNKRKHIAPEDVRKSSKEVLFG
>d1d2na_ c.37.1.13 (A:) Hexamerization domain of N-ethylmaleimide-sensitive fusion (NSF) protein {Chinese hamster (Cricetulus griseus)}
EDYASYIMNGIICKWGDGVTRVLDDGELLVQQTNSDRTPLVSVLLEGPPHSKGKTLAAKIAEESNPFPIKICSPDK
MIGFSETAKCQAMKKIFDDAYKSQQLSCVVVDIERLLDYVPIGPRFSNLVLQALLVLLKAPPQGRKLLIIGTTSRK
DVLQEMEMLNAFSTTIHVPNIATGEQLLEALELLGNFKDKERTTIAQQVKGKKWIGIKKLLMLIEMSLQMDPE
YRVRKFALLREEGASPLD
>d1e32a2 c.37.1.13 (A:201-458) Membrane fusion atpase p97, D1 domain {Mouse (Mus musculus)}
VGYDDVGGCRKQLAQIKEMVELPLRHPALFKAIGVKPPRGILLYGPPGTGKTLIARAVANETGAFFLINGPEIMS
KLAGESESNLRAFEEAEKNAPAIIFIDEIADAIAPKREKTHGEVERRIVSQLTLMGLKQRAHVIVMAATRPNS
IDPALRRGFRFDREVDIGIPDATGRLEILQIHTKNMKLADDVDLEQVANETHGHVGADLAALCSEAALQAIRKK
MDLIDLEDETIDAEMVMSLAVTMDDFRWALSQ
>d1g6oa_ c.37.1.13 (A:) Hexameric traffic ATPase, HP0525 {Helicobacter pylori}
LSAEDKKFLEVERALKEAALNPLRHATEELFGDFLK MENITEICYNGNKVVWVLKNNGEWQPFDRKAFSLS
RLMHFARCCASFKKKTIDNYENPILSSNLANGERVQIVLSPVTNDETISISIRIPSKTTYPHSFFEEQGFYNLLDNK
EQAISAIKDGIAIGKNVIVCGGTGSGKTTIYSIMEFIPKEERIISIEDTEEIVFKHHKNYTQLFFGGNITSADCLKSCL
RMRPDRIILGELRSSEAYDFYNVLCSGHKGTLTLHAGSSEEAFIRLANMSSNSAARNIKFESLIEGFKDLIDMIV
HINHHHKQCDEFYIK
>d1ht1e_ c.37.1.13 (E:) HslU {Escherichia coli}

HSEMTPREIVSELDKHIIGQDNAKRSVIALRNRWRRMQLNEELRHEVTPKNILMIGPTGVGKTEIARRLAKLA
NAPFIKVEATKFTEVGYVGKEVDSIIRDLTAAVKMVRVQAIEKNRYRAEELAERILDVLIPPAKNNWGQTEQQ
QEPSAARQAFRKKLREGQLDDKEIEIDLAAAPMGVEIMAPPGMEEMTSQLQSMFQNLGGQKQKARKLKIKD
AMKLILLIEEAALKVNPEELQDAIDAVEQHGIVFIDEIDKICKRGESSGPDVSRGVQRDLPLVEGCTVSTKHG
MVKTDHILFIASGAFQIAKPSDLIPELQGRLPIRVELQALTSDFERILTEPNASITVQYKALMATEGVNIEFTDSGI
KRIAEEAWQVNESTENIGARRLHTVLERLMEEISYDASDLSGQNITIDADYVSKHLDALVADEDLSRFIL
>d1g41a_c.37.1.13 (A:) HsIU {Haemophilus influenzae}
SEMPREIVSELDQHIIQGADAKRAVAIALRNRWRRMQLQEPLRHEVTPKNILMIGPTGVGKTEIARRLAKLAN
APFIKVEATKFTEVGYVGKEVDSIIRDLTDSAMKLRQQEIKNRARAEDVAEERILDALLPPAKNQWGEVENH
DSHSSTRQAFRKKLREGQLDDKEIEIDVSAGVSMGVEIMAPPGMEEMTNQLQSLFQNLGSDKTKRKMKIKD
ALKALIDDEAAKLINPEELQKAIDAVEQNGIVFIDEIDKICKKGEGYSGADVSREGVQRDLPLVEGCTVSTKHGM
VKTDHILFIASGAFQVARPSDLIPELQGRLPIRVELTALSAADFERILTEPHASLTEQYKALMATEGVNIAFTDAV
KIAEAAFRVNEKTENIGARRLHTVMERLMDKISFSASDMNGQTVNIDAAYVADALGEVVENEDLSRFIL
>d1g8pa_c.37.1.13 (A:) ATPase subunit of magnesium chelatase, Bchl {Rhodobacter capsulatus}
RPVFPFAIVGQEDMKLALLTAVDPGIGGVLFQDRGTGKSTAVRALAALLPEIEAVEGCPVSSPNVEMIPDWA
TVLSTNVIRKPTPVVLPLGVSEDREVGAIDIERAISKGEKAFPGLLARANRGYLYIDECLNLEDHVLDLLVAQ
SGENVVERDGLSIRHPARFVLVSGNPREEGDLRPQLLDRFGLSVEVSPRDVETRVEVIRRRTDYDADPKAFLEE
WRPKDMDIRNQILEARERLPKVEAPNTALYDCAALCIALGSDGLRGELLLRSARALAALEGATAVGRDHLKRVA
TMALSHRLRRDPLDEAGSTARVARTVEETLP
>d1a1va1 c.37.1.14 (A:190-325) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}
PPAVPQSFQVAHLHAPTGSGKSTKVPAAAYAAQGYKVLVLPNSVAATLGFAYMSKAHGVDPNIRTGVRTITTGS
PITYSTYGKFLADGGCSGGAYDIICDECHSTDATSIIGITVLDQAETAGARLVVLATATP
>d1a1va2 c.37.1.14 (A:326-624) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}
PGSVTVPHPNIEEVALSTTGEIPFYGKAIPLEVIKGGRHIFCHSKKKDELAALKVALGINAVAYYRGLDVSIVIPTS
GDVVVATDALMTGFTGDFDSIDCNCVTQTVDFSLDPTFTIETTLPQDAVSRTQRRGRTGRGKPGIYRFVA
PGERPSGMFDSSVLCCEYDAGCAWYELTPAETTVRLRAYMNTPGLPVCQDHLEFWEGVFTGLTHIDAHFLSQ
KQSGENFPYLVAYQATVCARAQAPPSWDQMWKCLIRLKPTLHGPTPLYRLGAVQNEVTLHPITKYIMTCMS
>d1cu1a3 c.37.1.14 (A:326-631) HCV helicase domain {Human hepatitis C virus (HCV), different isolates}
PGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIRGGRHLIFCHSKKKDELAALKSLGLGINAVAYYRGLDVSIVIPTIG
DVVVATDALMTGTYGDFDSIDCNCVTQTVDFSLDPTFTIETTVPQDAVSRSQRRGRTGRGRRGIYRFVTP
GERPSGMFDSSVLCCEYDAGCAWYELTPAETSVRLRAYNTPGLPVCQDHLEFWESVFTGLTHIDAHFLSQTKQ
AGDNFPYLVAYQATVCARAQAPPSWDQMWKCLIRLKPTLHGPTPLYRLGAVQNEVTLHPITKYIMACMSA
DLEVVT
>d1gkub1 c.37.1.16 (B:1-250) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}
AAAAAAAAAAAAAAAAAAAAASLCLFPEDFLKEFVEFFRKCVGEPRAIQKMWAKRILRKES
FAATAPTVGKTSFGLAMSLFLALKGKRCYVIFPTSLVIQAAETIRKYAEKAGVGTEENLIGYYHGRIPKREKENFM
QNLRNFKIVITTTQFLSKHYRELGHFDFIFVDDVDAILKASKNVDKLLHLLGFHYDLKTSWVGARGCLMVSTA
TAKKGKKAELFRQLLNFDIGSSRIT
>d1gkub2 c.37.1.16 (B:251-498) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

VRNVEDVAVNDESISTLSSILEKLGTTGGIYARTGEEAEIYESLNKFRIGIVTAKKGDYEKFVEGEIDHLIGTAHY
GTLVRGLDLPERIRFAVFVGCPSPRVIEDIDSLSQMVKLLAYLYRNVDEIERLLPAVERHIDEVREILKKVMGKER
PQAKDVVVREGEVIFPDLRTYIQGSGRTSRLFAGGLTKGASFLLLEDDSELLSAFIERAKLYDIEFKSIDEVDFEKLSR
ELDESRDRYRRR

>d1gl9b1 c.37.1.16 (B:2-250) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus fulgidus}

IPVVYSNLCPVCGGDLESKEIEKHVCFRKRSCLFPEDFLLKEFVEFFRKCVGEPRAIQKMWAKRILRKFESFAATA
PTGVGKTSFLAMSLFLALKKRCYVIFPTSLLVIQAAETIRKYAEKAGVGTEENLIGYYHGRIPKREKENFMQNLR
NFKIVITTTQFLSKHYRELGHDFIFVDDVDAILKASKNVDKLLHLLGFHYDLKTKSWVGEARGCLMVSTATAKKG
KKAELFRQLLNFDIGSSRIT

>d1ble_ c.38.1.1 (-) Fructose permease, subunit IIb {Bacillus subtilis}

MNIVLARIDDRFIHGQILTRWIKVHAADRIIVVSDDIAQDEMRTKLILSVAPS NVKASAVSVSKMAKFHS PRYE
GVTAMILLFENPSDIVS LIEAGVPIKTVNVGGMRFENHRRQITKS VTEQDIKAFETLSDKGVKLELRQLPSDASE
DFVQILRNVT

>d1d0va_ c.39.1.1 (A:) Nicotinate mononucleotide:5,6-dimethylbenzimidazole phosphoribosyltransferase (CobT) {Salmonella typhimurium}

LHALLRDIPAPDAEAMARTQQHQIDGLLKPPGSLGRLETLAVQLAGMPGLNGTPQVGEKAVLVMCADHGVWD
EGVAVSPKIVTAIQAANMTRGTTGCVLAAQAGAKVHVIDVGIDAEP IPGVVNMRVARGCGNIAVGPAMS RL
QAEALLLEVSR YACDLAQRGVTLFGVGE LGMAN TTPAAMVSVFTGSDAKEVVGIGANLPPS RIDNKV DVVRR
AIAINQP NPRDGIDVLSKVGGFDLVGMTGVLGAARCGLPVLDGFLSYA ALAACQIAPAVRPYLIPSHFSAEK
GARIALAHLSMEPYLHMAMRLGE GSGAALAMP IVEAACAMFHNM GELAASNIVLP

>d1chd_ c.40.1.1 (-) Methyl esterase CheB, C-terminal domain {Salmonella typhimurium}

LLSSEK LIAIGASTGGTEAIRHVLQPLPLSSPAVIITQHMPPGFRSFAERLNKLCQISVKEAEDGERVLP GHAYIAP
GDKH MELARSGANYQIKIHDGPPVNRHPSVDVLHFSVAKHAGR NAVG VILTGMGNDGAAGMLAMYQAG
AWTIAQNEASC VVFGMPREAINMGGVSEVV DLSQVS QQMLAKISAGQAIRI

>d1csee_ c.41.1.1 (E:) Subtilisin {Bacillus subtilis, carlsberg}

AQTV PYGIPLIKADKVQAQGF KG ANVKVAVL DTG I QASHPD LN VGGASFVAGEAYNTDNGNGH GT HVAGTV A
ALDNTTGVLGVAPS VSLYAVKVLN SSGSGSYGIVS GIEWATTNGMDV INMSLGGASG STAMKQAVDNAY ARG
VVVVAAGNSGNSGSTNTIGYPAKYDSVIAVGAVD SNSNRAS FSSVGAELEV MAPGAGVYSTYPTNTYATLNG
TSMASPHVAGAAA LILSKHPNLSASQ VRNRLSSTATY LGSSF YYGKGLINVEAAA Q

>d1bh6a_ c.41.1.1 (A:) Subtilisin {Bacillus licheniformis}

AQTV PYGIPLIKADKVQAQGYKG ANVKVGI IDTG IASSHTDLKV VGGASFVGESYNTDNGNGH GT HVAGTV A
LDNTTGVLGVAPN VSLYAI KV LNS SGSGSYA IVSGIEWATQ NGLDV INMSLGGPSG STALKQAVD KAY ASGIV V
VAAAGNSGNSGSQ NTIGYPAKYDSVIAVGAVD SNSNRAS FSSVGSE LEV MAPGAGVYSTYPSNTY TS LNGT SM
ASPHVAGAAA LILSKYPTLSASQ VRNRLSSTATNL GDSF YYGKGLINVEAAA Q

>d1gci_ c.41.1.1 (-) Subtilisin {Bacillus l entus}

AQSVPWG ISRVQAPAAHN RGLTGS GVKA VLD TGISTH PDLN IRGGASFV PGEP STQDG NGH GT HVAGTIA AL
NN SIGV LGVAP SAELYAVKVLGAS GSGSVSSIAQGLE WAGN NGM H V ANLS GSPSPSAT LEQAV NSAT SRGV LV
VAASGN SGAGSI SYPAR YANAM AVGATD QNN RAS FSQY GAGL DIVAPGV NVQSTY PGSTY ASLNGT SMAT P
HVAGAAA LVKQKNP SWNS NVQIRNHLKNTATSLG STNLYGSGL VN AEAAT R

>d1s01_ c.41.1.1 (-) Subtilisin {Bacillus amylo liquefaciens, Novo/BPN'}

AQSVPYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSH PDLKVAGGASFV PSETPNFQDDNS HGTHVAGTV A

ALDNSIGVLGVAPSSALYAVKVLGDAGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVASG
VVVVAAGNEGSTGSSSTVGYPGKYPVIAVGAVDASNQRASFSSVGPELDVMAPGVUSICSTLPGNKYGAKSG
TSMASPHVAGAAALILSKHPNWTNTQVRSSLQNTTKLGDSFYKGKLINVQAAAQ
>d1sue_ c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}

AKCVSYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHDLNVAGGASFVPSETNPFDQDNNSHGHVAGTVL
AVAPSASLYAVKVLGADGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVASGVVVAAAG
NEGTGSSSTVGYPGKYPVIAVGAVDSSNQRASFSSVGPELDVMAPGVUSICSTLPGNKYGAKSGTSMASPHV
AGAAALILSKHPNWTNTQVRSSLLENTTCLGDSFYKGKLINVQAAAQ

>d1sup_ c.41.1.1 (-) Subtilisin {Bacillus amyloliquefaciens, Novo/BPN'}

AQSVPYGVSQIKAPALHSQGYTGSNVKVAVIDSGIDSSHDLKVAGGASMVPSETNPFDQDNNSHGHVAGTV
AALNNSIGVLGVAPSASLYAVKVLGADGSGQYSWIINGIEWAIANNMDVINMSLGGPSGSAALKAAVDKAVAS
GVVVVAAAGNEGSTGSSSTVGYPGKYPVIAVGAVDSSNQRASFSSVGPELDVMAPGVSIQSTLPGNKYGAYN
GTSMASPHVAGAAALILSKHPNWTNTQVRSSLLENTTCLGDSFYKGKLINVQAAAQ

>d1meea_ c.41.1.1 (A:) Messentericopeptidase {Bacillus mesentericus}

AQSVPYGISQIKAPALHSQGYTGSNVKVAVIDSGIDSSHDLNRGGASFVPSETNPYQDGSSHGHVAGTIAA
LNNSIGVLGVAPSASLYAVKVLDSLTSQYQYSWIINGIEWAIANNMDVINMSLGGPTGSTALKTVVDKAVSSGIVV
AAAAGNEGSSGSTSTVGYPAKYPSTIAVGAVNSANQRASFSSAGSELDVMAPGVSIQSTLPGGTGAYNGTSM
ATPHVAGAAALILSKHPTWTNAQVRDRLESTATYLGSFFYYKGKLINVQAAAQ

>d1dbia_ c.41.1.1 (A:) Thermostable serine protease {Bacillus sp., AK.1}

WTPNDTYQQYQYGPQNTYTDYAWDVTKGSSGQEIAVIDTGVDYTHPDLDGKVIKGDFVDNDYDPMDLNN
HGTHVAGIAAAETNNATGIAGMAPNTRILAVRALDRNGSGTLSADIADAIYAADSGAEVINLSLCDCHTTLEN
AVNYAWNKGSSVVAAGNNGSSTTFEPASYENVIAVGAVDQYDRLASFSNYGTWVDVVAPGVDIVSTITGNR
YAYMSGTSMASPHVAGLAALLASQGRNNIEIRQAIEQTADKISGTGTYFKYGRINSNAVTV

>d1thm_ c.41.1.1 (-) Thermitase {Thermoactinomyces vulgaris}

YTPNDPYFSSRQYGPQKIQAPQAWDIAEGSGAKIAIVDTGVQSNHPDLAGKVVGGWDFVDNDSTPQNGNG
HGTHCAGIAAAVTNSTGIAGTAPKASILAVRVLDNSGSGTWTAVANGITYAADQGAKVISLSGGTVGNGLQ
QAVNYAWNKGSSVVAAGNAGNTAPNYPAYSNIAIAVASTDQNDNKSSTYGSWVDVAAPGSSIYSTYPTST
YASLSGTSMATPHVAGVAGLLASQGRSASNIRAAIENTADKISGTGTYWAKGRVNAYKAVQY

>d1ic6a_ c.41.1.1 (A:) Proteinase K {Fungus (Tritirachium album), strain limber}

AAQTNAPWGLARISSTSPGTSTYYDESAGQGSCVYVIDTGEASHPEFEGRAQMVKYYYSSRDGNGHGTHC
AGTVGSRTYGVAKKTQLFGVKVLDNGSGQYSTIIAGMDFVASDKNNRNCPKGVASLSGGYSSVNSAAA
RLQSSGMVAVAAGNNNADARNYSPASEPSVCTVGASDRYDRSSFSNYGSVLDIFGPGTDILSTWIGGSTRSI
SGTSMATPHVAGLAAYLMTLGKTTAACRYIADTANKGDLNSIPFGTVNLAYNNYQA

>d1ga6a_ c.41.1.2 (A:) Serine-carboxyl proteinase PSCP {Pseudomonas sp.}

AGTAKGHNPTEFPTIYDASSAPTAANTVGIITIGGSQTLQDLQQFTSANGLASVNTQTIGTSSNGDYSDDQ
QQQGEWDLDSQSIVSGAGGAQVQLLFYMAQDQSASGNTLQAFNQAVSDNVAKVINVSLGWCEDANAD
GTLQAEDRIFATAAAQGQTFSVSSGDEGVYECNRGYPDGSTYSVSWPASSPNIAVGGTTLYTSAGAYSNET
VWNEGLDSNGKLWATGGGVSYESKPSWQSVSGTPGRRLLPDISFDAAQGTGALIINYGQLQQIGGTLASP
IFVGLWARLQSANSNSLGFPAAFSYASSTPSLVHDVKSGNNNGYGGYGYNAGTGWDPWGSLDIAKLSAYI
RSNGF

>d1d3va_ c.42.1.1 (A:) Arginase {Rat (Rattus norvegicus)}

KPIEIGAPFSKGQPRGGVEKGAALRKAGLVEKLKETEYNRDHGLAFVDVPNDSPFQIVKNPRSVGKANEQ
LAAVVAETQKNGTISVVLGGDHSMAIGSISGHARVHPDLCVIWVDAHTDINTPLTSSGNLHGQPVAFLKELK
GKFPDVPGFSWVTPCISAKDIVYIGLRDVDPEHYIIKTLGIKYFSMTEVDKLIGKVMEETFSYLLGRKKRPIHLS

FDVDGLDPVFTPATGTPVVGGLSYREGLYITEEYKTGLLSGLDIMEVNPTLGKTPPEVTRTVNTAVALTSCFGTK
REGNHK

>d2ceva_c.42.1.1 (A:) Arginase {Bacillus caldovelox}

KPISIIGVPMDLGQTRRGVDMGPSAMRYAGVIERLERLHYDIEDLGDIPIGKAERLHEQGDSRLRNLKAVAЕANE
KLAAAVDQVVQRGRFPLVGGDHSAIGTLAGVAKHYERLGVWYDAHDVNTAETSPSGNIHGMPALAASLG
GHPALTQIGGYSPKIKPEHVVILIGVRSLSDEGEKKFIREKGKIKIYTMEVDRGMTRVMEETIAYLKERTDGVL
DLDGLDPSDAPGVGTPVIGGLTYRESHLAMEMLAEAQIITSAEEFVEVNPILDERNKTASVAALMGSLFGEKLM

>d1c3pa_c.42.1.2 (A:) HDAC homologue {Aquifex aeolicus}

KKVKLIGTLDYGKYRYPKNHPLKIPRVSSLRFKDAMNLIDEKELIKSRPATKEELLFHTEDYINTLMEAERCQCVP
KGAREKYNIGGYENPVSYAMFTGSSLATGSTVQAIEFLKGNVAFNPAGGMHHAFKSANGFCYINNPAGVIEY
LRKKGFKRILYIDLDAHCDGVQEAFYDTDQVFVSLHQSPPEYAFPFEGFLEEIGEGKGKGYNLNIPPKGLNDN
EFLFALEKSLEIVKEVFEPEVYLLQLGTDPLLEDYLSKFNSNAFLKAFNIVREVFGEGVYLGGGGYHPYALARAW
TLIWCESGREVPEKLNNAKELLKSIDFEEFDEVDRSYMLETLKDPWRGGEVRKEVKDTLEKAKA

>d1hf2a2_c.102.1.1 (A:1-99) Cell-division inhibitor MinC, N-terminal domain {Thermotoga maritima}

MVDFKMTKEGLVLLIKDYQNLEEVLNAlSARITQMGGFFAKGDRISLMIENHNKHSQDIPRIVSHLRNLGLEVSQ
ILVGSTVEGKENDLKQSQRTTVE

>d1jkea_c.110.1.1 (A:) D-Tyr tRNA_{Tyr} deacylase {Escherichia coli}

MIALIQRVTRASVTVEGEVTGEIGAGLLVLLGVEKDDDEQKANRLCERVLGYRIFSDAEGKMNLNVQQAGGSVL
VVSQFTLAADTERGMRPSFSKGASPDRAEALYDYFVERCRQQEMNTQTGRFAADMQSVLVNDGPVTFWLQV

>d1nocb_c.43.1.1 (B:) Chloramphenicol acetyltransferase {Escherichia coli}
ITGYTTVDISQWHRKEHFEAQSVAQCTYNQTVQLDITAFLKTVKKNKHKFYPAPIHILARLMNAHPEFRMAMK
DGEVIVWDSVHPCYTVFHEQTETFSSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVS
FTSFDLNVANMDNFFAPVFTMGKYYTQGDVKLMLPAIQVHHAVCDGFHVGRMLNELQQYCDEWQG

>d3cla_c.43.1.1 (-) Chloramphenicol acetyltransferase {Escherichia coli}

MNYTKFDVKNWVRREHFEFYRHLPCGFSLTSKIDITLKKSLDDSSAYKFYPVMIYliaQAVNQFDELRMAIKDD
ELIVWDSVDPQFTVFHQETETFSALSCPYSSIDQFMVNLSVMERYKSDTKLFPQGVTPENHLNISALPWVNF
DSFNLNVANFTDYFAPIITMAKYQQEGDRLLLPLSVQVHHAVCDGFHVVARFINRLQELCNSKLK

>d1eaf_c.43.1.1 (-) Dihydrolipoamide acetyltransferase {Azotobacter vinelandii}

IPPIPPVDFAKYGEIEEVPMTRLMQIGATNLHRSWLNVPHTQFESADITEALEFRVAQKAVAKKAGVKLTVLPL
LLKACAYLLKELPDFNSSLAPSGQALRKYYHIGFAVDTDGLLVPVIRNVQDKSLLQLAAEAAELAEKARSKKLG
ADAMQGACFTISSLGHIGGTAFTPIVNAPEVAILGVSKASMQPVWDGKAFQPRMLPLSLSYDHRVINGAAAA
RFTKRLGDLADIRAILL

>d1b5sa_c.43.1.1 (A:) Dihydrolipoamide acetyltransferase {Bacillus stearothermophilus}

AAAKPATTEGEFPETREKMSGIRRAIAKAMVHSKHTAPHVTLMDEADVTKLVAHRKKFKAIAEKGIKLTFLPYV
VKALVSALREYPVLNTSIDDETEIIQKHYYNIGIAADTDRLGLVPVIKHADRKPIFALAQEINELAEKARDGKLTPG
EMKGASCTITNIGSAGGQWFTPVINHPEVAILGIGRIAEKPIVRDGEIVAAPMLALSFDHMRIDGATAQKALN
HIKRLLSDPELLM

>d1e2o_c.43.1.1 (-) Dihydrolipoamide succinyltransferase {Escherichia coli}

ARSEKRVPMTRLRKRAERLLEAKNSTAMLTTFNEVNMKPIMDLRKQYGEAFEKRHGIRLGFMFSFYVKAVVEA
LKRYPEVNASIDGDDVVYHNYFDVSMAVSTPRGLVTPVLRDVDTLGMADIEKKIKELAVKGRDGKLVEDLTGG
NFTITNGGVFGSLMSTPIINPPQSAILGMHAIKDRPMAVNGQVEILPMMYLALSYDHRLIDGRESVGFLVTIKEL
LEDPTRLLDV

>d1phr_ c.44.1.1 (-) Tyrosine phosphatase {Cow (Bos taurus)}

VTKSVLVCLGNICRSPIAEVFRKLVDQNIISDNWVIDSGAVSDWNVGRSPDPRAVSCLRNHGINTAHKARQ
VTKEDFTFDYILCMDESNLRLNRKSNQVKNCRAKIELLGSYDPQKQLIIEDPYYGNDADFETVYQQCVRCCR
AFLEKVR

>d5pnt_ c.44.1.1 (-) Tyrosine phosphatase {Human (Homo sapiens)}

AEQATKSVLFCLGNICRSPIAEVFRKLVDQNISENWRVDSAATSGYEIGNPPDYRGQSCMKRHGIPMSHVA
RQITKEDFATFDYILCMDESNLRLNRKSNQVKTCKAKIELLGSYDPQKQLIIEDPYYGNDSDFETVYQQCVRCCR
AFLEKAH

>d1d1qa_ c.44.1.1 (A:) Tyrosine phosphatase {Baker's yeast (Saccharomyces cerevisiae)}

IEKPKISVAFIALGNFCRSPMAEAIFKHEVEKANLENRFNKIDSFGTSNYHVGESPDHRTVSICKQHGVKINHKGK
QIKTKHFDEYDYIIGMDESNIINNLKKIQPEGSKAKVCLFGDWNTNDGTQTIIEDPWYQDIQDFEYNFKQITYFS
KQFLKKE

>d1jf8a_ c.44.1.1 (A:) Arsenate reductase ArsC {Staphylococcus aureus}

DKKTIYFISTGNSARSQMAEGWGKEILGEGWNVYSAGIETHGVNPKAIEAMKEVDidisNHTSDLIDNDILKQS
DLVVTLCSDADNNCPILPPNVKKEHWGFFDPAGKEWSEFQRVRDEIKLAIKFKLR

>d1jl3a_ c.44.1.1 (A:) Arsenate reductase ArsC {Bacillus subtilis}

NKIIYFLCTGNSCRSQLMAEGWAKQYLGDEWKVYSAGIEAHGLNPNAVKAMKEVGIDISNQTSIDIIDSDILNNA
DLVVTLCGDAADKCPMTPPHVKEHWGFFDPAGKEWSEFQRVRDEIGNRLKEFAETGK

>d1iiba_ c.44.2.1 (A:) Enzyme IIB-celllobiose {Escherichia coli}

KKHIYLSSAGMSTSLLVSKMRAQAEKYEVPIIEAFPETLAGEKGQNADVLLGPQIAYMLPEIQRLLPNKPVEV
IDSLLYGVGDGLGVLKAAVAAIKAAA

>d1vhra_ c.45.1.1 (A:) VH1-related dual-specificity phosphatase, VHR {Human (Homo sapiens)}

SVQDLNDLLSDGSGCYSLPSQPCNEVPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSMHVNTNANFYKD
SGITYLGKANDTQEFLNLSAYFERAADFIDQALAQKNGRVLHCREGYSRSPTLVIAYLMMRQKMDVKSALSIVR
QNREIGPNDGFLAQCLQLNDRLAKEGKLKP

>d1mkp_ c.45.1.1 (-) Mapk phosphatase Pyst1 (mkp3) {Human (Homo sapiens)}

ASFPVEILPFLYLGCAKDSTNLDVLEFGIKYILNVTPNLPNLFENAGEFKYKQIPISDHWSQNLSQFFPEAISFIDE
ARGKNCGVLVHSLAGISRSVTVTAYLMQKLNLSMDAYDIVKMKKSNIISPNFNMGQLDFERTL

>d1d5ra2 c.45.1.1 (A:14-187) Phosphoinositide phosphatase Pten (Pten tumor suppressor), N-terminal domain {Human (Homo sapiens)}

RRYQEDGFDDLTYIYPNIIAMGFPAAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNLCAERHYDTAKFNCRVAQY
PFEDHNPPQLELIKPFCEDLDQWLSEDDNHVAIHKAGKGRGVMICAYLLHRGKFLKAQEALDFYGEVRTR
DKKGVTIPSQRRYVYYSYLLKNHLD

>d1i9sa_ c.45.1.1 (A:) mRNA capping enzyme, triphosphatase domain {Mouse (Mus musculus)}

KIPPRWLNCPRRGQPVAGRFLPLKTMGPRYDSQVAEENRFHPSMLSNYLKSLKVKMSLLVDTNTSRFYDRN
DIEKEGIKYIKLQCKGHGECPTTENTETFIRLCERFNERSPPELIGVHCTHGFNRTGFLICAFLVEKMDWSIEAAVA
TFAQARPPGIYKGDYLKEFRRYGDIEEAPPPVLPDWCFEDED

>d1fpza_ c.45.1.1 (A:) Kinase associated phosphatase (kap) {Human (Homo sapiens)}

TPIHISWLSLRVNCSQFLGLCALPGCKFKDVRRNVQKDTEELKSCGIQDIFVFCTRGELESKYRVPNLLDLYQQCG
IITHHHPIADGGTPDIASCCEIMEELTCLKNYRKTЛИHSYGGLGRSCLVAACLLYLSDTISPEQAIDSRLDLRGSGA
IQTICKQNYLHEFRDKLA AHL

>d1eeoa_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), 1B}

EMEKEFEQIDKSGSWAAIYQDIRHEASDFPCRVAKLPKNKNRNRYRDVSPFDHSRRIKLHQEDNDYINASLIKME

EAQRSYILTQGPLPNTCGHWEMVWEQKSRGVVMLNRVMEKGLKCAQYWPQKEEKEMIFEDTNLKTLISE
DIKSYYTVRQLELENLTQETREILHFHYTTWPDFGPESPASFLNFLFKVRESGLSPEHGPVVHSSAGIGRSG
TFCLADTCLLMMDKRKDPSVDIKVLLEMRKFRMGLIQTADQLRFSYLAVIEGAKFIMGDSSVQDQWKELSHE
D

>d1rpma_c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), mu}

AIRVADLLQHITQMKCAEGYGFKEEYESFFEGQSAPWDSAKDENRMKNRYGNIIAYDHSRVRLQTIEGDTNSD
YINGNYIDGYHRPNHYIATQGPMQETIYDFWRMVWHENTASIIMVTNLVEGRVKCKYWPDDEIYKDIKVT
LIETELLAEVIRTFAVEKRGVHEIREIRQFHFTGWPDHGVPYHATGLGFVRQVSKSPPSAGPLVVHCSAGAG
RTGCFIVIDIMLDMAEREGVVDIYNCVRELRSRRVNMVQTEEQYVFIHDAILEACL

>d1yfoa_c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus)}

KYPPLPVDKLEEEINRRMADDNKLFREEFNALPACPIQATCEAASKEENKEKNRYVNILPYDHSRVHLTPVEGVP
DSDYINASFINGYQEKNKFIAAQGPKEETVNDFWRMIWEQNTATIVMVTNLKERKECKCAQYWPDPQGCWTY
GNVRVSVEDVTVLVDYTWRKFCIQQQVGVDVTNRKPQRLITQFHFTSWPDFGVFTPPIGMLKFLKKVACNPQYA
GAIVVHCSAGVGRGTGTFVVIDAMLDMMHSERKVVDVYGFVSIRIRAQRQCQMVTDMQYVFIYQALLEHYLY

>d2shpa1_c.45.1.2 (A:219-525) Tyrosine phosphatase {Human (Homo sapiens), shp-2}

TRINAAEIESRVRELSKLAETTDVKQGFWEETLQQQECKLLYSRKEGQRQENKNKNRYKNILPDFHTRVVLH
DGDPNEPVSDYINANIIMPEFETKCNSPKKSYIATQGCLQNTVNDFWRMVFQENSRVIVMTTKEVERGKSK
CVKYWPDEYALKEYGVMVRVNVKESAHDYTLRELKLSKGQGNTERTVWQYHFRTPDHGVPSDPGGVL
DFLEEVHHKQESIMDAGPVVVHCSAGIGRTGTFIVIDILIDIIREKGVDCIDVPKTIQMVRQRSGMVQTEAQY
RSIYMAVQHYIETL

>d1fpra_c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), shp-1}

GFWEEFESLQKQEVKNLHQRLEGQR PENKGKNRYKNILPDFHSRVI LQGRDSNIPGS DYINANYIKNQLLGPDE
NAKTYIASQGCLEATVNDFWQMAWQENS RVIVMTTREVEKGRNKCVPYWPEVGMQRAYGPYSVTNGEH
DTTEYKLRTLQVSPLDNGDLIREIWHYQYLSWPDHGV PSEPGVLSFLDQINQRQESLPHAGPIIVHSSAGIGRT
GTIIVIDMLMENISTKGLCDIDIQKTIQMVR AQRSGMVQTEAQYKFIYVAIAQFIETTKKLEVL

>d1jlna_c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus), ptp-sl/br7}

GSPREKVAMEYLQSASRVLTRSQLRDVVASSHLLQSEFMEIPMN FVDPKEIDIPRHGT KNRYKTILPNPLSRVCL
RPKNITDSLSTYINANYIRGYSGKE KAFIATQGPMINTVND FWQM VQEDSPVIVMITLKEKNEKCVLYWPE
KRGIGKVEVLTGVTECDNYTIRNLVLKQGSHTQHVKH YWTSWPDHKTPDSAQPLLQLMLDVEEDRLASEG
RGPVV HCSAGIGRTGCFATSIGCQQLKEEGVVDALSIVCQLRVDRGGMVQTSEQYEFVHALCLFESRLSPET
V

>d1ypta_c.45.1.2 (A:) Tyrosine phosphatase {Yersinia enterocolitica}

PEARAE LSSRLT LNRN TLPATNDPRYLQACGGEKLNRF RD IQCRR QTA VRADLN ANYIQVGNTR TIACQYPLQS
QLESHFRMLAEN RTPV LAVLASS SEIANQRFGMPDYFRQSGTY GSITVESKMTQQV GLGDGIMAD MYTLTIRE
AGQKTISVPV VHGNWP DQTA VSSE VT KALAS LV DQTA ET KRN M YESKG SSA ADDSKL RPV IHC RAGV GRTA
QLIGAMCMN DRSN SQLS VEDM VSQMR VQR NGIMV QKDE QL DV LIKLA EGQ GRPL LNS

>d1g4us2_c.45.1.2 (S:297-539) SptP tyrosine phosphatase, catalytic domain {Salmonella typhimurium}

PQTMSGPTLGLARFAVSSIPINQQTQVKLSDGMPVPVNTLFDGKPVALAGSYPKNTPALEAHMKMLLEKEC
SCLVVL TSEDQM QAKQLPPYFRGSY TFGEVHTNSQKVSSASQGEAIDQYNMQLSCGEKRYTIPVLHVKNWPD
HQPLPSTDQLEYLADR VKN SNQNGAPGRSS SDKHL PMIHCLGGVGR GTMAA ALVLKD NPHSN LEQV RA DF
RDSRNNR NMLED ASQF VQLK AMQA QLLM

>d1lara1_c.45.1.2 (A:1307-1623) RPTP Lar {Human (Homo sapiens)}

MITDLADNIERLKANDGLKFSQEYESIDPGQQFTWENSLEV NKPKNRYANVIYDHSRVILTSIDGVPGSDYIN

ANYIDGYRKQNAYIATQGPLPETMGDFWRMVWEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVT
LLDTVELATYVRTFALKSGSSEKRELRQFQFMAWPDHGVPEYPTPILAFLRRVKACNPLDAGPMVVHCSAG
VGRTGCFIVIDAMLERMKHEKTVDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEATCGHTEVPARNLYAH
QKLGQVPPGESVTAMELEFKLASS

>d1lara2 c.45.1.2 (A:1628-1876) RPTP Lar {Human (Homo sapiens)}

SRFISANLPCNKFKNRLVNIMPYELTRVCLQPIRGVEGSDYINASFLDGYRQQKAYIATQGPLAESTEDFWRMLW
EHNSTIIVMLTKLREMGREKCHQYWPAERSARYQYFVDPMAEYNMPQYILREFKVTNDARDGQSRTIRQFQFT
DWPEQGVPKTGE GFIDFIGQVHKTKEQFGQDGPIVHCSAGVGRTGVITLSIVLERMRYEGVVDMFQTVKTL
RTQRPAMVQTEDQYQLCYRAALEYLGSF

>d1larb1 c.45.1.2 (B:1340-1623) RPTP Lar {Human (Homo sapiens)}

TWENSNLEVNPKNRYANVIAYDHSRVILTSIDGVPGSDYINANYIDGYRKQNAYIATQGPLPETMGDFWRMV
WEQRTATVMMTRLEEKSRVKCDQYWPARGTETCGLIQVLLDTVELATYVRTFALKSGSSEKRELRQFQF
MAWPDHGVPEYPTPILAFLRRVKACNPLDAGPMVVHCSAGVGRTGCFIVIDAMLERMKHEKTVDIYGHVTC
MRSQRNYMVQTEDQYVFIHEALLEATCGHTEVPARNLYAHIQKLGQVPPGESVTAMELEFKLASS

>d1c25_ c.46.1.1 (-) CDC25a {Human (Homo sapiens)}

MLIGDFSKGYLFHTVAGKHQDLKYISPEIMASVNGKFANLIKEFVIIDCRYPYEYEGGHIKGAVNLHMEEEVEDF
LLKKPIVPTDGKRVIVVFHCEFSSERGPRMCRYVRERDRLGNEYPKLHPELYVLKGGYKEFFMKCQSYCEPPSYR
PMHHEDFKE

>d1qb0a_ c.46.1.1 (A:) CDC25b {Human (Homo sapiens)}

DHRELIGDYSKAFLLQTVDGKHQDLKYISPETMVALITGKFSNIVDKFIVDCRYPYEYEGGHIKTAVNLPLERDA
ESFLKSPIAPCSLDKRVILIFHCEFSSERGPRMCRFIRERDRAVNDYPSLYYPEMYILKGGYKEFPQHPNFCEPQ
DYRPMNHEAFKDELKTFRLKTRSWA

>d1hzma_ c.46.1.1 (A:) Erk2 binding domain of Mapk phosphatase m kp-3 {Human (Homo sapiens)}

MIDTLRVPFASEMAISKTVawlNEQLELGNERLLLMDCRPQELEYSSHIESAINVAIPGIMLRRLQKGNNLPVRA
LFTRGEDRDRFTRRCGTDVVLYDESSSDWNENTGGESLLGLKKLDEGCRAFYLEGGFSKFQAEFLHCETN
LDGS

>d1gmxa_ c.46.1.3 (A:) Sulfurtransferase GlpE {Escherichia coli}

MDQFECINVADAHQKLQEKEAVLVDIRDQSFAMGHAVQAFHLNTLGA FMRDNDFTPVVMVCYHGN
SSKGAAQYLLQQGYDVVSIDGGFEAWQRQFPAEVAYGA

>d1rhs_1 c.46.1.2 (1-149) Rhodanese {Cow (Bos taurus)}

VHQVLYRALVSTKWLAESVRAGKVGPGLRVLDASWYSPGTREARKEYLERHVP GASFFDIECRDKASPYEVML
PSEAGFADYVGSLGISNDTHVVYDGDDLGSFYAPRVWWMFRVFGHRTSVLNGGFRNWLKEGHPVTSEPS
RPEP

>d1rhs_2 c.46.1.2 (150-293) Rhodanese {Cow (Bos taurus)}

AIFKATLNRSLLKTYEQVLENLESKRFQLVDSRAQGRY LGTQPEPD AVGLDSGH IRGS VNM PF MNFLTEDGFEKS
PEELRAMFEAKKVDLT KPLIATCRKGVTACHIA AYLCGKPD VAIYDGSW FEWFH RAPPETW VSQGKG

>d1e0ca1 c.46.1.2 (A:1-135) Sulfurtransferase {Azotobacter vinelandii}

MDDFASLPLVIEPADLQARL SAPELILV DLTSAARYAEGH HIPGAR FVDPKRTQLGQPPAPGLQPPREQLES LF GEL
GHRPEAVYVYDDEGGGWAGR FIWLLD VIGQQRYHYLNGGL TAWLAEDRPLS RELPAPA

>d1e0ca2 c.46.1.2 (A:136-271) Sulfurtransferase {Azotobacter vinelandii}

GGPVALSLHDEPTASRDYLLGRLGAADLAIWDARSPQEYRGEKVLA AKGGH I P GAVNFEWTAAMDPSRALRIR
TDIAGRLEELGITPDKEIVTHCQTHRS GLTYIA KALGYPRVKG YAGSWGEWGNHPDTPVEL

>d2trxa_ c.47.1.1 (A:) Thioredoxin {Escherichia coli}

SDKIIHLTDDSFDTDVLKADGAILVDFWAEWC GPC KMI API DEIADEYQGKLTVA KLNIDQNP GTAPK YGIRGIP

TLLLFKNGEVAATKVGALSKGQLKEFLDANLA
>d1thx__ c.47.1.1 (-) Thioredoxin {Anabaena sp., pcc 7120}
SKGVITITDAEFESEVLKAEQPVLVYFWASWCPCQLMSPLINLAANTYSDRLKVVKLEIDPNPTTVKKYKVEGV
PALRLVKGEQILDSTEGVISDKLKSFLDTHLN
>d1dbya_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}
MEAGAVNDDTFKNVVLESSVPVLDFWAPWCPCRIIAPVVDEIAGEYKDKLKCVKLNTDESPNVASEYGIRSI
PTIMVFKGKKTETIIGAVPKATIVQTVEKYLN
>d1ep7a_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}
GGSVIVIDSAAWDAQLAKGKEEHKPIVVDFTATWCPCCKMIAPLFETLSNDYAGKVIFLKVDVDAVAAVAEEAA
GITAMPTFHVKDGKVADDLVGASQDKLKALVAKHAAA
>d1quwa_ c.47.1.1 (A:) Thioredoxin {Bacillus acidocaldarius}
ATMTLT DANFQQAIQGDKPVLVDFWAAWCPCRMMA PVLEEEFAEAHADKVTVAKLNVDENPETTSQFGIM
SIPTLILFKGGGRPVKQLIGYQPKEQLEAQLADVLQ
>d1f9ma_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin F}
MEAIVGVTEVNKDTFWPIVKAAGDKPVVLD MFTQWCPCCKM APLFETLSNDYAGKVIFLKVDVDAVAAVAEEAA
KELGIRVVP TF KILKENS VVG EVTGAKYDKLLEAIQAARS
>d1fb6a_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin M}
VQDVNDSSWKEFVLESEVPVMVDFWAPWCPC KLIAPVIDELAKEYSGKIAVYKLNTDEAPGIATQYNIRSIPT
VLFFKNGERKESIIGAVPKSTLTDSIEKYL
>d1erv__ c.47.1.1 (-) Thioredoxin {Human (Homo sapiens)}
MVKQIESKTA FQE ALDAAGDKLVVDFS ATWCPCCKM I KPF HSLSEKYSNV IFLEV DVDDC QDVASECEVKS
MPTFQFFKKGQKVGEFGANKEKLEATINELV
>d1aba_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Bacteriophage T4}
MF KVYGYDSNIHKCGPCDNAKRLLTVKKQPFEFINIMPEKG VFD DEKIAELLTKLGRDTQIGLTMPQVFAPDGSH
IGGF DQLREYFK
>d1qfna_ c.47.1.1 (A:) Glutaredoxin (Thioltransferase) {Escherichia coli}
MQTVIFGRSGCPYSVRAKDLAEKLSNERDDFQYQYVDIRAEGITKEDLQQKAGKPVETVPQIFVDQQHIGGYT
DFAAWVKENLDA
>d3grx_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Escherichia coli, GRX3}
AN VEI YT KET CPY SHRAK ALLSSKGVSFQELPIDGNAAKREEMIKRS GRTTVPQIFIDAQHIGGYDDLYALDARGG
LDPLKK
>d1kte_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Pig (Sus scrofa)}
AQAFVNSKIQPGKVVVFIKPTCPFCRKTQELLSQLPFKEGLLEFDITATSDTNEI QDYLQQLTGARTVPRVFIGKE
CIGGCTDLES MHKR GELLTRLQQVGAVK
>d1jhb_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Human (Homo sapiens)}
AQEFVNCKIQPGKVVVFIKPTCPYCRRAQEILSQLPIKQGLLEFDITATNHTNEI QDYLQQLTGARTVPRVFIGKD
CIGGCS DLVSLQQSGELLTRLKQIGALQ
>d1h75a_ c.47.1.1 (A:) Glutaredoxin-like NRDH-redoxin {Escherichia coli}
MRITIYTRNDCVQCHATKRAMENRGFD FEMINVDRVPEAAEALRAQGFRQLPVVIAGDLSWSGFRPDMINRL
HPAP
>d1fo5a_ c.47.1.1 (A:) MJ0307, thioredoxin/glutaredoxin-like protein {Archaeon Methanococcus
jannaschii}
MSKV KIELFTSPMC PHCPAAKRVVEEVANEMPDAVEVEYINV MENPQKAMEY GIMA VPTI VINGDVE FIGAPT
KEALVEAIKKRL

>d1iloa_ c.47.1.1 (A:) MTH985, a thioredoxin {Archaeon Methanobacterium thermoautotrophicum}
MMKIQIYGTGCANCQMLEKNAREAVKELGIDAEFEKIKEMDQILEAGLTALPGLAVDGEKIMGRVASKEEIKKI
LS

>d1gh2a_ c.47.1.1 (A:) Thioredoxin-like protein, N-terminal domain {Human (Homo sapiens)}
VGVKPVGSDPDFQPELSGAGSRLAVVKFTMRGCGPCLRIAPAFSSMSNKYPQAVFLEVVDVHQCGTAATNNIS
ATPTFQFRNKRVIDQYQGADAVGLEEKIKQHLE

>d1bjx_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}
AATTLPDGAAAESLVESSEVAIGFFKDVESDSAKQFLQAAEAIDDIPFGITSNSDVFSKYQLDKDGVVLFKFDE
GRNNFEGEVTKENLLDFIKHNQLPLVIEFTEQTA

>d1mek_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (Homo sapiens)}
DAPEEEDHVLVLRKSNAEALAAHKYLLVEFYAPWCGHCKALAPEYAKAAGKLAEKGSEIRLAKVDATEESDLAQ
QYGVRGYPTIKFFRNGDTASPKEYTAGREADDIVNWLLKKRTGPAA

>d1a8l_1 c.47.1.2 (1-119) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}
MGLISDADKKVIKEFFSKMVNPVKLIVFVRKDHCQYCDQLKQLVQELSETDKLSYEIVDFDTPEGKELAKRYRI
DRAPATTITQDGKDFGVRYFGLPAGHEFAAFLEDIVDVSREET

>d1a8l_2 c.47.1.2 (120-226) Protein disulfide isomerase, PDI {Archaeon Pyrococcus furiosus}
NLMDETKQAIRNIDQDVRILVFVTPTCPYCPLAVRMAHKFAIENTKAGKGKILGDMVEAIEYPEWADQYNVMA
VPKIVIQVNGEDRVEFEGAYPEKMFLEKLLSALS

>d1hyua3 c.47.1.2 (A:1-102) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}
MLDTNMKTQLRAYLEKLTKPVELIATLDDSAKSAEIKELLAELIAEAEKILGDMVEAIEYPEWADQYNVMA
FAGSPLGHEFTSLVALLWTGGHPS

>d1hyua4 c.47.1.2 (A:103-198) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {Salmonella typhimurium}
KEAQSLLEQIRDIDGDFEFETYYSLSCHNCPDVVQALNLMAVLNPRIKHTAIDGGTFQNEITERNVMGVPAVFV
NGKEFGQQGRMTLTEIVAKVDTG

>d1a8y_1 c.47.1.3 (3-126) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
GLDFPEYDGVDRVINVNAKNYKNVFKKYEVLLALLYHEPPEDDKASQRQFEMEEELILEAAQVLEDKGVGFGLVD
SEKDAAVAKKLGTEEDSIYVFEDEVIEYDGEFSADTLVEFLDVLED

>d1a8y_2 c.47.1.3 (127-228) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
VELIEGERELQAFENIEDEIKLIGYFKNKDSEHYKAFKEAAEEFHPYIPFFATFD SKVAKKLTLKLNEIDFYEA FMEEP
VTIPDKPNSEEIVNFVEEHRRS

>d1a8y_3 c.47.1.3 (229-347) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
TLRKLKPESMYETWEDDMMDGIHIVAFAAEADPDGYEFL EILKSVAQDNTDNP DLSIIWIDPDDPLL VPYWEKTF
DIDLSAPQIGVVNVTDADSVWMEMDDEEDLPSAEELEDWLEDVL

>d1fvka2 c.47.1.4 (A:1-64,A:129-188) Disulphide-bond formation facilitator (DSBA)
{Escherichia coli}
AQYEDGKQYTTLEKPVAGAPQVLEFFSFFCPHCYQFEEVLHISDNVKKLPEGVKMTKYHVNF MXFVV KSLVAQ
QEKAADVQLRGVPAMFVN GKYQLNPQGM DTSNMDV FVQQYADTV KYLSEK

>d1bed_2 c.47.1.4 (1-62,127-181) Disulphide-bond formation facilitator (DSBA)
{Vibrio cholerae}
AQFKEGEHYQVLKTPASSSPV VSEFFSFYCPHCNTFEP II AQLKQQLPEGAKFQKNHVSFMGXFAVDSMVRRFD

KQFQDSGLTGVPAVVNNRYLVQGQSVKSLDEYFDLVNYLLTK
>d1aqwa2 c.47.1.5 (A:1-76) Glutathione S-transferase {Human (Homo sapiens), class pi}
PPYTIVYFPVRGRCAALRMLLADQGQSWKEEVVTETWQEGSLKASCLYQQLPKFQDGLTLYQSNTILRHLG
RTL
>d2gsra2 c.47.1.5 (A:1-76) Glutathione S-transferase {Pig (Sus scrofa), class pi}
PPYTIVYFPVRGRCEAMRMLLADQDQSWEVVTMETWPPLKPSCLFRQLPKFQDGLTLYQSNAIRHLGRS
FGL
>d1glqa2 c.47.1.5 (A:1-78) Glutathione S-transferase {Mouse (Mus musculus), class pi}
PPYTIVYFPVRGRCEAMRMLLADQGQSWKEEVVTIDTMQGLLKPTCLYQQLPKFEDGDLTLYQSNAIRHLG
RSLGL
>d1gtua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
PMILGYWDIRGLAHAIRLLLEYTDSSYEKKYTMGDAPDYDRSQWLNEFKFLGLDFPNLPYLIDGAHKITQSNAI
LCYIARKHN
>d1hna_2 c.47.1.5 (1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
PMTLGYWNIRGLAHSIRLLLEYTDSSYEKKYTMGDAPDYDRSQWLNEFKFLGLDFPNLPYLIDGTHKITQSNAI
LRYIARKHN
>d3gtub2 c.47.1.5 (B:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
SCESSEMVLGWDIRGLAHAIRLLLEFTDTSYEEKRYTCGEAPDYDRSQWLVDVKFKLDFPNLPYLIDDGKNKITQ
SNAILRYIA
>d2gst2 c.47.1.5 (A:1-84) Glutathione S-transferase {Rat (Rattus norvegicus), class mu}
PMILGYWNVRGLTHPIRLLLEYTDSSYEKKRYAMGDAPDYDRSQWLNEFKFLGLDFPNLPYLIDGSRKITQSNAI
MRYLARKHH
>d1gsua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Chicken (Gallus gallus), class mu}
VVTLGYWDIRGLAHAIRLLLEYTETPYQERRYKAGPAPDFPSDWTEKEKLGLDFPNLPYLIDGDKLTQSNAI
RYIARKHN
>d1gsea2 c.47.1.5 (A:2-80) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}
AEKPKLHYFNARGKMESTRWLLAAAGVEFEKKFIKSAEDLDKLRNDGYLMFQQVPMVEIDGMKLVQTRAILN
YIASKYN
>d1gula2 c.47.1.5 (A:4-80) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}
RPKLHYPNGRGRMESVRWVLAAGVEFEEFLETKEQLYKLQDGNHLLFQQVPMVEIDGMKLVQTRSILHYIA
DKHN
>d1f3aa2 c.47.1.5 (A:1-79) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-1)}
AGKPVLHYFNARGRMECIRWLLAAAGVEFEKKFIQSPEDEKLKKDGNLMFDQVPMVEIDGMKLAQTRAILN
YIATKYD
>d1b48a2 c.47.1.5 (A:2-79) Glutathione S-transferase {Mouse (Mus musculus), class alpha (a1-4)}
AAKPKLYYFNNGRGRMESIRWLLAAAGVEFEEFLETREQYEKMQKDGHLLFGQVPLVEVEGLTLHQSLAIARYLT
AAKY
>d1ljra2 c.47.1.5 (A:1-79) Glutathione S-transferase {Human (Homo sapiens), class theta}
MGLELFSDLVSQPSRAVYIFAKKNGIPLELRTVDLVKGQHKSKEFLQINSLGKLPTLKDGDFILTESSAIIYLSCKYQ
>d1pd212 c.47.1.5 (1:1-75) Glutathione S-transferase {Rat (Rattus norvegicus), class sigma}
MPNYKLLYFNMRGRAEIIRYIFAYLDIKYEDHRIEQADWPKIKPTLPGKIPVLEVEGLTLHQSLAIARYLT
KNT
>d2gsq_2 c.47.1.5 (1-75) Glutathione S-transferase {Squid (Ommastrephes
sloani pacificus), class sigma}
PKYTLHYFPLMGRAELCRFVLAHGEEFTDRVEMADWPNLKATMYSNAMPVLDIDGTKMSQSMCIARHLA

REFG

>d1eema2 c.47.1.5 (A:5-102) Glutathione S-transferase {Human (Homo sapiens), class omega}
SARSLGKGSAPPGPVPEGSIRIYSMRFCPFAERTRLVLAKGIRHEVININLKNKPEWFFKNPGLVPVLENSQG
QLIYESAITCEYLDEAPGKKL

>d1fw1a2 c.47.1.5 (A:5-87) Glutathione S-transferase {Human (Homo sapiens), class zeta}
KPILYSYFRSSCSWRVRIALALKIDYKTVPINLIKDGQQFSKDFQALNPMKQVPTLKIDGITIHQSIAIYELETR
PTPR

>d1duga2 c.47.1.5 (A:1-80) Glutathione S-transferase {Schistosoma japonicum}
SPILGYWKIKGLVQPTRLLEEKYEEHYERDEGDKWRNKKFELGLEFPNLPPYYIDGDVKLTQSMAIIRYIADK
HNM

>d1fhe_2 c.47.1.5 (1-80) Glutathione S-transferase {Fasciola hepatica}
PAKLGWKLRLGLAQPVRLFLEYLGEEYEEHLYGRDDREKWMSEKFNMGLDLPNLPYYIDDKCKLTQSVAIMRYI
ADKHGM

>d2fhea2 c.47.1.5 (A:1-80) Glutathione S-transferase {Fasciola hepatica}
PAKLGWKRGLQQPVRLLEYLGEKYEEQIYERDDGEKWFSKFELGLDPNLPYYIDDKCKLTQSLAILRYIADK
HGM

>d1gnwa2 c.47.1.5 (A:2-85) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}
GIKVFHPASIATRRVLIALHEKNLDFELVHVELKDGEHKKEPFLSRNPFGQVPAFEDGDLKLFESENQYIAHRY
ENQGTNL

>d1axda2 c.47.1.5 (A:1-80) Glutathione S-transferase {Maize (Zea mays), type I}
APMKLYGAVMSWNLRCATALEEAGSDYEIVPINFATAEHKSPEHLVRNPFGQVPAQDGDLYLFESRAICKYAA
RKNKP

>d1aw9_2 c.47.1.5 (2-82) Glutathione S-transferase {Maize (Zea mays), type III}
APLKLYGMPLSPNVVRVATVNEKGLDFEIVPVDLTTGAHKQPDFLALNPFGQIPALVDGDEVLFESRAINRYIAS
KYASE

>d1e6ba2 c.47.1.5 (A:8-87) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana), class zeta}
KLKLYSYWRSSCAHRVRIALALKLDYEYIPVNLLKGDDQFDSDFKINPMGTVPALVDGDDVVINDSFAIMYLDEK
YPEP

>d1a0fa2 c.47.1.5 (A:1-80) Glutathione S-transferase {Escherichia coli}
MKLFYKPGACSLASHITLRESGKDFTLVSDLMKKRENGDDYFAVNPKGQVPALLDDGTLTEGVAIMQYLA
DSVPDR

>d1pmt_2 c.47.1.5 (1-80) Glutathione S-transferase {Proteus mirabilis}
MKLYYTPGSCSLSPHIVLRETGLDFSIERIDLRTKTESGKDFLAINPKGQVPVLQLDNGDILTEGVAIQYLADLKP
DR

>d1f2ea2 c.47.1.5 (A:1-80) Glutathione S-transferase {Sphingomonas paucimobilis}
MKLFISPGACSLAPHIALRETGADFEAVKVDLAVRKTEAGEDFLTVNPSGKVPALTDSGETLTENPAILLYIADQN
PAS

>d1g7oa2 c.47.1.5 (A:1-75) Glutaredoxin 2 {Escherichia coli}
MKLYIYDHCPYCLKARMIFGLKNIPVELHVLLNDDAETPTRMVGQKQVPILKQDDSRYMPESMDIVHYVDKLD
GK

>d1k0da2 c.47.1.5 (A:109-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}

QPLEGYTLFSRASPNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVPNARVPALIDHGMDNLSIWESGA

ILLHLVNVKYYKETGNPL

>d1k0dd2 c.47.1.5 (D:99-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (*Saccharomyces cerevisiae*)}

YSRITKFQEQPLEGYTLFSRSAPNGFKVAIVLSELGFHYNTIFLDNLGEHRAPEFVSVPNPARVPALIDHGMD
NLSIWESGAILLHLVNVKYYKETGNPL

>d1k0ma2 c.47.1.5 (A:6-91) Chloride intracellular channel 1 (clic1) {Human (*Homo sapiens*)}

PQVELFKAGSDGAKIGNCPFSQRLFMVLWLKGVTNVTTDKRRTEVQKLCPGGELPFLYGTEVHTDTNK
IEEFLEAVLCPP

>d2trcp_c.47.1.6 (P:) Phosducin {Rat (*Rattus norvegicus*)}

EGQATHGPKGVIDWRKFKESEDGDSIPPSKKEILRQMSSPQRDDKDSKERMSRKMSIQEYELIHQDKED
GCLRKYRRQCMQDMHQKLSFGPRYGFVYELETGEQFLETIEKEQKVTTIVVNIYEDGVRGCDALNSSLECLAAE
YPMVKFCKIRASNTGAGDRSSDVLPULLVYKGGELISNFISAEQFAEDFFAADVESFLNEYGLLPER

>d1a0rp_c.47.1.6 (P:) Phosducin {Cow (*Bos taurus*)}

FEGQASHTGPKGVIDWRKFKESEDSDSVAHSKKEILRQMSSPQRDDKDSKERFSRKMSVQEYELIHDKDE
DENCLRKYRRQCMQDMHQKLSFGPRYGFVYELESGEQFLETIEKEQKITTIVVHIYEDGIKGCDALNSSLICLAAE
YPMVKFCKIKASNTGAGDRSSDVLPULLVYKGGELLSNFISVTEQLAEEFTGDVESFLNEYGLLPEK

>d1g7ea_c.47.1.7 (A:) Endoplasmic reticulum protein ERP29, N-domain {Rat (*Rattus norvegicus*)}

LHTKGALPLDTVTFYKVIPSKFVLFVKFDTQYPYGEKQDEFKRLAENSASSDLLVAEVGISDYGDKLNMELSEKY
KLDKESYPVFYLFRDGDFENPVYSGAVKVGAIQRWLKGQGVYLG

>d1qgva_c.47.1.8 (A:) spliceosomal protein U5-15Kd {Human (*Homo sapiens*)}

SYMLPHLHNGWQVDQAILSEEDRVVIRFGHDWDPTCMKMDEVLYSIAEKVKNFAVIYLVDITEVPDFNKM
ELYDPCTVMFFFNRNKHIMIDLGTGNNNKINWAMEDKQEMVDIETVYRGARKGRGLVSPKDYST

>d1eeja1_c.47.1.9 (A:61-216) Disulfide bond isomerase, DsbC, C-terminal domain {Escherichia coli}

NVTNKMLLKQLNALEKEMIVYKAPQEKKHVITVFTDITCGYCHKLHEQMADYNALGITVRYLA
FPRQGLDSAEMKAIWCACKNKAFFDVMAGKSVAPASCDVDIADHYALGVQLGVSGTPAVVLSNGTLVPGYQPPKEMKEFL
DEHQKMTSGK

>d1gp1a_c.47.1.10 (A:) Glutathione peroxidase {Cow (*Bos taurus*)}

RTVYAFSARPLAGGEFPNLSSLRGKVLLIENVASLXGTTVRYTQMNDLQRLGPRGLVLFPCNQFGHQENA
KNEEILNCLKYVRPGGGFEPNMLFEKCEVNGEKAHPLFAFLREVLPTPSDDATALMTDPKFITWSPVCRNDVS
WNFEKFLVGPDPGVPRRYSRRLFTIDIEPDIELLSQ

>d1qk8a_c.47.1.10 (A:) Tryparedoxin I {Crithidia fasciculata}

GLDKYLPGIEKLRRGDGEVEVKSLAGKLVFFYFSASWCPPCRGFTPQLIEFYDKFHESKNFEVVFC
TWDCEEDGFAFYAKMPWLAVPFAQSEAVQKLSKHFNVESIPTLIGVDADSGDVTRARATLVKDPEGEQFWKDA

>d1i5ga_c.47.1.10 (A:) Tryparedoxin II {Crithidia fasciculata}

SGLKKFPYSTNLKGAAADIALPSLAGKTVFFYFSASWCPPSRAFTPQLIDFYKAHAEKKNF
EVMLISWDESAE DFKDYYAKMPWLALPFEDRKGMELTTGFDVKS
IPTLGVVEADSGNIITQARTMVVKDPEAKDFPWPN

>d1e2ya_c.47.1.10 (A:) Tryparedoxin peroxidase (thioredoxin peroxidase homologue) {Crithidia fasciculata}

GAAKLNHPAPEFDDMALMPNGTFKKVSLSSYKGKYVVLFFYPMDFTFVC
CPTEIIQFSDDAKRFAEINTEVISCSC DSEYSHLQWTSVDRKKGGLGPMAIPMLADKT
KAIARAYGVLEDGSVAYRGVFIIDPNGKLRQIIINDMPIGRN VEEVIRLVEALQFVEEHG

>d1qq2a_c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys peroxiredoxin) {Norway rat (*Rattus norvegicus*)}

SGNAKIGHPAPSFKATAVMPDGQFKDISLDYKGKYVVFYPLDFTVCPTEIFASDRAEFKKLNCQVIGASV
DSHFSHLAWINTPKKQGGLGPMNIPLVSDPKRTIAQDYGVLKADEGISFRGLIIDDKGILRQITINDLPGRSVD
EILRLVQAFQFTDKHGEVCPA
>d1qmva_ c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys peroxiredoxin) {Human (Homo sapiens)}
SGNARIGKPAPDFKATAVVGDGAFKEVKLSDYKGKYVVLFFYPLDFTVAPTEIIAFSNRAEDFRKLGEVLGVSVD
SQFTHLAWINTPRKEGGLGPLNIPLLADVTSSLSEDYGVLTDEGIAYRGLFIIDGKGVLQRQITVNDLPGRSVD
ALRLVQAFQYTDEHGEVCPAGWKPGSDTIKPNVDDSKHNF
>d1hd2a_ c.47.1.10 (A:) Peroxiredoxin 5 {Human (Homo sapiens)}
APIVGDAIPAVEVFECEPGNKVNLAELFKGKKGVLFGVPGAFTPGCSKTHLPGFVEQAEALKAKGVQVVACLS
VNDAFVTGEWGRAHKAEGKVRLAADPTGAFGKETDLLLDSLVSIFGNRRLKRFMSMVQDGIVKALNVEPDGT
GLTCSLAPNIISQL
>d1prxa_ c.47.1.10 (A:) HorF6 peroxidase {Human (Homo sapiens)}
LLLGDVAPNFEANTTVGRIRFHDFLGDSWGLFSHPRDFTPVCTTELGRAAKLAPEFAKRNVLIALSIDVEDHL
AWSKDINAYNSEEPTEKLPFPPIDDRNRELAILGMILDPAEKDEKGMPTARVVFGPDKKLKSILYPATTGRN
FDEILRVVISLQLTAEKRVATPWDKGDSVMVLPTIPEEEAKKLFPGVFTKELPSGKKYLRYTPQP
>d1kyga_ c.47.1.10 (A:) Alkyl hydroperoxide reductase AhpC {Salmonella typhimurium}
SLINTKIKPKNQAFKNGEFIEVTEKDTGTRWSVFFFYPADFTVCPTELGDVADHYEELQKLGVDVYSVSTDTHF
THKAWHSSSETIAKIKYAMIGDPTGALTRNFDNMREDEGLADRATFVVDPQGIIQAIIEVTAEGIGRDASDLLKI
KAAQYVAAHPGEVCP
>d1jfua_ c.47.1.10 (A:) Membrane-anchored thioredoxin-like protein TlpA, soluble domain {Bradyrhizobium japonicum}
TGDPACRAAVATAQKIAPLAHGEVAALTMASAPLKLPLAFEDADGKPKLSDRGKTLVNLWATWCPCRKE
MPALDELQGKLSGPNEVVAINIDTRDPEPKTFLKEANTRLGYFNDQKAKVFQDLKAIGRALGMPTSVLVDP
QGCEIATIAGPAEWASEDALKLIRAATG
>d1foha3 c.47.1.10 (A:462-662) Phenol hydroxylase, C-terminal domain {Soil-living yeast (Trichosporon cutaneum)}
NLVTDKKSSQELAKNCVVGTRFKSQPVVRHSEGLWMHFGDRLVTDGRFRIIVFAGKATDATQMSRIKKFSAYL
DSENSVISLYTPKVSDRNSRIDVITIHSCHRDDIEMHDFPAPALHPKWQYDFIYACDSWHHPHPKSYQAWGV
DETKGAVVVVRPDGYTLSVTDLEGTAEIDRYFSGILVEPKKEGSAQTEADWTKS
>d1f37a_ c.47.1.11 (A:) Thioredoxin-like 2Fe-2S ferredoxin {Aquifex aeolicus}
AEFKHVFVCVQDRPPGHPQGSQAQRGSREVQAFMEIQTDPQLFMTTVITPTGCMNACMMGPVVVYPD
GVWYGQVKPEDVDEIVEKHLKGGEPPERLVIISKGPXPGM
>d1j9ba_ c.47.1.12 (A:) Arsenate reductase ArsC {Escherichia coli}
NITIYHNPAAGTSRNTLEMIRNSGTEPTIILYLENPPSRDELVKLIADMGISVRALLRNVEPYEQLGLAEDKFTDD
QLIDFMLQHPILINRPIVVTPLGTRLCRPSEVVLQDAQKGAFTKEDGEKVVDEAGKRL
>d1qmha1 c.47.2.1 (A:185-279) RNA 3'-terminal phosphate cyclase, RPTC, insert domain {Escherichia coli}
ERGNIVQMRGEVLLAGVPRHVAEREIATLAGSFLHEQNIHNLPRDQGPGNTVSLEVESENITERFFVGEKRV
SAEVVAAQLVKEVKRYLASTA
>d1gpua3 c.48.1.1 (A:535-680) Transketolase {Baker's yeast (Saccharomyces cerevisiae)}
EGSSIESASKGGYVLQDVANPDIILVATGSEVLSVEAAKTLAAKNIKARVVSLPDFFTDFKQPLEYRLSVPDNVPI
MSVEVLATTCWGKYAHQSFGIDRFGASGKAPEVFKFFGFTPEGVAERAQKTIIFYKGDKLISPLKKAF

>d1dtwb2 c.48.1.2 (B:205-342) Branched-chain alpha-keto acid dehydrogenase {Human (Homo sapiens)}

PYNIPLSQAEVIQEGSDVTLVAWGTQVHVIREVASMAKEKLGVSCEVIDLRTIIPWDVDTICKSVIKTGRLLISHEA
PLTGGFASEISSTVQEECFLNLEAPISRVCYDTPFPHFIFEPFYIPDKWKCYDALRKMINY

>d1qs0b2 c.48.1.2 (B:206-339) 2-oxoisovalerate dehydrogenase E1b {Pseudomonas putida}

YYTVPLDKAAITRPGNDVSLTYGTTVYVAQVAAEESGVDAEVIDLRLSLWPLLDLTIVESVKKTGRCVVHEATR
TCGFGAELVSLVQEHCFFHLEAPIERVGTWDTYPHAQEWAYFPGPSRVGAALKVMEV

>d1ik6a2 c.48.1.2 (A:192-326) E1-beta subunit of pyruvate dehydrogenase {Archaeon Pyrobaculum aerophilum}

DYVVEIGKARVAREGDDVTLVYGAHHKALEAAERVKASVEVVDLQTLNPLDFDTVLKSLSKTGRLLIAHDSPK
TGGLGAEVRALVAEKALDRLTAPVIRLAGPDVPQSPIAADAAAYAPTVERIIKAIEYVMRY

>d1keka3 c.48.1.3 (A:259-415) Pyruvate-ferredoxin oxidoreductase, PFOR, domain II {Desulfovibrio africanus}

KLFDYVGAPDAERVIVSMGSSCETIEEVINHLAAKGEKIGLIKVRLYRPFVSEAFFAALPASAKVITVLDRTKEPGAP
GDPLYLDVCSAFVERGEAMPKILAGRYGLGSKEFSPAMVKSVDNMSGAKKNHFTVGIEDDVGTSLPVDNFA
ADTPK

>d1a49a3 c.49.1.1 (A:396-530) Pyruvate kinase, C-terminal domain {Rabbit (Oryctolagus cuniculus)}

ELARSSHSTDLMEAMAMGSVEASYKCLAAALIVLTESGRSAHQVARYRPRAPIIAVTRNHQTARQAHLYRGIFP
VVCKDPVQEAWAEDVDLRVNLAMNVGKARGFFKKGDVVIVLTGWRPGSGFTNTMRVVPVP

>d1pkla3 c.49.1.1 (A:358-498) Pyruvate kinase, C-terminal domain {Leishmania mexicana}

NEYVFFNSIKKLQHIPMSADEAVCSSAVNSVYETKAKAMVVLNTGRSARLAKYRPNCPICVTTRLQTCRQL
NITQGVESVFFDADKLGHDEGKEHRVAAGVEFAKSKGYVQTGDYCVVIADHKVKGYANQTRILLVE

>d1a3wa3 c.49.1.1 (A:367-500) Pyruvate kinase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

DMRNCTPKPTSTTETVAASAVAAVFEQKAKAIIVLSTSGTTPRLVSKYRPNCPIILVTRCPRAARFSHLYRGVFV
FEKEPVSDWTDDVEARINFOIEKAKEFGILKKGDYVSIQGFKAGAGHSNTLQVSTV

>d1e0ta3 c.49.1.1 (A:354-470) Pyruvate kinase, C-terminal domain {Escherichia coli}

ITEAVCRGAVETAEKLDAPLIVVATQGGKSARAVRKYFPDATILATTNEKTAHQLVLSKGVPQLVKEITSTDDFY
RLGKELALQSGLAHKGDVVVMVSGALVPSGTTNTASVHVL

>d1e79g_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Cow (Bos taurus)}

ATLKDIRRLKSNIQKITKSMKMVAAKYARAERELKPARVYVGVLALYEKADIKPEDKKHLLIGVSSDRGL
CGAIHSSVAKQMKEAANLAAAGKEVKIIGVGDKIRSILHRTHSDQFLVTFKEVGRPPFTGDASVIALELLNSGY
EFDEGSIIFNFRSVISYKTEEKPIFSLDTISSAESMSIYDDIDADVLRNYQEYSLANIIYSLKESTTSEQSARMTAM
DNASKNASEMIDKLTTFNRTRQAVITKELIEIISGAAALD

>d1mabg_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Rat (Rattus norvegicus)}

RDTIRRLKSNIQKITKSMKMVAAKYARAERELKPARVYGTGSLALYEKAEIKGPEDKKHLLIGVSSDRGLCGAI
HSSVAKQMNDMAALTAAGKEVMIVGIGEKIKSILYRTHSDQFLVTFKEVGRPPFTGDASVIALELLNSGYEFD
EGSIIFNQFKSVISYKTEEKPIFSFSTVVAENMSIYDDIDADVLRNYQEYNLANIIYSLKESTTSEQSARMTAMD
NASKNASDMIDKLTTFNRTRQAVITKELIEIISGAAALD

>d1fs0g_ c.49.2.1 (G:) ATP syntase (F1-ATPase), gamma subunit {Escherichia coli}

KITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGNGLEYKHPYLEDRDVKRGVGYLVSTDRLGLCG
GLNINLFKLLAEMKTWTDKGVQCDLAMIGSKGVFFFNSVGGNVVAQVTGMGDNPSSLIGPVKVMLQAY
DEGRLDKLYIVSNKFINTMSQVPTISQLLPLPASDDDLKHKSWDYLYEPDPKALLDTLRRYVESQVYQGVVEN
LASEQAARMVAMK

>d1lam_1 c.50.1.1 (1-159) Leucine aminopeptidase, N-terminal domain {Cow (Bos taurus)}
TKGLVLGIYSKEEDEPQFTSAGENFNKLVSGKLREILNISGPPKAGKTRTFYGLHEDFPSVVVGLGKKTAGID
EQENWHEGKENIRAAVAAGCRQIQDLEIPSVEVDPCGDAQAAAEGAVLGLYEYDDLQKRKVVVSAKLHGSE
DQEAWQRGV

>d1kmma1 c.51.1.1 (A:326-424) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Escherichia coli}
DPVVDIYLVASGADTQSAAMALAERLRDEPGVKLMTNHGGGNFKQFARADKWGARVAVVGESEVANGT
AVVKDLRSGEQTAVAQDSVAAHLRTLLG

>d1qe0a1 c.51.1.1 (A:326-420) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Staphylococcus aureus}
IEENLDLFIVTMGDQADRYAVKLLNHLRHNGIKADKDYLQRKIKGQMKQADRLGAKFTIVGDQELENNKIDVK
NMTTGESETIELDALVEYFKK

>d1h4vb1 c.51.1.1 (B:326-421) Histidyl-tRNA synthetase (HisRS), C-terminal domain {Thermus thermophilus}
EKGPDLYIPLTEEAFAEFLAEALRPRLRAEYALAPRKPAKGLEALKRGAAFAGFLGEDELRAGEVTLKRLATG
EQVRLSREEVPGYLLQALG

>d1latia1 c.51.1.1 (A:395-505) Glycyl-tRNA synthetase (GlyRS), C-terminal domain {Thermus thermophilus}
QLAPIKVAVIPLVKNRPEITEYAKRLKARLLALGLGRVLYEDTGNIGKAYRRHDEVGTPFAVTVDYDTIGQSKDGTT
RLKDTVTVRDRDTMEQIRLHVDELEGFLRERLRW

>d1qf6a1 c.51.1.1 (A:533-642) Threonyl-tRNA synthetase (ThrRS), C-terminal domain {Escherichia coli}
FPTWLAPVQVVIMNITDSQSEYVNELTQKLSNAGIRVKADLRNEKIGFKIREHTLRRVPYMLVCGDKEVESGKV
AVRTRRGKDLGSMDVNEVIEKLQQEIRSRSLKQLEE

>d1hc7a1 c.51.1.1 (A:277-403) C-terminal domain of ProRS {Thermus thermophilus}
RGLVLPPRЛАPIQVVIVPIYKDESРЕRVLEAAQGLRQALLAQGLRVHЛDDRDQHTPGYKFHEWELKGVPFRVEL
GPKDLEGGQAVALASRLGGKETLPLAALPEALPGKLDАFHEELYRRALAFREDH

>d1g5ha1 c.51.1.1 (A:343-469) The aaRS-like accessory subunit of mitochondrial polymerase gamma, C-terminal domain {Mouse (Mus musculus)}
RKVLKLHPCLAPIKVALVGKGPТVELRQVCQGLLNELLENGISVWPGYSETVHSSLEQLHSKYDEMСVLFSVLV
TETTLENGLIQLRSRDTTMKEMMHISKLDFLVKYLASASNVAALDHHHHH

>d1crza2 c.51.2.1 (A:7-140) TolB, N-terminal domain {Escherichia coli}
DSGVDSGRPIGVVPFQWAGPGAAPEDIGGIVAADLRNSGKFNPldrарlpQQPGSAQEVPAAWSALGIDA
VVVGQVTPNPDGSYNVAYQLVDTGGAPGTVLAQNSYKVNQWLRYAGHTASDEVFEKLТGИK

>d1eexb_c.51.3.1 (B:) Diol dehydratase, beta subunit {Klebsiella oxytoca}
GFLTEVGЕARQGTQQDEVIIAVGPAFGLAQTVNIVGIPHKSILREVIAGIEEEGIKARVIRCFKSSDVAFVAVEGNR
LSGSGISIGIQSKGTTVIHQQGLPLSNLELPQAPLLTLEYRQIGKNAARYAKRESPQPVPTLNDQMARPKYQ
AKSAILHIKETKYVVTGKNPQELRVA

>d1b78a_c.51.4.1 (A:) XTP pyrophosphatase {Archaeon Methanococcus jannaschii}
KIYFATGNPNKIKEANIIKLKDЛVEIEQIKISYPEIQGTLEEVAEFGAKWVYNILKKPVIVEDSGFFVEALNGFPГTY
SKFVQETIGNEGILKLEGKDNRNAYFKTIVGYCDENGVRLFKGIVKGRVSEEIRSKGYGFAYDSIFIPEEEERTFAE
MTTEEKSQISHRKKAФEEFKKFLLDRI

>d1ex2a_c.51.4.2 (A:) Maf protein {Bacillus subtilis}
MTKPLILASQSPRRKELL DLLQLPYSIIVSEVEEKLNRNFSPEENVQWLAKQAKAVADLHPHAIVIGADTMVCL

DGECLGKPQDQEEAASMLRRLSGRSHSVITAVSIQAENHSETFYDKTEAFWSLSEEEIWTYIETKEPMKDAGA
YGIQGRGALFVKKIDGDYYSVMLPISKTMRALRHF

>d1ihna_ c.103.1.1 (A:) Hypothetical protein MT938 (MTH938) {Archaeon Methanobacterium thermoautotrophicum}

SHMFSDCRFGSVTYRGREYRSIVVHVDGSVTPRKEISRKYGTSHVMAEEELEELLEEKPESIIIGSGVHGALE
TGFRSDATVLPTCEAIKRYNEERSAGRRAVIIHVTC

>d1ckqa_ c.52.1.1 (A:) Restriction endonuclease EcoRI {Escherichia coli}

SQGVIGIFGDYAKAHDLAVGEVSKLVKKALSNEYPQLSFRYRDSIKKTEINEALKKIDPDGGTLFVNNSSIKPDGGI
VEVKDDYGEWRVVLVAEAKHQGKDIINIRNGLVGKRGDQDLMAAGNAIERSHKNISEIANFMLSESHFPVLF
LEGSNFLTENISITRPDGRVVNLLEYNSGILNRLDLTAANYGMPINSNLCKFVNHKDKSIMLQAASIYTQGDG
REWDSKIMFEIMFDISTTSRLVGRDLFEQLTSK

>d1az3a_ c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia coli}

SLRSDLINALYDENQKYDVCIGIISAEGKIPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEPKQQNHYPDFTLYKPS
EPNKKIAIDIKTYYTNKENEKIKFTLGGYTSFIRNNTKNIVYPFDQYIAHWIIGYVYTRVATRKSSLKTYNINELNEIP
KPYKGVKVFLQDKWVIAGDLAGSGNTTNGSIHAHYKDFVEGKGIFDSEDEFLDYWRNYERTSQLRNDKYN
EYRNWIYRGRK

>d1eona_ c.52.1.2 (A:) Restriction endonuclease EcoRV {Escherichia coli}

SLRSDLINALYDENQKYDVCIGIISAEGKIPLGSDTKVLSTIFELFSRPIINKIAEKHGYIVEEPKQQNHYPDFTLYKPS
EPNKKIAIDIKTYYTNKENEKIKFTLGGYTSFIRNNTKNIVYPFDQYIAHWIIGYVYTRVATRKSSLKTYNINELNEIP
KPYKGVKVFLQDKWVIAGDLAGSGNTTNGSIHAHYKDFVEGKGIFDSEDEFLDYWRNYERTSQLRNDKYN
EYRNWIYRGRK

>d1bam__ c.52.1.3 (-) Restriction endonuclease BamHI {Bacillus amyloliquefaciens}

MEVEKEFITDEAKELLSKDKLIQQAYNEVKSICSPIWPATSKTFTINNTEKNCNGVVPIKECYTLLEDTNWYRE
KPLDILKLEKKGGPIDVYKEFIENSELKRVGMEFETGNISSAHRSMNKLLGLKHGEIDLAIILMPIKQLAYLTDR
VTNFEELEPYFELTEGQPFIFIGFNAAEAYNSNVPLPKGSDGMSKRSIKKWKDKVENK

>d1dmua_ c.52.1.4 (A:) Restriction endonuclease BglII {Bacillus subtilis}

MYNLHREKIFMSYNQNQKQYLEDNPEIQEKIELYGLNLLNEVISDNEEEIRADYNEANFLHPFWMNYPPLDRKG
MPKGDQIPWIEVGEKAVGSKLTRLVSQREDITVREIGLPTGPDERYLTSPTIYSLTNGFTDSIMMFVDIKSVGPR
DSDYDLVSPNQVSGNGDWAQLEGGIQNNQQTIQGPRSSQIFLPTIPPLYILSDGTIAPVVHLFIKPIYAMRSLTK
GDTGQSLYKIKLASVPNGLGLFCNPYAFDSAYKFLFRPGKDDRTKSLLQKRVRVDLRVLKIGPRVMTIDMDK

>d1dfma_ c.52.1.5 (A:) Restriction endonuclease BglIII {Bacillus subtilis}

MKIDITDYNHADEILNPQLWKEIEETLLKMPHLVKASDQASKVGSLIFDPVGTNQYIKDELVPKHWKNNIPIPKR
FDLGLTDIDFGKRDTLVEQFSNYPFLNNNTVRSELFHSNMDIDEEGMKVIIITKGHMFPASNSSLYEQAQN
QLNSLAENVFDVPIRLVGLIEDFETDIDIVSTTYADKRYSRITKRDVKGVIDTNTPNTRRKRGTVTY

>d3pvia_ c.52.1.6 (A:) Restriction endonuclease Pvull {Proteus vulgaris}

SHPDLNKLLELWPHIQEYQDLALKHGINDIFQGNGGKLLQVLLITGLTVLPREGNDAVDNAGQEYELKSINIDL
TKGFSTHHHMNPVIIAKYRQPWIFAIYRGIAIEAIYRLEPKDLEFYYDKWERKWYSDGHKDINNPKIPVKYVME
HGTKIY

>d1cfr__ c.52.1.7 (-) Restriction endonuclease Cfr10I {Citrobacter freundii}

MDIISKSGEGNKYTINSIAFVAYASHIDINTTEFSKVLSGLRDFINDEAIRLGGKISDGFSFNKCNGDWYEWLIGIR
AIEFFLESETNFIVVAKMPNATSFVMSIYKSCLSEFIYDLRSKLSNNVNLITSNPDFSIIDIRGRREELKSMLKDISFS
NISLSTISEIDNLYKNFIDYAELEHIKSFLSVTTFRPDRLQLAHEGSLMKALYTHLQTRWTINPTGIRYYAAATSI
GNADVIGLKVATHSITDVKSLSQSAVDEIFKINSVLDVDSCLSHIL

>d1knva_ c.52.1.7 (A:) Restriction endonuclease Bse634I {Bacillus stearothermophilus}

NLTNSNCVEEYKENGKTKIRIKPFNALIELYHHQTPTGSIKENLDKLENYVKDVKAKGLAIPSGAFSNTRGTWF

EVMIAIQSWNYRVKRELNDYLIIKMPNVKTFDFRKIFDNETREKLHQLEKSLLTHKQQVRLITSNPDLIIRQKD
KSEYNLPINKLTHEIDVALTLFDIEGKCKWDSLAVAGVGLKTSLRPDRLQLVHEGNILKSLFAHLKMRYWNPKA
EFKYYGASSEPVSKADDDALQTAATHIVNVNSTPERAVDDIFSLSFEDIDKMLDQI

>d1d02a_c.52.1.8 (A:) Restriction endonuclease MunI {Eubacteria (Mycoplasma unidentified)}
LSGRLNWQALAGLKASGAEQNLYNVFNAVFEGTKVLYEKPKHLKNLYAQVVLPPDDVIKEIFNPLIDLSTTQWG
VSPAFAIENTETHKILFGEIKRQDGWVEGKDPSAGRGAHERSCKLFTPGLLKAYRTIGGINDEEILPFVVVFEG
DITRDPKRVREITFWYDHQDNYFMWRPNESGEKLVQHFNEKLKKYD

>d1ev7a_c.52.1.9 (A:) Restriction endonuclease Nael {Nocardia aerocolonigenes}
EPDDDLERVRATLYSLDPDGDRTAGVLRDTLDQLYDGQRTGRWNFDQLHKTEKTHMGTIVEINLHREFQFGD
GFETDYEIAGVQVDCKFSMSQGAWMPPESIGHICLVIWASDQQCAWTAGLVKVIPQFLGTANRDLKRRLTPE
GRAQVVKLWPDHGKLQENLLHIPGDVRDQIFSAKSSRGNQHGQARVNELRRVHGRIGRAVIATVAQQDD
FMKRVRGSGGARSILRPEGIILGHQDNPKVANDGLPVRKGQVVAARVVADEGDQRQTAEIQGRRWA
AVPGDPIVEAPVV

>d1fiua_c.52.1.10 (A:) Restriction endonuclease NgoIV {Neisseria gonorrhoeae}
MQPLFTQERRIFHKLLDGNILATNNRGVVSNADGSNTRSFNIAGIADLLHSETVSERLPQTSGNAFEAICSE
FVQSAFEKLQHIRPGDWNVKQVGSNRLEIARYQQYAHLTALAKAAEENPEAAALGSDYTITPDIIVTRNLIAD
AEINRNEFLVDENIATYASLRAGNGNMPLLHASISCKWTIRSDRAQNARSEGTLVNRNRKRLPHIVVTAEPTP
SRRISSIALGTGEIDCVYHFALYEQILQSLNYEDALDLFYIMVNGKRLKDISDPLPLD
AV

>d1dc1a_c.52.1.11 (A:) Restriction endonuclease Bsobi {Bacillus stearothermophilus}
KPFENHLKSVDLKTYYEYRAGFIAFALEKNKRSTPYIERARALKVAASVAKTPKDLYLEDIQDALLYASGISDKA
KKFLTEDDKKESINNLIENFLEPAGEEFIDEYLFRYLLFQGDSLGGTMRNIAGALAQQKLTRAISALDIANIPYKWL
DSRDKKYTNWMDKPEDDYELETFAKGISWTINGKHRTLMYNITVSLVKKNDICLFNCEPEIYTPQKVHQ
YLLLGEKGGIDPAGADEHWKTANTALTRIRNKFSEKGLSPKTFIGAAIEHSMAEIIDQLOQSGSLNSANLT
EQVGSLCRWIINI

>d1kc6a_c.52.1.19 (A:) Restriction endonuclease HinII {Haemophilus influenzae}
SFIKPIYQDINSILIGQKVKRPKGTLGHAAGEPFKLYKFLKENLSDLTFKQYEYLNDLFMKNP
AIIGHEARYKL
FNSPTLLFLSRGKAATENWSIENLFEEKQNDTADILLVKDQFYELLDVKTRNISK
SAQAPNIISAYKLAQTC
AKMIDNKEFDLFDINYLEVWDWELNGEDLVCVSTSFAELFKSE
PSELYINWAAAMQI
QFHV
RDLDQGFNGT
REEWA
K
YLKH
FVT
QAEQRA
ISMIDKFV
KPFKKYIL

>d2foka4_c.52.1.12 (A:387-579) Restriction endonuclease FokI, C-terminal (catalytic) domain {Flavobacterium okeanokoites}
KSELEEKSELRHKLKYVPHEYIELIEIARNSTQDRILEMKVMEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYS
GGYNLPI
GQA
DEM
QRY
VEEN
QTRN
KHINP
NEW
WKV
YPSS
TEF
KFL
VSG
HF
KGN
YKA
QLTRL
NHITNC
NGAVL
SVE
ELLIG
GEMI
KAG
TLE
EVRR
KFNN
GEINF

>d1avqa_c.52.1.13 (A:) lambda exonuclease {Bacteriophage lambda}
SHMTPDIIQLQRTGIDVRAVEQGDDAWHKLRLGVITASEVHNVI
AKPRSGKKWPDMKMSYFHTLLAEVCTGVAP
EVNAKALAWGKQYENDARTLFEFTSGVNVTESPIIYRDESMRTACSPDGLCSDGNGLELKCP
FTSRDFMKFRLG
GFEAI
KSAYMA
QVQYS
MWV
TRK
NAWY
FANYD
P
RMK
REG
LHY
VV
IER
DEK
YMAS
F
DEI
V
PEF
IEK
M
DEALAEI
GFV
FGE
QWR

>d1azo_c.52.1.14 (-) DNA mismatch repair protein MutH from {Escherichia coli}
PRPLLSPPETEEQLLAQAQQQLSGYTLGELAALVGLTPENLKRDKGWIGVLLEI
LGASAGSKPEQDF
AALGVEL
KTIPVDSL
GRPLETT
FVC
APLT
GNS
GTW
ETSH
VRH
KL
K
VL
WIP
VE
GE
ASI
PLA
QRR
VG
SP
L
W
SP
NE
EDRQ
L
RED
WE
EL
MD
M
IV
LG
Q
VER
ITAR
H
GE
YL
Q
IR
PKA
A
AN
AK
LT
EA
IG
G
AR
GE
R
IL
T
L
P
RG
F
Y
L
K
K
N
F
T
S
A
L
L
A
R
H
F
L
I
Q

>d1cw0a_c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {Escherichia coli}

ADVHDKATRSKNMRAIATRDTAIKEKLASLLTGQGLAFRVQDASLPGRPDFVVDEYRCVIFTHGCFWHHHHCY
LFKVPATRTEFWLEKIGKNVERDRDISRLQELGWRVLIVWECALRGREKLTDALTERLEEWICGEGASAQIDT
QGIHLLA
>d1vsra_c.52.1.15 (A:) Very short patch repair (VSR) endonuclease {Escherichia coli}
AIEKRLASLLTGQGLAFRVQDASLPGRPDFVVDEYRCVIFTHGCFWHHHHCYLFKVPATRTEFWLEKIGKNVER
DRRDISRLQELGWRVLIVWECALRGREKLTDALTERLEEWICGEGASAQIDTQGIHLLA
>d1f1za2 c.52.1.16 (A:8-168) TnsA endonuclease, N-terminal domain {Escherichia coli}
FSEVQIARRIKEGRGQGHGKDYIPWLTQEVPSGRSHRIYSHKTGRVHLLSDLEAVFLSLEWESSVLDIREQF
PLLPSDTRQIAIDSGIKHPVIRGVQVMSTDFLVDCDKGPFEQFAIQVKPAAALQDERTLEKLELERRYWQQKQI
PWFIITDKEI
>d1fzra_c.52.1.17 (A:) Endonuclease I (Holliday junction resolvase) {Bacteriophage T7}
SGLEDKVSKQLESKGKIKFEYEEWKPVYVIPASNHTYTPDFLLPNGIFVTKGLWESDDRKKHLLIREQHPELDIRIV
FSSSRTKLYKGSPTSYGEFCEKHGKIKFADKLIPAEWIKEPKKEVPFDRLKRK
>d1gefa_c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Pyrococcus furiosus}
MYRKGAQAERELIKLEKHGFAVVRASGSKKVDSLAVANGKKYLIEVKVTKDHLYVGKRDGMRLIEFSRRFGGI
PVLAVKFLNVGWRFIEVSPKIEKFVFTPSSGSLEVLLGIQKTLE
>d1hh1a_c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Sulfolobus solfataricus}
SAVERNIVSRLRDKGFAVVRAPASGSKRKDPIPDIIALKNGVIIIELMSRKDIEGKIYVRREQAEGIIEFARKSGGSL
FLGVKKPGVLKFIPFEKLRRTETGNYVADSEIEGLDLEDLVRVLEAKISRTL
>d1a79a1_c.52.2.1 (A:83-179) tRNA splicing endonuclease, C-terminal domain {Archaeon
Methanococcus jannaschii}
ERLCLKYLVYKDLRTRGYIVKTGLKYGADFRYYERGANIDKEHSVYLVKVFPEDSSFLSELTFVRAHSVRKKLLI
AIVDADGDIVYYNMTYVKP
>d1dzfa1_c.52.3.1 (A:5-143) Eukaryotic RPB5 N-terminal domain {Baker's yeast
(Saccharomyces cerevisiae)}
NERNISRLWRAFRTVKEMVKDRGYFITQEEVELPLEDFKAKYCDSMGRPQRKMMMSFQANPTEESISKFPDMG
SLWVEFCDEPSVGVKTMKTFVIHQEKNFQTGIFVYQNNITPSAMKLVPSIPPATIETFNEAALVNN
>d1gta2 c.53.1.1 (A:1-140) gamma,delta resolvase, catalytic domain {Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALDKAGVKANRIFTDKASGSSSDRKGLDLMKVEEGDVILVKKLDRLGRDTA
DMIQLIKEFDAQGVSIWFDDGISTDGEKGK
>d1hx7a_c.53.1.1 (A:) gamma,delta resolvase, catalytic domain {Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALDKAGVKANRIFTDKASGSSSDRKGLDLMKVEEGDVILVKKLDRLGRDTA
DMIQLIKEFDAQGVSIWFDDGISTDGEKGK
>d2rsla_c.53.1.1 (A:) gamma,delta resolvase, catalytic domain {Escherichia coli}
MRLFGYARVSTSQQSLDIQVRALDKAGVKANRIFTDKASGSSSDRKGLDLMKVEEGDVILVKKLDRLGRDTA
DMIQLIKEFDAQGVSIWFDDGISTDGEKGK
>d1tf_2 c.53.1.2 (12-180) T4 RNase H {Bacteriophage T4}
KEGICLIDFSQIALSTALVNFPDKEKINLSMRHLILNSIKFNVKKAKTLGYTKIVLCIDNAKSGYWRRDFAYYYKKN
RGKAREESTWDWEFYFESSHKVIDELKAYMPYIVMDIDKYEADDHIAVLVKKFSLEGHKILIISSDGDFQLHKYP
NVKQWSPMHKKWVKI
>d1bgxt2 c.53.1.2 (T:1-173) 5' to 3' exonuclease domain of DNA polymerase {Thermus aquaticus}
MRGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTSRGEPVQAVYGFAKSLLKALKEDGDAVIVFDAKAPSFR
HEAYGGYKAGRAPTPEDFPRQLALIKELVDLLGLARLEVPGYEADDVLASLAKKAEGYEVRILTADKLYQLLS
DRIHVLHPEGYLITPAWLWEKYG

>d1xo1a2 c.53.1.2 (A:19-185) T5 5'-exonuclease {Bacteriophage T5}

RRNLMIVDGTNLGFRKHNNSSKKPFASSYVSTIQSLAKSYSARTTIVLGDKGSVFRLEHLPEYAGRDEKYAQR
TEEEKALDEQFFEYLKDAFELCKTTFTIRGVEADDMAAYIVKLIGHLYDHVWLISTGDWDTLLTDKVSRSF
TTRREYHLRDMYEHHN

>d1a77_2 c.53.1.2 (2-208) Flap endonuclease-1 {Archaeon Methanococcus jannaschii}

GVQFGDFIPKNIISFEDLKGKKVAIDGMNALYQFLTSIRLDGSPLRNKRGEITSAYNGVFYKTIHLLENDITPIWVF
DGEPPKLKEKTRKVREMKEKAELKMKEAIKKDFEEAAKYAKRVSYLTGKVNENCKYLLSMGIPYVEAPSEGE
AQASYMAKKGDVWAVVSQDYDALLYGAPRVVRNLTTKEMPELIEVLEDLR

>d1b43a2 c.53.1.2 (A:1-219) Fen-1 nuclease {Archaeon Pyrococcus furiosus}

GPPIGEIIPRKEIELENLYGKKIAIDALNAIYQFLSTIRQKDGTPLMDSKGRITSHLSGLFYRTINLMEAGIKPVYVFD
GEPPEFKKKELEKRREAREEAEKWREALEKGEIEEARAKYAQRATRVNEMLIEDAKLLEMGIPIVQAPSEGEA
QAAYMAAKGSVYASASQDYDSLLFGAPRLVRNLITGKRKLPGNVVVEIKPELILEEVLKELK

>d1ekja_c.53.2.1 (A:) beta-carbonic anhydrase {Pea (*Pisum sativum*)}

EASERIKTGFLHFKEKYDKNPALYGELAKGQSPPFMVFACSDSRVCPSHVLDQPGEAFFVVRNVANLVPPYDQ
AKYAGTAGAAIEYAVLHLKVSNIIVIGHSACGGIKLLSFDPGTYSTDFIEEWVKIGLPAKAVKAQHGDAPFAEL
CTHCEKEAVNASLGNLLTYPFVREGLVNKTLALKGGYYDFVKGSFELWGLEFGLSSTFSV

>d1g5ca_c.53.2.1 (A:) beta-carbonic anhydrase {Archaeon *Methanobacterium thermoautotrophicum*}

IIKDILRENQDFRFRDLSDLKHSPKLCIITCMDSRLIDLRLALGIGRGDAKVIKNAGNIVDDGVIRSAAVAIYALGD
NEIIIIVGHTDCGMARLDEDLIVSRMRELGVEEEVIENFSIDVLNPVGDEFENVIEGVKRLKSSPLIPESIGVHGLIID
INTGRLKPLYLDE

>d1i6pa_c.53.2.1 (A:) beta-carbonic anhydrase {Escherichia coli}

KDIDTLISNNALWSKMLVEEDPGFFEKLAAQAKPRFLWIGCSDSRVPAERLTGLEPGELFVHRNVANLVHTDNL
CLSVVQYAVDVLEVEHIICGHYCGGGVQAAVENPELGLINNWLHIRDIFKHSSLLGEMPQERRLDTLCELNV
MEQVYNLGHSTIMQSAWKRGQKVTIHGWAYGIHDGLLRDLDVTATNRETLEQRYRHGISNLKLK

>d1ddza1_c.53.2.1 (A:84-325) beta-carbonic anhydrase {Red alga (*Porphyridium purpureum*)}

VMSDLEKKFIELEAKLVAQPAGQAMPGKSНИFANNEAWRQEMLKQDPFFNRLANGQSPEYLWIGCADSRVP
ANQLLDL PAGEVFVHRNIANQCIHS DISFLSVLQYAVQYLKVKHILVCGHYCGGAKAALGDSRLGLIDNWLRHI
RDVRRMNAKYLDKCKDGDEELNR LIELNVLEQVHNVCATSIVQDAWDAGQELTVQGVVYGVGDGKLRLD LGV
VVNSSDDISKFYRTKSDSGALKAG

>d1ddza2_c.53.2.1 (A:326-564) beta-carbonic anhydrase {Red alga (*Porphyridium purpureum*)}

NPNAPLVQVTKGGESELSTMEKLTAELVQQTPGKLKEGANRVFVNNENWRQKMLQDPQFFSNLAHTQTP
EILWIGCADSRVPANQIINLPAGEVFVHRNIANQCIHS DISMSFLSVLQYAVQYLKVKR VVCGHYACGGCAA ALG
DSRLGLIDNWLRHIR DVRRHNQAELS RITDPKDSLNR LIEINVLEQMHNVCATSIVQDAWDAGQELEVQGVVY
GVGDGKL RDGMGVVAKANDIG

>d1pdo_c.54.1.1 (-) IIA domain of mannose transporter, IIA-Man {Escherichia coli}

TIAIVIGTHWAAEQLLKTAEMLLGEQENVGWIDFVPGENAETLIEKYNAQLAKLDTKGVLFLVDTWGSPFN
AASRIVVDKEHYEVIAGVNIPMLVETLMARDDDPSFDELVALAVETGREGVKALK

>d1bupa1_c.55.1.1 (A:4-188) Heat shock protein 70kDa, ATPase fragment {Cow (Bos taurus)}

GPAVGIDLGSTYSCGVFQHGKVEIIANDQGNRTTPSYAFTDTERLIGDAAKNQVAMNPTNTVFDAKRLIGRR
FDDAVVQSDMKHWPMVVNDAGR PKVQVEYKGETKS F YPEEVSSMVLTKMKEIAEAYLGKTVNAV VTV PAY
FNDSQRQATKDAGTIAGLNVLR IINEPTAAIA YGLD KK

>d1bupa2_c.55.1.1 (A:189-381) Heat shock protein 70kDa, ATPase fragment {Cow}

(Bos taurus)}

VGAERNVLIFDLGGGTFDVSILTIEDGIFEVKSTAGDTHLGGEFDNRMVNHFIAEFKRKHKKDISENKRAVRL
RTACERAKRTLSSSTQASIEIDSLYEGIDFYTSITRARFEELNADLFRGTLDPVEKALRDAKLDKSQIHDLVVGSTR
IPKIQKLLQDFNGKELNKSINPDEAVAYGAAVQAIALS

>d1hjoa1 c.55.1.1 (A:3-188) Heat shock protein 70kDa, ATPase fragment {Human (Homo sapiens)}
KAAAIGIDLGTTSCGVVFQHGKVEIIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNPQNTVFDAKRLIGR
KFGDPVQVSDMKHWPFQVINDGDKPKVQVSYKGETKAFYPEEISSMVLTKMKEIAEAYLGYPVTNAVITVPAYF
NDSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDRT

>d1hjoa2 c.55.1.1 (A:189-382) Heat shock protein 70kDa, ATPase fragment {Human (Homo sapiens)}

GKGERNVLFIDLGTTFDVSILTIDDGIFEVKATAGDTHLGGEFDNRLVNHFVEEFKRKHKKDISQNKRAVRL
RTACERAKRTLSSSTQASIEIDSLFEGIDFYTSITRARFEELCSDLFRSTLEPVKEKLDKAQIHDILVVGSTR
IPKVQKLLQDFNGRDLNKSINPDEAVAYGAAVQAIALMG

>d1dkgd1 c.55.1.1 (D:3-185) Heat shock protein 70kDa, ATPase fragment {Escherichia coli, gene dnaK}

KIIGIDLGTTNSCVAIMDGTTPRVLENAEGDRTPSIIAYTQDGETLVGQPAKRQAVTNPQNTLFAIKRLIGRRFQ
DEEVQRDVSIIMPKIIAADNGDAWVEVKGQKMAPPQISAEVKKMKKTAEDYLGEPVTEAVITVPAYFNDAQR
QATKDAGRIAGLEVKRIINEPTAAALAYGLDKGT

>d1dkgd2 c.55.1.1 (D:186-383) Heat shock protein 70kDa, ATPase fragment {Escherichia coli, gene dnaK}

GNRTIAVYDLGGGTFDISIIIDEVDGEKTFEVLATNGDTHLGGEFDDSLRLINYLVEEFKKDQGIDLRLNDPLAMQR
LKEAAEKAKIELSSAQQTDVNLPIYADATGPKHMNIKVTRAKLESLVEDLNRSEILLKVALQDAGLSVSDIDDVI
LVGGQTRMPMVQKKVAEFFGKEPRKDVPNDEAVAIGAAVQGGVLT

>d1j6za1 c.55.1.1 (A:4-146) Actin {Rabbit (Oryctolagus cuniculus)}

ETTALVCDNGSGLVKAGFAGDDAPRAVFPSIVGRPRHQGMVGMGQKDSYVGDEAQSKRGILTLKYPIEHGIIT
NWDDMEKIWHHTFYNELRVAPEEHPTLLEAPLNPKANREKMTQIMFETFNPAMYVAIQAVLSLYASG

>d1j6za2 c.55.1.1 (A:147-372) Actin {Rabbit (Oryctolagus cuniculus)}

RTTGIVLDSGDGVTHNVPIYEGYALPHAIMRLDLAGRDLTDYLMKILTERGYSFTTAEREIVRDIKEKLCYVALDF
ENEMATAASSSLEKSYELPDGQVITIGNERFRCPETLFQPSFIGMESAGIHETTYNSIMKCDIDIRKDLYANNVM
SGGTTMYPGIADRMQKEITALAPSTMKIKIAPPERKYSVWIGGSILASLSTFQQMWITKQEYDEAGPSIVHR

>d1d4xa1 c.55.1.1 (A:4-146) Actin {Nematode (Caenorhabditis elegans)}

EVAALVVVDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGMVGMGQKDSYVGDEAQSKRGILTLKYPIEHGI
VTNWDDMEKIWHHTFYNELRVAPEEHPTLLEAPLNPKANREKMTQIMFETFNPAMYVAIQAVLSLYASG

>d1d4xa2 c.55.1.1 (A:147-375) Actin {Nematode (Caenorhabditis elegans)}

RTTGIVLDSGDGVTHVPIYEGYALPHAILRLDLAGRDLTDYLMKILTERGYSFTTAEREIVRDIKEKLCYVALDF
QEMATAASSSLEKSYELPDGQVITVGNERFRCPEAMFQPSFLGMESAGIHETSYNSIMKCDIDIRKDLYANTVL
SGGTTMYPGIADRMQKEITALAPSTMKIKIAPPERKYSVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHRKC
F

>d1c0fa1 c.55.1.1 (A:1-146) Actin {Slime mold (Dictyostelium discoideum)}

DGEDVQALVIDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHTGKDSYVGDEAQSKRGILTLKYPIEHGIITNWD
DMEKIWHHTFYNELRVAPEEHPTLLEAPLNPKANREKMTQIMFETFNPAMYVAIQAVLSLYASG

>d1dga2 c.55.1.1 (A:147-375) Actin {Slime mold (Dictyostelium discoideum)}

RTTGIVMDSGDGVSHTVPIYEGYALPHAILRLDLAGRDLTDYMMKILTERGYSFTTAEREIVRDIKEKLAYVALDF
EQEMATAASSSALEKSYELPDGQVITIGNERFRCPEALFQPSFLGMESAGIHETTYNSIMKCDVDIRKDLYGNVV

LSGGTTMFPGIADRMNKELTALAPSTMKIKIAPPERKYSVWIGGSILASLSTFQQMWISKEEYDESGPSIVHRKF
F

>d1yaga1 c.55.1.1 (A:4-146) Actin {Baker's yeast (Saccharomyces cerevisiae)}
EVAALVIDNGSGMCKAGFAGDDAPRAVFPSIVGRPRHQGIMVMGQKDSYVGDEAQSKRGILTLYPIEHIV
TNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAMNPKNREKMTQIMFETFNVPAFYVSIQAVSLYSSG

>d1yaga2 c.55.1.1 (A:147-375) Actin {Baker's yeast (Saccharomyces cerevisiae)}
RTTGVLDSDGVTWVPIYAGFLPHAILRIDLAGRDLTDYLMKILSERGYSFSTAEREIVRDIKEKLCYVALDF
QEMQTAAQSSSIEKSYLEPDGQVITIGNERFRAPEALFHPsvglesagidqttynsimkcdvdvrkelygnivm
SGGTTMFPGIAERMQKEITALAPSSMKVKIIAPPERKYSVWIGGSILASLTFQQMWISKQEYDESGPSIVHHKF
F

>d1jcfa1 c.55.1.1 (A:1-140) Prokaryotic actin homolog MreB {Thermotoga maritima}
MLRKDIGIDLGTANTLVFLRGKGIVVNEPSVIAIDSTTGEILKVGLEAKNMIGKTPATIKAIRPMRDGVIADYTVL
VMLRYFINKAKGGMNLFKPRVVIGVPIGITDVERRAILDAGLEAGASKVFLIEEPMAAAIGSN

>d1jcfa2 c.55.1.1 (A:141-336) Prokaryotic actin homolog MreB {Thermotoga maritima}
LNVEEPGNMVVDIGGGTTEAVISLGSIVTWESIRIAGDEMDEAIVQYVRETYRVAIGERTAERVKIEIGNVFP
KENDELETTVSGIDLSTGLPRKLTKGGEVREALRSVVAIVESVRTTLEKTPPELVDIERRGIFLTGGSLLRGLDT
LLQKETGISVIRSEEPLTAVAKGAGMVLKDVKVNILKKLQGAG

>d1k8ka1 c.55.1.1 (A:3-160) Actin-related protein 3, Arp3 {Cow (Bos taurus)}
GRLPACVVDCGTGYTKLGAGNTEPQFIIPSCIAIKESAKVGDQAQRRVMKGVDLDFFIGDEAIEKPTYATKWP
IRHGIVEDWDLMERFMEQVIFKYLRAEPEDHYFLLTEPPLNTPENREYTAEIMFESFNVPGLYIAVQAVLALAAS
WTSRQVGE

>d1k8ka2 c.55.1.1 (A:161-418) Actin-related protein 3, Arp3 {Cow (Bos taurus)}
RTLTGTVIDSGDGVTWVIPVAEGYVIGSCIHKIPIAGRDTITYFIQQLLRDREVGPPEQSLETAKAVKERYSYVCPDL
VKEFNKYDTDGSWKWIKQYTGINAIISKKEFSIDVGYERFLGPEIFFHPEFANPDFTQPISEVVDEVIQNCPIDVRRPL
YKNIVLGGSTMFRDFGRRLQRDLKRTVDARLKLSEELSGGRLKPKPIDVQVITHHMQRYAVWF GGSM LASTP
EFYQVCHTKKDYEELGPSICRHNPVFGVMS

>d1k8kb1 c.55.1.1 (B:154-343) Actin-related protein 2, Arp2 {Cow (Bos taurus)}
GVVVDSGDGVTHICPVYEGFLPHLRRLDIAGRDTTRYLIKLLRGYAFNHSADFETVRMIKEKLCYVGYNIEQE
QKLALETTVLVESYTLPDGRIIKVGERFEAPEALFQPHLINVEGVGAELLFTIQAADIDTRSEFYKHIVLSGGST
MYPGLPSRLERELKQLYLERVLKGDVEKLSKFKIR

>d1e4ft1 c.55.1.1 (T:7-199) Cell division protein FtsA {Thermotoga maritima}
TVFYTSDIGSRYIKGLVLGKRDQEWEALAFSSVKSRLDEGEIKDAIAFKESVNTLLKEEEQLQKSLRSDFVISFSS
VSFEREDTVIERDFGEEKRSITLDILSEMQSEALEKLKENGKTPLHIFS KRYLLDDERIVFNPLDMKASKIAEYTSIV
VPLKVYEMFYNFLQDTVKSPFQLKSSLVSTAEGVL

>d1e4ft2 c.55.1.1 (T:200-390) Cell division protein FtsA {Thermotoga maritima}
TTPEKDRGVVVVNLGYNFTGLIAYKNGVPIKISYVPVGMKHVKDVAVLTSFEESERLIITHGNAVYNDLKEEEI
QYRGLDGNTIKTTAKKLSVIIHARLREIMS SKKKFREVEAKIVEEGEIGIPGGVLTGGAKIPRINELATEVFKS
PVRTGCYANSDRPSIINADEVANDPSFAAAGGNVFA

>d1huxa_ c.55.1.5 (A:) Hydroxyglutaryl-CoA dehydratase component A {Acidaminococcus fermentans}
SIYTLGIDVGSTASKCIILKGKEIVAKSLVAVGTGTSGPARSISEVLEN AHMKKEDMAFTLATGYGRNSLEGIADK
QMSELSCHAMGASFIPWNVHTVIDGGQDVKVIHVENTMTNFQMNDKCAAGTGRFLDVMANILEVKSD
LAEGLGAKSTKRAISSTCTVFAESEVISQLSKGTDKIDIAGIHRVASRVIGLANRVGIVKDVVMTGGVAQNYGVR
GALEEGLGVEIKTSPQAQYNGALGAALYAYKKA AK

>d1g99a1 c.55.1.2 (A:1-156) Acetate kinase {Archaeon Methanoscincus thermophila}
MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIITQKKFDGKLEKLTDLPTHKDAEEVVKALTDEFG
VIKDMGEINAVGHRVVGGEKFTTSALYDEGVEKAIKDCFELAPLHNPPNMMGISACAEIMPGTPMVIVFDTA
FHQTMP

>d1g99a2 c.55.1.2 (A:157-398) Acetate kinase {Archaeon Methanoscincus thermophila}
PYAYMYALPYDLYEKHGVRKYGFHGTSHKYVAERAALMLGKPAEETKIITCHLNGNGSSITAVEGGKSVENTSMGFT
PLEGLAMGTRCGSIDPAIPFLMEKEGLTREIDLTMNKSGVLGVSGSNDFRDLDEAASKGNRKAELALEIFA
YKVKKFIGEYSAVLNGADAVVFTAGIGENSASIRKRILTGLDGIGIKIDDEKNKIRGQEIDISTPDAKVRVFVPTNEE
LAIARETKEIVET

>d1ig8a1 c.55.1.3 (A:18-224) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}
DVPKELMQQIENFEKIFTVPTETLQAVTKHFISELEKGLSKGGNIPMIPGVWVMDPFTGKESGDFLAIDLGGTNL
RVVVLVKLGGDRTFDTTQSQYRLPDAMRTTQNPDELWEFIADSLKAFIGEQFPQGISEPIPLGFTFSFPASQNKINE
GILQRWTKGFDIPNIENHDVVPMLQKQITKRNIPIEVVALINDTTGTLVASYYTDP

>d1ig8a2 c.55.1.3 (A:225-486) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}
ETKMGVIFGTGVNGAYDVCS DIEKLQGKLSDDIPPSAPMA INCEYGSFDNEHV VLPRTKYDITIDEESPRPGQQ
TFEKMSGGYYLGEILRLALMDMYKQGFIFKNQDLSKFDKPFVMDTSY PARIEEDPFENLED TDDLFQNEFGINTT
VQERKLIRRLSELIGARAARLSVCGIAICQKRGYKTGHIAADGSVYNRYPGFKEKAANALKDIY GWTQTS LDDY
PIKIVPAEDGSGAGAAVIAALA AQKRIAEGKSVGIIGA

>d1bdg_1 c.55.1.3 (13-222) Hexokinase {Blood fluke (Schistosoma mansoni)}
FSDQQLFEKVVEILKPFDSLVDYEEICDRMGESMRLGLQKSTNEKSSIKMFPSYVT KTPNGTETGNFLALDLGG
TNYRVLSVTLEGKGKSPRIQERTYCIPA EKMSGSGTELFKYIAETLADFL ENNGM KDKFDLGFTSFPCVQKGLT
HATLVRWTKGFSADGV EGHNV AELLQTEL DKREL NVKCVA VVNDTV GTLASCALED P

>d1bdg_2 c.55.1.3 (223-460) Hexokinase {Blood fluke (Schistosoma mansoni)}
KCAVGLIVGTGTNVAYIEDSSKVELMDGVKEPEVVINTEWGAFGEKGE LDCWRTQFDKSMIDSLHPGKQLYE
KMVSGM YLGE VRHII VLV EQK ILFRGDL PERL KV RNS LLTRY LTDVER DP A HLL NTHYML TDD LH VP VE PID
NRIVRYACEMVV KRAAYLAGAGIACILRRINRSEVTVGVDGSLYKFHPKFCERMTDMV DKLKPKNTRFCLRLSE
DGSGKGAAAIAASC

>d1czan1 c.55.1.3 (N:16-222) Mammalian type I hexokinase {Human (Homo sapiens)}
DDQVKKIDKYLYAMRLSDETLIDIMTRFRKEMKNGLSRDFNPTATVKMLPTVRSIPDGSEK GDFIA LD LGG SSF
RILRVQVNHEKNQNVHMESEVYDTPENIVHGSGSQLFDHVAECLGDFMEKRKIKDKKLPGFTSFPCQ QSKI
DEAILITWTKRFKASGVEGADVVKLLNKAIIKRGDYDANIVAVVNDTV GTMMTCGYDDQ

>d1czan2 c.55.1.3 (N:223-465) Mammalian type I hexokinase {Human (Homo sapiens)}
HCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRAIDAYS LNP GKQL F EKM
VSGMYLGE VR LILV KMAKEGLLFEGRITPELLTRGKFNTSDV SAI EKNKE GLHNAKE ILTRLGVEPS DDC VSVQ
HVCTIVSFRSANLVAATLGAILNRLRDNKGT PRL RTTVGVDGSLYKTHPQYSR RHF KTLRLV PDSDV RFLL SESG
SGKGAA MVT AVAY RLA E

>d1czan3 c.55.1.3 (N:466-670) Mammalian type I hexokinase {Human (Homo sapiens)}
QHRQIEETLAHFHTKDMLEVKKRMRAEMELGLRKQTHNNAVV KMLPSFVR RTPDGTENGDFLA LD LGG TN
FRVLLVKIRSGKKRTVEMHNKIYAIP EIMQGTGEELFDHIVSCISDFLDYMGIGKPRMPLGFTSFPCQ QTSL DA
GILITWTKGFKATDCVGHDV VTLL RDAIKRREEFDLDV VAVVNDTV GTMMTCAYEEP

>d1czan4 c.55.1.3 (N:671-913) Mammalian type I hexokinase {Human (Homo sapiens)}
TCEVGLIVGTGSNACYMEEMKNVEMVEGDQGQMCINMEWGA FGDN GCLDDIRTHYDRLVDEYSLNAGKQ
RYEKMISGM YLGE VR NI LIDFTKKGFLFRGQISETLKTRGIFETKFLSQIES DR ALLQV RAILQQLGLN STC DDSIL

VKTCGVVSRRAAQLCAGMAAVVDKIRENRGLDRLNVTVGVDGTLYKLHPHFSRIMHQTVKELSPKCNVSFL
LSEDGSGKGAALITAVGVRLRT

>d1bg3a1 c.55.1.3 (A:1-222) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
MIAAQLLAYYFTELKDDQVKKIDKYLYAMRLSDEILIDLTRFKEMKNGLSRDYNPTASVKMLPTFVRSIPDGSEK
GDFIALDLGGSSFRILRVQVNHEKNQNVSMESEIYDTPENIVHSGSTQLFDHVADCLGDFMEKKIKDKKLPVG
FTFSFPCRQSKIDEAVLITWTKRFKASGVEGADVVKLLNAIKKRGDYDANIVAVVNDTVGTMMTCGYDDQ

>d1bg3a2 c.55.1.3 (A:223-465) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
QCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRELDRGSLNPGKQLFEK
MVSGMYMGEVRLILVKMAKEGLLFEGRITPELLTRGKFNTSDVSAIEKDKEGIQNAKEILTRLGVEPSDVDCVS
VQHICITVSFRSANLVAATLGAILNRLRDNKTPRLRTVGVDGSLYKMHPQYSRRFHKTLLRRLVPDSDFVRFLSE
SGTGKAAMVTAVAYRAE

>d1bg3a3 c.55.1.3 (A:466-670) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
QHIRQIEETLAHFRLSKQTLMEVKKRLRTEMEMGLRKETNSKATVKMLPSFVRSIPDGTEHGDFLALDLGGTNF
RVLLVKIRSGKKRTVEMHNKIYSIPLEIMQGTGDELFDHIVSCISDFLDYMGIKGPRMPLGFTSFPCHQTNLDCG
ILISWTKGFKATDCEGHVASLLRAVKRREEFDLVAVVNDTVGTMMTCAYEEP

>d1bg3a4 c.55.1.3 (A:671-911) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
TCEIGLIVGTGTNACYMEEMKNVEMVEGNQGQMCINMEWGAFGDNGCLDDIRTDFKVVDEYSLNSGKQR
FEKMISGMYLGEIVRNILIDFTKGFLFRGQISEPLKTRGIFETKFLSQIESDRLALLQVRAILQQQLGLNSTCDDSLV
KTCVGVSKRAAQLCAGMAAVVEKIRENRGLDHLNVTVGVDGTLYKLHPHFSRIMHQTVKELSPKCTVSFLS
EDGSGKGAALITAVGVRL

>d1bu6o1 c.55.1.4 (O:3-253) Glycerol kinase {Escherichia coli}
KKYIVALDQGTTSSRAVVMHDANIISVSQREFEQIYPKPGWVEHDPMEIWATQSSTLVEVLTKADISSDQIAAI
GITNQRETTIVWEKETGKPIYNAIVWQCRTAEICEHLKRDGLEDYRSNTGLVIDPYFSGTKVKWILDHVEGSRE
RARRGELLFGTVDTWLIWKMTQGRVHVTDYTNASRTMLFNIHTLDWDDKMLEVLDIPREMLPEVRRSSEVY
GQTNIGGKGGTRIPISGIAGDQQAALFGQ

>d1bu6o2 c.55.1.4 (O:254-499) Glycerol kinase {Escherichia coli}
LCVKEGMANKTYGTGCFMLMNTGEKAVKSENLTTIACGPTGEVNYALEGAVFMAGASIQWLRDEMKLIND
AYDSEYFATKVQNTNGVYVVAFTGLGAPYWDPYARGAIFGLTRGVNANHIIRATLESIAYQTRDVLEAMQADS
GIRLHALRVGGAVANNFLMQFQSDILGTRVERPEVREVTALGAAYLAGLAVGFWQNLDELQEKAVIDERFRP
GIETTERNYRYAGWKKAVKRAMAWEEH

>d1chma1 c.55.2.1 (A:2-156) Creatinase {Pseudomonas putida}
QMPKTLIRNGDKVRSTFSQAQEYANRQARLRAHAAENIDAAIFTSYHNINYYSDFLYCSFGRPYALVVTEDDVIS
ISANIDGGQPWRRTVGTDNIVYTDWQRDNYFAAIQQALPKARRIGIEHDHNLQNRDKLAARYPDAELVDVA
AACMRMR

>d1az9_1 c.55.2.1 (1-176) Aminopeptidase P {Escherichia coli}
SEISRQEFPQQRQALVEQMPGPGSAALFAAPEVTRSADSEYPYRQNSDFWYFTGFNEPEAVLVLIKSDDTHNHS
VLFNRVRDLTAEIWFGRRLGQDAAPEKLGVDRALAFSEINQQLYQLLNGLDVYHAQGEYAYADVIVNSALEKL
RKGSRQNLTAPATMIDWRPVVHEMRLF

>d1jl1a_c.55.3.1 (A:) RNase H (RNase HI) {Escherichia coli}
KQVEIFTAGSALGNPGPGGYGAILRYGREKTFASAGYRTTNNRMELMAAIVALEALKEHAEVILSTDSQYVRQ
GITQWIHNWKRGWKTADKKPVKNVDLWQRLDAALGQHQIKWEWVKGHAGHPENERADELARAAMNP
TLEDTGYQVE

>d1ril__ c.55.3.1 (-) RNase H (RNase HI) {Thermus thermophilus}
RKRALFTDGACLGNPGPGWAALLRFHAHEKLLSGGEACTTNNRMELKAAIEGLKALKEPCEVDLYTDSHYL

KKAFTEGWLEGWRKRGWRTAEGKPVKNRDLWEALLAMAPHRVRFHVKGHTGHPENERVDREARRQAQS
QAKT

>d1jl2a_c.55.3.1 (A:) RNase H (RNase HI) {Chimeric (Escherichia coli/Thermus thermophilus)}

KQVEIFTDGSALGNPGPGGYGAILRYRGREKTFSAKYTRTTNNRMELKAAIEGLKALKEPAEVLDLYTDSHYLKKA
FTEGWLEGWRKRGWRTAEGKPVKNRDLWEALLAMAPHRVRFHVKGAGHPENERADELARAAMNPT
LEDTGY

>d1ekea_c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Methanococcus jannaschii}

MIIIGIDEAGRGPVLGPMVVCAFAIEKEREELKKLGVKDSKELTKNKRAYLKKLENLGYVEKRILEAEEINQLMN
SINLNNDIEINAFSKVAKNLIEKLNRDDEIEIYIDACSTNTKFEDSFKDIEDIINKERNLNKIIAEHKADAKYPVVSAA
SIIAKAERDEIIDYYKKIYGDIGSGYPSDPKTIFLEDYFKKKLPDIARTHWTCKRILDKSKQT

>d1i39a_c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Archaeoglobus fulgidus}

MKAGIDEAGKGCVIGPLVVAVGAVCSDEDRLRKLGVKDSKKLSQRREELAEIRKICRTEVLKVSPENLDERMAA
KTINEILKECYAEIILRLKPEIAYVSDPVIPERLSRELEETGLRVVAEHKADEKYPLVAAASIIAKVEREREIERLKEF
GDFGSGYASDPRTRVLKEWIASGRIPSCVRMRWKTWSNLRQK

>d1io2a_c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Thermococcus kodakaraensis}

MKIAGIDEAGRGPVIGPMVIAAVVDENS LPKLEELKVRDSKKLTPKRREKLFNEILGVLDYVILELPPDVIGSRE
GTLNEFEVENFAKALNSLKVKPDVYADAADVDEERFARELGERLNFEAVVAKHKADDIFPVVSAASILAKVTR
DRAVEKLKEEYGEIGSGYPSDPRTAFLENYYREHGEFPPIVRKGWKTLLKIAEKVESEKK

>d1c9ra1 c.55.3.1 (A:430-558) HIV RNase H (Domain of reverse transcriptase)
{Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANAATKLGKAGYVTNKGRQKVPLNTTNQKTELQAIYLALQDSGLEVNIVTDSQYAL
GIIQAQPDKSESELVNQIIEALIKKEAVYLA WVPAHAGIGGNAAVDALVSAGIAA

>d1hrha1 c.55.3.1 (A:432-556) HIV RNase H (Domain of reverse transcriptase)
{Human immunodeficiency virus type 1}

EPIVGAETFYVDGAANRET KLGKAGYVTNKGRQKVPLNTTNQKTELQAIYLALQDSGLEVNIVTDSQYALGII
QAQPDKSESELVNQIIEQLIKKEKVYLA WVPAHKGIGGNEQVDKLV SAGI

>d1jlaa1 c.55.3.1 (A:430-553) HIV RNase H (Domain of reverse transcriptase)
{Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANRET KLGKAGYVTNRGRQKVPLNTTNQKTELQAIYLALQDSGLEVNIVTDSQYAL
GIIQAQPDQSESELVNQIIEQLIKKEKVYLA WVPAHKGIGGNEQVDKLV S

>d1vrta1 c.55.3.1 (A:430-539) HIV RNase H (Domain of reverse transcriptase)
{Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANRET KLGKAGYVTNRGRQKVPLNTTNQKTELQAIYLALQDSGLEVNIVTDSQYAL
GIIQAQPDQSESELVNQIIEQLIKKEKVYLA WVPAH

>d1asu_ c.55.3.2 (-) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian
sarcoma virus)}

PLREPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAQHHWATAIAVLGRP KAI KT
DNGSCFTSKSTREW LARW GIAHTTGIPGNSQGQAMVERANRLLKDKIRV LAEGDGFMKRIPTSKQGELLAKA
MYALNHFERGENTKTNL

>d1c0ma2 c.55.3.2 (A:49-216) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV,
avian sarcoma virus)}

GVNPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSVAQHHWATAIAVLGRP KAI KT
DNGSCFTSKSTREW LARW GIAHTTGIPGNSQGQAMVERANRLLKDRIRV LAEGDGFMKRIPTSKQGELLAKA
YALNHKER GENTKTPIQKHW RPT

>d1cxqa_c.55.3.2 (A:) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV, avian sarcoma virus)}

GRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDTASSAIVVTQHGRVTSAAQHHWATAIAVLGRPKAIKTDNG
SCFTSKSTREWLARWIAHTTGIPGNSQGQAMVERANRLLDKIRVLAEGDGFMKRIPTSKQGELAKAMYAL
NH

>d1exqa_c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}

SSPGIWQLDCTHLEGKVLVAHVVASGYIEAEVIPAETGQETAYFLLLAGRWPVKTIHTDNGSNFTGATVRAAC
DWAGIKQEDGIPYNPQSQGVESMNKELKKIIGQVRDQAELKTAQMAVFIHNKKRKGGIGGYSAGERIVDII
ATDIQ

>d1hyva_c.55.3.2 (A:) Retroviral integrase, catalytic domain {Human immunodeficiency virus type 1}

SPGIWQLDCTHLEGKVLVAHVVASGYIEAEVIPAETGQETAYFLLLAGRWPVKTVHTDNGSNFTTTVKAAC
WWAGIKQEFGIPYNPQSQGVIESMNKELKKIIGQVRDQAELKTAQMAVFIHNKKRKGGIGGYSAGERIVDII
ATDIQT

>d1c6va_c.55.3.2 (A:) Retroviral integrase, catalytic domain {Simian immunodeficiency virus}

NSDLGTWQMDCTHLEGKIVIVAHVVASGFIEAEVIPQETGRQTAFLLKLGRWPITHLHTDNGANFASQEVK
MVAWWAGIEHTFGVPYNPQSQGVVEAMNHHLKNQIDRIREQANSVETIVLMAVHCMNHRRGGIGDMTP
AERLINMITTEQEIQFQ

>d1bco_2 c.55.3.3 (258-480) mu transposase, core domain {Bacteriophage mu}

EHLDAMQWINGDGYLHNVFVRWFNGDVIRPKTWFWQDVKTRKILGWRCRVSENIDSIRLSFMDVVTRYGIP
EDFHITIDNTRGAANKWLTGGAPNRYRFVKEDDPKGLFLMGAKMHWTsvAGKGWGQAKPVERAFGVG
GLEEYVDKHPALAGAYTGPNPQAKPDNYGDRAVDAELFLKTLAEGVAMFNARTGRETEMCGGKLSFDDVFER
EYARTIVRKP

>d1b7ea_c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}

SAEAIRKAGAMQTVKLAQEFPPELLAIEDTTSLSYRHQVAEELGKLGSIQDKSRGWWVHSVLLLEATTFRVGLLH
QEWWMRPDDPADADEKESGKWAAAATSLRMGSMSNVIAVCDREADIHAYLQDKLAHNERFVVRSKH
PRKDVESGLYLYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPARKASLSLRSGRITLKQGNITLNAVLAEEINP
PKGETPLKWLLTSEPVESLAQALRVIDIYTHRWRIEEFHKAWKTGAGAERQRMEEPDNLERMVSILSFVAVRLL
QLRESFLPQALRAQGGLKEAEHVESQSAETVTPDECQLLGYLDKGKRKRKEKGSQWAYMAIARLGGFMDSK
RTGIASWGALWEGWEALQSKLDGFLAAKDLMAQ

>d1f3ia_c.55.3.4 (A:) Transposase inhibitor (Tn5 transposase) {Escherichia coli}

ALHRAADWAKSVFSSAALGDPRTARLVNAAQLAKYSGKSITISSEGSKAAQEGAYRFIRNPVSAEAIRKAGA
MQTVKLAQEFPPELLAIEDTTSLSYRHQVAEELGKLGSIQDKSRGWWVHSVLLLEATTFRVGLLHQEWWMRP
DDPADADEKESGKWAAAATSLRMGSMSNVIAVCDREADIHAYLQDKLAHNERFVVRSKHPRKDVESGLY
LYDHLKNQPELGGYQISIPQKGVVDKRGKRKNRPARKASLSLRSGRITLKQGNITLNAVLAEEINPPKGETPLKW
LLTSEPVESLAQALRVIDIYTHRWRIEEFHKAWKTGAGAERQRMEEPDNLERMVSILSFVAVRLLQLRESFLPQ
ALRAQGGLKEAEHVESQSAETVTPDECQLLGYLDKGKRKRKEKAGSLOWAYMAIARLGGFMDSKRTGIASWG
ALWEGWEALQSKLDGFLAAKDLMAQGKIG

>d1kfsa1 c.55.3.5 (A:324-518) Exonuclease domain of prokaryotic DNA polymerase {Escherichia coli}

MISYDNYVTILDEETLKAWIAKLEKAPVFAFDTETDSLNIANLVGLSFAIEPGVAAYIPVAHDYLDAPDQISRER
ALELLKPLLEDEKALKVGQNLKYDRGILANYGIELRGIAFDTMLESYILNSVAGRHDMDSLAERWLKHKTITFEI
AGKGKNQLTFNQIALEEAGRYAAEDADVTQLQLHLMWPDLQK

>d1qtma1 c.55.3.5 (A:293-422) Exonuclease domain of prokaryotic DNA polymerase {Thermus aquaticus}

ALEEAAPWPPPPEGAFVGFVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGLLAKDLSVLALREGI
GLPPGDDPMILLAYLLDPSNTTPEGVARRYGEWTEAGERAALSERLFANLWGRLEG

>d1xwl_1 c.55.3.5 (297-468) Exonuclease domain of prokaryotic DNA polymerase {Bacillus stearothermophilus, newly identified strain as yet unnamed}

AKMAFTLADRVTTEEMILADKAALVVVEENYHDAPIVGIAVNVNEHGRFFLRPETALADPQFVAWLGD**E**TKKS
MFDSKRAAVALKWKGIELCGVSFDLLAAYLLDPAQGVDDVAAA**K**MQYEAVRPDEAVYGKGAKRAVPDEP
VLAEHLVRKAAAIWE**L**ERPFLDELRRN

>d1t7pa1 c.55.3.5 (A:1-210) Exonuclease domain of T7 DNA polymerase {Bacteriophage T7}
MIVSDIEANALLESVTKFHCGVIYDYSTA**E**YVSYRPSDFGAYLDALEAEVARGGLIVFHNGHKYDVPALT**K**LAKLQ
LNREFHILPRENCIDTLVLSRLIHSNLKD**T**DMGLLRGKLPAGEAWGYRLGEMKGEYKDDFKRMLEE**Q**GEYVD
GM**E**WWNFNEEMMDYNVQDVVTKALLEKLLSDKH**Y**FPP**E**IDFTDVGYTTFWSES

>d1noya_ c.55.3.5 (A:) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Bacteriophage T4}

DEFYISIETVGN*N*IVERYIDENGKERTREVEYLPTMFRHC**E**ESKYKDIY**G**KNCAPQKFPSMKDARDWMKRME
DIGLEALGMND**F**KLAYISDTY**G**SEIVYDRKFVRVANCDIEVTGDKFPDPMKA**E**YEIDAITHYDSIDDRFYVFDLL
SMYGSVSKWD**A**KLAKLDCEGG**D**EV**P**QEILD**R**VIYMPFDNERDMLMEYINLWEQKRP**A**IFT**G**WNIEGFDV**P**
IMNRVKM**I**LGERSMKRFSPIGRV**K**SKLLQNMYGS**K**E**I**YSIDGV**S**ILDYLDLYKKFAFTNLPSFSLESVAQHETKK**G**
LPYDGPI**N**KLRET**N**H**Q**RY**I**SY**N**IID**V**ESV**Q**A**I**D**K**IRGF**I**DL**V**MSYYAKMP**F**SGVM**S**PIKTWD**A**I**I**FN**S**LK**G**

>d1ih7a1 c.55.3.5 (A:1-375) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Bacteriophage RB69}

MKEFYLTVEQIGDSIFERYIDSNGRERTREVEYKPSLFAHC**P**ESQAT**K**YFDIY**G**KPCTRKL**F**ANMRDASQWIKRM
EDIGLEALGMDDFKLAYISDTY**N**YE**I**KYDHTKIRVAN**F**DI**E**VTSPDG**P**EP**S**QAKHP**I**DAITHYDSIDDRFYVFDLL
NSPYGNVEEWSIEIA**A**KL**Q**E**Q**GG**D**EV**P**SE**I**DKIIYMPFD**N**E**K**ELL**M**E**Y**LNFWQQKTPV**I**LT**G**WN**V**ES**F**DIP**V**
NRIKNIFGESTAKRLSPHRKTRV**K**VIEN**M**Y**G**S**R**E**I**IT**L**FG**I**S**V**LDY**I**DLYKK**F**ST**N**Q**P**SY**S**LD**I**Y**I**SE**F**EL**N**VG**K**L**K**YD
GPISKLRESNH**Q**RY**I**SY**N**IID**V**Y**R**VL**Q**IDA**K**RQ**F**IN**L**DM**Y**AK**I**Q**S**V**F**PIKTWD**A**I**I**FN**S**L**K**E

>d1tgoa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Thermococcus gorgonarius}

MILD**T**DYITED**G**KP**V**IR**I**FK**K**EN**E**FK**I**YD**R**N**F**EP**I**Y**A**LL**K**DD**S**A**I**ED**V**KK**I**TA**E**R**H**G**T**V**V**R**V**R**A**E**K**V**KK**F**L**
PIEVW**K**LY**F**TH**P**Q**D**V**A**IR**D**K**I**KE**H**PA**V**D**I**Y**E**D**I**P**F**AK**R**Y**L**D**K**GL**I**P**M**EG**D**E**E**L**K**ML**A**FD**I**ET**L**Y**H**E**G**EE**F**A**E**
ILM**I**SY**A**DEEGARV**I**T**W**KN**I**D**L**P**Y**V**D**V**V**STE**K**E**M**I**K**R**F**LV**V**KE**K**D**P**D**V**L**I**TY**N**GD**N**FD**F**AY**L**KK**R**SE**K**LG**V**K**F**
REG**S**EP**K**I**Q**RM**G**DR**F**AV**E**V**K**G**R**I**H**F**D**L**P**V**I**R**R**T**I**N**L**P**T**Y**T**LE**A**Y**E**A**I**F**G**QP**K**E**K**V**Y**A**E**E**I**A**Q**W**E**T**G**EL**R**VA
RYS**M**ED**A**K**V**T**Y**EL**G**KE**F**FP**M**EA**Q**LS**R**LV**G**Q**S**L**W**D**V**RS

>d1qhta1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Thermococcus sp., 9on-7}

MILD**T**DYITED**G**KP**V**IR**I**FK**K**EN**E**FK**I**YD**R**T**F**EP**I**Y**A**LL**K**DD**S**A**I**ED**V**KK**I**TA**E**R**H**G**T**V**V**K**V**R**A**E**K**V**Q**KK**F**
GR**P**IEVW**K**LY**F**HN**H**P**Q**D**V**PAIR**R**DR**I**RA**H**PA**V**D**I**Y**E**D**I**P**F**AK**R**Y**L**D**K**GL**I**P**M**EG**D**E**E**L**T**ML**A**FA**I**AT**L**Y**H**E**G**EE**F**
TG**P**IL**M**ISY**A**D**G**SE**A**RV**I**T**W**KK**I**D**L**P**Y**V**D**V**V**STE**K**E**M**I**K**R**F**LV**V**RE**K**D**P**D**V**L**I**TY**N**GD**N**FD**F**AY**L**KK**R**CE**E**LG**I**
TLGRDG**S**EP**K**I**Q**RM**G**DR**F**AV**E**V**K**G**R**I**H**F**D**L**P**V**I**R**R**T**I**N**L**P**T**Y**T**LE**A**Y**E**A**I**F**G**KP**K**E**K**V**Y**A**E**E**I**A**Q**W**E**SG**E**GLE
RVARY**S**ME**A**K**V**T**Y**EL**G**RE**F**FP**M**EA**Q**LS**R**LV**G**Q**S**L**W**D**V**RS

>d1d5aa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Desulfurococcus tok}

MILD**A**DYITED**G**KP**V**IR**I**FK**K**EN**E**FK**I**YD**R**D**F**EP**I**Y**A**LL**K**DD**S**A**I**ED**I**KK**I**TA**E**R**H**G**T**V**V**R**T**RA**E**R**V**KK**F**
LGRDG**S**EP**K**I**Q**RM**G**DR**F**AV**E**V**K**G**R**I**H**F**D**L**P**V**I**R**R**T**I**N**L**P**T**Y**T**LE**A**Y**E**A**I**F**G**KP**K**E**K**V**Y**A**E**E**I**A**Q**W**E**SG**E**GLE

PVEVWKLYFTHPQDPAIRDKIREHPAIRVVDIYEYDIPFAKRYLIDRGLIPMEGDEELRMLAFDIETLAHAGAAAG
AGPILMISYADEEGARVITWKNIDLPGESVSTEKEMIKRFLKVIEQKDPDVILITYNGDNFDFAYLKKRSEMLGVK
FILGRDGSEPKIQRMGDRFAVEVKGRIHFIDLYPVIRRTINLPTYLETYEPVFGQPAEKVYAAEIAEAWASGEGLE
RVARYSMEDAKATYELGKEFFPMEAQLSRLVGQSLWDVSRS

>d1gcxa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon Pyrococcus kodakaraensis}

MILDTDYITEDGKPVIRIFKKENGEFKIEYDRTFEPFYALLKDDSAIEEVKKITAERHGTVVTVKRVEKVQKKFLGR
PVEVWKLYFTHPQDPAIRDKIREHPAIRVVDIYEYDIPFAKRYLIDKGLVPMEGDEELKMLAFDIETLYHEGEEFAEG
PILMISYADEEGARVITWKNIDLPGESVSTEKEMIKRFLRVVKEKDPDVILITYNGDNFDFAYLKKRCEKLGINFA
LGRDGSEPKIQRMGDRFAVEVKGRIHFIDLYPVIRRTINLPTYTLEAVYEAvgqpKEKvyaeeittawetgenler
VARYSMEDAKVTYELGKEFLPMEAQLSRLIGQSLWDVSRS

>d1fxxa_c.55.3.5 (A:) Exonuclease I {Escherichia coli}

QSTFLHDYETFGTHPALRPAQFAAIRTDSEFNIVGEPEVFYCKPADDYLPCPGAVLITGITPQEAKGENEAA
FAARIHSLFTVPKTICLGYNNVRFDDEVTRNIFYRNFYDPYAWSWQHDNSRWDLDDVMRACYALRPEGINWP
ENDDGLPSRFRLHLTKANGIEHSNAHDAMADVATIAMAKLVKTRQPRLFDTLFRNKHKLMALIDVPQMKP
LVHVSGMFGAWRGNTSWVAPLAWHPEVNRAVIMVDSLADISPLLELDSDTLRERLYTAKTDLGDNAAVPVKL
VHINKCPVLAQANTLRPEDADRLGINRQHCLDNLKILRENPNQVREKVVIAFAEAEPFTPSDNVDAQLYNGFFSD
ADRAAMKIVLETEPRNLPALDITFVDKRIEKLNFNYRARNFPGTLDYAEQQRWLEHRRQVFTPEFLQGYADELQ
MLVQQYADDKEKVALLKALWQYADEIVEH

>d1hjra_c.55.3.6 (A:) RuvC resolvase {Escherichia coli}

AIILGIDPGSRVTGYGVIRQVGRQLSYLGSGCIRTKVDDLPSRLKLIYAGVTEITQFQPDYFAIEQVFMAKNADSAL
KLGQARGVAIAAVNQELPVFEYAARQVKQTVGIGSAKSQVQHMVRTLLKLPANPQADAADALAIATHCH
VSQNAMQ

>d1kcfa2 c.55.3.7 (A:39-256) Mitochondrial resolvase ydc2 catalytic domain {Fission yeast (Schizosaccharomyces pombe)}

TSRVLGIDLGIKNFSYCFASQNEDSKVIIHNWSVENLTEKNGLDIQWTEDFQPSSMADLSIQLFNTLHEKFNPBV
ILMERQRYSRSGIATIPEWTLRVNMLESMLYALHYAEKRNSIEQKIQYPFLLSLSPKSTYSY WASV LNTKASFSKKKS
RVQMVKELIDGQKILFENEALYKWNNNSRVEFKKDDMADSALIASGWMRWQAQLKHYRNFCQFL

>d1jj2m_c.55.4.1 (M:) Ribosomal protein L18 (L18p) {Archaeon Haloarcula marismortui}

ATGPRYKVMRRRREARTDYHQRLRLKSGKPRLVARKSNKHVR AQLVTLGPNGDDTLASAHSSDLAEYGWEA
PTGNMPSAYLTGLLAGLRAQEAGVEEAVLDIGLNSPTPGSKVFAIQEGAIDAGLDIPHNDDVLA DWQRTRGAHI
AEYDEQLEPLYSGFDAADLPEHDELRETLLDGIEL

>d1fjgk_c.55.4.1 (K:) Ribosomal protein S11 {Thermus thermophilus}

KRQVASGRAYIHASYNNNTIVTIDPDGNPITWSSGGVIGYKGSRKTPYAAQLAALDAKKAMAYGMQSVDVI
VRGTGAGREQAIRALQASGLQVKSVDDTPVPHNGCRPKKKFRKAS

>d1dt9a1 c.55.4.2 (A:143-276) Middle domain of eukaryotic peptide chain release factor subunit 1, ERF1 {Human (Homo sapiens)}

DSKFGFVIDGSGALFGTLQGNTREVLHKFTVDPKKHGRGGQSLRFARLRMEKRHNYVRKVAETAVQLFISG
DKVNAGLVLAGSADFKELSQSDMFDQRLQSKV LKV D ISYGGENG FNQAI ELSTE VLS

>d1eo1a_c.55.5.1 (A:) Hypothetical protein MTH1175 {Archaeon Methanobacterium thermoautotrophicum}

MKIAIASSGTDLGSEVSRRFFGRAPYFMIVEMKKGNIESSEVIENPSASASGGAGIRTAQIIANNGVKAVIASSPGP
NAFEVLNELGIKIYRATGTSVEENLKLFTEGNLEEIRSPGSGRGRRRR

>d1ewqa3 c.55.6.1 (A:121-266) DNA repair protein MutS, domain II {Thermus aquaticus}
LLQESLLPREANYLAAIATGDGGLAFLDVSTGEFKGTVLKSALYDELFRRPAEVLLAPELLENGAFLDEFRK
RFPVMLSEAPFEPEGEPLAARRARGALLAYAQRTQGGALSLQPFRFYDPGAFMRLPEATLRALEVFEPL

>d1e3ma3 c.55.6.1 (A:117-269) DNA repair protein MutS, domain II {Escherichia coli}
GTISDEALLQERQDNLLAAIWQDSKGFGYATLDISSLRFRRLSEPADRETMAAELQRTNPAELLYAEDFAEMSLIEG
RRGLRRRPLWEFEIDTARQQLNLQFGTRDLVGFVENAPRGLCAAGCLLQYAKDTQRTTLPHIRSITMEREQDSI
IM

>d1sfe_2 c.55.7.1 (12-92) Ada DNA repair protein {Escherichia coli}
LAVRYALADCELGRCLVAESERCICAILLGDDDATLISELQQMFPAADNAPADLMFQQHVREVIASLNQRDTPLT
LPLDIR

>d1qnta2 c.55.7.1 (A:6-91) O6-alkylguanine-DNA alkyltransferase {Human (Homo sapiens)}
EMKRTTLDSPLGKLELSGCEQLHIEIKLLGKGTSAADAVEVPAPAAVLGGPEPLMQCTAWLNAYFHQPEAIEEF
PVPALHHPVFQQ

>d1mgta2 c.55.7.1 (A:1-88) O6-alkylguanine-DNA alkyltransferase {Archaeon Pyrococcus kodakaraensis}
MLSVEKFRVGERVVWIGVIFSGRVQGIAFAFDRGTLMKRIHDLAELHGKRGVSISLDVQPSDYPEKVFVVLIGEL
DNASFLRELSFEG

>d1cfza_c.56.1.1 (A:) Hydrogenase maturing endopeptidase HybD {Escherichia coli}
MRILVLGVGNILLTDEAIGVRIVEALEQRYILPDYVEILDGGTAGMELLGDMANRDHLIIADAIVSKKNAPGTMM
ILRDEEVPALFTNKISPHQLGLADVLSALRFTGEFPKKLTIVGVIPESLEPHIGLTPTVEAMIEPALEQVLAALRESG
VEAIPRSDS

>d1c8ba_c.56.1.2 (A:) Germination protease {Bacillus megaterium}
MEKEELDSQYSVRTDLAVEAKDIALENQPKPNQNQSEIKGVIVKEKEEQGVKISMVEITEEGAIAIGKKGRYVTLE
SVGIREQDTEKQEEAMEEVFAKELNFFIKSLNIPDDASCLVVGGLNLSVTPDALGPKAVIDNLLITRHLFELQPESV
QDGFRPVSIAVPGVMGMTGIETSDIIFGVVKVNPDFIIADALAARSIERVNATIQISDSGIHPGSVGNKRKEIS
YETLGIPVIAIGIPTVVDAVSITSIDFILKHFGREMKEQGKPSKLLPSGMTFGEKKKLTEDDLPNEEQRQTYLG
MIGTLPDEEKRRLIHEVLAPLGHNLMTPKEVDMFIEDMANVAGGLNAALHHEVDQENFGAYTH

>d1ulb_c.56.2.1 (-) Purine nucleoside phosphorylase, PNP {Human (Homo sapiens)}
MENGYTYEDYKNTAEWLLSHTKHRPQVAICSGGLGGTDKLTQAQIFDYSEIPNFPRSTVPGHAGRLVFGFLNG
RACVMMQGRFHMYEGLPWLKVTFPVRFHLLGVDTLVNAAGGLNPKEVGDIMLIRDHINLPGFSGQNP
LRGPNDERFGDRFPAMS DAYDRTMRQRALSTWKQMGEQRELQEGTYVMVAGPSFETVAECRVLQKLGADA
VGMSTVPEVIVARHCGLRVFGSLITNKVIMDYESLEKANHEEVLAAGKQAAQKLEQFVSLMASIPLPDKAS

>d1b8oa_c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cow (Bos taurus)}
NGYTYEDYQDTAKWLLSHTEQRPQVAICSGGLGGLVNKLTQAQTFDYSEIPNFPESTVPGHAGRLVFGILNGR
ACVMMQGRFHMYEGLPWLKVTFPVRFRLLGVETLVTNAAGGLNPFEVGDIMLIRDHINLPGFSGENPLR
GPNEERFGVRFPAMS DAYDRTMRQKAHSTWKQMGEQRELQEGTYVMLGGPNFETVAECRLLRNGLGADAVG
MSTVPEVIVARHCGLRVFGSLITNKVIMDYESQGKANHEEVLEAGKQAAQKLEQFVSLMASI

>d1k9sa_c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Escherichia coli}
ATPHINAEMGDFADVVLMMPGDPLRAKYIAETFLEDAREVNNVRGMLGFTGTYKGRKISVMGHGMGIPCSIYT
KELITDFGVKKIIRVGSCGAVLPHVKLRDVIGMGACTDSKVNIRFKDHDFAAIADFDMVRNAVDAAKALGD
ARVGNLFSADLFYSPDGEFDVMEKYGILGVEMEAAGIYGVAAEFGAKALTICTVSDHIRTHEQTTAAERQTTF
NDMIKIALESVLLGDK

>d1qe5a_c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cellulomonas sp.}
PPLDDPATDPFLVARAADHIAQATGVEGHDMALVLGSGWGAAELLGEVVAEVPTHEIPGFSSVTRSIRVERA

DGSVRHALVLGSRTHLYEGKGVRAVVGVRTAAATGAETLILTNGCGGLNQEWGAGTPVLLSDHINLTARSPLE
GPTFVDLTDVYSPRLRELAHRVDPTLPEGVYAQFPGPHYETPAEVRMAGILGADLVMSTTLEAIAARHCGLEV
LGVSLVTNLAAGISPTPLSHAEVIEAGQAAGPRISALLADIKR

>d1g2oa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Mycobacterium tuberculosis}

DPDELARRAAQVIADRTGIGEHDVAVVLGSGWLPAVAALGSPTTVLPQAELPGFPPTAAGHAGELLSVPIGAH
RVLVLAGRIHAYEGHDLRYVVHPVRAARAAGAQIMVLNAAGGLRADLQVQGPVLISDHNLNTARSPLVGGEF
VDLTDAYSPLRELARQSDPQLAEGVYAGLPGPHYETPAEIRMLQTLGADLVMSTVHETIAARAAGAEVLGV
LVTNLAAGITGEPLSHAEVLAAGAASATRMGALLADVIARF

>d1k3fa_ c.56.2.1 (A:) Uridine phosphorylase {Escherichia coli}

MSKSDVFHLGLTKNDLQGATLAIVGDPDRVEKIAALMDKPVKLASHREFTTWRAELDGKPVICSTGIGGPST
SIAVEELAQLGIRTFLRIGTTGAIQPHINVGDVLVTTASVRLDGASLHFAPLEPPAVADFFECTTALVEAAKSIGATTH
VGVTASSDTFYPGQERYDTYSGRVVRHFKGSMEEWQAMGVMNYEMESATLLMCASQGLRAGMVAGVIV
NRTQQEIPNAETMKQTESHAVKIVVEAARRLL

>d1cb0a_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Human (Homo sapiens)}
AVKIGIIGGTGLDDPEILEGRTEKYVDTDPFGKPSDALILGKIKNVDCVLLARHGRQHTIMPSKVNYQANIWALKEE
GCTHVIVTTACGSLREEIQPGDIVIIDQFIDRTTMRPQSFYDGSHSCARGVCHIPMAEPFCPKTREVLIELTAKKLG
LRCHSKGTMVTIEGPRFSSRAESFMFRWGADVNMVVPEVVAKEAGICYASIAMATDYDCWKEHEEEAVSV
DRVLTTLKENANKAKSLLTTIPQIGSTEWSETLHNKNMAQFSVLLP

>d1je0a_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Archaeon Sulfolobus solfataricus}

PVHILAKKGEVAERVLVVGDGRARLLSTLLQNPKLTNENRGFLVYTGKYNGETVSIATHGIGGPSIAIVLEELAM
LGANVFIRYGTGALVPYINLGEYIIVTGASYNQGGLFYQYLRDNACVASTPDFELTNKLVTSFSKRNLKYYVGNVF
SSDAFYAEDEEFVKKWSSRGNIAVEMECATLFTLSKVKGWKSATVLVSDNLAKGGIWITKEELEKSVMGDAKA
VLDLTS

>d2pth_ c.56.3.1 (-) Peptidyl-tRNA hydrolase {Escherichia coli}

TIKLIVGLANPGAEYAATRHNAAGAWFDLLAERLRAPLREEAKFFGYTSRVTLGGEDVRLVPTTFMNLSGKAVA
AMASFRINPDEILVAHDELDLPPGVAKFKLGGGHGNGLKDIISKLGNPNFHRLRIGIGHPGDKNKVVGFV
LGKPPVSEQQLIDEAARCTEMWFTDGLTKATNRLHAFKAQ

>d1a2za_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Archaeon Thermococcus litoralis}

MKKVLITGFEPFGGDSKNPTEQIAKYFDRKQIGNAMVYGRVLPVSVKRATIELKRYLEEIKPEIVINLGLAPTYNSI
TVERIAVNIIDARIPIPNDGYQPIDEKIEEDAPLAYMATLPVRAITKTLRDNGIPATISYSAGTYLCNYVMFKTLHFSK
IEGYPLKAGFIHVPTPDQVNKFFLLGKNTPSMCLEAEIKIAELAVKVSLDYLEKDRDDIKIPL

>d1auga_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Bacillus amyloliquefaciens}

MEKKVLLTGFDPFGGETVNPSWEAVKRLNGAAEGPASIVSEQVPTVFYKSLAVLREAIIKHQPDIIICVGQAGGR
MQITPERVAINLNEARIPDNEGNQPVGEDISQGGPAAYWTGLPIKRIVEEIKKEGIPAAVSYTAGTFVCNHLFYGL
MDEISRHHPHIRGGFIHIPYIPEQTLQKSAPSLSLDHITKALKIAAVTAAVHEDDIETG

>d1iofa_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Archaeon Pyrococcus furiosus}

MKVLVTGFEPFGGEKINPTERIAKDLGIKIGDAQVFGRVLPVFGKAKEVLEKTEEIKPDIAIHVGLAPGRSAISI
ERIAVNAIDARIPIPNEGKKIEDEPIVPGAPTAYFSTLPIKKIMKKLHERGIPAYISNSAGLYLCNYVMYLSLHHSATK
GYPKMSGFIHVPTYIPEQIIDKIGKGQVPPSMCYEMELEAVKVAIEVALELL

>d2ctc__ c.56.5.1 (-) Carboxypeptidase A {Cow (Bos taurus)}

ARSTNTFNYATYHTLDEIYDFMDLLVAEHPQLVSKLQIGRSYEGRPIYVLKFSTGGSNRPAIWIDLGIHSREWITQA
TGVWFAKKFTEDYGQDPSFTAILEDSDMIDIFLEIVTPNPDGFATHSQNRLWRKTRSVTSSLCVGVDANRNWDAG
FGKAGASSSPCSETYHGKYANSEVEVKSVDFVKDHGNFKAFLSIHYSQLLYPYGYTTQSIPDKTELQNQVAKSA
VEALKSLYGTSYKGSIITIYQASGGSIDWSYNQGKYSFTFELRTGRTGRYGFLLPASQIPTAQETWLGVLTIMEHT
LNN

>d1pca_1 c.56.5.1 (1-308) Carboxypeptidase A {Pig (Sus scrofa)}

ARTTSTFNYATYHTLEEYDFMDILVAEHPALVSKLQIGRSYEGRPIYVLKFSTGGSNRPAIWIDSGIHSREWITQAS
GVWFACKITENYGNNSFTAILEDSDMIDIFLEIVTPNPDGFATHSQNRLWRKTRSVTSSLCVGSDSNRNWDAGF
GGAGASSSPCAETYHGKYPNSEVEVKSVDFVKNNNGNIKAFISIHSYSQLLYPYGYKTQSPADKSELNQIAKSAVA
ALKSLYGTSYKGSIITIYQASGGVIDWTYNQGKYSFTFELRTGRTGRYGFLLPASQIPTAQETWLALLTIMEHTLN
NS

>d1dtda_c.56.5.1 (A:) Carboxypeptidase A {Human (Homo sapiens)}

FNFGAYHTLEEISQEMDNLVAEHPGLVSKVNIGSSFENRPMNVLFSTGGDKPAIWLDAGIHAREWVTQATAL
WTANKIVSDYKGKDPSTSILDALDIFLLPVTPNPDGYFSQTKNRMWRKTRSKVSAGSLCVGVDPNRNWDAGFG
GPGASSNPSCSDSYHGPSANSEVEVKSVDFIKSHGKVKAFLHHSYSQLLMFPYGYKCTKLDDFDELSEVAQKAAQ
SLSRLHGTKYKVGPICSVYQASGGSIDWSYDYGKYSFAFELRTGRTGRYGFLLPARQILPTAEETWLGLKAIMEHVR
DHPY

>d1nsa_1 c.56.5.1 (4-308) Carboxypeptidase B {Pig (Sus scrofa)}

TTGHSYEKYNWETIEAWTEQVTSKNPDLISRASIGTTFDGDNIYLLKVGKPGSNKPAIFMDCGFHAREWISQA
FCQWFVRDAVRTGYEAHMTEFLDNLDFYLPVLNIDGYIYTWTKNRMWRKTRSTNAGSSCTGTDPNRNFN
AGWCTVGASVNPCCNETYCGSAAESEKETKALADFIRNNLSSIAYLTIHSYSQMILYPYSYDYKLPENDAELNSLA
KGAVKELASLYGTSYGPGSTTIYPAAGGSDDWAYNQGKYSFTFELRDKGRTGFVLPESQIQATCQETMLAVK
YVTNYTLEHL

>d1cpb__ c.56.5.1 (-) Carboxypeptidase B {Cow (Bos taurus)}

TTGHSYEKYNWETIEAWTEQVASENPDLISRASIGTTFLGNTIYLLKVGKPGSNKPAVFMDCGFHAREWISPA
FCQWFVREXXXXXXEIHMTEFLDKLDFYLPVVNIDGYIYTWTKNRMWRKTRSTAGSSCTGTDLNRFDA
GWCSIGASNNPCSETYCGSAAESEKESKAVADFIRNHLSKIAYLTIHSYSQMILYPYSYDYKLPKNNVELNTLAK
GAVKKLASLHGTTYSYGPAGATTIYPASGGSDDWAYDQGKYSFTFELRDKGRTGFVLPESQIQPTCEETMLAIKYV
TSVLEHL

>d1h8la2 c.56.5.1 (A:4-304) Carboxypeptidase D, catalytic domain {Crested duck (Lophonetta specularioides)}

QAVQPVDFRHHFSDMEIFLRRYANEYPSITRLYVGKSVELRELYVMEISDNPGIHEAGEPEFKYIGNMHGNE
VVGRELLNLIEYLCKNFGTDPEVTDLVQSTRIHIMPSMNPDGYEKSQEGDRGGTVGRNNSNNYDLNRNFPD
QFFQVTDPQPETLAVMSWLKTYPFVLSANLHGGSLVNVYPFDDDEQGIAIYSKSPDDAVFQQLALSYSKENKK
MYQGSPCKDLYPTEYFPHGITNGAQWYNVPGGMQDWNYLNTNCFEVTIELGCVKYPKAELPKYWEQRSS
LLQFIKQVHR

>d1obr__ c.56.5.2 (-) Carboxypeptidase T {Thermoactinomyces vulgaris}

DFPSYDSGYHNYNEMVNKINTVASNYPNIVKKFSIGKSYEGRELWAVKISDNVGTDENEPVLYTALHHAREHLT
VEMALYTLDFLTQNYNLDSRITNLVNNREIYIVFNINPDGGEYDISSGSYKSWRKNRQPNSSYVGTDLNRNY
GYKWGCCGGSSGSPSSETYRGRAFSAPETAAMRDFINSRVVGGKQQIKTLITFHTYSELILYPYGYTYTDVPSD
MTQDDFNVFKTMANTMAQTNGYTPQQASDLYITDGDMDTDWAYGQHKIFAFTFEMYPTSYNPGFYPDEVI
GRETSRNKEAVLYVAEKADCPSVIGKSC

>d1lam_2 c.56.5.3 (160-484) Leucine aminopeptidase, C-terminal domain {Cow (Bos taurus)}

FASGQNLARRLMETPANEMLPTKFAEIVEENLKSASIKTDVFIRPKSWIEEQEMGSFLSVAKGSEEPVFLEIHYK
GSPNASEPPLVFGKGITFDGGISIKAAANMDLMRADMGGAACTCSAIVSAAKLDLPINIVGLAPLCENMPG
KANKPGDVVRARNGKTIQVDNTDAEGRILADALCYAHTFNPKVIIINAATLTGAMDIALSGATGVFTNSSWL
WNKLFEASIETGDRVWRMPLFEHYTRQVIDCQLADVNNIGKYRSAGACTAAFLKEFVTHPKWAHLDIAGVM
TNKDEVPLYLRKGAGRPTRTLIEFLFRSQ

>d1amp_ c.56.5.4 (-) Aminopeptidase {Aeromonas proteolytica}

MPPITQQATVTAWLQPQVDASQITGTISSLESFTNRFYTTSGAQASDWIASEWQALSASLPNASVKQVSHSGY
NQKSVVMTITGSEAPDEWIVIGGHLDSTIGSHTNEQSVAPGADDDASGIAAVTEVIRVLSENNFQPKRSIAFMA
YAAEVGLRGSQDLANQYKSEGKNVVSALQLDMTNKGSAQDVFITDYTDNSFTQYLQTLMDYLPSTYGF
DTCGYACSDHASWHNAGYPAMPFESKFNDYNPRIHTTQDTLANSPTGSHAKKFTQLGLAYAIEMSATG

>d1qq9a_ c.56.5.4 (A:) Aminopeptidase {Streptomyces griseus}

APDIPLANVKAHLTQLSTIAANNNGRNRAHGRPGYKASVDYVAKLDAAGYTTLQQFTSGGATGYNLIANWP
GGDPNKVLMAGAHLDSVSSGAGINDNGGSAAVLETALAVSRAGYQPDKHLRFWWGAELGLIGSKFYVN
NLPSADRSSLAGYLNFDMIGSPNPGYFVYDDPVIEKTFKNYFAGLNVPTEIETEGDGRSDHAPFKNVGPVG
GLFTGAGYTKSAAQAQKWGQTAGQAFDRCYHSSCDLSNINDALDRNSDAAAHAIWTLSS

>d1cg2a1 c.56.5.4 (A:26-213,A:327-414) Carboxypeptidase G2, catalytic domain
{Pseudomonas sp., strain rs-16}

QKRDNVLFQAAATDEQPAVIKTLKLVNIETGTGDAEGIAAAGNFLEAEKLNLGFTVTRSKSAGLVGDNIVGKIK
GRGGKNLLMSHMDTVLKGILAKAPFRVEGDKAYGPGIADDKGGNAVILHTLKLKEYGVRDYGTTVLFNTD
EEKGSFGSRDLIQFEAKLADYVLSFEPTSAGDEKLSLGTXFNAGEGGKKLVDKAVAYYKEAGGTLGVEERTGGGT
DAAYAALSGKPVIESGLPGFGYHSDKAEYVDISAIPIRRLYMAARLIMDLGAG

>d1de4c3 c.56.5.5 (C:122-189,C:383-608) Transferrin receptor ectodomain, protease-like domain {Human (Homo sapiens)}

LYWDDLKRKLSEKLDSTDFSTKLLNENSYVPREAGSQKDENCALYVENQFREFKLSKVWRDQHFVXEIKILNI
FGVIKGFVEPDHYVVGAQRDAWGPAAKSGVGTTALLKLAQMFSMDVLKDGFPQPSRIIFASWSAGDFGSV
GATEWLEGYLSSLHLKAFTYINLDKAVLGTNSFKVSASPLLYTIEKTMQNVKHPVTGQFLYQDSNWASKVEKLT
DNAAFPFLAYSGIPAVSFCFCEDTDYPYLGTTMDTYKELIERIPELNKVARAAEVAGQFVILHDVELN

>d1boub_ c.56.6.1 (B:) LigB subunit of an aromatic-ring-opening dioxygenase LigAB {Pseudomonas paucimobilis}

ARVTTGITSSHIPALGAAIQTGTSNDYWGPVFKGYQPIRDWIKQPGNMPDVVILVYNDHASAFDMNIIPTFAI
GCAETFKPADEGWGPRVPDVKGHPDLAWHIAQSLILDEFDMTIMNQMDVDHGCTVPLSMIFGEPEEWPC
KVIPFPVNVTYPPPSGKRCFALGDSIRAAVESFPEDLNVHVWGTGGMSHQLQGPRAGLINKEFDLNFIDKLIS
DPEELSKMPHIQYLRESGSEGVELVMWLIMRGALPEKVRDLYTFYHIPASNTALGAMILQPEETAGTPLEPRKV
MSGHSL

>d1di6a_ c.57.1.1 (A:) MogA {Escherichia coli}

ATLRIGLVSISDRASSGVYQDKGIPALEEWLTSALTPFELETRLIPDEQAIIEQLCELVDEMSCHLVLTTGGTGP
RDVTPDATLAVADREMPGFGEQMRQISLHFVPTAILSRQVGIRKQALILNLPGQPKSIKETLEGVKDAEGNV
VHGIFASVPYCIQLLEGPYVETAPEVVAFRPKSARR

>d1jlja_ c.57.1.1 (A:) Gephyrin N-terminal domain {Human (Homo sapiens)}

HQIRVGVLTVSDSCFRNLAEDRSGINLKDLVQDPSLLGGTISAYKIVPDEIEEIKETLIDWCDEKELNLITGGTGF
APRDVTPEATKEVIEREAPGMALAMLMGSLNVTPLGMLSRPVCGIRGKTLIINLPGSKGSQECFQFILPALPHA
IDLLRDAIVKVKEVHD

>d1eava_ c.57.1.1 (A:) Plant CNX1 G domain {Mouse-ear cress (Arabidopsis thaliana)}

GPEYKVAILTVSDTVSAGAGPDRSGPRAVSVDSSSEKLGGAKVVATAVPDEVERIKDILQKWSDVDEMDLILT
LGGTGFTPRDVTPPEATKKVIERETPGLLVMMQESLKTPFAMLSRSAAGIRGSTLIINMPGNPNAVAECMEALL
PALKHALKQI

>d1g8la3 c.57.1.2 (A:178-326) MoeA, central domain {Escherichia coli}
VRVALFSTGDELQLPGQPLGDGQIYDTNRLAVHLMLEQLGCEVINLGIIRDDPHALRAAFIEADSQADVVISSGG
VSVGEADYTKTILEELGEIAFWKLAIKPGKPFAGKLSNSWFCGLPGNPVSATLFYQLVQPLLAKGNTASG

>d1bgva2 c.58.1.1 (A:1-194) Glutamate dehydrogenase {Clostridium symbiosum}
SKYVDRVIAEVEKKYADEPEFVQTVEEVLSLGPVVDAHPEYEEVALLERMVIPERVIEFRVPWEDDNGKVHVN
TGYRVQFNAGIGPYKGLRFAPSVNLSIMKFLGFEQAFKDSLTLPMGGAKGGSDFDPNGKSDREVMRFCQAF
MTELYRHIGPDIDVPAGDLGVGAREIGYMYGQYRKIVGGFYNGVLTG

>d1gtma2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}
ADPYEIVIKQLERAACQYMEISEEAEFLKRQRQRIEVTPVEMDDGSVKVFTGFRVQHNWARGPTKGIRWHPE
ETLSTVKALAAWMTWKAVMDLPYGGGKGGIIVDPKKLDREKERLARGYIRAIYDVISPYEDIPAPDVYTNPQI
MAWMMDEYETISRRTKPAFGITGKPLSI

>d1euza2 c.58.1.1 (A:4-180) Glutamate dehydrogenase {Archaeon Thermococcus profundus}
IDPFEMAVKQLERAACQYMDISEEAELEWLKKPMRIVEVSVPIEMDDGSVKVFTGFRVQHNWARGPTKGIRW
HPAETLSTVKALATWMTWKAVAVDLPYGGGKGGIIVNPKELSEREQERLARAYIRAVYDVIGPWTIDIPAPDVYT
NPKIMGWMMDEYETIMRRKGPAFGVITGKPLS

>d1bvua2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Thermococcus litoralis}
QDPFEIAVKQLERAACQYMDISEEAELEFLKRQRQRIEVSPVEMDDGSVKVFTGFRVQYNWARGPTKGIRWHP
ETLSTVKALAAWMTWKAVMDLPYGGGKGGVICNPKEMSDREKERLARGYVRAIYDVISPYTDIPAPDVYT
PQIMAWMMDEYETISRKDPSFGVITGKPPSV

>d1b26a2 c.58.1.1 (A:4-178) Glutamate dehydrogenase {Thermotoga maritima}
SLYEMAVEQFNRAASLMLESQDIAEVLRPKRVLIVEFPVRMDDGHVEVFTGYRVQHNWARGPAKGGIRYHP
DVTLDEVKALAFWMTWKAVMNLPFGGGKGGVRDPKKLSRNELERLSRRFFSEIQVIIGPYNDIPAPDVNTN
ADVIAYMDTYSMVNVGHTVLGIVTGKPVEL

>d1hwxa2 c.58.1.1 (A:1-208) Glutamate dehydrogenase {Cow (Bos taurus)}
ADREDDPNFFKMVEGFFDRGASIVEDKLVEDLKTTRQTQEQRKNRVRGILRIKPCNHNVLSSLSPIRRDDGSWEVI
EGYRAQHSHQRTPKGGIRYSTDVSVDEVKALASLMTYKCAVVDPFGGAAGVKINPKNYTDEDLEKITRRFT
MELAKKGFIGPGVDVPAPNMSTGEREMSWIADTYASTIGHYDINAHACVTGKPISQGGI

>d1leha2 c.58.1.1 (A:1-134) Leucine dehydrogenase {Bacillus sphaericus}
MEIFKYMELYEQQLVFCQDEASGLKAVIAIHDTTLGPALGGARMWTYNAEEEAIEDALRLARGMTYKNAAG
LNLLGGGKTVIIGDPFADKNEDMFRALGRFIQGLNGRYITAEDVGTTVDDMDLIHQETDYVT

>d1c1da2 c.58.1.1 (A:1-148) Phenylalanine dehydrogenase {Rhodococcus sp., M4}
SIDSALNWDGEMTVTRFDAMTGAHFVIRLDSTQLGPAAGGTRAACQYSNLADALTAGKLAGAMTLKMAVSN
LPMGGGKSVIALPAPRHSIDPSTWARILRIHAENIDKLSNYWTGPDVNTNSADMDTLNDTEVFGRSLERG
GAGS

>d1a4ia2 c.58.1.2 (A:2-126) Tetrahydrofolate
dehydrogenase/cyclohydrolase {Human (Homo sapiens)}
APAEILNGKEISAQIRARLKNQVTQLKEQVPGFTPRLAILQVGNRDDSNNLYINVKLKAAEEIGIKATHIKLPRTTES
EVMKYITSLNEDSTVHGFLVQLPLDSENSINTEEVINAIAPEKDVDG

>d1b0aa2 c.58.1.2 (A:2-122) Tetrahydrofolate

dehydrogenase/cyclohydrolase {Escherichia coli}
AAKIIDGKTIAQQVRSEVAQKVQARIAAGLRAPGLAVLVGSNPASQIYVASKRACEEVGFVRSYDLPETTSEA
ELLELIDTLNADNTIDGILVQLPLPAGIDNVKVLERIHPDKDVDG

>d1edza2 c.58.1.2 (A:3-148) Tetrahydrofolate
dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}
KPGRTILASKVAETFNTEIINNVEEYKKTHNGQGPLVGFLANNDPAAKMYATWTQKTSESMGFRYDLRVIEDK
DFLEEAIQANGDDSVNGIMVYFPVFGNAQDQYLQQVCVKEDVEGLNHVYYQNLYHNVRYLDKENRLKSIL
>d1do8a2 c.58.1.3 (A:21-279) Mitochondrial NAD(P)-dependent malic enzyme {Human (Homo sapiens)}
IKEKGKPLMLNPRNTKGMATLQERQMLGLQGLPPKETQDIQALRFHRNLKKMTSPLKEKYIYIMGIQERNEK
LFYRILQDDIESLMPIVYPTPTVGLACSQYGHIFRRPKGLFISIDRGHVRSIVDNWPNHVKA
VVTDGERILGLG
DLGVYGMGIPVGKLCYTACAGIRPDRCPLVCIDVGTNDNIALLKDPFYMGLYQKRDRTQQYDDLIDEFMKAITD
RYGRNTLIQFEDFGNHNAFRFLRKYREKYCTFNDD

>d2uaga2 c.59.1.1 (A:298-437) UDP-N-acetyl muramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}
GLPHRFEVVLEHNGVRWINDSKATNVGSTEALNLHVDGTLHLLGGDGKSADFSPLARYLNGDNVRLYCFG
RDGAQLAALRPEVAEQTETMEQAMRLAPRVQPGDMVLLSPACASLDQFKNFEQRGNEFARLAKELG

>d1e8ca2 c.59.1.1 (A:338-497) UDP-N-acetyl muramyl tripeptide synthetase MurE {Escherichia coli}
VCGRMVEVFTAPGKPTVVVDYAHPTDALEKALQAARLHCAGKLWCVFGCGGDRDKGKRPLMGAIAEEFADVA
VVTDDNPRTEEPRAIINDILAGMLDAGHAKVMEGRAEAVTCAVMQAKENDVVLVAGKGHEDYQIVGNQRLD
YSDRVTVARLLGVIARSH

>d1gg4a1 c.59.1.1 (A:313-447) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}
VPGRLFPIQLAENQLLDDSYNANVGSMTAAVQVLAEMPGYRVLVVGDMAELGAES EACHHVQVGEAAKAAGI
DRVLSVGKQSHAISTASGVGEHFADKTALTRLKLLIAEQQVITILVKGSRSAAMEEVVRALQ

>d1jbwa1 c.59.1.2 (A:297-425) Fatty polyglutamate synthetase, C-terminal domain {Lactobacillus casei}
WPARLEKISDTPLIVIDGAHNPDGINGLITALKQLFSQPITVIAGILADKDYAAMADRIFTVYLPVPGTPRA
LPEAGYEALHEGRLKDSWQEALAASLNDVDPQPIVITGSLYLASAVRQTLLG

>d1qhfa_ c.60.1.1 (A:) Phosphoglycerate mutase {Baker's yeast (Saccharomyces cerevisiae)}
PKLVLVRHGQSEWNEKNLFTGWVDVKLSAKGQQEAARAGELLKEKKVYPDVLYTSKLSRAIQTANIALEKADRL
WIPVNRSWRLNERHYGDLQGKDKAETLKKFEEKFNTYRRSFDPVVPPPIDASSPFSQKGDERYKYVDPNVLPET
ESLALVIDRLLPYWQDVIAKDLLSGKTVMIAAHGNSLRLGLVKHLEGISDADIAKLNIPPTGIPLVFELDENLKPSKPS
YYLDPEAAAAGAAAAV

>d3pgm_ c.60.1.1 (-) Phosphoglycerate mutase {Baker's yeast (Saccharomyces cerevisiae)}
PKLVLVRHGQSEWNEKNLFTGWVDVKLSAKGQQEAARAGELLKEKGVNVLVDYTSKLSRAIQTANIALEKADRL
WIPVNRSWRLNERHYGDLQGKDKAETLKKFEEKFNTYRRSFDPVVPPPIDASSPFSQKGDERYKYVDPNVLPET
TESLALVIDRLLPYWQDVIAKLVGKTSMIAAHGNSLRLGLVKHLEGISDADIAKLNIPPGTILVFELDENLKPSKPSYY
LDPEA

>d1fzta_ c.60.1.1 (A:) Phosphoglycerate mutase {Yeast (Schizosaccharomyces pombe)}

MTTEAAPNLLVLTRGESEWNKLNLFWGKDPALSETGIKEAKLGGERLKSRGYKFIAFTSALQRAQKTCQIILE
EVGEPNLETIKSEKLNERYYGDLQGLNKDDARKKGAEQVQIWRRSYDIAPPNGESLKDTAERVLV рука
HILKGEKVLAAGNSLRALIMDLEGITGDQIVKRELATGVPIVYHLDKGKYV рука
IDN

>d1e58a_c.60.1.1 (A:) Phosphoglycerate mutase {Escherichia coli}

AVTKLVLVRHGESQWNKENRTGWYDVLSEKGVSEAKAAGKLLKEEGYSFDFAYTSVLKRAIHTLWNVLDELD
QA WLPVEKSWKLNERHYGALQGLNKAETAEKYGDEQVKQWRRGFAVTPPELT KDDERYPGHDPRYAKLSEKE
LPLTESLALTIDRVIPYWNETILPRMKSGERVIIAAHGNSLRALVKYLDNMSEEELNIPTGVPLV рука
YEFDENFKPL

KRYYLGNADEIAAKAAAVANQGK

>d1ebba_c.60.1.1 (A:) Broad specificity phosphatase YhfR {Bacillus stearothermophilus}

ATTLYLTRHGETKWNVERRMQGWQDSPLTEKGRQDAMRLGKRLEAVELAAIYTSTSGRALETAEIVRGGR LIPI
YQDERLREIHLGDWEGKTHDEIRQMDPIAFDHFWQAPHLYAPQRGERFCDVQQRALEAVQSIVDRHEGETVLI
VTHGVVLKTLMAAFKDTPLDHLWSPPYMYGTSVTIIEVDGGTFHV рука
AVEG DVS HIE

>d1rpa_c.60.1.2 (-) Acid phosphatase {Rat (Rattus norvegicus)}

KELKFVTLVFRHGDRGPIETFPNDPIKESSWPQGFGQLTKWMGMQHYELGSYIRRRYGRFLNNSYKHDQV рука
YRS TDVDR LMSAMTNLAALFPPEGNSIWNPRLWQPIP VHTV рука
LSEDRLLYLPFRDCP RFQELKSETLKSEEFLKRL
QPYKSFIDTLP SL SGFD EQDLF EIWS RLYD PLY CESVHNFTLPTWATEDAMTKLKESELSSLYGIHKQKEKSRLQ
GGVLVNEILKNM KLA TQPQ KARKLIM YSAHDTVSGLQMA LDVYNGLLPPYASCHIMELYQDNGGHFV рука
EMYY RNETQNEPYPLTLPGCTHSCPLEKFAELDPVIPQDWATECMG

>d2hpaa_c.60.1.2 (A:) Acid phosphatase {Human (Homo sapiens)}

KELKFVTLVFRHGDRSPIDTFPTDPIKESSWPQGFGQLTQLGM EQHYELGEYIRKRYRKFLNESYKHEQV рука
YIRSTD VDRTLMSAMTNLAALFPPEGNSIWNPILLWQPIP VHTV рука
PLSEDQLLYLPFRNCPRFQELESETLKSEEFLKRLHP
YKDFIATLGKLSGLHGQDLFGIWSKV рука
YD PLY CESVHNFTLPTWATEDAMTKLRELSELSSLYGIHKQKEKSRLQ
GVLVNEILNHMKRATQIPSYKKLIM YSAHDTVSGLQMA LDVYNGLLPPYASCHIMELYFEKGEYFV рука
EMYYRNET QHEPYPLMLPGCSPSCPLERFAELVGVPVIPQDWSTE CMT

>d1ihp_c.60.1.3 (-) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus ficuum}

SCDTV DQGYQCFSETSHLWGQYAPFFSLANESVISPEVAGCRVFAQVLSRH GARYPTDSKGKKY SALIEEIQQ
NATT FDGKYAFLKT NYSLGADDLTPFGEQELVNSGIKFYQRYESLTRNIVPFIRSSGSSRVIASGKKFIEGFQSTKL
KDPRAQPGQSSPKIDVVISEASSNNLDPGTCTVFEDSELADTV EANFTATVPSIRQRLENDLSGVTLTDTEVT
YLMDMCSFDTISTSTVDTKLSPCDLFTHDEWINYDYLQLSKYYHGAGNPLGPTQGVGYANELIARLTHSPV
HDDTSSNHTLDSSPATFPLNSTLYADFHDNGIISILFALGLYNGTKPLSTTVENITQTDGFSSAWTVFASRLYVE
MMQCQAEQEPLVRVLVNDRVVPLHCPVDALGRCTRDSFVRGLSFARSGGDWAECFA

>d1qfxa_c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus niger}

KQFSQEFRDGYSILKHYGGNGPYSERVS YGIARDPPTSCEVDQVIMVKRHGERYPSPSAGKDIEEALAKV рука
YINT TEYKGDLAFLNDWTYYVPNECYYNAETTSGPYAGLLDAYNHGNDYKARYGHLWNGETV рука
PFFSSGYGRVIETA RKGEGFFGNYNSTNAALNIISESEVMGADSLPTCDTNDQTTCDNLTYQLPQFKV рука
AAARLNSQNPGMNLTA SDVYNLMVMASFELNARPFSNWINAFTQDEWV рука
SFYVEDLNYYYCAGPGDKNMAAVGAVYANASLTLNQ GPKEAGSLFFNFAHDTNITPILAALGV рука
LIPNEDLPLDRAFGNPYSIGNIVPMGGHLTIERLSCQATALSDEGTYVR
LVLNEAVLPNDCTSGPGYSCPLAN YTSILNKLPDYTTCNVSASYPQYLSFWWNYNTTELNYRSSPIACQEG
DAMD

>d1dkla_c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Escherichia coli}

SEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPV рука
KLGWLPRGGELIAYLGHYQRQRLVADGLLAK

KGCPQSGQVIIADVDERTRKTGEAAGLAPCAITVHTQADTSSPDPLNPLKTGVCCQLDNANVTDAILSRA
GGSIADFTGHRQTAFRELERVNFPQSNLCLKREKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQ
QAQGMPEPGWGRITDSHQWNTLLSHNAQFYLLQRTPEVARSRATPLLDIKTALTPHPPQKQAYGVTLPSTSVL
FIAGHDTNLANLGGALELNWTLPQPDNTPPGELVFERWRLSDNSQWIQVSLVFQTLQQMRDKTPLSLNT
PPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL

>d1bif_2 c.60.1.4 (250-468) 6-phosphofructo-
2-kinase/fructose-2,6-bisphosphatase, phosphatase domain {Rat (*Rattus norvegicus*)}

SIYLCRHGESELNLKGRIGGDPLSPRGREFSKHLAQFISDQNICKDLKVFTSQMKRTIQTAEALSVPYEQFKVLNEI
DAGVCEEMTYEEIQDHYPLEFALRDQDKYRYRYPKGESYEDLVQRLEPVIMELERQENVLVICHQAVMRCLLAY
FLDKAAEELPYLKCPPLHTVLKLTPVAYGCKVESIFLNVAAVNTHRDRPQNVDIRPSEEALTVPAHQ

>d1fbta_ c.60.1.4 (A:) 6-phosphofructo-
2-kinase/fructose-2,6-bisphosphatase, phosphatase domain {Rat (*Rattus norvegicus*)}

RSIYLCRHGESELNLRGRIGGDGLSARGKQYAYALANFIRSGQISSLKVWTSHMKRTIQTAEALGVPYEQWKAL
NEIDAGVCEEMTYEEIQEHYPEEFALRDQDKYRYRYPKGESYEDLVQRLEPVIMELERQENVLVICHQAVMRCLL
AYFLDKSSDELPYLKCPLHTVLKLTPVAYGCRVESIYLNV

>d1nula_ c.61.1.1 (A:) Xantine-guanine PRTase (XPRTase) {Escherichia coli}
EKYIVTWDMQLQIHARKLASRLMPSEQWKGIIAVSRGGLVPGALLARELGIRHVDTVCISSYDHDNQRELKVLKR
AEGDGEGFIVDDLVDTGGTAVAIREMYPKAHFVTIFAKPAGRPLVDDYVVDPQDTWIEQPWDMGVVFVPPIS
GR

>d1hgxa_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Tritrichomonas foetus}
MDDLERVLYNQDDIQKRIRELAELTEFYEDKNPVMICVLTGAVFFYTDLLKHLDfqLEPDYIICSSYSGTKSTGNL
TISKDLKTNIEGRHVLVVEDIITGLTMYQLNNLQMRKPASLKVCCTLCDKDIGKKAYDVPIDYCGFVENRYIIGY
GFDFHNKYRNLPVIGILKE

>d1fsga_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Toxoplasma gondii}
GSHMASKPIEDYGKGKGRIEPMYIPDNTFYNADDFLVPPHCKPYIDKILLPGGLVKDRVEKLAYDIHRTYFGEELH
IICILKGSRGFFNLLIDYLATIQKYSRESSVPPFEHYVRLKSYQNDNSTGQLTVLSDDLSIFRDKHVLIVEDIVDTG
FTLTEFGERLKAVGPKSMRIATLVEKRTDRSNSLKGDFVGFSIEDVVIVGCCYDFNEMFRDFDHVAVLSDAARKK
FEK

>d1gph11 c.61.1.1 (1:235-465) Glutamine PRPP amidotransferase, C-terminal domain
{Bacillus subtilis}

ICSMYEIYFSRPDSNIDGINVHSARKNLGKMLAQESAVEADVVTGVPDSSISAIGYAETGIPYELGLIKNRVVG
RTFIQPSQALREQGVRMKLSAVRGVVEGKRVVMVDDSIVRGTTSRRIVTMLREAGATEVHVKISSPPIAHPCFY
GIDTSTHELIASSHSVDEIRQEIGADTLSFLSVEGLKGIGRKYDDSNCGQCLACFTGKYPTEIYQDTVLPHVKEA
VLTK

>d1ecfa1 c.61.1.1 (A:250-492) Glutamine PRPP amidotransferase, C-terminal domain
{Escherichia coli}

NPCLFEYVYFARPDSFIDKISVYSARVNMGTKLGEKIAREWEDLDIDVVIPIPETSCDIALEIARILGKPYRQGFVK
NRVGRFTIMPQQQLRRKSVRKLNANRAEFRDKNVLLVDDDSIVRGTTSEQIEMAREAGAKKVYLASAAPEIR
FPNVYGDMPSATELIAHGREVDEIRQIIGADGLIFQDLNDLIDAVRAENPDIQQFECVFNGVYVTKDVDQGYL
DFLTLRNDDAKAVQRQ

>d1dqna_ c.61.1.1 (A:) Guanine PRTase {Giardia lamblia}
MICSVTGKPVKDVLSFFFDRNDVLESEVKKFHLLATFEECKALAADTARRMINEYYKDVAEPVTLVALLTAYLYA
SLLTVHLTFPYTLHFVVKSSYKGTRQESVVFDEEDLKQLKEKREVVLIDEYVDSGHTIFSIQUEQIKHAKICSCFVKDV
DAIKKHSALADTKMFYGYTPMPKGWSLIGFGLDDNGLRRGWAHLFDINLSESEVTEFRRRLTEHIKGLNINGVN

RY

>d1bzya_c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGprtase) {Human (Homo sapiens)}

SPGVVISDDEPGYDLDLFCIPNHYAEDLERVFIPHGLIMDRTERLARDVMKEMGGHHIVALCVLKGGYKFFADLL
DYIKALNRNSDRSIPMTVDFIRLKSYCNDQSTGDIKVIGGDDLSTLTGKNVLIVEDIIDTGKTMQTLLSLVRQYNPK
MVKVASLLVKRTPRSVGYPKPDFVGFEIPDKFVVGYALDYNEYFRDLNHVCIVSETGKAKYKA

>d1cjba_c.61.1.1 (A:) Hypoxantine-guanine PRTase (HGprtase) {Plasmodium falciparum}

PIPNNPGAGENAFDPVFVNDDGYDLSFMIPAHYKKYLTKVLVNGVIKNRIEKLAYDIKKVYNNEEFHILCLLK
GSRGFFTALLKHLRSIHNSAVETSKPLFGEHYVRVKSVCNDQSTGTLEIVSEDLSCLKGKHVLIVEDIIDTGKTLVK
FCEYLKKFEIKTVIAACLFIKRTPLWNGFKADFVGFSIPDHVVGYSLDYNEIFRDLDHCCLVNEGKKKYKAT

>d1tc1a_c.61.1.1 (A:) Hypoxanthine PRTase {Trypanosoma cruzi}

YEFAEKILFTEEEIRTRIKEVAKRIADDYKGKGLRPYVNPLVLISVLKGSFMFTADLCRALCDFNVPVRMEFICVSSY
GEGLTSSGQVRMLLDTRHSIEGHHLIVEDIVDTALTINLYHMYFTRRPASLKTVVLLDKREGRRVPSADYVVA
NIPNAFVIGYGLDYDDTYRELRDIVVLRPE

>d1qb7a_c.61.1.1 (A:) Adenine PRTase {Leishmania donovani}

PFKEVSPNSFLDDSHALSQLLKKSYRWYSPVFSRVNPRFADVSSITESPETLKAIRDQLVQRYRAMSPAPTHILG
FDARGFLFGPMIAVELEIPFVLMRKADKNAGLLIRSEPYEKEYKEAAPEVMTIRYGSIGKGSRVVLDDVLATGGT
ALSGLQLVEASDAVVVEMVSILSIPFLKAAEKIHSTANSRYKDIKFISLLSDDALTEENCGDSDKNYTGPRVLSCGDVL
AEHPH

>d1g2qa_c.61.1.1 (A:) Adenine PRTase {Baker's yeast (Saccharomyces cerevisiae)}

MPIASYAQELKLALHQYPNFPSEGILFEDFLPIFRNPGLFQKLIDAFKLHLEAFPEVKIDYIVGLESRGFLFGPTLAI
ALGVGFVPVRKAGKLPGECKATYEKEYGSDLFEIQKNAIPAGSNVIIVDDIIATGGSAAAAGELVEQLEANLLEYN
FVMELDFLKGRSKLNAPVFTLL

>d1oroa_c.61.1.1 (A:) Orotate PRTase {Escherichia coli}

MKPYQRQFIEFLSKQVLKFGEFTLKSGRKSPYFFNAGLNTGRDLALLGRFYAEALVDGIEFDLLFGPAYKGIPIA
TTAVALAEHHDLDPYCFNRKEAKDHGEGGNLVGSALQGRVMLVDDVITAGTAIRESMEIIQANGATLAGVLIS
LDRQERGRGEISAIQEVERTDYNCKVISIITLKDIALEEKPEMAEHAAVKAYREEFGV

>d1a3c_c.61.1.1 (-) Uracil PRTase {Bacillus subtilis}

QKAVILDEQAIRRRLTRIAHEMIERNKGMMNCILVGKIKTRGIYLAKRLAERIEQIEGNPVTVGEIDITLYRDDLSKKT
SNDEPLVKGADIPVDITDQKVILVDDVLYTGRTVRAGMDALDVGRPSSIQLAVLVDRGHRELPIRADYIGKNIPT
SKSEKVMVQLDEVTDQNDLVAIYEN

>d1bd3a_c.61.1.1 (A:) Uracil PRTase {Toxoplasma gondii}

QEESILQDIITRFPNVVLMKQTAQLRAMMTIIRDKETPKEEFYADRLIRLLIEALNELPFQKKEVTTPLDVSYH
GVSFYSKICGVSVRAGESMESGLRAVCRGVRIGKILIQRDETTAEPKLIYEKLPADIRERWVMLLDPMCATAGSV
CKAIEVLLRLGVKEERIIFVNILAAPQGIERVFKEYPKVRMVTAAVDICLNSRYIVPGIGDFGDRYFGTM

>d1dkra1_c.61.1.2 (A:8-166) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}

NLKIFSLNSNPELAKEIADIVGVQLGKCSVTRFSDGEVQINIEESIRGCDCYIIQSTSDFPVNEHIMELLIMVDALKRA
SAKTINIVIPYYGYARQDRKARSREPITAKLFANLLETAGATRVIALLHAPQIQGFFDIPIDHLMGVPIGEYFEGK
NLE

>d1dkra2_c.61.1.2 (A:167-316) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}

DIVIVSPDHGGVTRARKLADRLKAPIAIIDKRRRPNVAEVMNIVGNIEGKTAILIDDIIDTAGTITLAANALVENG
AKEVYACCTHPVLSGPVERINNSTIKELVVTNSIKLPEEKKIERFKQLSVGPLLAEAIIRVHEQQSVSYLFS

>d1lfaa_c.62.1.1 (A:) Integrin CD11a/CD18 (Leukocyte function associated antigen-1, LFA-1) {Human (Homo sapiens)}

GNVDLVFLFDGSMSLQPDEFQKILDFMKDMKKLSNTSYQFAAVQFSTS YKTEFDFSDYVKRKDPMALLKHVK

HMILLNTFGAINYVATEVFREELGARP DATKVLIIIDGEATDSGNIDA AKDIIRYIIGIGKHFQTKESQETLHKFAS
KPASEFVKILDTEKLKDLFTELQKKIYVIE

>d1atza_c.62.1.1 (A:) von Willebrand factor A3 domain {Human (Homo sapiens)}

QPLDVILLDGSSFPASYFDEMKSFAKAFISKANIGPRLTQVSVLQYGSITTIDVPWNVVPEKAHLLSLVDVMQR
EGGPSQIGDALGFAVRYLTSEMHGARPGASKAVVILVTDSVDAADAARSNRVTVPPIGIGDRYDAAQLR
ILAGPAGDSNVVKLQRIEDLPTMVTLGNFLHKL

>d1fnsa_c.62.1.1 (A:) von Willebrand factor A1 domain {Human (Homo sapiens)}

MYCSRLLDLVFLDGSSRLSEAEFEVLKAFVVDMMERLRSQKWVRVAVVEYHDGSHAYIGLKDRKRPS ELRRI
ASQVKYAGSQVASTSEVLKYTLFQIFS KIDRPEASRI ALLMASQEPQRMSRN FVRYVQGLKKKKVIVIPVGIGPH
ANLKQIRLIEKQAPENKAFVLSSVDELEQQRDEIVSYLCDLAPEAP

>d1ido_c.62.1.1 (-) Integrin CR3 (CD11b/CD18, Mac-1), alpha subunit {Human (Homo sapiens)}
DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKSKTLFSLMQYSEEFRIHFTKEFQNNPNPRSLVKPITQLLGR
THTATGIRKV VREL FNITNGARKNAFKILV VITDGEKFGDPLGYEDV IPEADREGVIRYVIGVGDAFRSEKS RQELN
TIASKPPRDHV FQVNNFEALKTIQNQLREK

>d1qc5a_c.62.1.1 (A:) Integrin alpha1-beta1 {Human (Homo sapiens)}

STQLDIVVLDGSNSIYPWDSVTAFLNDLLERMDIGPKQTQVGIVQYGENVTHEFNLNKYSSTEEVLVAAKKIVQ
RGGRQTMALGIDTARKEAFTEARGARRGVKKVMVITDGE SHDNHRLKKVIQDCEDENIQRFSIAILGHSYRN
GNLSTEKFVEEIKSIASEPTEKHFFNVSDELALVTIVKALGERIFA

>d1ck4a_c.62.1.1 (A:) Integrin alpha1-beta1 {Rat (Rattus norvegicus)}

TQLDIVVLDGSNSIYPWESVIAFLNDLLKRM DIGPKQTQVGIVQYGENVTHEFNLNKYSSTEEVLVAANKIGRQ
GGLQTMTALGIDTARKEAFTEARGARRGVKKVMVITDGE SHDNHRLKKVIQDCEDENIQRFSIAILGHYNRG
NLSTEKFVEEIKSIASEPTEKHFFNVSDELALVTIVKALGERIFA

>d1aoxa_c.62.1.1 (A:) Integrin alpha2-beta1 {Human (Homo sapiens)}

SCPSLIDVVVCDESNSIYPDAVKNFLEKFVQGLDIGPTKTQVG LIQYANNPRVVFNLNTYKTKEEMIVATSQT
SQYGGDLNTFGAIQYARKYAYSAASGGRRSATKVMVVTDGE SHDGSM LKAVIDQCNC HDNILRGIAVLGYL
NRNALDTKNLKEIKAIASIPTERYFFNVSDEA ALLEKAGTLGEQIFSIEGGT

>d1jv2b2_c.62.1.1 (B:107-354) Integrin beta A domain {Human (Homo sapiens)}

VEDYPVDIYLMDSL SYSMKDDLWSIQNLGK LATQMRKLTNSL RIGFGAFV DKPVSPY MYS PPEALEN PCYDM
KTTCLPMFGYKHVLT TDQVTRFNEEVKKQSVSRN RDAP EGGFDAIM QATVCDEKIGWRNDASHLLVFTTDAK
THIALDGRLAGIVQPNDGQCHVGSDNHY SASTMD YPSLGMTEKLSQKNINLIFAVTENVNLYQNYSELIPG
TTVGVLSDSSNVLQLIVDAYKIRSK

>d1poia_c.63.1.1 (A:) Glutaconate-CoA transferase alpha {Acidaminococcus fermentans}

SKVMTLKDIAK YVHSGDHIALGGFTT DRKP YAAVFEILRQG ITDLTGLGGAAGGDW DMLIGNGRV KAY INCYT
ANS GVTNV SRRFRK WFEAGKLT MEDY SQDV IYMM WHAA ALGLPFLPV TL MQGSGLT DEWG ISKE VRK TLDK
VPDDKFKYIDNP FKPG EKV VAVPV P QVDV AI HAQQ AS PDGT VR IWGGK FQD VDIA EA AKY TIVT CEEI SDEE IR
RDPTKNDI PGMC VDAV VLAP YGAH PSQ CYGLYDYD NPFL KV YDK VS KT QED F DAF CKEW VF DLK DHDE YLNK
LGATR LNL KV VP GLG YHID MTKE

>d1poib_c.63.1.1 (B:) Glutaconate-CoA transferase beta {Acidaminococcus fermentans}

DYTNYTNKEMQAVTIAKQIKNGQV VTGTLPLIGASVAKRVYAPDCHIIVESGLMDCSPVEV PRS VGDLRFM
AHCGCIWP NVRFVG FEINEY LHKA NRLIA FIGGAQ IDPYGNVN STSIGDYHH PKTRFTGSGGANGI ATYSNTIIM
MQHEKRRFMN KIDYV TSPGWIDGP GG RERL GLP GDV GPQLV TDKG ILKF DEK T KRM YLA YYPTSS PEDV LE
NTGF DLDV SKA VEAPDPAV KLI REEIDPGQAFI QVP

>d1keka4 c.64.1.1 (A:416-668) Pyruvate-ferredoxin oxidoreductase, PFOR, domain III {Desulfovibrio africanus}
GTIQCQFWGLGADGTVGANKQAIKIIGDNTDLFAQGYFSYDSKSGGITISHLRFGEKPIQSTYLVNRADYVACH
NPAYVGIVYDILEGIKDGGTFVLNSPWSSLEDMDKHLPNGIKRTIANKKLFYNIDAVKIATDVLGGGRINMIMQT
AFFKLAGVLPFEKAVDLLKKSIIHKAGKKGEKIVKMNTDAVDQAVTSLQEFKYPDSWKDAPAETKAEPMTNEFF
KNVVVKPILTQQGDKLPVSAFEADGRFPLG

>d1jkxa_c.65.1.1 (A:) Glycinamide ribonucleotide transformylase, GART {Escherichia coli}
MNIVVLISGNGSNLQAIIDACKTNKIKGTVRAVFSNKADAFGLERARQAGIATHTLIASAFDSREAYDRELIHEID
MYAPDVVVLAGFMRLSPAFVSHYAGRLLNIHPSLLPKYPGLHTRQALENGDEEHGTSVHFVTDELGGPVIL
QAKVPVFAGDSEDDITARVQTQEHAIYPLVISWFADGRLKMHENAAWLDGQRLPPQGYA

>d1fmta2 c.65.1.1 (A:1-206) Methionyl-tRNAfmet formyltransferase {Escherichia coli}
SESLRIIFAGTPDFAARHLDALLSSGHNVGVFTQPDRPAGRGKKLMPSPVKVLAEEKGLPVFQPVSRLPQENQ
QLVAELQADVMVVVAYGLILPKAVLEMPRLGCINVHGSLLPRWRGAAPIQRSLWAGDAETGVTIMQMDVGLD
TGDMILYKLSCPITAEDTSGTLYDKLAEGLPQGLITTLKQLADGTAKPEVQDETIVTYAEK

>d1vid_c.66.1.1 (-) Catechol O-methyltransferase, COMT {Rat (Rattus norvegicus)}
TKEQRILRYVQQNAKPGDPQSYLEADTYCTQKEWAMNVGDAKGQIMDAIREYSPSLVLELGAYCGYSAVRM
ARLLQPGARLLTMEMNPDYAAITQQMLNFAGLQDKVTILNGASQDLIPQLKKYDVDTLDMVFLDHWDKDRYL
PDTLLKEKGLLRKGTVLLADNVIVPGTPDFLAYVRGSSSFECTHYSSYLEYMKVVDGLEKAIYQGPS

>d1fp1d2 c.66.1.12 (D:129-372) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}
RGYLASFPTFLCYPALLQVWMNFKEAVVDEDIDLFKNVHGVTKYEFMGKDKKMNQIFNKSMDVCATEMKR
MLEIYTGFEGISTLVDVGGGSGRNLELIISKYPLIKGINFDLPQVIENAPPLSGIEHVGDMFASVPQGDAMILKA
VCHNWSDEKCIKLSNCHKALSPNGKVIIVEFILPEEPNTSEESKLVSTLDNLMFITVGGRERTEKQYEKLSKLSGF
SKFQVACRAFNLSLGVMIFYK

>d1fp2a2 c.66.1.12 (A:109-352) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}
LCLAPMVECVLDPTLSGSYHELKKWIYEEDLTLFGVTLSGFWDFLDKNPEYNTSFNDAMASDSKLINLALRDC
DFVFDGLESIVDVGTTAKIICETFPKLKICIVFDRPQVVENLSGSNNLTYVGGDMFTSIPNADAVLLKYILHN
WTDKDCRLKKCKEAVTNDGKRGKVTIIMVIDKKDENQVTQIKLLMDVNMACLNGKERNEEEWKKLFIEA
GFQHYKISPLTGFLSLIEIY

>d1ej0a_c.66.1.2 (A:) RNA methyltransferase FtsJ {Escherichia coli}
GLRSRAWFKLDEIQQSDKLKFPGMTVVDLGAAPGGWSQYVVTQIGGKGRIIACDLLPMMDPIVGVDLQGDFR
DELVMKALLERVGDSKVQVVMSDMAPNMSGTPAVDIPRAMYLVELALEMCRDVLAPGGSFVVKVFQGEKF
DEYLREIRSLFTKVKVRKPDSRARSREVYIVATGRKP

>d1fbna_c.66.1.3 (A:) Fibrillarin homologue {Archaeon Methanococcus jannaschii}
MEDIKIKEIFENIYEVDLGDGLKRIATKSIVGKKVYDEIIKIGDEEYRIWNPNSKLAACCIKGLKVMPIKRDSKILY
LGASAGTTPSHVADIADKGIVYAIYEYAPRIMRELLACAERENIIPILGDANKPQEYANIVEKVDVIYEDVAQPNQ
AEILIKNAKWFLLGGYGMIAKARSIDVTKDPKEIFKEQKEILEAGGFKIVDEVIEPFEDHVMFVGIWEGK

>d1dusa_c.66.1.4 (A:) Hypothetical protein MJ0882 {Archaeon Methanococcus jannaschii}
FSEKPTTKSDVKIVEDILRGKKLKFTDSGVFSYGKVDGKTKILVENVVVDKDDILDLCGYGVIGIALADEVKST
TMADINRRAIKLAKENIKLNLDNYDIRVHSDLYENVKDRKYNKIITNPPIRAGKEVLHRIIEEGKELLKDNGEI
WVVIQTKQGAKSLAKYMKDVFGNVETVTIKGGYRVLKSKKL

>d1im8a_c.66.1.14 (A:) Hypothetical protein HI0319 (YecO) {Haemophilus influenzae}
FIFDENVAEVFPDMIQRSPVPGYSNIIAIGMLAERFVTADSNVYDLGCSRGAATLSARRNINQPNVKIIGIDNSQP
MVERCRQHIAAYHSEIPVEILCNDIRHVEIKNASMVLNFTLQFLPPEDRIALLTKIYEGLNPNGVVLSEKFRFEDT

KINHLLIDLHHQFKRANGYSELEVSQKRTALENVMRRTDSIETHKVRKLNVGFSQVELWFQCFNFGSMIAVK
>d1d2ha_ c.66.1.5 (A:) Glycine -methyltransferase {Rat (Rattus norvegicus)}
TAEYKAWLGLLRQHGCHRVLVDACGTGVDSIMLVEEGFSVTSVDASDKMLKYALKERWNRRKEPAFDKWVIE
EANWLTLDKDVPGDGFDAVICLGNFAHLPSKGQDQSEHRLALKNIASMVRPGGLVIDHKNYDYILSTGCAP
PGKNIYYKSDLTKDITTSVLTVNNKAHMVTLDYTQVPGAGRDPAGFSKFRLSYYPHCLASFTELVQEAFGGR
CQHSVLGDFKPYRPGQAYVPCYFIHVLKKTG
>d1xvaa_ c.66.1.5 (A:) Glycine -methyltransferase {Rat (Rattus norvegicus)}
VDSVYRTRSLGVAEGLPQYADGEAARVWQLYIGDTRSRTAEYKAWLGLLRQHGCHRVLVDACGTGVDSIM
LVEEGFSVTSVDASDKMLKYALKERWNRRKEPAFDKWVIEEANWLTLDKDVPGDGFDAVICLGNFAHLPS
KGQDQSEHRLALKNIASMVRPGGLVIDHRNYDYILSTGCAPPGKNIYYKSDLTKDITTSVLTVNNKAHMVTLDYT
VQVPGAGRDPAGFSKFRLSYYPHCLASFTELVQEAFGGRCQHSVLGDFKPYRPGQAYVPCYFIHVLKKTG
>d1hnna_ c.66.1.15 (A:) Phenylethanolamine N-methyltransferase, PNMTase {Human
(Homo sapiens)}
AVASAYQRFEPRAYLRNNYAPRGDLCNPNGVGPWKLRLAQTATGEVSGRTLIDIGSGPTVYQLLSACSHFE
DITMTDFLEVNRQELGRWLQEEPGAFNWSMYSQHACLIEKGKECWQDKERQLRARVKRVLPIDVHQPLG
AGSPAPLPADALVSACLEAVSPDLASFQRALDHITLLRPGGHLLIGALEESWYLAGEARLTVVVPVSEEEVREAL
VRSGYKVRDLRTYIMPAHLQTGVDDVKGVFFAWAQKVGL
>d1khha_ c.66.1.16 (A:) Guanidinoacetate methyltransferase {Rat (Rattus norvegicus)}
RWETPYMHSLAAAASRGGRVLEVGFGMAIAASRVQQAPIKEHWIIECNDGVFQRLQNWLKQPHKVVPLK
GLWEEVAPTLPDGHFDGILYDTYPLSEETWHTHQFNFIKTHAFRLLKPGGILTYCNLTSGELMKSKYTDITAMF
EETQVPALLEAGFQRENICTEVMALVPPADCYYAFPQMTPVTKH
>d1g6q1_ c.66.1.6 (1:) Arginine methyltransferase, HMT1 {Baker's yeast (Saccharomyces
cerevisiae)}
DYYFDSDHYGIHEEMLQDTVRTLSYRNAAIQNKDLFKDKIVLDVCGTGILSMFAAKHGAKHVIGVDMSSIEM
AKELVELNGFSDKITLLRGKLEDVHPFPKVDIISSEWMGYFLYESMMDTVLYARDHVLVEGGLIFPDKCSIHLAG
LEDSQYKDEKLNYWQDVYGFDSYSPFVPLVHEPIVDTVERNNVNTSDKLIEFDLNTVKISDLAFKSNFKLTAKRQ
DMIINGIVTWFDIVFPAPKGKRPVEFSTGPHAPYTHWKQTIFYFPDDLDAETGDTIEGELVCSPNEKNNRDLNIKI
SYKFESNGIDGNSRSRKNEGSYLMH
>d1f3la_ c.66.1.6 (A:) Arginine methyltransferase, HMT1 {Rat (Rattus norvegicus)}
DLQEDEDGVYFSSYGHYGIHEEMLKDKVRTESYRDFIYQNPHEFKDKVVLVDVCGTGILSMFAAKAGAKKVI
DQSEILYQAMDIIRLNKLEDTIVLIKKGKIEEVSLPVEKVDVIISSEWMGYFLFESMLDSVLYAKSKYLA
GGSVYPDI
CTISLVAVDVSKHADRIAFWDDVYGFNMSCMKKAVIPEAVVEVDHKTLSIDPCDIKHIDCHTSISD
LEFSSDF
TLRTTKTAMCTAVAGYFDIYFEKNCHNRVFSTGPQSTKTHWKQTIFLLEKPFPVKAGEALKGKITV
HKNKKDPR
SLIVTTLNSSTQTYSLQ
>d1dl5a1 c.66.1.7 (A:1-213) Protein-L-isoaspartyl O-methyltransferase
{Thermotoga maritima}
MREKLFWILKKYGVSDHIKAFALEIPREEFLTSYPLSYVYEDIVLVSYDDGEYSTSSQPSLMAFM
EWVGLDKG
MRVLEIGGGTGYNAAVMSRVGEKGLVVSEYSRKICEIAKRNRVERLG
IENVFVCGDGYYYGVPEFSPYDVIFVT
VGVDVPETWFTQLKEGGRVIVPINLKLSSRRQPAFLFKKKDPYLV
GNYKLETTRFITAGGNLG
>d1jg1a_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Archaeon Pyrococcus furiosus}
EKELYEKWMRTVEMILKAEGIIRSKEVERAFLKYPRYLSVEDKYKKYAHIDEPLPIPAGQTVSAPHMVA
IMLEIANL
KPGMNILEVGTGSGWNAALISEIVKTDVYTIERIPELVEFAKRNL
ERAGVKNVHVLGDGSKGFPKAPYDVII
AGAPK
IPEPLIEQLKIGGKLIIPVGSYHLWQELLEVRKTKDG
IKIKNHGGVAFVPLIGEYGWK
>d1kr5a_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Human (Homo sapiens)}

ASHSELIHNLRKNGIICKDKVFEVMLATDRSHYAKCNPYMDSPQSIGFQATISAPHMHAYALELLFDQLHEGAKA
LDVGSGSGILTACFARMVGCTGKVIGIDHIKEVLDSVNNVRKDDPTLSSGRVQLVGDGRMGYAAEAPYDAI
HVGAAPVVPQALIDQLPKPGGLILPVGPAAGNQMIEQYDKLQDGSIKMKPLMGVIYVPLTDKEKQWSR
>d1i9ga_ c.66.1.13 (A:) Probable methyltransferase Rv2118c {Mycobacterium tuberculosis}
TGPF SIGERVQLTDAKGRRTMSLTPGA EFHTHRGSIAHD A VIGLEQGSVVKS NGALFLVLRPLL DVVMSMP
RG PQV IYPK DAAQIV HEGD IFPG ARV LEAGAG SGALT SLLRAV GPAG QVIS YQRAD HA EHARRN VSGCYGQ
PPDNW RL VV SLD ADSEL PDGS VDRAV LDM LAPWE VLD AVS RL VAGG VL MVY VATV TQL SRI VEA LRA KQCW
TEPRAW ETLQR GWNVV GLAV RPQ HS M RGH TAFLV AT RRLA PGAVA
>d1af7_2 c.66.1.8 (92-284) Chemotaxis receptor methyltransferase CheR, C-terminal domain {Salmonella typhimurium}
NLTAFFREAHHF PILAEHARRRHGEYRVWSAAASTGEEPYSIAITLADALGMAPGRWKVFASDIDTEVLEKARS
GIYRLSELKTLSPQQQLQRYFMRG TG PHEGLV RVRQ E ANYEFSSVNLL EKQYNVPGP F DAIFCRNVM IYFDKTT
QEDILRRFVPLLKPDGLLFAGHSENFSNLVREFSLRGQT VYALS
>d3mag_ c.66.1.9 (-) Polymerase regulatory subunit VP39 {Vaccinia virus}
MDVVSLDKP FMYFEEIDNE LDYEPESANEVAKL PYQGQLKLLGELFFLSKLQRHGILDGATV VYIGSAPGTHIR
YLRDH FYNLGVII KWMLIDGRHH DPILNGL RDVT LVTRF VDEEYLRSIKQLHPSKII LISD VRSPKR GGNE STADL
LSNYALQNV MISILNPVASSLK WRCFPDQWIKDFYI PHGNKMLQPFAPS YSAEMRLLSIYTGENMRLTRVTKS
DAV NYEK KMYYLN KIVRN KVVNF DYPNQEYDYF HMYFML RTVYC NKTFPTTAKVLF LQQSIFRFLNIP
>d1yub_ c.66.1.9 (-) rRNA methyltransferase {Streptococcus pneumoniae, Ermam}
MNKN IKSQ NF LTSEK VLNQ IQLNLKETDTVYEIGTGKGHLTTKLA KISKQV TSIE LD SHLF NLSSEK LKL NTRV
T LIHQD ILQF QFPN KQRYK IVGN IPYHLSTQI KKV FESRASDIY LIVEEGFYKRTLDI HRTL GLL HTQV SIQQLL KLP
AE CFHPKPKVNSV LIKTRHTT DVP DKYW KLYTYF VS KWVN REYRQLFTKNQFH QAMK HA KVNNL STITYEQV
LSIFNSYLLFNGRK
>d1qama_ c.66.1.9 (A:) rRNA methyltransferase {Bacillus subtilis, Ermc'}
QNFITSKHNIDKIMTNIRLNEHDNIFEIGSGKGHFTLELVQRCNFVTAIEIDHKLCKTENKLVDHDNFQVLNKDIL
QFKFPKNQSYKIFGNIPYNISTDIIRKIVFDSIADEIY LIVEYGFAKRLN TKRS LAFLMAEV DISILSMV PREYFHPK
PKVNSSI RLNRKK SRISHKDQK YN FVMK WVNKEY KKIFTKNQF NN SLKHAG IDDL NN ISFEQFLSF NSYKL
NK
>d1i4wa_ c.66.1.9 (A:) Transcription factor sc-mtTFB {Baker's yeast (Saccharomyces cerevisiae)}
PIPGIKDISKLKFFYGF KYLWNPTVYNKIFDKLDTKTYKHPEELKVL DLYPGVG IQSAIF YNK YCPRQ YS LLEKRSSL
YKFLNAKF EG SPLQ I LKRD PYDW STY SNL IDEER IFVPEV QSSD HINDKFLT VAN VT GEG SEGL IMQWL S CIGNK
NWLYRFGKVKMILLWMPSTTARKLLARPGMHSRSKCSVVREAFTDTKLIAISDANELKGFD SQCIEEWDPILFSA
AEIWPTKGK PIALVEMDPIDFDFDV NW DYVTRHLMILKRTPLNTVMDSLGHGGQQYFNSR ITDK DLLKKCPI
DLTNDEFIYLT KLFMEWPFKP
>d6mhta_ c.66.1.10 (A:) DNA methylase Hhal, coenzyme-binding domain {Haemophilus haemolyticus}
MIEIKDKQLTGLRFIDL FAGLGGFRLA ESGAECVYSNEWDKYA QEVYEMNFGEKPEGDITQVNEKTI PDHDIL
CAGFPCQAFSISGKQKG FEDSRG TLFF DIARI VREKKPKV VFMENVKNFASHDNGNTLEVVKNTMNE LDY SFH
AKVLN ALD YGIPQKRERI YMICFRNDL NIQNFQFPKP FELNTFVKD LLLPDSEVEH LVIDRKD LVMTNQ EIEQ TTP
KTVRLGIVGKGGQGERIYSTRGIAITLSAYGGIFAKTGGYLNGKTRKLH PRECARVMGYPDSYK VHPSTS QAY
KQFGNSVVINLQYIAYNIGSSLNFKPY
>d1g38a_ c.66.1.10 (A:) DNA methylase Taql, coenzyme-binding domain {Thermus aquaticus}
VETPPEVVDFMVSLAEAPRGGRVLEPACAHGPFLRAFREAHGTGYRFVGVEIDPKALDLPPWAEGILADFLWE

PGEAFDLILGNPPYIVGEASKYPIHVKAVKDALYKKAFSTWKGKYNLYGAFLEKAVRLLKPGGVLFVVPATWLV
LEDFAALLREFLAREGKTSVYYLGEVFPQKKSAVVIRFQKSGKGLSLWDTQESESGFTPILWAEPHWEGEIIRFET
EETRKLEISGMPLGDFLHIRFAARSPEFKHPAVRKEPGPGLVPVLGRNLKPGWVDYEKNHSGLWMPKERAKE
LRDFYATPHLVVAHTKGTRVVAAWDERAYPWREEFHLLPKEGVRLDPSSLVQWLNEAMQKHVRTLYRDFVP
HTLRLMLERLPVRREYGFHT

>d1dcta_c.66.1.10 (A:) DNA methylase HaeIII, coenzyme-binding domain {Haemophilus aegyptius}
MNLISLFGAGGLDGFQKAGFRIICANEYDKSIWKTYESNHSAKLIKGDISKISSDEFPKCDGIIGGPPCQSWS
GGSLRGIDDPRGKLFYEYIRILKQKKPIFFLAENVKGMMMAQRHNKAVQEFIQEFDNAGYDVHIILLNANDYGV
QDRKRVFYIGFRKELNINYLPPIPHLIKPTFKDVIWDLKDNPPIPALKNKNTNGKCIYPNHEYFIGSYSTIFMSRNR
VRQWNEPAFTVQASGRQCQLHPQAPVMLVSKNLNKVEGKEHLYRRLTRECARVQGFPDDFIFHYESLND
GYKMIGNAVPVNLAYEIAKTIKSAL

>d2dpma_c.66.1.10 (A:) DpnM DNA adenine methyltransferase {Streptococcus pneumoniae}

TLQPFTKWTGGKRQLLPVIRELIPKTYNRYFEPFVGGAFFDLAPKDAVINDNAELINCYQQIKDNPQELIEILK
VHQEYNSKEYYLDLRSADRDERIDMMSEVQRAARILYMLRVNFNGLYRVNSKNQFNVPYGRYKNPKIVDEELIS
AISVYINNNQLEIKVGDFEKAIVDVRTGDFVYFDPPYIPLSETSAFTSYTHEGFSFADQVRLRDAFKRLSDTGAYV
MLSNSSSALVEELYKDFNIHYVEATRTNGAKSSSRGKISEIIVTNYEK

>d1g55a_c.66.1.10 (A:) DNMT2 {Human (Homo sapiens)}

EPLRVLELYSGVGGMHHALRESCIPAQVVAIDVNTVANEVYKYNFPHTQLLAKTIEGITLEEFDRLSFDMILMSP
PCQPFTTRIGRQGDMTDSRTNSFLHILDILPRLQKLPKYILLEENVKGFEVSSTRDLIQTIENCGFQYQEFLLSPTSLG
IPNSRLRYFLIAKLQSEPLPFQAPGQVLMFEPKIEIHRKNQQDSDLSVKMLKDFLEDDTDVNQYLLPPKSLLRYAL
LLDIVQPTCRRSVCFTKGYGSYIEGTGSVLQTAEDVQVENIYKSLTNLSQEEQITKLLILKRYFTPKEIANLLGFPPE
FGFPEKITVKQRYRLLGNSLNVHVVAKLIKILYE

>d1booa_c.66.1.11 (A:) m.Pvull N4 cytosine-specific DNA methyltransferase
{Proteus vulgaris}

NFGKKPAYTTSNGSMYIGDSLELESFPEESISLVMTPSPFALQRKKEYGNLEQHEYVDWFLSFAKVVNKKLKPD
GSFVVFDFGGAYMKGPARSIIYNFRVLIRMIDEVGFFLAEDFYWFNPSKLPSPIEWVNKRKIRVKDAVNTVWWF
SKTEWPKSITKVLAPEYSRMRMKKLIEDPDFKTFPKTRPSGHDIGKSFSDKDNGGSIPPNLLQISNSENGQYLANC
KLMGIKAHPARFPAKLPEFFIRMILTEPDDLVDIFGGSNTTGLVAERESRKWISFEMKPEYVAASAFRFLDNNISE
EKITDIYNRILNGESLDLNSI

>d1eg2a_c.66.1.11 (A:) m.Rsrl N6 adenosine-specific DNA methyltransferase
{Rhodobacter sphaeroides}

GTTRHVYDVCDCDLTLAKLPDDSVQLIICDPPYNIMIADWDDHMDYIGWAKRWLAEAERVLSPTGSIAIFGGL
QYQGEAGSGDLISIISHMRQNSKMLLANLIIWNYPNGMSAQRFANRHEEIAWFAKTKYFFDLDARPYDE
ETKAAYMKDKRLNPESVEKGRNPTNVWRMSRLNGNSLERVGHPTQKPAAVIERLVRALSHPGSTVLDFFAGSG
VTARVAIQEGRNSICTDAAPVKEYYQKQLTFLQDDGLIDKARSYEIVEGAANFGAALQR

>d1inla_c.66.1.17 (A:) Spermidine synthase {Thermotoga maritima}

RTLKELERELQPRQHLWYFEYYTGNNVGLFMKMNRIYSGQSDIQRIDIFENPDGLVVFALDGITMTTEKDEF
MYHEMLAHVPMFLHPNPKKVLIIGGGDGGTLREVLKHDSEKAILCEVDGLVIAARKYLKQTSCGFDDPRAEI
VIANGAEYVRKFKNEDVIIIDSTDPTAGQGGHLTEEFYQACYDALKEDGVFSAETEDPFYDIGWFKLAYRRISK
VFPITRVYLGFMTPSGMWSYTFASKGIDPIKDFPKEVKRNKELKYYNEEVHVASFALPNFVKKELGLM

>d1kpga_c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1 {Mycobacterium tuberculosis}
DELKPHFANVQAHYDLSDDFFRLFLDPTQTYSCAYFERDDMTLQEAQIAKIDLALGKLGLQPGMTLLDVGCGW
GATMMRAVEKYDVNVVGLTLSKNQANHVQQLVANSENLRSKRVLLAGWEQFDEPVDRIVSIGAFEHFGHERY

DAFFSLAHL PADGVMLLHTITGLHPKEIHERGLPMSFTARFLKFIVTEIFPGGRLPSIPMVQECASANGFTVT
RVQLQPHYAKTLDLWSAALQANKGQAIALQSEEVYERYMKYLTCGAEMFRIGYIDVNQFTCQK

>d1kzia_c.66.1.18 (A:) Mycolic acid cyclopropane synthase CmaA1 {Mycobacterium tuberculosis}
QLKPPVEAVRSHYDKSNEFFKLWLDPSMTYSACAYFERPDMLTLEEAQYAKRKLAQKLNLEPGMTLLDIGCGWG
STMRHAVAEDVNIGLTLSENQYAHDKAMFDEVDSPRRKEVRIQGWEFDEPVDRIVSLGAFEHFADGAGD
AGFERYDTFFKKFYNLTPDDGRMILLHTIPDKEEAQELGLTSPMSLLRFIKFILTEIFPGGRLPRISQVDYYSSNAG
WKVERYHRIGANYVPTLNAWADALQAHKDEAIALKGQETCDIYMHYLRCGSDLFRDKYTDVCQFTLVK
>d7aata_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken (Gallus gallus), mitochondria}
SSWWSHVEMGPPDPILGVTEAFKRDTNSKKMNLGVGAYRDDNGKPYVLNCVRKAEAMIAAKKMDKEYLPIA
GLADFTRASAELALGENSEAFKSGRYVTVQGISGTGSLRVGANFLQRFFKFSRDVYLPKPSWGNHTPIFRDAGL
QLQAYRYYDPKTCSDLFTGAMEDISKIPEKSIILLHACAHNPTGVDPHQEWKELASVVKKRNLLAYFDIMAYQG
FASGDIINRDAWALRHFIEQGIDVVLSQLSYAKNMGLYGERAGAFTVICRDAEEAKRVESQLKILIRPMYSNPPMN
GARIASLILNTPELRKEWLVEVKGMADRIISMRTQLVSNLKKEGSSHWNQHITDQIGMFCTGLKPEQVERLTK
EFSIYMTKDGRISVAGVASSNVGYLAHAIHQVTK

>d2csta_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Chicken (Gallus gallus), cytosolic form}
AASIFAAVPRAAPPVAVFKLTADFREDGDSRKVN LGVGAYRTDEGQPWLPVVRKVEQLIAGDGSLNHEYLPILG
LPEFRANASRIALGDDSPAIAQKRVGSVQGLGGTGALRIGAEFLRRWYNGNNNTATPVYVSSPTWENHNSVF
MDAGFKDIRTYRYWDAKRGQLDQGLDDMEKAPEFSIFILHACAHNPTGTDPTDEWKQIAAVMKRRCFLP
FFDSAYQGFASGSLDKDAWAVRYFVSEGFEFLCAQSFSKNFGLYNERVGNLSVVGKDEDNVQRVLSQMEKIVR
TTWSNPPSQGARIVATTITSPQLFAFWKDNVKTMDRVL MRSELRSRLES LGTPGTWNHITDQIGMFSTGL
NPKQVEYMIKEKHIYLMASGRINMCGLTTKNLDYVAKSIHEAVTKIQ

>d1ajsa_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Pig (Sus scrofa), cytosolic form}
APPSVFAEVPAQPVLFKLIADFREDPDRKVNLGVGAYRTDDCQPWLPVVRKVEQRIANNSSLNHEYLPIL
GLAEFRTCASRLALGDDSPALQEKRVGGVQSLGGTGALRIGAEFLARWYNGTNNKDTPVYVSSPTWENHNGV
FTTAGFKDIRSYRYWDTEKRGQLDQGLSDLENAPEFSIFVLHACAHNPTGTDPTPEQWKQIASVMKRRFLFPFF
DSAYQGFASGNLEKDAWAIRYFVSEGFEFLCAQSFSKNFGLYNERVGNLTVAKEPDSILRVL SQMQKIVRVTW
SNPPAQGARIVARTLSDPELFHEWTGNVKTMDRILSMRSELRARLEALKTPGTWNHITDQIGMFSTGLNP
QVEYLINQKHIYLLPSGRINMCGLTTKNLDYVATSIHEAVTKIQ

>d1yaaa_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Baker's yeast (Saccharomyces cerevisiae), cytosolic form}
SATLFNNIELLPPDALFGIKQRYGQDQRATKVDLGIGAYRDDNGKPWVLPSVKAEEKLIIHDSSYNHEYLGITGL
PSLT SNAAKIIFGTQSDALQEDRVISVQSLSGTGALHISAKFFSKFFPDKLVYLSKPTWANHMAIFENQGLKTATYP
YWANETKS LLDNGFLN AIQKAP EGSI FVLHS CAHNPTGLDPTSEQWVQIVDAIA SKNHIALFDTAYQGFATGDL
DKDAYAVRLGVEKLSTVSPFVFCQSFAKNAGMYGERVGCFLALT KQ AQNKT IKA VTSQ LAKI IRSEV SNPPAY
GAKIVAKLLETPEL TEQWHKDMVTMSSRITKMRHAL RDHLVKG TPGNWDHIVNQCGMFSFTGLTPQMVK
LEETHAVYLVASGRASIAGL NQGNVEYVAKAIDEV VRFYA

>d1qisa_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Escherichia coli}
MFENITAAPADPILGLADLFRADERPGKINLGIGVYKDET GKT PVLTSVKKAEQYLL ENETK NYL GIDGIPEFGRC
TQELLFGKGSALINDKRARTAQTPGGT GALRVAADFLAKNTSVKRVWVSNPSWP NHK SVF NSAG LEVRE YAY
DAENHTLDFDALINSLNEAQAGDVVLFHGFCHNPTGIDPTLEQWQTLAQLSVEKGWPLDFAYQGFARGLEE
DAEGLRAFAAMHKELIVASSYSKNFGLYNERVGA CLTVAADSETV DRAFSQ MKAAIRAN YSNPPA HGA SVVATI
LSNDAL RAIWEQELTDMRQRIQMRQLFVN TLQEKGANRDFS FI IKQNGM FSGLTKEQV RLREEFGVYAVA
SGRVNVAGMTPDNMAPLCEAIVAVL

>d1bjwa_c.67.1.1 (A:) Aspartate aminotransferase, AAT {Thermus thermophilus}

MRGLSRRVQAMKPSATVAVNAKALELRRQGVDLVALTAGEPDFDTPEHVKEAARRALAQGKTKYAPPAGIPEL
REALAEKFRRENGLSVTPEETIVTGGKQALFNLQAILDPGDEVILSPYWVSYPEMVRFAGGVVEVETLPEE
GFVPDPERVRAITPRTKALVVNSPNPTGAVYPKEVLEALARLAVEHDFVLSDIEYHLLYEGEHFSPGRVAPE
HTLTNGAAKAFAMTGWRIGYACGPKEVIKAMASVSSQSTTSPDTIAQWATLEALTNQEASRAFVEMAREAYR
RRRDLLLEGTLGLKAVRPSGAFYVLMDSPIAPDEVRAAERLLEAGVAVVPGTFAAFGHVRLSYATSEENLRK
ALERFARVL

>d2ay1a_c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Paracoccus denitrificans}
MLGNLKPKQAPDKILALMGEFRADPRQGKIDLGVGVYKDATGHTPIMRAVHAAEQRMLETTKTYAGLSGEP
EFQKAMIGELIGDGLKSETTATLATVGGT GALRQALELARMANPDLRVFVSDPTWPVNHSIMNFMLPVQTY
RYFDAETRGVD FEGMKADLA AKKGDMVLLHGCHNPTGANL TDQWA EIASILEKTGALPLIDAYQGFGDG
LEEDAAGTRLIASRIPEV LIAASC SKNFGIYRERTGCLLAC ADAATRELAQGAMAFLNRQTYSFPPFHGAKIVSTV
LTTP ELRADWMAE LEAV RSGML RLREQ LAGEL RDLSGS DRFGF VAEHR GMFS RLGA TPEQV KRIKEE FG IYMV
GDSRINIAGLNDNTIPILARAII EVGV

>d3tata_c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Escherichia coli}
MFQKV DAYAGDP ILT M ER FK ED PR SD KV NLS IGL YNED G IIP QL QAV AE A E AR L N A Q P H G A S LY LP M E GL NC
YRHAIAPLLFGADHPVLQQRVATIQLGGSGALKVGADFLKRYFPESGVWVSDPTWENHVAIFAGAGFEVSTY
PWYDEATNGVRFNDLLATLKLTPARSIVLLHPCCHNPTGADLTNDQWD AVIEILKARELIPFLDIAYQGFGAGME
EDAYAIRAIASAGLPALVSNSFSKIFS L YGERVGGLSVM CEDA EAAGRVLGQLKATVRRN YSSPPNFGAQVVA AV
LNDEALKASWLAEV EEMRTRILAMRQELVKV LSTEMPERNF D YLLNQ RGMFS YTGLSAAQVDR LREEFGVYI
ASGRMCVAGLNTANVQRVAKAFAAVM

>d1gdea_c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Archaeon Pyrococcus horikoshii}

ALSDRLELV SASEIRKLF DIAAGM KDVISLGIGEPDFDTPQHIKEYAKEALDKGLTHYGP NI GLLELREAIAEKLKKQ
NGIEADPKTEIMVLLGANQAFLMGLSAFLKDGEELIPTPAF VS YAPAVI LAGGKP VEVPTYEEDEFRLNVDELKK
YVTDKTRALIINSPCNPTGAVL KK DLEE IADF VVEHDLIV ISDEV YEHFIYDDARHYSIASLDGMFERTITVNGFSK
TFAMTGWR LGFVAAPSWI IERMV KFQMYNATCPVTFIQYAAKALKDERSWKAVEEMRKEYD RRRKLV WKR
LNEMGLPTVKPKGAFYI FPR IRDTGLTSKKFSELMLKEARVAVVPGSAFGKAGEGYVRISYATAYE KLEEAMD RM
ERVLKERKLV

>d1bw0a_c.67.1.1 (A:) Tyrosine aminotransferase (TAT) {Trypanosoma cruzi}
WDV SMSN HAGL VFNP IRTVSDNAKPSPKPIIKL SGDPTLDKNLLT SAAQIKKLKEAIDSQECNGYFPTVGSP
EAREAVATWWRNSFVHKEELKSTIVKDNV VLCGGSHGILMAITAICAGDYALVPQPGFPHYETVCKAYGIGM
HFYNCRPENDWEADLDEIRRLKDDKTKLIVTNPSNCGSNFSRKHVEDIVRLAELRLPLFSDEIYAGMVFKGK
DPNATFTS VADFETTVPRVILGGTAKNLVPGWRLGWL VD PHNGN GPSFLEG LKRVGM LVCGPCTVQ AAL
GEALLNTPQEHLDQIVAKIEESAMYLYNHIGECIGLAPTM PRGAMYLMSRIDLEYRDIKTDVEFFEKL LEEENV
QLPGTIFHAPGFTRL TTRPVEVY REAVERIKAFCQRHAA

>d1fg7a_c.67.1.1 (A:) Histidinol-phosphate aminotransferase {Escherichia coli}
TVTITDLARENVRNLT PYQSARRLGGNGDVWL NAN EYPTA VE FQLTQQT LNRYPECQPKAVIENYA QYAGVKP
EQVLVSRGADEGIELLIRAFCEPGK DAILYCP PTYGM YSV AETIGVEC RTVPTLDNWQLDQGISDKLDGVKV
YVCSPNNPTGQLINPQDFRTLLELTRGKAI VVADEAYIEFC PQASLAGWLA EYPHLAI RLSKAFA LA GLRCGFTL
ANEEVINLLMKVIA PYPLSTPVADIAAQALSPQGIVAMRERVAQIIAEREY LIAALKEIPC VEQFDSETNYI LARF
KASSAVFKSLWDQGIILRDQNKQPSLSGCLR ITVG TREESQRVIDALRAEQV

>d1kusa_c.67.1.1 (A:) L-threonine-O-3-phosphate decarboxylase CobD {Salmonella enterica}
HGGNI REPATV LGISPDQ LLDF SANINPLGMPV SVKRAL IDNL DCI EYPDAD YFHLHQ ALR HHQ VPAS WI
GNGETESIFTVASGLKPR RAMIVTPGFAEYGR ALA QSGCEIRRWSLREADGWQLTDAILEALTPDLDCLFLC TPN

NPTGLLPERPLLQAIADRCKSLNINLILDEAFIDFIPHETGFIPALKDNPHIWVRLSLTKFYAIPGLRLGYLVNSDDAA
MARMRRQQMPWSVNALAALAGEVALQDSAQQATWHWLREEGARFYQALCQLPLTVPGGRANYLLRC
EREDIDLQRRLTQRILRSCANYPGLSRYRVAIRSAQNERLLAALRNVLTGIAP

>d1jg8a_c.67.1.1 (A:) Low-specificity threonine aldolase {Thermatoga maritima}

MIDLRSVTKPKTEEMRKAMAQAEVGDDVYGEDPTINELERLAAETFGKEAALFVPSGTMGNQVSIMAHTQR
GDEVILEADSHIFWYEVGAMAVLSGVMPHPVPGKNGAMDPPDVRKAIRPRNIHFPRTSLIAIENTHNRSGGR
VVPLENIKEICTIAKEHGINVHIDGARIFNASIASGVPVKEYAGYADSVMFCLSKGLCAPVGSVVGDGRDFIERAR
KARKMLGGGMRQAGVLAAAGIIALTAKMVDRLKEDHENARFLAKLKEIGYSVNPEDVKTNMVILRTDNLKVN
AHGFIEALRNSGVLANAVSDTEIRLVTHKDVSrndIEEALNIFEKLFRKFS

>d1tpla_c.67.1.2 (A:) Tyrosine phenol-lyase {Citrobacter intermedius}

MNYPAAEPFRIKSVEVTSMIPRDERLKKMQEAGYNTFLNSKDIYIDLTDSTNAMSDKQWAGMMMGDEAY
AGSENFYHLERTVQELFGFKHVPTHQGRGAENLLSQLAIKPGQVAGNMVKNGAVFVDIVRDEAHAGLNIA
FKGDidLKKLQKLIDEKGAEANIYICLAVTVNLAGGQPVS MANMRAVRELTAAHGIVFYDATRCVENAYFIKEQ
EQGFENKSIAEIVHEMFSYADGCTMSGKKDCLVNIGGFLCMNDDEMSSAKELVVVYEGMPSYGGLAGRDME
AMAIGLREAMQYIEHDRVVKQVRYLGDKLKAAGVPIVEPVGGHAVFLDARRCEHTQDEFPAQSLAASIYVET
GVRSMERGIKLETVRLTIPRRVYTYAHMDVVADGIIKLYQHKEDIRGLKFIYFFTARFDYI

>d1ax4a_c.67.1.2 (A:) Tryptophan indol-lyase (tryptophanase) {Proteus vulgaris}

AKRIVEPFRIKMVEKIRVPSREERAALKEAGYNPFLPSSAVYIDLTDSTNAMSDHQAAMITGDEAYAGSR
NYYDLKDKAKELFNYDYIIPAHQGRGAENILFPVLLKYKQKEGKAKNPVFISNFHFTAAHVELNGCKAINIVTE
KAFDSETYDDWKGDFDIKKLKENIAQHGADNIVAIYSTVTCNSAGGQPVSMSNLKEVYEIAKQHGIFVVMDSA
RFCENAYFIKARDPKYKNATIKEVIFDMYKYADALTMSAKKDPLLNIIGGLVAIRDNEEIFTLARQRCVPMEGFVTY
GGLAGRDMAMVQGLEEGTEEEYLHYRIGQVKYLGDRLEAGIPIQYPTGGHAVFVDCKKLVPQIPGDQFPAQ
AVINALYLESGVRAVEIGSFLLGRDPATGEQKHADMEFMRITIARRVYTNDHMDYIADALIGLKEKFATLKLEFE
YEPPVLRHFTARLKPI

>d1js3a_c.67.1.6 (A:) DOPA decarboxylase {Pig (Sus scrofa)}

MNASDFRRRGKEMVDYMADELEGIEGRQVYPDVQPGYLRPLIPATAPQEPDTFEDILQDVEKIIMPGVTHWH
SPYFFAYFPTASSYPAMLADMLCGAIGCIGFSWAASPACELETVMMDWLGMQLPPEAFLAGEAGEEGGGVI
QGSASEATLVALLAARTKVVRLQAASPGLTQAVLEKLVAYASDQAHSVERAGLIGGVKLKAIPSDGKFAMRA
SALQEALERDKAAGLIPFFVATLTTSCSFNLLEVGPICHEEDIWLHVDAAYAGSAFICPEFRHLLNGVEFAD
SFNFNPHKWLNFDCSAMWVKRTDLTGAKLDPVYLKHSHQGSLITDYRHWQLPLGRRFRSLKMWVF
RMYGVKGLQAYIRKHVQLSHEFEAFVLQDPRFEVCAEVTLGLVCRLKGSDGLNEALLERINSARKIHLVPCRLRG
QFVLRFACSRKVESGHVRLAWEHIRGLAAELLA

>d1cl1a_c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Escherichia coli}

KLDTQLVNAGRKKYTLGAVNSVIQRASSLVFDSVEAKKHATRNRANGELFYGRRGTLTHFSLQQAMCELEGGA
GCVLFPCGAAAVANSILAFIEQGDHVLMTNTAYEPSQDFCSKILSKLGVTTSWFPLIGADIVKHLQPNTKIVFLE
SPGSITMEVHDVPAIVAARSVVPDAAIMDNTWAAGVLFKALDFGIDVSIQAATKYLGHSDAMIGTAVCNAR
CWEQLRENAJLMQMVADATAYITSRGLRTLGVRLRQHHESSLKVAEWLAEPQVARVNHPALPGSKGHEF
WKRDFTGSSGLFSVLLKKLNNEELANYLDNFSLFSMAYSWGGYESLILANQPEHIAIRPQGEIDFSGTLIRLHI
GLEDVDDLIADLDAGFARIV

>d1ibja_c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Thale cress (Arabidopsis thaliana)}

ASVSTLLVNLNDNKFDPF DAMSTPLYQTATFKQPSAIENG PYDYTRSGN PTRDALESLLAKLDKADRAFCFTSGMA
ALSAVTHLIKNGEEIVAGDDVYGGSDRLLSQVPRSGVVVKRVNTKLDEVAAAIGPQTKLVWLESPTNPRQQI
SDIRKISEMAHAQGALVLVDNSIMSPVLSRPLELGADIVMHSATKFIAGHSDVMAGVLAVKGEKLAKEVYFLQN
SESGGLAPFDCWLCLRGIKTMALRIEKQQENARKIAMYLSSHPRVKKVYYAGLPDHPGHHLHSQAKGAGSVF

SFITGSVALSKHLVETTKYFSIAVSFGSVKSLISMPCFMHSASIPAEVREARGLTEDLVRISAGIEDVDDLISDLDIAF

KTFPL

>d1cs1a_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Escherichia coli}
RKQATI AVRSGLNDDEQYGCVPPPIHLSSTYNFTGFNEPRAHDYSRRGNPTRDVVQRALAELEGGAGAVLTNT
GMSAIHLVTTVFLKPGDLLVAPHDCYGGSYRLFDLSAKRGCYRVLFDQGDEQALRAALAEKPKLVLVESPSNPL
LRVV DIAKICHLAREVGAVSVVDNTFLSPALQNPLALGADLVLSCTKYLNGHSDVVAGVVIAKDPDVTELAW
WANNIGVTGGAFDSYLLRLRTLVRPMELAQRNAQAIVKYLQTQPLVKLYHPSLPENQGHEIAARQQKGFG
AMLSFELDGDEQTLRRFLGGSLFTLAESLGGVESLISHAATMTHAGMAPEARAAAGISETLLRISTGIEDGEDLI
ADLENGFRAANKG

>d1qgna_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Common tobacco (Nicotiana tabacum)}

MKYASFLNSDGSVAIHAGERLGRGIVTDAITTPVVNTSAYFFNKTSELIDFKEKRRASFEYGRYGNPTTVLEEKIS
ALEGAESTLLMASGMCASTVMLLALVPAGGHIVTTDCYRKTRIFIETILPKMGITATVIDPADVGCALELALNQKK
VNLFTE SPTNPFLRCVDIELVSKLCHEKGALVCIDGTATPLNQKALALGADLVLSATKFLGGHNDVLAGCISGP
LKLVEIRNLHHILGGALNPNAAYLIIRGMKTLHLRVQQQNSTALRMAEILEAHPKVRVYYPGLQSHPEHHIAK
KQMTGFGGAVSFEDGDLTTAKFVDALKIPIYIAPSFGGCESIVDQPAIMSYWDLSQSDRAKYGIMDNLVRFSF
GVEDFDDLKADILQALDSI

>d1e5ea_ c.67.1.3 (A:) Methionine gamma-lyase, MGL {Trichomonas vaginalis}

ERMTPATACIHANPQKDQFGAAIPPIYQTSTFVFDNCQQGGNRAGQESGYIYTRLGNPTVSNLEGKIAFLEKTE
ACVATSSGMGAIAATVLTILKAGDHLISDEC LYGCTHALFEHALTKFGIQVDFINTAIPGEVKKHMKPNTKIVYFET
PANPTLKIIDMERVCKDAHSQEGLVLIADNTFCSPMITNPVDFGVVVHSATKYINGHTDVVAGLICGKADLL
QQIRMVGIKDIRGSVISPHDAWLITRGLSTLNIRMKAESENAMKVAEYLKSHPAVEKVYYPGFEDHEGHDIAKK
QMRMYGSMITFILKSGFEGAKL LDNLKLITLAVSLGGCESLIQHPASMTHAVVPKEEREAGITDGMIRLSVGI
EDADELIADFKQGLDALLR

>d1d2fa_ c.67.1.3 (A:) Modulator in mal gene expression, MalY {Escherichia coli}
LLPFTISDMDFATAPCIIEALNQQLMHGVFGYSRWKNDEF LAIAHWFSTQHYTAIDSQTVVYGPSVIYMVSELI
RQWSETGEGVVIHTPAYDAFYKAIEGNQRTVMPVALEKQADGWFCDMGKLEAVLAKPECKIMLLCSPQNPTG
KVVTCDELEIMADLCERHGVRVISDEIHMDMVWGEQPHIPWSNVARGDWALLSGSKSFNIPALTGAYIIEN
SSSRDAYLSALKGRDGLSSPSVLALTAHIAAYQQGAPWLDALRIYLKDNLTYIADKMNAAFPELNWQIPQSTYLA
WLDLRPLNIDDNALQKALIEQEKAIMPETYGEEGRGFVRLNAGCPRS KLEKGVAGLINAIRAVR

>d1c7na_ c.67.1.3 (A:) Cystalysin {Treponema denticola}

MIYDFTTKISRKNLGLSKWDLMSQNPEVGNEVPLSADMEFKNPPELIEGLKKYLDETVLGYTGPTEEYKKT
VKKWMKDRHQWDIQTDWIINTAGVVP AVFNAVREFTKPGDGVIITPVYYPFFMAIKNQERKII ECELLEKDGY
YTIDFQKLEKLSKDKNNKALLFCSPHNPVGRVWKD EQLQKIKDIVLKS DLM IWSDEIHFDLIMPGYEHTVFQSID
EQLADKTITFTAPS KTFNIAGMGMSNIIKNPDIRERFTKSRDATSGMPFTTLYKACEICYKECGKWL DGCIVI
DKNQRIVKDF FEVN HPEIKA PLEGTYLQWIDFRALKMDHKAMEEFMIHKAQIFFDEGYIFGDGGIGFERINLA
APSSVIQESLERLNKALKDLK

>d1eg5a_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Thermotoga maritima}
MRVYFDNNATTRVDDRVLEEMIVFYREKYGNPNSA HGMGIEANLHMEKAREK VAKVLGVSPSEIFFTSCATESI
NWILKTV AETFEKRKRTIITTPIEHKAVLETMKYLSMKGFKV KYVPVDSRGVVKLEELEKLVD EDTFLVSIMAANN
EVGTIQPVEDVTRIVKKKNKETLVHVDAVQTIGKIPFSLEKLEV DYASFSAHKFHGPKGVGITYIRKGVPIRPLIHGG
GQERGLRS GTQN VPGIVGAARAMEIAVEELSEA KHM EKLR SKLVSGLMNLGAHIITPLEISLPNTL VSFPNIR
GSTLQNLLSGYGYVSTSSACTSKDERLRHVLDAMGVDRRIAQGAI RISLCKYNTEEEVDYFLKKIEEILSFL

>d1jf9a_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Escherichia coli}

IFSVDKVRADFPVLSREVNGLPLAYLDSAASAQKPSQVIDAEAEFYRHGYAAVHRIHTLSAQATEKMENVRK
ASLFINARSAEELVFVRGTTEGINLVANSWGNNSNRAGDNIIISQMEHHANIVPWQMLCARVGAELRVIPLNP
DGTQLQETLPTLFDEKTRLLAITHVSNVLGNTENPLAEMITLAHQHGAKVLVDGAQAVMHPVDVQALDCDFYV
FSGHKLYGPTGIGILYVKEALLQEMPPWEGGGSMIATVSLSEGTTWTKAPWRFEAGTPNTGGIIGLGALEYVS
ALGLNNIAEYEQNLMHYALSQLESVPDLTLYGPQNRLGVIAFNLGKHAYDGSFLDNYGIAVRTGHHCAMPL
MAYYNVPAMCRASLAMYNTHEEVDRVTGLQRIHRLLG

>d1elua_c.67.1.3 (A:) Cystine C-S lyase {*Synechocystis* sp.}

QFPGLANKTYNFNGGQGILPTVALEAITAMYGYLQENGPFSAANQHQIQQQLAQLRQALAETFNVDPNTITIDN
VTTGCDIVLWGLDWHQGDEIILTDCEHPGIIAVQIAARFGITYRFFPVAATLNQGDAAAVLANHLGPKTRLVIL
SHLLWNTGQVLPLAEIMAVCRRHQGNYPVRVLVDGAQSAGSLPLDFSRLEV DYYAFTGHKW FAGPAGVGGLYI
HGDCLGEINPTYVGWSRITYGAKGEPTGWAEGGKRFEVATSAQPQYAGLAAQLHQQRQGTAEERYQAICQRS
EFLWRLNQLPHVHCLATSAPQAGLVSFTVDSPLGHRAIVQKLEEQRYLRTIADPDCIRACCHYTDEEEINHLL
ARLADFGP

>d2dkb_c.67.1.4 (-) Dialkylglycine decarboxylase {*Pseudomonas cepacia*}

LNDDATFWRNARHHLVRYGGTFEPMIERAKGSFVYDADGRAILDFTSGQMSAVLGHCHPEIVSVIGEYAGKLD
HLFSEMLSRPVVDLATRLANITPPGLDRALLSTGAESNEAIRMAKLTGKYEIVGFAQSWHGMTGAAASATY
SAGRKGVGPAAVGSFAIPAPFTYRPRFERNGAYDYLAELDYAFDLIDRQSSGNLAAFIAEPILSSGGIELPDGYMA
ALKRKCEARGMILLDEAQTVGVRTGTMFACQRDGVTDPIDLTSLKTLGAGLPLAAITSAEERAHGELGYLFYT
HVSDPLPAAVGLRVLDVVQRDGLVARANVMGDRLLRGLLDERFDICGDVRGRGLLGVEIVKDRRTKEPAD
GLGAKITRECMNLGSMNIVQLPGMGGVFRIAPPLTVSEDEIDLGLSLLGQAIERAL

>d2gsaa_c.67.1.4 (A:) Glutamate-1-semialdehyde aminomutase (aminotransferase)
{*Synechococcus* sp., strain GR6}

FKTIKSDEIFAAAQKLMPGGVSSPVRAFKSVGQPIVFDRVKD DAYAWDVGNRYIDYVGTWGPAICGHAHPEV
IEALKVAMEKGTSFGAPCALENVLAEMVNDAVPSIEMVRFVNSGEACMAVLRLMRAYTGRDKIICKFEGCYHG
HADMFLVKAGSGVATLGLPSSPGVPKKTTANTLTPYNDLEAVKALFAENPGEIAGVILEPIVGNSGFIVPDAGFL
EGLREITLEHDALLVDEVMTGFRIAYGGVQEKGVTDPDLTTLGKIIGGLPVGAYGGKREIMQLVAPAGPMYQA
GTLGNPLAMTAGIKTLELLRQPGTYEYLDQITKRLSDGLLAIAQETGHAACGGQVSGMFGFFFTEGPVHNYED
AKKSDLQKFSRFHRGMLEQGIYLAPSQFEAGFTSLAHEEDIDATLAAARTVMSAL

>d2oata_c.67.1.4 (A:) Ornithine aminotransferase {Human (*Homo sapiens*)}

GPPTSDDIFEREYKYGAHNYHPLPVALERGKGIYLWDVEGRKYFDLSSYSAVNQGHCHPKIVNALSQVDKLT
TSRAFYNNVLGEYEEYITKLFNYHKVLPMTGVEAGETACKLARKWGYTVKGIQKYKAKIVFAAGNFWGRTLSA
ISSSTDPTSYDGFMPGFDIIPYNDLPALERALQDPNVAAMVVEPIQGEAGVVVDPGVLMGVRELCTRHQ
VLFIADEIQTGLARTGRWLAVDYENVRPDIVLLGKALSGGLYPVSAVLCDDDIMLTIKPGEHGSTYGGNPLGCRV
AIAALEVLEEEENLAENADKLGIIIRNELMKLPSDVVTAVRGKGLLNAIVIKETKDWDWKVCLLRDNGLLAKPT
HGDIIRFAPPLVIKEDELRESIEIINKTILSF

>d1gtxa_c.67.1.4 (A:) 4-aminobutyrate aminotransferase, GABA-aminotransferase {Pig (*Sus scrofa*)}

FDYDGPLMKTEVPGPRSRELMKQLNIIQNAEAVHFFCNYESRGNYLVDVDGNRMQLDLYSQISSIPGYSHPALV
KLVQQPQNVSTFINRPALGILPPENFVEKLRESLLSVPKGMSQLITMACGSCSNENAFKTIFMWYRSKERGQS
AFSKEELETCMINQAPGCPDYSILSFMGAFHGRMGCLATHSKAIHKIDIPSFDWPAPIFPRLKYPEEFVKEN
QQEEARCLEEVEDLIVKYRKKKTVAGIIVEPIQSEGDNHASDDFFRKLRDISRKHGCAFLDEVQTGGGSTGK
FWAHEHWGLDDAADVMTFSKKMMTGFFFKEEFPNAPYRIFNTWLGDPSKNLLAEVINIIKREDLLSNA
HAGKVLLTGLLDLQARYPQFISRVGRGTFCSFDTPDESIRNLISIARNKGVMILGGCGDKSIRFRPTLVFRDHHA
HLFLNIFSDILADFK

>d1bt4a_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Bacillus circulans, subsp. alkalophilus}

SERAYNPNAGPAALPLEVLERAQAEFVDYQHTGMSIMEMSHRGAVYEAVHNEAQARLLALLGNPTGYKVLFIQGGASTQFAMIPMNFLKEGQTANYVMTGSWASKALKEAKLIGDTHVAASSEASNYMTLPKLQEIQLOQDNAAYLHLTSNETIEGAQFKAFPDTGSVPLIGDMSSDILSRPFDLNQFGLVYAGAQKNLGPSGVVVIVREDLVAESPKHPTMLRYDTYVKNNNSLYNTPPSFGIYMVNEVLKWIEERGGLEGVQQANRKKASLIYDAIDQSGGFYRGCDVDSRSDMNITFRILASEELEKEFVKASEQEGFVGLKGHRSGVGLRASIYNAVPYESCEALVQFMEEHFKRSRG

>d1bjna_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {Escherichia coli}QIFNFSSGPAMLPAEVLKQAQQELRDWNGLGTSMEVSHRGKEFIQVAEEAKDFRDLNVPSNYKVLFCHGGRGQFAAVPLNILGDKTTADYDAGYWAASAIKEAKKYCTPNVFDAKVTVDGLRAVKPMREWQLSDNAAYMHCPNETIDGIAIDETPDFGADVVAADFSSTLSRPIDVSRYGVIYAGAQKNIGPAGLTIVVREDLLGKANIACPSILDYSILNDNGSMFNTPPTFAWYLSGLVFKWLKANGVAEMDKINQQKAELLYGVIDNSDFYRNDVAKRNRSRMNVPFQLADSALDKLFLEESFAAGLHALKGHRVVGGMRASIYNAMPLEGVKALTDFMVEFERRHG

>d1cj0a_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Rabbit (Oryctolagus cuniculus)}

WSSHEQMLAQPLKDSDAEVYDIKKESNRQRVGLELIASENFASRAVLEALGSCNNKYSEGYPGQRYYGGTEHIDELETLCQKRALQAYGLDPQCWCNVNPYSGSPANFAVYTALVEPHGRIMGLDLPDGHLTHGFMTDKKISATSIFFESMAYKVNPDTGYIDYDRLEENARLFHPKLIAGTSCYSRNLDYGRLRKIADENGAYLMADMAHISGLVAGVVPSPFEHCHVTTTHKTLRGCRAGMIFYRRGVRSVDPKTGKEILYNLESLINSAVFPGLQGGPHNHAIAGVAVALQAMTPEFKEYQRQVVCNRLSAAVLELGYKIVTGGSDNHLILVDLRSKGTDGGRAEKVLEACSIACNKNTCPGDKSALRPSGLRLGTPALTSRGLLEKDFQKVAHFIHRGIELTVQIQDDTGPRATLKEFKEKLAGDEKHQRAVRALRQEVEVESFAALFPLPGLPGF

>d1ejia_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Mouse (Mus musculus)}

MADRDATLWASHEKMLSQPLKDSDAEVYIIKKESNRQRVGLELIASENFASRAVLEALGSSLNNKYSEGYPGQRYYGGTEFIDELEMICQKRALQAYHLDPQCWCNVNPYSGSPANFAVYTALVEPHGRIMGLDLPDGHLTHGFMTDKKKISATSIFFESMPYKVYPETGYINYDQLEENARLFHPKLIAGTSCYSRNLDYARLRKIADENGAYLMADMAHISGLVAAGVVPSPFEHCHVTTTHKTLRGCRAGMIFYRKGVRSVDPKTGKETYYELESLINSAVFPGLQGGPHNMAIAGVAVALQAMTTEFKIYQLQLVANCRLSDALTELGYKIVTGGSDNHLILMDLRSKGTDGGRAEKVLEACSIACNKNTCPGDKSALRPSGLRLGTPALTSRGLLEDFQKVAHFIHRGIELTLQIQSHMATKATLKEFKEKLAGDEKIQSATLREEVENFASNFSLPGLPDF

>d1bj4a_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Human (Homo sapiens)}

DADLWSSHDAQPLKDSDVEVYNIKKESNRQRVGLELIASENFASRAVLEALGSCNNKYSEGYPGQRYYGGTEFIDELETLCQKRALQAYKLDPQCWCNVNPYSGSPANFAVYTALVEPHGRIMGLDLPDGHLTHGFMTDKKKISATSIFFESMPYKVNPDTGYINYDQLEENARLFHPKLIAGTSCYSRNLEYARLRKIADENGAYLMADMAHISGLVAAGVVPSPFEHCHVTTTHKTLRGCRAGMIFYRKGVKSVPATGKEILYNLESLINSAVFPGLQGGPHNHAIAGVAVALQAMTLEFKVYHQVVCNRLSAAVLELGYKIVTGGSDNHLILVDLRSKGTDGGRAEKVLEACSIACNKNTCPGDRSALRPSGLRLGTPALTSRGLLEKDFQKVAHFIHRGIELTLQIQSDTGVAATLKEFKERLAGDKYQAAVQALREEVESFASLFPGLPGL

>d1dfa_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Escherichia coli}

LKREMNIADYDAELWQAMEQEKFVRQEEHIELIASENYTSRVMQAQGSQLTNKYAEGYPGKRYYGGCEYVDIVEQLAIDRAKELFGADYANVQPHSGSQANFAVYTALLEPGDTVLGMNLAHGGHLTHGSPVNFSGKLYNIVPYGIDATGHIDYADLEKQAKEHKPKMIIGGFSAYSGVVDWAKMREIADSIGAYLFVDMAHVAGLVAAGVYPNPVPHAHVTTTHKTLAGPRGGYLAKGGSEELYKKLNSAVFPGGQGGPLMHVIAGKAVALEMEPEFKTYQQQVAKNAKAMVEVFLERGYKVSGGTNDNLFLVLDVKNLTGKEADAALGRANITVNKNVPNDPKSPFVTSGIRVGT

PAITRRGFKEAEAKELAGWMCDVLD\$INDEAVIERIKGVLDICARYPVY

>d1b9ha_ c.67.1.4 (A:) 3-amino-5-hydroxybenzoic acid synthase (AHBA synthase) {Amycolatopsis mediterranei}

KAPEFPAPQYDDAERNGLVRALEQQQWWRMGGDEVNSFEREFAAHGAAHALAVTNGTHALELALQVM
GVPGPTEVIVPAFTFISSSQAAQRGAVTPVDVDAATYNLDPEAVAAVTPTKVIMPVHMAGLMADMAL
AKISADTGVLQDAAHGARWQGKRVGELDSIATFSQNGKLMTAGEGGAVVFPDGETEKYETAFRHSC
GRPRDDRRYFHKIAGSNMRLNEFSASVLAQLRDLDEQIAVRDERWTLLSRLGAIDGVVPQGGDVRADRS
HYMAMFRIPGLTEERRNALVDRIVEAGLPAAFAFRAIYRTDAFWELGAPDESVDIAARRCPNTDAISSDCVWLH
HRVLLAGEPELHATAEIIADAVARA

>d1fc4a_ c.67.1.4 (A:) 2-amino-3-ketobutyrate CoA ligase {Escherichia coli}

GSHMRGEFYQQLTNDLETARAEGLFKEERIITSAQQAQDITVADGSHVINFCANNYGLANHPDLIAAKAGMD
SHGFGMASVRFCIGTQDSHKELEQKLAALFLGMEDAILYSSCFDANGGLFETLLGAEDAIISDALNHASIIDGVRLC
KAKRYRYANNDMQUELEARLKEAREAGARHVLIAATDGVFSMDGVIANLGVCVLADKYDALVMVDDSHAVGF
VGENGGRSHEYCDVMGRVDIITGTLGKALGGASGGYTAARKEVVEWLRQRSRPYLFSNLAPAIVAASIKVLEM
VEAGSELRDRLLWANARQFREQMSAAGFTLAGADHAIIPVMLGDAVVAQKFARELQKEGIYVTGFFYPVVPKG
QARIRTQMSAAHTPEQITRAVEAFTRIGKQLGVIA

>d1bs0a_ c.67.1.4 (A:) PLP-dependent acyl-CoA synthase (8-amino-7-oxonanoate synthase, AONS) {Escherichia coli}

SWQEKINAALDARRAADALRRYPVAQGAGRWLVADDRQYLNFSNDYLGLSHHPQIRAWQQGAEQFGIG
SGGSGHVGYSVVHQALEEEFELAEWLGYSRALLFISGFAANQAVIAAMMAKEDRIAADRLSHASLLEAASLSPSQ
LRRFAHNDVTHLARLLASPCPGQQMVVTEGVFSMDGSAPLAEIQQVTQQHNGWLMVDDAHGTGVIGEQ
GRGSCWLQVKVKEPLLVTGKFGVGSAAVLCSSTVADYLLQFARHLIYSTSMSPPAQALRASLAVIRSDEGD
ARREKLAALITRFRAGVQDLPFTLADSCSAIQPLIVGDNSRALQAEKLQQGCWVTAIRPPTVPAGTARLRLT
AAHEMQDIDRLLEVHGNG

>d1qj5a_ c.67.1.4 (A:) Adenosylmethionine-8-amino-7-oxononanoate aminotransferase, BioA {Escherichia coli}

MTTDDLAQFDQRHILHPYTSMTSPLPVYPVVAEGCELISDGRRLVDMSSWWAAIHGYNHPQLNAAMKSQI
DAMSHVMFGGITHAPAIELCRKLVAMTPQPLECVFLADSGSVAEVAMKMAQYWQAKGEARQRFLTFRNG
YHGDTFGAMSVCDFDNMSHSLWKGYPENLFAPAPQSRMDGEWDERDMVGFARLMAAHRHEIAAVIEPIV
QGAGGMRMYHPEWLKRIRKICDREGILLADEIATGGRTGKLFACEHAEIAPDILCLGKALTGGTMTLSATLTT
EVAETISNGEAGCFMHGPTFMGNPLACAAANASLAILESGDWQQQVADIEVQLREQLPARDAEMVADVRV
LGAIGVVEVTHPVNMAALQKFFVEQGVWIRPGKLIYLMPPYIILPQQQLQRLTAANRAVQDETFFCQ

>d1b8ga_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {Apple (Malus domestica)}

MLSRNATFNSHGQDSSYFLGWQEYEKNPYHEVHNTNGIIQMGLAENQLCFDLLESWLAKNPEAAFKKNGES
IFAEALALFQDYHGLPAFKKAMVDFMAEIRGNKVTDPNHLVLTAGATSANETFIFCLADPGEAVLIPTYYPGFDR
DLKWRGVEIVPIHCTSSNGFQITETALEEAYQEAERNLRVKGVLVTNPNSNPLGTTMTRNELYLLSFVEDKGH
LISDEIYSGTAFSSPSFISVMEVLDKRNCDENSEVWQRHVVYSLSKDLGLPGFRVGAIYSNDDMVAAATKMS
SFGLVSSQTQHLLSAMLSDDKKLTKNYIAENHKRLKQRQKKLVSGLQKSGISCLNGNAGLFCWVDMRHLLRSNTF
EAEMELWKKIVYEVHLNISPSSCHCTEPGWFRVCFANLPERTLDLAMQRLKAFVG

>d1iaya_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {Tomato (Lycopersicon esculentum)}

ILSKLATNEEHGENSPYFDGWKAYDSDPFHPLKNPNGVIQMGLAENQLCLDLIEDWIKRNPKGSICSEGIKSFA
IANFQDYHGLPEFRKAIKFMEKTRGGRVRFDPERVMAGGATGANETIIFCLADPGDAFLVPSYPYPAFNRLD

RWRTGVQLIPIHCESNNFKITSKAVKEAYENAQKSNIKVGLILTNPSNPLGTTLDKDTLKSVL
SFTNQHNIHLVC
DEIYAATVFDTDPQFV ріа ЕІЛДЕQEMTYCNKDLV HIVYSLSKDMGLPGFRVGIIYSFNDDVVNCARKMSSGLVST
QTQYFLAAMLSDEKFVDNFLRESAMRLGKRHKHFTNGLEVVGIKCLKNNAGLFCWMMDLRPLLRESTFDSEMSL
WRVIINDVKLNVSPGSSFECQE PGWFRVCFA NMDDGTVDIALARI RRFVGVEK

>d1c4ka2 c.67.1.5 (A:108-569) Ornithine decarboxylase major domain {Lactobacillus sp., strain 30a}
PPFFKSLKEYVSRYLIQFDCPGHQGGQYYRKHPAGREFYDFFGETVFRADLCNADVALGDLLIHEGPAVAEKH
AARVYNADKTYFVLGGSSNANNTVTSALSVNGDLVLFDRNNHKSYNSALAMAGGRPVYLQTNRNPYGFIGG
IYDSDFDEKKIRELA AKVDPERAKWKRPFRLAVIQLGTYDGTIYNAHEVVKRIGHLCDYIEFDSAWVGYEQFIPM
MRNSSPLLIDDLGPEDPGIIVVQS VHKQQAGFSQTSQIHKKDSHIKGQLRYCDHKHFNFNSNLFMSTSPFPMY
AA LDVNAAMQEGEAGRKLWHDLLITIEARKKLIKAGSMFRPFVPPVNGKKWEDGDTEDMANNIDYWRFE
KGAKWHAYEGYGDNQYYVDPNKFM LTPGINPETG DYEDFGVPATIVANYLRDHGIIPEKSDLNSILFLMTPAET
PAKMNNLITQLLQLQR LIEED

>d1qg8a_ c.68.1.1 (A:) Spore coat polysaccharide biosynthesis protein SpsA {Bacillus subtilis}
PKVSVIMTSYNKSDYVAKSISSILSQTFSDFELFIMDDNSNEETLN VIRPFLNDNRVRFYQSDISGVKERTEKTRYA
ALINQAIEMAEGEYITYATDDNIYMPDRLK MVRELDTHPEKAVIYSASKTYHLNENRDIVKETVRPAAQVTWN
APCAIDHCSV MHRYSVLEK VKEKFGSYWDESPAFYRIGDARFFWRVNHFYPF YPLDEELDNYITDQSIHFQLFE
LEKNEFVRNLPPQRNCRELRESLKKLG MG

>d1j8wb_ c.68.1.2 (B:) beta 1,4 galactosyltransferase (b4GalT1) {Cow (Bos taurus)}
TACPEESPLLVGPMLIEFNIPVDLKLVEQQNPKVKGGRYTPMDCISPHKVAIIPFRNRQEHLK YWLYLHPILQR
QQLDYGIYVINQAGESMFNRAKLLNVGFKEALKDYDYNCFVFSVDLIPMNDHNTYRCFSQPRHISVAMD KFG
FSLPYVQYFGGSALS KQQFLSINGFPNNYWG WGGEDDDIYNRLA FRGMSVSRPNAVIGKCRMIRHSRD KKN
EPNPQRFDRIAHTKETMLS DGLNSLTYMVLEVQRYPLYTKITV DIGTPS

>d1ezia_ c.68.1.3 (A:) CMP acylneuraminate synthetase {Neisseria meningitidis}
MEKQNIAVILARQNSKGLPLK NLRKMNGISLLGHTINAAISSKCFDRIIVSTDGLIAEEAKNFGVEVVL RPAELAS
DTASSISGVIA LETIGNSGTVTLLQPTSPLRTGAHIREA FSLFDEKIKGSV VSACPMEH HPLKTLLQINNGEYAP
MRHLS DLEQPRQQLPQA FRPNGAIYINDTASLI ANNCFFIAPT KLYIMSHQD SIDIDTE LDLQQAENILN

>d1ga8a_ c.68.1.4 (A:) Galactosyltransferase LgtC {Neisseria meningitidis}
MDIVFAADD NYAAYL CVA AKSVEA AHPD TEIR FHVL DAGISEAN RAAV AANLRGGGGNIRFIDVN P EDFAGFPL
NIRHIS ITTYAR LKLGEYIACDKVLYLDIDV LVRDSLPLWDTDLGD NWLG ASIDL FVER QEGYKQ KIGMADGEY
YFNAGVLL INLKKWRRHDIFKMSSEW VEQYK DVMQYQD QDILNGLF KG GVCYANSRFN MPTN YAFMANW
FASRHTDPLYRDR TNTV MPV AVSH YCGPAK PWH RDCT AWGA ERFTE LAGSL TTVP EEW RGKL

>d1g93a_ c.68.1.9 (A:) alpha-1,3-galactosyltransferase catalytic domain {Cow (Bos taurus)}
KLK LSDW FNPF KRPEV VTMT KW KAPV VWE GTYNRAV LDN YYAK QK I TVGLTV FAV GRYIEHY LEEFL TSANKHF
MVGH PVI FYIMV DDV SRMPLIELGPLRSFKV FKIK PKE KRW QD ISMMRM KTIGE HIA HIQHEV DFLCMDV D
QVFQDKFGVETLGE SVAQLQAWWYKADPNDFTYERRKESAAYIPFGE GDYYHAA IFGGTPTQVL NITQECFK
GILKDKKNDIEAQW HDE SHLN KYFLLN KPTK ILSPEY CW DYHIGLPADIKL VKMSWQT

>d1hv9a2 c.68.1.5 (A:4-251) N-acetylglucosamine 1-phosphate uridyltransferase
GlmU, N-terminal domain {Escherichia coli}
NAMS VVILAAGKGTRMYS DLPKVLHTLAGKAMVQH VIDAANELGAAHVHLVY GHGG DLLKQ ALKDDN LN
VLQAEQLGTGHAMI QQAAPFF FADDED IMLYGDVPLIS VETLQRLRDAK P QGGI GLLT V KLDD PTG YGRITRENG
KVTGIVEHK DATDE QRQI QEINTG ILIANGADM KRWLAKL NNNAQGE YYITDII ALAY QEG REIV AVHP QRLSE
VEGVNNRLQLS RL SERV YQSE QA EKLLA G

>d1hm9a2 c.68.1.5 (A:2-251) N-acetylglucosamine 1-phosphate uridyltransferase
GlmU, N-terminal domain {Streptococcus pneumoniae}

SNFAIILAAGKGTRMKSDLPKVLHKVAGISMLEHVFRSGAIQPEKTVVGHKAELVEEVLAGQTEFVTQSEQL
GTGHAVMMTEPILEGLSGHTLVIAGDTPLITGESLKNLIDFHINHKNVATILTAETDNPFGYGRIVRNDNAEVLR
VEQKDATDFEKQIKEINTGTYVFDNERLFEALKNINTNNAQGEYYITDVIGIFRETGEKVGAYTLKDFDESLGVND
RVALATAESVMRRRINHKHMVNG

>d1fxoa_c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Pseudomonas aeruginosa}
KRKGIILAGGSGTRLHPATLAISKQLLPVYDKPMIYYPLSTLMLAGIREILIIISTPQDTPRFQQLLGDGSNWGLDLQ
YAVQPSPDGLAQAFIQLIGESFIGNDLSALVLDGNLYYGHDFHELLGSASQRQTGASVFAYHVDPERYGVVEFDQ
GGKAISLEEKPLEPKSNYAVTGLYFYDQQVVDIARDLKPSPRGELEITDVNRAYLERGQLSVEIMGRGYAWLDTG
THDSLLEAGQFIATLENRQGLKVACPEEIAQRKWIDAQLEKLAAPLAKNGYQYLKRLLTETVY

>d1iina_c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Salmonella enterica}
MKTRKGIIILAGGSGTRLYPVTMAVSQQLPIYDKPMIYYPLSTLMLAGIRDILIISTPQDTPRFQQLLGDGSQWGW
LNHQYKVQPSPDGLAQAFIIGEEFIGHDDCALVLDNIFYGHDLPLKMEAAVNKESGATVFAYHVNDPERYGVV
EFDQKGTAWSLEEKPLQPKSNYAVTGLYFYDNSVVEAMAKNLKPSARGELEITDINRIYMEQGRLSVAMMGRGYA
WLDTGTHQSLIEASNFIATIEERQGLKVSCPEEIAFRKNFINAQVIELAGPLSKNDYGYKLLKMV

>d1h5ra_c.68.1.6 (A:) glucose-1-phosphate thymidylyltransferase RmlA {Escherichia coli}
KMRKGIIILAGGSGTRLYPVTMAVKQLLPIYDKPMIYYPLSTLMLAGIRDILIISTPQDTPRFQQLLGDGSQWGLN
LQYKVQPSPDGLAQAFIIGEEFIGGDDCALVLDNIFYGHDLPLKMEAAVNKESGATVFAYHVNDPERYGVVEF
DKNGTAISLEEKPLEPKSNYAVTGLYFYDNDVVQMAKNLKPSARGELEITDINRIYLEQGRLSVAMMGRGYAWL
DTGTHQSLIEASNFIATIEERQGLKVSCPEEIAFRKGIFIDVEQVRKLAVALPLLDKPNQFDSTAPRGHLESSLLSHLVDP
KDLEPRAANCTRVLVWHTRTEKPKMKQEEQLQRQGRGSDPAIEV

>d1fgga_c.68.1.7 (A:) 1,3-Glucuronyltransferase I (glcAT-II) {Human (Homo sapiens)}
MTIYVVTPTYARLVQKAELVRLSQTLSVPRHLWLLVEDAEGPTPLVSGLLAASGLLFTHLVLTPKAQQLREGEPE
GWVHPRGVEQRNKALDWLRGRGGAVGGEKDPPPGTQGVVFADDNTYSRELFEEMRWTRGVSVWPV
GLVGLRFEGPQVQDGRVVGHTAWEPSRPFPVDMAGFAVALPLLDKPNQFDSTAPRGHLESSLLSHLVDP
KDLEPRAANCTRVLVWHTRTEKPKMKQEEQLQRQGRGSDPAIEV

>d1fo8a_c.68.1.10 (A:) N-acetylglucosaminyltransferase I {Rabbit (Oryctolagus cuniculus)}
LAVIPILVIACDRSTVRRCLDKLLHYRPSAELFPIIVSQDCGHEETAQVIASYGSAVTHRQPDLSNIAVQPDHRKFQ
GYYKIAHWYRALGQIFHNFNYPAAVVEDDLEVAPDFFEFQATYPLLKADPSLWCVAWNDNGKEQMVD
SKPELLRTDFPGLWLLAELWAELEPKWPKAFLWDDWMRRPEQRKGRACVRPEISRTMTGRKGVSHGQ
FFDQHLKFIKLNNQQFVPTQLDLSYLQQEAYDRDFLARVYGAAPQLQVEKVRTNDRKELGEVRVQYTGRDSFKAF
AKALGVMDDLKSGVPRAGYRGIVTFLFRRRVHLAPPQTWDGYDPSWT

>d1e5ka_c.68.1.8 (A:) Molybdenum cofactor biosynthesis protein MobA {Escherichia coli}
MTTITGVVLAGGKARRMGGVDKGLLENGKPLWQHVADALMTQLSHVVNNANRHQEIQASGLKIEDSLA
DYPGPLAGMLSVMQEAGEWFPCPCDTPYIPPDLAARLNHQRKDAPVWWVHDGERDHPTIALVNRAIEPLL
LEYLQAGERRMVFMRLAGGHAVDFSDHKDAFNVNTPEELARWQ

>d1i52a_c.68.1.13 (A:) 4-diphosphocytidyl-2-c-methylerythritol (CDP-me) synthase (YgbP)
{Escherichia coli}

HLDVCVVPAAGFRRMQTECPKQYLSIGNQTILEHSVHALLAHPRVKRVVIAISPGDSRFAQLPLANHPQITVV
DGGDERADSVLAGLKAAGDAQWVVLVHDAARPCLHQDDLARLLALSETSRTGGILAAPVRDTMKRAEPGKNAI
AHTVDRNGLWHALTPQFFPRELLHDCLTRALNEGATITDEASALEYCGFHPQLVEGRADNIKVTRPEDLALAEFY
LTR

>d1h7ea_c.68.1.13 (A:) CMP:2-keto-3-deoxy-manno-octonic acid (CMP-KDO)synthetase,
KdsB {Escherichia coli}

SKAVIVIPARYGSSRLPGKPLLDIVGKPMIQHRYERALQVAGVAEVWVATDDPRVEQAVQAFGGKAIMTRNDH
ESGTDRLVEVMHKVEADIYINLQGDEPMIRPRDVETLLQGMRDDPALPVATLCHAISAAEAEPESTVKVVVNTR

QDALYFSRSPIPYPRNAEKARYLKHVGIVAYRRDVLQNYSQLPESMPEQAESLEQLRLMNAGINIRTFEVAATGP
GVDTPACEKVRALMAQELAENA

>d1jyka_c.68.1.13 (A:) CTP:phosphocholine cytidylytransferase LicC {Streptococcus pneumoniae}
EIRVKAIILAAAGLTRLRPLTENTPKALVQVNQKPLIEYQIEFLKEKGINDIIIVGYLKEQFDYLKEKYGVRLVFNDKY
ADYNNFSLYLVKEELANSYVIDADNYLFKNMFRNDLRTSTYFSVYREDCTNEWFLVYGDDYKVQDIIVDSKAGR
ILSGVSFWDAPTAEKIVSFIDKAYVSGEFVDLYWDNMVKDNIKELDVYVEELEGNSIYEIDSQDYRKLEEILK
>d1jw9b_c.111.1.1 (B:) Molybdenum cofactor biosynthesis protein MoeB {Escherichia coli}
AELSDQEMLRYNRQIILRGFDGDQEAALKDSRVLIVGLGGLGCAASQYLASAGVGNLTLLDFDTVLSNLQRQTL
HSDATVGQPKVESARDALTRINPHIAITPVNALDDAELAALIAEHDLVLDCTDNVAVRNQLNAGCFAAKVPLVS
GAAIRMEGQITVFTYQDGEPYCRLSRLFGENALTCVEAGVMAPLIGVIGSLQAMEAIKMLAGYGKPASGKIV
MYDAMTCQFREMKLMRNPNGCEVCG

>d1ea5a_c.69.1.1 (A:) Acetylcholinesterase {Electric ray (Torpedo californica)}
SELLVNTSGKVMGTRVPVLSHISAFLGIPFAEPPVGNMRFRREPKKPWSGVWNASTYPNNCQQYVDEQF
PGFSGSEMWNPNREMSEDCLYLNIWVPSPRPKSTTVMVWIYGGGFSGSSTLDVNGKLAYTEEVVLVSLSY
RVGAFGFLALHGSQEAPGNVGLLDQRMALQWVHDNIQFFGGDPKTVTIFGESAGGASVMHILSPGSRDLF
RRAILQSGSPNCPWASVSAEGRRAVELGRNLNCNLSDEELIHLREKKPQELIDVEWNVLPFDSIFRFSFVP
VIDGEFFPTSLESMLNSGNFKKTQILLGVNKDEGSFFLLYGAPGFSKDSESKISREDFMSGVKLSVPHANDGLDA
VTLQYTDWMDDNNNGIKNRDGLDDIVGDHNVICPLMHFVNKYTKFGNGTYLYFFNHRASNLVWPEWMGVIH
GYEIFVFGPLVKELNYTAEEEALSRRIMHYWATFAKTGNPNEPHSQESKWPLFTTKEQKFIDLNTEPMKVHQ
RLRVQMCVFWNQFLPKLLNAT

>d1maaa_c.69.1.1 (A:) Acetylcholinesterase {Mouse (Mus musculus)}
EDPQLLVRVRGGQLRGLRGLKAPGGPVSAGLIPFAEPPVGSRRFMPPEPKRPWSGVLDATTFQNVYCQYVDTLY
PGFEGTEMWNPNRELSEDCLYLNWTPYPRPASPTPVLIWIYGGGFSGAASLDVYDGRFLAQVEGAVLVSM
NYRVGTFGLALPGSREAPGNVGLLDQRLALQWVQENIAAFGGDPMSVTFGESAGAASVGMHILSPSRSLF
HRAVLQSGTPNGPWATVSAGEARRRATLLARLVCPPGGAGGNDTELIACLRTRPAQDLVDHEWHVLPQESIF
RFSFPVVDGDFLSDTPEALINTGDFQDLQVLGVVVKDEGSYFLVYGVPGFSKDNESLISRAQFLAGVRIGVPQA
SDLAAEAVVLHYTDWLHPEDPTHLDAMS AVVG DHN VCPVAQLAGRLAAQGARVYAYIFEHRASLTWPL
WMGVPHGYIEIFIFGLPLDPSLNYYTTEERIFAQRLMKYWTNFARTGDPNDPRDRKSPQWPYTTAAQQYVSL
NLKPLEVRRGLRAQTCAFWNRFPLKLLSAT

>d1f8ua_c.69.1.1 (A:) Acetylcholinesterase {Human (Homo sapiens)}
DAELLVTVRGGRLRGLKTPGGPVSAGLIPFAEPPMGPRRFPLPPEPKQPWSGVVDATTFQSVYCQYVDTLYP
GFEGETEMWNPNRELSEDCLYLNWTPYPRPTSPTPVLIWIYGGGFSGASSLDVYDGRFLVQAERTVLVSMNY
RVGAFGFLALPGSREAPGNVGLLDQRLALQWVQENVAAFGGDPTSVTFGQSAGAASVGMHLLSPSRGLFH
RAVLQSGAPNGPWATVGMGEARRRATQLAHVGCPPGGTGGNDTELVACLRTRPAQVLNHEWHVLPQESV
FRFSFPVVDGDFLSDTPEALINAGDFHGLQVLGVVVKDEGSYFLVYGVPGFSKDNESLISRAEFLAGVRVGVPQ
VSDLAAEAVVLHYTDWLHPEDPARLREALSDVVGHDHN VCPVAQLAGRLAAQGARVYAYFEHRASLTWPL
WMGVPHGYIEIFIFGIPLDPSRNYTAEEKIFAQRLMRYWANFARTGDPNEPRDPKAPQWPYTAGAQQYVSL
DLRPLEVRRGLRAQACAFWNRFPLKLLSAT

>d1dx4a_c.69.1.1 (A:) Acetylcholinesterase {Fruit fly (Drosophila melanogaster)}
DRLVVQTSSGPVRGRS VTVQGREVHVTGIPYAKPPVEDLRFRKPVPAEPWHGVLDATGLSATCVQERYEYFPG
FSGEEIWNPNNTNVSEDCLYINVWAPAKARL RHR GANGGEHPNGKQADTDH LIHNGNPQNTTNGLPIIWIY
GGGFMTGSATLDIYNADIMA AVGNVIVASFQYRVGAFGFLHLAPEMPSEFAEEAPGNVGLWDQALAIRWLKD
NAHAGGNPEWMLFGESAGSSSVNAQLMSPVTRGLVKRGMMQSGTMNAPWSHMTSEKA V EIGKALIND
CNCNASMLKTNPAHVMSCMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAFLPADPMTLMKTADLKDYDILM

GNVRDEGYFLLYDFIDYFDKDDATALPRDKYLEIMNNIFGKATQAEREAIFQYTSWEGNPGYQNQQQIGRAV
GDHFFTCPTNEYAQALAERGASVHYYFTHRTSTSLWGEWMGVHGDEIEYFFGQPLNNSLQYRPVERELGKR
MLSAVIEFAKTGNPAQDGEEWPNSKEDPVYIFSTDICKLARGPLAARCSFWNDYLPKVRSW

>d2bce_ c.69.1.1 (-) Bile-salt activated lipase (cholesterol esterase) {Cow (Bos taurus)}
AKLGSVYTEGGFVEGVNKLSLFGDSVDIFKGIPFAAAPKALEKPERHPGWQGTLAKSFKKRCLQATLTQDSTY
GNEDCLYLNIVPQGRKEVSHDPVMIWIYGGAFIMGASQGANFLSNLYDGEIATRGNVIVTFNYRVGPL
GFLSTGDSNLPGNYGLWDQHMAIAWKRNIIEAFGGDPDNITLFGESAGGASVSLQTLSPYNKGLIKRAISQSG
VGLCPWAIQQDPLFWAKRIAEKVGCPVDDTSKMAGCLKITDPRALTLAYKPLGSTEYPKLHYLSFVPPVIDGDFIP
DDPVNLYANAADVYIAGTNDMDGHLFVGMDVPAINSNKQDVTEEDFYKLVSGLTVTKGLRGANATYEVYTE
PWAQDSSQETRKKTMDLETDLFLIPTKIAVAQHKSHAKSANTTYLFSQPSRMPYPKWMGADHADDLQYV
FGKPFATPLGYRAQDRTVSKAMIAYWTNFARTGDPNTGHSTVANWDPYLEDDNYLEINKQMDNSMKLHL
RTNYLQFWTQTYQALPTVTSAGASLPPEDNSQASPVPADNSGAPTEPSAGDSEVAQMPVIGF

>d1f6wa_ c.69.1.1 (A:) Bile-salt activated lipase (cholesterol esterase) {Human (Homo sapiens)}

AKLGAVYTEGGFVEGVNKLLGDSVDIFKGIPFAAPTKALENPQPHPGWQGTLAKNFKKRCLQATITQDST
YGDEDCLYLNIVPQGRKQVSRLDPVMIWIYGGAFIMGSGHGANFLNNYLYDGEIATRGNVIVTFNYRVG
PLGFLSTGDSNLPGNYGLRDQHMAIAWKRNIIEAFGGDPDNITLFGESAGGASVSLQTLSPYNKGLIRRAISQS
GVALSPWVIQKNPLFWAKKVAEKVGCPVDAARMAQCLKVTDPRALTLAYKVLPLAGLEYPMLHYVGFVPVID
GDFIPDDPINLYANAADIDYIAGTNMDGHIFASIDMPAINGNKKVTEEDFYKLVSEFTITKGLRGAKTTFDVYT
ESWAQDPSQENKKKTVDFETDVLFLVPTEIALAQHRANAKSAKTYAYLFSHPSRMPVYPKWVGADHADDIQY
VFGKPFATPTGYRPQDRTVSKAMIAYWTNFAKTGDPNGDSAVPTHWEPYTTENSGYLEITKKMGSSSMKRS
LRTNFLRYWTLTYLALPTV

>d1qe3a_ c.69.1.1 (A:) Thermophytic para-nitrobenzyl esterase (PNB esterase) {Bacillus subtilis}

THQIVTTQYKGKVTENGVHKWKGIPYAKPPVGQWRFKAPEPPEVWEDVLDATAVGPICPQPSDLSLSYTEL
PRQSEDCLYVNVPADTPSQNLPMVWIHGGAFYLGAGSEPLYDGSKLAAQGEVIVVTLNYRLGPGFLHLSSF
DEAYSNDLGLDQAAALKWVRENISAFGGDPNVTVFGESAGGMSIAALLAMPAAKGLFQKAIMESGASRTM
TKEQAASAAFLQLVGINESQLDRLHTVAAEDLLKAADQLRIAEKENIFQLFFQPALDPKTLPEEPEKSIAEGAA
SGIPLLIGTRDEGYLFFTPSDVHSQETLDAALEYLLGKPLAEGAADLYPRSLESQIHMMTDLLWRPAVAYASA
QSHYAPVWMYRFDWHEPEKPPYNKAFHALELPVFGNLDGLERMAKAEITDEVKQLSHTIQSAWITFAKTGNP
STEAVNWPAYHEETRETVILDSEITIENDPESEKRQKLF

>d1jkma_ c.69.1.2 (A:) Carboxylesterase {Bacillus subtilis, brefeldin A esterase}

PGRLGDESSGPRTDPRFSPAMVEALATFGDAVAAAAPPVSASDDLPTVLA AVGASHDGFQAVYDSIALDLPTDR
DDVETSTETILGVDGNEITLHVFRPAGVEGLPGLVYTHGGMTILTTDNRVHRRWCTDAAAGSVVMVDF
RNAWTAEGHHFPFSGVEDCLAALWVDEHRESLGLSGVVQGESGGNLAIATLLAKRRGRRLDAIDGVASI
PYISGGYAWDHERRLTELPSLVENDGYFIENGGMALLVRAYDPTGEHAEDPIAWPYFASEDELRGLPPFVVAVN
ELDPLRDEGIAFARRLARAGDVAARVNIGLVHGADVIFRHWLPAALESTVRDVAGFAADRARLR

>d1evqa_ c.69.1.2 (A:) Carboxylesterase {Alicyclobacillus acidocaldarius}

LDPVIQQVLDQLNRMPAPDYKHLFAQFRSQQLFPPVKKEPVAEVREFDMDLPGRTLKVRYRPEGVEPPY
PALVYYHGGWVVGDETHDPVCRVLAKDGRAVVFSVDYRLAPEHKFPAAVEDAYDALQWIAERAADFHLDP
ARIAVGGDSAGGNLAATSVILAKERGGPALAFQQLIYPSTGYDPAHPPASIEENAEGYLLTGGMMLWFRDQYLN
SLEELTHPWFSVPVLYPDLSGLPPAYIATAQYDPLRDVGKLYAEALNKAGVKVEIENFEDLIHGFAQFYSLSPGATKA
LVRIAEKLRDALA

>d1jjia_ c.69.1.2 (A:) Carboxylesterase {Archaeon Archaeoglobus fulgidus}

MLDMPIDPVYYQLAEYFDSPKFDQFSSAREYREAINRIYEERNRQLSQHERVERVEDRTIKGRNGDIRVRVYQ

QKPDSPVLVYYHGGGFVICSIESHALCRIARLSNSTVSVDRALAPEHKPAAVYDCYDATKWVAENAEELRI
DPSKIFVGGDSAGGNLAAAVSIMARDSGEDFIKHQILIYPVVFVAPTPSLLEFGEGLWILDQKIMSWFSEQYFS
REEDKFNPLASVIFADLENLPPALIITAEDPLRDEGEVFGQMLRAGVEASIVRYRGVLHGFINYYPVLKAARDAI
NQIAALLVFD

>d1jjfa_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase z {Clostridium thermocellum}

SLPTMPPSGYDQVRNGVPRGQVVNISYFSTATNSTRPARVYLPPGYSKDKYSVLYLLHGIGGSENDWFEGGGR
ANVIADNLIAEGKIKPLIIVTPNTNAAGPGIADGYENFTKDLLNSLIPIYESNSVYTDREHRAIAGLSMGGGQSF
NIGLTNLDKFAYIGPISAAPNTYPNERLFPDGGKAAREKLKLLFIACGTNDSLIGFGQRVHEYCVANNINHVYWL
QGGGHDFNVWKPGLWNFLQMADEAGLTD

>d1gkla_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase y {Clostridium thermocellum}

SFKYESAVQYRPAPDSYLNPCPQAGRIVKETYTINGTKSLNVLPYGYDPNKKYNIFYLMHGGGENENTIFSND
VKLQNILDHAIMNGELEPLIVVTPTFNGGNCTAQNFYQEFRQNIPVESKYSTYAESTTPQGIAASRMHRGFG
GFAMGLTTWYVMVNCLDYAYFMPQLSGDYWGNGSPQDKANSIAEAINRSGLSKREYFVFAATGSEDIAYAN
MNPQIEAMKALPHFDYTSDFSKGNFYFLVAPGATHWWGYVRHYIYDALPYFFHELEHHHHHH

>d1f0na_ c.69.1.3 (A:) Antigen 85b {Mycobacterium tuberculosis}

SRPGLPVEYLQVPSPSMGRDIKVQFQSGGNNSPAVYLLDGLRAQDDYNGWDINTPAFEWYYQSGLSIVMPVG
GQSSFYSDWYSPACGKAGCQTYKWETFLTSELPQWLSANRAVKPTGSAIIGLSMAGSSAMILAAYHPQQFIYA
GSLSALLDPSQGMGPSSLIGLAMGDAGGYKAADMWGPSSDPAWERNDPTQQIPKLVANNTRLWVYCGNGTP
NELGGANIPAEFLENVRSSNLKFQDAYNAAGGHNAVNFPPNGTHSWEYWGAQLNAMKGDLQSSLGAG

>d1dqza_ c.69.1.3 (A:) Antigen 85c {Mycobacterium tuberculosis}

RPGLPVEYLQVPSASMGRDIKVQFQGGGPHAVYLLDGLRAQDDYNGWDINTPAFEEYYQSGLSVIMPVGGQS
SFYTDWYQPSQSNGQNYTYKWETFLTREMPAWLQANKGVSPTGNAAVGLSMSGGSALILAAYPQQFPYAA
SLSGFLNPSESWWPTLIGLAMNDSGGYNANSMWGPSSDPAWKRNDPMVQIPRLVANNTRIWVYCGNGTPS
DLGGDNIPAKFLEGTLRTNQTFRDTYADGGRNGVFNFPPNGTHSWPYWNEQLVAMKADIQHVNLG

>d1ju3a2 c.69.1.21 (A:5-351) Bacterial cocaine esterase N-terminal domain {Rhodococcus sp. mb1}
NYSVASNVMVPMRDGVRLAVDLYRPDADGPVPVLLVRNPYDKFDVFAWSTQSTNWLEFVRDGYAVVIQDTR
GLFASEGEFVPHVDDEADAEDTLSWILEQAWCDGNVGMFGVSYLGVTQWQAAVSGVGLKAIAPSMASAD
LYRAPWYGPALSVEALLGWSALIGTGLITSRSDARPEDAADFVQLAAILNDVAGAASVTPLAEQPLLGRIP
WVIDQVVDHDPNDESWQSIISLERLGGLATPALITAGWYDGFVGESLRTFVAVKDNDARLVVGPWSHSNLT
GRNADRKFIAATYPIQEATTMHKAFFDRHLRGETDALAGVPKVRLFVMGIDEWRDETDW

>d1qfma2 c.69.1.4 (A:431-710) Prolyl oligopeptidase, C-terminal domain {Pig (Sus scrofa)}

DASDYQTQIFYPSKDGTKIPMFIVHKKGIKLDGSHPAFLGYGGFNISITPNYSVSRLIFVRHMGGVLAVANIRG
GGEYGETWHKGGILANKQNCDDFQCAAELYIKEGYTSPKRLLTINGGSNGGLLVATCANQRPDLFGCVIAQVG
VMDMLKFHKYTIGHAWTTDYGCSDSKQHFEWLKYSPLHNVKLPEADDIQYPSMLLTADHDDRVVPLHSLKFI
ATLQYIVGRSRKQNNPLLIHVDTKAGHGAGKPTAKVIEEVDMSAFIARCLNIDWIP

>g1wht.1 c.69.1.5 (A;B:) Serine carboxypeptidase II {Wheat (Triticum vulgaris)}

GHAADRIARLPGQPAVDFDMYSGYITVDEGAGRSLFYLLQEAPEDAQPAPLVLWLNNGPGCSSVAYGASEELG
AFRVKPRGAGLVLNEYRNWKVANVLFLDSPAGVGFSYNTSSDIYSGDNRTAHDSYAFLAKWFERFPHYKYRD
FYIAGESYAGHYVPELSQLVHRSKNPVINLKGMVGNGLIDDYHDYVGTFEFWNHGIVSDDTYRRLKEACLH
DSFIHPSPACDAATDVATAEQGNIDMYSLYTPVCNIXSYDPCTERYSTAYNRRDVQMALHANVTGAMNYTWA
TCSDTINTHWHDAPRSMLPIYRELIAAGLRIWVFSGDTDADVPLATRYSIGALGLPTTSWYPWYDDQEVG

WSQVYKGLTLVSRGAGHEVPLHRPRQALVLFQYFLQGKPMMPGQ

>d1cpy_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (Saccharomyces cerevisiae)}
KIKDPKILGIDPNVTQYTGYLDVEDEDKHFFFWTFESRNDPAKDPVILWLNGPGCSSLTGLFFALGPSSIGPDLK
PIGNPYSWNSNATVIFLDQPVNVGFSYSGSSGVNTVAAGKDVFNFLELFFDQFPEVNKGQDFHIAGASYAG
HYIPVFASEILSHKDRNFnLTSVLIGNGLDPLTQYNNYEPMACGEALLEPSVLPSEECSAMEDSLERCLGLIESCYD
SQSVWSCVPATIYCNAQLAPYQRTGRNVYDIRKDCEGGNLCPYLQDIDDYLNQDYVKEAVGAEVDHYESCN
FDINRNLFAGDWMKPYHTAVTDLLNQDLPILVYAGDKDFICNWLGNAWTDVLPKYDEEFASQKVRNWT
ASITDEVAGEVKSYKHFTYLRVFNGGHMVPFDVPENALSMVNEWIHGGFSL

>d1ac5_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (Saccharomyces cerevisiae)}, kex1(delta)p}

LPSSEYYKVAYELLPGLEVPDPSNIPQMAGHIPLRSEDADEQDSSDLEYFFWKFTNNDSNGNVDRPLIIWLN
GGPGCSSMDGALVESGPFRVNSDGKLYLNEGWSISKGDLLFIDQPTGTGSVEQNKEGKIDKNKFDEDLEDV
TKHFMDFLENYFKIFPEDLTRKIILSGESYAGQYIPFFANAILHNHKFSKIDGDTYDLKALLINGWIDPNTQSLSYL
PFAMEKKLIDESNPNFKHLTNNAHENCQNLINSASTDEAAHFSYQECENILNLLSYTRESSQKTADCLNMYNFN
LKDSYPSCGMNWPKDISFVSKFFSTPGVIDSLHLDSDKIDHWKECTNSVGTLSNPISKPSIHLLPGLLESGIEIVL
FNGDKDLCNNKGVLDTIDLKWGGIKGFSDDAVSFDWIHKSKSTDSEEFSGYVKYDRNLTFSVYNASHMV
PFDKSLVSRGIVDIYSNDVMIIDNNNGKNVMITT

>d1ivya_ c.69.1.5 (A:) Human 'protective protein', HPP {Human (Homo sapiens)}

APDQDEIQRLPGLAKQPSFRQYSYGLKSSGSKHLHYWFVESQKDPENSPVVLWLNGPGCSSLDGLTEHGPF
LVQPDGVTEYNPSWNLIANVLYLESPAGVGFSYSDKFYATNDTEVAQSNFEALQDFRFLFPEYKNNKLFLTG
ESYAGIYIPTLAVLVMQDPSMNQGLAVGNGLSSYEQNDNSLVYFAYYHGLGNRLWSSLQTHCCSQNKCNFY
DNKDLECVTNLQEVARIVGNSGLNIYNYAPCAGGVPSPHRYEKDTVVVQD LGNIFTRLPLKRMWHQALLRSG
DKVRMDPPCTNTTAASTYLNPNPYVRKALNIPEQLPQWDMCNFLVNQYRRLYRSMNSQYKLSSQKYQILLY
NGDVDMACNFMGDEWFVDSLQNQKMEVQRRPWLVKYGDSGEQIAGFVKEFSHIAFLTIGAGHMVPTDKPL
AAFTMFSRFLNKQPY

>d1hlga_ c.69.1.6 (A:) Gastric lipase {Human (Homo sapiens)}

SPEVTMNIISQMITYWGYPNEEYEVVTEDGYILEVNRIPIYGKKNSGNTGQRPVFLQHGLLASATNWISNLPNN
SLAFILADAGYDVWLGNNSRGNTWARRNLYYSPDSVEFWAFSDEMAKYDLPATIDFIVKKTGQQLHYVGHQSQ
GTTIGFIAFSTNPSLAKRIKTFYALAPVATVKYTKSLINKLRFVPQSLFKFIFGDKIFYPHNFFDQFLATEVCSREMLN
LLCSNALIFIICGFDKSNFNTSRLDVYLSHNPAGTSVQNMFHWTQAVKSGKFQAYDWGSPVQNRMHYDQSQP
PYYNVTAMNPIAVWNGGKDLLADPQDVGLLPKLPNLIYHKEIPFYNHLDFIWAMDAPQEYNDIVSMISED
KK

>d1azwa_ c.69.1.7 (A:) Proline iminopeptidase {Xanthomonas campestris, pv. citri}

MRTLYPEITPYQQGSLKVDDRHTLYFEQCGNPHGKPVMLHGGPGGGCNDKMRRFHDPAKYRIVLFDQRGS
GRSTPHADLVDTTWDLVADIERLRTHLGVDRWQVF GGSGGSTLALAYAQTHPQQVTELVRGIFLLRRFELE
WFYQEGASRLFPDAWEHYLNAIPPVERADLMSAFHRRLTSDDEATRLAAAKAWSVWEGATSFLHVDEDFTVG
HEDAHFALAFARIENHYFVNGGFFEVEDQLLRAHRIADIPGVIVHGRYDVVCPLQSAWDLHKAWPKAQLQIS
PASGHSAFEPEVNDAVLVRATDGFA

>d1qtra_ c.69.1.7 (A:) Proline iminopeptidase {Serratia marcescens}

LRGLYPPLAAYDSGWLDTGDGHRIYWELSGNPNGKPAVFIHGGPGGGISPHRQLFDPERYKVLLFDQRGCGR
SRPHASLDNNTTWHLVADIERLREMAGVEQWLVF GGSGGSTLALAYAQTHPERVSEMVLRGIFTLRKQRLHW
YYQDGASRFFPEKWERVLSILSDDERKDVIAYRQRILTSADPQVQLEAAKLWSVWEGETVTLLPSRESASFGED
DFALAFARIENHYFTHLGFLESDDQLLRNVPLIRHIPAVIVHGRYDMAQVQNAWDLAKAWPEAELHIVEGAG
HSYDEPGILHQLMIATDRFAGK

>d1b6g_ c.69.1.8 (-) Haloalkane dehalogenase {Xanthobacter autotrophicus}
MVNAIRTPDQRFSNLDQYPFSPNYLDDLPGYPGPLRAHYLDEGNSDAEDVFLCLHGEPTWSYLYRKMPVFAES
GARVIAPPDFFGKGKSDKPVDEEDEYTFFHRNFLALIERLDRNITLVVQDWGGFLGLTPMADPSRFKRLIIMN
ACLMTPVTQPAFSAFVTQPADGFTAWKYDLVTPSDLRLDQFMKRWAPTLTEAEASAYAAPFPDTSYQAGVRK
FPKMVAQRDQACIDISTEISFWQNDWNGQTFMAIGMKDKLLGPDMYPMKALINGCPEPLEIADAGHFVQ
EFGEQVAREALKHFAETE

>d1bn7a_ c.69.1.8 (A:) Haloalkane dehalogenase {Rhodococcus sp.}
IGTGFDFPHYVEVLGERMHYVDVGPRDGTPVLHGNPTSSYLWRNIIPHVAPSHRCIAPDLIGMGKSDKPDL
DYFFDDHVRYLDAFIEALGLEEVVLVIHDWGSALGFHWAKRNPERVKGIACMEFIRPIWTDEWPEFARETFQ
AFRTADVGRELIIDQNAFIEGVLPKCVVRPLTEVEMDHYREPFLKPVDREPLWRFPNEIPIAGEPANIVALVEAYM
NWLNHQSPVPKLLFWGTPGVLIPIAAEARLAESLPNCKTVDIGPGLHYLQEDNPDLIGSEIARWLPGLA

>d1cv2a_ c.69.1.8 (A:) Haloalkane dehalogenase {Sphingomonas paucimobilis, UT26, LinB}
GAKPFGEKKFIEIKGRRMAYIDEGTGDPILFQHGNPTSSYLWRNIMPHCAGLGRLIACDLIGMGDSKLDPSGP
ERYAYAEHRDYLDALWEALDGLDRVVLVHVHDWGSALGFDWARRHRERVQGIAYMEAIAPIEWADFPEQDR
DLFQAFRSQAGEELVLQDNVFVEQVLPGILRPLSEAEMAAYREPFLAAGEARRPTLSWPRQIPIAGTPADVVAI
ARDYAGWLSESPIPKLFINAEPGALTGRMRDFCRTWPQNQTEITVAGAHFIQEDSPDEIGAAIAFVRLLRPA

>d1din_ c.69.1.9 (-) Dienelactone hydrolase {Pseudomonas sp., B13}
MLTEGISIQSYDGHTFGALVGSPAKAPAPVIVIAQEIFGVNAFMRETWSWLVLDQGYAAVCPDLYARQAPGTALD
PQDERQREQAYKLWQAFDMEAGVGDEAAIRYARHQPSNGKVGLVGYALGGALAFLVAAKGYDRAVGYYG
VGLEKQLNKVPEVKHPALFHMGQDHFPAPSRLQITEGFGANPLLQVHWYEEAGHSARTSSSGYVASAAAL
ANERTLDFLAPLQS

>d1c4xa_ c.69.1.10 (A:) 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (BPHD)
{Rhodococcus sp., strain rha1}
TVEIIEKRFPSTLASHALVAGDPQSPAVVLLHGAGPGAHAASNWRPIIPDLAENFFVVAPDLIGFGQSEYPETY
PGHIMSWVGMRVEQILGLMNHFIEKSHIVGNSMGGAVTLQLVVEAPERFDKVALMGSVGAPMNARPPPEL
ARLLAFYADPRLTPYRELIHSFVYDPENFPGMEEIVKSRFEVANDPEVRRIQEVMFESMKAGMESLVIAPPATLGRL
PHDVLVFHGRQDRIVPLDTSLYLTKHLKHAELVVLDCRGHWAQLERWDAMGPMILMEHFRA

>d1ek1a2 c.69.1.11 (A:226-544) Mammalian epoxide hydrolase, C-terminal domain
{Mouse (Mus musculus)}

LPVPCNPNDVSHGYVTVKPGIRLHFVEMGSGPALCLCHGFPESWFSWRYQIPALAQAGFRVLAIDMKGYGDSS
SPPEIEEYAMELLCKEMVTFLDKLGIPQAVFIGHDWAGVMVWNMALFYPERVRAVASLNTPFMPDPDVSP
MKVIRSIPVFNQLYFQEPGVAEAELEKNMSRTFKSFRASDETGFIAVHKATEIGGILVNTPEDPNLSKITTEEEIE
FYIQQFKKTGFRGPLNWYRNTERNWKWSCKGLRKILVPALMVTAEKDIVLRPEMSKNMEKWIPFLKRGHIED
CGHWTQIEKPTEVNQILIKWLQTE

>d1ehya_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Agrobacterium radiobacter}
AIRRPEDFKHYEVQLPDVKIHVREGAGPTLLLHGWPFWWEWSKVGPLAEHYDVIPDLRGFGDSEKPD
NDLSKYSLDKAADDQAALLDALGIEKAYVGHDFAAIVLHKFIRKYSDRVIAAIFDPIQPDFGPVYFLGHVHES
WYSQFHQLDMAVEVGSSREVCKKYFKHFFDHWSYRDELLTEEELEVHDNCMKPDNIHGGFNYYRANIRPD
AALWTDLHDHTMSDLPVTMIWGLGDTCPVYAPIEFVPKYYSNYTMETIEDCGHFLMVEKPEIAIDRIKTAFR

>d1qo7a_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Aspergillus niger}
KAFAKFPPSSASISPNTVSIPDEQLDDLKTLVRLSKIAPPTYESLQADGRFGITSEWLTTMREKWLSEFDWRPFE
ARLNSFPQFTTEIEGLTIHFAALFSEREDAVPIALLHGWPGSFVEFYPILQLFREETYPTELPFHLVVPSLPGYTFSSG
PPLDKDFGLMDNARVVQDQLMKDLGFGSGYIQQGGDIFSFGVGRLLGVGFACKAVHNLCARAPPEGPSIESL

SAAEKEGIARMEKFMTDGLAYAMEHSTRSTIGHVLSSPIALLAWIGEKYLQWVDKPLPSETILEMVSPLYWLTE
SFPRAIHTYRETTPTASAPNGATMLQKELYIHKPFGSFFPKDLCPVPRSWIATTGNLVFFRDHAEGGHFAALERP
RELKTDLTAFVEQVW

>d1brt_ c.69.1.12 (-) Bromoperoxidase A2 {*Streptomyces aureofaciens*}

PFITVGQENSTSIDLYYEDHTGQPVLIHGFLSGHSWERQSAALLDAGYRVTYDRRGFGQSSQPTGYDYD
TFAADLNTVLETDLQDAVLVGFBGTGEVARYVSSYGTARIKVAFLASLEPFLKTDDNPDGAAPQEFDGIV
AVKADRYAFYTGFNFDFYNLDENLGTRISEEAVRNSWNTAASGGFFAAAAAPTTWYTDFRADIPRIDVPALILH
GTGDRTLPIENTARVFHKALPSAEYVEVEGAPHGLLWTHAEEVNTALLAFLAK

>d1a8q_ c.69.1.12 (-) Bromoperoxidase A1 {*Streptomyces aureofaciens*}

PICTTRDGVEIFYKDWGQGRPVVFIHGWLNGDAWQDQLKAVVDAGYRGIAHDRRGHGHSTPVWDGYDFD
TFADDLNDLTDLRLDVTLVAHSMGGELARYVGRHGTGRLSAVLLSAIPPVMIKSDKNPDGVPEVFDALK
NGVLTERSQFWKDTAEGFFSANRPGNKTQGNKDAFWYMAMAQTIEGGVRCVDAFGYTDFTEDLKKFDIPT
LVVHGDDDVQVVPIDATGRKSAQIIPNAELKVYEGSSHGIAVPGDKEKFNRDLLEFLNK

>d1a88a_ c.69.1.12 (A:) Chloroperoxidase L {*Streptomyces lividans*}

GTVTTSDGTNIFYKDWGPRDGLPVFHHWPLSADDWDNQMLFLSHGYRVIAHDRRGHGRSDQPSTGHD
MDTYAADVAALTEALDLRGAVHIGHSTGGGEVARYVARAEPGRVAKAVLVSAVPPVMVKSDTNPDGLPLEVFD
EFRAALAANRAQFYIDVPSGPFYGFNREGATVSQGLIDHWLQGMMGAANAHYE CIAAFSETDFTDDLKRID
VPVLVAHGTDDQVVPYADAAPKSAELLANATLKSYEGLPHGMLSTHPEVLPNPDLLAFVKS

>d1a8s_ c.69.1.12 (-) Chloroperoxidase F {*Pseudomonas fluorescens*}

TTFTTRDGTQIYYYKDWGSGQPIVFSHGWLPLNADSWEQMIFLAAQGYRVIAHDRRGHGRSSQPWSGNDMD
TYADDLAQLIEHLDLRDAVLFGFSTGGGEVARYIGRHGTARVAKAGLISAVPPLMLKTEANPGGLPMEVFDGIR
QASLADRSQLYKDLASGPFFGFNQPGAKSSAGMVDWFWLQGMAAGHKNAYDCIKAFSETDFTEDLKKIDVPT
LVVHGDADQVVPIEASGIASAALVKGSTLKIYSGAPHGLTDTHKDQLNADLLAFIKG

>d1thta_ c.69.1.13 (A:) Myristoyl-ACP-specific thioesterase {*Vibrio harveyi*}

QCCTIAHVLRVNNNGQELHVWETPPKENVPFKNNTLIASGFARRMDHFAGLAEYLSTNGFHVFRYDSLHHVGL
SSGSIDEFTMTTGKNSLCTVYHWLQTKGTQNIGLIAASLSARVAYEVISDLELSFLITAVGVVNLRDTLEKALGFDY
LSLPIDELPNLDLFEGHKLGSEFVRDCFEHHWDTLDSTLDKVANTSVPPIAFTANNDDWVKQEEVYDMLAHI
RTGHCKLYSLGSSHDLGENLVLRNFYQSVTKAAIAMDGGSLEIDVDFIEPDEQLTIATVNERRLKAEIENRTPE
MA

>d1ei9a_ c.69.1.13 (A:) Palmitoyl protein thioesterase 1 {Cow (*Bos taurus*)}

DPPAPLPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIHVLSEIGKTLREDVENSFLNVNSQVTVCQILAK
DPKLQQGYNAMGFSQGGQFLRAVAQRCPSPPMVNLSIVGGHQGVFGLPRCPGESSHICDFIRKTLNAGAYN
KAIQERLVQAELYWDPIREDIYRNHSIFLADINQERGVNESYKKNLALKFVMVKFLNDTIVDPVDSEWFGFY
RSGQAKETIPLQESTLYTQDRLGLKAMDKAQQLVFLALEGDHLQLSEEWFYAHIIIPFLE

>d1auoa_ c.69.1.14 (A:) Carboxylesterase {*Pseudomonas fluorescens*}

MTEPLILQPAKPADACVIWLHGLGADRYDFMPVAEALQESLLTRFVLPQAPTRPVTINGGYEMPSWYDIKAM
SPARSISLEELEVSAKMVTDLIEAQKRTGIDASRIFLAGFSQGGAVVFHTAFINWQGPLGGVIALSTYAPTFGDEL
ELSASQQRIPALCLHGQYDDVVQNAMEGRSAFEHLKSRGVTWTQEYPMGHEVLPQEIIDGAWLAARLG

>d1fj2a_ c.69.1.14 (A:) Acyl protein thioesterase 1 {Human (*Homo sapiens*)}

MDPEFMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAEAFAGIRSSHIKYICPHAPVRPVTLNMNVAMPSWF
DIIGLSPDSQEDESGIKQAAENIKALIDQEVKNGIPSRIILGGFSQGGALSYTALTTQQKLAGVTALSCWLPLRA
SFPQGPPIGGANRDISILQCHGDCDPLVPLMFGSLTVEKLKTLVNPANVTFKTYEGMMHSSCQQEMMDVKQFI
DKLLPPI

>d1qlwa_ c.69.1.15 (A:) A novel bacterial esterase {*Alcaligenes sp.*}

VPKTPAGPLTLSGQGSFFVGGRDVTSETLSLSPKYDAHGTVTVDQMYVRYQIPQRACKRYPITLIHGCLTGMTW
ETTPDGRMGWDEYFLRGYSTYVIDQSGRGRSATDISAINAVKLGKAPASSLPDLFAAGHEAAWAIFRGPRYP
DAFKDTQFPVQAQAEWLQQMVPDWLGSMPNPTVANLSKLAIKLDGTVLLSHSQSGIYPFQTAAMNPKGIT
AIVSVEPGECPKPEDVKPLTSIPVLVFGDHIEFPRWAPRLKACHAFIDALNAAGGKGQLMSLPALGVHGNSH
MMMQRDRNNLQVADLILDWIGRNTA

>d1jfra_ c.69.1.16 (A:) Lipase {Streptomyces exfoliatus}

NPYERGPAPTNASIEASRGPYATSQTSVSSLVASGFGGTIYYPSTADGTGAVVISPGFTAYQSSIAWLGPRLAS
QGFVVFTIDTNTLDQPDPSRGRQLLSALDYLQRSSVRTRVDATRLGVMGHSMGGGSLEAAKSRTSLKAAIPL
TGWNNDKWTPELRTPTLVVGADGDTVAPVATHSKPFYSLPGSLDKAYLELRGASHFTPNTSDTTIAKYSISWLK
RFIDSDTRYEQFLCPIPRPSLTIAEYRGTCPHTS

>d1tca_ c.69.1.17 (-) Triacylglycerol lipase {Yeast (Candida antarctica), form b}
LPSGSDPAFSQPKSVLDAGLCQGASPSSVKPILLVPGTGTGQSFDSNWIPSLTQLGYTPCWISPPPMLND
TQVNTEYMVNAITALYAGSGNNKLPVLTWSQGGLVAQWGLTFPSIRSKVDRDMAFAPDYKGTVLAGPLALA
VSAPSvwQQTGSALTTALRNAGGLTQIVPTTNLYSATDEIVQPQVSNSPLDSSYLFNGKNVQAQAVCGPLFVI
DHAGSLTSQFSYVGRSALRSTGQARSADYGITDCNPLPANDLTPEQKVAAAALLAPAAAAIVAGPKQNCEPD
LMPYARPFAVGKRTCSGIVTP

>d3tgl_ c.69.1.17 (-) Triacylglycerol lipase {Rhizomucor miehei}

GIRAATSQEINELTYTTLANSYCRTVIPGATWDCIHCDATEDLKIICKTWSTLIYDTNAMVARGDSEKTIYIVFRGS
SSIRNWIADLTFVPSYPPVSGTKVHKGFLDSYGEVQNELVATVLDQFKQYPSYKVAVTGHSLGGATVLLCALDLY
QREEGLSSNLFLYTQGQPRVGDPAFANYVSTGIPYRTVNERDIVPHLPPAAGFLHAGEEYWITDNSPETVQ
VCTSDELTSDCNSIVPFTSVLDHLSYFGINTGLCT

>d1tia_ c.69.1.17 (-) Triacylglycerol lipase {Penicillium camembertii}

DVSTSELDQFEFWVQYAAASYEADYTAQVGDKLSCSKGNCPVEATGATVSYDFSDSTITDTAGYIAVDHTNSA
VVLAFRGSYSVRNWVADATFVHTNPGLCDGCLAEGLFWSSWKLVRDDIIKELKEVVAQNPNYELVVVGHSLGA
AVATLAATDLRGKGYPSAKLYAYASPRVGNAALAKYITAQGNFRFTHTNDPVPKLPLSMGYVHVSPEYWITSP
NNATVSTSDIKVIDGDVSFDGNTGTGLPLTDFAEHIAWYFVQVDAGKG

>d1tib_ c.69.1.17 (-) Triacylglycerol lipase {Thermomyces (Humicola) lanuginosa}

EVSQDLFNQFNLFQAQYSAAYCGKNNDAPAGTNITCTGNACPEVEKADATFLYSFEDSGVGDVTFGLALDNTN
KLIVLSFRGSRSIENWIGNLNFDLKEINDICSGCRGHDGFTSSWRSAIDLQKVEDAVREHPDYRVFTGHSLG
GALATVAGADLRGNGYDIDVFSYGAJPRVGNAFAELTVQTGGTLYRITHNDIVPRLPPREFGYSHSSPEYWIK
SGTLVPVTRNDIVKIEGIDATGGNNQPNIPDIPAHLYWYFGLIGTCL

>d1lgya_ c.69.1.17 (A:) Triacylglycerol lipase {Rhizopus niveus}

KVVAATTAAQIQEFTKYAGIAATAYCRSVVPGNKWDCVQCQKWVPGKIITFTSLLSDTNGYVLRSDKQKTIYL
FRGTONSFRSAITDIVFNFSDYKPKVKGAKVHAGFLSSYEQVNDYFPVVQEQLTAHPTYKVITGHSLGQAQALLA
GMDLYQREPRLSPKNLSIFTVGGPRVGNPTFAYYVESTGIPFQRTVHKRDIVPHVPPQSFGLHPGVESWIKSGT
SNVQICTSEIETKDCNSIVPFTSILDHLSYFDINEGSCL

>d1thg_ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (Geotrichum candidum)}, ATCC 34614}

EAPTAVLNGNEVISGVLEGKVDTFKGIPFADPPLNDLRFKHPQPFITGSYQGLKANDFSPACMQLDPGNSTLLD
KALGLAKVIPEEFRGPLYDMAKGTVSMNEDCLYLNVFRPAGTKPDAKLPVMVWIYGGAFVYGSAAYPGNSYV
KESINMGQPVVFVSINYRTGPGFLGGDAITAEGNTNAGLHDQRKGLEWVSDNIANFGGDPDKVMIFGESAG
AMSVAHQLIAYGGDNTYNGKKLFHSAILQSGGPLPYHDSSVGPDISYNRFAQYAGCDTSASANDTLECLRSKSS
SVLHDAQNSYDLKDLFGLLPQFLGFGPRPDGNIIPDAAYELFRSGRYAKVPIISGNQEDEGTAFAPVALNATTP
HVKKWLQYIFYDASEASIDRVLSLYPQTLSVGSPFRTGILNALTPQFKRVAAILSDMLFQSPPRVMMLSATKDVR

WTYLSTHLHNLVPFLGTFHGNEIFQFNVNIGPANSYLRYFISFANHHDPNVGTNLLQWDQYTDEGKEMLEIH
MTDNVMRTDDYRIEGISNFETDVNLYG

>d1lpp_ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (*Candida rugosa*), formerly *Cylindracea*}

APATLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYSGLDGQKFTSYGPSCMQQNPEGTYEENLPK
AAALDLMQSKVFEAVSPSSEDCLTINVVRPPGTKAGANLPVMLWIFGGGFEVGGTSTFPPAQMITKSIAMGKPI
IHVSVNYRVSSWGFAGDEIKAEGSANAGLKQRLGMQWVADNIAFGGDPTKVTIFGESAGSMSVMCHIL
WNDGDNTYKGKPLFRAGIMQSGAMVPSDAVDGIYGNEIFDLLASNAGCGSASDKLACLRGVSSDTLEDATNN
TPGFLAYSSLRLSYLPRPDGVNITDDMYALVREGKYANIPVIIGDQNDEGTFFGTSSLNVTTDAQAREYFKQSFVH
ASDAEIDLTLMTAYPGDITQGSPFDTGILNALTPQFKRISAVLGLGFTLARRYFLNHYTGGTKYSFLSKQLSGLPVL
GTFHSNDIVFQDYLLGSGSLIYNNAFIAFATDLDPTAGLLVKWPEYTSSSQSGNNLMMINALGLYTGKDNRFTA
GYDALFSNPPSFFFV

>d1clea_ c.69.1.17 (A:) Type-B carboxylesterase/lipase {*Candida cylindracea*, cholesterol esterase}

APATAKLANGDTITGLNAIINEAFLGIPFAEPPVGNLRFKDPVPYSGLDNGQKFTSYGPSCMQQNPEGTFEEENLGK
TALDLVMQSKVFOAVLPQSEDCLTINVVRPPGTKAGANLPVMLWIFGGGFEIGSPTIFPPAQMVTKSVMGKPI
IHVAVNYRVASWGFAGDDIKAEGSGNAGLKQRLGMQWVADNIAGFGGDPSKVTFGESAGSMSVLCHIL
WNDGDNTYKGKPLFRAGIMQSGAMVPSDPDVGTYGNEIYDLFVSSAGCGSASDKLACRSASSDTLLDATNN
TPGFLAYSSLRLSYLPRPDGKNITDDMYKLVRDGKYASVPVIIGDQNDEGTVFGLSSLNVTTNAQARAYFKQSFV
HASDAEIDLTLMAAYPQDITQGSPFDTGIFNAITPQFKRISAVLGLAFIHARRYFLNHFQGGTKYSFLSKQLSGLPV
MGTFHANDIVWQDYLLGSGSVIYNNAFIAFATDLDPTAGLLVNWPKYTSSSQSGNNLMMINALGLYTGKDNR
FRTAGYDALMTNPSSFFFV

>d1i6wa_ c.69.1.18 (A:) Lipase A {*Bacillus subtilis*}

HNPVVMVHGIGGASFNFAGIKSYLVSQGWSRDKLYAVDFWDKTGTNYNNNGPVLRFVQKVLDETGAKKVDIV
AHSMGGANTLYYIKNLDGGNKVANVVTLGGANRLTTGKALPGTDPNQKILYTSISSLADMIVMNYLSRLDGAR
NVQIHGVGHIGLLYSSQVNSLIKEGLNGGGQNTN

>d4lipd_ c.69.1.18 (D:) Lipase {*Burkholderia cepacia* (formerly *Pseudomonas cepacia*)}
DNYAATRYPILVHGLTDKYAGVLEYWYGIQEDLQQRGATVYVANLSGFQSDDGPNGRGEQLLAYVTVLAA
TGATKVNVLVHSQGGLTSRYAAVAPDLVASVTTIGTPHRGSEFADFVQGVLAYDPTGLSSTVIAAFVNFGILTS
SSNNTNQDALAALKLTTAQATYNQNYPAGLGAPGSCQTGAPTEVGGNTHLLYSWAGTAIQPTISVFGVT
GATDTSTIPLVDPANALDPSTIALFGTGTVMVNRGSGQNDGVVKCSALYGQVLSTSYKWNHLDEINQLLGVR
GANAEADPVAVIRTHANRLKLAGV

>d1ex9a_ c.69.1.18 (A:) Lipase {*Pseudomonas aeruginosa*}

STYTQTKPIVLAHGMLGFDNLGVWFGIPSALRRDGAQVYVTEVSQLDTSEVRGEQLLQQVEEIVALSGQP
KVNIGHSHGGPTIRYVAAVRPDLIASATSVGAPHKGSDTADFLRQIPPGSAGEAVLSGLVNSLGALISFLSSGSTG
TQNSLGSLESLNSEGAAFRNAKYPQGIPTSACGEGAYKVNGVSYYWSGSSPLTNFLPSDAFLGASSLTFKNGT
ANDGLVGTCSSHLGMVIRDNYRMNHDEVNQVFGLTSFETSPVSVYRQHANRLKNASL

>d1cvt_ c.69.1.18 (-) Lipase {*Chromobacterium viscosum*}

ADTYAATRYPVILVHGLAGTDKFANVVVDYWYGIQSDLQSHGAKVYVANLSGFQSDDGPNGRGEQLLAYVQVL
AATGATKVNIGHHSQGGLTSRYAAVAPQLVASVTTIGTPHRGSEFADFVQDVLTDPGLSSTVIAAFVNFGT
LVSSSHNTDQDALAALRTLTTAQATYNRNFPSAGLGAPGSCQTGAATETVGGSQHLLYSWGGTAIQPTSTVLG
VTGATDTSTGTLDVANVTDPSTLALLATGAVMINRASGQNDGLVSRCSLLFGQVISTSYHWNHLDEINQLLGVR
GANAEADPVAVIRTHVNRLKLQGV

>d1hpla2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Horse (*Equus caballus*)}

NEVCYERLGCFSDDSPWAGIVERPLKILPWSPEKVNRFLYTENPDNFQEIVADPSTIQSSNFNTGRKTRFIH
GFIDKGEESWLSTMQCQNMFKVESVNCICVDWKSGSRTAYSQASQNVRIVGAEVAYLVGLQSSFDYSPSNVHII
GHSLGSHAAGEAGRRTNGAVGRITGLDPAEPCFQGTPELVRLDPSDAQFVDVIHTDIAPFIPNLGFGMSQTAG
HLDFFPNNGKEMPGCQKNVLSQLIVIDGIWQGTRDFAACNHLRSYKYYTDSILNPDGFAGFSCASYSDFTANK
CFPCSSEGCPQMGMHYADRFPGRTKGVGQLFYLNTGDASNFA

>d1etha2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Pig (Sus scrofa)}
SEVCFPRLGCFSDDAPWAGIVQRPLKILPWSPKDVTFLYTQNQNQNNYQELVADPSTITNSNFRMDRKTRFI
HGFIDKGEEDWLSNICKNLKVESVNCICVDWKGGSRGTYTQASQNIRIVGAEVAYFVEVLKSSLGYSPSNVHVI
GHSLGSHAAGEAGRRTNGTIERITGLDPAEPCFQGTPELVRLDPSDAKFVDVIHTDAAPIPNLGFMSQTVGHL
DFFPNNGKQMPGCQKNILSQLIVIDGIWEGTRDFVACNHLRSYKYYADSILNPDGFAGFPCDSYNVFTANKCFP
CPSEGCPQMGMHYADRFPGRKTNGVSQVFYLNTGDASNFA

>d1lpbb2 c.69.1.19 (B:1-336) Pancreatic lipase, N-terminal domain {Human (Homo sapiens)}
KEVCYERLGCFSDDSPWSGITRPLHILPWSPKDVTFLYTENPNNFQEVAADSSSISGSNFKTRFI
GFIDKGEENWLANVCKNLKVESVNCICVDWKGGSRGTYTQASQNIRIVGAEVAYFVEFLQSAFGYSPSNVHVI
GHSLGAHAAGEAGRRTNGTIGRITGLDPAEPCFQGTPELVRLDPSDAKFVDVIHTDGAPIPNLGFMSQVVG
HLDFFPNNGVEMPGCKKNILSQLIVIDGIWEGTRDFVACNHLRSYKYYTDSIVNPDGFAGFPCASYNVFTANKC
FPCPSGGCPQMGMHYADRYPGKTNDVGQKFYLDTGASNFA

>d1gpl_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain {Guinea pig (Cavia porcellus)}
AEVCYSHLGCFSDEKPWAGTSQRPIKSLPSDPKKINTRFLYTENQNSYQLITATDIATIKASNFNLNRKTRFI
FTDSEGENSWLSDMCKNMFKQVEKVN CICVDWKGGSKAQYSQASQNIRVVAEVAYLVQLSTS NYAPENVH
IGHSLGAHTAGEAGKRLNGLVGRITGLDPAEPYFQDTPEEVRLDPSDAKFVDVIHTDISPILPSLGFMSQKVGH
MDFFPNNGKDMMPGCKTGISCNHHSIEYYHSSILNPEGFLGYP CASYDEFQESGCFPCPAKGCPKM GHFADQY
PGKTN AVEQTFFLNTGASDNFT

>d1rp1_2 c.69.1.19 (1-336) Pancreatic lipase, N-terminal domain {Dog (Canis familiaris)}
KEVCYEQIGCFSDAEPWAGTAIRPLKVL WS PERIGTRFLYTENPNNFQTLPSDPSTIGASNFQTDKKTRFI
GFIDKGEENWLLDMCKNMFKVEEVNCICVDWKGGSQTSYTQAANNVRV V GAQVAQMLSMSLANSYSPSQ
VQLIGHSLGAHVAGEAGSRTPGLGRITGLDPVEASFQGTPEEVRLDPTDADFVDVIHTDAAPLIPFLGFGTSQQ
MGHLDFFPNNGEEMPGCKKNALSQLIVDLDGIWEGTRDFVACNHLRSYKYYSESILNPDGFASYP CASYRAFES
NKCFPCPDQGCPQMGMHYADKFAQKYFLNTGDSSNFA

>d1bu8a2 c.69.1.19 (A:1-336) Pancreatic lipase, N-terminal domain {Rat (Rattus norvegicus)}
KEVCYGHLCFSNDKPWAGMLQRPLKIFPWSPEDIDTRFLYTENPNNYQKISATEPDTIKFSNFQLDRKTRFI
VHGFI DKG EDGWLLDMCKMFQVEKVN CICVDWRRGSRTEY TQASYNTRV V GAEIAFLVQLSTEMGYSPEN
VHLIGHSLGAHVVG EAGRRL EGHVGRITGLDPAEPCFQGLPEEVRLDPS DAMFVDVIHTDSAPIPYLGFGMSQ
KVGHLDFFPNNGKEMPGCQKNILSTIVDINGIWE GTQNFVACNHLRSYKYYASSILNPDGF LGYP CSSY EKFQQ
NDCFPCPEEGCPKMGMHYADQFEGKTATVEQT VYLNTGD SGNFT

>d1qj4a_c.69.1.20 (A:) Hydroxynitrile lyase {Rubber tree (Hevea brasiliensis)}
AFAHFVLIHTICHGAWIWHKLKPLLEALGHKVTALDLAASGV D PRQIEEIGSFDEYSEPLLT FLEALPPGEK VILVG
ESCGGLNIAIAADKYCEKIAAAVFHSVLPDTEHCPSYVVDKLM EVFPDWKDTYFTYTKDGKEITGLKLGF TLL
RENLYTLCGPEEYELAKMLTRKGSLFQNILA KRPFFTKEGYGSIKKIYVWTDQDEIFLPEFQLWQIENYKPKDKVYK
VEGGDHKLQLT KTKEIAEILQEVADTYN

>d1e89a_c.69.1.20 (A:) Hydroxynitrile lyase {Cassava (Manihot esculenta)}
PISKMVTAHFVLIHTICHGAWIWHKLKP ALERAGHK VTALDMAASGIDPRQIEQINSFDEYSEPLLT FLEKLPQGE
KVIIVGEACAGLNIAIAADRYVDKIAAGVFHNSLLPDTVHSPSYTVEKLLESFPDWRDTEYFTFTNITGETIT MKL
GFVLLRENLFTKCTDGEYELAKMVMRKGSLFQNVLAQRPKFTEKG YGSIKK VYI WTDQDKI FLPDFQ RWQIAN

YKPDKVYQVQGGDHKLQLTKTEEVAHILQEVA DAYA

>d1keza_ c.69.1.22 (A:) Erythromycin polyketide synthase {Saccharopolyspora erythraea}

SSALRDGYRQAGVSGRVRSYLDLLAGLSDFREHFDGSDGFSLDLMADGPGEVTVICAGTAISGPHEFTRL
AGALRGIA PVRAV P QPGYEEG EPLPSSMAAA VQADAVIR TQGD KPFV VAGHSAGA LMAYA LATE LLDRGHP
PRGVVLIDVYPPGHQDAMNAWLELTATLF DRET VRMDDTRL TALGAYDRLTGQWRPRETGLPTLLVSAGEPM
GPWPDDSWKPTWPFEHDTVAVPGDHFTMVQE HADAIARHIDAWLGGG

>d2masa_ c.70.1.1 (A:) Inosine-uridine nucleoside N-ribohydrolase, IU-NH {Crithidia fasciculata}
AKKIILD CDPGLDDAVAILAHGNPEIELLA ITTVVG NQTLAKVTRNAQLVADIAGITGVPIAAGCDKPLVRKIMTA
GHIHGESGMGT VAYPAEFKNVDERHVNLIIDLVMSHEPKTITL VPTGGLTNIAMAARLEPRIVDRVKEVVL
GGGYHEGNATSVAE FNII DPEAAHIVFNESWQVTMVG LDTHQALATPPI LQRVKEVDTNPARF MILEIMDYYT
KIYQSNRYMAAAVHDPCA VAYVIDPSVMTTERVPVDIELTGKLTG MTVADFRNPRPEHCHTQAVAKLDFEKK
WGLVLDALERIGDP

>d1ezra_ c.70.1.1 (A:) Nucleoside hydrolase {Leishmania major}

PRKIILD CDPGIDD AVALFA HGNPEIELLA ITTVVG NQSLEK VTNQARL VADVAGIVGV PVAAGCTKPLVRGV RN
ASHIHGETGMGNVSY PP EFKTKL DGRH AVQ LIDL IM SHEPKTITL VPTGGLT NIAMA VRLE PRIVDRV KEVVL
GGGYHTGNASPVAE FN FIDPEAAHIVFNESWNV TMVG LDTH LALATPAVQK RVREV GTKPAA FMLQ I DFY
TKVYEKEHDTY GK VHD PCA VAYVIDPTV MTT ERVPV DIEL NGALT GMTVADFRYPRPKNCRTQVAVKLD FDKF
WCLVIDALERIGDP

>d1hoza_ c.70.1.1 (A:) Inosine-adenosine-guanosine preferring nucleoside hydrolase
{Trypanosoma vivax}

GSAKNVVLHDGNLDDFVAMVLLASNTKVR LIGAL CT DADCF VENG FNV TGKIMCLMHNNMNLPLFPIGKS
ATAVNPFPKEWRCLAKNMDDMPILNIPENVELWDKIKAE NEKYEGQQLLADLVMNSEEKVTCVTGPLSNVA
WCID KYGEKFTSKVEECVIMGGAVDVRGNVFLPSTDGTAEWNIY WDP PASAKTVFGCPGLRRIMFSLDSTNTVP
VRSPYVQRFGEQTNFLLSILVGT MWAM CTHCELL RDGD GYYAW DALTAAYVVDQKVANVDPV PIDVVVDKQP
NEGATVRTDAENYPLTF VARNPEAEFFLDMILLRSARAC

>d1ra9_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Escherichia coli}

MISLIAALAVDRVIGMENAMPWNLPADLAWFKRNTLDKPVIMGRHTWESIGRPLPGRKNIILSSQPGTDDRV
TWVKSVDEAIAACGDVPEIMVIGGRVYEQFLPKAQKLYLTHIDA EVEGDT HF PDYEPDDWESVFSEFHADA
QNSHSYCFEILERR

>d3dfr_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Lactobacillus casei}

TAFLWAQN RNR NLIGKDGH LPWHL PDD LH YFRA QT VGKIMV VGR RTYESFPKRPLP ERTNV VLTHQ QEDYQA QG
AVV VHDVA AVFAYAKQHLDQELVIAGGAQI FTAFKDDVDTL VTR LAGSFEGDTK MIPLN WDDFT KVSS RTVED
TNP ALTH TYEVWQKKA

>d1df7a_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Mycobacterium tuberculosis}
MVGLIWAQATSGVIGRGGDIPWRLPEDQAHFREITMGHTIVMGRRTWDSLPAKVRPLPGRRN VLSRQADF
MASGAEVVG SLEE ALTSPETW VIGGGQVYALALPYATRCEVTEV D IGLP REAGDALAPV LDETWR GETGEWRF
SRSGLRYRLYSYHRS

>d1d1ga_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Thermotoga maritima}

AKVIFV LAMD VSGK IASS VESW SSSFEDRKNFR KITTEIGNV VMGRIT FEEIGRPLPERL NVV LTR RP KTSNNPSLV
FFNGSPADV VKFLEGKGYER VA VIGGKT VFTEFLREKL VDEF VTVE PYVFGK GIP FFDEF EGYFPLK LLEM RRLNE
RG TLFLKYS VE

>d1vdra_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Haloferax volcanii}

ELV SVA ALAEN RVIG RDGEL PWPSI PADK KQYRSRI ADDPV VLGR TT FESMR DD LGPSAQIVMSRSERSFSVDTA

HRAASVEEAVDIAASLDAETAYVIGGAAIYALFQPHLDRMVLSPGEYEYEGDTYYPEWDAEWELDAETDHEG
FTLQEWRVS

>d8dfr_c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Chicken (Gallus gallus)}
VRSLSNSIVAVCQNMIGKDGNLWPPLRNEYKYFQRMTSTSHVEGKQNAVIMGKKTWFSIPEKNRPLKDRINI
VLSRELKEAPKGAHYLSKSLDDALALLDSPELKSKVDMVVIVGGTAVYKAAMEKPINHRLFVTRILHEFESDTFFF
EIDYKDFKLLTEYPGVPADIQEEDGIQYKFEVYQKSV

>d1hfq_c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Human (Homo sapiens)}
VGSLNCIVAVSQNMIGKNGDLPWPPLRNESRYFQRMTTSSVEGKQNLVIMGKKTWFSIPEKNRPLKGRINL
VLSRELKEPPQGAHFLSRLDDALKLQEPELANKVDMVVIVGGSSVYKEAMNHPGHLKLKVTRIMQDFESDT
FFPEIDLEKYKLLPEYPGVLSDVQEEKGIKYKFEVYEKND

>d1dyr_c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Fungus (Pneumocystis carinii)}
NQQKSLTLVALTTSYGIGRSNSLPWKLKEISYFKRVTSFVPTFDSFESMNVLGMGRKTWEIPLQFRPLKGRIN
VVITRNESLDLNGNIHSAKSLDHALELLYRTYGSSESVQINRIFVIGGAQLYKAAMDHPKLDrimatiyKDIHCDV
FFPLKFRDKEWSSVWKKEKHSDLESVGTKVPHGKINEDGFDYEFEMWTRDL

>d1aoe_c.71.1.1 (A:) Dihydrofolate reductases, eukaryotic type {Yeast (Candida albicans)}
MLKPNVAlVAALKPALGIGYKGKMPWRLRKEIRYFKDVTRTKPNTRNAVIMGRKTWEIPQKFRPLPDRLN
ILSRSYENEIIDDNIIHASSESSLNLVSDVERVFIIGGAEIYNELINNSLVSHLLITEIEHPSPESIEMDTFLKFPLESWT
KQPKSELQKFVGDTVLEDDIKEGDFTYNTLWTRK

>d1ekqa_c.72.1.2 (A:) Hydroxyethylthiazole kinase (THZ kinase, ThiK) {Bacillus subtilis}
MDAQSAAKCLTA VRRHSPLVHSITNNVVTNFTANGLLALGASPVMAYAKEEVADMAKIAGALVNLIGTLSKESV
EAMIIAGKSANEHGVPVILDVGAGATPFRTESARDIIREVRLAAIRGNAEIAHTVGVTDWLIKGVDAEGGGG
DIIRLAQQAAQKLNTVIAITGEVDVIADTSHVYTLHNGHKLLTKVTGAGCLLTSVVGAFCAVEENPLFAAIAAISSY
GVAAQLAAQQTADKGPGSFQIELLNKLSTVTEQDVQEWTIERV

>d1jxha_c.72.1.2 (A:) 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate kinase
(HMP-phosphate kinase, ThiD) {Salmonella typhimurium}
MQRINALTIAGTDPGGAGIQADLKTFSALGAYGCSVITALVAENTCGVQSVYRIEPDFVAAQLDSVSDVRIDTT
KIGMLAETDIVEAVAERLQRHHVRNVVLDTVMLAKSGDPLLPSAIETLRVRLLPQVSLITPNLPEAAALLDAPH
ARTEQEMLAQGRALLAMGCEAVLMKGHHLEDAQSPDWLFTRGEQRFSAPRVNTKNTHTGCTLSAALAAL
RPRHRSWGETVNEAKAWLSAALAQADTLEVKGKIGPVHHFHAWW

>d1rkd_c.72.1.1 (-) Ribokinase {Escherichia coli}

AGSLVVLGSINADHILNLQSFTPGETVTGNHYQVAFGGKGANQAVAAGRSGANIAFIACGTGDDSIGESVRQQL
ATDNIDITPVSIVKGESTGVALIFVNGEGENVIGHAGANAALSPALVEAQRERIANASALLMQLESPLESVMAAA
KIAHQNKIVALNPAPARELPDELLALVDIITPNETEAELTGIRVENDEDAAKAAQVLHEKGIRTVLITLGSRGVW
ASVNGEGQRVPGFRVQAVDTIAAGDTFNGALITALLEKPLPEAIRFAAAAAIAVTRKGAQPSVPWREEIDAFL
DRQR

>d1bx4a_c.72.1.1 (A:) Adenosine kinase {Human (Homo sapiens)}

VRENILFGMGNPLLDISAVVDKDFLDKYSKPNDQILAEDKHKELFDELVKKFKVEYHAGGSTQNSIKVAQWMI
QQPHKAATFFCIGIDKFGEILKRKAAEAHVDAHYEQNEQPTGTCAACTGDNRSLIANLAAANCYKKEKHD
LEKNWMLVEKARVCYIAGFFLTSPESVLKVAHHASENNRIFTLNSAPFISQFYKESLMKVMPYVDILFGNETE
AATFAREQGFETKDIKEIAKKTQALPKMNSKRQRIVIFTQGRDDTIMATESEVTAFAVLDDQDQKEIIDNGAGDA
FVGGFLSQLVSDKPLTECIRAGHYAASIIIRRTGCTFPEKPDFH

>d1dgxa_c.72.1.1 (A:) Adenosine kinase {Toxoplasma gondii}

GPMRVAIGNPILDVAEVPSFLDEFFLKRGDATLATPEQMRIYSTLDQFNPTSLPGGSALNSVRVVQKLLRK
GSAGYMGAIQDDPRGQVLKELCDKEGLATRFMVAPGQSTGTCAVLINEKERTLCTHLGACGSFIPENWTTFA

SGALIFYATAYLTATPKNALEVAGYAHGIPNAIFTLNLSAPFCVELYKDAMQSLLHTNILFGNEEEFAHLAKVHNL
VAAEKVALSVANKEHAVEVCTGALRLTAGQNTGATKLVMTRGHNPVIAAEQTADGTVVVHEGVGPVVAE
KIVDTNGAGDAFVGGLYGLSQGKTVKQCIMCGNACAQDVIQHVGFSLSF
>d1gc5a_ c.72.1.3 (A:) ADP-dependent glucokinase {Archaeon Thermococcus litoralis}
MKESLKDRIRLWKRLYVNAFENALNAIPNVKGVLAYNTNIDAIKYLDADDLEKRVTEKGKEKVFEIENPPEKISSI
EELGGILRSIKLGKAMEWFVSEEVRRYLREWGWDLREGGQAGIMANLLGGVYRIFTIVHPQNPKLQAELF
VDGPIYVPVFEGNKLKLVHPKDAIAEEEELIHYIYEPRGFQVFVQAPRENRFIANADDYNARVYMRREFREGF
EEITRNVELAIISGLQVLKEYYPDGTTYKDVLDRVESHLNLINRYNVKSHFEFAYTANRRVREALVELLPKFTSVGLN
EVELASIMEIIGDEELAKEVLEGHIFSVIDAMNVLMDETGIERIHFTYGYYLALTQYRGEEVRDALLFASLAAA
AMKGNLERIEQIRDALSPTNERAIVLEEELEKEFTEFENGLIDMVDRQLAFVPTKIVASKSTVIGDITSSAFV
SEFGMRKR
>d2uaga3 c.72.2.1 (A:94-297) UDP-N-acetyl muramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}
DIELFCREAQAPIAVITGSNGKSTVTLVGEAMAKAAGNVGVGGNIGLPALMILLDECELYVLELSSFQLETTSSL
QAVAATILNVTEDHMDRYPFGLQQYRAAKLRIYENAKVCVNADDALTMPIRGADERCVSFGVNMGDYHLN
HQQGETWLRVKGEKVLNVKEMKLSGQHNYTNALAALALADAAGLPRASSLKALTTFT
>d1e8ca3 c.72.2.1 (A:88-337) UDP-N-acetyl muramyl tripeptide synthetase MurE {Escherichia coli}
QLNERLSALAGRFYHEPSDNLRIVGVTGNGKTTTQLAQWSQLGEISAVMGTVGNGLLGKVIPTENTTG
AVDVQHELAGLVDQGATFCAMEVSSHGLVQHRVAALKFAASVFTNLSRDHLDYHGDMEHYEAKWLLYSEH
HCGQAINADDEVGRRWLAKLPDAVAVSMEDHINPNCHGRWLKATEVNYHDSGATIRFSSWDGGEIESHLM
GAFNVSNLLALATLLALGYPLADLLKTAARLQP
>d1gg4a4 c.72.2.1 (A:82-312) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}
DTRLAFGELAAWVRQQVPARVVALTGSSGKTSVKEMTAAILSQCGNTLYTAGNLNNNDIGVPMTLLRLTPEYDYA
VIELGANHQGEIAWTVSLTRPEAALVNNLAAAHLEGFGSLAGVAKAKGEIFSGLPENGIAIMNADNNDWLNW
QSVIGSRKVWRFSPNAANSDFATNIHVTSHGTEFTLQTPTGSVDVLLPLPGRHNIANALAAAALMSMSVGATLD
AIKAGLANLKA
>d1jbwa2 c.72.2.2 (A:1-296) Folylpolyglutamate synthetase {Lactobacillus casei}
MNYTETVAYIHSFPRLAKTGDHRRILTLHALGNPQQQQGRYIHTGTNGKGSAANIAAHVLEASGLTVGLYTSPP
IMRFNERIMIDHEPIPDAALVNAVAFVRAALERLQQQQADFNTEFEPITALAYWYFRQRQVDVAVIEVGIGGD
TDSTNVITPVVSVLTEVALDHQKLLGHTITAIAKHKAGIIKRGIPVVTGNLVPDAAAVVAKVATTGSQWLFDR
DFSVPKAKLHGWGQRFTYEDQDGRISDLEVPLVGDYQQRNMAIAIQTAKVYAKQTEWPLTPQNIRQGLAASH
>d1jzta_c.104.1.1 (A:) Hypothetical protein YNL200c (YN00_YEAST) {Baker's yeast (Saccharomyces cerevisiae)}
LKVSSKLAEEIDKELMGPQIGFTLQQMLMEAGFSVAQAVCRQFPLRGKTETEKKGKHVFVIAGPGNNGGDGLV
CARHLKLFGYNPVVFYPKRSERTEFYKQLVHQLNFFKVPVLSQDEGNWLEYLKPEKTLIVDAIFGFSFKPPMRE
PFGKIVEELCKVQNIPIVSDVPTGWDVKGPISQPSINPAVLVSLTPKPCSSHIRENQTTHYVGGRFIPRFAN
KFGFEPFGYESTDQILKL
>d1b7ba_c.73.1.1 (A:) Carbamate kinase {Enterococcus faecium}
GKKMVVALGGNAILSNDASAHQQQQALVQTSAYLVHLIKQGHRLIVSHGNGPQVGNLLLQQQAADSEKNPA
MPLDTCVAMTQGSIGYWLSNALNQELNKAGIKKQVATVLTQVVVDPADEAFKNPTKPIGPFLTEAEAKEAMQA
GAIFKEDAGRGRWRKVVPSPKPIDIHEAETINTLIKNDIITSCGGGGIPVVGQELKGVEAVIDKDFASEKLAELVDA

DALVILTGVDYVCINYGKPDEKQLTNVTVAELEEYKQAGHFAPGSMPLKIEAAIQFVESQPNQAIITSLENLGSM
SGDEIVGTVV

>d1e19a_ c.73.1.1 (A:) Carbamate kinase {Archaeon Pyrococcus furiosus}
GKRVVIALGGNALQQRGQKGSYEEMMDNVRKTARQIAEIARGYEVVITHGNGPQVGSLLLHMDAGQATYGI
PAQPMDVAGAMSQGWIGYMIQQALKNELRKRGMEKKVVTIQTIVDKNDPAFQNPTKPVGPFYDEETAKRL
AREKGWIVKEDSGRGWRRVVPSPDPKGHVEAETIKLVERGVIVIASGGGGVPVILEDGEIKGVEAVIDKDLAG
EKLAEEVNADIFMILTDVNGAALYYGTEKEQWLREVKVEELRKYYEEGHFKAGSMGPVKLAAIRFIEWGGERAII
AHLEKAVEALEGKTGTQVLP

>d1eqja1 c.105.1.1 (A:77-310) 2,3-Bisphosphoglycerate-independent phosphoglycerate
mutase, substrate-binding domain {Bacillus stearothermophilus}
QSLTRINIAIREGEFDRNETFLAAMNHVKQHGTSLHLFGLLSDGGVHSIHHLYALLRLAAKEGVKRVYIHGLD
GRDVGPQTAPQYIKEIQLQEKIKEYGVGEIATLSGRYYSMRDKRWDRVEKAYRAMVYGEPTYRDPLECIEDSYK
HGYDEFVLPSIVREDGRPVATIQDNDIIFYNFRPDRAIQISNTFTNEDFREFDRGPKHPKHLFFVCLTHFSETV
AGYVAFKP

>d1eqja2 c.76.1.3 (A:3-76,A:311-510) 2,3-Bisphosphoglycerate-independent phosphoglycerate
mutase, catalytic domain {Bacillus stearothermophilus}
KKPVALIILDGFALRDETYGNAVAQANKPNFDYWNEYPHTLKACGEAVGLPEGQMGNSEVGLHNIGAGRIV
YXTNLDNTIGEVLSQHGLRQLRIAETEKYPHTFFMSGGREEEFPGEDRILINSPKVPTYDLKPEMSAYEVTDALL
KEIEADKYDAIIINYANPDMDVGHSGKLEPTIKAVEAVDECLGVVDAILAKGGIAITADHGNNADEVLTPDGKPQT
AHTTNPVPVIVTKGIKLRDGGILGDLAPTMDDLLGLPQPKEMTGKSLIV

>d1ed8a_ c.76.1.1 (A:) Alkaline phosphatase {Escherichia coli}
TPEMPVLENRAAQGDITAPGGARRLTGDTAALRDSLSDKPAKNIILLGDGMGDSEITAARNYAEGAGGFFKGI
DALPLTGQYTHYALNKKTGKPDYVTDASAASATAWSTGVKTYNGALVDIHEKDHTILEMAKAAGLATGNVSTA
ELQDATPAALVAHVTSRKCYGPSATSEKCPGNALEKGGKGSITEQLLNARADVTLGGGAKTFAETATAGEWQGK
TLREQAQARGYQLVSDAASLNSVTEANQQKPLLGLFADGNMPVRWLGPKATYHGNIDKPAVTCTPNPQRNDS
VPTLAQMTDKAIELLSKNEKGGFLQVEGASIDKQDHAAANPCGQIGETVLDDEAVQRALEFAKKEGNTLVITAD
HAHASQIVAPDTKAPGLTQALNTKDGAJVVMVMSYGNSEEDSQEHTGSQLRIAAYGPHAANVVGTDQTDLFYT
MKAALGLK

>d1ew2a_ c.76.1.1 (A:) Alkaline phosphatase {Human (Homo sapiens)}
IIPVEEENPDFWNREAAEALGAAKKLQPAQTAKNLIIFLGDGMGVSTVTAARILKGQKKDKLGPEIPLAMDRFP
YVALSKTYNVDKHVPDSGATATAYLCGVKGNFQTIGLSAARFNQCNTTRGNEVISVMNRAKKAGKSGVVT
TRVQHASPAGTYAHTVNRNWYSDADVPASARQEGCQDIATQLISNMIDVILGGGRKYMFRMGTDPPEYPD
DYSQGGTRLDGKNLVQEWLAKRQGARYVWNRTELMQASLDPSVTHLMGLFEPGDMKYEIHRDSTLPSLM
EMTEAALRLLSRNPRGFFLFVEGGRIDHGHESRAYRALTETIMFDDAIERAGQLTSEEDTLSVTADHSHVFSF
GGYPLRGSSIFGLAPGKARDKAYTVLLYNGNGPGYVLKDGPVTESESPEYRQQSAVPLDEETHAGEDVA
VFARGPQAHLVHGVQEQTIAHVMAFAACLEPYTACDLAPP

>d1auk_ c.76.1.2 (-) Arylsulfatase A {Human (Homo sapiens)}
RPPNIVLIFADDLGYGDLGCYGHPSSTTPNLDQLAAGGLRFTDFYVPVSLCTPSRAALLTRGLPVRMGMYPGVL
VPSSRGLPLEEVTVAEVLAARGYLTMAGKWHLGVGPEGAFLPPHQGFHRLGIPYSHDQGPCQNLTCFPPA
TPCDGGCDQGLVPIPLLANLSVEAQPWPGLEARYMAFAHDLMADAQRQDRPFFLYASHHTHYPQFSGQS
FAERSGRGPFGDSLIMEELAAVGLMTAIGDGLLEETLVIFTADNGPETMRMSRGCGSLLRCGKGTTYEGGV
REPALAFWPGHIAPGVTHELASSLDLLPTLAALAGAPLPNVTLGFDLSPLLLGTGKSPRQLFFYPSYPDEVRGV
FAVRTGKYKAHFFTQGSAHSDDTADPACHASSLTAHEPPLYDLSKDPGENYNLLGGVAGATPEVLQALKQLQ

LKAQLDAAVTFGPSQVARGEDPALQICCHPGCTPRPACCHCP

>d1fsu_ c.76.1.2 (-) Arylsulfatase B (4-sulfatase) {Human (Homo sapiens)}

SRPPHLVFLADDLGWNDVGFHGSIRTPHLDALAAGGVLLDNYTQPLXPSRSQLTGRYQIRTGLQHQIIW
PCQPSCVPLDEKLLPQLLKEAGYTTHMVGKWHGMYRKECLPTRRGFDTYFGYLLGSEDYYSHERCTLIDALNV
TRCALDFRDGEETATGYKNMYSTNIFTKRAIALITNHPPKEPLFLYALQSVHEPLQVPEEYLKPYDFIQDKNRHH
YAGMVSLMDEAVGNVTAALKSSGLWNNTVFIFSTDNGQTLAGGNWPLRGRKWSLWEGGVRGVGFVAS
PLLKQKGVKNRELIHISDWLPTLVKLARGHTNGTKPLDGFDVWKTISEGSPSPRIELHNIDPNFVDSSPCPRNS
MAPAKDDSSLPEYSAFNTSVHAIRHGNWKLLTGYPGCGWFPPPSQYNVSEIPSSDPPTKTLWLFIDRDPEE
RHDLREYPHIVTKLLSRLQFYHKHSVVPVYFPQAQDPRCDPKATGVWGPWM

>d1hdha_ c.76.1.2 (A:) Arylsulfatase B (4-sulfatase) {Pseudomonas aeruginosa}

KRPNFLVIVADDLGFSIDAFGGEIATPNLDALAIAGLRLTDFTASTCSPTRSMLLTGTDHHIAGIGTMAEALTPE
LEGKPGYEGHLNERVVALPELLREAGYQTLMAGKWHGLKPEQTPHARGFERSFSLLPGAANHYGFEPPYDEST
PRILKGTPALYVEDERYLDTLPEGFYSSDAFGDKLLQYLKERDQSRRFFAYLPFSAPHWPLQAPREIVEKYRGRYD
AGPEALRQERLARLKEGLVEADVEAHPVALTREWEALEDEERAKSARAMEVYAMVERMDWNIGRVVDYL
RRQGELDNTFVLFMSDNGAEGALLEAFPKFGPDLLGFLDRHYDNSLENIGRANSYVWYGRWAQAATAPSRL
YKAFTTQGGIRVPAVLVRYPRLSRQGAISHAFATVMDVTPTLTLAGVRHPGKRWRGREIAEPRGRSWLGWLSG
ETEAAHDENTVTGWELFGMRAIRQGDWKAVYLPAPVGPATWQLYDLARDPGEIHDLADSQPGKLAELIEHW
KRYVSETGVV

>d1k30a_ c.112.1.1 (A:) Glycerol-3-phosphate (1)-acyltransferase {Cushaw squash (Cucurbita moschata)}

SHSRKFLLDVRSEEELLSCIKKETEAGKLPPNVAAGMEELYQNYRNAVIESGNPKADEIVLSNMTVALDRILLVED
PFVFSHHKAIREPDFYYIFGQNYIRPLIDFGNSFVGNLNSFKDIEEKLQQGHNVVLISNHQTEADPAIISLLLEKTN
PYIAENTIFVAGDRVLATPLCKPFSIGRNLCVYSKKHMFDIPELTETKRKANTRSLKEMALLRGGSQLIWIAPSG
GRDRPDPSTGEWYPAPFDASSVDNMRRRIQHSVDVPGHLFPLALLCHDIMPPPSQVEIEIGEKVIAFNGAGLSV
APEISFEEIAATHKNPEEVREAYSKALFDSVAMQYNVLKTAISGKQGLGASTADVSLSQPW

>d1e4bp_ c.74.1.1 (P:) L-fuculose-1-phosphate aldolase {Escherichia coli}

MERNKLARQIIDTCLEMTRLGLNQGTAGQSVRYQDGMLITPTGIPYEKLTESHVIFDNGNGKHEEGKLPSEW
RFHMAAQSRPDANAVVHNNAVHCTAVSILNRSPAIHYMIAAAGGNSIPCACYATFGTRELSEHVALALKNR
ATLLQHHGLIACEVNLEKALWLAHEVEVLAQLYLTTAITDPVPVLSDEEIAVVLEKF

>d1jdia_ c.74.1.1 (A:) L-ribulose-5-phosphate 4-epimerase {Escherichia coli}

MLEDLKRVQLEANLALPKHNLVLTWGNVSADVDRERGVFIKPSGVVDYSIMTADDMVVSIETGEVVEGAKKP
SSDTPTHRLYQAFPSIGGIVHTHSRHTIWAQAGQSIPATGTTADYFYGTIPCTRKM TDAEINGEYEWETGNV
IVETFEKQGIDAAQMPGVLVSHGPFAWGKNAEDAVHNAIVLEEVAYMGIFCRQLAPQLPDMQQTLNKHYL
RKH

>d1j9la_ c.106.1.1 (A:) SurE homolog TM1662 (TM107 ?) {Thermotoga maritima}

MRLVTNDDGIQSKGIIVLAELLSEEHEVFVVAAPDKERSATGHSITIHPVLMKKFISERVVAYSTTGT PADCVKL
AYNVVMDKRVDLIVSGVNRGPNMGMDILHSGTVSGAMEAMMNIPSIAISSANYESPDFEGAARFLIDFLKE
FDFSLDDPFTMLNINVPAGEIKGWRFRTRQSRRWNDYFEERVSPFGEKYYWMGEVIEDDDRDDVDYKAVR
EGYVSITPIHPFLTNEQCLKLREVYD

>d1cjya2 c.75.1.1 (A:142-721) Cytosolic phospholipase A2 catalytic domain {Human (Homo sapiens)}

PDLRFSMALCDQEKTFRQQRKEHIRESMKLLGPKNSEGLHSARDVPVAILGSGGGFRAMVGFSVMKALY
ESGILDCATVAGLSGSTWYMSTLYSHPDFPEKGPEEINEELMKNVSHNPLLLTPQKVKRYVESLWKKSSGQP
VTFTDIFGMLIGETLIHNRMNTLSSLKEKVNTAQCPLPLFTCLHVKPDVSELMFADWVEFSPYEIGMAKYGT

MAPDLFGSKFFMGTVVKKYEENPLHFLMGVWGSAFSILFNRVLGVSGSQSRGSTMEELENITTKHIVSNDDSS
DSDDESHEPKGTEINEDAGSDYQSDNQASWIHRMIMALVSDSALFNTREGRAGKVHNFMGLNLNTSYPLSPL
SDFATQDSFDDDELDAAVADPDEFERIYEPLDVSKKIHVVDSGLTFNLPLYPLIRPQRGVLDLISFDFSARPSDSSP
PFKEELLAEKWAKMNKLFPKIDPYVFDREGLKECYVFKPKNPDMEKDCPTIIHFVLANINFRKYKAPGVPRETE
EEKEIADFDIFDDPESPFSTFNFQYPNQAFKRLHDLMHFTNLNNIDVIKEAMIVESIEYRRQ

>d1xaa_ c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Thermus thermophilus}
MKVAVLPGDGIGPEVTEAALKVLRALDEAEGLGLAYEVFPFGGAIDAFGEPEPFRKGVEEAEAVLLGSVGGP
KWDGLPRKIRPETGLLSLRKSQDLFANLRPAKVFPLERLSPLKEEIARGVDLIVRELGGIYFGEPRGMSEAEA
WNTERYSKPEVERVARVAFEAARKRKRKHVVSVDKANVLEVGEFWRKTVEEVGRGYPDVALEHQYVDAMAM
HLVRSPARFDVVVTGNIFGDILSDLASVLPGSLGLPSASLGRGTPVFEPVHGSAPIAGKGIANPTAAILSAAMM
LEHAFAGLVELARKVEDAVAKALLETPPPDLGGSAGTEAFTATVLRHLA

>d1xad_ c.77.1.1 (-) 3-isopropylmalate dehydrogenase, IPMDH {Chimera (Thermus thermophilus) and (Bacillus subtilis)}

MKVAVLPGDGIGPEVTEAALKVLRALDEAEGLGLAYEVFPFGGAIDAFGEPEPFRKGVEEAEAVLLGSVGGP
KWDQNPRELRPEKGLLSIRKQLDLFANLRPVKFESLSDASPLKEYIDNVDFLIVRELGGIYFGEPRGMSEAEA
WNTERYSKPEVERVARVAFEAARKRKRKHVVSVDKANVLEVGEFWRKTVEEVGRGYPDVALEHQYVDAMAM
HLVRSPARFDVVVTGNIFGDILSDLASVLPGSLGLPSASLGRGTPVFEPVHGSAPIAGKGIANPTAAILSAAMM
LEHAFAGLVELARKVEDAVAKALLETPPPDLGGSAGTEAFTATVLRHLA

>d2ayqa_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Bacillus coagulans}
MKMKLAVALPGDGIGPEVMDAAIRVLKTVLDNDGHEAVFENALIGGAAIDEAGTPLPEETLDICRRSDAILLGAV
GGPKWDHNPASLRPEKGLLRLKEMGLFANLRPVKAYATLLNASPLKRERVENVDLIVRELGGLYFGRPSERR
GPGENEVVDTLAYTREEIERIIEKAFAQLAQIRRKKLASVDKANVLESSRMWREIAETAKYPDVELSHMLVDSTS
MQLIANPGQFDVITENMFGDILSDEASVITGSLGMLPSASLRSDRGMYEPVHGSAPIAGQGKANPLGTVL
SAALMLRYSFGLEKEAAAIEKAVDDVLQDGYCTGDLQVANGKVVSTIELDRRIEKLN

>d1a05a_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Thiobacillus ferrooxidans}

MKKIAIFAGDGIGPEIVAAARQVLDADVQAAHLGLRCTEGLVGGAAALDASDDPLPAASLQLAMAADAVILGAV
GGPRWDAYPPAKRPEQGLLRLKGQLDLYANLRPAQJFPQLLDASPLRPELVRDVDILVVRELTDIYFGQPRGLEV
IDGKRRGFNTMVYDEDEIRRIAHVAFRAAQGRRKQLCSVVDKANVLETTRLWREVTEARDYPDVRLSHMYV
DNAAMQLIRAPAQFDVLLTGNMFGDILSDEASLTGSIGMLPSASLGEGRAMYEPIHGSAPIAGQDKANPLA
TILSVAMMLRHSLNAEPWAQRVEAAVQRVLDQGLRTADIAAPGTPVIGTKAMGAAVVNALNLK

>d1cnza_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Salmonella typhimurium}

MSKNYHIAVLPDGIGPEVMAQALKVMDAVRSRFDMRITTSHYDVGGIAIDNHGHPLPKATVEGCEQADAIL
FGSGGGPKWENLPPESQPERGALLPLRKHFKLFSNLRPAKLYQGLEAFCPLRADIAANGFDILCVRELGGIYFGQ
PKGREGSGQYEKAFDTEVYHRFEIERIARIAFESARKRRKVTSIDKANVLQSSILWREIVNDVAKTYPDVELAHM
YIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMITGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGKNIANPI
AQILSLALLRYSLDANDAATAIEQAINRALEEGVRTGDLARGAAAVSTDEMGIARYVAEGV

>d1cm7a_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Escherichia coli}

MSKNYHIAVLPDGIGPEVMTQALKVLDAVRNRFAMRITTSHYDVGGAAIDNHGQPLPPATVEGCEQADAVL
FGSGGGPKWEHLPPDQQPERGALLPLRKHFKLFSNLRPAKLYQGLEAFCPLRADIAANGFDILCVRELGGIYFG
QPKGREGSGQYEKAFDTEVYHRFEIERIARIAFESARKRRKVTSIDKANVLQSSILWREIVNEIATEYPDVELAH
MYIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMITGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGKNIA
NPIAQILSLALLRYSLDADDAACAIERAINRALEEGIRTGDLARGAAAVSTDEMGIARYVAEGV

>d1iso_c.77.1.1 (-) Isocitrate dehydrogenase, ICDH {Escherichia coli}
SKVVVPAQGKKITLQNGKLNVPENPIIPYIEGDGIGVDTPAMLKVVDAAVEKAYKGERKISWMEIYTGEKSTQV
YQQDVWLPAETLDLIREYRAIKGPLTPVGGGIRSLNVALRQELDLYICLRPVRYQQGTPSPVKHPELDMVIFRE
NSEDIYAGIEWKADSADAEEKVIKFLREEMGVKKIRFPEHCGIGIKPMSEEGTKRLVRAAIEYAIANDRDSVTLVHK
GNIMKFTEGAFKDHWGYQLAREEFGGELIDGGPWLKVKNPNTGKEIVKDIADAFLQQILLRPAEYDVIACMNL
NGDYISDALAAQVGGIGIAPGANIGDEYALFEATHGTAPDIAGQDKANPGSIILSAEMMLRHMGWTEAADLIV
KGMEAGAINAKTVTKDFESLMDGAKLLKCSEFGDAIIENM

>d1hqsa_c.77.1.1 (A:) Isocitrate dehydrogenase, ICDH {Bacillus subtilis}
MAQGEKITVSNGVLNVNPNNPIIPFIEGDTGPDIWNAASKVLEAAVEKAYKGEKKITWKEVYAGEKAYNKTGE
WLPAETLDVIREYFIAIKGPLTPVGGGIRSLNVALRQELDLFVCLRPVRYFTGVPSPVKRPEDTDMVIFRENTEDI
YAGIEYAKGSEEVQKLISFLQNELNVNKIRFPETSGIGIKPVSEEGTSRLVRAAIDYIAEHGRKSVTLVHGNIMKFT
EGAFKNWGYELAEKEYGDKVFTWAQYDRIAEEQGKDAANKAQSEAEAAGKIIKDSIADIFLQQILTRPNEFDVV
ATMNLNGDYISDALAAQVGGIGIAPGANINYETGHAIFEATHGTAPKYAGLDKVNPPSVILSGVLLHEHLGWNE
AADLVIKSMEKTIASKVVTYDFARLMGATEVKCSEFGEELIKNMD

>d1ekxa1 c.78.1.1 (A:1-150) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}
ANPLYQKHIISINDLSRDDNLVLATAAKLKANPQPELLKHKVIASCFFEASTRTRLSFETSMHRLGASVVGFSDSA
NTSLGKKGTELADTISVISTYVDAIVMRHPQEGAARLATEFSGNVPVLNAGDGSNQHPTQLLDFTIQETQG

>d1ekxa2 c.78.1.1 (A:151-310) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}
RLDNLHVAMVGDLKYGRTVHSLTQALAKFDGNRFYFIAPDALAMPQYILDMLDEKGIAWSLHSSIEEVMAEVD
ILYMTRVQKERLDPSEYANVKAQFVLRASDLHNKANMKVLHPLPRVDEIATVDKTPHAWYFQQAGNGIFA
RQALLALVNRDLVL

>d2atca2 c.78.1.1 (A:151-305) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}
RLNNLHVAMVGDLKYGRTVHSLTQALAKFDGNRFYFIAPDALAMPEYILDMLDEKGIAWSLHSSIEEVMTRVQ
KERLDPSEYABVKAQFVLVRANSLGGLHNKANMKVLHPLPRVDEIATVDKTPHAWYFQQAGNGIFARQALL
ALVLRNDLVL

>d2at2a1 c.78.1.1 (A:1-144) Aspartate carbamoyltransferase catalytic subunit {Bacillus subtilis}
MKHLTTMSELSTEEIKDLLQTAQELKSGKTDNQLTGKFAANLFFEPSTRTRFSFEVAEKKLGMNVNLNDGTSTSV
QKGETLYDTIRTLESIGVDVCVIRHSEDEYYEELVSQVNIPILNAGDGCQHPTQSLLDLMTIYEFNT

>d2at2a2 c.78.1.1 (A:145-295) Aspartate carbamoyltransferase catalytic subunit {Bacillus subtilis}
FKGLTVSIHGDIKHSRVARSNAEVTRLGARVLFGPSEWQDEENTFGTYVSMDEAVESSDVVMLLRIQNERHQ
SAVSQEGLNKYGLTVERAERMKRHAIIMHPAPVNRGEIDDLSVESEKSIRFKQMKGNGFIRMAVIQCALQTN
VKR

>d1dxha1 c.78.1.1 (A:1-150) Ornithine transcarbamoylase {Pseudomonas aeruginosa}
AFNMHNRNLLSLMHSTRELRYLLDLRDLKRAKYTGTEQQHLKRKNIALIFEKTSTRTRCAFEVAAYDQGANV
TYIDPNSSQIGHKESMKDTARVLGRMYDAIEYRGFKQEIVEELAKFAGVPVFNGLTDEYHPTQMLADVLTMR
HSD

>d1dxha2 c.78.1.1 (A:151-335) Ornithine transcarbamoylase {Pseudomonas aeruginosa}
KPLHDISYAYLGDARNMGNSSLIGAKLGMDVRIAAPKALWPHDEFVAQCKKFAEESGAKLTEDPKEAVKG
VDFVHTDVWVSMGEPVEAWGERIKELPYQVNMEIMKATGNPRAKFMHCLPAFHNSSETKVGKQIAEQYPNL
ANGIEVTEDVFESPYNIAFEQAENRMHTIKAILVSTLADI

>d1duvg1 c.78.1.1 (G:1-150) Ornithine transcarbamoylase {Escherichia coli}
SGFYHKHFLKLLDFTPAELNSLLQLAALKADKKSGKEEAKLTGKNIALIFEKDSTRTRCSFEVAAYDQGARVTYLG
PSGSQIGHKESIKDTARVLGRMYDGIQYRGYQQEIVETLAEVASPVWNGLTNEFHPTQLLADLLTMQEHLPG
>d1duvg2 c.78.1.1 (G:151-333) Ornithine transcarbamoylase {Escherichia coli}
KAFNEMTLVYAGDARNNMGNMNSLEAAALTGLDLRLVAPQACWPEAALVTECRALAQQNGGNITLTDVAKG
VEGADFIYTDVVVSMGEAKEKWAERIALREYQVNSKMMQLTGNPEVKFLHCLPAFHDDQTTLGKKMAEEF
GLHGGMEVTDEVFESAASIVFDQAENRMHTIKAVMVATLSK
>d1a1s_1 c.78.1.1 (1-150) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}
VVSLAGRDLCLQDYTAEEIWILETAKMFKIWQKIGKPHRLLEGKTLAMIFQKPSTRTRVSFEVAMAHLGGHAL
YLNAQDLQLRRGETIADTARVLSRYVDAIMARVYDHKDVEDLAKYATPVINGLSDFSHPCQALADYMTIWEKK
G
>d1a1s_2 c.78.1.1 (151-313) Ornithine transcarbamoylase {Archaeon Pyrococcus furiosus}
TIKGVVVYVGDGNNVAHSLMIAGTKLGADVVAPEGYEPDEKVIKWAEQNAAESGGSFELLHDPVKAVKD
ADVIYTDVWASMGQEAEAEERRKIFRPFQVNKDLVKHAKPDYMFMHCLPAHRGEEVTDDVIDSPNSVVWDQ
AENRLHAQKAVLALVMGGIK
>d1otha1 c.78.1.1 (A:34-184) Ornithine transcarbamoylase {Human (Homo sapiens)}
KVQLKGDRLLTKNFTGEEIKYMLWLSADLKFRKQKGEYLPLLQGKSLGMIFEKRSTRTRLSTETGFALLGGHPCF
LTQDIHLGVNESLTD TARVLSSMADAVLARVYKQSDLDTLAKEASIPIINGLSDLYHPIQILADYLTQEHYS
>d1otha2 c.78.1.1 (A:185-354) Ornithine transcarbamoylase {Human (Homo sapiens)}
SLKGLTLSWIGDGNNILHSIMMSAAKFGMHLQAATPKGYEPDASVTKLAEQYAKENGTKLLLTDPLEAHGG
NVLITDTWISMGREREKKRQLQAFQGYQVTMKTAKVAASDWTFLHCLPRKPEEVDEVFYSRSLVFPEAENR
KWTIMAVMVSLLTDYSPQLQPKF
>d1b74a1 c.78.2.1 (A:1-105) Glutamate racemase {Aquifex pyrophilus}
MKIGIFDSGVGGTLVKAIRNRYRKVDIVYLGDTARVPYGIRSKDTIIRYSLCAGFLDKGVDIIVVACNTASAYAL
ERLKKEINVPVFGVIEPGVKEALKSR
>d1b74a2 c.78.2.1 (A:106-252) Glutamate racemase {Aquifex pyrophilus}
NKKIGVIGTPATVKSGAYQRKLEEGGADVFAKACPLFAPLAEEGLLEGEITRKVVEHYLKEFKGKIDTLILGCTHYPL
LKKEIKKKFLGDAEVVDSSEALSLHNFIKDDGSSSLELFFTDSPNLQFLIKLILGRDYPVKAEGVF
>d1qopb_c.79.1.1 (B:) Tryptophan synthase, beta-subunit {Salmonella typhimurium}
TTLLNPYFEGGMYVPQILMPALNQLEEAfvSAQKDPEFQAQFADLLKNYAGRPTALTCKQNITAGTRTTLYLK
REDLLHGAHKTNQVLGQALLAKRMGKSEIIAETGAGQHGVASALASALLGLKRIYMGAKDVERQSPNVFR
MRLMGAEVIPVHSGSATLKDACNEALRDWSGSYETAHYMLGTAAGPHPYPTIVREFQRMIGEETKAQILDKEG
RLPDAVIACVGGGSNAIGMFADFINDTVGLIGVEPGGHGIETGEHGAPLKHGRVGIYFGMKAPMMQTADG
QIEESYSISAGLDFPSVGPQHAYLNSIGRADYVSITDDEALEAKTLCRHEGIIPALESSHALAHALKMMREQPEK
EQLLVVNLSGRGDKDIFTVHDIL
>d1fcja_c.79.1.1 (A:) O-acetylserine sulfhydrylase (Cystein synthase) {Salmonella typhimurium}
SKIYEDNSLTIGHTPLVRLNRIGNGRILAKVESRNPSFSVKCRIGANMIWDAEKRGVLKPGVELVEPTNGNTGIAL
AYVAAARGYKLTLMETMSIERRKLLKALGANLVLTEGAKGMKGAIQKAEEIVASDPQKYLLQQFSNPANPEI
HEKTTGPEIWEDTDGQDVFISVGVTGGTLGVTRYIKGTGKTDLITVAEPTDSPVIAQALAGEEIKPGPHKIQ
GIGAGFIPGNLDLKLIDKVVGITNEEAISTARRLMEEEGILAGISSGAAVAAALKLQEDESFTNKNIVVILPSSG
>d1tdj_1 c.79.1.1 (5-335) Allosteric threonine deaminase N-terminal domain {Escherichia coli}
QPLSGAPEGAELYRALVRAPVYEAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLRGAYAMMAGLTEEQ
KAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRGFGGEVLLHGAFDEAKAKAIELSQQQG
FTWVPPFDHPMVIAGQGTIALELLQQDAHDRVFPVGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAA

LDAGHPV ррр VГЛ FAEGV AVKRIGDETFR LCQЕY LDDIITV DSAICAAMKDLFEDVRAVAEP SGAL ALAGMK
KYIALHNIRGERLAHILSGANVNФHGLRYV SERCELGE

>d1e5xa_ c.79.1.1 (A:) Threonine synthase {Mouse-ear cress (*Arabidopsis thaliana*)}
IETAVKPHRTEDNIRDEARRNRSNAVNPFSAKYVPFNAAPGSTESYSLDEIVYRSRSGLLDVEHDMEALKRFD
GAYWRDLFDSRVGKSTWPYGSVWSKKEWVLPEIDDDDIVSAFEГNSNLFWAERFGKQFLGMNDLWVKHC
GISHTGSFKDLGMTVLVSQVNRLRKMRPVVGCASTGDTSAALSAYCASAGIPSIVFLPANKISMAQLVQPIA
NGAFVLSIDTDFGCMKLIREITAELPIYLANSLSNRLEGQKTAACIEILQQFDWQVPDWIVPGGNLGNIYAFYK
GFKMCQELGLVDRIPRMVCAQAANANPLYLHYKSGWKDFKPMTASTTFASAIQIGDPVSIDRAVYALKCNGI
VEEATEEEELMDAMAQADSTGMFICPHTGVALTALFKLRNQGVIAPTDRTVVVSTAHLKFTQSKIDYHSNAIPD
MACRFSNPPDVKA DFGAVMDVLKS YLGSNTLTS

>d1f2da_ c.79.1.1 (A:) 1-aminocyclopropane-1-carboxylate deaminase {Yeast (*Hansenula saturnus*)}
AGVAKFAKYPLTFGPSPISLNRLSQHLGSKVNVYAKREDCNSGLAFGGNKLKLEYIVPDI VEGDYTHLVSIGGR

QSNQTRMVAALAAKLGKKCVLIQEDWVPIPEAEKD VYNRVGNIELSRIMGADVRVIEDGF DIGMRKS FANALQ
ELEDAGHKPYPIPAGCSEHKYGGLGFGVFADEVINQEVELGIKFDKIVVCCVTGTTAGILAGMAQYGRQDDVIA
IDASFTSEKTKEQTLRIANNTAKLIGVEHEFKDFTLDTRFAYPCYGVNEG TIEAIRTCAEQEGVLTDPVYEGKSMQ
GLIALIKE DYFKPGANVLYVHLGGAPALSAYSSFFPTKTA

>d1jbqa_ c.79.1.1 (A:) Cystathionine beta-synthase {Human (*Homo sapiens*)}
WIRPDAPS RCTWQLGRPASESPHHHTAPAKSPKILPDILKKIGDTPMVRINKIGKKFGLKCELLAKCEFFNAGGSV

KDRISLRMIEDAERDGTLPKGDTII EPTSGNTGIGLALAAVRGYRCIIVMPEKMSSEKVDVLRALGAEIVRPTN
ARFDSPESHVGVAWRLKNEIPNSHILDQYRNASNPLAHYDTTADEILQQCDGKLDMLVASVGTGGTITGIARKL
KEKCPGCRIIGVDPEGSILAEPEELNQTEQTTVEGIGYDFIPTVLDRTVVDKWFKS NDEEAFTFARMLIAQEGL
LCGGSAGSTVAVAVKAAQELQEQQRCVVI LPDSVRNYMTKFLSDRWMLQKGFL

>d1jeoa_ c.80.1.3 (A:) Probable 3-hexulose-6-phosphate isomerase MJ1247 {Archaeon *Methanococcus jannaschii*}
LEELDIVSNNILILKKFYTNDEWKNKLDLSIDRIIKAKKIFIFGVGRSGYIGRCFAMRLMH LGFKSYFVG ETTTPSYE

KDDLLILISGSGRTESVLT VAKKAKNINNNIIAIVCECGNVVEFADLTI PLEVKKSKYLPM GTT FEETALIFLDLVIAEI
MKRNLNLD ESEIIKRHCNLL

>d1moq_ c.80.1.1 (-) "Isomerase domain" of glucosamine 6-phosphate synthase (GLMS) {Escherichia coli}
GDKG IYRH YM QK EY EQPNAIKNLTGRISHGQV DLSELGPNADELLSKVEHIQILACGT SYNSGMV SRYWFESL

AGIPCDV EIASEF RYR KSA VRN SLM ITLSQSGETADT LAGLRLS KELGYLGSLAICNV PGSS LVRES DLA M TNA
GTEIGVASTKAFTTQLTVLLMLVAKLSRLKG LDASIEHDIVHGLQALPSRIEQMLSQDKRIE ALAEDFSDKHHALFL
GRGDQYPIALEGALKLKEISYIHA EAYAAGE LKHGPLA LIDADMPV IVVAPN NELLEKLKS NIIE VRARGG QLYVF
ADQDAGFVSSDNM HII EMPH VEEVIAPIFYTVPLQLAYHVALIKGTDVDQPRNLAKSVTVE

>d1g98a_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Rabbit (*Oryctolagus cuniculus*)}
AALTRNPQFQKLQQWHREHGSELNRHLFDTDKERFNHFSLNTNHGHILLDYSKNL VTEVMHM LLDLAKS

RGVEAARESMFNGEKINSTEDRAVLHVALRNRSNTPIVDGKDV MPEV NKVLDKMKAFCQR VRSGD WKG YT
GKTITD VINIGIGGSDLGPMVTEALKPYSSGGPRVWFVSNIDG THIAK TLACLNPESSLIIASKTFTT QETITNAK
TAKDWFLSAKDPSTVAKHFVALSTNTAKVKEFGIDPQNMFE FW DWVGG RYSLWSAIGLSIALHVGFDNFEQL
LSGAHWMDQHFRTT PLEKNAPVLLAMI LGIWIYNCFGCETQAVLPYDQY LHRFAAYFQQGDMESNG KYITKSG
ARVDHQ TGPIVW GEPGTNGQHAFYQ LIHQ GTK MIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMKGKS
TEE ARKELQAAGKSPEDLMKLLPHKV FEGNRPTNSIVFTKLTPFILGALI AMYEHK IFVQGVVWDINSFDQWG V

ELGKQLAKKIEPELDGSSPVTS HD SSTNGLINFIKQQREAK

>d1iata_c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Human (Homo sapiens)}

AALTRDPQFQKLQQWYREHRSENLRRLFANKDRFNHFSLNTNHGHILVDYSKNLVEDVMRMLVDLAKS
RGVEAARERMFNGEKINYTEGRALVALRNRSNTPILDGKDVMPNVKVLDMKSFQVRSGDWKGYT
GKTITDVINIGIGGSQDLGPLMVTEALKPYSSGGPRVWVSNIDGTHIAKTLAQLNPESLIIASKTFTQETITNA
ETAKEWFLQAQKDPASAVAKHFVALSTNTKVKEFGIDPQNMFEFWVGGRYSLSAIGLSIALHVGFDNFE
QLLSGAHWMDQHFRTPLEKNAPVLLALLGIWYINCFCETHAMLPYDQYLHRAAYFQQGDMESNGKYITK
SGTRVDHQTPGIVWGEPGTNGQHAFYQLIHQGTMIPCDFLIPVQTQHPIRKGLHHKILLANFLAQTEALMRG
KSTEEARKELQAAGKSPEDLERLLPHKVFEGRPTNSIVFTKLTDFMLGALVAMYEHKIFVQGIIWDINSFDQWG
VELGKQLAKKIEPELDGSAQVTSHDASTNGLINFIKQQREARV

>d1c7qa_c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Bacillus stearothermophilus}
AISFDYSNALPFMQENELDYLSFVKAAHHMLHERKGPGSDFLGWVWDWPIRYDKNEFSRIKQAAERIRNHSDA
LVVIGIGGSYLGARAAIEALSHTFHQMNDTTQIYFAGQNISSTYISHLLDVLEGKDSLINVISKSGTTPEAIAFR
FRDYM EKKYGKEEAR KRIYVTTDR TKGALKKLADQEGYETFVIPDNIGGRY SVLTAVGLPIAVAGLNIDRMMEG
AASAYHKYNNPDLLNESYQYAA VRN ILYRKGKAI ELLV N YEPS LHYVSEWWKQLFGESEGKDQKGLFPASVDF
TDLHSMGQYVQEGRRLIETVLHVKKPQIELTIQEDPENIDGLNFLAGKTLDEVNKKAFQGTLLAHVDGGVPNL
IVEDEMNEYTFGEMVYFFEKA CGISGHLLGVNPFDQPGVEAYKKNMFALLGKPGFEDEKA ALMKRL

>d1eu1a2 c.81.1.1 (A:4-625) Dimethylsulfoxide reductase (DMSO reductase)
{Rhodobacter sphaeroides}

ANGEVMSGCHWGVFKARVENGRAVAFEPWDKDPAPSHQLPGVLDIYSPTRIKYPMVRREFLEKGVNADRS
TRNGDFVRVTWDEALDLVARELKRVQESYGP GTFGGSYGWKSPGRLHNCQVLMRRALNLAGGFVNSSGD
YSTAAAQIIMPHVMG TLEVYEQQTAWPVVVENTDLMVFWAADPMKTNEIGWVIPDHGAYAGM KALKEKGT
RVIAINPVRTETADYFGADV VSPRPQTDVALMLGMAHTLYSEDLHDKDFLENCTTGFDLFAAYLTGESDGTPKTA
EWAAEICGLPAEQIRELARSFVAGRTMLAAGWSIQRMHHGEQAHWMLVTLASMIQIGLPGGGFGLSYHYS
NGGSPTSDGPALGGISDGGKAVEGA AWLSESGATSIPCARVVDMLLNPGGEFQNGATATYPDVKLA WAGG
NPFAHHQDRNRMLKAWE KLET FIVQDFQWTATARHADIVLPATT SYERNDIESVG DYSNRAILAMKKVVDPL
EARS DYDIFAALAERLGKGA EFT EG RDEM GWI SSFYEA AVKQAE FKNVAMP SFED FWSE GI EFPITEGANF
YADFREDPLFNPLGTPSGLIEIYSK NIEKMGYDDCPA HPTW M EPA

>d1dmr_2 c.81.1.1 (3-625) Dimethylsulfoxide reductase (DMSO reductase) {Rhodobacter capsulatus}

LANGTVMSGSHWGVTATVENGRATAFTPWEKDPHPSPMLAGVLDIYSPTRIKYPMVRREFLEKGVNADRS
TRNGDFVRVSWDQALDLVAAEVKRVEETYPEGVFGGSYGWKSPGRLHNCQVLMRRMLTLAGGYVNGAGD
YSTGAAQVIMPHVVGTLEVYEQQTAWPVLAENTE VMVFWAADPIKTSQIGWVPIEHGAYPGLEALKAKGT
VIDPVRTKTVEFFGAEHITPKPQTDVAIMLGMAHTLVAEDLYDKDFIANYTSGFDKFLPYLDGETDSTPKTA
EGISGVPAETIKELARLFESKRTMLAAGWSMQRMHGEQAHWMLVTLASMLGQIGLPGGGFGLSYHSGGG
TPSTSGPALAGITDGGATKGPEWLAASGASVIPVARVDMILENPGAEFD FNGTRSKFPDV KMAYWVGGNPF
VHHQDRNRMVKAWEKLET FVHD FQWT TARHADIVLPATT SYERNDIETIGDYSNTGILAMKKIVEPLYEARS
DYDIFA AVAERLGKGA EFT EG KDEM GWI SKFYDDA AKQGKAAGVQMPA FDFWAEGI EFPV TDGAD FV
SFREDPLLNPLGTPTGLIEIYSK NIEKMGYDDCPA HPTW M EPA

>d1aa6_2 c.81.1.1 (1-564) Formate dehydrogenase H {Escherichia coli}

MKKVVTVCPCASGCKINLVVDNGKIVRAEAAQGKTNQGTLC LGYYGWFINDTQILT PRLKTPMIRRQRGG
KLEPVSWDEALNYVAERLSAIKEK YGPDAI QTGSSRG TGNET NYV MQKFARAVIGTNNVDC CARVCHGPSVA
GLHQSVNGAMSNAINEIDNTLVFVFGYNPADSHPIVANHVINAKRNGAKIIVCDPRKIETARIADMHIALKN
GSNIA LLNAMGHVII ENLYDKAFVASRTEGFEYRKIVEGYTPESV EDITGV SASEIRQA ARMYA QAKSA AILWG

MGVTQFYQGVETVRSLSLAMLTGNLGPAGVNPRGQNNVQGACDMGALPDYPGYQYVKDPANREKF
AKAWGVESLPAHTGYRISELPRAAHGEVRAAYIMGEDPLQTDAELSAVRKAFEDLELVIVQDIFMTKASAAD
VILPSTSWGEHEGVFTAADRGFQRFFKAVEPKWDLKTDWQIISEIATRMGYPMHYNNTQEIWDELRLHLCPDFY
GATYEKMGEGLFIQWPCRDTSDADQGTSYLFKEKFDTPNGLAQFFTCDWVA

>d1tmo_2 c.81.1.1 (5-631) Trimethylamine N-oxide reductase {Shewanella massilia}

NEDEWLTGSHFGAFKMKRKNGVIAEVKPFDLKYPTDMINGIRGMVYNPSRVRYPMVRLDFLKGHSNTH
QRGDFRFVRTWDKALTFLKHSDEVQTQYGPSGLHAGQTGWRATGQLHSSTSHMQRAVMHGNYVKKIG
DYSTGAGQTILPYVLGSTEVYAQGTSWPLILEHSDTIVLWSNDPYKNLQVGWNAETHESFAYLAQLKEKVKGK
IRVISIDPVVTKTQAYLGCEQLYVNPQTDVTMLAIAHEMISKLYDDKFIQGYSLGFEEFPYVMGTDGVAKTP
EWAAPICGVEAHVIRDLAKTLVKGRTQFMMGWCIQRQQHGEQPYWMAAVLATMIGQIGLPGGGISYGHY
SSIGVPSSGAAAPGAFPRNLDENQKPLFDSSDFKGASSTIPVARWIDAILEPGKTIDANGSKVVYPDIKMMIFSG
NNPWNHHQDRNRMKQAFHKLECVVTVDVNWTATCRFSDIVLPACTTYERNDIDVYGAYANRGILAMQKMV
EPLFDSSLDFEIFTRFAAVLGKEKEYTRNMGEMEWLETLYNECKAANAGKFEMPDFATFWKQGYVHFGDGEV
WTRHADFRNDPEINPLGTPSGLIEIFSRKIDQFGYDDCKGHPTWMEKT

>d1g8ka2 c.81.1.1 (A:4-682) Arsenite oxidase large subunit {Alcaligenes faecalis}
NDRITLPPANAQRTNMTCHFCIVGCGYHVYKWPELEEGGRAPEQNALGLDFRKQLPPLAVTLPAMTNVVTE
HDGARYDIMVVPDKACVVNSGLSSTRGGKMASYMYTPTGDGKERLSAPRLYAADEWVDTTWDHAMALYAG
LIKKTLDKDPQGVFFSCFDHGGAGGGFENTWGTGKLMFSAIQTPMVRIHNPAYNSECHATREMGIGELNN
AYEDAQLADVIWSIGNNPYESQNTYFLNHWLPNLQGATTSKKERFPNENIFPQARIIFVDPRETPSVAIARHVA
GNDRVLHLIAIEPGTDTALFNGLFTYVVEQGWIDKPFIEAHTKGFDAAVTKNRLSDECSENITGVPVDMLKRAAE
WSYKPKASQGQAPRTMHAYEKIIWGNNDNYVIQSALLDLVIATHNVGRGTGCVRMGGHQEGYTRPPYPGDK
KIYIDQELIKGKGRIMTWWGNNFQTSNNAQALREAILQRSIAVKQAMQKARGATTEEMVDVIYEATQNGGL
FVT SINLYPTKLAEAAHMLPAAHPGEMNLTSMNGERRIRLSEKFDPPGTAMADCLIAARIANALRDMYQKD
GKAEMAAQFEGFDWKTEEDAFNDGFRRAQQPGAPAIDSQGGSTGHLVTYDRLRKSGNNGVQLPVVSWDES
KGLVGTEMLYTEGKFDTDDGKAHFKPAPWNG

>d2napa2 c.81.1.1 (A:4-600) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}
RPEKWVKGVCRYCGTGCGLVGVKDGKAVAIQGNPNHHNAGLLCLKSLLIPVLSKERTVQPLVRRHKGKGL
EPVSWDEALDLMASRFRSSIDMYGPNSVAWYGSQCLTEESYVANKIFKGGFTNNVDGNPRLCMASAVGG
YVTSFGKDEPMGTYADIDQATCFFIIGSNTSEAHPVLRRARRKQVEPGVKIIIVADPRRTNTSRIADMHVAFRP
GTDLAFMHMSMAWVIIINEELDNPWFQRYVNFM DAEGKPSDFEGYKAFLENYRPEKVAEICRPVVEQIYGAAR
AFAESAATMSLWCMGINQRVQGVFANNLIHNLHITGQICRPGATSFSLTGQPNA CGGVRDGGALSHLLPAGR
AIPNAKHRAEMEKLWGLPEGRIAPEPGYHTVALFEALGRGDVKCMIICETNPAHTLPNLNKVHKAMSHPESFIV
CIEAFDAVTLEYADLVLPPFWCERDGVYVGCGERRYSLTEKAVDPPGQCRPTVNTLVEFARRAGVDPQLVNFR
NAEDVWNEWRMVSKGTTYDFWMTRERLRKESGLIWPCPSEDHPGTSRLYVRGQDPCVPADHPDRFFFYG
KPDGRAVIWMRPAKG

>d1ad3a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus norvegicus)}
SISDTVKRAREAFNSGKTRSLQFRIQQLEALQRMINENLKSISGALASDLGKNEWTSYYEEVAHVLEELDTTIKE
PDWAEDEPVAKTRQTQQDDLYIHSEPLGVVLVIGAWNYPFNLTIQPMVGAVAAGNAVILKPSEVSGHMADLL
ATLIPQYMDQNLVVKGGVPETTELLKERFDHIMYTGSTAVGKIVMAAAAKHLTPVTLELGGKSPCYVDKDCD
LDVACRRIAWGKFMNSGQTCVAPDYILCDPSIQNQIVEKLKSLKDFYGEDAKQS RDYGRINDRFQRVKGLID
NQKVAHGGTWDQSSRYIAPTILVDVDPQSPVMQEEIFGPVMPIVCVRSLLEAIQFINQREKPLALYVFSNEKVI
KKMIAETSSGGVTANDVIVHITVPTLPFGGVGNNSGMGAYHGKKS FETFSHRRSCLVKSLNNEAHKARYPPSPA
>d1bi9a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (Rattus norvegicus)}, retinal

type II}

MASLQLLPSPTPNLEIKYTKIFINNEWQNSESGRVFPVCNPATGEQVCEVQEADKVDIDKAVQAARLAFLSGV
WRRMDASERGRLLDKLADLVERDRATLATMESLNGGKPFLQAFYIDLQGVIKTLRYAGWADKIHGMTIPVDG
DYFTFTRHEPIVGCGQIIPWNFPLLMFTWKIAPALCCGNTVVIKPAEQTPLSALYMGALIKEAGFPPGVNLPGY
GPTAGAAIASIGIDKIAFTGSTEVGKLIQEAGRSLKRVTLELGGKSPNIIFADADLDYAVEQAHQGVFFNQG
QCCTAGSRIFVEESIYEVFVRSVERAKRIVGSPFDPTTEQGPQIDKKQYNKILELIQSGVAEGAKLECGGKGLGR
KGFFIEPTVFSNVTDMMRIAKEEIFGPVQEILRFKTMDDEVIERANNSDFGLVAAVFTNDINKALMVSSAMQAGT
VWINCYNALNAQSPFGGFMSGNGREMGEFGLREYSEVKTVKIPQKNS

>d1ag8a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Cow (Bos taurus), mitochondrial}

VPTPNQQPEVLYNQIFINNEWHDAVSKTFPTVNPOSTGDVICHVAEGDKADVDRAVKAARAAFQLGSPWRR
MDASERGRLLNRALDLIERDRTYLAALETLDNGKPVIISYLVLDLDMVLKCLRYAGWADKYHGKTIPIDGDYFSYT
RHEPVGVCQIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVNVIPGFGP
AGAAIASHEVDKVAFTGSTEVGHLIQVAAGKSNLKRVTLEIGGKSPNIIMSDADMDWAVEQAHFALFFNQG
QCCCAGSRTFVQEDIYAEFVERSVARAKSRVVGNPFDSTEQGPQVDETQFKVLGYIKSGKEEGLKLLCGGG
AADRGYFIQPTVFGDLQDGMTIAKEEIFGPVMQILKFMSMEVVGRANNSKYGLAAAVFTKDLDKANYLSQAL
QAGTVVVNCYDVFGAQSPFGGYKLSGSGRELGEYGLQAYTEVKTVTVRPQKNS

>d1cw3a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Human (Homo sapiens), mitochondrial}

AVPAPNQQPEVFCNQIFINNEWHDAVSRKTFPTVNPOSTGEVICQVAEGDKEDVDKAVKAARAAFQLGSPWRR
MDASHRGRLLNRLADLIERDRTYLAALETLDNGKPVISYLVLDLDMVLKCLRYAGWADKYHGKTIPIDGDFSY
TRHEPVGVCQIIPWNFPLLMQAWKLGPALATGNVVVMKVAEQTPLTALYVANLIKEAGFPPGVNVIPGFGP
TAGAAIASHEVDKVAFTGSTEIGRVIQVAAGSSNLKRVTLEIGGKSPNIIMSDADMDWAVEQAHFALFFNQG
QCCCAGSRTFVQEDIYDEFVERSVARAKSRVVGNPFDSTEQGPQVDETQFKKILGYINTGKQEGAKLLCGGG
AADRGYFIQPTVFGDVQDGMTIAKEEIFGPVMQILKFKTIEEVVGRANNSTYGLAAAVFTKDLDKANYLSQALQ
AGTVVVNCYDVFGAQSPFGGYKMSGSGRELGEYGLQAYTEVKTVTVKVPQKNS

>d1bxsa_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Sheep (Ovis aries)}

DVPAPLTNLQFKYTKIFINNEWHSSVSGKKFPVFNPATTEKLCEVEEGDKEDVDKAVKAARQAFQIGSPWRTM
DASERGRLLNKADLIERDRLLATMEAMNGGKLFSNAYLMDLGGCIKTLRYCAGWADKIQGRTIPMDGNFFT
YTRSEPVGVCQIIPWNFPLLMFLWKGPAKSCGNTVVVKPAEQTPLTALHMGSLIKEAGFPPGVNVIPGYGP
TAGAAISHMDVDKVAFTGSTEVGKLIKEAGKSNLKRVSLELGGKSPCIVFADADLDNAVEFAHQGVFYHQGQ
CCIAASRLFVEESIYDEFVRSVERAKYVLGNPLTPGSQGPQIDKEQYEKILDIESGKKEGAKLECGGGPWGN
KGYFIQPTVFSVTDDMRIAEEIFGPVQQIMKFKSLDDVIKRANNTFYGLSAGIFTNDIDKAITVSSALQSGTV
WVNCYSVVAQCPFGFKMSGNGRELGEYGFHEYTEVKTVTIKISQKNS

>d1a4sa_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Baltic cod (Gadus callarias)}

AQLVDSMPSASTGSVVVTDDLNYWGGRRIKSKDGTTEPVFEPATGRVLCQMVPAGEEVQAVQSAQAAYL
KWSKMAGIERSRMVLEARIERRDNIAKLEVINGKTITEAEYDIDAAWCQIEYYAGLAPTLSQHQIQLPGGA
FAYTRREPLGVCAGILAWNYPFMIAAWKCAPALACGNAVFKPSPMTPVTGVILAEIFHEAGVPVGLNVVQG
GAETGSSLCHHPNVAKSFTGSVPTGKKVEMSAKTVKHTLELGGKSPLIFKDCELENAVRGALMANFLTQ
GQVCTNGTRVVFVQREIMPQFLEEVVKRTKAIIVVGDPLLTETRMGGLISKPQLDKVLGFVAQAKKEGARVLCGG
EPLTPSDPKLKNGYFMSPCVLDNCRDDMTCKEEIFGPVMSVLPFDTEEEVLQRANNTFGLASGVFTRDISRA
HRVAANLEAGTCYINTYSISPVEVPGGGYKMSGFGRENGQATVDYYSQLKTVIVEMGDVDSL

>d1euha_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Streptococcus mutans}

TKQYKNYVNGEWKLSENEIKIYEPASGAELGSPAMSTEEVVDYVYASAKKAQPAWRALSYIERAAYLHKVADILM

RDKEKIGAILSKEVAKGYKSAVSEVVRTAEIINYAAEGLRMEGEVLEGGSFEEASKKIAVVRRREPVLVLAISPF
NYPVNLAGSKIAPALIAGNVIACKPPTQGSISGLLAEAAEAGLPAGVFNTITGRGSEIGDYIVEHQAVNFINTG
STGIGERIGKMGMRPIMLELGGKDSAIVLEDADLELTAKNIIAGAFGYSQRCTAVKRVLVMESVADELVEKIRE
KVLALTIGNPEDDADITPLIDTKSADYVEGLINDANDKGATALTEIKREGNLICPIFDKVTTDMRLAWEEPFGPVL
PIIRVTSEEAEISNKSEYGLQASIFTNDFPRAFGIAEQLEVGTVHINNKTQRGTDNFPFLGAKKSGAGIQGVKYS
IEAMTTVKSVVFDIK

>d1ez0a_c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Vibrio harveyi}
TDNVFYATNAFTGEALPLAFPVHTEVEVNQAATAAKVARDFRLNNSKRASLLRTIASELEARSDIIARAHLET
ALPEVRLTGEIARTANQLRLFADVVNSGSYHQAIIDTPNPTRAPLPKDIRRQQIALGPVAVFGASNPLAFSAA
GGDTASALAAGCPVIVKGHTAHPGTSQIVAECEQALKQEQLPQAIFTLLQGNQRALGQALVSHPEIKAVGFTGS
VGGGRALFNLAAHERPEPIPFGELGAINPTFIFPSAMRAKADLADQFVASMTMCGQFCFKPGVVFALNTPET
QAFIETAQSLIRQQSPSTLLTPGIRDSYQSQQVSRGSDDGIDVTFSQAESPCVASALFVTSSENWRKHPAEEEIF
GPQSLIVVCENVADMILSLEMILAGSLTATIHATEEDYPQVSQLIPREELIAGRLVFNGLWPTGVEVGYAMVHGPP
YPASTHSASTSVGAEAIHRWL RPVAYQALPESLLPDSLKAENPLEIARAVDGKAA

>d1k75a_c.82.1.2 (A:) L-histidinol dehydrogenase HisD {Escherichia coli}
NTIIDWNSCTAEQQQRQLLMRPAISASESITRTVNDILDNVKARGDEALREYESAKFDKTTVTALKVSAEEIAASER
LSDELKQAMAVAVKNIETFHTAQKLPPVDVETQPGVRCQQVTRPVASVGLYIPGGSAPLFSTVLMLATPASIAGC
KKVVLCSPPIADEIILYAAQLCGVQDVFNVGAQIAALAFGTESVPKVDKIFGPGNAFVTEAKRQVSQRDGA
AIDMPAGPSEVLVIADSGATPDFVASDLSQAEHGPDSQVILLTPAADMARRVAEAVRQLAELPRAETARQAL
NASRLIVTKDLAQCVEISNQYGPHELIQTRNARELVDSITSAGSVFLGDWSPEASAGDYASGTNHVLPTYGYTATC
SSLGLADFQKRMTVQELSKEGFSALASTIETLAAAERLTAHKNAVTLRVNALKEQA

>d1aco_2 c.83.1.1 (2-528) Aconitase, first 3 domains {Cow (Bos taurus)}
RAKVAMSHFEPHEYIRYDLLEKNIDIVRKRLNRPLTLSEKIVYGHLDPPANQEIERGKTYLRLRPDRVAMQDATA
QMAMILQFISSGLPKVAVPSTIHCDSLIEAQQLGGEKDLRRAKDINQEYVNFLATAGAKYGVGFWRPGSGIIHQIIL
ENYAYPGVLLIGTDSHTPNGGLGGICIGVGGADAVVMAGIPWELKCPKIVGVKLTGSLSGWTSPKDVLKVA
GILTVKGGTGAIVEYHGPVDSISCTGMATICNMGAEGATTSPYNNHRMKKYLSKTGRADIANLADEFKDHL
VPDSGCHYDQLEINLSELKPHINGPFTPDLAHPVAEVGSVAEKEGWPLDIRVGLIGSCTNSSYEDMGRSAAVAK
QALAHGLKCKSQFTITPGSEQIRATIERDGYAQVLRDVGIVLANACGPCIGQWDRKDIKGEKNTIVTSYNRNF
TGRNDANPETHAFVTSPEIVTALAIAGTLKFNPETDFLTGKDGFKKLEAPDAELPRAEFDPGQDTYQHPPKDS
SGQR

>d3pmga1 c.84.1.1 (A:1-190) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}
VKIVTVKTKAYPDQPGTSGLRKRVKFQSSNTYAENFIQSIISTVEPAQRQEATLVVGGDGRFYMKEAIQLIVRI
AAANGIGRLVIGQNGILSTPAVSCIIRKIKAIIGGIILTASHNPGGNGDFGIKFNISNGGPAPEAITDKIFQISKTIEEY
AICPDLKVDLGVLGKQQFDLENKFKPFTVEIVDS

>d3pmga2 c.84.1.1 (A:191-303) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

VEAYATMLRNIFDFNALKELLSGPNRLKIRIDAMHGVVGPYVKKILCEELGAPANSANCVPLEDFGGHHPDPN
LTYAADLVTMKSGEHDFGAADFDDGDRNMLGKHGFFV

>d3pmga3 c.84.1.1 (A:304-420) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}

NPSDSVAVIAANIFSIPYFQQTGVRGFARSMPTEGALDRVANATKIALYETPTGWKFFGNLMDASKLSCGEESF
GTGSDHIREKDGLWAVLAWLSILATRKQSVEDILKDHWHKFG

>d1kfia1 c.84.1.1 (A:3-205) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

QVIPAPRVQVTQPYAGQKPGTSLRKKVSEATQPNYLENFVQSIFNTRKDELKPKNVLVGGDGRYFNRQAIF
SIIRLAYANDISEVHVGQAGLMSTPASSHYIRKVNEEVNCIGGIILTASHNPGGKEHGDFGIKFNVRTGAPAPED
FTDQIYTHTTKIKEYLTVDYEFEKHINLDQIGVYKFGTRLEKSHFEVKVVDT
>d1kfia2 c.84.1.1 (A:206-323) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}
VQDYTQLMQKLFDLKLGLFSNKDFSFRFDGMHGVAAGPYAKHIFGTLLGCSKESLLNCDPSEDFGGGHPDPN
LTYAHDLVELLDIHKKKDVGTVQFGAACDGDADRNMILGRQFFV
>d1kfia3 c.84.1.1 (A:324-443) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}
TPSDSLAVIAANANLIFKNGLGAARSMPTSGALDKVAAKNGIKLFETPTGWKFFGNLMDAGLINLCGEESFGT
GSNHIREKDGIVAWLTLAHKNNTDHFVTVEEVTQYWQQFG
>d1k2yx1 c.84.1.1 (X:5-154) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}
KAPTLPASIFRAYDIRGVVVGDTLTAETAYWIGRAIGSES LARGEPVC AVGRDGRLSGP ELVKQLIQGLVDCGCQVS
DVGMVPTPVLYAANVLEGKSGVMLTGAHNPPDYNFKIVVAGETLANEQIQLRERIEKNDLASGVGSVEQV
D
>d1k2yx2 c.84.1.1 (X:155-258) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}
ILPRYFKQIRDDIAMAKPMKVVVDCGNGVAGVIAPQLIEALGCSVIPYCEVDGNFPNHHPDPGK PENLKDLIA
KVKAENADLGLAFDGDGDRGVVVTNTGTII
>d1k2yx3 c.84.1.1 (X:259-367) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}
YPDRLLLMFAKDV VSRNPGADI FDVKCTRRLIALISGYGGRPV MWKTGHSLIKKKMKG ELAGEMSGHVFF
KERWFGFDDGIYSAARLLEILSQDQRDSEHVFSAF
>d1k2yx4 c.84.1.1 (X:368-463) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}
PSDISTPEINITVTE SKFAII EALQRDAQW GEGNIT TLDGV RV DYPKG WGLVRAS NTTPV LRF EA DTEEELERI
KTVFRNQLKAVDSSL PVF
>d1fua2 c.85.1.1 (A:1-355) L-fucose isomerase, N-terminal and second domains {Escherichia coli}
MKKISLPKIGIRPVIDGRRMGVRESLEEQT MNMAKATAALLTEKLRHACGA AVECVIS DTCIAGMAAAACEEK
FSSQNVGLTITVTPCWCYGSETIDMDPTRPKAIWGFGNTERPGAVYLA AALAAHSQKGIPAFSIYGH DVQDAD
DTSIPADVEE KLLRFARAGLAVASMKGKSYLSGGVSMGIAGSIVDHNFFESWLGMKVQAVDMTELRRRIDQKI
YDEAELEMALAWADKNFRYGEDENN KQYQRNAE QSR A VLRES LLMAM CIRDMMQGNSKLADIGRVE ESLG
NAIAAGFQGQRHWTDQY PNGDTAE AILN SSFDWNGVREPFVV ATENDS LNGVAML GHQLTGT
>d1fw8a_ c.86.1.1 (A:) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}
SKYSLAPVAKELQSLLGKDV TLN DCVGPEVEAAV KASAPG SVILLE NRYHIEEGSRKVDGQ KV KASKEDVQK
FRHE LSSLA DVYINDA FGTA HRAHSSMVGF DLPQ RAGFL EKEL KYFG KALEN P TRPFL A I LGGAKVAD KIQLID
NL LDKVDSI IGGGMAFT FKKVLEN TEI GD SIF DKAG AEIVPKLMEKA KAGV E VVLPVDFI IADAFSADANTKTV
TDKE GIPAGWQGLDNGPESRKLFAATVAKAKTIVWNGPPGV FEFK FAAGT KALLDEVK SSAAGNTVIIGGG
DTATVAKKYGVTDKISHVSTGGGASLELLEGKELPGV AFLSEKKS LSSKLSVQD DLKDKR VFIRVDFN VP LDGKKI
TSNQRIV AALPTIKYV LEHHPRYVV LASHL GRPNGERN
>d1qpg_ c.86.1.1 (-) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SLSSKLSVQDSDLKD KR V FIR V DF N VPL DG K KITSN Q R IVA AL P T I KY V LE HH P R Y V VLASHLGQPNGERNEK Y S L APVAKELQSLLGKDVTFLNDCVGPEVEAAVKASAPGSVILLENLYHIEEGSRKV D GQ KV KASKEDVQKFRHEL
SSLADVYINDAFGT ARAHSSMVGFDLPQRAAGFLLEKELKYFGKALENPTRPFLAILGGAKVADKIQ LIDNLLD
KVDSIIIGGGMAFTKKVLENTEIGDSIFDKAGAEIVPKLMEKA KAGVEVVL PVDI IADAFSADANTKTVTDKE
GIPAGWQGLDNGPESRKLFAATVAKAKTIVWNGPPGV FEF EKFAAGTKALLDEVVKSSAAGNTVIIGGGDTATV
AKKYGVTDKISHVSTGGGASLELEGKELPGVAFLSEKK

>d1php_ c.86.1.1 (-) Phosphoglycerate kinase {Bacillus stearothermophilus}
MNKKTIRDVDVRGKRVFCRDFNVPMEQGAITDDTRIRALPTIRYLIEHGAKVILASHLGRPKGKVVEELRLDA
VAKRLGELLERPVAKTNEAVGDEVKAAVDRNLNEG D VLLLEN VRFYPGEEKNDPELA K AFA ELADLYVNDAFGAA
HRAHASTEGIAHYLPAVAGFLMEKELEV LGKALSNPDRPFTAIGGAKVKDKIGVIDNLLEKVDNLIIGGGLAYTFV
KALGH DVGKS LLEEDKIELAKSFMEKAKEKG VRFYMPDV VVADR FANDANTKVVPI DAI PADWSALD IGP KTR
ELYRDVIRESKLVVWNGPMGVFEMDAFAHGTKAIAEALAEALDTYSVIGGGDSAAA VEV KGLADKMDHISTGG
GASLEFM EGKQLPGVVALEDK

>d1vpe_ c.86.1.1 (-) Phosphoglycerate kinase {Thermotoga maritima}
EKMTIRDVDLKGKRVIMRVDFNVPVKNGKITNDYRIRSA PLTLKKVLT EGGSCVLM SHLGRPKGEPSP EF SLAPV
AKRLSELLGKEVKFVPAVG D E V K K A V E E L K E G E V L L E N T R F H P G E T K N D P E L A K F W A S L A D I H V N D A F G T A H
RAHASNVGIAQFIPSVAGFLMEKEIKFLSKV TYNPEKPYVVVLGGAKVSDKIGVITNLMEKADRILIGGAMMFT
LKALGKEVGSSRVEEDKIDLAKELVEKAKEKG VEVLPVDAVIAQKIEPGV EKKVVRDDGIP EGWMGL DIGPETI
ELFKQKLSDAKTVVWNGPMGVFEIDDFAEGTKQVALAIAALTEKGAITV VGGGD SAAA VNKFGLEDKF SHV ST
GGGASLEFLEGKELPGIASMR IKKA

>d16pk_ c.86.1.1 (-) Phosphoglycerate kinase {Trypanosoma brucei}
EKKSINECDLKGKKVLRVDFNVPVKNGKITNDYRIRSA PLTLKKVLT EGGSCVLM SHLGRPKGIPMAQAGKIRST
GGVPGFQQKATLKPVAKRLSELLRPVT FAPDCLNAADV VSKMSPGDVVLLEN VRFYKEEGSKKAKDREAMAK
ILASYGDVYISDAFGTAHRDSATMTGIPKILGNGAAGYLMEKEISYFAKVLGNPPRPLVAI VGGAKVSDKIQLLDN
MLQRIDYLLIGGAMAYTFLKAQGYSIGKSCEESKLEFARSLLKAEDRKVQVILPIDHVCHTEFKAVD SPLITEDQ
NIPEGHMA LDIGPKTIEKYVQTIGCKCSAIWNGPMGVFEMVPYSKGTFAIAKAMGRGTHEHGLMSIIGGGDSA
SAAELSGEAKRM SHVSTGGGASLELEGKTLPGVTVLDDK

>d1hdia_ c.86.1.1 (A:) Phosphoglycerate kinase {Pig (Sus scrofa)}
NKLTLKLNVKGKR VVM RVDFNVPMAAAQITNNARIKA AVPSIKFCL DDGAKSVVLM SHLGRPDGSPMPD KY
SLQPVAELKSALGKAVLFLKDCVGP AVEKACADPAAGSVILLE NLRHVEEGKGKDASGNKAAGEPAKIAFR
ASLSALGDVYVND AFGTAHRAHSSMVG VNLPKKAGAFLMKKELNYFAAAAESPERPFLAILGGAKVADKIQ LIN
NMILDKVNEMIIGGGMAFTFLKVLNNMEIGTSLFDEAGKKIVKNLMSKAAANGVKITLPDFVTADKFDEQAKI
GQATVASGIPAGWMGLDCGPKSSAKYSEA VARAKQIVWNGPVG VFEWEAFAQGT KALMDEVVKATSRCITI
IGGGDTATCCA KWN TEDNVSHVSTGGGASLELEGKVLPGVDALSNV

>d1jixa_ c.87.1.1 (A:) beta-Glucosyltransferase (DNA-modifying) {Bacteriophage T4}
MKIAIINMGNNVINFKTVPSSETIYLFKVI SEMGLNVDIISLKG VYT KSF DEV D VNDYDRLIVV NSSINFFGGKP
NLAI LS AQKFMAKYKSKIYLFDTIRLPFSQS WP NVKNRPWAYLYTEEELIKSPIKVISQGINLDIAAHKKVDN
VIEFEYFP IEQYKIH MNDFQLSKPTK TLDVYGG SFRSGQRES KMVEFLDTGLNIEFFGNAREKQFKNPKYPW
TKAPVFTG KIPM NMVSEKNSQAIAALIIGDKNYNDNFITLRVWETMASDAVMLIDE FDTKHRIINDARFYVN
NRAELIDRVNELKHS DVLRK EM LSIQHDILNKTRAKKA E WQDAFKAIDL

>d1f0ka_ c.87.1.2 (A:) Peptidoglycan biosynthesys glycosyltransferase
MurG {Escherichia coli}
KRLMV MAGGTGGHVF PG LAVAHH LMAQGWQVRWL GTADRMEADL VP K H GIEIDFIRISGLRGKG I KALIAA
PLRIFNAWRQARAIMKAYKPDVVLGMGGYVSGPGGLAAWSLGIPVVLHEQNGIAGLTNKWLAKIATKVMQA

FPGAFPNAEVVGNPVRTDVLALPLPQQQLAGREGPVRVLVGGSGARILNQTMPQVAAKLGDSVTIWHQS
GKGSQSQVEQAYAEAGQPQHKVTEFIDDMAAAYAWADVVVCRSGALTSEIAAGLPALFVPFQHKDRQQY
WNALPLEKAGAAKIIEQPQLSVDAVANTLAGWSRELLTMAERARAASIPDATERVANEVSRVARAL
>d1f6da_ c.87.1.3 (A:) UDP-N-acetylglucosamine 2-epimerase {Escherichia coli}
MKVLTIVFGTRPEAKMAPLHALAKDPFEAKCVTAQHREMLDQVLKLFISIVPDYDLNIMQPGQGLTEITCRIL
EGLKPILAEFKPDVVLVHGDTTTLATSLAAFYQRIPVGHVEAGLRTGDLYSPWPEEANRTLGHAMYHFSPT
TSRQNLLRENVADSRIFITGNTVIDALLWVRDQMSSDKLSELANYFIDPDKKMILVTGHRRESFGRGFEI
CHALADIATTHQDIQIVYPVHLNPNVREPVNRLGHVKNVILIDPQEYLPFWLMNHAWLILTDGGIQEEAPSL
GKPVLVMDRTERPEAVTAGTVRLVGTDKQRIVEEVTRLKDENEYQAMSRAHNPyGDGQACSRILEALKNNR
ISL

>d1iira_ c.87.1.5 (A:) UDP-glucosyltransferase GtfB {Amycolatopsis orientalis}
MRVLLATCGSRGDTEPLVALAVRVRDLGADVRMCAPPDAERLAEGVPHVPGPSARAPIQRAKPLTAEDVR
RFTTEAIATQFDEIPAAAEGCAAVTTGLAAAIGVRSVAEKLGIPIFYAFHCPSYVSPYPPPLGEPESTQDTIDI
PAQWERNNQSAYQRYGGLLNSHRDAIGLPPVEDIFTFGYTDHPWVAADPVLAQPTDLDAVQTGAWILPDE
RPLSPELAFLDAGPPPVLGFGLGAPADAVRAIDAIRAHGRRVILSRGWADLVLPPDGADCFAIGEVNHQV
LFGRVAAVIHGGAGTTHVAARAGAPQILLPMADQPYYAGRVAELGVGVAHDGPIPTFDLSAALATALTPET
HARATAVAGTIRTGAAVAARLLDAVSRE

>d1em6a_ c.87.1.4 (A:) Glycogen phosphorylase {Human (Homo sapiens)}
ENVAELKKSFRHLHFTLVKDRNVATTRDYYFALAHTVRDHVLGRWIRTQQHYYDKCPKRVYYLSLEFYMGRTL
QNTMINGLQNAACDEAIYQLGLDIEELEEIFEDAGLNGNGGLGRLAACFLDSMATLGLAAYGYGIRYEGIFNQKIR
DGWQVEEADDWLRYGNPWEKSPEFMLPVHFYKVEHTNTGKWIDTQVVLALPYDTPVPGYMNNVTNT
MRLWSRAPNDFNLRDFNVGDDYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQEYFVVAATLQDIIRRFKASK
FGSTRGAGTVFDAFPDQVAIQLNDTHPALAIPLEMRIVDIEKLPSKAWELTQKTFAYTNHTVLPEALERWPV
DLVEKLLPRHLEIYYEINQKHLDIVALFPKDVRLLRMSLIEEGSKRINMAHLCIVGSHAVNGVAKIHSIVKTK
VFKDFSELEPDFQNKNTNGITPRRWLLLNPGLAELIAEKIGEDYVKDSLSQLTKLHSFLGDDVFLRELAKVKQENK
LKFSQFLETEYKVKNPSSMFVDVQVKRIHEYKRQLLNCLHVITMYNRIKKDPKKLFPRTVIIGGKAAPGYHMAK
MIIKLITSVADVNNNDPMVGSKLVIFLENYRVSLAEKVIPATDLSEQISTAGTEASGTGNMKFMLNGALTIGTM
DGANVEMAEAGEENLFIFGMRIDDVAAALKGYEAKEYEALPELKLVIDQIDNGFFSPKQPDFKDIINMLFY
HDRFKVFADYEAYVKCQDKVSQLYMNPKAWNTMVLKNIAASGKFSSDRTIKEYAQNIWNVEPS

>d1a8i_ c.87.1.4 (-) Glycogen phosphorylase {Rabbit (Oryctolagus cuniculus)}
QEKRKQISVRGLAGVENVTELKKNFNRHLHFTLVKDRNVATPRDYFYFALAHTVRDHVLGRWIRTQQHYYEKDP
KRIYYLSLEFYMGRTLQNTMVNLALENACDEATYQLGLDMEELEEIEEDAGLNGNGGLGRLAACFLDSMATLGLA
AYGYGIRYEGIFNQKICGGWQMEEADDWLRYGNPWEKARPEFTLPVHFYGRVEHTSQGAKWVDTQVVL
MPYDTPVPGYRNNVVNTMRLWSAKPNDFNLKDFNVGGYIQAVLDRNLAENISRVLYPNDNFFEGKELRLKQ
EYFVVAATLQDIIRRFKSSKFGCRDPVRTNFDAPDKVAIQLNDTHPSLAIPELMRVLVDLERLDWDKAWEVTVK
TCAYTNHTVIPEALERWPVHLLETLPRHLQIYEINQRFLNRVAAAFPGDVRLLRMSLVEEGAVKRINMAHLC
IAGSHAVNGVARIHSEILKKTIFKDFYELEPHKFQNKTNGITPRRWVLVLCNPGLAEIIAERIGEEYISLDQLRKLLS
YVDDEAFIRDVAKVKQENKLKFAAYLEREYKVHINPNSLFDVQVKRIHEYKRQLLNCLHVITLYNRIKEPNKFV
PRTVMIGGKAAPGYHMAKMIKLITAIGDVVNHDPPVGDRRLRIVIFLENYRVSLAEKVIPAAIDLSEQISTAGTEAS
GTGNMKFMLNGALTIGTMDGANVEMAEAGEENFFIFGMRVEDVDRLLDQRGYNAQEYDRIPELRQIEQLS
SGFFSPKQPDFKDIVNMLMHDRFKVFADYEYVKCQERSALYKNPREWTRMVRNIATSGKFSSDRTIAQY
AREIWGVVEPSRQRLP

>d1ygpa_ c.87.1.4 (A:) Glycogen phosphorylase {Baker's yeast (Saccharomyces cerevisiae)}

TRRLTGFLPQEIKSIDTMIPPLSRALWNKHQVKKFNAEDFQDRRIDHVETTLARSLYNCDDMVAYEAASMSIRD
NLVIDWNKTQQKFTTRDPKRVYLYSLEFLMGRALDNALINMKIEDPEDPAASKGKPREMIKGALDELGFKLEDV
LDQEPDAGLNGNGLGRLAACFVDSMATEGIPAWGYGLRYEYGIFAQKIIDGYQVETPDYWLNNSGNPWEIERNE
VQIPVTFYGYVDRPEGGKTTLSASQWIGGERVLAVAYDFPVPGFKTSNVNNRLWQARPTEFDLNKFNNGDY
KNSVAQQQRAESITAVLVPNDNFAQGKELRLKQQYFWCAASLHDILRRFKKSKRWPTEFPDQVAIQLNDTHPTL
AIVELQRVLVDLEKLDWHEAWDIVTKTFAYTNHTVMQEALEKWPRLFGHLLPRHLEIYDINWFFLEDVAKKF
PKDVLSSRISIIEENSPERQIRMAFLAIVGSHKVNGVVELHSELIKTTIFKDFIKFYGPSKFVNVTNGITPRRWLKQ
ANPSLAKLISETLNDPTEEYLLDMAKLTLQLEKYVEDKEFLKKWNQVKLNNKIRLVDLIKKENDGVDIINREYDDT
LFDMQVKRIHEYKRQQLNVFGIYRYLAMIKNMLKNGASIEEVARKYPRKVSIFGGKSAPGYYMAKLIKLINCA
DIVNNDESIEHLLKVVVFADYNVSKAEIIIPASDLSEHISTAGTEASGTSNMKFVMNGGLIIGTVGANVEITREIG
EDNVFLFGNLSENVEELRYNHQYHPQDLPSSLDVSYIESGQFSPEPNFEPKPLVDSIKYHGDYLVSDDFESYL
ATHELVDQEFHNQRSEWLKSVSLANVGFFSSDRCIEEYSDTIWNVEPVT

>d1qm5a_c.87.1.4 (A:) Maltodextrin phosphorylase (MALP) {Escherichia coli}

SQPIFNDKQFQEALSRQWQRYGLNSAAEMTPRQWWLAVSEALAEMLRAQPFAKPVANQRHVNYISMEFLIG
RLTGNLLNLGKYQDVQDSLKAYDINLTDLEEEIDPALGNGGLGRLAACFLDSMATVGQSATGYGLNYQYGLF
RQSFVDGKQVEAPDDWHRSNYPWFRHNEALDVQVGIGGKVTKDRWEPEFTITGQAWDLPVVGYRNGVA
QPLRLWQATHAHPFDLTNFNDGFLRAEQQQGINAEKLTKVLYPNDNHTAGKKLRLMQQYFQCACSVADILRRH
HLAGRKLHELADYEVIQLNDTHPTIAPELLRVLIDEHQMSWDDAWITSKTFAYTNHTLMPEALERWDVKLVK
GLLPRHMQIINEINTRFKTLVEKTWPGDEKVWAKLAVVHDQVHMANLCVVGGAFAVNGVAALHSDLVVKDLF
PEYHQLWPNKFHNTNGITPWRWIKQCNPALAALLDKSLQEWANDLDQLINLEKFADDAKFRDQYREIKQAN
KVRLAEFKVRTGIEINPQAIFDIQIKRLHEYKRQHLLNLLHILALYKEIRENPQADRVPRVFLFGAKAAPGYYLAKN
IIFAINKVADVINNDPLVGDKLKVFLPDYCVAEEKLIPEADISEQISTAGKEASGTGNMKLALNGALTVGTLDG
ANVEIAEKVGEENIFIFGHTVEQVKAILAKGYDPVKWRKKDKVLDVLKELESGKYSQGDKHAFDQMLHSIGKQ
GGDPYLVMMADFAAYVEAQKQDVLYRDQEAWTRAAILNTARCGMFSSDRSIRDYQARIWQAKR

>d4ecaa_c.88.1.1 (A:) Asparaginase type II {Escherichia coli}

LPNITILATGGTIAGGGDSATKSNTVGVGVENLVNAVPLKDIANVKGEQVNVNIGSQDMNDNVWLTAKKI
NTDCDKTDGFVITHGVDTMEETAYFLDLTVKCDKPVVMVGAMRPSTSMSADGPFNLYNAVTAADKASANR
GVLVMMNDTVLDGRDVTKTNTTDVATFKSVNYGPLGYIHNGKIDYQRT PARKHTSDTPFDVSKLNELPKVGIVY
NYANASDLPKALVDAGYDGIVSAGVGNGLYKSFDTLATAAKTGTAVVRSSRVPTGATTQDAEVDDAKYGFV
ASGTLNPQKARVLLQLALTQTKDPQQIQQIFNQY

>d1wsaa_c.88.1.1 (A:) Asparaginase type II {Wolinella succinogenes}

KPQVTILATGGTIAGSGESSVKSSYSAAGAVTVDKLLAAVPAINDLATIKGEQISSIGSQEMTGKVWLKLAKRVNEL
LAQKETEAVIITHGTDTMEETAFFNLTVKSQKPVVLVGAMRPGSSMSADGPMNLYNAVVAINKASTNKGVV
IVMNDEIHAAREATKLNTTAVNAFASPNTGKIGTVYYGKVEYFTQSVRPTHASEFDISKIEELPRVDILYAHPPDT
DVLVNAALQAGAKGIIHAGMGNGNPFLTQNALEKAAKSGVVVARSSRVSGSTTQEAEVDDKKLGFBATESL
NPQKARVLLMLALTSDREAIQKIFSTY

>d1jsra_c.88.1.1 (A:) Asparaginase type II {Erwinia chrysanthemi}

LPNIVILATGGTIAGSAATGTQTTGYKAGALGVDTLINAVPEVKKLANVKGEQFSNMASENMTGDVVLKLSQRV
NELLARDDVGVVITHGTDTVEESAYFLHLTVKSDKPVVFVAAMRPATAISADGPMNLLAEVRVAGDKQSRGR
GVMVVINDRIGSARYITKTNASTLDTFRANEEGYLGVIIGNRIYYQNRIDKLHTRSVFDVRLTSPLKVDILYGYQ
DDPEYLYDAAIQHGKGIVYAGMGAGSVVRGIAGMRKALEKGVVVMRSTRTGNGIVPPDEELPLGLVSDSLNP
AHARILLMLALTRSDPKVIQEYFHTY

>d1agx_c.88.1.1 (-) Glutaminase-asparaginase {Acinetobacter glutaminasificans}

KNNVVIVATGGTIAGAGASSTSNTSATYSAAKVPVDALIKAVPQVNDLANITGIQALQVASESITDKELLSLARQVN

DLVKKPSVNGVVITHGTDMEETAFFLNLVHTDKPIVLGSMRPSTALSADGPLNLYSAVALASSNEAKNKGV
MVLMNDSIFAARDVTKGINIHTHAFVSQW GALGTLEVKPYWFRSSVKKHTNNSEF NIEKIQGDALPGVQIVY
GSDNMMPDAYQAFAKAGVKAIHAGTGNGS MANYLVPEVRKLHDEQGLQIVRSSRVAQGFVLRNAEQPDDK
YGWIAAHDLNPQKARLLMALALTKTNDAKEIQNMFWNY

>d4pgaa_c.88.1.1 (A:) Glutaminase-asparaginase {Pseudomonas sp., 7A}

KLANVVILATGGTIAGAGASAANSATYQA AKVGVDKLIAGVPELADLANVRGEQVMQIASESITNDLLKGKR
VAELADSNDVDGIVITHGTDLEETAYFLNLVQKTDKPIVVVGSMRPGTAMSADGMLNLYNAVASNKDSRG
KGVLVTMND EIQSGRDVS KSINIKTEAFKSAWGPLGMVVEGKS YWFRLPAKRHTVNSEFDIKQISSLPQVDIAYS
YGNVTDAYKALAQN GAKALI HAGTGNGSVSSRVPALQQLRKNGTQI RSSHVNQGGFVLRNAEQPDDKND
WVVAHDLNPEKARILAMVAMTKTQDSKELQRIFWEY

>d1pfka_c.89.1.1 (A:) Phosphofructokinase {Escherichia coli}

MIKKIGVLTSGGDAPGMNAAIRGVVRSALTEGLEVMGIYDGYLGLYEDRMVQLDRYSVSDMINRGGTFLGSAR
FPEFRDENIRAVAIENLKKRGIDALV VIGGDGSYMGAMRLTEMGFPCIGLPTIDNDIKGTDYTIGFTALSTVVE
AIDRLRDTSSHQRISVVEVMGRYCGDLTAAA IAGGCEFVVVPEVEFSRE DLVNEIKAGIAKGKKHAIVAITEHM
CDVDELAHFIEKETGRETRATVLGH IQRGGSPTVYDRILASRMGAYAIDL LLAGYGGRCVGIQNEQLVHHDIDAI
ENMKRPFKGDWLDCAKKLY

>d3pfk_c.89.1.1 (-) Phosphofructokinase {Bacillus stearothermophilus}
MKRIGVLTSGGDSPGMNAAIRSVVRKAIYHGVEVYGVYHGYAGLIAGNIKLEVGDVGDIIHRGGTILYTCPE
FKTEEGQKKGIEQLKKHGIQGLV VIGGDGSYQGAKKLTEHGFPCVGVP GTIDNDIPGTDFTIGFDTALNTVIDAID
KIRD TATSHERTYVIEVMGRHAGDIALWSGLAGGAETI LIPEADYDMNDVIARLKRGHERGKKHSIIVAEGVGS
GVDFGRQI QEATGFETR VTVLGHVQRGGSPTAFDRV LASRLGARAVELLLEGKGGRCVGIQNNQLVDHDIAEAL
ANKHTIDQRMYALSKELSI

>d1cbf_c.90.1.1 (-) Cobalt precorrin-4 methyltransferase CbiF {Bacillus megaterium}

GLVPRGSHMKLYIIGAGPGDPDLTVKGLKLLQQADVVLYADSLVSQD LIAKS KPGAEVLKTAGMHEEMVGT M
LDRMREGK MVVRVHTGDPAMYGAIMEQM VLLKREGVDIEIVPGVTSVFAAAAAAE AELTIPDLTQTVILTRA E
GRTPVPEFEK LTD LAKHKCTIALFLSSTL KKVMKEFINAGWSE DTPVVVYKATWPDEKIVRTTVKDLDAM R
TNGIRKQAMILAGWALDP

>d1i74a_c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase
(family II) {Streptococcus mutans}

SKILVFGHQNPDSAIGSSMAYAYLKRQLGVDAQVALGNPNEETAFVLDYFGIQAPPVVKSAQAEGAKQVILT
DHNEFQQSIADIREVEVVEVVDHHRVANFETANPL YMRLEPVGSASSIVR LYKENGVAIPKEAGVMLS GLISD
TLLKSP THASDPAVAEDLAKIAGV DLQEYGLAMLKAGTNLASKTA AQLVDIDAKTFELNGSQVRVAQVNTVDI
NEVLERQNEIEEA IKASQAANGY SDFVLMITDILNSNSEILA GSNMDKVEAFNFTLKN NHAFLAGAVSRKKQV
VPQLTESFNG

>d1k20a_c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase
(family II) {Streptococcus gordonii}

SKILVFGHQNPDSAIGSSYAFAYLAREAYGLTEAVALGEPNEETAFVLDYFGVAAPRVITS AKAEGAEQVILTDH
NEFQQSVADIAEVEVYGVVDHHRVANFETANPL YMRLEPVGSASSIVR MFKEHSV AVSK EAGL MSLG LISDTL
LLKSP THPTDKAIAP ELAELAGVNLEEYGLAMLKAGTNLASKSAEELIDIDAKTFELNGNNVRVAQVNTVDIAE
VLERQAEIEAAIEKAIADNGY SDFVLMITDILNSNSEILA GSNMDKVEAFNFTLKN NHAFLAGAVSRKKQV
QLTESFNA

>d1k23a_c.107.1.1 (A:) Manganese-dependent inorganic pyrophosphatase
(family II) {Bacillus subtilis}

MEKILIFGHQNPDTDTCSAIA YADLKNKLG FNAEPVRLGQVN GETQYALDYFKQESP RL VETAANEVNGVILVD

HNERQQSIKDIIEVQVLEVIDHHRIANFETAEPLYYRAEPVGCTATILNKMYKENVKIEKEIAGLMSAIISDSLLFKSPTCTDQDVAAAKELAEIAGVDAEEYGLNMLKAGADLSKKTVEELISDAKEFTLGSKKVEIAQVNTVDIEDVKKRQAELEAVISKVVAEKNLDLFLVITDILENDLALAINNEAAKVEKAFTNLLENNTALLKGVVSRKKQVVPVLTDAM

>d1ayl_1 c.91.1.1 (228-540) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy- liase) {Escherichia coli}

IASMHC SANVGEKGD VAVFFGLSGTGKTTLSTDPKRRLIGDDEHG WDDGVNFEGG CYAKTI KLSKEAEPEIYNAIRR DALLE NVT VREDGTIDFDDGSKTENTRVSYPIHIDNIVKPVSKAGHATKVIFLTADAFGVLPV SRLTAD QTQYHF LSGFTAKLAGTERGITEPTPTFSACFGAAFLSLHPTQYA EVLV KRMQAAGAQAYLVNTGWNGTGKRISIKDTRAIIDAILNGSLDNAETFTLPMFNLAIPTEPGVDTKILDPRNTYASPEQWQEKAETLA KLFIDNFDKYTDTPAGAALVAAGPKL

>d1ii2a1 c.91.1.1 (A:201-523) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy- liase) {Trypanosoma cruzi}

HLCMHASANVGKQGD VTVFFGLSGTGKTTLSADPHRN LIGDDEHVWTDRGVF NI EGGC YAKAIGLNPKTEKDIYDAVRGAVAENCVLDKRTGEIDFYDESICKNTRVAYPLSHIEGALKAIAGHPKNVIFLTNDAGVMPPVARLTS AQAMFWFVFMGYTANVPGV EAGGTR TARP IFSSCFGGPFLVRHATFYGEQLAEKMQKHNSRVWLNTGYAGGRADRGAKRMPLRVTRAIIDAIHDGTLDRTEYEYPGWLHIPKYVAKVPEHLLNPRKAWKDVRQFNETS KELVAMFQESFSARFAAKASQEMKS A VPRYVEFA

>d1khba1 c.91.1.1 (A:260-622) Cytosolic phosphoenolpyruvate carboxykinase (GTP- hydrolysing) {Human (Homo sapiens)}

WLAEHMLVLGITNPEGEKKYLAAA FPSACGKTNLAMMNPSLPGWKVECVGDDI AWMKF DAQGH LRAINPE NGFFGVAPG TSVKTNPNAIKTIQKNTIFTNVAETSDGGVYWE GIDEPLASGV TITSWK NKEWSSE DGEPCAH PNSRFCTPASQCPIIDA AWESPEGVPIEGIIFGGRRPAGVPLVYEALSWQHGVFVGAAMRSEATAAEHKGKIM HDPFAMRPFFGYNFGKYL AHWLSMAQH PAAKLPKIFHV NWFRKDKEGKFLWPGFGENSRVLEWMFNRIDG KASTKLTPIGYIPKEDALNLKGLGHINMMELFSISKE FW DKEVEDIEKYLVDQVNADLPCEI EREI LALKQRISQM

>d1jb1a_ c.91.1.2 (A:) HPr kinase HprK C-terminal domain {Lactobacillus casei} ERRSMHGVLVDIYGLGV LITGDSGV GKSETALELVQRGHRLIADDRVDVYQQDEQTIVGAAPPILSHLLEIRGLII DVMNLFGAGAVREDTTISLIVHLENWTPDKTFDRLGS GEQTQLI FDPVVPK ITVPVKVGRNLAIIEVAAMNFRA KSMGYDATKTFEKNLNH LIEH

>d1ayl_2 c.109.1.1 (1-227) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy- liase) {Escherichia coli}

MRVNNGLTPQE LEAYGISDVHDIVNPSYDL YQEELDPSLTGYERGVLTNLGAVAVDTGIFTGRSPKDKYIVRDD TTRDTFWWADKGKGKNDNKP LSPETWQHLKGLVTRQLSGKRLFVVDAFCGANPDTRLSVRFITEVAWQAHF VKNM FIRPSDEELAGFKPDFIVMNGAKCTNPQWKEQGLNSENFVAFNLTERMQLIGGTWYGGEMKKGMFS MMNYLLPLKG

>d1ii2a2 c.109.1.1 (A:2-200) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate carboxy- liase) {Trypanosoma cruzi}

PPTIHRNLLSPELVQWALKIEKDSRLTARGALAVMSYAKTGRSPLDKRIVDTDDVRENVDWGKVNMKLSEESFA RVRKIAKEFLDTREH L FV DCFAGH DERYRLKVRVFTTRPYHALFMRDMLIVPTPEELATFGE PDYVIYAGECK ADPSIPGLTSTTCVALNFKTREQVILGTEYAGEMKKGILT VMFELMPQMN

>d1khba2 c.109.1.1 (A:10-259) Cytosolic phosphoenolpyruvate carboxykinase (GTP- hydrolysing) {Human (Homo sapiens)}

NLSAKV VQGS LDSL P QAVREFLENNAELCQPDHIICDGSEEENG RLLGQMEEEGILRRLKKYDN CWLALT DPR DVARI ES KTV I VTQEQ RDTV PIPKTGLSQL GRWMSEEDFEKA FNARFP GCMKG RTM YVIPFSM GPLGSPLSKIG

IELTDSPYVVASMRIMTRMGTpvLEALGDGEFVKCLHSVGCPLPLQKPLVNNWPCNPELTIAHLPDRREIISFG
SGYGGNSLLGKKCFALRMASRLAKEEG

>d1doza_c.92.1.1 (A:) Ferrochelatase {Bacillus subtilis}

SRKKMGLVMAYGTPYKEEDIERYYTHIRRGRKPEPEMLQDLKDRYEAGGISPLAQITEQQAHNLEQHLNEIQR
EITFKAYIGLKHIEPFIEDAVAEMHKDGITEAVSIVLAPHFSTFSVQSYNKRAKEEAELGGLTITSVESWYDEPKFV
TYWVDRVKETYASMPEDERENAMLIVSAHSLPEKIKEFGDPYPDQLHESAKLIAEGAGVSEYAVGWQSEGNTP
DPWLGPDVQDLTRDLFEQKGYQAFVYVPVGFDADLEVLYDNDYECKVVTDDIGASYYRPEMPNAKPEFIDAL
ATVVLKKLGR

>d1hrka_c.92.1.1 (A:) Ferrochelatase {Human (Homo sapiens)}

RKPKTGILMLNMGGPETLGDVHDFLRLFLDRDLMTLPIQNKLAPFIKRTPKIQEQYRRIGGGSPIKIWTSKQ
GEGMVKLLDELSPTAPHKYYIGFRYVHPTEEAIEEMERDGLERAIAFTQYPQYSCSTTGSNLAIYRYYNQVGR
KPTMKWSTIDRWPTHHLIQCFAHILKELDHFPLEKRSEVVILFAHSPLMSVNRGDPYPQEVSATVQKVME
RLEYCNPYRLWQSKVGPMPWLGQPQTDESIKGLCERGRKNILLVPIAFTSDHIETLYEIDIESQVLAKECGVENI
RRAESLNGNPLFSKALADLVHSHIQSNELCSKQLTSCPLCVNPVCRETKSFFTSQQL

>d1qgoa_c.92.1.2 (A:) Cobalt chelatase CbiK {Salmonella typhimurium}

KKALLVVFSGTSYHDTCEKNIVACERDLAASCPRDRLRAFTSGMIIRKLRQRDGIDIDTPLQALQKLAAGQYQD
VAIQSLHIINGDEYEKIVREVQLLRPLFTRLGVPLLSSHNDYVQLMQALRQQMPSLRQTEKVVFMGHGASHH
AFAAYACLDHMMTAQRFPARVGAVESYPEVDILIDSRLDEGVTGVHLMPLMLVAGDHAINDMASDDGDSWK
MRFNAAGIPATPWLSGLGENPAIRAMFVAHLHQALNM

>d1efd_c.92.2.1 (N:) Periplasmic ferric siderophore binding protein FhuD {Escherichia coli}

GIDPNRIVALELPVELLLALGIVPYGVADTINYRLWVSEPLPDSVIDVGLTEPNLELLTEMKPSFMVWSAGY
GPSPEMLARIAPGRGFNFSDGKQPLAMARKSLTEMADLLNLQSAETHLAQYEDFIRSMKPRFVKRGARPLLLT
TLIDPRHMLVFGPNSLFQEILDEYGIPNAWQGETNFWGSTAVSIDRLAAYKDVDVLCFDHDNSKMDALMATP
LWQAMPFVRAGRFQRVPAVWFYGTLSAMHFVRVLDNAIG

>d1toaa_c.92.2.2 (A:) Periplasmic zinc binding protein TroA {Treponema pallidum}

GKPLVVTIGMIADAVKNIAQGDVHLKGMLPGVDPHLYTATAGDVEWGNADLILYNGLHLETKMGEVFSKL
RGSRLVVAVSETIPVSQRSLLEAEFDPHVWFDVKLWSYSVKAVYESLCKLLPGKTREFTQRYQAYQQQLDKLDA
YVRRKAQSLPAERRVLTAHDAFGYFSRAYGFEVKGLQGVSTASEASAHDQMELAAFIQAQRKLPAIFIESSIPHKN
VEALRDAVQARGHVVQIGGELFSDAMGDAGTSEGTYVGMVTHNIDTIVAALAR

>d1psza_c.92.2.2 (A:) Pneumococcal surface antigen PssA {Pneumococcus (Streptococcus pneumoniae)}

KKDTTSGQKLKVATNSIIADITKNIAGDKIDLHSIVPIGQDPHEYEPLPEDVKTSEADLIFYNGINLETGGNAWF
TKLVENAKKTENKDYFAVSDGVDVIYLEGQNEKGKEDPHAWLNLENGIIFAKNIAKQLSAKDPNNKEFYEKNLKE
YTDKLDKLDKESKDKFNKIPAEKKLIVTSEGAFKYFSKAYGVPSAYIWEINTEEGTPEQIKTLVEKLRTQKVPSLFV
ESSVDDRPMKTVSQDTNIPYAQIFTDSIAEQGKEGDSYYSMKYNLDKIAEGLAK

>d1mioa_c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}

SENLKDEILEKYIPKTKKTRSGHIVIKTEETPNPEIVANRTVPGIITARGCAYAGCKGVVMGPIKDMVHITHGPIG
CSFYTWGRRFKSKPENGTLNFNEYVFSTDMQESDIVFGGVNKLDAIHEAYEMFHAAAIGVYATCPVGLIGD
DILAVAATASKEIGIPVHAFSCEGYKGVSQSAGHHIANNTVMTDIIGKGNKEQKKYSINVGEYNIGGDAWEMD
RVLEKIGYHVNATLTGDATYEKVQNADKADLNVLQCHRSINYIAEMMETKYGIPWIKCNFIGVDGIVETLRDMA
KCFDDPELTKRTEEVIAEEIAIQDDLDYFKEKLQGKTACLYVGGRSHTYMNMLKSFGVDSLVAGFEFAHRDDY
EGREVIPTIKIDADSKNIPEITVTPDEQKYRVVIPEDKVEELKKAGVPLSSYGGMMKEMHDGTILIDDMNHHD
EVVLEKLKPDMFFAGIKEKFVIQKGGVLSKQLHSYDNGPYAGFRGVVNFGHELVNGIYTPAWKMITPPWKKA

SSES

>d1miob_c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium pasteurianum}

LDATPKEIVERKALRINPAKTCQPGAMYAALGIHNCLPHSGSQGCCSYHRTVLSRHFKEPAMASTSSFTEGAS
VFGGGSNIKTAVKNIFSLYNPDIIAVHTTCLSETLGDDLPTYISQMEDAGSipeGLVIHTNTPSYVGSHVTGFAN
MVQGIVNYLSENTGAKNGKINVIPGFVGPADMREIKRLFEAMDIPIYIMFPDTSGVLDGPTTGEYKMYPEGGT
IEDLKDTGNSDLTLSGSYASDLGAKTLEKKCKVPFKTLRTPIGVSATDEFIMALSEATGKEVPASIEERGQLIDLMI
DAQQYLQGKKVALLGDPDEIIALSKFIIELGAIPKYVVTGPGMKFQKEIDAMLAEGSKVKVEGDFDVHQ
WIKNEGVDLLISNTYGKFIAREENIPFVRFGPIMDRYGHYYNPKVGKGAIHLVEEITNVILDKIERCTEEDFEV

VR

>d2mina_c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}

SREEVESLIQEVLLEVYPEKARKDRNKHLAVNDPAVTQSKKCIISNKSQPGMLTIRGCAYAGSKGVVWGPIKDMI
HISHGPVGCGQYSRAGRNNYYIGTTGVNAFTMNFTSDFQEKDIFGGDKKLAKLIDEVETLFPLNKGISVQSEC
PIGLIGDIESVSKVKGAEALKTIVPRCEGFRGVSQLGHHIANDAVRDWVLGKRDEDTTFASTPYDVAIIGDYN
IGGDAWSSRILLEEMGLRCVAQWSGDGSISEIELTPKVKLNLVHCYRSMNYISRHMEEKYGIPWMEMNFNGPTK
TIESLRAIAAKFDESIQKCEEVIAKYKPEWEAVVAKYRPRLEGKRVMLYIGGLRPRHVIGAYEDLGMEVVGTGYE
FAHNDDYDRTMKEMGDSTLYDDVTGYEFEEFVKRIKPDLIGSGIKEKFIFQKMGIPFREMHSWDYSGPYHGF
DGFAIFARDMDMTLNPCWKKLQAPWE

>d2minb_c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}

SQQVDKIKASYPLFLDQDYKDMIAKKRDGFEEKYPQDKIDEVFQWTTTKEYQELNFQREALTVNPAKACQPLG
AVLCALGFETKMPYVHGSQGCVAYFRSYFNRHFREPVCVSDSMTEDAAVFGQQQNMKDGLQNCKATYKPD
MIAVSTTCMAEVIGDDLNAFINNSKKEGIFPDEFPVPAHTPSFGSHVTGWDNMFEGLARYFTLKSMDKVV
GSNKKINIVPGFETYLGFRVIRMLSEMVGVGSSLSDPEEVLDTPADGQFRMYAGGTTQEEMKDAPNALNTV
LLQPWHLETKKFVEGTWKHEVPKLNIPMGLDWTDEFLMKVSEISGQPIPASLTKERGLVDMMMTDSHTWLH
GKRFALWGDPDFVMGLVKFLLELGCEPVHLCHNGNKRWKAVDAILAASPYGKNATVYIGKDLWHLRSLVFT
DKPDFMIGNSYGKFIQRDTLHKGKEFEVPLIRIGFPIFDRHHLHRSTTLGYEGAMQILTTLVNSILERLDEETRG
QATDYNHDLVR

>d1qqua_c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Klebsiella pneumoniae}

TNATGERNLALIQEVLEVFPETARKERRKHMMSDPKMKSVGKCIISNRKSQPGVMTVRGCAYAGSKGVVFGP
IKDMAHISHGPVGCGQYSRAGRNNYTGVSGVDSFGTLNFTSDFQERDIVFGGDKKLSKIEEMELLFPLTKGITI
QSECPVGLIGDDISAVANASSKALDKPVIPRCEGFRGVSQLGHHIANDVVRDWLNNREGQPFETTPYDVAII
GDYNIGGDAWASRILLEEMGLRVVAQWSGDGTLVEMENTPFVKLNLVHCYRSMNYIARHMEEKHQIPWME
YNFFGPTKIAESLRKIADQFDTIRANAEEAVIARYEGQMAIIAKYRPRLEGKVLLYMGLRPRHVIGAYEDLG
MEIIAAGYEFAHNDDYDRTLPDLKEGTLLFDDASSYELEAFVKALKPDLIGSGIKEKYIFQKMGVPFRQMHSWD
YSGPYHGDGFAIFARDMDMTLNNAWNELTAPWL

>d1qgub_c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Klebsiella pneumoniae}

SQTIDKINSYCPLFEQDEYQELFRNKRQLEEAHDQAQRVQEVAWTTAEYEALNFRREALTVDPKAQACQPLGAV
LCSLGFANTLPYVHGSQGCVAYFRTYFNRHFKEPIACVSDSMTEDAAVFGNNNMNLQNASALYKPEIIAVS
TTCMAEVIGDDLQAFIANAKKDGFVDSSIAVPHAHTPSFIGSHVTGWDNMFEGLFAKTFTADYQGQPGKLPKL
NLVTGFETYLGFRVLKRMMEQMAVPCSSLSDPSEVLDTPADGHYRMYSGGTTQQEMKEAPDAIDTLLQP

WQLLSSKKVQEMWNQPATEVAIPLGLAATDELLMTVSQLSGKPIADALTLEGRGLVDMMMLDSHTWLHGKKF
GLYGDPDFVMGLTRFLLEGCEPTVILSHNANKRWQKAMNKMLDASPYGRDSEVFINCDLWHFRSLMFRQP
DFMIGNSYGKFICRDTLAKGKAFEVPLIRLGFLDRHHLHRQTTWGYEGAMNIVTTLVNAVLEKLSDTSQLG
KTDYSFDLVR

>d1jr2a_c.113.1.1 (A:) Uroporphyrinogen III synthase (U3S, HemD) {Human (Homo sapiens)}
MKVLLLKDAKEDDCGQDPYIRELGLYGLEATLIPVLSFEFLSPFSEKLSHPEDYGGLIFTSPRAVEAAELCLEQNN
KTEVWERSLKEKWNAKSVYVVGNTASLVSIGLDTEGETCGNAEYICSRESSALPLLPCGNLKREILPKAL
DKGIAMESITVYQTVAHPGIQGNLNSYYSSQGVPAITFFSPSGLTYSLKHIQELSGDNIDQIKFAAIGPTTARAL
AAQGLPVSCATAESPTPQALATGIRKALQ

>d2dri_c.93.1.1 (-) D-ribose-binding protein {Escherichia coli, strain k-12}
KDTIALVVSTLNPNPFVSLKDGAQKEADKLGYNLVLDQSQQNPAKELANVQDLTVRGTKILLINPTDSDAVNAV
KMANQANIPVITLDRQATKGEVVSHIASDNVLGGKIAGDYIAKKAGEGAKVIELQGIAGTSAARERGEGFQQAV
AAHKFNVLASQPADFDRIKGLNVMQNLLTAHPDVQAVFAQNDEMAGALRALQTAGKSDVMVVGFDGTPD
GEKAVNDGKLAATIAQLPDQIGAKGVETADKVLGEVKQAKYPVDLKLVVKQ

>d8abp_c.93.1.1 (-) L-arabinose-binding protein {Escherichia coli}
NLKLGFLVKQPEEPWFQTEWKFADKAGKDLGFEVIKIAVPDGEKTLNAIDS LAASGAKGFVICTPDPKLGSAIVA
KARGYDMKVIAVDDQFVNAGKGPMDTVPLVMAATKIGERQQGELYKEMQKRGWDVKE SAVMAITANELD
TARRRTTGSMDALKAAGFPEKQIYQVPTKSNDIPGAFDAANSMLVQHPEVKHWLIVGMNDSTVLGGVRATEG
QGFKAADIIGINGVDAVSELSKAQATGFYGSLLPSPDVHGYKSSEMLYNWWAKDVEPPKTEVTDVVLITRDN
FKEELEKKGLGGK

>d1rpja_c.93.1.1 (A:) D-allose-binding protein {Escherichia coli}
AAEYAVVLTLSNPFWVDMKKGIEDEAKTLGVSVDFASPSEGDFQSQLQLFEDLSNKNYKGIAFAPLSSVNLM
PVARAWKKGIYLVLNDEKIDMDNLKKAGGNVEAFVTDNVAVGAKGASFIDKLGAE GG EVAIIEGKAGNASGE
ARRNGATEAFKKASQIKLVASQPADWDRIKALDVATNVLQRNPNIKAIYCANDTMAMGVAQAVANAGKTGKV
LVVGTDGIPEARKMVEAGQMTATVAQNPADIGATGLKLMVDAEKGKVIPLDKAPEFKLVDSLVTQ

>d2gbp_c.93.1.1 (-) Galactose/glucose-binding protein {Escherichia coli}
ADTRIGVTIYKYDDNFMSVVRKAIEQDAKAAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAINLVDPA
AGTVIEKARGQNVPVFFFNKEPSRKALDSYDKAYYVGTDSKESGIIQGDLIAKHWAANQGWDLNKDGQIQFV
LKGEPGHPDAEARTTYVIKELNDKGIKTEQLQLDTAMWDTAQAKDKMDAWLSGPNANKIEVVIANNDAMA
MGAVEALKAHNKSSIPVFGVDALPEALALVKSGALAGTVLNDANNQAKATFDLAKNLADGKGAADGTONWKID
NKVVRVPYVGVDKDNLAEFSKK

>d1gca_c.93.1.1 (-) Galactose/glucose-binding protein {Salmonella typhimurium, strain lt2}
ADTRIGVTIYKYDDNFMSVVRKAIEKDGKSAPDVQLLMNDSQNDQSKQNDQIDVLLAKGVKALAINLVDPA
GTVIEKARGQNVPVFFFNKEPSRKALDSYDKAYYVGTDSKESGVIQGDLIAKHWAANQGWDLNKDGKIQYVL
LKGEPGHPDAEARTTYVVKELNDKGIKTEQLALDTAMWDTAQAKDKMDAWLSGPNANKIEVVIANNDAMA
MGAVEALKAHNKSSIPVFGVDALPEALALVKSGAMAGTVLNDANNQAKATFDLAKNLADGKGAADGTONWKIE
NKIVRVPYVGVDKDNLSEFTQK

>d1pea_c.93.1.1 (-) Amide receptor/negative regulator of the amidase operon (AmiC)
{Pseudomonas aeruginosa}

PLIGLLFSETGVTADIERSQRYGALLAVEQLNREGGVGGRPIETLSQDPGGDPDRYRLCAEDFIRNRGVFLVG
MSHTRKAVMPVVERADALLCYPTPYEGFEYSPNIVYGGPAPNQNSAPLAAYLIRHYGERVVFIGSDYIYPRESNH
VMRHLYRQHGGTVLEEIYIPLYSDDDLQRAVERIYQARADVVFSTVVGTVTAELYRAIARRYGDGRPPIASLT
SEAEVAKMESDVAEGQVVVAPYFSSIDTPASRAFVQACHGFFPENATITAWAEAAYWQTLLGRAAQAGNW
RVEDVQRHLYDIDIDAPQGPVRVERQNNHSRLSSRIAEDARGVFQVRWQSPEPIRPDPYVVVHNLLDW

>d1jx6a_c.93.1.1 (A:) Quorum-sensing signal (autoinducer-2) binding protein LuxP {Vibrio harveyi}
GYWGYQEFLDEFPEQRNLTNALSEAVRAQPVPLSKPTQRPIKISVYPGQQVSDYVRNIASFKEKRLYKLNINY
QLNQVFTRPNADIKKQQLSLMEALKSKSDYLIFTLDTRHRKFVEHVLDSNTKLILQNITTPVREWDKHQFLY
VGFDAEGSRELATEFGKFFPKHTYSVLYFSEGYISDVRGDTFIHQVNRDNNFELQSAYTAKTQSGYDAAKA
SLAKHPDVDFIYACSTDVALGAVDALAELGREDIMINGWGGGSAELDAIQKGDLITVMRMNDDGIAMAEAI
KWDLEDKPVPTVSGDFEIVTKADSPERIEALKKRAFRYSD

>d1dbqa_c.93.1.1 (A:) Purine repressor (PurR), C-terminal domain {Escherichia coli}
KSIGLLATSSEAAYFAEIIEAVEKNCFQKGYTLLGNNAWNNEKQRAYLSMMAQKRVGGLVMCSEYPEPLLAML
EEYRHIPMVVMWDGEAKADFTDAVIDNAFEGGYMAGRYLIERGHREIGVIPGPLERTGAGRLAGFMKAME
EAMIKVPESWIVQGDFEPESGYRAMQQILSQPHRPTAVFCGGDIMAMGALCAADEMGLRPVQDVSLIGYDN
VRNARYFTPALTTIHQPKDSLGETAFNMLLDRIVNKREEPQSIEVHPRIERRSVADGPFRDYRR

>d1jyea_c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}
LLIGVATSSLALHAPSQIVAAILSRADQLGASVVSMVERSGVEACKTAVHNLLAQRVSGLIINYPLDDQDAIAVE
AACTNVPALFLDVSDDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLAGPLSSVSARLRLAGWHKYLTRNQIQP
AEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMRAITESGLRVGADISVVGYDDTEDSSCYI
PPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNNQLPVSLVKRKTTLAP

>d1tlfa_c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {Escherichia coli}
SLLIGVATSSLALHAPSQIVAAIKSRADQLGASVVSMVERSGVEACKAVHNLLAQRVSGLIINYPLDDQDAIAVE
AAACTNVPALFLDVSDDQTPINSIIFSHEDGTRLGVEHLVALGHQQIALLAGPLSSVSARLRLAGWHKYLTRNQIQP
IAEREGDWSAMSGFQQTMQMLNEGIVPTAMLVANDQMALGAMRAITESGLRVGADISVVGYDDTEDSSCYI
PPLTTIKQDFRLLGQTSVDRLLQLSQGQAVKGNNQLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRL

>d1byka_c.93.1.1 (A:) Trehalose repressor, C-terminal domain {Escherichia coli}
SDKVVAAIVTRLDSLSENLAQTMPLAFYEQGYDPIMMESQFSPQLVAEHLGVLKRRNIDGVVLFGFTGITEEML
AHWQSSLVLLARDAKGFASCVYDDEGAIKILMQRLYDQGHRNISYLGVPHSVTTGKRRHEAYLAFCKAHKLHP
VAALPGlamKQGYENVAKVITPETTALLCATDTLALGASKYLQEQRIDLQLASVGNTPLMKFLHPEIVTVDPGY
AEAGRQAACQLIAQVTGRSEPQQIIIPATLS

>d2liv_c.93.1.1 (-) Leucine-,isoleucine-,valine-binding (LIV) protein {Escherichia coli}
EDIKVAVVGAMSGPVAQYGDQEFTGAEQAVADINAKGGIKGNKLQIAKYDDACDPKQAVAVANKVNDGIKY
VIGHLCSSSTQPASDIYEDEGILMITPAATAPELTARGYQLILRTTGLSDQGPTAAKYILEKVKPQRIAIVHDKQQY
GEGLARAVQDGLKKGNANVFFDGITAGEKDFSTLVARLKKENIDFVYYGGYHPEMGQILRQARAAGLKTQFM
GPEGVANVLSNIAGESAEGLLVTPKNYDQVPANKPIVDAIKAKKQDPSGAFWTTYAALQLQAGLNQSDD
PAEIAKYLKANSVDTVMGPLTWDEKGLKGFEFGVFDWHANGTATDAK

>d2lbp_c.93.1.1 (-) Leucine-binding protein {Escherichia coli}
DDIKVAVVGAMSGPIAQWGIMEFNGAEQQAIDINAKGGIKGDKLGVVEYDDACDPKQAVAVANKIVNDGIKY
VIGHLCSSSTQPASDIYEDEGILMISPGATAPELTQRGYQHIMRTAGLDSSQGPTAAKYILETVKPQRIAIIHDKQQ
YGEGLARSVQDGLKAANANVFFDGITAGEKDFSTLALARLKKENIDFVYYGGYHPEMGQMLRQARSVGLKTQFM
MGPEGVGNASLSNIAGDAAEGMLVTMPKRYDQDPANQGIVDALKADKKDPSGPYVWITYAAVQLATALERT
GSDEPLALVKDLKANGANTVIGPLNWDEKGLKGFDGFVQFWHADGSSTKAK

>d1dp4a_c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Rat (Rattus norvegicus)}

SDLTVAVVPLNTSYPWSWARVGPVELALARVKARPDLPGWTVMVLGSSENAAGVCSDTAAPLAADV
WEHSPAVFLPGCVYSAAPVGRFTAHWRVPLTAGAPALGIGVKDEYALTTRGSPHVKGDFVTALHRR
HQALVYADRLGDDRPCFFIVEGLYMRVRERLNITVNHQEFVEGDPDHYPKLLRAVRRKGRVIYICSSPDAFRNL
MLLALNAGLTGEDYVFFHLDVFGQLKSAQGLVPQKPERGDGQDRSARQAFQAAKIITYKEPDNP
EYLEFLK

QLKLLADKKFNFTVEDGLKNIIPASFHDGLLYVQAVTETLAQGGTVTDGENITQRMWNSRFQGVGTYLKIDRN
GDRDTDFSLWDMDPETGAFRVVLNYNGTSQELMAVSEHKLYWPLGYPPPDVPKCGF

>d1jdpa_c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Human (Homo sapiens)}

EALPPQKIEVLVLLPQDDSYLFLSITRVRPAIEYALRSVEGNGTGRRLPPGTRFQVAYEDSDCGNRALFSLDRVAA
ARGAKPDLILGPVCEYAAPVARLASHWDLPMISAGALAAGFQHKDSEYSHLTRVAPAYAKMGEMLALFRH
HHWSRAALVYSSDKLERNCYFTLEGVHEVFQEEGLHTSIYSFDETLDLLEDIVRNIQASERVVIMCASSDTIRSI
MLVAHRHGMTSGDYAFFNIELFNSSSYGDGSWKRGDKHDFEAKQAYSSLQTVTLRTVKPEFEKFSMEVKSSVE
KQGLNMEDYVNMFVEGFHDAILYVLALHEVLRAGYSKKDGGKIIQQTWNRTFEGIAGQVSIDANGDRYGDVS
VIAMTDVEAGTQEVIDYFGKEGRFEMRP

>d1ewka_c.93.1.1 (A:) Metabotropic glutamate receptor subtype 1 {Rat (Rattus norvegicus)}
RSVARMDGDIIGALFSVHHQPPAEKVPERKCGEIREQYGIQRVEAMFHLDKINADPVLLPNITLGSEIRDSCW
HSSVALEQSIEFIRDSLISIRDEKDGLNRCLPDGQTLPPGRTKKPIAGVIGPGSSSVAIQVQNLLQLFDIPQIAYSATS
IDLSDKTLYKYFLRVVPSDTLQARAMLDIVKRYNWTVSAVHTEGNYGESGMDAFKELAAQEGLCIAHSDFKIYS
NAGEKSFDRLLRKLERLPKARVVCFCEGMDVRLGLSAMRRLGVGEFSLIGSDGWADRDEVIEGYEVEANG
GITIKLQSPEVRSFDDYFLKLRLDTNTRNPWFPEFWQHRFQCRLPGHLLENPNFKVCTGNESLEENYVQDSK
MGFVINAIYAMAHLQNMHHALCPGHVGLCDAMKPIDGRKLLDFLIKSSFVGVSCEEWFDEKGDAPGRYDI
MNLQYTEANRYDYVHVGTVWHEGVLNIDDYKI

>d1jeta_c.94.1.1 (A:) Oligo-peptide binding protein (OPPA) {Salmonella typhimurium}
ADVPAGVQLADKQTLVRNNGSEVQSLDPHKIEGVPESNVSRLFEGLLISDVEGHPSPGVAEKWENKDFKVWT
FHLRENAKWSDGTPVTAHDFVYSWQRLADPNTASPASYLQYGHIANIDIIAGKKPATDLGVKALDDHTFEVT
LSEPVYPFYKLLVHPSPVPKSAVEKFGDKWTQPANIVTNGAYKLKNVVNERIVLERNPQYWDNAKTVINQ
VTYLPISSEVDVNRYRSGEIDMTYNNMPIELFQKLKEIPNEVRVDPYLCTYYEINNQKAPFNDVRVTALKLA
LDRDIIVNKVNQGDLPAYSTPPYTDGAKLVEPEWFKWSQQKRNEEAKLLAEAGFTADKPLTFDLYNTSDLH
KKLAIAVASIWKKNLGVNVNLENQEWEKTFLDTRHQGTFDVARAGWCADYNEPTSLNTMLSDSSNNTAHYKS
PAFDKLIADTLVADDTQRSELYAKAEQQLDKDSAIVPVYYYVNARLVKPWVGGYTGKDPLDNIYVKNLYIIKH

>d1pda_1 c.94.1.1 (3-219) Porphobilinogen deaminase
(hydroxymethylbilane synthase), N-terminal domain {Escherichia coli}

DNVLRIATRQSPLALWQAHYVKDKLMASHPGLVVELPMVTRGDVILDPLAKVGGKGLFVKELEVallenRA
DIAVHSMKDVPVEFPQGLGLVTICEREDPRDAFVSNNYDSLDALPAGSIVGTSSLRRCQLAERRPDLIIRSLRGN
VGTRLSKLDNGEYDAIIILAVAGLKRLGLESRIRAALPPEISLPAVGQGAVGIECRLEDDSRTRLEAAL

>d1lst_c.94.1.1 (-) Lysine-,arginine-,ornithine-binding (LAO) protein {Salmonella typhimurium}

ALPQTVRIGTDPTYAPFSSKDAKGEFIGFDIDLGNECKRMQVKCTWVASDFDALIPSLAKKIDAISSLSITDKR
QQEIAFSDKLYADSRLIAAKGSPIQPTLESLKGKHGVVLQGSTQEAYANDNWRTKGVDVVAYANQDLIYSDLTA
GRLDAALQDEVAASEGFLKQPGKEYAFAGPSVKDKYFGDGTGVGLRKDDTELKAFFDKALTELRQDGTYDK
MAKKYFDFNVYGDK

>d1sbp_c.94.1.1 (-) Sulphate-binding protein {Salmonella typhimurium}
KDIQLLNVSYDPTRELYEQYNKAFSAHWKQETGDNVVIDQSHGGSGKQATSVINGIEADTVTLALAYDVNAIAE
RGRIDKNWIKRLPDDSAPYTSTIVFLVRKGNPQKQIHDWNDLIKPGVSITPNPKSSGGARWNYLAAWGYALHH
NNNDQAKAEDFVKALFKNVEVLDGARGSTNTFVERGIGDVLIWENEALLATNELGDKDFEIVTPSESILAEP
VSVVDKVEKKDTKAVAECAYLKYLYSPEGQEIAKNFYRPRDADVAKYDDAFPKLKLFTIDEVFGGWAKAQKD
HFADGGTFDQISK

>d1ixh_c.94.1.1 (-) Phosphate-binding protein {Escherichia coli}

EASLTGAGATFPAPVYAKWADTYQKETGNKVNYQGIGSSGGVKQIIANTVDFGASDAPLSDEKLAQEGLFQFPT
VIGGVVLAVNIPGLKSGELVDGKTLGDIYLGKIKKWDDEAIAKLNPGKLPSQNIAVRRADSGTSFVFTSYLA
KVNEEWKNNVTGSTVKWPIGLGGKNDGIAAFVQLPAGAIGYVEYAYAKQNNLAYTKLISADGKPVSPTEEN
FANAAGKADWSKTFQAQDLTNQKGEDAWPITSTTFLIHKDQKKPEQGTEVLKFFDWAYKTGAQANDLDYASL
PDSVVEQVRAAWKTNIKDSSGKPLY

>d3mbp_c.94.1.1 (-) D-maltodextrin-binding protein, MBP {Escherichia coli}
KIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIFWAHDRFGGYAQSGL
LLAEITPDKAQDKLYPFTDAVRYNGKLIYPIAVEALSLIYNKDLLPNPPKTWEIPALDKELKAKGKSALMFNL
QEPYFTWPLIAADGGYAFKYENGKYDIKDVGVDNAGAKAGLTFVLVDLKHNKHMNADTDYSIAEAANKGETAM
TINGPWAWSNIDTSKVNYGTVLPTFKGQPSKPFVGVLISAGINAASPNKELAKEFLENYLLTDEGLEAVNDKPL
GAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDDEALKDAQTRITK
>d1elja_c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Pyrococcus furiosus}
MKIEEGKVVWHAMQPNELEVQSLAEEYMALCPEVEIVFEQKPNLEDALKAAIPTGQGPDLFIWAHDWIGKF
AEAGLLEPIDEYVTEDLLNEFAPMAQDAMQYKGHHYALPFAAETVAIYNKEMVSEPPKTFDEMKAIMEKYYDP
ANEKYGIAWPINAYFISIAAQAFGGYYFDDKTEQPGLKPETIEGFKFFFTEIWPMAPTDYNTQQSIFLEGRA
PMMVNGPWSINDVKKAGINFGVVPLPPIIKDGKEYWPRPYGGVKLIYFAAGIKNKDAAWKFAKWLTSEESIK
TLEALELGYIPVLTKVLDDEIKNDPVIYGFQAVQHAYLMPKSPKMSAVWGGVDGAINELQDPQNADIEGILKK
YQQEILNNMQ

>d1eu8a_c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Thermococcus litoralis}
IEEGKIVFAVGGAPNEIEYWKGVIAEFEEKYKPGVTVELKRQATDTEQRRLDLVNALRGKSSDPDVFLMDVAWLQ
QFIASGWLEPLDDYVQKDNYDLSVFFQSVINLADKQGGKLYALPVYIDAGLLYRKDLLEKYGYSKPPETWQELV
EMAQKIQSGERETNPFWGFWQGKQYEGLVCDFVEYVYNSNGGSLGEFDKGKWWPTLNKPENVEALQFMV
DLIHKYKISPPNTYTEMTEEPVRLMFQQGNAAFERNWPYAWGLHNADDSPVKGKVGVAPLPHFGHKSAATL
GGWHIGISKYSDNKALAWEFVKFVESVQKGFMNLGNPGRVDVYDDPAVVSKSPHLKELRAVFENAVPR
PIVPYYPQLSEIIQKYVNSALAGKISPQEALDKAQKEAEELVKQ

>d3thia_c.94.1.1 (A:) Thiaminase I {Paenibacillus thiaminolyticus}
ITLKVAIYPYVPDPARFQAAVLQWQRQEPGVKLEFTDWDSYADPPDDLDFVLDISIFLSHFVDAGYLLPFGS
QDIDQAEDVLPFALQGAKRNGEVYGLPQILCTNLLFYRKGDLKIGQVDNIYELYKKIGTSHSEQIPPPQNKGLLIN
MAGGTTKASMYLEALIDVTGQYTEYDLPPLDPLNDKVRGLRLINMAGEKPSQYVPEDGDAYVRASWFAQG
SGRAFIGYSESMMRMGDYAEQVRFKPISSAGQDPLFYSDDVSVNSKTAHPELAKKLANVMASADTVEQALR
PQADGQYPQYLLPARHQVYEALMQDYPYSELAQIVNKPSNRVFRGPEVRTWLKDAKQLPEALG

>d1mrp_c.94.1.1 (-) Ferric-binding protein {Haemophilus influenzae}
DITVYNGQHKEATAVAKAFEQETGIKVTLNSKSEQLAGQLKEEGDKTPADVFTEQTATFADLSEAGLLAPISE
QTIQQTAQKGVPPLAKKDWIALSGRSRVVYDHTKLSEKDMEKSVLDYATPKWKGKIGYVSTSGAFLEQVVALS
KMKGDKVALNWLKGLKENGKLYAKNSVALQAVENGEVPAALINNNYWHAFAREKGVQNVHTRLNFVRHDPG
ALVYSGAAVLKASKNQAEAKFVDFLAGKKGQEAQKPLRADVSPNLEPYEKLAPVVSATTQDKE
HAIKLIIEAGLK

>d1d9ya_c.94.1.1 (A:) Ferric-binding protein {Neisseria gonorrhoeae}
DITVYNGQHKEAAQAVADAFTTRATGIKVKLNCAKGDQLAGQIKEEGSRSPADVYSEQIPALATLSAANLLEPLP
ASTINETRGKGVPAAKKDWWALSGRSRVVYDTRKLSEKDLKSVLYATPKWKNRIGYVPTSGAFLEQIVAI
KLKGEAAALKWLKGLKEYGKPYAKNSVALQAVENGEIDAALINNNYWHAFAREKGVQNVHTRLNFVRHDPG
ALVTYSGAAVLKSSQNDEAKKFVAFLAGKEGQRALTAVRAEYPLNPHVVSTFNLEPIAKLEAPQVSATTVSEKE
HATRLLEQAGMK

>d1dpe_c.94.1.1 (-) Dipeptide-binding protein {Escherichia coli}

KTLVYCSEGSPEGFNPQLFISGTTDASSVPLYNRLVEFKIGTTEVIPGLAEKWEVSEDGKTYTFHLRKGVKWHDN
KEFKPTRELNADDVVFSFDRQKNAQNPYHKVSGGSYEYFEGMGLPELISEVKVDDNTVQFVLTRPEAPFLADL
AMDFASILSKEYADAMMKAGTPEKLDNPIGTGPQLQQYQKDSRIRYKAFDGYWTGPQIDTLVFSITPDASV
RYAKLQKNECQVMPPNPADIARMKQDKSINLMEMPGLNVGYLSYNQKKPLDDVKVRQALTYAVNKDAIIK
AVYQGAGVSAKNLIPPTMWGYNDDVQDYDPEKAKALLKEAGLEKGFSIDLWAMPVQRPNPNARRMAE

MIQADWAKVGVQAKIVTYEWGEYLKRAKDGEHQTVMMGWTGDNGDPDNFFATEFSCAASEQGSNSYKW
CYKPFEDLIQPARATDDHNKRVELYKQAQVVMHDQAPALIIAHSTVFEPVRKEVKGYVVDPGLKHHFENVSIE
>d1hsla_c.94.1.1 (A:) Histidine-binding protein {Escherichia coli}

AIPQKIRIGTDPTYAPFESKNAQGELVGFIDILAKELCKRINTQCTFVENPLDALIPSLKAKKIDAIMSSLSITEKRQ
QEIAFTDKLYAADSRLVVAKSNDIQPTVASLGKRVGVVLQGTTQETFGNEHWAPKGIEIVSYQGQDNIYSDLTAG
RIDAAFQDEVAASEGFLKQPVGKDYKFGGPAVKDEKLFGVGTGMGLRKEDNELREALNKAFAEMRADGTYEKL
AKKYFDVDVYGG

>d1pot_c.94.1.1 (-) Spermidine/putrescine-binding protein PotD {Escherichia coli}

NNTLYFYNWTEYVPPGLLEQFTKETGIKVYSTYESNETMYAKLKTYKDGAYDLVPSTYYVDKMRKEGMIQKID
KSKLTNFNLDPDMLNKPFDPPNDYSIPIWGATAIGVNGDAVDPKSVTSWADLWPKPEYKGSLLTDDAREVF
QMALARLGSGNTDPKEIEAAYNELKKLMPNVAAFNSDNPANPYMEGEVNLGMIWNGSAFVARQAGTPID
VVWPKEGGIFWMDSLAI PANAKNKEGALKLINFLRPDVAKQVAETIGYPTPNLAARKLLSPEVANDKLYPDA
ETIKNGEWQNDVGAASSIYEYYYQKLKAG

>d1a99a_c.94.1.1 (A:) Putrescine receptor (PotF) {Escherichia coli}

QKTLHIYNWSDYIAPDTVANFEKETGIKVYDVFDNSEVLEGKLMAGSTGFDLVPSASFLERQLTAGVFQPLDK
SKLPEWKNLDPPELLKLVAKHDPDNKFAMPYMWATTGIGYNVDKVKAVALGENAPVDSWDLILK PENLEKLKSCG
VSFLDAPEEVFATVNLNYLGKDPNSTKADDYTGPATDLLLKLRPNIRYFHSSQYINDANGDICVAIGWAGDVWQ
ASNRAKEAKNGVNVSFSIPKEGAMAFFDVFAMPADAKNDEAYQFLNYLLRPDVVAHISDHVFYANANKAATP
LVSAEVRENPGIYPPADVRALKFTLKVQDPKIDRVRTRAWTKVKSG

>d1wdna_c.94.1.1 (A:) Glutamine-binding protein {Escherichia coli}

KLVVATDTAFVPFEFKQGDLVGFVDLWAAIAKELKLDYELKPMDFSGIIPALQTKNVDLALAGITITDERKKAID
FSDGYYKSGLLVMVKANNNDVKSVKLDGKVVAVKSGTGSVDYAKANIKTKDLRQFPNIDNAYMELGTNRAD
AVLHDTPNILYFIKTAGNGQFKAVGDSLEAQQYGIAPFKGSDEL RDKVNGALKTLRENGTYNEIYKKWFGTEPK
>d1ftka_c.94.1.1 (A:) Glutamate receptor ligand binding core {Rat (Rattus norvegicus), GluR2}
KTVVVTITLESPYVMMKKNHEMLEGNERYEYCVDLAAEIAKHC GFKYKLTIVGDGKYGARDADTKIWNGMV
GELVYGKADIAIAPLTITLVREEVIDSKPMSLGISIMIKPGTDGNPIESAEDLSKQTEIAYGTLDSGSTKEFRRS
KIAVFDKMWTYMRSAPSVFVRTTAEGVARVRKSKGKYAYLLESTMNEYIEQRKPCDTMKVGGNLD SKGYGIA
TPKGSSLGNANVLKLNEQGLLDKLKNKWWYDKGEC

>d1ii5a_c.94.1.1 (A:) Glutamate receptor ligand binding core {Synechocystis sp., GluR0}

GSAMALKVGVGNPPFVFYGEGKNAFTGISLDVWRAVAESQKWNSEYVRQNSISAGITAVAEGELDILGPIS
VTPERAIAIEGITFTQPYFSSGIGLLIPGTATPLFRSVGDLKNKEVAVVRDTTAVDWANFYQADVRETNNLTAITLL
QKKQVEAVMFDRPALIYYTRQNPNLNLEVTEIRVSLEPYGFVLKENSPLQKTINVEMLNLLSRVIAEFTERWLG

>d1amf_c.94.1.1 (-) Molybdate-binding protein, ModA {Escherichia coli}

GKITVFAAASLTNAMQDIATQFKKEKGVDVSSFASSTLARQIEAGAPADLFISADQKWM DYAVDKKAIDTATR
QTLLGNSL VVVA PKASVQKDFTIDS KTNW TSLL NGG RLAV GDPEH VPAGI YAKE AL QKL GAW DT LSP KLA PAED
VRGALALVERNEAPLGIVYGS DAV ASKG V KV V AT FP ED SH KK VEY P AV V EGH NNATV KAFYDYLKG P QAA EIF
KRYGFTIK

>d1atg_c.94.1.1 (-) Molybdate-binding protein, ModA {Azotobacter vinelandii}

ELKVVATNFLGTLQLAGQFAKQTGHAVVISSGSSGPVYAQIVNGAPYNVFFSADEKSPEKLDNQGFALPGSRFTYAIGKVLWSAKPGLVDNQGKVLAGNGWRHIAISNPQIAPYGLAGTQLTHLGLLDKLTAQERIVEANSGQAHSQTASGAADLGVALAQIIQAAAKIPGSHWFPPANYEPIVQQAVITKSTAEKANAEQFMSWMKGPKAVAIKAAAGYVLPQ

>d1al3_ c.94.1.1 (-) Cofactor-binding fragment of CysB {Klebsiella aerogenes}

TWPDKGSLYVATHTQARYALPGVIKGFIERYPRVSLHMHQGSPTQIAEAVSKGNADFAIATEALHYDDLVMPLCYHWNRISVVTPEHPLATKGSVIEELAQYPLVTYTFGFTGRSELDTAFNRAGLTPRIVFTADAVIKTYVRLGLGVGVIASMAVDPVSDPDLVKLDANGIFSHSTTKIGFRRSTFLRSYMYDFIQRFAPHLTRDVVDTAVALRSNEDIAMFKDIKLPEK

>d1i6aa_ c.94.1.1 (A:) Hydrogen peroxide-inducible genes activator OxyR, regulatory domain {Escherichia coli}

ETMSGPLHIGLIPTVGPYLLPHIIPMLHQTFPKLEMYLHEAQTHQLLAQLDSGKLDLAVILALVKESEAFIEVPLFDEPMLLAIYEDHPWANREAVPMADLAGEKLLMLEDGHCLRDQAMGFCFEAGADEDTHFRATSLETLRNMVAA

GSGITLLPALAVPPERKRDGVVYLPAIKPEPRRTIGLVYRPGSPLRSRYEQLAEAIRARMDGHFD

>d1kwha_ c.94.1.1 (A:) Alginate-binding periplasmic protein AlgQ2 {Sphingomonas sp.}

KEATWVTDKPLTLKIHMHFRDKWWDENWPVAKESFRLTNVKLQSVANKAATNSQEQQNLMMASGDLPDVVGGDNLKDKFIQYGQEGAFVPLNKLDQYAPHIKAFFKSHPEVERAIKAPDGNIYFIPYVPDGVVARGYFIREDWKKLNLKPPQNIDEYTVLKAFKEKDPMNGNGKADEVFPIDRHPDEVFRVLVNFWGARSSGSDNYMDFYIDNGRVKHPWAETAFRDGMKHVAQWYKEGLIDKEIFTRKAKAREQMFGGNLGGFTHDWFASTMTFNEGLAKTVPGFKLIPIAPPNTSKGQRWEEDSRQKVRPDGWAITVKNKNPVETIKFFDFYFSRPGRDISNFGVPGVTYDIKNGKAVFKDSVLKSPQPVNQNLYDMGAQIPIGFWQDYDYERQWTTPEAQAGIDMYVKGKYVMPGFEGVNMTREERA

IYDKYWADVRTYMYEMGQAWVMGTDVDTWDEYQRQLKLRGLYQVLQMMQQAYDRQYKN

>d1cb6a2 c.94.1.2 (A:1335-1691) Lactoferrin {Human (Homo sapiens)}

EEEVAARRARVVCAVGEQELRKCNQWSGLSEGSVTCSSASTTEDCIALVLGEADAMSLDGGYVYTAGKCGLVPVLAENYKSQQSSDPDPNCVDRPVEGYLAVAVVRRSDTSLTWSVKGKKSCHTAVDRTAGWNIPMGLLFNQ

TGSCKFDEYFSQSCAPGSDPRSNLCALCIGDEQGENKCVPNSNERYYGTGAFRCLAENAGDVAFKVVDVTVLQ

NTDGNNEAWAKDLKLADFALLCLDGKRKPVTEARSCHLAMAPNHAVVSRMDKVERLKQVLLHQQAQKFGNGSDCPDKFCFLQSETKNLLFDNTECLARLHGKTTYEYLGPQYVAGITNLKKCSTSPLLEACEFLRK

>d1lct_ c.94.1.2 (-) Lactoferrin {Human (Homo sapiens)}

RSVQWCASNPEATKCFWQRNMRKVRGPPVSCIKRDSPIQCIAENRADAVTLDGGFIYEAGLAPYKLRPVAAEVYGTTERQPRTHYYAVAVVKKGGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLRFLNWTGPPEPIEAAVARFFSASCVPGADKGARFFSASCVPGADKGQFPNLCLRCAGTGENKCAFSSQEPYFSYSGAFKCLRDGAGDVAFIRESTVFEDLSDEAERDEYELLCPDNTRKPVDKFKDCHLARVPSHAVVARSVNGKEDAIWNLRLQAQEKFQDKSPKFQLFGSPSGQD

LLFKDSAIGFSRVPPRIDSGLYLGSFYTA

>d1lgbc_ c.94.1.2 (C:) Lactoferrin {Human (Homo sapiens)}

HYYAVAVVKKGGSFQLNELQGLKSCHTGLRRTAGWNVPIGTLRFLNWTGPPEPIEAAVARFFSASCVPGADKGQFPNLCLRCAGTGENKCAFSSQEPYFSYSGAFKCLRDGAGDVAFIRESTVFEDLSDEAERDEYELLCPDNTRKPD

DKFKDCHLAR

>d1ce2a1 c.94.1.2 (A:1-333) Lactoferrin {Domestic water buffalo (Bubalus arnee bubalis)}

APRNVRWCTISQPEWLKCHRWQWRMKKLGAPSITCVRRASVLECIRAIITEKKKADAVTLDGGMVEAGRDPYKLRPVAAEIYGTKEQPQTHYYAVAVVKKGSNFQLDQLQGRNSCHTGLGRSAGWNIPMGILRPYLSWTESLEPLQGAVAKFFSASCVPCVDRQAYPNLCQLCKGEGENQCACSPREPYFGYSGAFKCLQDGAGDVAFVKETTVFENLP

EKADRDQYELLCLNNTRAPVDAFKECHLAQVPSHAVVARSVDGKEDLIWKLLSKAQEKFQDKSPKFQLFGSP

PGQRDLLFKDSALGFLRIPSKVDSALYLGSRYLALKNLRE

>d1ce2a2 c.94.1.2 (A:334-689) Lactoferrin {Domestic water buffalo (*Bubalus arnee bubalis*)}
TAEEVQARRARVVWCAVGPEEQKKCQQWSQQSGQIVTCATASTTDDCIALVLGEADALSLDGGYIYTAKCG
LPVLAENRKSSKHSSLDCVLRPTEGYLAVAVVKANEGLTWNSLKGKKSCHTAVDRTAGWNIPMGLIANQTGS
CAFDEFFSQSCAPGADPKSRLCALCAGDDQGLDKCVPNSKEYYGYTGAFRCLAEDVGDAFVKNDTVWENT
NGESTADWAKNLNREDFRLCLDGTRPVTEAQSCHLAVAPNHAVVLSERAAHVEQVLLHQQALFGENGKN
CPDKFCLFKSETKNLLFNDNTECLAKLGGRPTYEEYLGTEYVTIAIANLKKCSTSPLLEACAFLTR

>d1b1xa1 c.94.1.2 (A:1-333) Lactoferrin {Horse (*Equus caballus*)}
APRKSVRWCTISPAEAAKCAKFQRNMKKVRGSPVSCIRKTSSFECIQAIAANKADAVENTLDGLVYEAGLHPYKLR
PVAAEVYQTRGKPQTRYYAVAVVKKGSGFQLNQLQGVKSCHTGLGRSAGWNIPIGTLRPLYLNWTGPPEPLQKA
VANFFSASCVPCADGKQYPNLRCAGTEADKCACSSQEPYFGYSGAFKCLENGAGDVAFVKDSTVFENLPDEA
ERDKYELLCPDNTRKPVDKFECHLARVPSHAVVARSVDGREDLIWKLHRAQEEFGRNKSSAFQLFGSTPGEQ
DLLFKDSALGFVRIPSQIDSGLYLGANYLTATQNLRE

>d1b1xa2 c.94.1.2 (A:334-689) Lactoferrin {Horse (*Equus caballus*)}
TAAEVAARRERVWCAVGPEEERKCKQWSDVSNRKVACASASTTEECIALVLGEADALNLDGGFIYAGKCGL
VPVLAENQKSQNSNAPDCVHRPPEGYLAVALVRKSDADLTWNNSLSGKKSCHTGVGRTAAWNIPMIGLLFNQT
GSCKFDKFFSQSCAPGADPQSSLALCVGNNEENKCMNPSEERYGYTGAFRCLAEKAGDVAFVKDVTVLQ
NTDGKNSEPWAQDLKQEDFELLCLDGTRKPVAEAESCHLARAPNHAVVSQSDRAQHLKKVLFLQQDQFGGN
GPDCEPGKCLFKSETKNLLFNDNTECLAEQGKTTYEQYLGEYVTSITNLRRCSSPLLEACAFTRA

>d1dtza1 c.94.1.2 (A:1-333) Lactoferrin {Arabian camel (*Camelus dromedarius*)}
ASKKSVRWCTTSPAESKKCAQWQRRMKVVRGSPVTCVKKTSRFECIQAISTEKADAVENTLDGLVYDAGLDPYKL
RPIAAEVYGTENQPQTHYYAVAIKKGTNFQLNQLQGLKSCHTGLGRSAGWNIPMGLRPFLDWTGPPEPLQK
AVAKFFSASCVPCVDGKEYPNLCQLCAGTGENKCACSSQEPYFGYSGAFKCLQDGAGDVAFVKDSTVFESLPAK
ADRQYELLCPNNTRKPVDASFQECHLARVPSHAVVARSVNGKEDLIWKLVKAQEKFGRGKPSAFQLFGSPAG
QKDLLFKDSALGLLIPKKIDSGLYLGSNYITAIRGLRE

>d1dtza2 c.94.1.2 (A:334-689) Lactoferrin {Arabian camel (*Camelus dromedarius*)}
TAAEVELRAQVVWCAVGSDEQLKCQEWSRQSNQSVVCATASTTEDCIALVLGEADALSLDGGIYIAGKCGL
VPVLAESQQSPESSGLDCVHRPVKGYLAVALVRKANDKITWNSLRGKKSCHTAVDRTAGWNIPMGPLFKDTD
SCRFDFFSQSCAPGSDPRSKLCALCAGNEEGQLKCVPNSSERLYGYTGAFRCLAENVGDVAFVKDVTLDNTD
GKGTEQWAQDLKLQDFELLCLNGTRKPVTEAESCHLPVAPNHAVVSRIDKVAHLRQVLLRQQAHFGRNGEDCP
GKFCLFQSXTKNLLFNDNTECLAKLQGKTTYEYLGPQYVTAIAKLLRCSTSPLLEACAFLMR

>d1dot_1 c.94.1.2 (1-334) Ovotransferrin {Duck (*Anas platyrhynchos*)}
APPKTTVRWCTISSAEKKCNSLKDHMQQERTLSCVQKATYLCIKAISNEADAISLDGGQVFEAGLAPYKL
KPIAAEVYERSGGSTSYYAVAVVKKGTDPMIKDLRGKTSCHTGLGRSAGWNIPIGTLIHREDIEWEGIESGISEQ
AVAKFFSASCVPGATIEQKLCRQCKGDAKTKCLRNGPYSYSGAFQCLKGDKGDVAFVKHTTVQENAEEKDEY
ELLCLDGSRQPVDSYKTCNWARVAAHAVVARDDSKIDDIFSFLGMQAYSLGVDTTSDFHLFGPPGKKDPVLKD
LLFKDSAIMLKRVPELMDSQLYLGFEYYSAIQLRKD

>d1dot_2 c.94.1.2 (335-686) Ovotransferrin {Duck (*Anas platyrhynchos*)}
QLTVGPRENKIQWCAVGKDEKSCKDRWSVVSNGEVECTILDDNKDCIVKITGEADAISLDGGFVTAGVCGLV
PVVGESYEDETQCSKDEEQPAYYFAVAVVKSSAITWNNLQGKKSCHTAVGRTAGWNIPMGLIHNKTGSCDFD
DYFSEGCAPGSPPNSRLCKLCQGSGENLLEKCVASSHEKYYGYTGALRCLVEQGDVAFIKHTVGENVGSNKD
DWAKGLTRDDFELLCTNGKRAKTMDYKTCHLAKVPTHAVVARPEKANKIRELLEGQEKLFGHGTEKERFMMF
QSQTKDLLFKALTCLVKLQRQGITYKEFLGDEYYASVASLNTCNPSDLLQVCTFLEDK

>d1gv8a_c.94.1.2 (A:) Ovotransferrin {Duck (*Anas platyrhynchos*)}
SYYAVAVVKKGTDPMIKDLRGKTSCHTGLGRSAGWNIPIGTLIHRGDIEWEGIESGSVEQAVAKFFSASCVPGAT

TEQKLCRQCKGDAKTKCLRNAPYSGYSGAFQCLKGKDGVAFVKHTTVQENAPEEKDEYELLCLDGTRQPVDS

YKTCNWARVAA

>d1ieja_c.94.1.2 (A:) Ovotransferrin {Chicken (Gallus gallus)}

KSVIRWCTISSPEEKCNNLRLDTQQERISLTCVQKATYLDCAIKAIANNEADAITLDGGQVFEAGLAPYKLPIAAEVYEHTEGSTTSYYAVAVVKKGTEFTVNDLQGKTSCHTGLGRSAGWNIPIGTLLHRAIEWEGIESGSVEQAVAKFFSASCVPGATIEQKLCRQCKGDPKTKCARNAPYSGYSGAFHCLKDGKDGVAFVKHTVNENAPDQKDEYELLCLDGSRQPVNDYKTCNWARVAAHAVVARDDNKVEDIWSFLSKAQSDFGVDTKSDFHLFGPPGKKDPVLKDLLFKDSAIMLKRVPSLMDSQLYLGFEYYSAIQSMR

>d1iq7a_c.94.1.2 (A:) Ovotransferrin {Chicken (Gallus gallus)}

RIQWCAVGKDESKCDRWSVVSNGDVETVVDET KDCIIMKGEADAVALDGGLVYTAGVGLVPVMAERY DDESQCSTDERPASYFAVAVARKDSNVNNLKGKKSCHTAVGRTAGWVPMGLIHNRGTCNFDEYFSEG CAPGSPNSRLCQLCQGSGGIPPEKCVASSHEKYFGYT GALRCLVEKGDVAFIQHSTVEENTGGKNADWAKNLQMDDFELLCTDGRANVMDYRECNLAEVPTHAVVRPEKANKIRDLLERQEKRFGVNGSESKFMMFESQN KNDLLFKDLTKCLFKVREGTTYKEFLGDKFYTVISSLKTCNPSDLQMCSFLEGK

>d1jnf a1 c.94.1.2 (A:3-334) Transferrin {Rabbit (Oryctolagus cuniculus)}

EKTVRWCAVNDHEASKCANFRDSMKKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLADGLVHEAGLTPNN LKPVVAEFYGSKENPKTFYYAVALVKKGSNFQLNELQGKKSCHTGLGRSAGWNIPIGLLCDLPEPRKPLEKAVAS FFSGSCVPCADGADFPQLCQLCPGCGCSSVQPYFGYSGAFKCLKDGLGDVAFVKQETIFENLPSKDERDQYELL CLDNTRKPVDEYEQCHLARVPSHAVVARSVDGKEDLIWELLNQAQEFGKDKSGDFQLFSSPHGKNLLFKDSA YGFFKVPPRMDANILYLGYEYVTAVRNLREGICPDP

>d1jnf a2 c.94.1.2 (A:335-676) Transferrin {Rabbit (Oryctolagus cuniculus)}

LQDECKAVKWCAKGHHERLKCDEWSVTSGGLIECESAETPEDCIAKIMNGEADAMSLDGGYVYIAGQCGLVPV LAENYESTDCKKAPPEEGYLSVAVVKSNP DINWNNLEGKKSCHTAVDR TAGWNIPMGLLYNRINHCRFDEFFR QGCAPGSQKNSSLCELCVGP SVCAPNNREGYYGTGAFRCLVEKGDVAFVKQETIFENLPSKDERDQYELLCL EEDFELLCLDGTRKPVSEAHNCHLAKAPN HAVVSRDKAACVKQKLLDLQVEFGNTVADCSSKFCMFHSKTDL LFRRDDTKCLVDLRGKNTYEKYLGADYIKAVSNLRKCSTSRLLEACTFHKH

>d1tf d __ c.94.1.2 (-) Transferrin {Rabbit (Oryctolagus cuniculus)}

VRWC AVNDHEASKCANFRDSMKKVLPEDGPRIICVKKASYLDCIKAIAAHEADAVTLADGLVHEAGLTPNNLKP VVAEFYGSKENPKTFYYAVALVKKGSNFQLNELQGKKSCHTGLGRSAGWNIPIGLLCDLPEPRKPLEKAVASFFS GSCVPCADGADFPQLCQLCPGCGCSSQPYFGYSGAFKCLKDGLGDVAFVKQETIFENLPSKDERDQYELLCL NTRKPVDEYEQCHLARVPSHAVVARSVDGKEDLIWELLNQAQEFGKDKSGDFQLFSSPHGKNLLFKDSAYGF FK

>d1a8e_c.94.1.2 (-) Transferrin {Human (Homo sapiens)}

DKTVRWCAVSEHEATKCQSFRDHMKSVIPSDGPSVACVKKASYLDCIRAI AANEADAVTLADGLVYDAYLAPNN LKPVVAEFYGSKEDPQT FYYAVAVVKKDSGFQMNQLRGKKSCHTGLGRSAGWNIPIGLLCDLPEPRKPLEKAV ANFFSGSCAPCADGTD FPQLCQLCPGCGC STLNQYFGYSGAFKCLKDGA GDVAFVKHSTIFENLANKADR DQY ELLCLDNTRKPVDEYKDCHLAQVPSHTVVARSMGGKEDLIWELLNQAQEFGKDKSKEFQLFSSPHGKD LFK DSAHGFLKVPPRMDAKMYLGYEYVTAIRNLREGTC

>d1h76a1 c.94.1.2 (A:3-333) Transferrin {Pig (Sus scrofa)}

QKTVRWCTISNQEANKCSSFRENMSKAVKNGPLVSCVKKSSYLDCAIKAIRDKEADAVTLADGLVFEAGLAPYNL KPVVAEFYQKDNPQTHYYAVAVVKKGSNFQWNQLQGKRSCHTGLGRSAGWIIPMGLLYDQLPEPRKPIEKA VASFSSSCVPCADPVNFPKLCQQCAGKGAEKCACSNHEPYFGYAGAFNCLKEDAGDVAFVKHSTVLENLPDK ADRDQYELLCRDNTRRPVDDYENCYLAQVPSHAVVARSVDGQEDSIWELLNQAQEFG RDKSPDFQLFSSSH GKDLFKDSANGFLKIPSKMDSSLYLGYQYVTALRNLEE

>d1h76a2 c.94.1.2 (A:342-687) Transferrin {Pig (Sus scrofa)}

ECKKVRWCAIGHEETQKCDAWSINSGGKIECVSAENTEDCIAKIVGEADAMSLDGGYIYAGKGLVPVLAENY
KTEGENCVNTPEKGYLVAVVKKSSGPDLNWNNLKGKKSCHTAVDRTAGWNIPMGLLYNKINSCKFDQFFGE
GCAPGSQRNSSL CALCIGSERAPGRECLANNHERYYYGTGAFRCLVEKGDVAFVKDQVQQNTDGKNKDDW
AKDLKQMDFELLCQNGAREPVDNAENCHLARAPNHAVVARDDKVCVAEELLKQQAQFGRHVTDCSSFCM
FKSNTKDLLFRDDTQCLARVGKTTYESYLGADYITAVANLRKCSTSKLLEACTFHSA

>d1afwa1 c.95.1.1 (A:25-293) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

KNSLLEKRPEDVVVIVAANRSAIGKGFKGAFKDVTNDYLLYNFLNEFIGRFPEPLRADLNLIIEVACGNVLNVGAGA
TEHRAACLASGIPYSTPFVALNRQCSSLTAVNDIANKIKVGQIDIGLALGVESMTNNYKNVNPLGMISSEELQK
NREAKKCLIPMGITNENVAANFKISRKDQDEFAANSYQKAYKAKNEGLFEDEILPIKLPDGSICQSDEGPRPNVT
AESLSSIRPAFIKDRGTTAGNASQVSDGVAGVLLARRSVANQ

>d1afwa2 c.95.1.1 (A:294-417) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

LNLPVLGRYIDFQTGVVPPEIMGVGPAYAIPKVLEATGLQVQDIDIFEINEAAFAQALYCIHKLGIDLNVNPRGG
AIALGHPLGCTGARQVATILRELKKDQIGVVSMCIGTGMGAAAIFIKE

>d1qfla1 c.95.1.1 (A:4-268) Biosynthetic thiolase {Zoogloea ramigera}

SIVIASAARTAVGSFNGAFANTPAHELGATVISAVLERAGVAAGEVNEVLGQVLPAGEGQNPQPARQAAMKAGVP
QEATAWMNQLCGSGLRAVALGMQQIATGDASIIVAGGMESMSMAPCAHLRGGVKMDFKIDTMIKD
GLTDAFYGYHMGTTAENVAKQWQLSRDEQDAFAVASQNKAEEAAQKDGRFKDEIVPFIVKGRKGDTVDAEYI
RHGATLDSMAKLRPAFDKEGTVTAGNASGLNDGAAAALLMSEAEASRRG

>d1qfla2 c.95.1.1 (A:269-392) Biosynthetic thiolase {Zoogloea ramigera}

IQPLGRIVSWATVGVDPKVMGTGPIPASRKALERAGWKIGDLDLVEANEAAFAQACAVNKDLGWDPSPNVN
GGAIAIGHPIGASGARILNLLFEMKRRGARKGLATLCIGGGMGVAMCIESL

>d1ek4a1 c.95.1.1 (A:1-253) Beta-ketoacyl-ACP synthase I {Escherichia coli}

MKRVVITGLGIVSSIGNNQQEVLASLREGRSGITFSQELKDSGMRSHVWGNVKLDTTGLIDRKVVRFMSDASIY
AFLSMEQAIADAGLSPEAYQNNPRVGLAGSGGGSPRFQVFGADAMRGPRGLKAVGPYVVTKAMASGVSC
LATPFKIHGVNYSISSASATSAAHCIGNAVEQIQLGKQDIVFAGGGEELCWEMACEFDAMGALSTKYNDTPEKAS
RTYDAHRDGFVIAGGGGMVVVEELEHALARGAH

>d1ek4a2 c.95.1.1 (A:254-406) Beta-ketoacyl-ACP synthase I {Escherichia coli}

YAEIVGYGATSDGADMVAPSSEGAVRCMKMAMHGVDTPIDYLNHSHTPVGDKELAAIREVFGDKSPAIS
ATKAMTGHSLGAAGVQEAIYSLMLEHGFIAPI SINIEELDEQAAGLNIVTETTDRELTTVMSNSFGFGGTNATLV
MRKLKD

>d1kas_1 c.95.1.1 (2-251) Beta-ketoacyl-ACP synthase II {Escherichia coli}

KRRVVVTGLGMLSPVGNTESTWKALLAGQSGISLIDHFDT SAYATKFAGLVKDFNCEDIISRKEQRKMDAFIQY
GIVAGVQAMQDGSLEITEENATRIGAAIGSGIGGLGLIEENHTSLMNGGPRKISPFFVPSTIVNMVAGHLTIMYG
LRGPSISIATACTSGVHNIGHAARIIAYGDADVMVAGGAEKASTPLGVGGFGAARALSTRNDNPQAASRPWDK
ERDGFVLGDGAGMLVLEEYEHAKKRG

>d1kas_2 c.95.1.1 (252-412) Beta-ketoacyl-ACP synthase II {Escherichia coli}

KIYaelvgfgmssdayhmtspengagaalamanalrdagieasqigyvnahgtstpagdkaeaqavktifge
AASRVLVSSTKSMTGHLLGAAGAVESIYSLALRDQAVPPTINLDNPDEGCDDFVPHEARQVSGMEYTLCSNF
GFGGTNGSLIFKKI

>d1e5ma1 c.95.1.1 (A:6-255) Beta-ketoacyl-ACP synthase II {Synechocystis sp.}

KKRVVVTGLGAIPIGNTLQDYWQGLMEGRNGIGPITRFDASDQACRFGGEVKDFDATQFLDRKEAKRMDRF
CHFAVCASQQAINDAKLVINELNADEIGVILGTGIGGLKVLEDQQTIILDKGPSRCSPFMIPMMIANMASGLTAI
NLGAKGPNNCTVTACAAGSNAIGDAFRLVQNGYAKAMICGGTEAAITPLSYAGFASARALSFRNDDPLHASRPF

DKDRDGFMGEGSGILILEELESALARGA

>d1e5ma2 c.95.1.1 (A:256-416) Beta-ketoacyl-ACP synthase II {Synechocystis sp.}
KIYGEMVGYAMTC DAYHITAPVDPGRGATRAIAWALKDSGLKPEMVS YINAHTSTPANDVTETRAIKQALGN
HAYNIAVSSTKSMTGHLLGGGGIEAVATVMAIAEDKVPTINLENPDPECDLDYVPGQSRALIVDVALNSFGF
GGHNVTLAFKKYQ

>d1hnja1 c.95.1.1 (A:1-174) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}
MYTKIIGTGSYLPEQVRTNADLEKMVDTSD EWIVTRTGIRERHIAAPNETVSTMGF EAATRAIEMAGIEKDQIG
LIVVATTSA THAFPSAACQIQSMILGIKGCPAFDVAAACAGFTYALSVADQYVKG AVKYALVVGSDVLARTCDPT
DRGTIIIFGDGAGAAVLAASEEPM

>d1hnja2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}
ISTHLADGSYGE LTLPNADRVNPENSIH LT MAGNEVFKVAVTEL A HIVDET LA ANNLD RSQLDW LVP HQANL
RIISATAKLGMSMDNVV VTLD RGNTS AASV PCALDEA VRDG RI PGQL VLLEAF GGGFT WGS ALV RF
>d1hzpa1 c.95.1.1 (A:-10-174) Ketoacyl-ACP synthase III (FabH) {Mycobacterium
tuberculosis}

MTEIATTSGAR SVG LLSVGAYR PER VVT NDEIC QHID SSDE WIY TRG IKTR RFA ADDES AAS MATE ACRR ALS N
AGLSAADIDGVIVTTNT HFLQ TPPA PMVA ASLG AKG I LGF DLS AGCAG FG YALG AAADM IRGG AATML VVG
TEKLSPTID MYDRGNC FIFADGAA VVVGETPFQGI

>d1hzpa2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Mycobacterium
tuberculosis}
GPTVAG S DGEQ ADAIR QD IDW ITFA QN P SGPR PFVR LEGPA VFRWA FKM GDV GR RAM DAAG V RPD QID V
FVPHQANSR INELLV KNLQLRP DAVV VANDIE HTGNTS AASIPLAMA ELL TTGA KPG DL ALLI GY GAG LS YAA QV
VRM

>d1bi5a1 c.95.1.2 (A:1-235) Chalcone synthase {Alfalfa (Medicago sativa)}
MVS VSEIRKA QRAEGPATILA IGTANPANC VEQSTY PDFY FKITNSEHKTELKEKFQRMC DKSMIK RRYMLTE EI
LKENPNVCEYMAPSL DARQDMVVVEV PRLG KEEA V KAI KEWG QPK SKITHLIV CTTSGV DMPG ADY QLT KLL
GLRP YVKRYMMYQQG AFAG GTV RLAKDLA ENNK GARV LVC SEV TAVT FRG PSD THLD S LVG QAL FGD GAA
ALIVGSDPVPEIEKP

>d1bi5a2 c.95.1.2 (A:236-389) Chalcone synthase {Alfalfa (Medicago sativa)}
IFEMVWTAQTIAPDSEG AIDGHL REAGLTFHLLKD VPG I VSKN ITK ALVE AFEPLG ISD YNS IFWIAHPGG PAILDQ
VEQKLALKPEK MNATREVLSE YGNMSSACVLF ILDEM RKK STQNGLKT GEGLEWGV LFG FGP GLT IETV VLR S
VAI

>d1ee0a1 c.95.1.2 (A:20-235) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}
GLATILA IGTATPPNCVAQADYADYYFRVTKSEHMVDLKEFKRICEKTAIKKRYL ALTEDY LQENPTMCEFMAPS
LNARQDLVVTGVPM LGK EAAVKA IDEWGLPKSKITHLIFCTTAGV DMPGADYQLV KLLG LSPS V KRYMLYQQG
AAAGGT VRLA KDLA ENNK GS RVLIV CSEIT AILFH GPNE NHDSL V A QALFGD GAA ALIVGSGP H

>d1ee0a2 c.95.1.2 (A:236-395) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}
AVERPI FEIVSTDQ TILPD TEKAMKL HLREGGLTFQLH RDVPLM VAKNIENAAE KALSPLG I TDW NSV FW MVHP
GGRAILDQ VERKLN KEDKL RASR HV LSE YGNL ISACVLF IIDE VRK RSMA EGK STTGE GLDCGV LFG FGP GM TV
ETV VLR SRV RT

>d1feha1 c.96.1.1 (A:210-574) Fe-only hydrogenase, catalytic domain {Clostridium pasteurianum}
HMDRVKNALNAPEKH VIVAMIAPS VRASIGEL FMGFG DV TGKI YTALRQLGFD KIFD INF GAD MTIME EATE
LVQRIENNGPFPMTS CCPG WVRQAEN YYPELLNNLSSAKSPQ QIFGTASKTYYPSISGLDPKNVFTV MPCT
SKKFEADRPQM EKDGLR DIDA VITRELAK MIKDA KIPFA KLEDSEADP AMGE YSGAGA IFGATGGVMEA ALRS
AKDFAENAELEDIEYKQVRGLNGIKEAEVEINNNKYNVAVINGASNLFKFMKSGMINEKQYHFIEVMACHGGC

VNGGGQPHVNPKDLKEVKDIKKVRASVLYNQDEHLSRKSHENTALVKMYQNYFGKPGEGRAHEILHFKYKK
>d1hfel1 c.96.1.1 (L:87-398) Fe-only hydrogenase larger subunit, C-domain {Desulfovibrio desulfuricans}
WVPEVEKKLDGKVCKIAMPAPAVRYALGDAFGMPVGSVTTGKMLAALQKLGFAHCWDTEFTADVTIWEEGS
EFVERLTKSDMPLPQFTSCCPGWQKYAETYYPELLPHFSTCKSPIGMNGALAKTYGAERMKYDPKQVYTVSIM
PCIAKKYEGLRPELKSSGMRDIDATLTRELAYMIKKAGIDFAKLPDGKRDSLMGESTGGATIFGVGTGGVMEAAL
RFAYEAVTGKKPDSDWDFKAVRGLDGIKEATVN VGGTDVKAVVHGAKRFKQVCDDVKAGKSPYHFIYMACP
GGCVCGGGQPVMGVLEAM
>d1aln_1 c.97.1.1 (1-150) Cytidine deaminase {Escherichia coli}
MHPRFQTAFAQLADNLQSALEPIADKYFPALLGEQVSSLKSATGLDEDALAFALLPLAACARTPLSNFNVGAI
ARGVSGTWYFGANMEFIGATMQQTVAHQSAISHAWLSGEKALAAITVNYTPCGHCRQFMNELNSGLDLRI
HLP
>d1aln_2 c.97.1.1 (151-294) Cytidine deaminase {Escherichia coli}
GREAHALRDYL PDAFGPKDLEIKTLLMDEQDHGYALTGDALSQAAIAANRSHMPYSKSPSGVALECKDGRIFS
GSYAENAAFNPTLPLQGALILLNLKGYDYPDIQR AVALAEKADAPIQW DATSATL KALGCHSIDRVLLA
>d1g8ma2 c.97.2.1 (A:201-593) AICAR transformylase domain of bifunctional purine biosynthesis enzyme ATIC {Chicken (Gallus gallus)}
GVSQPLRLYGMNPHQSPAQLYTTRPKLPLTVNGSPGFINLC DALNAWQLV KELKQALGIPAAASF KVSPAGA
AVGIPLSEEEAQVCMVHDLHKTLPLASAYARS RGADMSSFGDFIALSDICDVPTAKIISREVSDGVVAPGYEEE
ALKILSKKKNGGYCVLQMDPNYEPPDNEIRTL YGLQLM QKRNNAVIDRS LFKNIVTKNKTLPESAVRDLIVASIAV
KYTQSNSVCYAKDGQVIGIGAGQQSRIHCTRLAGDKANSWWLRHHPRVLSMKFKAGVKRAEV SNAIDQYVT
GTIGEDEDLVKWQAMFEEVPAQLTEAEKKQWI AKLTAVSLSSDAFFPFRDNVDRAKRIGVQFIVAPSGSADEV
VIEACNELGITLIHTNLRLFHH
>d1rgea_d.1.1.1 (A:) RNase Sa {Streptomyces aureofaciens}
DVSGTVCL SALPPEATDTLNLIASDGPFPYSQDGVV FQNRESVLPTQSYGYYHEYTVITPGARTRGTRRIITGEAT
QEDYYTGDHYATFSLIDQTC
>d1fus_d.1.1.1 (-) RNase F1 {Fusarium moniliforme}
ESATT CGSTNYSASQVRAAANAACQYYQNDTAGS STYPHTNNYEGFD FSVSSPYEW P ILSSGDV YSGGSPG
ADR VVINTNCEYAGAITHT GAS GNNFVGCSGTN
>d1i0va_d.1.1.1 (A:) RNase T1 {Aspergillus oryzae}
ACDYTCGSNCYSSDVSTAQAAGYKLHEDGETVGSNSYPHKYNNYEGFD FSVSSPYEW P ILSSGDV YSGGSPG
ADR VVFNENNQLAGVITHT GAS GNNF VECT
>d1rtu_d.1.1.1 (-) RNase U2 {Ustilago sphaerogena}
CDIPQSTNCGGNVYNSDDINTAIQ GALDDVANGDRPDNYPHQYYXEASEDITLCCGSGPWSEFPLVNGPYYS
SRDNYVSPGPDRVIYQTNTGEFCATVHTGAASYDGFTQCS
>d1a2pa_d.1.1.1 (A:) Barnase/Binase {Bacillus amyloliquefaciens}
VINTFDGVADYLQTYHKLPDNYITKSEA Q ALGWVASKGNLADVAPGKSIGGDIFSNREGKLPKSGRTWREADI
NYTSGFRNSDRILYSSDWLIYKTTDHYQTFTKIR
>d1goua_d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}
AVINTFDGVADYLIRYKRLPDNYITKSQASALGWVASKGNLAEVAPGKSIGGDVFSNREGR LPSAGSRTWREADI
NYVSGFRNADRLVYSSDWLIYKTTDHYATFTRIR
>d2rbia_d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}
VINTFDGVADYLIRYKRLPDNYITKSQASALGWVASKGNLAEVAPGKSIGGDVFSNREGR LPSASGRTWREADI
NYVSGFRNADRLVYSSDWLIYKTTDNYATFTRIR

>d1rds__ d.1.1.1 (-) RNase Ms {Molsin (Aspergillus saitoi)}

ESCEYTCGSTCYWSSDVSAAKAKGYSLYESGDTIDDYPHEYHDYEGDFPVSGTYYEYPIMSDYDVYTGGSPGA
DRVIFNGDDELAGVITHGTGASGDDFVACSSS

>d0rst__ d.1.1.1 (-) RNase St {Streptomyces erythreus}

QAPCGDTSGFEEVRLADLPPEATDTYELIEKGGPYPYPEDGTVFENREGILPDCAEGYYHEYTVKTPSGDDRGAR
RFVVGDGGEYFYTEDHYESFRLTIVN

>d1aqza_ d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus restrictus), restrictocin}

ATWTCINQQLNPKTNKWEDKRLLYSQAKAESNSHHAPLSDGKTGSSYPHWFTNGYDGNGKLIKGRTPIKFGKA
DCDRPPKHSQNGMGKDDHYLLEFPTFPDGHDYKFDSSKKPKENPGPARVIYTPNPKVFCGIAHQQRGNQGDLR
LCSH

>d1de3a_ d.1.1.1 (A:) Ribotoxin {Fungus (Aspergillus giganteus), alpha-Sarcin}

AVWTCLNDQKNPKNKYETKRLLYNQNKAESNSHHAPLSDGKTGSSYPHWFTNGYDGDGKLPKGRTPIKFG
KSDCDRPPKHSKDNGKTDHYLLEFPTFPDGHDYKFDSSKKPKENPGPARVIYTPNPKVFCGIAHTKENQGELKL
CSH

>d1cnsa_ d.2.1.1 (A:) Plant class II chitinase {Barley (Hordeum vulgare)}

SVSSIVSRAQFDRMILLHRNDGACQAKGFYTYDAFAAAAAFSGFGTTGSADVQKREVAAFLAQTSHETTGGW
ATAPDGAFAWGYCFKQERGASSDYCTPSAQWPCAPGKRYYGRGPIQLSHNYNYGPAGRAIGVDLLANPDLVAT
DATVSFKTAMWFWMQAQPPKPSSHAVIVGQWSPSGADRAAGRVPFGVITNIINGGIECGHGQDSRVADRI
GFYKRYCDILGVGYGNLDCYSQRPFA

>d1dxja_ d.2.1.1 (A:) Plant class II chitinase {Jack bean (Canavalia ensiformis)}

DVGVIDASLFQDLLKHRNDPACEGKGFSYNAFTAARSFGGGFTGDTNTRKREVAAFLAQTSHETTGGAA
GSPDGPYAWGYCFVTERDKSNKYCDPGTPCPAGKSYYGRGPIQLTHNYNYAQAGRALGVLDLNNPDLVARDAV
ISFKTAIWFWMTPQGNKPSCHDVITNRWTPSAADVAANRTPGFGVITNIINGGIECGRGPSPASGDRIGFYKRY
CDVLHLSYGPNLNCRDQRPFGG

>d1lsg_1 d.2.1.2 (1-144) Lysozyme {Chicken (Gallus gallus)}

MKVGRCELAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRT
PGSRNLNCIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRLQQHHLGAKQA
GDV

>d3lzt__ d.2.1.2 (-) Lysozyme {Chicken (Gallus gallus)}

KVFGRCLEAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRT
GSRNLCNIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRNRCKGTDVQAWIRGCRL

>d1jse__ d.2.1.2 (-) Lysozyme {Turkey (Meleagris gallopavo)}

KVYGRCELAAMKRLGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRT
SKNLCNIPCSALLSSDITASVNCAKKIASGGNGMNAWVAWRNRCKGTDVHAWIRGCRL

>d1hh_ d.2.1.2 (-) Lysozyme {Guinea fowl (Numida meleagris)}

KVFGRCLEAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRT
GSRNLCNIPCSALQSSDITATANCAKKIVSDGDMNAWVAWRKHCKGTDVRVWIKGCRL

>d1ghla_ d.2.1.2 (A:) Lysozyme {Pheasant (Phasianus colchicus)}

GKVYGRCELAAMKRMGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGSTDYGILQINSRWWCNDGRT
PGSKNLCHIPCSALLSSDITASVNCAKKIVSDGNGMNAWVAWRKHCKGTDVNVWIRGCRL

>d1jsf__ d.2.1.2 (-) Lysozyme {Human (Homo sapiens)}

KVFERCELARTLKRLGMDGYRGISLANWMCLAKWESGYNTRATNYNAGDRSTDYGFQINSRYWCNDGKTPG
AVNACHLSCSALLQDNIADAVACAKRVVRDPQGIRAWVAWRNRCQNRDVRQYVQGCGV

>d2eql__ d.2.1.2 (-) Lysozyme {Horse (Equus caballus), milk}

KVFSKCELAHKLKAQEMDGFGGGYSLANWVCMAEYESNFNTRAFNGKNANGSSDYGLFQLNNKWCKDNK
RSSSNACNIMCSKLLDENIDDDISCAKRVVRDPKGMSAWKAWVKHCKDKDLSEYLASCNL
>d1qqya_d.2.1.2 (A:) Lysozyme {Dog (Canis familiaris), milk}
MKIFSKCELARKLKSMDGFGHGYSLANWVCMAEYESNFNTQAFNGRNSNGSSDYGIFQLNSKWWCKSNS
HSSANACNIMCSKFLDDNIDDDIACAKRVVKDPNGMSAWVAWVKHCKGKDLSKYLASCNL
>d1jug_d.2.1.2 (-) Lysozyme {Australian echidna (Tachyglossus aculeatus)}
KILKKQELCKNLVAQGMNGYQHITLPNVCTAFHESSYNTATNRNTDGSTDYGIFQINSRYWC HDGKTPGSK
NACNISCSKLLDDITDDLCAKKIAGEAKGLTPWVAWSKCRGHDL SKFKC
>d1lmg_d.2.1.2 (-) Lysozyme {Rainbow trout (Oncorhynchus mykiss)}
KVYDRCELARALKASGMDGYAGNSLPNVVCLSKWESSYNTQATNRNTDGSTDYGIFQINSRYWC DDGRTPG
AKNVCGIRCSQLTDDLTVAIRCAKRVVLDPNGIGAWVAWRLHCQNQDLRSYVAGCGV
>d1gd6a_d.2.1.2 (A:) Lysozyme {Silkworm (Bombyx mori)}
KTFTRCGLVHELRKHGFEENLMRNWVCLVEHESSRDTSKTNRNGSKDYGLFQINDRYWCSKGASPGKDCN
VKCSDLLTDDITKAACKAKKIYKRHRFDAWYGWKNHCQGS LPDISSC
>d1iiza_d.2.1.2 (A:) Lysozyme {Tasar silkworm (Antheraea mylitta)}
KRFTRCGLVNELRKQGF DENLMRDWVCLVENESARYTDKIANVNKNGSRDYGLFQINDKYWCSKGSTPGKDC
NVTCSQLTDDITVASTCAKKIYKRTKFDAWSGDHNHCNHSNPDISSC
>d1alc_d.2.1.2 (-) alpha-Lactalbumin {Baboon (Papio cynocephalus)}
KQFTKCELSQNL YDIDGYG RIALPEL ICTMFHTSGYDTQAIVENDESTEYGLFQISNALWCKSSQVPQSRNICDITC
DKFLDDDTDDIMCAKKI DIKGIDY WIAHKALCTEKLEQWLCEK
>d1b9oa_d.2.1.2 (A:) alpha-Lactalbumin {Human (Homo sapiens)}
KQFTKCELSQLK D IDGYGGI ALPEL ICTMFHTSGYDTQAIVENDESTEYGLFQISNKLWCKSSQVPQSRNICDITC
DKFLDDDTDDIMCAKKI DIKGIDY WLAHKALCTEKLEQWLCEK
>d1hfx_d.2.1.2 (-) alpha-Lactalbumin {Guinea pig (Cavia porcellus)}
KQLTKCALSH ELN LAGYR DITLPEWLCI IF HISGYDTQAIVKNSDHKEYGLFQINDKDFCESSTTVQSRNICDISC
DKL LDDDTDDIMCVKK I DIKGIDY WLAHKALCTEKLEQWLCEK
>d1fkqa_d.2.1.2 (A:) alpha-Lactalbumin {Goat (Capra hircus)}
MEQLTKCEVFQKLKDLKD YGGVSLPEWVCVAFHTSGYDTQAIVQNN DSTEYGLFQINN KIWCKDDQNPHSRN
ICNISCDKF LDDDTDDIVCAKKI LD KVGIN YWLAHKALCSEKLDQWLCEKL
>d1f6ra_d.2.1.2 (A:) alpha-Lactalbumin {Cow (Bos taurus)}
EQLTKCEVFRELKDLKG YGGVSLPEWVCTFHTSGYDTQAIVQNN DSTEYGLFQINN KIWCKDDQNPHSSNIC
NISCDKF LDDDTDDIMCVKK I DKGIDY WLAHKALCSEKLDQWLCEKL
>d1j8wa_d.2.1.2 (A:) alpha-Lactalbumin {Mouse (Mus musculus)}
TELT KCKVSHAIKDM DGYQGISLLEWTCVL FHTSGYDSQAVVNDNGSTEYGLFQISERFWCKSSEFP ESENICGI
SCDKL LDELD D DIVCAKKI VAIK GIDY WKA YKPM CSEKLEQWRCEKP
>d169la_d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRI DEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSEL DKAI GRNCNGVITKDEAEKLFN QDVDA VR
GILRNAKLKPVYDSLDAVRRCALINMV FQMGETGVAGFTNSLRMLQQKRWDAAA AAAAAA WAAATPNRA
KRVITTFRTGTW DAYK
>d174la_d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}
MNIFEMLRI DEGLRLKIYKDTEGYYTIGIGHLLAAAADLAAKA ALAAAIGRNTNGVITKDEAEKLFN QDVDA AV
RGILRNAKLKPVYDSLDAVRRCALINMV FQMGETGVAGFTNSLRMLQQKRWDAAA AAAAAA WAAATPNRA
AKRVITTFRTGTW DAYK NL
>d176la_d.2.1.3 (A:) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIEGLRLKIYKDTEGYYTIGIGHTLKVDGNSNAAKSELDKAIGRNTNGVITKDEAEKLFNQDVDAAV
RGILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRLQQKRWDEAAVNLAKSRWYNQTPNR
AKRVITTFRTGTWDAYKNL

>d189I__ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNLFEMLRIEGLRLKIYKDTEGYYTIGIGHLLTKSPDLNVAKSELDKAIGRNCNGVITKDEAEKLFNQDVDAAVR
GILRNPKLKPVYDSLDAVRRCALINMVFQMGETGVAGFTDSLRLQQKRWDEAAANLAKSRWYNQTPDRAK
RVITTFRTGTWDAYKNL

>d191I__ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKSELDKAIGRACAGAITKDEAEKLFNQDVDAAVR
GILRNAKLKPVYDSLDAVRRCALINMVFQMGETGVAGFTNSLRLQQKRWAAAAALAKSRWYNQTPNRA
KRVITTFRTGTWDAYK

>d192I__ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIEGLRLKIYKDTEGYYTIGIGHLLTKSPSLAAAKAALAAAIGRNTNGVITKDEAEKLFNQDVDAAVR
GILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRLQQKRWAAAAALAKSRWYNQTPNRA
KRVITTFRTGTWDAYK

>d217I__ d.2.1.3 (-) Phage T4 lysozyme {Bacteriophage T4}

MNIFEMLRIEGLRLKIYKDTEGYYTIGIGHLLTKSPSLNAAKEELDKAIGRNTNGVITKDEAEKLFNQDVDAAVR
GILRNAKLKPVYDSLDAVRRAALINMVFQMGETGVAGFTNSLRLQQKRWDEAAVNLAKSRWYNQTPNRA
KRVITTFRTGTWDAYK

>d1k28a3 d.2.1.3 (A:130-345) Tail-associated lysozyme gp5, catalytic domain {Bacteriophage T4}
NVLNQGGEVGYDSSNVIQDSNLDTAINPDDRPLSEIPTDDNPMSMAEMLRRDEGLRLKVYWDTEGYPTIG
IGHLIMKQPVRDMAQINKVLSKQVGREITGNPGSITMEEATTFLERDLADMQRDIKSHSKVGPVWQAVNRSR
QMALENMAFQMGVGGVAKFNTMLTAMLADWEKAYKAGRDSLWYQQTKGRASRTMIIITGNLESYGVEV
KT

>d1am7a_ d.2.1.4 (A:) Lambda lysozyme {Bacteriophage lambda}

MVEINNQRKAFLDMLAWSEGTDNGRQKTRNHGYDVIVGGEFTDYSDHPRKLVTLPKLNKSTGAGRYQLLSR
WWDAYRKQLGLKDFSPKSQDAVALQQIKERGALPMIDRGDIRQAIDRCNSNIWASLPGAGYGQFEHKADSLIAK
FKEAGGTVR

>d153I__ d.2.1.5 (-) Lysozyme {Goose (Anser anser anser)}

RTDCYGNVNRIDTTGASCKTAKPEGLSYCGVSASKKIAERDLQAMDRYKTIKKVGEKLCVEPAVIAGIISRESHAG
KVLKNGWGDRNGNGFGLMQVDKRSHKPQGTWNGEVHITQGTTILINFIKTIQKKFPSWTKDQQLKGGSAYNA
GAGNVRSYARMDIGTHDDYANDVVARAQYYKQHGY

>d1qsa2 d.2.1.6 (A:451-618) 70 kDa soluble lytic transglycosylase, SLT70 {Escherichia coli}

LAYNDLFKRYTSGKEIPQSYAMAIARQESAWNPKVKSPVGASGLMQIMP GTATHTVKMFSIPGYSSPGQLLD
ETNINIGTSYLQYVYQQFGNNRIFSSAAYNAGPGRVRTWLGN SAGRIDAFAVVESIPFSETRGYVKNV LAYDAYY
RYFMGDKPTLMSATEWGRRY

>d1qusa_ d.2.1.6 (A:) 36 kDa soluble lytic transglycosylase, SLT35 {Escherichia coli}

MVEPQHNVMQMGGDFANNPNAQQFIDKVMNKHGFDRQQLQEILSQAKRLDSVRLMDNQAPTTSVKPPS
GPNGAWLRYRKKFITPDNVQNGVVFWNQYEDALNRAWQVYGVPEIIVGIIGVETRWRGRVMGKTRILDALAT
LSFNYP RRAEYFSGELETFLLMARDEQDDPLNLKG SFAGAMGYGQFMPSSYKQYAVDFSGDGHINLWDPVDAI
GSVANYFKAHGWVKGDQVA VMANGQAPGLPNGFKT KYSISQLAAAGLTPQQPLGNHQQA SLLR LDVGTGY
QWYGLPNFYITTRYNHSTHYAMAVWQLQ AVALARVQ

>d1chka_ d.2.1.7 (A:) Endochitosanase {Streptomyces sp., strain N174}

AGAGLDDPHKKEIAM ELVSSAENSSL DWKAQYKYIEDIGDGRGYTGGIIGFCSTGDMILELVQHYTDLEPGN IL

AKYLPALKVNGSASHSGLGPFTKDWTAAKDTVFQQAQNDRDRVYFDPAVSQAKADGLRALGQFAYYDAI
VMHGPGNDPTSFGGIRKTAMKKARTPAQGGDETTYLNGFLDARKAAMLTEAAHDDTSRVDTEQRVFLKAGN
LDLNPPWKTYGDPYVINS

>d1qgia_d.2.1.7 (A:) Endochitosanase {Bacillus circulans}

ASPDDNFSPETLQFLRNNGLDGEQWNNIMKLINKPEQDDLNWIKYYGYCEDIEDERGYTIGLFGATTGGSRD
THPDGPDLFKAYDAAKGASNPSADGALKRLGINGKMKGSIIEIKDSEKVF CGKIKKLQNDAAWRKAMWETFY
NVYIRYSVEQARQRGFTSAVTIGSFVDTALNQGATGGSDTLQGLLARSGSSNEKTFMKNFHAKRTLVVDTNKY
NKPPNGKNRVKQWDTLVDMGMKMLKNVDSEIAQVTDWEMK

>d1aec_d.3.1.1 (-) Actininidin {Chinese gooseberry or kiwifruit (Actinidia chinensis)}

LPSYVDWRSAGAVVDIKSQGECGGCWAFSAITVEGINKIVTGVVLISLSEQELIDCGRTQNTRGCNGGYITDGFQ
FIINNGGINTEENPYTAQDGECNVDLQNEKYVTIDTYENVPNNEWALQTAVTYQPVSVALDAAGDAFKQYSS
GIFTGPCGTAIDHAVTIVGYGTEGGIDYWIVKNSWDTTGEEGYMRILRNVGGAGTCGIATMPSPVVKY

>d2act_d.3.1.1 (-) Actininidin {Chinese gooseberry or kiwifruit (Actinidia chinensis)}

LPSYVDWRSAGAVVDIKSQGECGGCWAFSAITVEGINKITSGSLISLSEQELIDCGRTQNTRGCDGGYITDGFQ
FIINDGGINTEENPYTAQDGDCDVALQDQKYVTIDTYENVPNNEWALQTAVTYQPVSVALDAAGDAFKQYA
SGIFTGPCGTAVDHAIVIVGYGTEGGVDYWIVKNSWDTTGEEGYMRILRNVGGAGTCGIATMPSPVVKY

>d1ppn_d.3.1.1 (-) Papain {Papaya (Carica papaya)}

IPEYVDWRQKGAVTPVKNQGSCGSCWAFSAVVTIEGIKIRTGNLNEYSEQELDCDRRSYGCNGGYPWSALQL
VAQYGIHYRNTYPYEGVQRYCRSREKGPYAAKTDGVRQVQPYNEGALLYSIANQPVSVVLEAAGKDFQLYRGGI
FVGPCGNKVDHAVAAGVYGPNYILIKNSWGTGWGEGNYIRIKRGTGNSYGVCGLYTSSFYPVKN

>d1pcia_d.3.1.1 (A:) Caricain (protease omega) {Papaya (Carica papaya)}

LTSTERLIQLFNSWMLNHNFYENVDEKLYRFEIFKDNLNYIDETNKKNSYWLGLNEFADLSNDEFNEKYVGSL
IDATIEQSYDEEFINEDIVNLPEVDWRKKAVTPVRHQGSCGSCWAFSAVATVEGINKIRTGKLVELSEQELVD
CERRSHGCKGGYPPYALEYVAKNGIHLRSKYPYAKQGTCKRAKQVGGPIVKTSVGRVQPNNEGNNLLNIAIKQ
PVSVVVESKGRPFQLYKGGIFEGPCGTVKDGAUTAVGYGKSGGKGYILIKNSWGTAWGEKGYIRIKRAPGNSPG
VCGLYKSSYYPTKN

>d1ppo_d.3.1.1 (-) Caricain (protease omega) {Papaya (Carica papaya)}

LPENVWDWRKKAVTPVRHQGSCGSCWAFSAVATVEGINKIRTGKLVELSEQELVDERRSHGCKGGYPPYALEY
VAKNGIHLRSKYPYAKQGTCKRAKQVGGPIVKTSVGRVQPNNEGNNLLNIAIKQPVSVVVESKGRPFQLYKGGI
FEGPCGTVKDHAUTAVGYGKSGGKGYILIKNSWGTAWGEKGYIRIKRAPGNSPGVCGLYKSSYYPTKN

>d1yal_d.3.1.1 (-) Chymopapain {Papaya (Carica papaya)}

YQPSIDWRAKGAVTPVKNQGACGSCWAFSTIATVEGINKIVTGNLLELSEQELVDCDKHSYGCKGGYQTTSLQY
VANNGVHTSKVYPYQAKQYKCRATDKPGPKVKITGYKRVPNSNCETSFLGALANQPLSVLVEAGGKPFQLYKSGV
FDGPGCTKLDHAUTAVGYGKSGGKGYILIKNSWGTAWGEKGYIRIKRAPGNSPGVCGLYKSSYYPTKN

>d1gece_d.3.1.1 (E:) Glycyl endopeptidase {Papaya (Carica papaya)}

LPESVDWRAKGAVTPVKHQGYCESCWAFSTVATVEGINKIKTGNLVELSEQELVDCDLQSYGCNRGYQSTS LQY
VAQNGIHLRAKYPYIAKQQTCRANQVGGPKVKTNGVGRVQSNNEGSLLNIAHQPVSVVVESAGRDFQNYK
GGIFEGSCGTVKDHAUTAVGYGKSGGKGYILIKNSWGPWGEGNYIRIRASGNPGVCGVYKSSYYPIKN

>d1cqda_d.3.1.1 (A:) Proline-specific cysteine protease {Ginger rhizome (Zingiber officinale)}

LPDSIDWRENGAVVPVKNQGGCGSCWAFSTVAAVEGINQIVTGDILISLSEQQLVDCTTANHGCRRGGWMNP
FQFIVNNGGINSEETYPYRGQDGICNSTVNAPVVSIDSYENVPSHNEQLQKAVANQPVSVTMDAAGRDFQLY
RSGIFTGSCNISANHALTVGYGTENDKDFWIVKNSWKGKNWGESGYIRAERNIENPDGKGITRFASYPVKK

>d3gcb_d.3.1.1 (-) Bleomycin hydrolase {Baker's yeast (Saccharomyces cerevisiae), Gal6}

AFQGAMASSIDISKINSWNKEFQSDLTHQLATTVLKNYNADDALLNKTRLQKQDNRVFNTVVSTDSTPVTNQK
SSGRAWLFAATNQLRLNVLSELNLKEFELSQAYLFFYDKLEKANYFLDQIVSSADQDIDSRLVQYLLAAPTEDGG
QYSMFLNLVKKYGLIPKDLYGDPYSTTASRKWNSLLTKLREFATLRTALKERSADDSSIITLREQMQREIFRML
SLFMDIPPVQPNEQFTWEYVDKDKKIHTIKSTPLEFASKYAKLDPSTPVSLINDPRHPYGKLKIDRLGNVLGGDA
VIYLNVDNETLSKLVVKRLQNNKAVFFGSHTPKFMDDKTGVMDIELWNYPAGYNLPPQQKASRIRYHESLMTH
AMLITGCHVDETSKLPLRYRVENSWGKDGGKDGLYVMTQKYFEYCFQIVVDINELPKELASKFTSGKEEPIVLPI
WDPMGALA

>d2cb5a_ d.3.1.1 (A:) Bleomycin hydrolase {Human (Homo sapiens)}

SSSGLNSEKVAALIQKLNSDPQFVLAQNVGTTHDLLICLK RATVQRAQHV FQH A VPQEGKP ITNQ KSSGR SWI
FSCLNVMR LP FMKKLNIEEF EFSQS YLFFWDKVERCYFFLSAFV DTAQRKE PED GRLVQ FLL MN PANDGG QW
DMLVNIV EKVGVIPKKCFPESYTTEATRRMNDILNHKMREFCIRLRNLVHSGATKG EISATQDVMMEEIFRVVCI
CLGNPPETFTWEYRDKDKNYEKIGPITPLEFYREHV KPLFN MEDKICLVNDPRPQKH KHN KLYTVEYLSNMVGGR
KTLYNNQPIDFLKKMVAASI KDG EAVWFGCDVGKHF NSKL GLSDM NLYDHELVFGVSLKNMNKAERLTFGESL
MTHAMTFTAVSEKDDQDGAF TKW RVEN SWGED HGHKG YLCMT DEWFSE YVYEV VVDRKHVPEEV LAVLE
QEPIILPAWDPGMALA

>d1f2aa_ d.3.1.1 (A:) Cruzain {Trypanosoma cruzi}

APAAVDWRARGAVTAVKDQGQCGSCWAFSAIGNVECQWFLAGHPLTNLSEQMLVSCDKTDSCGCSGLMNN
AFEWIVQENNGAVYTEDSYPYASGE GEGISPPCTTSGHTVGATITGHVELPQDEAQIAAWLAVNGPVA VADASS
WM TYTG GVM TSCVSE QLDHG VLLVG YNDS AAVPYWI KNS WTTQWGE EG YIRIA KGSN QCLVKE EASSA VVG
>d3pbh_ d.3.1.1 (-) (Pro)cathepsin B {Human (Homo sapiens)}

MRSRPSFHPLSDELVNYVNKRNTTWQAGHN FYNVDM SYLKRLCGTFLGGPKPPQRVMFTEDLKLPASFDARE
QWPQCPTIKEIRDQGSCGSCWAFGA VE A ISDRIC IHTNAH SVEV SAEDLLTCCGSMCGDG CNGGYPAEAWN
FWTRKG LVSGG LY ESHVGCR PYSIPPCEHHVNGSRPPCTGEGDTPKCSKIC EPGY SPTYKQDKHYGYN SYVSNS
EKDIMAEIYKNGPVEGAFSVYDFLLYKSGVYQHVTGEMMGHAIRILGWGVENGTPYWL VANSWNTDWG
DNGFFKILRGQDHCGIESEVVAGIPRTD

>g1huc.1 d.3.1.1 (A;;B;) (Pro)cathepsin B {Human (Homo sapiens)}

LPASFDAREQWPQCPTIKEIRDQGSCGSCWAFGA VE A ISDRIC IHTNXSVEV SAEDLLTCCGSMCGDG CNGG
YPAEAWNFWTRKG LVSGG LY ESHVGCR PYSIPPCEHHVNGSRPPCTGEGDTPKCSKIC EPGY SPTYKQDKHYGY
NSY SVS NSEK DIMAEIYKNGPVEGAFSVYDFLLYKSGVYQHVTGEMMGHAIRILGWGVENGTPYWL VANS
WNTDWGDNGFFKILRGQDHCGIESEVVAGIPRTD

>d1mira_ d.3.1.1 (A:) (Pro)cathepsin B {Rat (Rattus norvegicus)}

SDDMINYINKQNTTWQAGRNFYNDISYLKKLCGTVLGGPKLPERVGFSEDINLPESFDAREQWSNCPTIAQIR
DQGSCGSSWAFGA VE A M SDR IC IHTN GRV NVEV SAEDLLTCCG I QCGDG CNGGYPSGAWN FWTRKG LVSGG
VYNSHIGCLPYTIPPC EHHVNGARPPCTGEGDTPKCNKMCEAGY STSYKEDKHYG YTSVSD SEKEIMAEIYK N
GPVEGAFTVFSDFLTYKSGVYKHEAGDVMGGHAIRILGWGIENGVPYWL VANSWNA DWGDNGFFKILRGEN
HCGIESEIVAGIPRTQQYWGRF

>d1thea_ d.3.1.1 (A:) (Pro)cathepsin B {Rat (Rattus norvegicus)}

LPESFDAREQWSNCPTIAQIRDQGSCGSCWAFGA VE A M SDR IC IHTN GRV NVEV SAEDLLTCCG I QCGDG CNG
GGYPSGAWN FWTRKG LVSGG VYNSHIGCLPYTIPPC EHHVNGARPPCTGEGDTPKCNKMCEAGY STSYKEDK
HYG YTSVSD SEKEIMAEIYKNGPVEGAFTVFSDFLTYKSGVYKHEAGDVMGGHAIRILGWGIENGVPYWL V
NSWNA DWGDNGFFKILRGENHCGIESEIVAGIPRT

>d1qdqa_ d.3.1.1 (A:) (Pro)cathepsin B {Cow (Bos taurus)}

LPESFDAREQWPNCPTIKEIRDQGSCGSCWAFGA VE A ISDR IC IHSN GRV NVEV SAEDMLTCCGGECGDGCNG
GEP SGAWN FWTRKG LVSGG LYNSHVGCR PYSIPPCEHHVNGSRPPCTGEGDTPKCSKTC EPGYSPSYKEDKHF

GCSSYSVANNEKEIMAEIYKNGPVEGAFSVYSDFLLYKSGVYQHVSGEIMGGHAIRILGWGVENGTPYWLVANS
WNTDWGDNGFFKILRGQDHCGIESEIVAGMPCT

>d1cs8a_d.3.1.1 (A:) (Pro)cathepsin L {Human (Homo sapiens)}

SLTFDHSLEAQWTWKAMHNRLYGMNEEGWRRAVWEKNMKMIELHNQEYREGKHSFTMAMNAFGDMT
SEEFRQVMNGFQNRKPRKGKVFPQEPLFYEAPRSVDREKGYVTPVKNQGQCGSCWAFSATGALEGQMFRK
TGRLISLSEQNLVDCSGPQGNEGCNGGLMDYAFQYVQDNGGLDSEESYPYEATEESCKYNPKYSVANDAGFVD
IPKQEKALMKAVATVGPIVAIDAGHESFLYKEGIYFEPDCSSEDMDHGVLVVGXFESTESDNNKYWLKNS
WGEEWMGGYVKMAKDRRNHCIGIASASYPTV

>g1icf.1 d.3.1.1 (A;B:) (Pro)cathepsin L {Human (Homo sapiens)}

APRSVDWREKGYVTPVKNQGQCGSCWAFSATGALEGQMFRKTGRLISLSEQNLVDCSGPQGNEGCNGGLM
DYAFQYVQDNGGLDSEESYPYEATEESCKYNPKYSVANDTGFVDIPKQEKALMKAVATVGPIVAIDAGHESFLF
YKEGIYFEPDCSSEDMDHGVLVVGXFESTXNNKYWLKNSWGEEWMGGYVKMAKDRRNHCIGIASASY
PTV

>d1mem_a_d.3.1.1 (A:) (Pro)cathepsin K {Human (Homo sapiens)}

APDSVDYRKKGYVTPVKNQGQCGSCWAFFSGVALEGQLKKTGKLLNLSPQNLVDCVSENDGCGGGYMTNA
FQYVQKNRGIDSEDAYPYVGQEECMYNPTGKAACRGRYREIPEGNEKALKRAVARVGPVVAIDASLTSFQFY
SKGVYYDESCNSDNLNHAVLAVGYGIQKGNKHIIKNSWGENWGNKGYILMARNKNNACIANLASFPKM
>d7pcka_d.3.1.1 (A:) (Pro)cathepsin K {Human (Homo sapiens)}

LYPEEILDTHWELKKTHRQYNNKVDEISRRIWEKNLKYISIHNLEASLGVHTYELAMNHLDGDTSEEVVQK
MTGLKVPLSHRSNDTLYIPEWEGRAPDSVDYRKKGYVTPVKNQGQCGSCWAFFSGVALEGQLKKTGKLLNL
SPQNLVDCVSENDGCGGGYMTNAFQYVQKNRGIDSEDAYPYVGQEECMYNPTGKAACRGRYREIPEGNEK
ALKRAVARVGPVVAIDASLTSFQFYSKGVYYDESCNSDNLNHAVLAVGYGIQKGNKHIIKNSWGENWGNK
GYILMARNKNNACIANLASFPKM

>d8pcha_d.3.1.1 (A:) (Pro)cathepsin K {Pig (Sus scrofa)}

YPPSMDWRKKGNFVSPVKNQGSCGSCWTFSTTGALESAVAIATGKMLSLAEQQLVDCAQNFNNHGCQGGLP
SQAFEYIRYNGIMGEDTYPYKGQDDHCKFQPDKAIFVKDVANITMNDEEAMVEAVALYNPVSFAFEVTNDF
LMYRKGIYSSTSCHKTPDKVNHAVLAVGYGEENGIPYWIVKNSWGPQWGMNGYFLIERGKNMCGLAACASY
PIPLV

>d1fh0a_d.3.1.1 (A:) (Pro)cathepsin V {Human (Homo sapiens)}

LPKSVDWRKKGYVTPVKNQKQCGSCWAFFSATGALEGQMFRKTGKLVSLSEQNLVDCSRPQGNQCGNGFM
ARAFQYVKENNGLDSEESYPYAVDEICKYRPENSVAQDTGFTVVAvgKEKALMKAVATVGPIVAMDAGHSS
FQFYKSGIYFEPDCSSKNLDHGVLVVGXFEGANSNSKYWLKNSWGPQWGMNGYFLIERGKNMCGLAACASY
ASYPNV

>d1deua_d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}

RGQTCYRPLRGDGAPLGRRTYPRPHEYLSPADLPKSWDWRNVDGVNYASITRNQHIPQYCGSCWAHASTSA
MADRINIKRGAWPSTLLSVQNVIDCGNAGSCCEGGNDLSVWDYAHQHGIPDETNNYQAKDQECDKFNQC
GTCNEFKECHAIRNYTLWRVGDYGSLSGREKMMAEIYANGPISCGIMATERLANYTGGIYAELYQDTTYINHV
VAGWGISDGTEYWIVRNSWGPQWGMNGYFLIERGKNMCGLAACASY

>d1ef7a_d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}

LPKSWDWRNVDGVNYASITRNQHIPQYCGSCWAHASTSAMADRINIKRGAWPSTLLSVQNVIDCGNAGSC
EGGNDSLWVDYAHQHGIPDETNNYQAKDQECDKFNQCGTCNEFKECHAIRNYTLWRVGDYGSLSGREKM
MAEIYANGPISCGIMATERLANYTGGIYAELYQDTTYINHV
IVTSTYKDGKGARYNLAIEEHCTFDPIV

>d1cv8_d.3.1.1 (-) Staphopain {Staphylococcus aureus}

NEQYVNKLENFKIRETQGNNGWCAGYTMSALLNATYNTNKYHAEAVMRFLHPNLQQFQFTGLTPREMIY
FGQTQGRSPQLNRMTTYEVNDNLTKNNKGIAILGSRVESRNGMHAGHAMAVVGNAKLNGQEVIWNP
WDNGFMTQDAKNNVIPVSNGDHYQWYSSIFY

>d1dkia_ d.3.1.1 (A:) Streptococcal pyrogenic exotoxin B {Streptococcus
pyogenes}

LDKVNLGGELSGSNMYVYNISTGGFIVSGDKRSPEILGYSTSGSFVDNGKENIASFMESYVEQIKENKKLDSTYA
GTAEIKQPVVKSLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVGQHAATGSVATATAQIMKYHNYPNKGKD
TYTLSSNNPYFNHPKNLFAAISTRQYNWNNILPTYSGRESNVQKMAISELMADVGISVMDYGPSSGSAGSSR
VQRALKENFGYNQSVHQINRGDFSKQDWEAQIDKELSQNQPVYYQGVGKVGHHAFVIDGADGRNFYHVN
WGWWGGVSDGFFRLDALNPSALGTGGAGGFNGYQSAVVGKIP

>d1qmya_ d.3.1.2 (A:) FMDV leader protease {Foot-and-mouth disease virus}
MELTLYNGEKKTFYSRPNNHDNAWLAILQLFRYVEEPFFDWVYSSPENLTLEAIKQLEDLTGLELHEGGPPALVI
WNIKHLLHTGIGTASRPSEVCVVDGTDMSLADFHAGIFLKGQEHAVFACVTNSNGWYAIIDDEFYPWTPDPSD
VLVFVPYD

>d1qola_ d.3.1.2 (A:) FMDV leader protease {Foot-and-mouth disease virus}
MELTLYNGEKKTFYSRPNNHDNAWLAILQLFRYVEEPFFDWVYSSPENLTLEAIKQLEDLTGLELHEGGPPALVI
WNIKHLLHTGIGTASRPSEVCVVDGTDMSLADFHAGIFLKGQEHAVFACVTNSNGWYAIIDDEFYPWTPDPSD
VLVFVPYDQEPLNGEWAQVQRKLK

>d1kful3 d.3.1.3 (L:2-355) Calpain large subunit, catalytic domain (domain II) {Human (Homo sapiens)}

AGIAAKLAKDREAAEGLGSHERAIKYLNQDYEARNECLEAGTLFQDPSFPAPIPSALGFELGPYSSKTRGMRWK
RPTEICADPQFIIGGATRTDICQGALGDCWLLAIAASLTNEELARVVPNQSFQENYAGIFHFQFWQYGEWVE
VVVDDRLPTKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEGFEDFTGGIAEWYELKKPPPNLKI
IQKALQKGSLGCSDITSAADSEAITFQKLVKGHAYSVTGAEEVESNGSLQKLIRIRNPWGVEWTGRWNDNC
SWNTIDPEERERLRRHEDGEFWMSFSDFLRHYSRLEICNLTPDTLSDTYKK

>d1df0a3 d.3.1.3 (A:2-355) Calpain large subunit, catalytic domain (domain II) {Rat (Rattus norvegicus)}

AGIAMKLAKDREAAEGLGSHERAIKYLNQDYETLRNECLEAGALFQDPSFPALPSSLGFELGPYSSKTRGIEWK
RPTEICADPQFIIGGATRTDICQGALGDSWLLAIAASLTNEELARVVPPLDQSFQENYAGIFHFQFWQYGEWVE
VVVDDRLPTKDGELLFVHSAEGSEFWSALLEKAYAKINGCYEALSGGATTEGFEDFTGGIAEWYELRKPPPNLFK
IIQKALEKGSLGCSDITSAADSEAVTYQKLVKGHAYSVTGAEEVESGSLQKLIRIRNPWGQVEWTGKWNDNC
PSWNTVDPEVRANLTERQEDGEFWMSFSDFLRHYSRLEICNLTPDTLTCDSYKK

>d1f13a4 d.3.1.4 (A:191-515) Transglutaminase catalytic domain {Human (Homo sapiens)}
DAVYLDNEKEREEYVLNDIGVIFYGEVNDIKTRSWSYGQFEDGILDTCYVMDRAQMDSLGRGNPIKVSRVGSA
MVNAKDDEGVLVGSWDNIYAYGVPPSAWTGSVDILLEYRSSENPVRYGQCWFAGVFNTFLRCLGIPARIVTN
YFSAHNDNDANLQMDIFLEEDGNVNSKLTDSVWNYHCWNEAWMTRPDLPVGFGGWQAVDSTPQENSDG
MYRCGPASVQAikhGHVCFQFDAPVFAEVNSDLIYITAKKDGTVVENVDAHIGHKLIVTKQIGGDGMMDIT
DTYKFQEGQEEERLALETALMYGAKKPLNTEGVMKSR

>d1g0da4 d.3.1.4 (A:141-461) Transglutaminase catalytic domain {Red sea bream (Chrysophrys major)}

DMVYLPDESKLQEYVMNEDGVIYMGTWYDYLRSIPWNYGQFEDYVMDICFEVLDNSPAALKNSEMDIEHRSDP
VYVGRITAMVNSNGDRGVLTGRWEEPYTDGVAPYRWTGSVPILQQWSKAGVRPVKYGQCWFVAAVACTVL
RCLGIPTRPINFASAHDV DGNLSDFLNLERLESLSRQRSDSSWNFHCVVESWMSREDLPEGNDGWQVL
DPTPQELSDGEFCCGCPVAAIKEGNLGVKYDAPFVFAEVNADTIYWIVQKDGQRRKITEDHASVGKNISTKSV

YGNHREDVTLHYKYPEGSQKEREVYKKAGRVT
>d1e2ta_ d.3.1.5 (A:) Arylamine N-acetyltransferase {Salmonella typhimurium}
HMTSFLHAYFTRLHCQPLGVPTVEALRTLHLAHNCAIPFENLDVLLPREIQLDETAEEKLLYARRGGYCFELNGLF
ERALRDIGFNVRSLLGRVLISHPASLPPRTHRLLVDEEQWIADVGFGQTLAPRLQAEIAQQTPHGEYRL
MQEGSTWILQFRHHEHWQS MYCFDLGVQQQSDHVMGNFWSAHPQSHFRHLLMCRHLPDGGKLTN
HFTRYHQGHAVEQVNVPDVPSLYQLLQQQFGLGVNDVKHGFTEAELAAVMAAF
>d1uch_ d.3.1.6 (-) Ubiquitin C-terminal hydrolase UCH-I3 {Human (Homo sapiens)}
RWLPLEANPEVTNQFLKQLGLHPNWQFVDVYGM DPELLSMVPRPVCAVLLFPITEKYEVFRTEEEEKIKSQG
QDVTSSVYFMKQTISACGTIGLIHAIANNKDKMHFESGSTLKKFLEESVMSPEERARYLENYDAIRVTHETSA
HEGQTEAPSIDEKVDLHFIALVHDGHLYELDGRKPFPINHGETSDTLL EDIAEVCKKFMERDPDELRFNAIALS
AA
>d1cmxa_ d.3.1.6 (A:) Ubiquitin C-terminal hydrolase UCH-I3 {Synthetic, based on
Saccharomyces cerevisiae sequence}
RAVVPIESNPEVFTNFAHKGLKNEWAYFDIYSLTEPELLAFLPRPVKAIVLLFPINEDRKSSTSQQITSSYDVIWFK
QSVKNACGLYAILHLSNNQSLLEPGSDLDNFLKSQSDTSSSKNRFFDDVTTDQFVLNVIKENVQTFSTGQSEAPE
ATADTNLHYITYVEENGGIFELDGRNLSGPLYLGKSDPTATDLIEQELVRVRVASYMENANEEDVLFNAMLGLGP
N
>d1avpa_ d.3.1.7 (A:) Human adenovirus 2 proteinase {Mastadenovirus H2}
MGSSEQELKAIVKDLGCGPYFLGYDKRPGFVSPHKLACAIVNTAGRETGGVHWMAFAWNPRSKTCYLFEPP
GFSDQRKLQVYQFFEYESLLRRSAIASSPDRCITLEKSTQSVQGPNSAACGLFCMFLHAFANWPQTPMDHNPT
MNLITGVPNMLNSPQVQPTLRRNQEQLYSFLERHSPYFRSHSAQIRSATSFCHLKNM
>d1euva_ d.3.1.7 (A:) Ulp1 protease C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
GSLVPELNEKDDDQVQKALASRENTQLMN RDNIEITVRDFKTLAPRRWLNDTIEFFMKYIEKSTPNTVAFNSFF
YTNL SERGYQGVRRWMKRKTQIDKLDKIFTPINLNQSHWALGIIDLKKKTIGYVDSLNGPNAMSFAILDLQK
YVMEESKHTIGEDFDL IHLDCPQQPNGYDCGIYVCMNTLYGSADAPLDFDYKDAIRMRRFIAHLILTDALK
>d7ceib_ d.4.1.1 (B:) DNase domain of colicin E7 {Escherichia coli}
RNKPGKATGKGKPVNNKWLNNA GKD LGSPV DRIANKLRDKEFKSFDDFRKKFWE EVSKDPELSKQFSRNNN
DRMKVGKAPKTRTQDVSGKRTSFELHHEKPISQNGVYDMDNISVTPKRHIDIH
>d1emvb_ d.4.1.1 (B:) DNase domain of colicin E9 {Escherichia coli}
MESKRN KPGKATGKGKPVGDKWL DDAGKD SGAPIPDRIADKL RDKEFKSFDDFRKAVWEEVSKDPELSKNLN
PSNKSSVSKG YSPFTPKNQQVGGRKVYELHHDKPISQGGEVYDMDNIRVTPKRHIDIH
>d1ql0a_ d.4.1.2 (A:) Sm endonuclease {Serratia marcescens}
SIDNC AVGCPTGGSSKVSIVRHAYTLNNNSTTKFANWVAYHITKDTPASGKTRNWKTDPALNPADTLAPADYTG
ANAALKVDRGHQAPLASLAGVSDWESLN YLSNITPKS DLNQGA WARLEDQERKLIDRADISSVYTVGPLYE
RDMGKLPGTQKAHTIPSAYWKVIFINNSPAVNHYAAF LFDQNTPKGADFCQFRVTVDEIEKRTGLIIWAGLPDD
VQASLKSKPGVLPELMGCKN
>d1a73a_ d.4.1.3 (A:) Intron-encoded homing endonuclease I-Ppo1 {Slime mold (Physarum polycephalum)}
ALTNAQILAVIDSWEETVGQFPVITHVPLGGGLQGTLHCYEIPPLAAPYGVGFAKNGPTRWQYKRTINQVVHR
WGSHTVPFLLEPDNINGKTCTASHLCHNTRCHNPLHLCWESLDDNKGRNWCPGPNGGCVHAVVCLRQGPLY
GPGATVAGPQQRGSHFVV
>d1e7la2 d.4.1.5 (A:1-103) Recombination endonuclease VII, C-terminal and dimerization domains
{Bacteriophage T4}
MLLTGKLYKEEKQKFYDAQNGKCLICQRELNPDVQANHLDHDHELNGPKAGKVRG LLCNLCAAEGQMKHKF

NRSGLKQGVVDYLEWLENLLTYLKSODYTQNN

>d1dy5a_d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KETAAAKFERQHMDSTSAAASSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTN
CYQSYSITDCRETGSSKYPNCAYKTTQANKHIIVACEGNPYVPVHFDASV

>d1h8xa_d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KESAAAKFERQHMDSGNSPSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNVCFQEKTCKNGQ
GNCYKSNSSMHITDCRLTNGSRYPNCAERTSQKERHIIVACEGSPYVPVHFDASVE

>d1rbd_d.5.1.1 (-) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

SSSNYCQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTN CYQSYSITDCRETGSSKY
PNCAYKTTQANKHIIVACEGNPYVPVHFDASV

>g1d5d.1 d.5.1.1 (A;B;) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}

KETAAAKMERQHLDSDSSPSSSTYCNQMMKSRNLTKDRCKPVNTFVHESLADVQAVCSQKNVACKNGQTN CYQSYSITDCRETGSSKY
MSITDCRETGSSKYPNCAYKTTQANKHIIVACEGNPYVPVHFDASV

>d1e21a_d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Human (Homo sapiens), des1-7}

AFQRQHMDSDSSPSSSTYCNQMMRMRNMTQGRCKPVNTFVHEPLVDVQNVCFQEKTCKNGQGNCYKS
NSSM HITDCRLTNGSRYPNCAERTSPKERHIIVACEGSPYVPVHFDASVE

>d1rraa_d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Rat (Rattus norvegicus)}

AESSADKFKRQHMDEGPSKSSPTYCNQMMKRQGMTKGSCPKVNTFVHEPLEDVQAICSQGQVTCKNGRNN
NCHKSSSTLRITDCRLKGSSKYPNCDYTTDSQKHIIACDGNPYVPVHFDASV

>d1onc_d.5.1.1 (-) P-30 protein {Frog (Rana pipiens)}

EDWLTFQKKHITNTRDVDCDNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLTSEFYLSDCNVTSRPCK
YKLKKSTNKFCVTCENQAPVHFVGVGSC

>d1bc4_d.5.1.1 (-) Cytotoxic ribonuclease {Bullfrog (Rana catesbeiana)}

ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVINMNVLSTTRFQLNTCTRTSIT
PRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP

>d11bga_d.5.1.1 (A:) Seminal ribonuclelease {Cow (Bos taurus)}

KESAAAKFERQHMDSGNSPSSSTYCNLMMCCRKMTQGKCKPVNTFVHESLADVKA VCSQKKVTCNGQTN
CYQS KSTM RITDCRETGSSKYPNCAYKTTQANKHIIVACGGKPSPVHFDASV

>d1b6va_d.5.1.1 (A:) Hybrid between ribonuclease A and seminal ribonuclease {Cow (Bos taurus)}

KETAAAKFERQHMDSTSAAASSNYCNQMMKSRNLTKDRCKPVNTFVHESLADVKA VCSQKKVTCNGQTN
CYQS KSTM RITDCRETGSSKYPNCAYKTTQANKHIIVACGGKPSPVHFDASV

>d1dyta_d.5.1.1 (A:) Eosinophil cationic protein (ECP), ribonuclease 3 {Human (Homo sapiens)}

RPPQFTRAQWFQHISLNPPRCTIAMRAINNYWRCKNQNTFLRTTFANVVNVCGNQSIRCPHNRTLNNCH
RSRFRVPLLHCDLINPGAQNISNCRYADRGRRFYVACDNRDPRDSPRYPVVPVHLDTTI

>d1hi2a_d.5.1.1 (A:) Eosinophil-derived neurotoxin (EDN) {Human (Homo sapiens)}

MKPPQFTWAQWFETQHINMTSQQCTNAMQVINNYQRRCKNQNTFLRTTFANVVNVCGNPNMTCPSNKTR
KNCHHSGSQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRRDPPQYPVVPVHLDRII

>d1rnfa_d.5.1.1 (A:) Ribonuclease 4 {Human (Homo sapiens)}

MQDGMYQRFLRQHVHPEETGGSDRYCNLMMQRRKMTLYHCKRFNTFIHEDIWNIRSICSTTNIQCKNGKM
NCHEGVVKVTDCRTGSSRAPNCRYRAIASTRVVIACEGNPQVPVHFDG

>d1b1ia_d.5.1.1 (A:) Angiogenin {Human (Homo sapiens)}

EDNSRYTHFLTQHYDAKPQGRDDRYCESIMRRRGLTSPCKDINTFIHGNKRSIKAICENKGNPHRENLRISKSS
FQVTTCKLHGGS PWPPCQYRATAGFRNVVVACENGLPVHLDQSFRRP

>d1agi_d.5.1.1 (-) Angiogenin {Cow (Bos taurus)}

AQDDYRYIHFLTQHYDAKPGRNDEYCFNMMKNRRLTRPCDRNTFIHGNKNDIKAICEDRNGQPYRGDLRIS
KSEFQITICKHKGSSRPPCRYGATEDSRVIVGCENGLPVHFDESFITPRH
>d1ag2__ d.6.1.1 (-) Prion protein domain {Mouse (Mus musculus)}
GLGGYMLGSAMSRPMIHFGNDWEDRYRENMYRYPNQVYYRPVDQYSQNQNNFHDGVNITIKQHTVTTT
KGENDFTEDVKMMERVVEQMCVTQYQKESQAYY
>d1b10a_ d.6.1.1 (A:) Prion protein domain {Golden hamster (Mesocricetus auratus)}
LGGYMLGSAMSRPMMHFGNWEDRYRENMNRYPNQVYYRPVDQYNNQNNFHDGVNITIKQHTVTTT
TKGENFTEDTIKIMERVVEQMCITQYQKESQAYYDG
>d1fo7a_ d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}
LGGYMLGSAMSRPIIHFGSDYEDRYRENMRYPNQVYYRPMDEYSQNQNNFHDGVNITIKQHTVTTTKGE
NFTKTDVKMMERVVEQMCITQYERESQAYYQRGSS
>d1i4ma_ d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}
GAVVGGLGGYMLGSAMSRPIIHFGSDYEDRYRENMRYPNQVYYRPMDEYSQNQNNFHDGVNITIKQHTV
TTTKGENFTEDVKMMERVVEQMCITQYERESQAYY
>d1dwya_ d.6.1.1 (A:) Prion protein domain {Cow (Bos taurus)}
GLGGYMLGSAMSRPLIHFGSDYEDRYRENMRYPNQVYYRPVDQYSQNQNNFHDGVNITVKEHTVTTTK
GENFTEDTIKMMERVVEQMCITQYQRESQAYYQ
>d1i17a_ d.6.1.1 (A:) Prion-like protein Doppel {Mouse (Mus musculus)}
RVAENRPGAFIKQGRKLDIDFGAEGNRYYAANYWQFPDGIYYEGCSEANVTKEMLVTSCVNATQAANQAEFS
REKQDSKLHQRLWLRIKEICSAKHCDFWLERGAA
>d1e01a_ d.7.1.1 (A:) Membrane-bound lytic murein transglycosylase D, MltD {Escherichia coli}
DSITYVRKGDSLSSIAKRHGVNIKDVMRWNSDTANLQPGDKLTLFVK
>d1hywa_ d.186.1.1 (A:) Head-to-tail joining protein W, gpW {Bacteriophage lambda}
MTRQEELAAARAALHDLMTGKRVATVQKDGRVEFTATSVDLKKYIAELEVQTGMTQ
>d1ejra_ d.8.1.1 (A:) Urease, gamma-subunit {Klebsiella aerogenes}
MELTPREKDKLLFTAALVAERRLARGLKLNPESVALISAFIMEGARDGKSASLMEEGRHVLREQVMEGVPE
MIPDIQVEATFPDGSKLTVHNPII
>d4ubpa_ d.8.1.1 (A:) Urease, gamma-subunit {Bacillus pasteurii}
MHLNPAEKEKLQIFLASELLRRKARGLKLNPPEAVAIITSFIMEGARDGKTVAMLMEEGKHLTRDDVMEGVP
EMIDDIAEATFPDGTKLTVHNPII
>d1e9ya2 d.8.1.1 (A:1-105) Urease, gamma-subunit {Helicobacter pylori}
MKLTPKELDKLMLHYAGELAKRKEKGKLNVEAVALISAHIMEEARAGKKAAELMQEGRTLLKPDVMDG
VASMIHEVGIEAMFPDGTKLTVHPIEANGK
>d1qe6b_ d.9.1.1 (B:) Interleukin-8, IL-8 {Human (Homo sapiens)}
AKERCRCQCIKYSKPFHPKFIKERVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVEKFLKRAENS
>d3il8_ d.9.1.1 (-) Interleukin-8, IL-8 {Human (Homo sapiens)}
LRCQCQCIKYSKPFHPKFIKERVIESGPHCANTEIIVKLSDGRELCLDPKENWVQRVVEKFLKRAENS
>d1plfa_ d.9.1.1 (A:) Platelet factor 4, PF4 {Cow (Bos taurus)}
LQCVCLKTTSGINPRHISSLEVIGAGLHCPSQLIATLKTGRKICLDQQNPLYKKIIKRLLK
>d1pfma_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}
MSAKELRCQCVKTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNGRKICLDLQAPLYKKIIKKLLES
>d1rhpaa_ d.9.1.1 (A:) Platelet factor 4, PF4 {Human (Homo sapiens)}
DLQCLCVKTTSQVRPRHITSLEVIKAGPHCPTAQLIATLKNGRKICLDLQAPLYKKIIKKLLES

>d1mgsa_d.9.1.1 (A:) Melanoma growth stimulating activity (MGSA) {Human (Homo sapiens)}
ASVATELRCQCLQTLQGIHPKNIQSVDNVKSPGPHCACQTEVIATLKNGRKACLNTPASPIVKIIEKMLNSDKSN
>d1roda_d.9.1.1 (A:) IL-8/MGSA chimeric protein CIL-8M {Human (Homo sapiens)}
SAKELRCQCICKTYSKPFHPKFIKERVIESGPHCANTEIIVKLSDGRELCLEDPASPIVKIIEKMLNSDKSN
>d1huna_d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens), 1-beta}
APMGSDPPTACCFSYTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWVQEYVYDLELN
>d1b50a_d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens), 1-alpha}
SLAADTPTACCFSYTSRQIPQNFIAYFETSSQCSKPGVIFLTKRSRQVCADPSEEWVQKYVSDLELSA
>d1ha6a_d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Mouse (Mus musculus), ccl20/mip-3a}
ASNYDCCLS YIQTPLPSRAIVGFRQMADEACDINAIIFHTKKRKSVCADPKQNWKRAVNLLSRVKKM
>d1cm9a_d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Kaposi's sarcoma herpes virus, VMIP-II}
SWHRPDKCLGYQKRPLPQVLLSSWYPTSQLCSKPGVIFLTKRGQVCADKS KDWVKKLMQQLPVTAR
>d1b3aa_d.9.1.1 (A:) RANTES (regulated upon activation, normal T-cell expressed and secreted) {Human (Homo sapiens)}
PYSSDTTPCCFAIARPLPRAHIKEYFYTSGKCSNPAVV FVTRKNRQVCANPEKKWVREYINSLEMS
>d1doka_d.9.1.1 (A:) Monocyte chemoattractant protein-1 (MCP-1, MCAF) {Human (Homo sapiens)}
MQPDAINAPVTCCYNFTNRKISVQR LASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWVQDSMDHLDKQT
>d1esra_d.9.1.1 (A:) Monocyte chemoattractant protein-2 (MCP-2) {Human (Homo sapiens)}
EPDSVSIPITCCFNVINRKIPIQRLEYTRITNIQCPKEAVIFKTQRGKEVCADPKERWVRDSMKHLDQIFQNLKP
>d1el0a_d.9.1.1 (A:) CC chemokine I-309 {Human (Homo sapiens)}
SKSMQVPFSRCCFSFAEQEIPLRAILCYRNTSSICSNEGLIFKLKRGKEACALDTVGVWQRHRKMLRHCP SKRK
>d1eot_d.9.1.1 (-) Eotaxin {Human (Homo sapiens)}
GPASVPTTCCFNLANRKIPLQRLESYRRITSGKCPQKAVIFKTKLAKDICADPKKKWVQDSM KYLDQKSPTPKP
>d1eiha_d.9.1.1 (A:) Eotaxin-2 {Human (Homo sapiens)}
VVIPSPCCMFVSKRIPENRVSYQLSSRSTCLKAGVIFTKKGQQSCGDPKQE WVQR YMKNLDAKQKKASPR
>d1j9oa_d.9.1.1 (A:) Lymphotactin {Human (Homo sapiens)}
VGSEVSDKRTCVSLTTQRLPVSRKTYTITEGSLRAVIFITKRLKVCADPQATWVRDV VRSMDRKS NTRNNMIQ
TKPTGTQQSTNTAVTLG
>d1bo0_d.9.1.1 (-) Monocyte chemoattractant protein-3 (MCP-3) {Human (Homo sapiens)}
QPVGINTSTTCYRFINKKIPKQRLESYRRTTSSHC PREAMIFKT KLDKEICADPTQKWVQDFMKHLDKKTQTPKL
>d1b2ta_d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}
MQHHGVTKCNITCSKMTSKIPVALLIHYQQNQASC GKRAIILETRQHRLFCADPK EQWVKDAMQHLD RQAAA
LTRNG
>d1f2la_d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}
VTCKCNITCSKMTSKIPVALLIHYQQNQASC GKRAIILETRQHRLFCADPK EQWVKDAMQHLD RQ
>d1tvxa_d.9.1.1 (A:) Neutrophil-activating peptide-2 (NAP-2) {Human (Homo sapiens)}
LRCLCIKTTSGIHPKNIQSLEVIGKGTHCNQVEVIATLKDG R KICLDPDAPRIKKIVQKKLAGD
>d1tvxb_d.9.1.1 (B:) Neutrophil-activating peptide-2 (NAP-2) {Human (Homo sapiens)}
DSDLYAELRCLCIKTTSGIHPKNIQSLEVIGKGTHCNQVEVIATLKDG R KICLDPDAPRIKKIVQKKLAGD
>d1a15a_d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}
KPVSLSYRCPCRFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN

>d1a15b_d.9.1.1 (B:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}
RCPCRFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIQEYLEK
>d1qg7a_d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}
SYRPCRFFESHVARANVKHLKILNTPNCALQIVARLKNNNRQVCIDPKLKWIQEYLEKALN
>d1mi2a_d.9.1.1 (A:) Macrophage inflammatory protein-2 {Mouse (Mus musculus)}
AVVASELRCQCLTKLPRVDFKNIQSLSVTPPGPHCAQTEVIATLKGQQKVCLDPEAPLVQKIIQKILNKKGKAN
>d2hcc_d.9.1.1 (-) Chemokine hcc-2 (macrophage inflammatory protein-5) {Human (Homo sapiens)}
HFAADCCTSYISQSIPCSLMKSYFETSSECSKPGVIFLTKKGRQVCAKPSGPGVQDCMKKLKPYSI
>d1qnka_d.9.1.1 (A:) Gro beta {Human (Homo sapiens)}
TELRCQCLQTLQGIHLKNIQSVVKSPGPHCAQTEVIATLNGQKACLNPAASPMVKIIEKMLKNGKSN
>d1g91a_d.9.1.1 (A:) Myeloid progenitor inhibitory factor-1 (MPIF-1) {Human (Homo sapiens)}
MDRFHATSADCCISYTPRSIPCSLLESYFETNSECSKPGVIFLTKKGRRFCANPSDKQVQCMRMLKLDTRIKTRK
N
>d1bf4a_d.9.2.1 (A:) DNA-binding protein {Archaeon Sulfolobus solfataricus, Sso7d}
ATVKFKYKGEEKEVDISKIKKVVWRVGKMSFTYDEGGGKTGRGAVSEKDAPKELLQMLEKQKK
>d1azpa_d.9.2.1 (A:) DNA-binding protein {Archaeon Sulfolobus acidocaldarius, Sac7d}
MVVKFKYKGEEKEVDTSKIKKVVWRVGKMSFTYDDNGKTGRGAVSEKDAPKELLDMLARAEREKK
>d1ap0_d.9.2.2 (-) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}
HMVEEVLEEEEEEYVVEKVLDRVVKGKVEYLLKWKGFSDEDNTWEPEENLDCPDLIAEFLQSQKTAHETDKS
>d1dz1a_d.9.2.2 (A:) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}
HMKEESEKPRGFARGLEPERIIGATDSSGELMFLMKWKNSDEADLVPAKEANVKCPQVVISFYERLTWH
>d1e0ba_d.9.2.2 (A:) HP1 homologue SWI6 {Fission yeast (Schizosaccharomyces pombe)}
QVENYDSWEDLVSSIDTIERKDDGTLEIYLTKNGAISHHPSTITNKKCPQKMLQFYESHL
>d1g6za_d.9.2.2 (A:) Histone methyltransferase clr4 chromo domain {Fission yeast (Schizosaccharomyces pombe)}
ISSPKQEEYEVERIVDEKLRNGAVKLYRIRWLNYSSRSDTWEPPENLSGCSAVLAEWKRRKRRLKGSNS
>d1bb8_d.10.1.1 (-) DNA-binding domain from tn916 integrase {Enterococcus faecalis}
EKRRDNRGRILKTGESQRKDGRYLYKYIDSFGEPQFVYSWKLVATDRVAGRKDCISLREKIAELQKDIHD
>d1gcca_d.10.1.2 (A:) GCC-box binding domain {Mouse-ear cress (Arabidopsis thaliana)}
KHYRGVRQRPWGKFAAEIRDPAKNGARVWLGTETAEDAALAYDRAAFMRGRSRALLNFPLRV
>d1qk9a_d.10.1.3 (A:) Methyl-CpG-binding protein 2, MECP2 {Human (Homo sapiens)}
ASASPKQRRIIRDRGPMYDDPTLPEGWTRKLQRKSGRSAGKYDVYLINPQGKAFRSKVELIAYFEKVGDTSDL
PNDFDFTVTGRGSGSGC
>d1d9na_d.10.1.3 (A:) Methylation-dependent transcriptional repressor MBD1/PCM1 {Human (Homo sapiens)}
MAEDWLDCPALGPWKRREVFRKSGATGRSDTYYQSPTGDRIRSKVELTRYLGPACDLTLDFKQGILCYPAPK
>d1k25a1_d.11.1.1 (A:632-692) Penicillin-binding protein 2x (pbp-2x), c-terminal domain {Streptococcus pneumoniae}
TESSYAMPSIKDISPGE LAEALRRNIVQPIVVGTTKIKETSVEEGTNLAPNQQVLLSDK
>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}

QSPYPMPMPSVKDISPGDLAELRRNLVQPIVGTGKIKNSSAEEGKNLAPNQQVLILSDK

>d1qmea2 d.11.1.1 (A:693-750) Penicillin-binding protein 2x (pbp-2x), c-terminal domain
{Streptococcus pneumoniae}

AEEVPDMYGWTKETAETLAKWLNLIEFQGSGSTVQKQDVRANTAIKDIKKITLTD

>d1jj2r_d.12.1.1 (R:) Ribosomal protein L23 {Archaeon Haloarcula marismortui}

SWDVIKHPHVTEKAMNDMDQFNKLQFAVDDRASKGEVADAVEEQYDVTVEQVNTQNTMDGEKKAVVRLSE
DDDAQEVASRI

>d1ffki_d.12.1.2 (I:) Ribosomal protein L15e {Archaeon Haloarcula marismortui}

MKSMYAYIREAWKRPYEGYVGELMWHLRQLQKWRREPAVVRIPRPTRLDRARALGYKAKKGIVVVRVIRGGRR
ATRPNKGRSKKMMVNRRPRKKNLQWIAERANRKYPNMEVLNSYWVGEDGRYKWFELVDRDHPAIKSD
PQLSWVSRTGRVYRGLTSAGRKARGLRRKGRAEKVRPSLRANFRKKRR

>d1jj2l_d.12.1.2 (L:) Ribosomal protein L15e {Archaeon Haloarcula marismortui}

ARSAYSYIREAWKRPKEGQIAELMWHRMQEWRNEPAVVRIERPTRLDRARSLGYKAKQGIIVVRAIRKGSSRR
TRFNKGRRSKRMMVNTRKKNIQRIAERANRKFPNLRVLNSYSVGEDGRHKWHEVILIDPDHPAIKSDDQLS
WISRTRHRLRTFRGLTSAGRRCRGLRGQKGSEKVRPSLRVNGAKA

>d4rhn_d.13.1.1 (-) Histidine triad nucleotide-binding protein (HINT) {Rabbit (Oryctolagus cuniculus)}

RPGGDTIFGKIIKKEIPAKIIFEDDQCLAFHDISPQAPTHFLVIPKKHISQISAAEADESLLGHLIVGKKCAADLG
LKKGYRMVVNEGSDGGQSVDVHLVHLVLGGRQMNWPPG

>d1fit_d.13.1.1 (-) FHIT (fragile histidine triad protein) {Human (Homo sapiens)}

SFRFGQHLIKPSVVFALKTELSFALVNRKPVPGHVLCPLRPVERFHDLPDEVADLFQTTQRVGTVEKFHFHT
SLTFSMQDGPEAGQTVKHVHVHLVLPRKAGDFHRNDSIYEELQKHDKEDFPASWRSEEEMAAEAAALRVYFQ

>d1kpf_d.13.1.1 (-) Protein kinase C inhibitor-1, PKCI-1 {Human (Homo sapiens)}

DTIFGKIIKKEIPAKIIFEDDRCFLAFHDISPQAPTHFLVIPKKHISQISVAEDDDESLLGHLIVGKKCAADLGLNKGY
RMVVNEGSDGGQSVDVHLVHLVLGGRQMNWPPG

>d1emsa1 d.13.1.1 (A:281-440) NIT-FHIT fusion protein, C-terminal domain {Nematode (Caenorhabditis elegans)}

RSDLYTLHINEKSSETGGLKAFRFNIPADHIFYSTPHSFVFVNLKPVTGHVLVSPKRVVPRLTDLTAETADLFIVA
KKVQAMLEKHHNVTTICVQDGKDAGQTVPVHIIHLPRRAGDFGDNEIYQKLASHDKEPERKPRSNEQMA
EEAVVYRNLM

>d1guqa1 d.13.1.2 (A:2-177) Galactose-1-phosphate
uridylyltransferase {Escherichia coli}

TQFNPVDPHRYYNPLTGQWILVSPHRAKRWPQGAQETPAKQVLPAHDPPDCFLCAGNVRTGDKNPDTGT
YVFTNDFAALMSDTPDAPESHPLMRCQSARGTSRVICFSPDHSKTLPPELSVAALTEIVKTWQEQTAEGLKTY
WVQVFENKGAAAGCSNPHPGQIWANSFLPN

>d1guqa2 d.13.1.2 (A:178-348) Galactose-1-phosphate
uridylyltransferase {Escherichia coli}

EAEREDRLQKEYFAEQKSPMLVDYVQRELADGSRTVVEFHVLAVPYWAAPFETLLPKAHVLRITDLTA
QRSIDLALALKLTSRYDNLFQCSFPYSMGWHGAPFNGEENQHWQLHAHFYPPLLRSATVRKFMVGYEMLAE
TQRDLTAEQAAERLRAVSDIHFRESGV

>d1jyaa_d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}
YSFEQAITQLFQQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDEKETLLSHNIFSQDILKPILS
WDEVGGHPVLWRNRQPLNSLDNNNSLYTQLEMLVQGAERLQ
>d1k6za_d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}
SFEQAITQLFQQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDEKETLLSHNIFSQDILKPILS
DEVGGHPVLWRNRQPLNSLDNNNSLYTQLEMLVQGAERLQTSSLISPPRSFSHH
>d1jyoa_d.198.1.1 (A:) Virulence effector SptP secretion chaperone SicP {Salmonella typhimurium}
LQAHQDIIANIGEKLGLPLTFDDNNQCLLLSDIFTSIEAKDDIWLNGMIILSPVCGDSIWRQIMVINGELAA
NNEGTLAYIDAETLLIHAITDLNTYHIISQLESFVNQQEALKNILQEYAKV
>d1k3ea_d.198.1.1 (A:) Secretion chaperone CesT {Escherichia coli}
MSSRSELLLEKFAEKIGIGSISFNENRLCSFAIDEIYYISLSDANDEYMMIYGVCGFPTDNSNALEILNANLWFAE
NGGPYLCYEAGAQSLLLARFPPLDDATPEKLENIEVVVKSMENLYLVHNQGITLENEHMKIEEISS
>d1k3sa_d.198.1.1 (A:) Secretion chaperone SigE {Salmonella enterica}
MESLLNRLYDALGLDAPEDEPLLIIDDGIQVFNFESDHTLEMCCPFMPLPDDILTLQHFLRLNYTSAVTIGADADN
TALVALYRLPQTSTEEEALTGFELFISNVKQLKEHYA
>d1k8kf_d.198.2.1 (F:) ARPC4 (20 kDa subunit) {Cow (Bos taurus)}
TATLRPYLSAVRATLQAALCLENFSSQVVERHNKPEVEVRSSKELLQPVTISRNEKEVKVLEGINSVRVSIAVKQA
DEIEKILCHKFMRFMMRAENFFILRRKPVEGYDISFLITNFHTEQMYKHKLVDFVIHFMEIDKEISEMKLSVN
ARARIVAEFLKNF
>d1k8kd1_d.198.2.1 (D:1-120) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}
MILLEVNRIIEETLALKFENAAAGNKPEAVEVTFADFDRVLYHISNPNGDKTKVMVSISLKFYKELOQAHGADEL
LKRVYGSYLVNPESGYNVSLYDLENLPASKDSIVHQAGMLKRNC
>d1k8kd2_d.198.2.1 (D:121-284) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}
FASVFEKYFQFQEEGKEGENRAVIHYRDETMYVESKKDRVTVVFSTVFKDDDVIGKVFMQEFKEGRASH
TAPQVLFSHREPPLELKDTDAAVGDNIGYITFVLFPRHTNASARDNTINLIHTFRDYLHYHIKCSKAYIHTRMRAK
TSDFLKVLNRARPDA
>d1kafa_d.199.1.1 (A:) DNA-binding C-terminal domain of the transcription factor MotA {Bacteriophage T4}
MEITSDMEEDKDLMLKLLDKNGFVLKKVEIYRSNYLAILEKRTNGIRNFEINNNNGNMRIFGYKMMEHHIQKFT
DIGMSCKIAKGNVYLDIKRSAENIEAVITVASEL
>d1dar_3 d.14.1.1 (476-599) Elongation factor G (EF-G), domain IV {Thermus thermophilus}
VGKPQVAYRETITKPVDFEGKFIRQTGGRGQYGHVKIKVEPLPRGSGFEVNAIVGGVIPKEYIPAVQKGIEEAM
QSGPLIGFPVVDIKVTLYDGSYHEVDSSSEMAFKIAGSMAIKEAVQKGDP
>d1pkp_1 d.14.1.1 (78-148) Ribosomal protein S5, C-terminal domain {Bacillus stearothermophilus}
GTTIPHEVIGHFGAGEIILKPASEGTGVIAGGPARAVLELAGISDILSKSIGSNTPINMVRATFDGLKQLK
>d1fjge1 d.14.1.1 (E:74-154) Ribosomal protein S5, C-terminal domain {Thermus thermophilus}
GTIPHEIEVEFGASKIVLKPAPGTGVIAGAVPRAILELAGVTDLTKELGSRNPINIAYATMEALRQLRTKADVERL
RKG
>d1fgi_d.14.1.1 (I:) Ribosomal protein S9 {Thermus thermophilus}
EQYYGTGRRKEAVARVFLRPGNGKVTVNGQDFNEYFQGLVRAVAALEPLRAVDALGRFDAYITVRGGGKSGQI
DAIKLGIARALVQYNPDYRAKLKPLGFLTRDARVVERKKYGKHARRAPQYSKR
>d1a6f_d.14.1.2 (-) RNase P protein {Bacillus subtilis}
AHLKKRNRLKKNEDFQKVKHGTSVANRQFVLYTLDQPENDELRVGLSVSKKIGNAVMRNRIKRLIRQAFLEEK
ERLKEKDYIIIARKPASQLTYEETKKSLQHLFRKSSLYK

>d1d6ta_d.14.1.2 (A:) RNase P protein {Staphylococcus aureus}
MLLEKAYRIKKNADFQRIYKKGHSVANRQFVVYTCNNKEIDHFRLGISVKLGNALRNKIKRAIRENFKVHKS
HILAKDIIIVIARQPAKDMTTLQIQNSLEHVLIKIAKFVNKKK
>d1b63a1 d.14.1.3 (A:217-331) DNA mismatch repair protein MutL {Escherichia coli}
GTAFLEQALAIIEWQHGDLTLRGWVADPNHTTPALAEIQYCYVNGRMMRDRLINHAIRQACEDKLGADQQPA
FVLYLEIDPHQVDVNVHPAKHEVRFHQSRLVHDFIYQGVLSVLQ
>d1h7sa1 d.14.1.3 (A:232-365) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}
GQKQLQSLIPFVQLPPSDSVEEYGLSCSDLHNLFYISGFISQCTHGVGRSSTDQFFFINRRPCDAKVCRLVN
EVYHMYNRHQYPFVVLNISVDSECVDINVTPDKRQILLQEEKLLAVLKTSLIGMFDS
>d1ei1a1 d.14.1.3 (A:221-392) DNA gyrase B {Escherichia coli}
GIKAFVEYLKNKNTPIHPNIFYFSTEKDGGIGVEVALQWNDFQENIYCFNNIPQRDGUTHLAGFRAAMTRTLN
AYMDKEGYSKKAKVSATGDDAREGLIAVSVKVPDPKFSSQTDKKLVSSEVKAQEQQMNELLAEYLLLENPTDA
KIVVGKIIDAARAREAARRAREMT
>d1e3ha2 d.14.1.4 (A:3-151) Polynucleotide phosphorylase/guanosine pentaphosphate synthase
(PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}
NETHYAEAVIDNGAFGTRTIRFETGRALARQAGSAVAYLDDDTMVLATTASKNPKDQLDFPLTVDEERMYA
AGKIPGSFFRREGPSEDAILCRLIDRPLRPSFKKGLRNEIQVVATIMALNPDHLYDVVAINAASASTQLAGLP
>d1e3ha3 d.14.1.4 (A:346-482) Polynucleotide phosphorylase/guanosine pentaphosphate
synthase (PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}
TDIRTLAAEVEAIPRVHGSALFFERGETQILGVTLNMRMEQQQLTLSPVTRKRYMHNYNFPPYSVGETGRVGS
PKRREIGHGALAERAIVPVLPTREEFPYAIRQVSEALGSNGSTMGSVCASTMSLLNAGVPLK
>d1h72c1 d.14.1.5 (C:5-167) Homoserine kinase {Archaeon Methanococcus jannaschii}
MKVRVKAPCTSANLGVGFDVFLCLKEPYDVIEVAIDDKEIIIEVDDKNIPTDPDKNVAGIVAKKMIDDFNIGK
GVKITKKGVKAGSGLGSSAASSAGTAYAINELFKLNLDKLKLVDYASYGELASSGAKHADNVAPAIFGGFTMVN
YEPEVLHIPID
>d1fi4a1 d.14.1.5 (A:3-190) Mevalonate 5-diphosphate decarboxylase {Baker's yeast
(Saccharomyces cerevisiae)}
VYTASVTAPVNIATLKYWGKRDTKLNLTPTNSSISVTLSQDDLRTLSAATAPEFERDTWLNGEPHSIDNERTQNC
LRDLRQLRKEMESKDASLPTLSQWKLHIVSENNPTAACGLASSAAGFAALVSAIAKLYQLPQSTSEISRIARKGSGS
ACRSLFGGYVAWEMGKAEDGHDSMAVQIADSSDW
>d1c3ta_d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
MQLFVKTLTGKTLTVELEPSDTVENLAKAKIQLDKEGIPPDQQQLIFAGKQLEDGRTLSYNLQESTIHLVRLRGG
>d1gjza_d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
GSMQIFVKTLGKTITLEVEPSDTIENVKAKIQLDKEGIPPDQQQLIFAGKQLEDGRTLSYNLQESTIHLVRLRGG
>d1ubi_d.15.1.1 (-) Ubiquitin {Human (Homo sapiens)}
MQIFVKTLGKTITLEVEPSDTIENVKAKIQLDKEGIPPDQQQLIFAGKQLEDGRTLSYNLQESTIHLVRLRGG
>d1ud7a_d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
MQVFLKLTGKTITLEVEPSDTVENFKAKIQLDKEGIPPDQQQLIFAGKQLEDGRTLSYNLQESTIHLVRLRGG
>d1a5r_d.15.1.1 (-) SUMO-1 (smt3 homologue) {Human (Homo sapiens)}
GMSDQEAKPSTEDLGDKKEGEYIKLKVGQDSSEIHFKVKMTTHLKKLKESYCQRQGVPMNSLRFLFEGQRIA
DNHTPKELGMEEEDVIEVYQEQTGGHSTV
>d1euvb_d.15.1.1 (B:) SUMO-1 (smt3 homologue) {Baker's yeast (Saccharomyces
cerevisiae)}
PETHINLKVDGSSEIFFKIKKTTPLRRLMEAFAKRQGKEMDSLRFYDGIRIQAQDQTPEDLDMEDNDIIEAHREQ

IGG

>d1ndda_d.15.1.1 (A:) Nedd8 {Human (Homo sapiens)}
MLIKVKTGKEIEIDIEPTDKVERIKERVEEKEGIPPQQQLIYSGKQMNEKTAADYKILGGSVLHLVLALR
>d1vcba_d.15.1.1 (A:) Elongin B {Human (Homo sapiens)}
MDVFLMIRRHKTIFTDAKESSTVFLKRIVEGILKRPPDEQRPLYKDDQLDDGKTLGECGFTSQTARPQAPATV
GLAFRADDTEALCIEPFSSPPE
>d1bt0a_d.15.1.1 (A:) Rub1 {Mouse-ear cress (Arabidopsis thaliana)}
MLIKVKTGKEIEIDIEPTDTIDRIKERVEEKEGIPPVQQQLIYAGKQLADDKAKDYNIEGGSVLHLVLAL
>d1h8ca_d.15.1.2 (A:) Fas-assosiated factor 1, Faf1 {Human (Homo sapiens)}
NAEPVSKLIRTPSGEFLERRFLASNKLQIVFDFVASKGFPWDEYKLLSTFPRRDVTQLDPNKSLEVKLFPQETLF
LEAKE
>d1i42a_d.15.1.2 (A:) p47 {Rat (Rattus norvegicus)}
KASSSILINEAEPTTNIQIRLADGGRLVQKFNHSHRISDIRLIVDARPAMAATSFVLMTTFPNKELADENQLTKE
ANLLNAVIVQRLT
>d1eo6a_d.15.1.3 (A:) Golgi-associated ATPase enhancer of 16 kD, Gate-16 {Cow (Bos taurus)}
MKWMFKEDHSLEHRCVESAKIRAKYPDRVPVIVEKVSQSIVDIDKRKYLVPSDITVAQFMWIIRKRIQLPSEKA
IFLFVDKTVHQSSLTMGQLYEKEKDEDGFLYVAYSGENTFG
>d1gnua_d.15.1.3 (A:) GABA(A) receptor associated protein GABARAP {Human (Homo sapiens)}
MKFVYKEEHPKFEKRRSEGEKIRKKYPDRVPVIVEKAPKARIQDLDKKYLVPSDLTVGQFYFLIRKRIHLRAEDALF
FFVNNVIPPTSATMGQLYQEHHEDFFLYIAYSDESVYGL
>d1ef1a3 d.15.1.4 (A:4-87) Moezin {Human (Homo sapiens)}
TISVRVTTMDAELEFAIQPNTTGKQLFDQVVKTIGLREVWFFGLQYQDTKGSTWLKLNKKVTAQDVRESPLL
FKFRAKFYPE
>d1gc7a3 d.15.1.4 (A:1-87) Radixin {Mouse (Mus musculus)}
MPKPINVRVTTMDAELEFAIQPNTTGKQLFDQVVKTIGLREVWFFGLQYQDTKGSTWLKLNKKVTAQDVRESPLL
ENPLQFKFRAKFFPE
>d1gg3a3 d.15.1.4 (A:1-81) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
MHCKVSLDDTVYEVVEKHAKGQDLLKRVCEHLNLLEEDYFGLAIWDNATSKTWLDSAKEIKKQVRGVWPWN
FTFNVKFYP
>d1h4ra3 d.15.1.4 (A:20-103) Merlin {Human (Homo sapiens)}
KTFTVRIVTMADAEMEFNCEMKWKGKDLFLVCRTLGLRETWFGLQYTIKDTVAWLKMDKKVLDHDVSKEEP
VTFHFLAKFYPE
>d1c1yb_d.15.1.5 (B:) c-Raf1 RBD {Human (Homo sapiens)}
SNTIRVFLPNKQRTVVNRNGMSLHDCLMKALKVRGLQPECCAVFRLHEHKGKKARLDWNTDAASLIGEEL
QVDFL
>d1lfda_d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RaLGDS {Rat (Rattus norvegicus)}
GDCCIIRVSLVDNGNMYKSILVTSQDKAPT VIRKAMDKHNLDEDEPEDYELLQIISEDHKLKIPENANVFYAMN
SAANYDFILKRR
>d1raxa_d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RaLGDS {Human (Homo sapiens)}
QQVGDCCIIRVSLVDNGNMYKSILVTSQDKAPAVIRKAMDKHNLEEEPEDYELLQILSDDRKLKIPENANVFY
AMNSTANYDFVLKKRTFT
>d1rlf_d.15.1.5 (-) RalGDS-like factor, RIf {Mouse (Mus musculus)}
GSSDCRIIRVQMELEGDSVYKSILVTSQDKAPSVISRVLKKNNRDSA VASEFELVQLLPGDRELTI PHSANVFYA
MDGASHDFLLRQRR

>d1ef5a_d.15.1.5 (A:) Rgl {Mouse (Mus musculus)}

EDTCIIRISVEDNNGNMYKSIMLTSQDKTPAVIQRAMSKHNLESDPAEEYELVQVISEDKELVIPDSANVFYAMN
SQVNFDIFLRKKN

>d1e8xa3 d.15.1.5 (A:142-321) Phosphoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}

AASEETLAFQRQLNALIGYDVTDSNVHDDELFTRRLVTPRMAEVAGRDPKLYAMHPWVTSKPLPEYLLKKI
TNNCVFIVIHRSTTSQTIKSADDTPGTILQSFTKMAKKSLMDIPESQNERDFVLRCGRDEYLVGETPIKNFQ
WVRQCLKNGEEIHVLDTPPDPALDEVRK

>d1e8ya3 d.15.1.5 (A:143-322) Phosphoinositide 3-kinase (PI3K) {Human (Homo sapiens)}

MSEESQAFQRQLTALIGYDVTDSNVHDDELFTRRLVTPRMAEVASRDPKLYAMHPWVTSKPLPEYLWKI
ANNCFIVIHRSTTSQTIKVSPDDTPGAILQSFTKMAKKSLMDIPESQSEQDFVLRCGRDEYLVGETPIKNFQ
WVRHCLKNGEEIHVLDTPPDPALDEVRK

>d1i35a_d.15.1.5 (A:) Protein kinase byr2 {Yeast (Schizosaccharomyces pombe)}

CILRFIACNGQTRAVQSRGDYQKTLAIALKKFSLEDASKFIVCVSQSSRIKLITEEFKQICFNSSPERDRLIIVPKEK
PCPSFEDLRRSWEIE

>d1d4ba_d.15.2.1 (A:) Cell death-inducing effector B (CIDE-B), N-terminal domain {Human (Homo sapiens)}

MEYLSALNPSDLLRSVSNISSEFGRRVWTSAPPQRPFRVCDHKRTIRKGLTAATRQELLAKAETLLNGVLTVL
EEDGTAVDSEDFFQLLEDDTCLMVLQSGQSWSPTRSGVLHHHHHH

>d1c9fa_d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Mouse (Mus musculus)}

MCAVLRQPCKVLRALHSACKFGVAARSCQELLRGCVRFQLPMPGSRLCLYEDGTEVTDDCFPGLPNDAELLL
LTAGETWHGYVSD

>d1ibxa_d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Human (Homo sapiens)}

MLQPKSVKLRALRSPRKFGVAGRSCQEVLKGCLRFQLPERGSRLCLYEDGTELTEDYFPSVPDNAELVLLTGQ
AWQGH

>d1f2ri_d.15.2.1 (I:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Mouse (Mus musculus)}

MELSRGASAPDPDDVRPLKPCLLRRNHSRDQHGVAASSLEELRSKACELLAIDKSLTPITLVAEDGTIVDDDDYF
LCLPSNTKFVALACNEKWTYNSD

>d1ibxb_d.15.2.1 (B:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Human (Homo sapiens)}

SGEIRTLKPCLLRRNYSREQHGVAASCLEDLRSKACDILAIDKSLTPVTLVAEDGTIVDDDDYFLCLPSNTKFVALA
SNEKWAYNNSD

>d1ip9a_d.15.2.2 (A:) Bud emergence mediator Bmp1 {Baker's yeast (Saccharomyces cerevisiae)}

GAMGSSTSGLTTKIKFYKDDIFALMLKGDTTYKELRSKIAPRIIDTNFKLQTKLFDGSGEEIKTDSQVSNIQAK
LKISVHDI

>d1fm0d_d.15.3.1 (D:) Molybdopterin synthase subunit MoaD {Escherichia coli}

MIKVLFFAQVRELVGTDATEVAADFPTVEALRQHMAAQSDRWALALEDGKLLAAVNQTLVSFDHPLTDGDEV
AFFPPVTGG

>d1f0za_d.15.3.2 (A:) Thiamin biosynthesis sulfur carrier protein ThiS {Escherichia coli}

MQILFNDQAMQCAGQTVHELLEQLDQRQAGAALAINQQIVPREQWAQHIVQDGDQILLFQVIAGG

>d1jsba_d.15.3.2 (A:) Hypothetical protein MTH1743 {Archaeon Methanobacterium}

thermoautotrophicum}

MVIGMKFTVITDDGKKILESGAPRRIKDVLEIPIETVVVKKNGQIVIDEEIFDGDIIEVIRVIYGG

>d1czpa_d.15.4.1 (A:) 2Fe-2S ferredoxin {Cyanobacterium (*Anabaena* sp.), pcc 7119 and 7120}

ATFKVTLINEAEGTKHEIEVPDDEYILDAAEEQGYDLPSCRAGACSTCAGKLVSGTVQSDQFLDDQIEAGY
VLTCVAYPTSDVVIQTHKEEDLY

>d1frd_d.15.4.1 (-) 2Fe-2S ferredoxin {Cyanobacterium (*Anabaena* sp.), pcc 7119 and 7120}

ASYQVRLINKQDIDTTIEDEETTILDGAEEENGIELPFSCHSGSCSSCVGVVEGEVDQSDQIFLDDEQMGKGFA
LLCVTYPRSNCTIKTHQE PYLA

>d4fxc_d.15.4.1 (-) 2Fe-2S ferredoxin {*Spirulina platensis*}

ATYKVTLINAEGINETIDCDDDTYILDAAEEAGLDL PYSCRAGACSTCAGTITSGTIDQSDQSF LDDQIEAGYVL
TCVAYPTSDCTIKTHQE EGLY

>d1fxia_d.15.4.1 (A:) 2Fe-2S ferredoxin {Cyanobacterium (*Aphanothecae sacrum*)}

ASYKVTLKTPDGDNVITVPDDEYILDVAEEEGLDL PYSCRAGACSTCAGKL VSGPAPDEDQSFLDDQIQAGYILT
CVAYPTGDCVIETHKEEALY

>d1dox_d.15.4.1 (-) 2Fe-2S ferredoxin {*Synechocystis* sp., pcc 6803}

ASYTVKLITPDGESSIONCSDDTYILDAAEEAGLDL PYSCRAGACSTCAGKITAGSVDQSDQSF LDDQIEAGYVLTC
VAYPTSDCTIETHKEEDLY

>d2cjn_d.15.4.1 (-) 2Fe-2S ferredoxin {*Synechococcus elongatus*}

ATYKVTLVRPDGSETTIDVPEDEYILDVAEEQGLDLPFSCRAGACSTCAGKLLEG EVDQSDQSF LDDQIEKGFL
TCVAYPRSDCKILTNQEEFLY

>d1awd_d.15.4.1 (-) 2Fe-2S ferredoxin {*Chlorella fusca*}

YKVTLKTPSGEETIECPEDTYILDAAEEAGLDL PYSCRAGACSSCAGKVESGEVDQSDQSF LDDQIEKGFL
VAYPTSDVTILTHQE AALY

>d1frra_d.15.4.1 (A:) 2Fe-2S ferredoxin {*Equisetum arvense*}

AYKTVLKTPSGEFTLDVPEGTTILDAAEEAGYDLPFSCRAGACSSCLGVSGVDESEGSFLDDGQMKGFL
CIAIPESDLVIETHKEEELF

>d1doi_d.15.4.1 (-) 2Fe-2S ferredoxin {Archaeon *Haloarcula marismortui*}

PTVEYLNYEVVDDNGWDMYDDDVFGEASMDMLDEDYGSLEVNEGEYILEAAEAQGYDWPFSCRAGACAN
CAAIVLEGIDMDMQQILSDEEVEDKNVRLTCIGSPDADEVKIVYNNAKHLDYLQNRVI

>d1e0za_d.15.4.1 (A:) 2Fe-2S ferredoxin {Archaeon *Halobacterium halobium*}

PTVEYLNYETLDDQGWDMDDDLFEKAADAGLDGEDYGTMEVAEGEYILEAAEAQGYDWPFSCRAGACAN
CASIVKEGEIDMDMQQILSDEEVEEKDVR LTCIGSPADEVKIVYNNAKHLDYLQNRVI

>d1pf d.15.4.1 (-) 2Fe-2S ferredoxin {Parsley (*Petroselinum crispum*)}

ATYNVKLITPDGEVEFKCDDDVYLDQAEEEGIDLPSCRAGSCSSCAGKVVSGSIDQSDQSF LDDQIEMDAGYV
LTCHAYPTSDVVIETHKEEEIV

>d1a70_d.15.4.1 (-) 2Fe-2S ferredoxin {Spinach (*Spinacia oleracea*)}

AAVKVTLPTGNVEFQCPDDVYILDAAEEEGIDLPSCRAGSCSSCAGKLKTGSLNQDDQSF LDDQIEDEGWV
LTCAAYPVS DVTIETHKEEELTA

>d1gaqb_d.15.4.1 (B:) 2Fe-2S ferredoxin {Maize (*Zea mays*)}

ATYNVKLITPGEVELQVPDDVYILDQAEEEDGIDLPSCRAGSCSSCAGKVVSGVDQSDQSYLDDQIADGW
VLTCHAYPTSDVVIETHKEEELTG

>d1e9ma_d.15.4.1 (A:) Ferredoxin VI {*Rhodobacter capsulatus*}

AKIIFIEHNGTRHEVEAKPGTVMEAARDNGVPGIDADCGGACACSTCHAYVDPAWVDKLPKALPTETDMIDF
AYEPNPATSRLTCQIKVTSLLDGLVHLPEKQI

>d1put__ d.15.4.1 (-) Putidaredoxin {Pseudomonas putida}
SKVYYVSHDGTRRQLDADGVSLSMQAAVNGIYDIVGDCGGSASCATCHVYVNEAFTDKVPAANEREIGMLE
CVTAELKPNRLCCQIIMTPELDGIVVDVPDRQW

>d1b9ra_ d.15.4.1 (A:) Terpredoxin {Pseudomonas sp.}
PRVVFIDEQSGEYAVDAQDGQSLMEVATQNGVPGIVAECEGGSCVCATCRIEIDAWVEIVGEANPDENDLLQS
TGEPMTAGTRLSCQVFIDPSMDGLIVRVPLPA

>d1ayfa_ d.15.4.1 (A:) Adrenodoxin {Cow (Bos taurus)}
KITVHFINRDGETLTTKGKIGDSLLVVVQNNLDIDGFGACEGTLACSTCHLIFEQHIFEKLEAITDEENDMLDLAY
GLTDRSRLGCQICLTKAMDNMTRVLP

>d1feha2 d.15.4.2 (A:1-126) Fe-only hydrogenase, N-terminal domain {Clostridium pasteurianum}
MKTIIINGVQFNTDEDTTILKFARDNNNIDISALCFLNNCNNDINKCEICTVEVEGTGLVTACDTLIEDGMIINTNSD
AVNEKIKRSRISQLLDIHEFKCGPCNRRENCEFLKLVIKYKARASKPFLP

>d1hlra2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio gigas}
MIQKVITVNGIEQNLFVDAEALLSDVLRQQQLGLTVKGCEQGQCGACSVILDGKVVRACTKMKRVADGAQI
TTIEGVG

>d1dgja2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio desulfuricans}
METKTLIVNGMARRLLVSPNDLLDVLSQLQLTSVKVCGKGQCGACTVILDGKVVRACIKMSRVAENASVT
TLEGIG

>d1fo4a2 d.15.4.2 (A:3-92) Xanthine oxidase, N-terminal domain {Cow (Bos taurus)}
ADELVFFVNGKKVVEKNADPETTLLAYLRRKLGRLGCKLGCCEGGCGACTVMLSskyDRLQDKIIHFSANACLA
PICTLHHVAVTTVEGIG

>d1jroa2 d.15.4.2 (A:1-84) Xanthine dehydrogenase chain A, N-terminal domain {Rhodobacter capsulatus}
MEIAFLNGETRRVRIEDPTQSLLELLRAEGLTGTKEGCNEGDCGACTVMIRDAAGSRAVNACLMMLPQIAGK
ALRTIEGIAAP

>d1qj2a2 d.15.4.2 (A:3-81) Carbone monoxide (CO) dehydrogenase iron-sulfur protein, N-domain {Pseudomonas carboxydovorans}
KAHIETLINGHPVEALVEPRTLLIHFIREQQQNLTAHIGCDTSHCGACTVDLDGMSVKSCTMFAVQANGASITTIE
GMA

>d1ffva2 d.15.4.2 (A:3-81) Carbone monoxide (CO) dehydrogenase iron-sulfur protein, N-domain {Hydrogenophaga pseudoflava}
KKIITVNNGKAQEKAPEPRTLLIHFREELNLTAHIGCETSHCGACTVDIDGRSVKSCTHLAVQCDGSEVLTE
GLA

>d2pia_3 d.15.4.2 (224-321) Phthalate dioxygenase reductase, C-terminal domain {Pseudomonas cepacia, db01}
SFGATNTNARENTPFTVRLSRSGTSFEIPANRSILEVLDANVRVPSSCESGTCGCKTALCSGEADHRDMVLD
DEKGTQIMVCVSRRAKSAELVLD

>d1fumb2 d.15.4.2 (B:1-105) Fumarate reductase iron-sulfur protein, N-terminal domain {Escherichia coli}
AEMKNLKIEVVRYNPEVDTAPHSAFYEVPYDATTSLDALGYIKDNLAPDLSYRWSCRMAICGSCGMMVNNVP
KLACKTFLRDYTDGMKVEALANFPIERDLVVD

>d1qlab2 d.15.4.2 (B:1-106) Fumarate reductase iron-sulfur protein, N-terminal domain {Wolinella succinogenes}

MGRMLTIRVFYDPQSAVKPHFQEYKIEEAPSMTIFIVLN MIRETYDPDLNFDVCRAGICGSCGMMINGRPS
LACRTLT KDFEDGVITLLPLPAFKLIKDSLVD

>d1jq4a_ d.15.4.2 (A:) Methane monooxygenase reductase N-terminal domain {Methylococcus capsulatus}

MQRVHTITAVTEDGESLRFECRSDEDVITAALRQNIFLMSSCREGGCATCKALCSEG DYDLKGCSVQALPEEEE
EGLVLLCRTYPKTDLIELPYTH

>d1ssn_ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}

SSSF DKGKYKKGDDASYFEPTGPYLMVNVTGVDSKGNE LSPHYVEFPIKPGTTLTKEKIEYYVEWALDATA YKEF
RVVELDPSAKIEVTYYDKNKKKEETKSFPITEKGFVV PDLSEHIKNPGFNLTKV VIEKK

>d2sak_ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}

SYFEPTGPYLMVNVTGVDSKGNE LSPHYVEFPIKPGTTLTKEKIEYYVEWALDATA YKEFRVVELDPSAKIEVTYY
DKNKKKEETKSFPITEKGFVV PDLSEHIKNPGFNLTKV VIEKK

>d1bmlc1 d.15.5.1 (C:12-148) Streptokinase {Streptococcus equisimilis}

SVNNSQLVVSAGTV EGTNQDISLKFFIDLT SRPAHGGKTEQGLSPKSKPFATDSGAM PHKLEADLLKAIQEQ
LIANVHSNDDYFEVIDFASDATIDRNGKVYFADKGSVTLPTQPVQEFLLSGHVRVPYKE

>d1bmlc3 d.15.5.1 (C:285-372) Streptokinase {Streptococcus equisimilis}

DPFDRSHLKLFTIKYDVNTNELLKSEQLLTASERNLD FRDLYDPRD KAKL LYNLDAFGIMDYLTGKV EDNH
DTNRIITVYMGKR

>d1c4pc_ d.15.5.1 (C:) Streptokinase {Streptococcus equisimilis}

KPIQNQAKSVDVEYTVQFTPLNPDDDFRPGLKDTKLKTLAIGDTITSQELLAQAQSILNKTHPGYTIYERDSSIVT
HDNDIFRTILPMQDFEFTYHVKNREQAYEINKSGLNEEINNTDLISEKYYVLKKG

>d1qqra_ d.15.5.1 (A:) Streptokinase {Streptococcus equisimilis}

IQNQAKSVDVEYTVQFTPLNPDDDFRPGLKLT KLLKTLAIGDTITSQELLAQAQSILNKH PGYTIYERDSSIVT
DNDIFRTILPMQDFEFTYRVKNREQAYRINKSGLNEEINNTDLISEKYYVLKKGEKP YDPFD

>d1esfa2 d.15.6.1 (A:121-233) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}

EEKKVPI NLWLDGKQNTVPLETVKTNKKNVTVQELDLQARRYLQE KYNLYNSDVF DGKVQRGLIVFHTSTEPSV
NYDLFGAQGQYSNTLLRIYRD NK TINSEN NMHIDIYLYTS

>d1i4pa2 d.15.6.1 (A:121-239) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}

NHF DNGNLQNV LIRVYENKRNTISFEVQ TD KSVTAQELDIKARNFLINKN LYEFNSSPYETGYIKFIENNGNTF
WYDMMPAPGDKFDQSKYLM MYNDN KTVDSK SVKIEVHLTTKNG

>d3tss_2 d.15.6.1 (94-194) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}

LPTPIELPLKVKVHGKD SPLKYWP KFDK QLAISTLDFKIRHQLTQ THGLY RSSDKTGGYWK ITMNDGSTYQSDL
SKKFEYNTEKPPINIDEIKTIEAEIN

>d1sebd2 d.15.6.1 (D:127-235) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

DKYRSITRV FEDGKNLLSFDVQ TNKKVTAQELDYLTRH YLVKNKKLYETGYIKFIENENSFWYDMMPAPGDKF
DQSKYLM MYNDN KMVDSK DVKIEVYLT

>d3seb_2 d.15.6.1 (122-238) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}

NGNQLDKYRSITRV FEDGKNLLSFDVQ TNKKVTAQELDYLTRH YLVKNKKLYEFNNSPYETGYIKFIENENS
WYDMMPAPGDKFDQSKYLM MYNDN KMVDSK DVKIEVYLT

>d1enfa2 d.15.6.1 (A:102-213) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}

EKLAQERVIGANVWDGIQKETELIRTNKKNVTLQELDIKIRKILSD KYK IYYKDSEISKGLIEFDMKTP RDYSFDIY
DLKGENDYEIDKIYEDN KTLKSSDDISHIDVNLYT

>d1an8_2 d.15.6.1 (96-208) Streptococcal superantigen Spe-C {Streptococcus pyogenes}

NKVNHKLLGNLFISGESQQNLNKIILEKDIVTFQEIDFKIRKYLMNDNYKIYDATSPYVSGRIEIGTKDGKHEQIDLFDSPNEGTRSDIFAKYKDNRINMKNFSHFDIYLEK
>d1et9a2 d.15.6.1 (A:96-204) Streptococcal superantigen Spe-H {Streptococcus pyogenes}
EKKEIKVPVNWDKSKQQPPMFITVNPKVTAQEVDIKVRKLLIKYDIYNNREQKYSKGTVTLDLNSGKDIVFDLYYFGNGDFNSMLKIYSNNERIDSTQFHVDVSIS
>d1eu3a2 d.15.6.1 (A:97-209) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}
TSIPKNIPVNLWINGKQISVPYNEISTNKTTVTAQEIDLKVRKFLIAQHQLYSSGSSYKSGRLVFHTNDNSDKYSFDLFYVGYRDKESIFKVYKDNKSFNIDKIGHLDIEIDS
>d1bxta2 d.15.6.1 (A:120-234) Streptococcal superantigen SSA {Streptococcus pyogenes} QIEGKFPNITVKVYEDNENILSFDITNNKKQVTQELDCKTRKILSRKNLYEFNNSPYETGYIKFIESSGDSFWYD MMPAPGAIFDQSKYLMYNDNKTVSSAIAIEVHLTK
>d1fnua2 d.15.6.1 (A:108-221) Streptococcal pyrogenic exotoxin A1 {Streptococcus pyogenes} GNHLEIPKKIVVKSIDGIQSLSDIETNKKMVTAQELDYKVRKYTIDNKQLYTNGPSKYETGYIKFIPKNKESFWFDFFPEPEFTQSKYLMYKDNETLDNKTSQIEVYLTTK
>d1fcla_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
TTFKLIINGKTLKGETTTEAVDAATAEKVLQYINDNGIDGEWTYDDATKTWTVTE
>d1fd6a_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
MTTFKLIINGKTLKGETTTEAVDAATAEKVFKQYANDNGIDGEWTYDDATKTFTVTE
>d1gb4_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
MTTFKLIINGKTLKGETTIEAVDAAAEAKIFKQYANDNGIDGEWTYDDATKTFTVTE
>d1pgb_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
MTYKLILNGKTLKGETTTEAVDAATAEKVFQYANDNGVDGEWTYDDATKTFTVTE
>d1pgx_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
ELPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTEMVTEVPVA
>d1qkza_ d.15.7.1 (A:) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
VTTYKLVINGKTLKGETTTKAVDAATAEKVFQYANDNGVDGEWTYDDATKTFTVTEK
>d2igd_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
MTPAVTTYKLVINGKTLKGETTTKAVDAETAEKAFKQYANDNGVDGVWTYDDATKTFTVTE
>d2igg_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains {Streptococcus sp., group G}
LTPAVTTYKLVINGKTLKGETTTEAVDAATAEKVFQYANDNGVDGEWTYDDATKTFTVTEKPE
>d1heze_ d.15.7.1 (E:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}
EVTIKVNLIFADGKIQTAEFKGTSEEATAEARYRADLLAKVNGEYTADLEDGGNHMNIKFA
>d1hz6a_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L

{Peptostreptococcus magnus}

HHAMEEVТИKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVADKGYTLNIKFAG

>d1jmla_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

MHHHHHHGMEVTIKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVVPKAYTLNIKFAG

>d1k52a_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

MHHHHHHAMEEVТИKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEWTVDVADGGYTLNIKFAG

>d1kh0a_ d.15.7.1 (A:) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

EEVTIKANLIFANGSTQAEFKGTKEKALSEVLAYADTLKKDNGEWTIDKRVTNGVIIILNIKFAG

>d2ptl_ d.15.7.1 (-) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus magnus}

ENKEETPETPETDSEEETIKANLIFANGSTQAEFKGTFEKATSEAYAYADTLKKDNGEYTVDVADKGYTLNIKFA
G

>d1tif_ d.15.8.1 (-) Translation initiation factor IF3, N-terminal domain {Bacillus stearothermophilus}

KDFIINEQIRAREVRLIDQNGDQLGIKSQEALEIAARRNLDLVAPNAKPPVCRIMDYKFRFEQQKKEEARK

>d1f52a1 d.15.9.1 (A:1-100) Glutamine synthetase, N-terminal domain {Salmonella typhimurium}

SAEHVILMLNEHEVKFVDLRFTDTKGKEQHVTIPAHQVNAEFFEEGKMFDGSSIGGWKGINESDMVLMPDAS
TAVIDPFFADSTLIIRCILEPGTLQGY

>d1coy_2 d.16.1.1 (319-450) Cholesterol oxidase {Brevibacterium sterolicum}

GNNGNIMVGRANHMWDATGSKQATIPTMGIDNWADPTAPIFAEIAPLPAGLETYVSLYLAITKNPERARFQFN
SGTGKVDLTWAQSQNQKGIDMAKKVFDKINQKEGTIYRTDLFGVYYKTWGDDETYHPLG

>d1ijha2 d.16.1.1 (A:319-450) Cholesterol oxidase {Streptomyces sp.}

GPNGNIMTARANHMWNPTGAHQSSIPALGIDAWDNSDSSVFAEIAPMPAGLETWVSLYLAITKNPQRGTFVY
DAATDRAKLNWTRDQNAPAVNAAKALFDRINKANGTIYRYDLFGTQLKAFADDFCYHPLG

>d1k0ia2 d.16.1.2 (A:174-275) p-Hydroxybenzoate hydroxylase (PHBH) {Pseudomonas aeruginosa}

LKVFERVYPFGWLGLLADTPPVSHELIYANHPRGFALCSQRSATRSQYYVQVPLSEKVEDWSDERFWTELKARL
PSEVAEKLVGPSLEKSIAPLRSFVVEP

>d1foha4 d.16.1.2 (A:241-341) Phenol hydroxylase {Soil-living yeast (Trichosporon cutaneum)}

GEQTDYIWGVLDAPVSNFPDIRSRCAIHSAESGSIMIIPRENNLVRFYVQLQARAEGGGRVDRTKFTPEVVIAN
AKKIFHPYTFDVQQLDWFTAYHIGQR

>d1an9a2 d.16.1.3 (A:195-287) D-amino acid oxidase {Pig (Sus scrofa)}

LQPGRGQIIKVDAPWLKNFIITHDLERGIYNSPYIIPGLQAVLGGTFQVGNWNEINNIQDHNTIWECCRLEPT
LKDAKIVGEYTGFRPVRP

>d1c0pa2 d.16.1.3 (A:1194-1288) D-amino acid oxidase {Yeast (Rhodotorula gracilis)}

AEPIRGQTVLVKSPCKRCTMDSSDPASPAYIIPRGGEVICGGTYVGWDLSVPETVQRILKHCLRLDPTISSL
GTIEGIEVLRHNVGLRPAR

>d1el8a2 d.16.1.3 (A:218-321) Sarcosine oxidase {Bacillus sp., strain b0618}

LQPYRQVVGFFESDESKEYSDNDIFPGFMVEVPNGIYYGFPMSGCGKLGYHTFGQKIDPDTINREFGVYPEDES
NLRAFLEEMPGANGELKRGAVCMYTKTL

>d1i8ta2 d.16.1.7 (A:245-313) UDP-galactopyranose mutases {Escherichia coli}

EYRSLKFETERHEFPNFQGNAINFTDANPYTRIIIEHKHFDYVETKHTVVTKEYPLEWKVGDEPYYPV

>d1cf3a2 d.16.1.4 (A:325-520) Glucose oxidase {Aspergillus niger}
NLQDQTATVRSRITSAGAGQQAAWFATFNETFGDYSEKAHELLNTKLEQWAEEAVARGGFHNTTALLIQYE
NYRDWIVNHNVAYSELFDTAGVASFDVVDLLPFRGKVHILDKDPYLHHFAYDPQYFLNELDLLGQAAATQLA
RNISNSGAMQTYFAGETIPGDNLAYDADLSAWTEYIPYHFRPNYHGVGT

>d1gpea2 d.16.1.4 (A:329-524) Glucose oxidase {Penicillium amagasakiense}
NMQDQTTTVSSRASSAGAGQQAVFFANFTETFGDYAPQARDLLNTKLDQWAETVARGGFHNTALKVQ
YENYRNWLLEDVAFAELFMDTEGKINFDLWDLIPFRGSVHILSSDPYLWQFANDPKFLNEFDLLGQAAASK
LARDLTSQGAMKEYFAGETLPGYNLVQNATLSQWSDYVLQNFRPNWHAVSS

>d1b5qa2 d.16.1.5 (A:294-405) Polyamine oxidase {Maize (Zea mays)}
DMAVYTKIFLKFPKFWPEGKGREFFLYASSRRGYYGVWQEFEKQYPDANVLLVTVTDEESRRIEQQSDEQTKA
EIMQVLRKMFPGKDVPDATDILVPRWWSDRFYKGTFSN

>d1f8ra2 d.16.1.5 (A:320-432) L-amino acid oxidase {Malayan pit viper (Calloselasma rhodostoma)}

HYRSGTKIFLTCTTFWEDDGIHGGKSTTDLPSRFIYYPNHNFTNGVGVIAYGIGDDANFFQALDFKDCADIVF
NDLSQLPKKDIQSFCYPSVIQKWSLDKYAMGGITT

>d1gosa2 d.16.1.5 (A:290-401) Monoamine oxidase B {Human (Homo sapiens)}
PLGSVIKICIVYYKEPFWRKKDYCGTMIDGEEAPVAYTLDDTKPEGNYAAIMGFIKARLARLTKEERLKKCE
LYAKVLGSLEALEPVHYEEKNWCEEQYSGGCYTTY

>d1d5ta2 d.16.1.6 (A:292-388) Guanine nucleotide dissoiation inhibitor, GDI {Cow (Bos taurus)}

RKAGQVIRIICILSHPIKNTNDANSCQIIIPQNQVNRKSDIYVCMISYAHNVAAQGKYIAIASTTVETTDPEKEVEP
ALGLLEPIDQKFVAISDLYE

>d1mola_ d.17.1.1 (A:) Monellin, B & A chains together {Serendipity berry (Dioscoreophyllum cumminsii)}

GEWEIIDIGPFTQNLGKFAVDEENKIGQYGRLTNFNKIRPCMKKTIYENEREIKGYEYQLVVASDKLFRADISEDY
KTRGRKLLRFNGPVPPIP

>d1eqka_ d.17.1.2 (A:) Phytocystatin {Japanese rice (Oryza sativa), subsp. japonica, oryzacystatin-I}
MSSDGGPVGGVEPVGNENDLHLVDLARFAVTEHNKKANSLEFEKLVSVKQQVVAGTLYYFTIEVKEGDAKKL
YEAKVWEKPWMDFKELQEFKPVDASANA

>d1cewi_ d.17.1.2 (I:) Cystatin {Chicken (Gallus gallus)}

GAPVPVDENDEGLQRALQFAMAEYNRASNDKYSSRVRVISAKRQLVSGIKYILQVEIGRTTCPKSSGDLQSCEF
HDEPEMAKYTTCTVVYSIPWLNQIKLLESKCQ

>d1dvd_ d.17.1.2 (-) Cystatin A (stefin A) {Human (Homo sapiens)}

MIPGGLSEAKPATPEIQLQEVDFKVKPQLEEKTNETYGKLEAVQYKTQVVAGTNYYIKVRAGDNKYMHLKVFSLPG
QNEDLVTGYQVDKKNKDDELTF

>d1stfi_ d.17.1.2 (I:) Cystatin B (stefin B) {Human (Homo sapiens)}

MMMSGAPSATQPATAETQHIADQVRSQLEEKYNKKFPVFKAVSFKSQVVAGTNYFIKVHVGDEFVHLRVFQSL
PHENKPPLTLSNYQTNKAKHDELTYF

>d1g96a_ d.17.1.2 (A:) Cystatin C {Human (Homo sapiens)}

VGGPMMDASVEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNYFLDVELGRTTCKTQPNLD
NCDFHDQPHLKRKAFCSFQIYAVPWQGTMTLSKSTCQDA

>d1oaca2 d.17.2.1 (A:91-185) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

KRPHPNALTADIEIKQAVEIVKASADFKPNTRFEISLPPDKEAVWAFALENKPVDQPRKADVIMLDGKHIIAEV

VDLQNNKLLSWQPIKDAHG

>d1oaca3 d.17.2.1 (A:186-300) Copper amine oxidase, domains 1 and 2 {Escherichia coli}

MVLLDDFASVQNIINNSEFAAVKKRGITDAKKVITPLTVGYFDGKDGLKQDARLLKVISYLDVGDGNYWAH
PIENLVAVVDLEQKKIVKIEEGPVVPVPMTARPFDGRDRVA

>d1ksia2 d.17.2.1 (A:6-98) Copper amine oxidase, domains 1 and 2 {Pea seedling (Pisum sativum)}

VQHPLDPLTKEEFLAVQTIVQNKPISNNRLAFHYIGLDDPEKDHLRYETHPTLVSIPRKIFVVAIINSQTHEILNL
RIRSIIVSDNIHNGY

>d1ksia3 d.17.2.1 (A:99-206) Copper amine oxidase, domains 1 and 2 {Pea seedling (Pisum sativum)}

GFPILSVDEQSLAIKLPLKYPPFIDSVKKRGNLNLEIVCSSFTMGWFGEEKNVRTVRLCDFMKESTVNIYVRPITGI
TIVADLDMKIVEYHDRDIEAVPTAENTEYQ

>d1av4_2 d.17.2.1 (9-96) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ASPFRLASAGEISEVQGILRTAGLLGPEKRIAYLGVLDPARGAGSEAEDRRFRVFIHDVSGARPQEVTVSNTGTV
ISAVEELDTAATG

>d1av4_3 d.17.2.1 (97-211) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}

ELPVLEEEFEVVEQLLATDERWLKALAARNLDSVKRVAPLSAGVFYEAEERGRRLRGLAFVQDFPEDSAWAH
PVDGLVAYVDVVSKEVTRVIDTGVFPVPAEHGNYTDPELTG

>d1a2va2 d.17.2.1 (A:18-115) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula polymorpha)}

PARPAHPLDPLSTAEIKAATNTVKSYFAGKKISFTVTLREPARAKAYIQWKEQGGPLPPRLAYYVILEAGKPGVKE
GLVDLASLSVIETRALETVQPI

>d1a2va3 d.17.2.1 (A:116-236) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula polymorpha)}

LTVEDLCSTEEVIRNDPAVIEQCVLGIPANEMHKVYCDPWTIGYDERWGTGKRLQQALVYYRSDEDDSQYSHP
LDFCPIVDTEEKVIFIDIPNRRRKVKHKHANFYPKHMIEKGAMR

>d1eeja2 d.17.3.1 (A:1-60) Disulfide bond isomerase, DsbC, N-terminal domain {Escherichia coli}
DDAAIQQTAKMGIKSSDIQPAPVAGMKTVLNSGVLYITDDGKHIQGPMYDVSGTAPV

>d3stda_ d.17.4.1 (A:) Scytalone dehydratase {Fungus (Magnaporthe grisea)}

GEITFSYDYLGLMTCVYEWADSYDSKDWDRLRKVIAPTLRIDYRSFLDKLWEAMPAEFVGMVSSKQVLGDPTLR
TQHFFIGGTRWEKVS EDEVIGYHQLRPHQRYKDTTMKEVTMKGHAHSANLHWYKKIDGVWKAGLKPDIR
WGEFDFDRIFEDGRETGF

>d1ouna_ d.17.4.2 (A:) Nuclear transport factor-2 (NTF2) {Rat (Rattus norvegicus)}

GDKPIWEQIGSSFIQHYYQLFDNDRTQLGAIYIDASCLTWEGQQFQGKAAIVEKLSSLPFQKIQHSITAQDHQPT
PDSCIISMVVGQLKADEDPMGFMHQMFLLKNINDAWVCTNDMFRALAHNF

>d1jkga_ d.17.4.2 (A:) NTF2-related export protein 1 (p15) {Human (Homo sapiens)}

ASVDFKTYVDQACRAAEFVNYYTTMDKRRRLSRLYMGTATLVWNGNAVGQESLSEFFEMLPSEFQISV
VDCQPVHDEATPSQTTVLVICGSVKFEGNKQRDFNQNFI TAQASPSNTVWKIASDCFRFQDWAS

>d1jkgb_ d.17.4.2 (B:) NTF2-like domain of Tip associating protein, TAP {Human (Homo sapiens)}

APPCKGSYFGTENLKS LVLHFLQQYYAIYDSGDRQGLDAYHDGACCSLSIPFIPQNPARSSLAEYFKDSRNVKKL
KDPTLRFRLKKHTRLNVVAFLNELPKTQHDVNSFVVDISAQSTLLCF SNGVFKEVDGKSRDSLRAFRTFIAVP
ASNSGLCIVNDELFVRNASSEEIQRAFAMPAPTP

>d1qjga_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Comamonas testosteroni and Pseudomonas testosteroni}

MNTPEHMTAVVQRYVAALNAGDLDGIVALFADDATVENPVGSEPRSGTAIREFYANSLKLPLA VELTQEVR A

ANEAFAFIVSFYQGRKTVVAPIDHFRNGAGKVSMRALFGEKNIHAGA
>d1ea2a_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI {Pseudomonas putida}
NLPTAQEVQGLMARFIELVDVGDIIEAVQMYADDATVEDPFGQPPIHGREQIAAFYRQGLGGGKVRACLTGPV
RASHNGCGAMPFRVEMVWNGQPCALDVIDVMRFDEHGRITMQAYWSEVNLSV
>d1eg9b_ d.17.4.4 (B:) Naphthalene 1,2-dioxygenase beta subunit {Pseudomonas putida}
MINIQEDKLVSADAEELRFFNCHDSALQQEATTLLTQEAHLLDIQAYRAWLEHCVGSEVQYQVISRELRAASE
RRYKLNEAMNVYNENFQQLKVRVEHQLDPQNWNSPKLRFTRFITNVQAAMDVNDKELLHIRSNVILHRAR
RGNQDVDFYAAVEDKWKRGEGGVRKLVQRFDYPERILQTHNLVMFL
>d1euic_ d.17.5.1 (C:) Uracil-DNA glycosylase inhibitor protein {Bacteriophage pbs2}
QLVIQESILMLPEEEVIGNKPESDILVHTAYDESTDENVMLLSDAPEYKPWALVIQDSNGENKIKML
>d1ugia_ d.17.5.1 (A:) Uracil-DNA glycosylase inhibitor protein {Bacteriophage pbs2}
TNLSDIIKEKGKQLVIQESILMLPEEEVIGNKPESDILVHTAYDESTDENVMLLSDAPEYKPWALVIQDSNGE
NKIKML
>d1pcfa_ d.18.1.1 (A:) Transcriptional coactivator PC4 C-terminal domain {Human (Homo sapiens)}
AMFQIGKMRYSVRDFKGKVLIDIREYWMDPEGEMKPGKGISLNPEQWSQLKEQISDIDDAVRKL
>d1jb0d_ d.187.1.1 (D:) Photosystem I subunit Psd {Synechococcus elongatus}
TTLTGQPLYGGSTGGLLSAADTEEKYAITWTSPKEQVFEMPTAGAAVMREGENLVYFARKEQCLALAQQQLRP
RKINDYKIYRIFPDGETVLIHPKDGVPKEVKNGREAVNSVPRSIGQNPNSQLKFTGKKPYDP
>d3frua2 d.19.1.1 (A:1-178) Fc (IgG) receptor, alpha-1 and alpha-2 domains {Rat (Rattus norvegicus)}
AEPRLPLMYHLAAVSDLSTGLPSFWATGWLGAQQYLTYNNLRQEADPCGAWIWENQVSWYWEKETDLKS
EQLFLEAIRTLENQINGTFTLQGLLGCELPDNSSLPTAVFALNGEEFMRFNPRTGNWSGEWPETDIVGNLWM
KQPEAARKESFLLTSCPERLLGHLERGRQNLEW
>d1cd1a2 d.19.1.1 (A:7-185) CD1, alpha-1 and alpha-2 domains {Mouse (Mus musculus)}
NYTFRCLQMSSFANRSWSRTDSVVWGLDLQTHRWSNDSATISFTKPWSQGKLSNQQWEKLQHMFQVYRVS
FTRDIQELVKMMSPKEDYPIEIQSAGCEMPGNASESFLHVAFQGKYVVRFWGTSWQTVPGAPSWLDLPIKV
LNADQGTSATVQMLLNDTCPLFVRGLLEAGKSDLEK
>d1hdma2 d.19.1.1 (A:13-93) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}
LQNHTFLHTVYCQDGSPSVGLSEAYDEDQLFFFDFSQNTRVPRLPEFADWAQEQQDAILFDKEFCEWMQIQIP
KLDGKIPV
>d1hdmb2 d.19.1.1 (B:3-87) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}
FVAHVESTCLDDAGTPKDFTYCISFNKDLLCWDPEENKMAPCNSLANVLSQHLNQKDTLMQRLNGLQNCA
THTQPFWGSLTNR
>d1aqdb2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR1}
RPRFLWQLKFECHFFNGTERVRLLCIYNQEESVRFDSDVGEYRAVTELGRPDAEYWNSQKDLLEQRRAAVD
TYCRHNYGVGESFTVQ
>d1bx2b2 d.19.1.1 (B:3-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}
TRPRFLWQPKRECHFFNGTERVRLDRYFYNQEESVRFDSDVGEFRAVTELGRPDAEYWNSQKDILEQARA
DTYCRHNYGVVESFTVQ

>d1fv1a2 d.19.1.1 (A:3-81) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}
EEHVIIQAEFYLNPDQSGEFMFDFDGDEIFHVDMAKKETVWRLEFGRFASFEAQGALANIAVDKANLEIMTKRSNYTP

>d1fv1b2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR2}
GDTRPRFLQQDKYEHFFNGTERVRFHLRDIYNQEEDLRFSDVGEYRAVTELGRPDAEYWNSQKDFLEDRRAVDVTYCRHNYGVGESFTVQ

>d1a6ab2 d.19.1.1 (B:5-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR3}
PRFLEYSTSECHFFNGTERVRYLDRYFHQNQEENVRFDSDVGEFRAVTELGRPDAEYWNSQKDLLEQKRGDRVNDYCRHNYGVVESFTVQ

>d1d5zb2 d.19.1.1 (B:1-92) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR4}
GDTRPRFLEQVKHECHFFNGTERVRFLDRYFYHQEEYVRFDSDVGEYRAVTELGRPDAEYWNSQKDLLEQKRAAVDVTYCRHNYGVGESFTVQ

>d1jk8a2 d.19.1.1 (A:2-84) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}
VADHVASYGVNLYQSYGPSGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRDPQFALTNIAVLKHNLNIVIKRSNSTAATN

>d1jk8b2 d.19.1.1 (B:3-94) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}
SPEDFVYQFKGMCYFTNGTERVRLVTRYIYNREEVYARFDSDVGVYRAVTPLGPPAAEWNSQKEVLERTRAELDTVCRVNYEKTETPTSLR

>d1iaka2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}
IEADHVGSGITVYQSPGDIGQYTTEFDGDELFYVDLKKETVWMLPEFAQLRRFEPQGGLQNIATGKHNLIELTKRSNSTP

>d1iakb2 d.19.1.1 (B:5-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AK}
GSFVHQFQPCYFTNGTQRIRLVIRYIYNREEVYVRFDSDVGEYRAVTELGRPDAEYWNKQYLERTRAELDTVCRHNYEKTETPTSLR

>d1fnga2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}
IKEEHTIIQAEFYLLPDKRGEFMFDFDGDEIFHV DIEKSETIWRLEEFAKFASFEAQGALANIAVDKANLDVMKERSNNTP

>d1fnbg2 d.19.1.1 (B:4-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}
RPWFLEYCKSECHFYNGTQRVRLVRYFYNNLEENLRFDSDVGEFRAVTELGRPDAENWNSQPEFLEQKRAEVDTVCRVNYEIFDNFLVP

>d1i3rb2 d.19.1.1 (B:1-120) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}
GKKVITAFNEGLKGGGGSLVGGGGGGSRPWLFLEYCKSECHFYNGTQRVRLVRYFYNNLEENLRFDSDVGEFRAVTELGRPDAENWNSQPEFLEQKRAEVDTVCRVNYEIFDNFLVP

>d2iadb2 d.19.1.1 (B:5-93) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AD}
RHFVVQFKGECYYTNGTQRIRLVTRYIYNREEVRYDSDVGEYRAVTELGRPDAEYWNSQPEILERTRAEVDTAC
RHNYEGPETSTSLR

>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)}
DIEADHVGFYGTTVYQSPGDIGQYTHEFDGDELFYVLDKKTVWRLPEFGQLILFEPQGGLQNIAAEKHNLGI
LTKRSNFTPA

>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)}
RHFVHQFKGECYFTNGTQRIRLVTRYIYNREEVYLRFDSDVGEYRAVTELGRHSAEYYNKQYLERTRAELDTACRH
NYEETEVPTSLR

>d1k8ia2 d.19.1.1 (A:11-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}
QNHTFRHTLFCQDGIPNIGLSETYDEDELFSFDSQNTRVPRLPDFAEWAQGQGDASAIAFDKSFCEMLMREV
SPKLEGQIP

>d1k8ib2 d.19.1.1 (B:1-94) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}
GFVAHVESTCVLNDAGTPQDFTYCVSFNKLACWDPDVGKIVPCFGVLSRLAEIISNILNEQESLIHRLQNGL
QDCATHQPFWDVLTHRTR

>d1i4fa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-A2.1}
GSHSMRYFFTSVRPGRGEPRFIAVGYVDDTQFVRFDSAASQRMEPRAPWIEQEGPEYWDGETRKVKAHS
QTHRVDLGTLRGYYNQSEAGSHTVQRMYGCDSWRFLRGYHQYAYDGKDYLALKEDLSWTAADMAAQ
TTKHKWEAAHVAEQLRAYLEGTCTVEWLRRYLENGKETLQR

>d1hsaa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B2705}
GSHSMRYFHTSVSRPGRGEPRFITVGYVDDTLFVRFDSAASPREEPRAPWIEQEGPEYWDRETQICKAKAQT
DREDLRTLLRYYNQSEAGSHTLQNMGYGCDVGPGDGRLLRGYHQDAYDGKDYLALKEDLSWTAADTAAQITQR
KWEAARVAEQLRAYLEGECTVEWLRRYLENGKETLQR

>d1hsba2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-AW68}
GSHSMRYFYTTSVRPGRGEPRFIAVGYVDDTQFVRFDSAASQRMEPRAPWIEQEGPEYWDRNTRNVKAQS
QTDRVDLGTLRGYYNQSEAGSHTIQMMYGCDSGRFLRGYRQDAYDGKDYLALKEDLSWTAADMAAQIT
TKHKWEAAHVAEQWRAYLEGTCTVEWLRRYLENGKETLQR

>d1agda2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B0801}
GSHSMRYFDTAMSRPGRGEPRFISVGYVDDTQFVRFDSAASPREEPRAPWIEQEGPEYWDRNTQIFKTNTQ
TDRESLRNLRGYYNQSEAGSHTLQSMYGCDSVGPDGRLLRGHNQYAYDGKDYLALKEDLSWTAADTAAQITQ
RKWEAARVAEQDRAYLEGTCTVEWLRRYLENGKDTLER

>d1a1na2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B*3501}
GSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSAASPRTEPRPPWIEQEGPEYWDRNTQIFKTNTQ
TYRESLRNLRGYYNQSEAGSHIIQRMYGCDLGPDRLLRGHDQSAYDGKDYLALKEDLSWTAADTAAQITQR

KWEAARVAEQLRAYLEGLCWEWLRRYLENGKETLQR
>d1e27a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-B*5101}
GSHSMRYFYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRTEPAPWIEQEGPEYWDRNTQIFKTNTQ
TYRENLRILRYYNQSEAGSHTWQTMYGCDVGPDGRLRGHNQYAYDGKDYLIALNEDLSSWTAADTAACQITQ
RKWEAAREAEQLRAYLEGLCWEWLRRYLENGKETLQR
>d1efxa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-CW3}
GSHSMRYFYTAVSRPGRGEPHFIAVGYVDDTQFVRFDSDAASPRGEPRAPWVEQEGPEYWDRETQKYKRQA
QTDRVSLRNLRGYYNQSEAGSHIQRMYGCDVGPDGRLRGYDQYAYDGKDYLIALNEDLRSWTAADTAACQITQ
RKWEAAREAEQLRAYLEGLCWEWLRRYLNGKETLQR
>d1qqda2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-CW4}
SHSMRYFSTSWSWPGRGEPRFIAVGYVDDTQFVRFDSDAASPRGEPRPWVEQEGPEYWDRETQKYKRQAQ
ADRVLRLKGYYNQSEDGSHTLQRMFGCDLGPDRRLRGYNQFAYDGKDYLIALNEDLRSWTAADTAACQITQ
RKWEAAREAEQRRAYLEGTCWEWLRRYLENGKETLQR
>d1mhea2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-E}
SHSLKYFHTSVSRPGRGEPRFISVGYVDDTQFVRFDNDAASPRMVPRAPWMEQEGSEYWDRETRSARDTAQI
FRVNLRTLRGYYNQSEAGSHTLQWMHGCELGPDRRLRGYEQFAYDGKDYLTLNEDLRSWTAADTAACQISEQK
SNDASEAEHQRAYLEDTCWEWLHKYLEKGKETLLH
>d1de4a2 d.19.1.1 (A:4-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), hemochromatosis protein Hfe}
RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPTRPWVSSRISSQMWLQLSQSLKGWDHM
FTVDFWTIMENHNHSKESHTLQVILGCEMQEDNSTEGYWKGYDGQDHLEFCPTLDWRAAEPRAWPTKLE
WERHKIRARQNRAYLERDCPAQLQQLELGRGVLD
>d1fzka2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2KB}
GPHSLRYFVTAVSRPGLGEPRYMEVGYVDDTEFVRFDSDAENPRYEPRARWMEQEGPEYWERETQKAKGNE
QSFRVDLRTLGGYYNQSKGGSHTIQVISGCEVGSMSGDGRLLRGYQQYAYDGCDYLIALNEDLKTWTAAADMALITKH
KWEQAGAAEYYRAYLEGTCWEWLRRYLNGNATLLR
>d1jpfa2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2DB}
PHSMRYFETAVSRPGLGEPRYISVGYVDNKEFVRFDSDAENPRYEPRAPWMEQEGPEYWERETQKAKGQE
WFRVSLRNLLGGYYNQSAGGSHTLQQMSGCDLGSDWRLRGYLQFAYEGRDYIALNEDLKTWTAAADMAAQIT
RRKWEQSGAAEHYKAYLEGECWEWLHRYLKNGNATLLR
>d1mhca2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2M3}
GSHSLRYFHTAVSRPGRGEPRYISVGYVDDVQFQRCDSIEEIPRMEPRAPWMEKERPEYWKELKLKVKNIAQS
ARANLRTLLRYYNQSEGGSHILQWMVSCEVGPDMRLLGAHYQAAYDGSDYITLNEDLSSWTAADMVSQITKS
RLESAGTAEYFRAYVEGECLELLHRFLRNGKEILQR
>d1ld9a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2LD}
GPHSMRYFETAVSRPGLGEPRYISVGYVDNKEFVRFDSDAENPRYEPRAPWMEQEGPEYWERITQIAKGQE

WFRVNLRTLLGYYNQSAGGTHTLQWMYCDVGSDGRLLRGYEQFAYGCDYIALNEDLKTWTAAADMAAQIT
RRKWEQAGAAEYYRAYLEGECVEWLHRYLKNGNATLLR
>d1qo3a2 d.19.1.1 (A:2-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), H-2DD}
SHSLRYFVTAVSRPGFGEPRYMEVGYVDNTEFVRFDSAENPRYEPRARWIEQEGPEYWERETRRAKGNEQSFR
RVDLRTALYYNQSAGGSHTLQWMAGCDVESDGRLRGYWQFAYGCDYIALNEDLKTWTAAADMAAQITRR
KWEQAGAAERDRAYLEGECVEWLRRYLKNGNATLLR
>d1k8da2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Mouse (Mus musculus), IB QA-2}
GQHSLQYFHTAVSRPGLGEPWIFSVGYVDDTQFVRFDSAENPRMEPRARWMEQEGPEYWERETQIAKGHE
QSFRGSLRTAQSYNNQSKGGSHTLQWMYCDMGSDGRLRGYLQFAYGRDYIALNEDLKTWTAVDMAAQITRR
TRRKWEQAGIAEKDQAYLEGTCMQLRRLYLELGKETLLR
>d1ed3a2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Rat (Rattus norvegicus), RT1-AA}
GSHSLRYFYTAWSRPGLGEPRFIAVGYVDDTEFVRFDSAENPRMEPRARWMEREGPEYWEQQTRIAKEWEQIY
YRVDLRTLRYYNQSEGGSHIQEMYCDVGSDGSLRGYRQDAYGRDYIALNEDLKTWTAAADFAAQITRN
KWERARYAERLRAYLEGTCVEWLSRYLELGKETLLR
>d1zaga2 d.19.1.1 (A:5-183) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}
DGRYSILTYIYTGLSKHVDPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGMEDWKQDSQLQKAREDFMET
LKDIVEYYNSNGSHVLQGRFGCEIENNRSAGFWKYYDGKDYIEFNKEIPAWVPFDAAQITKQKWAE
PVYVQRAKAYLEEECPATLRKYLKYSKNILD
>d1hyrc2 d.19.1.1 (C:0-180) MHC I homolog {Human (Homo sapiens), Mic-a}
MEPHSLRYNLTVLSWDGSVQSGFLTEVHLDGQPFLRCRQKCRAPQGQWAEDVGNKTWDRETRDLTGNG
GKDLRMTLAHKDQKEGLHSLQEIRVCIEHDNSTRSSQHFYYDGELFSQNLETKEWTMPQSSRAQTLAMNV
RNFLKEDAMTKTHYHAMHADCLQELRRYLKSGVVLR
>d1c16a2 d.19.1.1 (A:1-180) MHC I homolog {Mouse (Mus musculus), t22}
GSHSLRYFYTAWSRPGLGEPWIFIIGYVDDMQVLRFSSKEETPRMAPWLEQEEADNWEQQTRIVTIQGQLSER
NLMTLVHFYNKSMDDSHTLQWLQGCDVEPDRHLCLWYNQLAYDSEDLPTLNENPSSCTVGNSTVPHISQDLK
SHCS DLLQKYLEKGKERLL
>d1exua2 d.19.1.1 (A:4-176) Class I MHC-related Fc receptor {Human (Homo sapiens)}
HLSLLYHHTAVSSPAPGTPAFWVSGWLGPQQYLSYNSLRGEAEPGAWVWENQVSWYWEKETDLRIKEKLFE
EAKALGGKGPYTLQGLLGCELPDNTSVPATAKALNGEEFMNFDLKQGTWGGDWPEALAIQRWQQQDKA
ANKELTFLLFSCPMLREHLERGRGNLEW
>d1kgc_d.19.1.1 (C:) Class I MHC-related molecule Ulbp3 {Human (Homo sapiens)}
DAHSLWYNFTIIHLPRHGQQWCEVQSQVDQKNFLSYDCGSDKVLSMGHLEEQLYATDAWGKQLEMLREVGQ
RLRLEADTELEDFTPSGPLTLQVRMSCECEADGYIRGSWQFSFDGRKFLLFDSNNRKWTVVHAGARRMKE
WEKDSLTTFFKMVSMRDCKSWLRDFLMHRKKRLE
>d1jfma_d.19.1.1 (A:) NK cell ligand RAE-1 beta {Mouse (Mus musculus)}
DAHSLRCNLTIKDPTPADPLWYEAKCFGEILILHLSNINKMTSGDPGETANATEVKKCLTQPLKNLCQKLRNK
SNTKVDTHKTNGYPHLQVTMIYPQSQGRTPSATWEFNISDSYFFTFTENMSWRSANDEGVIMNKWKDDG
EFVKQLKFLIHECSQKMDEFLKQSKEK
>d2aak_d.20.1.1 (-) Ubiquitin conjugating enzyme {Arabidopsis thaliana}
MSTPKRKLMRDFKRLQQDPPAGISGAPQDNINMLWNAVIFGPDTPWDGGTFKLSLQFSEDYPNKPPTVRF
VSRMFHNPNIYADGSICLILQNQWSPIYDVAAILTSIQSLLCDPNPNSPANSEAARMYSESKEYNRRV
RDVVEQ

SWT

>d1fzya_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc1}

SRAKRIMKEIQAVKDDPAAHITLEFVSESDIHHLKGTFLGPPGTPYEGGFVVVDIEVPMEYPFKPPKMQFDTKVY
HPNISSVTGAICLDILKNAWSVPITLKSALISLQALLQSPEPNPQDAEVAQHYLRDRESFNKTAALWTRLYAS

>d1ayza_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc2 (RAD6)}

STPARRRLMRDFKRMKDAPPGVSASPLPDNVMVWNAMIIGPADTPYEDGTFRLLLEFDEEYPNKPPHVKFLS
EMFHPN^VYANGEICLDILQNWRWTPTYDVASILTSIQLSFNDPNPASPANVEAATLFKDHSQYVKRVETVEKS
WEDDM

>d1qcqa_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc4}

MSSSKRIAKELSDLERDPPTCSAGPVGDDLYHWQASIMGPADSPYAGGVFFLSIHFPTDYPFKPPKISFTTKIYH
PNINANGNICLDILKDQWSPALTSLKVLLSICSLTDANPDDPLVPEIAHIYKTDRPKYEATAREWTKKYAV

>d2ucz_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc7}

SKTAQKRLLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPPDTPYADGVFNAKLEFPKDYLPSPPKLTFTPSIL
HPNIYPNGEV CISILHSPGDDPNMYELAEERWSPVQSVEKILL SVMMSMLSEPNIESGANIDACILWRDNRPEFER
QVKLSILKSLGF

>d1jata_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), ubc13}

AASLPKRIIKETEKLVSDPVGITAEPHDDNLRYFQVTIEGPEQSPYEDGIFEELYLPDDYPMEAPKVRFLTKIYHP
NIDRLGRICLDVLKTNWSPALQIRTVLLSIQALLASPNPNPNDPLANDVAEDWIKNEQGAKAKAREWTKLYAKKKP

>d1j7db_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc13}

AGLPRII^KETQRLLAEPVPGIKAEPDES^NARYFHVVIAGPQDSFEGGT^KLEFLPEYPMAAPKVRFMTKIYH
PNVDKLGRICLDILKDKWSPALQIRTVLLSIQALLSAPNPDDPLANDVAEQWKTNEAQAIETARA^WTRLYAMN

>d1jatb_ d.20.1.1 (B:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae), mms2}

SKVPRNFRLLEELEKGEKGFGPESCSYGLADSDDITMTKWNGTILGPPHSNHENRIYSLSIDCPNYPDSPPKVT
FISKINLPCVNPTTGEVQTDFHTLRDWKRAYTMETLLDLRKEMATPANKKLRQPKEGETF

>d1j7da_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), mms2}

GVKVRNFRLLLEELEEGQKGVG^DGTVSWGLEDDEDMLTRWTGMIIGPPRTNYENRIYSLKVECGPKYEAPP
SVRFVTKINMNGINNSGMVDARSIPVLA^KWQNSYSIKVVLQELRRLMMSKENMKLPQPPEGQTYNN

>d1c4zd_ d.20.1.1 (D:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch7}

SRRLMKELEEIRKG^MKNFRNIQVDEANLLTWQGLIVPDNPPYDKGAFRIEINFPAEYPFKPPKITFKTKIYHPNI
DEKGQVCLP^VISAENWKPATKTDQVIQSLIALVNDPQPEHPLRADLAEEYSKDRKKFC^KNAEEFTKKY

>d1u9aa_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc9}

LNMSGIALSRLAQRKAWRKDHPFGFVAVPTKNPDGT^MLNWCAIPGKKTPWEGGLFKRMLFKDDY
PSSPPKCKFEPLFHPNVYPSGT^VCLSILEEDKDWRPAITIKQILLGIQELLNEPNIQDPAQAEAYTIYCQRVEYEK
RVRAQAKKFAPS

>d1i7ka_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch10}

PVGKRLQQELMTLMMGDKG^IAFPESDNLFK^WVTI^GAAGTVYEDLRYKLSLEFPG^YPYNAPT^VKFLTPCY
HPNVDTQGNISLDILKEKWSALYDVRTILLSIQLSLGE^PNIDSPLNTHAAELWKNPTAFKKYLQETYSKQVT

>d2e2c_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Clam (Spisula solidissima), E-2C}

MTTSKERHSVSKRLQQELRTLLMSGDPGITAFPDGDNLFKWVATLDGPKDTVYESLKVKLTLEFPSDYPYKPPVV
KFTTPCWHPNVDQSGNICLDILKENWTASYDVRTILLSQLSLLGEPNNASPLNAQAADMWSNQTEYKKVLHEK
YKTAQSDK

>d1bwza1 d.21.1.1 (A:1-130) Diaminopimelate epimerase {Haemophilus influenzae}
MQFSKMHGLNDVFVVDGVTQNVFFPETIRRLANRHCIGFDQLLIVEAPYDPELFHYRIFNADGSEVSQC
GNGARCFARFVTLKGLTNKKDISVSTQKGKGNMVLTVKDMNQIRVNMGEPWEPAKIPF

>d1bwza2 d.21.1.1 (A:131-274) Diaminopimelate epimerase {Haemophilus influenzae}
TANKFEKNYILRTDIQTVLCGAVSMGNPHCVVQVDDIQTANVEQLGPLLESHERFPERVNAGFMQIINKEHIKL
RVYERGAGETQACGSGACA AVAVGIMQGLNNNVQVDLPGGSLMIEWNGVGHPLYMTGEATHIYDGFI TL

>d1h6ra_ d.22.1.1 (A:) Green fluorescent protein, GFP {Jellyfish (Aequorea victoria)}
SKGEELFTGVVPILVELGDVNGHKFSVSGEGEGDATYGKLTGFIVTTGKLPVPWPTLVTFAYGLQCFARYPDH
MKRHDDFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHCVYI
VADKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLQYQSALSKDPNEKRDHMVLEFVT
AAGITH

>d2emd__ d.22.1.1 (-) Green fluorescent protein, GFP {Jellyfish (Aequorea victoria)}
ELFTGVVPILVELGDVNGHKFSVSGEGEGDATYGKLTGFIVTTGKLPVPWPTLVTLSYGVQCFSRYPDHMKR
HDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNNSHNVYIMA
DKQKNGIKVNFKIRHNIEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSALSKDPNEKRDHMVLEFVTAA
GIT

>d1ggxa_ d.22.1.1 (A:) Red fluorescent protein (fp583 or dsred(clontech)) {Coral (Discosoma sp.)}

VIKEFMRFKVRMEGTNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPLFAWDILSPQFYGSKVYVKHPADIP
DYKKLSFPEGFKWERVMNFEDGGVVTQDSSLQDGCFIYKVFIGVNFP SDGPVMQKKTMGWEASTERLYP
RDGVLKGEIHKALKLKDGGHYLVEFKSIYMAKKPVQLPGYYYYDSKLDITSHNEDYTIVEQYERTEGRHHFL

>d1gl4a1 d.22.1.2 (A:399-631) Domain G2 of nidogen-1 {Mouse (Mus musculus)}
GSPQRVNGKVKGRI FVGSSQPVVFENTDLHSYVVMNHGRSYTAISTIPETVGYSLLPLAPIGGIIGWMFAVEQ
DGFKNGFSITGGEFTRQAETFLGHPGKLVLKQQFSGIDEHGHLTISTELEG RVPQIPY GASVHIEPYTELYHYSSS
VITSSSTREYTVMEPDQDGAAPSHTIYQWRQQTITFQECAHDDARPALPSTQQLSVDSVFLYNKEERILRYALS
NSIGPVR

>d1c8za_ d.23.1.1 (A:) Transcriptional factor tubby, C-terminal domain {Mouse (Mus musculus)}
GSVDIEVQDLEEFALRPAPQGITIKCRITRDKKGM DRGMFPTYFLHLDREDGKKVFLLAGRKRKKS KTSNYLISVD
PTDLSRGGSYIGKLRSNLMGTKFTYDNGVNPQKASSSTLES GTRLQELAACVYETNVLGFKGPRKMSVIVPG
MNMVHERVCIRPRNEHETLLARWQNKNTESIIELQN KTPVWNDDTQS YVLFHGRVTQASVKNFQIIHGND
PDYIVMQFGRVAEDVFTMD NYPLCALQAF AIA LSSFDSKLACE

>d2pil__ d.24.1.1 (-) Pilin {Gc (Neisseria gonorrhoeae)}
FTLIELMIVIAVGILAVALPAYQDY TARA QVSEAILAEGQKSAVTEYYLNHGKPENNTSAGVASPPSDIKGY
VKEVEVKNGVVTATMLSSGVNNEIKGKKLSLWARRENGSVKWF CGQP VRTDDDTVADAKDGKEIDTKHLP
TCRDNFD AK

>d1hpwa_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa}
ALEGTEFARAQLSEAMT LASGLKT KVS DIFS QDGSCPANT AATAGIEKDTDINGKYVAKVTTGGTAAASGGCTIV
ATMKASDVATPLRGKTLT LGNADKG SYTWACTSNADNK YLPKTC QTATTTP

>d1dzoa_ d.24.1.1 (A:) Pilin {Pseudomonas aeruginosa, type IV pilin, pak pilin}
GTEFARSEGASALASVNPLKTTVEE ALSRGWSVKG SG TGTEDATKKEVPLGVAADAN KLG TIALK PDPADGTADIT
LTFTMGGAGPKNKGKIITRTAADGLWKCTS DQDEQFIPKGCSR

>d1p32a_d.25.1.1 (A:) Acidic mitochondrial matrix protein p32 {Human (Homo sapiens)}
MHTDGDKA FVDFLSDEIKEERKIQKHKTLPKMSGGWELELNGTEAKLVRKVAGEKITVTFNINNSIPPTFDGE
PSQGQKVEEQEPELTSTPNFVVEVIKNDDGKKALVLDC HYPEDEVGQEDEAESDIFSIREVSFQSTGESEWKDT
NYTLNTDSL DWALYDHLMDFLADRGVDNTFADELVELSTALEHQEYITFLEDLKS FVKSQ

>d1bkf_d.26.1.1 (-) FK-506 binding protein (FKBP12), an immunophilin {Human (Homo sapiens)}
GVQVETISPGDGRTFPKRGQTCVVHYTGMLEDGKKFDSSRDKNPKFKMLGKQE VIRGWE EGVAQMSVGQR
AKLTISPDYAYGATGVPGIIPP HATLVFD VELLKLE

>d1c9ha_d.26.1.1 (A:) Calcineurin (FKBP12.6) {Human (Homo sapiens)}
GVEIETISPGDGRTFPKKGQTCVVHYTGMLQNGKKFDSSRDRNPKFRIGKQE VIKGFE EGAAQMSLGQRAK
LTCTPDVAYGATGHPGVIPP NATLIFDV ELLNLE

>d1yat_d.26.1.1 (-) Calcineurin (FKBP12.6) {Baker's yeast (Saccharomyces cerevisiae)}
SEVIEGNVKIDRISPGDGATFPKTGDLVTIHYTGTLENGQKFDSSVDRGSPFQC NIVGQVIKGWDVGIPKLSVG
EKARLTIPGPYAYGPRGFPG LIPPNSTL VF DVELLKVN

>d1pbk_d.26.1.1 (-) FKBP25 {Human (Homo sapiens)}
PKYTKSVLKKGD KTNFPKKGDVVHCWYTGTLDGTVFDTNIQTSAKKKKNAKPLSF KVVGK VIRGWDE ALLT
MSKGEKARLEIEPEWAYGKKGQPDAKIPPNAKLTFEVELVDID

>d1rot_d.26.1.1 (-) FKBP59-I, N-terminal domain {Rabbit (Oryctolagus cuniculus)}
GVDISPKQDEGVLKVIKREGTGTETPMIGDRV FVHYTG WLLDGTKFDSSL DRKDKFSFDLGKGEV IKA WDI A
TMKV GELCRITCKPEYAYGSAGSPPKIPP NATL VF EVEL FEFKG

>d1pina2 d.26.1.1 (A:45-163) Mitotic rotamase PIN1, domain 2 {Human (Homo sapiens)}
GKNGQGEPARVRC SHLLVKHSQSRRPSSWRQEKITRTKEE ALELINGYIQKIKSGEEDFESLASQFSDCSSAKAR
GDLGAFSRGQM QKPFEDASF ALRTGEMSGPVFTDSGIHIIL RTE

>d1eq3a_d.26.1.1 (A:) Parvulin {Human (Homo sapiens), hpar14}
NAV KVRHILCEKHGKIMEAMEKLKSGMRFNEVA AQYSED KARQGGDLGWMTRGSMVGPFQEA AFALPVSG
MDKP VFTDPPVKT KFGYHIIMVEGRK

>d1fd9a_d.26.1.1 (A:) Macrophage infectivity potentiator protein (MIP) {Legionella pneumophila}
TDKDKL S YSIGADLGKNFKNQGIDVNPEAMAKGMQDAMSGAQLALTEQQMKDVLNKFQKDLMAKRTAE FN
KKADEN KVKGEAFLTENKNKPGVVLP SGLQYKVINS GNGVKPGKSDTV VEY TGR LI DGT VFDSTEKTGKPATF
QVSQVIPGW TEALQLMPAGSTWEIYVPSGLAYGPRSVGGPIGPNETLIFKIHLISVKKS

>d1grj_2_d.26.1.2 (80-158) GreA transcript cleavage factor, C-terminal domain {Escherichia coli}
MPNNGRVIFGATVTVLNLD SDEEQTYRIVGDDEADFKQNLISVNSPIARGLIGKEEDDVVIKTPGGEV EFEV IK
VEYL

>d3eipa_d.26.2.1 (A:) Colicin E3 immunity protein {Escherichia coli}
GLKLDLTWF D KSTEDFKGEEYSKDFGDDGSVMESLGVPFKDNVNN GCFD VIAEWVPLLQPYFNHQI DISDNEY
FVSFDYRDGDW

>d1edqa3 d.26.3.1 (A:444-516) Chitinase A {Serratia marcescens}
YGRGWTGVNGYQNNIPFTGTATGPVKGTWENGIVDYRQIAGQFMSG E WQTYDATAEAPYVFKPSTGDLITF
D

>d1goia3 d.26.3.1 (A:292-379) Chitinase B {Serratia marcescens}
YGRAFKGVSGGNGGQYSSHSTPGEDPYPSTDYWL VGCEECVRDKDPRI ASYRQLEQMLQGNYGYQRLWNDK
TKTPYLYHAQNGLFVTY

>d1d2ka2 d.26.3.1 (A:293-354) Chitinase 1 {Fungus (Coccidioides immitis)}

YGRAFASTDGIGTSNGVGGGSWENGVWDYKDMPQQGAQVTELEDIAASYSYDKNKRYLISY

>d1e9la2 d.26.3.1 (A:267-336) Chitinase-like lectin ym1 {Mouse (Mus musculus)}

YGHTFILSDPSKTGIGAPTISTGPPGKYTDESGLLAYEVCTFLNEGATEVWDAPQEVPYAYQGNEWVGY

>d1fjgp_d.27.1.1 (P:) Ribosomal protein S16 {Thermus thermophilus}

MVKIRLARFGSKHNPHYRIVVTDARRKRDGKYIEKIGYYDPRKTPDWLKVDVERARYWLSVGAQPTDTARRLL
RQAGVFRQE

>d1fjgs_d.28.1.1 (S:) Ribosomal protein S19 {Thermus thermophilus}

PRSLKKGVFVDDHILLEKYLENAKGEKRLIKTWSRRSTIVPEMVGHIAVYNGKQHVPVYITENMVGHKLGEFA
PTRTYRGHGK

>d1qkha_d.28.1.1 (A:) Ribosomal protein S19 {Thermus thermophilus}

GVFVDDHILLEKYLENAKGEKRLIKTWSRRSTIVPEMVGHIAVYNGKQHVPVYITENMVGHKLGEFAPRTY

>d1jj2w_d.29.1.1 (W:) Ribosomal protein L31e {Archaeon Haloarcula marismortui}

ERVVTIPLRDARAEPNHKRADKAMILIREHLAKHFSVDEDAVRLPSINEAAWARGRANTPSKIRVRAARFEEE
GEAIVEAE

>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 griseus)}

DKAKQCIGTMTIEIDFLQKKNIDSNPYDTDKMAAEFIQQFNNQAFSGQQLVFSNDKLFGLLVKDIAMDPSI
LKGEPASGKRQKIEVGLVVGNNSQVAFEKAENSSLNLIGKAKT

>d1cr5a2 d.31.1.1 (A:108-210) C-terminal domain of NSF-N, NSF-Nc {Baker's yeast (Saccharomyces cerevisiae), sec18p}

SGKQSYLGSIDIDISFRARGKAVSTVFDQDELAKQFVRCYESQIFSPTQYLIMEFQGHFFDLKIRNVQAIDLGDIEP
TSAVATGIETKGILTQQTQINFFKGR

>d1cz4a2 d.31.1.1 (A:92-185) C-terminal domain of VAT-N, VAT-Nc {Archaeon Thermoplasma acidophilum}

TEIAKKVTLAPIIRKDQRLKFEGEIEYVQRALIRRPMLEQDNISVPGTLAGQTGLFKVVKTLPSKVPVEIGEETK
IEIREEPASEVLEEGG

>d1e32a3 d.31.1.1 (A:107-200) Membrane fusion atpase p97 domain 2, P97-Nc {Mouse (Mus musculus)}

DVKYGRKRIHVLPIDDTEGITGNLFEVYLKPYFLEAYRPIRKGDIFLVRGGMRAVEFKVVEVDPSPYCIVAPDTVIH
CEGEPIKREDEEESLNE

>d1qipa_d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Human (Homo sapiens)}

GGLTDEAALSCCSDADPSTKDFLLQQTMLRVKDPKSLDFYTRVLGMTLIQKCDFPIMKFSLYFLAYEDKNDIPKE
KDEKIAWLSRKATLELTHNWGTEDDETQSYYHNGNSDPRGFHIGIAVPDVYSACKRFEELGVKFVKKPDDKG
MKGLAFIQDPDGYWIEILNPNKMATLM

>d1f9za_d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Escherichia coli}

MRLLHTMLRVGDLQRSIDFYTKVLMKLLRTSENPEYKSLAFVGYPETEEAVIELTYNWGVDKYELGTAYGHI
ALSVDNAAEACEKIRQNNGGNVTREAGPVKGTTVIAFVEDPDGYKIELIEEKDAGRGLGN

>d1qtoa_d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptomyces verticillus}

MVKFLGAVPVLTAVDVPANVSFWVDTLGFEKDFGDRDFAGVRRGDIRLHSRTEHQIVADNTSAWIEVTDPDA
LHEEWARAVSTDYADTSGPAMTPVGESPAGREFAVRDPAGNCVHFTAGE

>d1byla_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptoalloteichus hindustanus}
FMAKLTSAVPVLTARDVAGAVEFWTDRLGFSRDFVEDDFAGVVRDDVTLFISAVQDQVVPDNTLAWVVVRGL
DELYAEWSEVVSTNFRDASGPAMTEIGEQPWGREFALEPAGNCVHFVAE

>d1ecsa_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Klebsiella pneumoniae}
TDQATPNLPSRDFDSTAAYERLGIVFRDAGWMILQRGDLMLEFFAHPGLDPLASWFSCCLRLDDLAEFYR
QCKSVGIQETSSGYPRIHAPELQGWGGTMAALVDPDGTLRLIQNEL

>d1jc4a_ d.32.1.4 (A:) Methylmalonyl-CoA epimerase
{Propionibacterium shermanii}
NEDLFICIDHVAYACPDADAEASKYYQETFGWHELHREENPEQGVVEIMMAPAAKLTEHMTQVQVMAPLNDES
TVAKWLAKHNGRAGLHHMAWRVDDIDAVSATLRERGVQLLYDEPKLGTGGNRINFMPKGKVLIETQYP
K

>d1gdga1 d.32.1.3 (A:1-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Pseudomonas sp.}
SIERLGYLGFAVKDVPWDHFLTKSGLMAAGSAGDAALYRADQRAWRIAVQPGEELDDLAYAGLEVDDAAALE
RMADKLQRQAGVAFTRGDEALMQQRKVMGLLCLQDPFGLPLEIYYGPAEIFHEPFLPSAP

>d1gdga2 d.32.1.3 (A:133-288) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Pseudomonas sp.}
VSGFVTGDQGIGHFVRCVPDTAKAMAFYTEVLGFVLSIDIQMGPETSVAHFLHCNGRHHTIALAAFPKRI
HHFMLQANTIDDVGYAFDRIDAAGRITSLLGRHTNDQTLSFYADTPSPMIEVEFGWGPRTVDSSWTVARHSRT
AMWGHKSV

>d1han_1 d.32.1.3 (2-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Burkholderia cepacia (formerly Pseudomonas cepacia)}
SIRSLGYMGFAVSDAAWRSFLTQKLGLMEAGTTDNGDLFRIDSRAWRIAVQQGEVDDLAFAFYEVADAAGL
AQMDKLKQAGIAVTTGDASLARRRGVTGLITFADPFGGLEIYYGASEVFEKPFLPGA

>d1han_2 d.32.1.3 (133-289) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Burkholderia cepacia (formerly Pseudomonas cepacia)}
AVSGFLTGEQGLGHFVRCVPDSDKALAFYTDVLGFQLSDVIDMKMGPDTVVPAYFLHCNERHHTLAAFPPLPK
RIHHFMLEVASLDDVGFAFDRVADGLITSTLGRHTNDHMVSFYASTPSGVEVEYGWSARTVDRSWVVVRHD
SPSMWGHKSVR

>d1mpya1 d.32.1.3 (A:1-145) Catechol 2,3-dioxygenase
(metapyrocatechase) {Pseudomonas putida, mt2}
MNKGVMRPGHVQLRVLDMSKALEHYVELLGLIEMDRDDQGRVYLKAWTEVDKFSLVLREADEPGMDFMGF
KVVDEDALRQLERDLMAYGCAVEQLPAGELNSCGRRVRFQAPSGHHFELYADKEYTGKWGLNDVNPEAWPR
DLKG

>d1mpya2 d.32.1.3 (A:146-307) Catechol 2,3-dioxygenase
(metapyrocatechase) {Pseudomonas putida, mt2}
MAAVRFDHALMYGDELPATYDLFTKVLGFYLAEQVLDENGTRVAQFLSLSTKAHDVAFIHPEKGRHHVFSHL
ETWEDLLRAADLISMTDTSIDIGPTRHGLTHGKTIYFFDPSGNRNEVFCGGDYNYPDHKPVTWTTDQLGKAIFY
HDRILNERFMTVLT

>d1cjxa1 d.32.1.3 (A:4-153) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas fluorescens}
YENPMGLMGFEFIEFASPTPGTLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILNNEPNSIASYFAAEHGPSVCG
MAFRVKDSQKAYNRAELGAQPIHIDTGPMEMLNPAIKGIGGAPLYLIDRFGEGSSIYDIDFVYLEGVERNPVG

>d1cjxa2 d.32.1.3 (A:154-356) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas fluorescens}
AGLKVIDHLTHNVYRGRMVYWANFYEKLNFREARYFDIKGEYTGLTSKAMSAPDGMIRIPLNEESSKGAGQIE
EFLMQFNQEIQHVAFLTDLVKTWDALKIGMRFMTAPPDTYYEMLEGRLPDHGEPVVDQLQARGILDGSS
VEGDKRLLLQIFSETLMGPVFFEFIQRKGDDGFEGNFKALFESIERDQVRGVLAT

>d1fx3a_ d.33.1.1 (A:) Bacterial protein-export protein SecB {Haemophilus influenzae}
QPVLQIQRIVVKDVSFEAPNLPHIFQQEWPKLGFDLSTETTQVGDDLYEVVLNISVETTLESDGVAFICEVKQ
AGVFTISGLEDVQMAHCLTSQCPNMLFPYARELVSNLVNRGTFPALNLSPVNFDALFVEYMRQQAEN

>d1bm8_ d.34.1.1 (-) DNA-binding domain of Mlu1-box binding protein MBP1 {Baker's yeast (Saccharomyces cerevisiae)}

QIYSARYSGVDVYEFIHSTGSIMRKKDDWVNATHILKAANFAKAKRTRILEKEVLKETHEKVQGGFGKYQGTW
VPLNIAKQLAEKFSVYDQLKPLFDF

>d1dk0a_ d.35.1.1 (A:) Heme-binding protein A (HasA) {Serratia marcescens}
AFSVNYDSSFGGYSIHDYLGQWASTFGDVNHTNGNVTDANSGGFYGGSLGSQYAISSSTANQVTAFVAGGNLT
YTLFNEPAHTLYGQLDSLFSFGDGLSGGDTSPYIQLVDPVSFGGLNLSSLQAQGHGTVHVHQVYGLMSGDTGAL
ETALNGILDDYGLSVNSTFDQVAAATA

>d1eyqa_ d.36.1.1 (A:) Chalcone isomerase {Alfalfa (Medicago sativa)}

SITAITVENLEYPAVVTSPVTGKSYFLGGAGERGLTIEGNFIKFTAIGVYLEDIAVASLAAKWKGSSEELLETLDFYR
DIISGPFEKLRGSKIRELSGPEYSRKVMENCVAHLKSVGTYGDAEAEAMQKFAEAFKPVNFPPGASVFYRQSPD
GILGLSFSPDTSIPEKEAALIENKAVSSAVLETMIGEHAVSPDLKRCLAARLPALLNE

>d1b3ob2 d.37.1.1 (B:112-159) Type II inosine monophosphate dehydrogenase {Human (Homo sapiens)}

QGFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRIVGIIS

>d1jr1a2 d.37.1.1 (A:113-155) Type II inosine monophosphate dehydrogenase {Chinese hamster (Cricetus griseus)}

GFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRIV

>d1jr1a3 d.37.1.1 (A:178-232) Type II inosine monophosphate dehydrogenase {Chinese hamster (Cricetus griseus)}

IMTKREDLVVAPAGITLKEANEILQRSKKGKLPIVNENDELVAIARTDLKKNRD

>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}

MTSEHLVTAAVGTDLETAERILHEHRIEKPLVDNSGRSLGLITIKDIEKVIEFPAAKDEF

>d1bvqa_ d.38.1.1 (A:) 4-hydroxybenzoyl-CoA thioesterase {Pseudomonas sp., CBS-3}

ARSITMQQRIEFGDCDPAGIVWYPNYHRWLDAASRNYFIKCGLPPWRQTVVERGIVGTPIVSCNASFVCTASY
DDVLTIELTCIKEWRRKSFVQRHSVSRTTPGGDVQLVMADEIRVFAMNDGERLRAIEVPADYIELC

>d1mkaa_ d.38.1.2 (A:) beta-Hydroxydecanol thiol ester dehydrase {Escherichia coli}

VDKRESYTKEDLLASGRGELFGAKGPQLPAPNMLMMDRVVKMTETGGNFDKGYVEAELDINPDLWFFGCHFI
GDPVMPGCLGLDAMWQLVGFYLGWLGGEGKGRALGVGEVKFTGQVLPTAKVTYRIHFKRIVNRRЛИMGLA
DGEVLVDGRLIYTASDLKVGLFQDTSAF

>d1c8ua1 d.38.1.3 (A:2-115) Thioesterase II (TesB) {Escherichia coli}

SQALKNLLTLLNLEKIEGLFRGQSEDLGLRQVF GGQVGQALYAAKETVPEERLVHSFHSYFLRPGDSKKPIYD
VETLRDGNSFSARRVAAIQNGKPIFYMTASFQAPEAGF
>d1c8ua2 d.38.1.3 (A:116-286) Thioesterase II (TesB) {Escherichia coli}
EHQKTMPSAPAPDGLPSETQIAQSLAHLLPPVLKDKFICDRPLEVRPVEFHNPPLKGHVAEPHRQVVIRANGSVP
DDL RVHQYLLGYASDLNLPVALQPHGIGFLEPGIQIATIDHSMWFHRPFNLNEWLLYSVESTSASSARGFVRGE
FY TQDGVLVASTVQE GVMRNHN
>d1cmia_d.39.1.1 (A:) Dynein light chain 8 (DLC8) {Human (Homo sapiens)}
KAVIKNADMSEEMQQDSVEC ATQALEKYNIEKDIAAHIKKEFDKKYNPTWHCIVGRNFGSYVTHETKHFIYFYL
GQVAILLFKSG
>d1csei_d.40.1.1 (I:) Eglin C {Leech (Hirudo medicinalis)}
KSFPEVVGKTV DQAREYFTLHYPQYFLPEGSPVTLDLRYNRVRFYNPGTNVVNHVPHVG
>d1egl_d.40.1.1 (-) Eglin C {Leech (Hirudo medicinalis)}
TEFGSELKSFP EVVGKTV DQAREYFTLHYPQYD VYFLPEGSPVTLDLRYNRVRFYNPGTNVVNHVPHVG
>d1ypci_d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}
MKTEWPELVGKS VAAAKVILQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAQVPRVG
>d2snii_d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}
LKTEWPELVGKS VEEAKVILQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAEVPRVG
>g1cq4.1 d.40.1.1 (A;B;) Chymotrypsin inhibitor CI-2 {Barley (Hordeum vulgare)}
KTEWPELVGKS VEEAKVILQDKPEAQIIVLPVGTIVX YRIDRVRLFVDKLDNIAQVPRVG
>d1tin_d.40.1.1 (-) Trypsin inhibitor V {Pumpkin (Cucurbita maxima)}
SSCPGKSSWPHL VGGSVAKAI ERQNP NVKAVILEEGTPVT KDFRCNRVRIWVN KRG LVSP PRIG
>d1dwma_d.40.1.1 (A:) Trypsin inhibitor LUTI {Flax (Linum usitatissimum)}
SRRC PGKNAWPELVGKSGN MAAATVERENRN VHAI VLKE GSAM T KDFRC DRV W VIVNDHG VVT SVPHIT
>d1jv2b3 d.200.1.1 (B:606-690) Integrin beta tail domain {Human (Homo sapiens)}
DACTFKKECVECKKF DREP YMTENTCN RYCRDEIESV KELDTGKD AVNCTYKN EDDCV VR FQYYEDSSG KSI LY
VVEEPEC PKG
>d1hlra3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio gigas}
DYGADL GLKMPAG TLHL AMVQAKVSHANIKGIDTSE ALT MPGVHSV ITHKDVKG KNR ITGLIT FPTNKG DGWD
RP IL CDEKV FQYGD CIALVCAD SEANAR AAAEKV KV DLE LPAY
>d1dgja3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {Desulfovibrio desulfuricans}
EFGADAALR MPENTLHL ALAQAKVSHALIKGIDTSEA EKMPGVYKV LHKDVKG KNR ITGLIT FPTNKG DGWER
PILND SKIF QYGD ALA IVCAD SEANAR AAAEKV KFD LELL PEY
>d1fiqc1 d.41.1.1 (C:571-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}
DTV GRPL PHLAAAMQ ASGEAVY CDDIPRYEN ELFL RLVT STRAHAKI KSIDV SEA QK VPGF CFS ADDI PGSNE
TGLF NDET VFAK DT C VGHII GAVVAD TPEHAERA AHVV KV TYEDLPA
>d1fo4a3 d.41.1.1 (A:537-694) Xanthine oxidase, domain 5 (?) {Cow (Bos taurus)}
KLD PTY TSAT LLFQ KHP PANIQLF QEV P NGS KEDT VGRPL PHLAAAMQ ASGEAVY CDDIPRYEN ELFL RLVT ST
RAHAKI KSIDV SEA QK VPGF CFS ADDI PGSNET GLF NDET VFAK DT C VGHII GAVVAD TPEHAERA AHVV K
V TYEDLPA
>d1jrob1 d.41.1.1 (B:2-123) Xanthine dehydrogenase chain B, N-terminal domain
{Rhodobacter capsulatus}
SVGKPLHDSARA HVTGQARYL DDLP C PANTLHL AFG LSTEASA AITGLD LE PVRESPG VIAVFTA ADLPHDN DA
SPAPSPEPV LATGEVHFVGQPIFLVAATSHRAARIAARKARITYAPR
>d1qj2b1 d.41.1.1 (B:10-146) Carbon monoxide (CO) dehydrogenase molybdo protein, N-domain

{Pseudomonas carboxydovorans}

TSAERAEKLQGMGCKRKRVEDIRFTQGKGNVDDVKLPGMLFGDFVRSSAHARIKSIDTSKAKALPGVFAVL
AADLKPLNLHYMPTLAGDVQAVLADEKVLFQNQEVAFFVAKDRYVAADAIELVEVDYEPLPVL

>d1ffvb1 d.41.1.1 (B:7-146) Carbon monoxide (CO) dehydrogenase molybdoprotein, N-domain {Hydrogenophaga pseudoflava}

DAEARELALAGMGASRLRKEDARFIQGKGNVDDIKMPGMLHMDIVRAPIAHGRIKKIHKDAALAMPGVHA
VLTAEDLKLHWMPTLAGDVAAVLADEKVHFQMIEVAIVIADDYIAADAVEAVKVEYDELPVVIDP

>d1qapa2 d.41.2.1 (A:8-129) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Salmonella typhimurium}

DDRRDALLERINLDIPAAVAQALREDLGGEVDAGNDITAQLLPADTQAHATVITREDGVFCGKRWVEEVFIQLA
GDDVRLTWVDDGDAIHANQTVFELQGPARNLLGERTALNFVQTLSG

>d1qpoa2 d.41.2.1 (A:2-116) Quinolinic acid phosphoribosyltransferase, N-terminal domain {Mycobacterium tuberculosis}

GLSDWELAAARAIIARGLDDELRYGPDVTTLATVPASATTASLVTRAGVVAGLDVALTLNEVLGTNGYRVLD
RVEDGARVPPGEALMTLEAQTRGLLTAERTMLNLVGHLSG

>d2tpt_3 d.41.3.1 (336-440) Thymidine phosphorylase {Escherichia coli}

TAMLTKAVYADTEGFVSEMDTRALGMAVVAMGGRRQASDTIDYSVGFTDMARLGDQVDGQRPLAVIHAK
DENNWQEAAKAVKAAIKLADKAPESTPTVYRRISE

>d1brwa3 d.41.3.1 (A:331-433) Pyrimidine nucleoside phosphorylase {Bacillus stearothermophilus}
KAAYTSTVTAAADGYVAEMAADDIGTAAMWLGAGRRAKKEDVIDLAVGIVLHKKIGDRVQKGEALATIHSNRPD
VLDVKEKIEAAIRLSPQPVARPPLIYETIV

>d1ffkf_d.41.4.1 (F:) Ribosomal protein L10e {Archaeon Haloarcula marismortui}

KPGAHFRNSIKPAYTRREYISGIPGKGIAQFKMGNNNGAGPTYPAPAQVENVVEKPVQIRHNALEAARNAANRFVQ
NSGAAANYKFRIRKFPHVIREQDGDMRAPFGKSGTAARSHGANHDFIAWVNPDPAVEFAWRAYMKVT
PTVNIDSSPAGNA

>d1jj2h_d.41.4.1 (H:) Ribosomal protein L10e {Archaeon Haloarcula marismortui}

KPGAMYRNSSKPAYTRREYISGIPGKKIAQFDGMNNNGAGPTYPAPAQVELVVEKPVQIRHNALEAARVAANRYVQ
NSGAAANYKFRIRKFPHVIRENKAADGMRAPFGKPGVTAARVHGANCHIFIAWVNPDPAVEFAWRAYMKVT
AWRRAKMKVTPTINIDSSPAGNA

>d1fm0e_d.41.5.1 (E:) Molybdopterin synthase subunit MoaE {Escherichia coli}

AETKIVVGPQPSVGEYPWLAERDEDGAVVTFTGKVRNHNLDGSVNALTLEHYPGMTEKALAEIVDEARNR
WPLGRVTVIHRIGELWPGDEIVFGVTSahrssafeagqfimdylktrapfwkreatpegdrwvaresdqq
AAKRW

>d1buoa_d.42.1.1 (A:) Promyelocytic leukemia zinc finger (PLZF) protein BTB domain {Human (Homo sapiens)}

MGMQLQNPSHTGLLCKANQMRLAGTLCDVVIMVDSQEFHAHRTVLACTSKMFEILFHRNSQHYTLDFLSP
KTFQQILEYAYTATLQAKAEDLDDLLYAAEILEIEYLEEQCLKMLETIQ

>d1vcbb_d.42.1.1 (B:) Elongin C {Human (Homo sapiens)}

MYVKLISSDGHEFIVKREHALTSGTIKAMILSGPGQFAENETNEVNFRIPSHVLSKVCMYFTYKVRYTNSTEIP
FPIAPEIALELLMAANFLDC

>d1hv2a_d.42.1.1 (A:) Elongin C {Baker's yeast (Saccharomyces cerevisiae)}

MSQDFVTLVSKDDKEYEISRSAAMISPTLKAMIEGPFRSKGRIELKQFD SHILEKAVEYLNYNLKYSGVSEDDDEI
PEFEIPTEMSLELLAADYLSI

>d1a68_d.42.1.2 (-) Shaker potassium channel {California sea hare (Aplysia californica)}

ERVVINVSGLRFETQLKTLNQFPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGRLRRPVNVPLD
VFSEEIKFYELG
>d1t1da_d.42.1.2 (A:) Shaker potassium channel {California sea hare (Aplysia californica)}
ERVVINVSGLRFETQLKTLNQFPDTLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQSGGRLRRPVNVPLD
VFSEEIKFYELGENAFERYREDEGF
>d3kvt_d.42.1.2 (-) akv3.1 voltage-gated potassium channel {California sea hare (Aplysia californica)}
ENRVIIINVGGIRHETYKATLKKIPATRLSRTEGMLNYDPVLNEYFFDRHPGVFAQIINYYRSGKLHYPTDVCGPLF
EEELEFWGLDSNQVEPCCWMTYTAHR
>d1exbe_d.42.1.2 (E:) KV1.1 {Rat (Rattus norvegicus)}
CERVVINISGLRFETQLKTLAQFPNTLLGNPKKRMRYFDPLRNEYFFDRNRPSFDAILYQQQSGGRLRRPVNVPL
DMFSEEIKFYELGEEA
>d1dsxa_d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}
ERVVINISGLRFEVQLKTLAQFPETLLGDPKKRMRYFDPLRNEYFFDRNRPSFDAILYQQQSGGRLRRPVNVPLDI
FSEEIRFYELGEEAMEMFREDEG
>d1qdva_d.42.1.2 (A:) Kv1.2 {Rat (Rattus norvegicus)}
ERVVINISGLRFETQLKTLAQFPETLLGDPKKRMRYFDPLRNEYFFDRNRPSFDAILYQQQSGGRLRRPVNVPLDI
FSEEIRFYELGEEAMEMFREDEG
>d1fs1b2 d.42.1.2 (B:2-68) Cyclin A/CDK2-associated p45, Skp1 {Human (Homo sapiens)}
PSIKLQSSDGEIIFEVDVIEAKQSVTIKTMLEDLGMDPVLPLNVAAILKKVIQWCTHHKDD
>d1efub2 d.43.1.1 (B:140-282) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}
DVLGSYQHGARIGVLVAAGADEELVKHIAMHVAASKPEFIKPEDVSAEVVEKEYQVQLDIAMQSGKPKEIAEK
MVEGRMKKFTGEVSLTGQPFVMEPSKTVGQLLKEHNAEVGTGIRFEVGEGIEKVETDFAAEVAAMSKQS
>d1efub4 d.43.1.1 (B:55-139) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}
VAADGVIKTIDGNYGIILEVNCQTDVAKDAGFQAFADKVLDAAVAGKITDVEVLKAQFEEERVALVAKIGENI
NIRVVAALEG
>d1tfe_d.43.1.1 (-) Elongation factor Ts (EF-Ts), dimerisation domain {Thermus thermophilus}
AREGIIGHYIHHNQRGVGLVELNCETDFVARNELFQNLAKDLAMHIAMMNPRYVSAEEIPAAELEKERQIYIQA
ALNEGKPQQIAEKIAEGRKKYLEEVVLLEQPFVKDDKVKVKELIQQAIKIGENIVVRRFCRFELGA
>d1i0ha2 d.44.1.1 (A:91-205) Mn superoxide dismutase (MnSOD) {Escherichia coli}
GTTLQGDLKAAIERDFGSVDNFKAEEFKAAASRGSGWAWLVLKGDKLAVVSTANQDSPLMGEAISGASFPI
MGLDVWEHAYFLKFQNRRPDYIKEFWNVNVWDDEAAARFAAKK
>d1mnga2 d.44.1.1 (A:93-203) Mn superoxide dismutase (MnSOD) {Thermus thermophilus}
GGAKEPVGELKKAIDEQFGGFQALKELTQAAMGRFGSGWAWLVKDPFGKLHLVSTPNQDNPMEGFTP
GIDVWEHAYYLKYQNRRADYLQAIWNVLNWDAEAEFFKKA
>d1ap6a2 d.44.1.1 (A:84-198) Mn superoxide dismutase (MnSOD) {Human (Homo sapiens)}
NGGGEPKGELLEAIKRDFGSFDKFKEKLTAASVGVQGSGWGWLFNKERGHLQIAACPNQDPLQGTTGLIPLL
GIDVWEHAYYLQYKNVRPDYLKAIWNVINWENVTERYMACKK
>d1kkca2 d.44.1.1 (A:98-213) Mn superoxide dismutase (MnSOD) {Aspergillus fumigatus}
EKSGGGKIDQAPVLKAAIEQRWGSFDKFKAFTNTLLGIQGSGWGWLVTDGPKGKLDITTHDQDPVTGAAP
VFGVDMWEHAYYLQYLNDKASYAKGIWNVINWAEAENRYIAGDK

>d1dt0a2 d.44.1.1 (A:84-197) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}
AGGQPTGALADAINAAFGSFDFKKEEFTKTSVGTGSGWGWL/KKADGLALASTIGAGCPLTIGDTPLLCDV
WEHAYYIDYRNLRPKYVEAFWNLNVNWFVAEQFEGKTYKV

>d3sdpa2 d.44.1.1 (A:84-190) Fe superoxide dismutase (FeSOD) {Pseudomonas ovalis}
DAGGQPTGALADAINAAFGSFDFKKEEFTKTSVGTGSGWA/WLVKADGLALCSTIGAGAPLTS/CDV
WEHAYYIDYRNLRPKYVEAFWNLNVNWFVAEEG

>d1isaa2 d.44.1.1 (A:83-192) Fe superoxide dismutase (FeSOD) {Escherichia coli}
NAGGEPTGKVAE/AIASFGSFADFKAQFTDAAIKNFGSGWTWL/KNSDGKLAIVSTS/NAGTPLTTDATPLLTVD
VWEHAYYIDYRNARPGYLEHF/WALVNWEFVAKNLAA

>d1idsa2 d.44.1.1 (A:86-199) Fe superoxide dismutase (FeSOD) {Mycobacterium tuberculosis}
NGGDKPTGELAAAIA/DAFGSFDFK/FRAQFHAAATT/QGSGWAALGWDTLNKLLIFQVYDHQTNFPLGIVPLL
LDMWEHAFYLQYK/NVKVDFAKAFWNVN/WADVQSR/YAAATS

>d1coja2 d.44.1.1 (A:91-212) Fe superoxide dismutase (FeSOD) {Aquifex pyrophilus}
GGKGEPESEALKKKIEEDIGGLACTNELKAAAMA/FRG/WAILGLDIFS/GRLVNGLDAHN/VNL/TGLIPLIVIDTYE
HAYYVDYKNKRPPY/DAFFKNINWDVVNERFEKAMKAYEALKDFIK

>d1sssa2 d.44.1.1 (A:93-208) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus solfataricus}
PSGKG/GKPGGALADLINKQYGSFDRFKQVF/TETANSLPGTG/WAVLYYDTESGNLQIMTFENHFQNHIAEIP/ILI
LDEF/EHAYYLQYK/NKR/DYVNAWWNVN/WDAEKKLQ/KYL

>d1b06a2 d.44.1.1 (A:93-210) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus acidocaldarius}
PAGKG/GKPGGALADLIDKQYGSFDRFKQVFSESANS/LPGSGWT/VLYYDNE/SGNLQIMTFENHF/MNHIAEIPV
ILIVDEFEHAYYLQYK/NKR/DYVNAWWNVN/WDAEKKRLQ/KYL/NK

>d1bsma2 d.44.1.1 (A:87-201) Cambialistic superoxide dismutase {Propionibacterium shermanii}
SAPERPTDELGAAIDEFFGSFDNMKAQFTAATGIQGSGWASLVW/DPLGKRINTLQFYDHQNNLPAGSIPLLQL
DMWEHAFYLQYK/NVKG/DYVKS/WNVN/WDDVALRFSEARVA

>d1qnna2 d.44.1.1 (A:85-191) Cambialistic superoxide dismutase {Porphyromonas gingivalis}
KGGA/PKGKLGEAIDKQFGSFEKFKEEFNTAGTTLFGSGWVWL/ASDANGKLSIEKEPNAGNPVRKG/LNPLLGF
VWEHAYYLTYQNRRADHLKDLWSIVDW/DIVESRY

>d1ctf_ d.45.1.1 (-) Ribosomal protein L7/12, C-terminal domain {Escherichia coli}
EFDVILKAAGANKVAVIKAVRGATGLGLKEAKDLVESAPAALKEGVSKDDAEALKKALEEAGAEVEVK

>d1dd3a2 d.45.1.1 (A:58-128) Ribosomal protein L7/12, C-terminal domain {Thermotoga maritima}
EFDVVLKSFQNKIQV/KVREITGLGLKEAKDLVEKAGSPDAVIKSGVSKEEAEIKKKLEEAGAEVELK

>d1ekta_ d.46.1.1 (A:) Transcription-state regulator AbrB, the N-terminal DNA recognition domain {Bacillus subtilis}
MKSTGIVRKVDELGRVVIPIELRRTLGIAEKDALEIYV/DDEKIILKKYKPNMT

>d1mmsa2 d.47.1.1 (A:8-70) Ribosomal protein L11, N-terminal domain {Thermotoga maritima}
QIKLQLPAGKATPAPPVGPA/LGQHG/VNIMEFCKRFNAETADKAGMILPVVITVYEDKSFTII

>d2reb_2 d.48.1.1 (269-328) RecA protein, C-terminal domain {Escherichia coli}
NFYGEVL/DLG/VKEK/LIEKAGAWYSYKGEKIGQGKANATAWLKDNPETAKEIEKKVRELL

>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)}

PQYQTWEFSRAAEKLYLADPMKARVVLKYRHSDGNLCVKVTDDLCLVCLVYKTDQAQDVKKIEKFHSQLMRLMVA

>d1e8ob_d.49.1.1 (B:) Signal recognition particle alu RNA binding heterodimer, SRP9/14 {Human (Homo sapiens)}

VLLESEQFLTELTRLFQKCRTSGSVYITLKKYDGRTPIPKKGTVEGFEPADNKCLLRATDGKKKISTVVSKEVNFKQMAYSNLLRANMDGLK

>d1914_d.49.1.1 (-) Signal recognition particle alu RNA binding heterodimer, SRP9/14 {Mouse (Mus musculus)}

MVLLESEQFLTELTRLFQKCRTSGSVFILKKYDGRTPIPKKSSVEGLEPAENKCLLRATDGKRKISTVVSKEVNFKQMAYSNLLRANMDGLKKRDKKNKSKKPAQGGEQKLISEEDDSAGSPMPQFQTWEFSRAAEKLYLADPMKVRVLKYRHDGNLCIKVTDDLCLVCLVYRTDQAQDVKKIEKFHSQLMRLMVAESRNV

>d1di2a_d.50.1.1 (A:) Double-stranded RNA-binding protein A, second dsRBD {Xenopus laevis}

MPVGSLQELAVQKGWRLPEYTVAQESGPPHKREFTITCRVETFVETGSGTSKQVAKRVAAEKLTKFKT

>d1ekza_d.50.1.1 (A:) Staufen, domain III {Fruit fly (Drosophila melanogaster)}

MDEGDKKSPISQVHEIGIKRNMTVHFVVLREEGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAEKMLVELQKL

>d1stu_d.50.1.1 (-) Staufen, domain III {Fruit fly (Drosophila melanogaster)}

PISQVHEIGIKRNMTVHFVVLREEGPAHMKNFITACIVGSIVTEGEGNGKKVSKKRAAEKMLVELQKL

>d1qu6a1 d.50.1.1 (A:1-90) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}

GSHMEMAGDLSAGFFMEELNTYRQKQGVVLKYQELPNNSGPPHDRRFTFQVIIDGREFPEGEGRSKKEAKNAAAKLAVEILNKEKKAVSPL

>d1qu6a2 d.50.1.1 (A:91-179) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}

LLTTTNSSEGLSMGNYIGLINRIAQKKRLTVNYEQCAGSVHGPEGFHYCKCMGQKEYSIGTGSTKQEAKQLAAKLAQLYLQILSEETGSGC

>d1pkp_2 d.50.1.2 (4-77) Ribosomal S5 protein, N-terminal domain {Bacillus stearothermophilus}

INPNKLELEERVVAVNRVAKVVKGRRRLRFSALVVGDKNGHVGFGTGKAQEVPPEAIRKAIEDAKKNLIEVPIV

>d1fjge2 d.50.1.2 (E:5-73) Ribosomal S5 protein, N-terminal domain {Thermus thermophilus}

DFEEKMILIRRARMQAGGRRFRFGALVVVGDRQGRVGLGFGKAPEVPLAVQKAGYYARRNMVEVPLQN

>d1ah5_2 d.50.2.1 (220-313) Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}

NHHETALRVTAERAMNTRLEGGCQVPIGSYAEILDGEIWLRALVGAPDGSQIIRGERRGAPQDAEQMGISLAEELLNNGAREILAEVYNGDAPA

>d1pda_2 d.50.2.1 (220-307) Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain {Escherichia coli}

NHHETALRVTAERAMNTRLEGACQVPIGSYAEILDGEIWLGLVGAPDGSQIIRGERRGAPQDAEQMGISLAEELLNNGAREILAEVY

>d1dq3a2 d.50.3.1 (A:336-414) PI-Pfui intein middle domain {Archaeon Pyrococcus furiosus}

GNFGLPLNFNAFKEWASEYGVEFKTNGSQTIAIINDERISLGQWHTRNRVSKAVLVKMLRKLYEATKDEEVKRM LHLIE

>d1jida_d.201.1.1 (A:) SRP19 {Human (Homo sapiens)}

AARSPADQDRFICIYPAYLNNKKTIAEGRIPISKAVENPTATEIQDVCSAVGLNVLEKNKMYREWNRDVQYR
GRVRVQLQEDGSLCLVQFPSRKSVMLYAAEMIPKLTR
>d1dt4a_d.51.1.1 (A:) Neuro-oncological ventral antigen 1, nova-1, KH3 {Human (Homo sapiens)}
MKDVVEIAVPENLVGAILGKGGKTLVEYQELTGRIQISKKGEFLPGTRNRKVITGTPAATQAAQYLITQRI
>d1dtja_d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}
MKELVEMAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGEFLPGTRNRRVTITGSPAATQAAQYLISQRVT
>d1ec6a_d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}
MKELVEIAVPENLVGAILGKGGKTLVEYQELTGARIQISKKGEFLPGTRNRRVTITGSPAATQAAQYLISQRVTYEQ
GVRASNPQKV
>d1vig__d.51.1.1 (-) Vigilin, KH6 {Human (Homo sapiens)}
INRMDYVEINIDHKFHRHLIGKSGANINRIKDQYKVSVRIPPSEKSNLIRIEGDPQGVQQAKRELLELAS
>d2fmr__d.51.1.1 (-) Fragile X protein, KH1 {Human (Homo sapiens)}
ASRFHEQFIVREDLMLGAIGTHGANIQQARKVPGVTAIDLDEDCTFHIYGEDQDAVKKARSFLE
>d1khma_d.51.1.1 (A:) HnRNP K, KH3 {Human (Homo sapiens)}
GSPNSYGLGGPIITQVTIPKDLARSIIGKGGQRIKQIRHESGASIKIDEPLEGSEDRIITITGTQDQIQNAQYLLQ
NSVKQYSGKFF
>d1k1ga_d.51.1.1 (A:) RNA splicing factor 1 {Human (Homo sapiens)}
TRVSDKVMIPQDEYPEINFVGLLIGPRGNTLKNIEKECNAKIMIRGKGSVKEGVGRKDQMLPGEDEPLHALV
TANTMENVKKAVEQIRNLKQGIETPEDQNDLRKMQLRELARLNGTLR
>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}
PQLKFAMQRDLGIFPTQLPQYLQTEKLARTQAAAIERFGAQFAGSWIERNEDGSFKLVAATSGARKSSTLGGV
EVRNVR
>d3proc2 d.52.1.1 (C:86-163) Alpha-lytic protease prodomain {Lysobacter enzymogenes}
YSLKQLQSAMEQLDAGANARVKGVSKPLDGVQSYYDPRSNAVVKVDDGATDAGVDFVALSGADSAQVRI
ESSPGKL
>d1gpma3_d.52.2.1 (A:405-525) GMP synthetase, C-terminal, dimerisation domain {Escherichia coli}
GPGLGVRVLGEVKKEYCDLRRADAIFIEELRKADLYDKVSQAFTVFLPVRSVGVMGDGRKYDWVVSLRAVETI
DFMTAHWAHLPYDFLGRVSNRIINEVNGISRVVYDISGKPPATIEWE
>d1fjgc1 d.52.3.1 (C:2-106) Ribosomal protein S3 N-terminal domain {Thermus thermophilus}
GNKIHPIGFRLGITRDWESRWYAGKKQYRHLLEDQRIRGLLEKELYASGLARVDIERAADNVAVTVHVAKPGV
VIGRGGERIRVLREELAKLTGKNVALNVQE
>d1egaa2_d.52.3.1 (A:183-295) GTPase Era C-terminal domain {Escherichia coli}
DYITDRSQRFMASEIIREKLMRFLGAELPYSVTVEIERFVSNERGGYDINGLILVEREGQKKMVIGNKGAKIKTIGI
EARKDMQEMFEAPVHLELWVKVKSGWADDERALRSL
>d1hh2p2_d.52.3.1 (P:199-276) Transcription factor NusA, C-terminal domains {Thermotoga maritima}
RVPEFVIGLMKLEIPEVENGIVEIKAIAREPGVRTKAVASNDPNVDPIGACIGEGGSRIAAILKELGEKLDVLKW
S
>d1hh2p3_d.52.3.1 (P:277-344) Transcription factor NusA, C-terminal domains {Thermotoga maritima}

DDPKQLIANALAPATVIEVEILDKENKAARVLVPPQLSLAIGKGGQNARLAALKTGWKIDIKPIMNL
>d1k0ra2 d.52.3.1 (A:184-262) Transcription factor NusA, C-terminal domains {Mycobacterium tuberculosis}
THPNLVRKLFSLEVPEIADGSVEIVAVAREAGHRSKIAVRSNVAGLNAKGACIGPMGQRVRNVMSLSGEKIDII
DYDD
>d1k0ra3 d.52.3.1 (A:263-329) Transcription factor NusA, C-terminal domains {Mycobacterium tuberculosis}
DPARFVANALSPAKVVSVSVIDQTARAARVVPDFQLSLAIGKEGQNNARLAARLTGWRIDIRGDAPP
>d1e3ha4 d.52.3.1 (A:579-632) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 6 {Streptomyces antibioticus}
APRIITVKIPVDKIGEVIGPKRQMINQIQEDTGAETIEDDGTYIYGAADGPAA
>d1fjgc2 d.53.1.1 (C:107-207) Ribosomal protein S3 C-terminal domain {Thermus thermophilus}
QNPNLSAPLVQAQRVAEQIERRFAVRRAIKQAVQRVMESGAKGVIVSGRIGGAEQARTEWAAQGRVPLHTLR
ANIDYGFALARTTYGVLGVKAYIFLGEV
>d1hh2p4 d.202.1.1 (P:1-126) Transcription factor NusA, N-terminal domain {Thermotoga maritima}
MNIGLLEALDQLEEKGISKEEVIPILEKALVSAYRKNFKNVNEVVIDRNTGNIKVYQLLEVVEEVEDPATQISLE
EAKKIDPLAEVGSIVKKELNVKNFGRIAQQTAQKVLIQRIRELEKEKQ
>d1k0ra4 d.202.1.1 (A:-4-99) Transcription factor NusA, N-terminal domain {Mycobacterium tuberculosis}
VSRRHMNIDMAALHAIERVDRGISVNELLTIKSALLTAYRHTQGHQTDARIEIDRKTGVVRVIARETDEAGNLISE
WDDTPEGFGRIAATTARQVMLQRFRDAE
>d1onea2 d.54.1.1 (A:1-141) Enolase {Baker's yeast (Saccharomyces cerevisiae)}
AVSKVYARSVYDSRGNPTVEVELTTEKGVFVRSIVPSGASTGVHEALEMRDGDKSKWMGKGVHAVKNVNDVI
APAFVKANIDVKDQKAVDDFLISLDGTANKSKLGANAILGVSLAASRAAAAEKNVPLYKHLADLSKSKT
>d1pdz_2 d.54.1.1 (1-139) Enolase {Lobster (Homarus vulgaris)}
SITKVFARTIFDSRGNPTVEVDLYTSKGLFRAAVPSGASTGVHEALEMRDGDKSKYHGKSVFNAVKNVNDVIVP
EIIKSGLKVTQQKECDEFMCKLDGTENKSSLGANAILGVSLAICKAGAAELGIPLYRHIANLANY
>d1e9ia2 d.54.1.1 (A:1-139) Enolase {Escherichia coli}
SKIVKIIGREIIDS RGNPTVEAEVHLEGGFGVGM AAPSGASTGSREALELRDGDKSRFLKGVTKAVA AVNGPIA
QALIGKDAKDQAGIDKIMIDLDTENKS KFGANAILAVSLANAKAAA AKGMPLYEHIAELNGT
>d1bqg_2 d.54.1.1 (12-143) D-glucarate dehydratase {Pseudomonas putida}
GAPVITDLKVVPA GHDSMLNLSGAHGPLTRNILITDSSGHVG VGEVPGGEGIRKTLEDARHLLINQSIGNY
QSLLNKVRNAFADRDVGGRGLQTFDLRIA HVAVTAVES ALLDLLGQHLQVPVA ALLG
>d1ec7a2 d.54.1.1 (A:5-137) D-glucarate dehydratase {Escherichia coli}
FTTPVVTEMQVIPVAGHDSMLNLSGAHAPFFTRNIVI KDNSGHTGVGEIPGGEKIRKTLED AIPLVVGKTLGE
YKNVLT VRNTFAD RDAGGRGLQTFDLRTTIHVVTGIEAAMLDLLGQHLGVNVASLLG
>d1fhua2 d.54.1.1 (A:1-99) O-succinylbenzoate synthase {Escherichia coli}
MRSAQVYRWQIPMDAGVVLRDRLKTRDGLYVCLREGEREGWGEISPLPGFSQETWEEAQSVLLAWVNNW
LAGDCELPQMPSVAFGVSCALAE LTD TLP
>d1muca2 d.54.1.1 (A:4-130) Muconate-lactonizing enzyme (cis muconate cycloisomerase)
{Pseudomonas putida}
ALIERIDAIIVDLPTIRPHKLAMHTMQQQTLVVLVRCS DGVEGIGEATTIGGLAYGYESPEGIKANIDAHLAPALI
GLAADNINAAMLKLDKLAKGNTFAKSGIESALLDAQGKRLGLPVSELLGG

>d2mnr_2 d.54.1.1 (3-132) Mandelate racemase {Pseudomonas putida}
EVLITGLRTRAVNVPLAYPVHTAVGTVGTAPLVLIDLATSAGVVGHSYLFAYTPVALKSLKQLDDMAAMIVNEPL
APVSLEAMILAKRFCLAGYTGLIRMAAAGIDMAAWDALGKVHETPLVKLLGANAR

>d2chr_2 d.54.1.1 (1-126) Chlormuconate cycloisomerase {Alcaligenes eutrophus}
MKIDAIEAVIVDVPTKRPIQMSITTVHQQSYIVRVYSEGLVGEGGSVGGPVWSAECAETIKIIVERYLAPHLL
GTDAFNVSGALQTMARAVTGNASAKAAVEMALLDKARALGVSIAELGG

>d1jpdx2 d.54.1.1 (X:-2-113) L-Ala-D/L-Glu epimerase {Escherichia coli}
GSHMRTVKVFEEAWPLHTPFVIARGSSEARVVVELEEEGIKGTGECTPYPRYGESDASVMAQIMSVVPQLE
KGLTREELQKILPAGAARNALDCALWDLAARRQQSQLADLIGI

>d1jpma2 d.54.1.1 (A:1-125) L-Ala-D/L-Glu epimerase {Bacillus subtilis}
MKIIRIETSRIA VPLTKPFTALRTVYTAESVIRTYDSGAVGWGEAPPTLVITGDSMDSIESAIHHVLKPALLGKS
AGYEAILHDIQHLLTGNSAKAAVEMALYDGWAQMCGLPLYQMLGG

>d1kcza2 d.54.1.1 (A:1-160) beta-Methylaspartase {Clostridium tetanomorphum}
MKIVDVLCPTGLTFYFDDQRAIKKGAGHDGFTYTGSTVTGFTQVRQKGESISVLLVEDGQVAHGDCAAVQY
SGAGGRDPLFLAKDFIPVIEKEIAPKLIGREITNFKPMAEEFDKMTVNGNRLHTAIRYGITQAILDAVAKTRKVTM
AEVIRDEYNP

>d1kkoa2 d.54.1.1 (A:1-160) beta-Methylaspartase {Citrobacter amalonaticus}
MKIKQALFTAGYSSFYFDDQQAIIKNGAGHDGFIYTGDPVTPGFTSRQAGECVSQLILENGAVAVGDCAAVQ
YSGAGGRDPLFLAEHFIPFLNDHIKPLLEGGRDVAFLPNARFFDKLRIDGNLLHTAVRYGLSQALLDATA
LSGRKTKEVVCDEWQL

>d1bxe_a_d.55.1.1 (A:) Ribosomal protein L22 {Thermus aquaticus, subsp. Thermus thermophilus}
MEAKAIARYVRISPRKVRLVVDLIRGKSLEARNILRYTNKRGAYFVAKVLESAAAANAVNNHDMLEDRLYVKAAY
VDEGPALKRVLPRARGRADIKKRTSHITVILGEK

>d1jj2q_d.55.1.1 (Q:) Ribosomal protein L22 {Archaeon Haloarcula marismortui}
GISYSVEADPDTTAKAMLRERQMSFKHSKAIAREIKGKTAGEAVDYLEAVIEGDQPVPFKQHNSGVGHKS
KVDGWDAGRYPEKASKAFDLLENAVGNADHQGFGEAMTIKHVAHKVGEQQGRKPRAMGRASAWNSPQVD
ELILEEP

>d1gd8a_d.188.1.1 (A:) Prokaryotic ribosomal protein L17 {Thermus thermophilus}
SSHRLALYRNQAKSSLTHGRITTVPKAKELRGFVDHLIHLAKRGDLHARRLVLRLQDVKLVRKLF
DEIAPRYRD RQGGYTRVLKLAERRRGDGAPLALVELVE

>d1oela3 d.56.1.1 (A:137-190,A:367-409) GroEL {Escherichia coli}
PCSDSKAIAQVGTISANSDETVGKLIAEAMDVKVGKEGVITVEDGTGLQDEL
DVXERVAKLAGGVAVIKVGAAT
EVEMKEKKARVEDALHATRAAVEE

>d1ioka3 d.56.1.1 (A:137-190,A:367-409) GroEL {Paracoccus denitrificans}
PVNDSSVEAQVGTISANGESFIGQQIAEAMQRVGNEG
VITVEENKG
METEV
EVVXERVAKLAGGVAVIRVGG
MTEIEV
KERKDRV
DDALN
ATRAAVQE

>d1a6da3 d.56.1.2 (A:146-214,A:368-403) Thermosome {Archaeon Thermoplasma acidophilum}
TDDATLRKIALTSGKNTGLSNDFLADLVKAVNAVAEV
RDGKTIVDT
TANIKV
DKNGGS
VNDTQ
FISXAV
SILI
RGGTD
HVV
SEVERAL
NDAIRV
VAITK
EDGK

>d1a6db3 d.56.1.2 (B:145-215,B:368-403) Thermosome {Archaeon Thermoplasma acidophilum}
GADEK
KALLK
MAQTS
LNSKS
ASVAK
DKLAE
ISYEAV
KSVAEL
RDGKYY
VDFDNI
QVVKK
QGGA
IDDT
QLINX
KAV
SILVR
GETEH
VVDEMERS
ITDSL
HVVAS
ALEDG

>d1h6ha_d.189.1.1 (A:) p40phox NADPH oxidase {Human (Homo sapiens)}
AVAQQLRAESDFEQLPDDVAISANIA DIEEKRGFTSHFVFIEVKTKGGSKYLIYRRYRQFHALQS KLEERFGPDS
KSSALACTLPTLPAKVYVGVKQEIAEMRIPALNAYMKSLLSLPVWVLMDEDVRIFFYQSPYDSEQVP
>d1gd5a_d.189.1.1 (A:) p47phox NADPH oxidase {Human (Homo sapiens)}
GSMGDT FIRHIALLGFEKF RVP SQHYV YMFLVKW QDLSEKVVYR RFT EYEFHKTLKEMFPIEAGAINPENRIIPH
LPAPKWF DGQR AENRQ GTL TEYC ST LMSLPTK ISRC PHLL DFFK VRP DDLKL P
>d1ji8a_d.203.1.1 (A:) DsrC, the gamma subunit of dissimilatory sulfite reductase {Archaeon Pyrobaculum aerophilum}
MPVKCPGEYQVDGKKVILD EDCFMQN PEDWDEKVAEWLARELEGIQKMTEEHWKLVYLREYWETFGTCPP
IKMVTKETGFSLEKIYQLFPSGPAHGACKVAGAPKPTGCV
>d1ghha_d.57.1.1 (A:) DNA damage-inducible protein Dnl {Escherichia coli}
MRIEV TIAK TSPL PAGA IDAL A LAGEL SRRIQ YAFPDNEG HVS VRYAA ANNLS VIGAT KEDK QRIS EILQ ETWES ADD
WVFSE
>d1fxd_d.58.1.1 (-) Ferredoxin II {Desulfovibrio gigas}
PIEVN DDCMACEACVEICPDVFEMNEEGDKAVV INPDSDLCD CEEAIDSCPAEAIVRS
>d1dura_d.58.1.1 (A:) Ferredoxin II {Peptostreptococcus asaccharolyticus}
AYVINDSCIACGACKPECPVNCIQEGSIYAI DADSCIDCGSCASVCPVGAPNPED
>d1fca_d.58.1.1 (-) Ferredoxin II {Clostridium acidi-urici}
AYVINEACIS CGACEPECPVDAISQ GGSRYVIDADTCIDCGACAGVCPVDAPVQA
>d2fdn_d.58.1.1 (-) Ferredoxin II {Clostridium acidi-urici}
AYVINEACIS CGACEPECPVNAI SSGDD RYVIDADTCIDCGACAGVCPVDAPVQA
>d1clf_d.58.1.1 (-) Ferredoxin II {Clostridium pasteurianum}
AYKIADSCVSCGACASECPVNAISQGDSIFVIDADTCIDCGNCANVCPVGAPVQE
>d1blu_d.58.1.1 (-) Ferredoxin II {Chromatium vinosum}
ALMITDECINCDVCEPECPNGAISQGDETYVIEPSLCTECVGHYETSQCVECPVDCI IKDPSHEETEDELRAKYE
RITG
>d7fd1a_d.58.1.2 (A:) Ferredoxin {Azotobacter vinelandii}
AFVVTDNCIKCKYTDCVECPVDCFYEGPNFLVIHPDECIDCALCEPECPAQAI FSEDEV P EMDMQE F IQLNAELAE
VWP NITEKKDPLPDAEDWDGVKGKLQHLER
>d1bc6_d.58.1.2 (-) Ferredoxin {Bacillus schlegelii}
AYVITEPCIGTKDASCVECPVDCIHEGEDQYYIDPDVCIDCGACEAVCPVSAIYHEDFVPEEWKSYI QKNRDFFK
K
>d1h98a_d.58.1.2 (A:) Ferredoxin {Thermus thermophilus}
PHVICEPCIGVKDQSCVECPVCIYDGGDQFYIHPEECIDCGACVPACPVNAIYPEEDVPEQWKS YIEKNRKLA
GL
>d1xer_d.58.1.3 (-) Ferredoxin {Archaeon Sulfolobus sp.}
GIDPNYRTNRQVVGEHSGHKVYGPVEPPKVLGIHGTIVGVDFDLCIADGSCINACPVN VFQWYDTPGH PASEK
KADPVNEQACIFCMACVNVC PVA AIDVKPP
>d1vfw_d.58.1.4 (-) Ferredoxin {Thermotoga maritima}
MKVRVDADACIGCGVCENLC PDVFQLGDDGKAKV LQPETDLP CAKDAADSCPTGAISVE
>d1fxra_d.58.1.4 (A:) Ferredoxin I {Sulfate-reducing bacteria (Desulfovibrio africanus)}
ARKFYVDQDECIA CESCVEI APGAFAMDPEIEKAYVKDVEGASQEE EAMTCPVQCIHW EDE
>d1iqza_d.58.1.4 (A:) Ferredoxin {Bacillus thermoproteolyticus}
PKYTIVDKETCIACGACGAAAPDIYDYDEDGIAYVTL DDNQGIVEVPDILIDDMMDA FEGCPTDSIKVADEPFDG

DPNKFE

>d1jb0c_ d.58.1.4 (C:) Photosystem I iron-sulfur protein PsaC {Synechococcus elongatus}

AHTVKIYDTCTIGCTQCVRACPTDVLEMVPWDGCKAGQIASSPRTEDCVGCKRCETACPTDFLSIRVYLGAEATTRSMGLAY

>d1feha3 d.58.1.5 (A:127-209) Fe-only hydrogenase, second domain {Clostridium pasteurianum} KDKTEYVDERSKSLTVDRTKCLLCGRCVNACGKNTETYAMKFLNKGKTIIGAEDEKCFDDTNLLCGQCIIACPVAALSEKS

>d1hfel2 d.58.1.5 (L:2-86) Fe-only hydrogenase larger subunit, N-domain {Desulfovibrio desulfuricans}

SRTVMERIEYEMHTPDPKADPKLHFVQIDEAKCIGCDTCSQYCPTAAIFGEMGEPHSIPHIEACINCQCLTHCPENAIYEAQSV

>d1keka5 d.58.1.5 (A:669-785) Pyruvate-ferredoxin oxidoreductase, PFOR, domain V {Desulfovibrio africanus}

TSQFEKRGVAINVPPQWVPENCIQCNQCAFVCPHSAILPVLAKEELVGAPANFTALEAKGKELKGYKFRIQINTLDCMGCGNCADICPPKEKALVMQPLDTQRDAQVPNLEYAARIP

>d1h7wa5 d.58.1.5 (A:845-1017) Dihydropyrimidine dehydrogenase, C-terminal domain {Pig (Sus scrofa)}

ELQGWDGQSPGTESHQKGKPVPIAELMGKKLPNFGPYLEQRKKIIAEEKMRLKEQNAAFPPLERKPFIPKKPIPAIKDVGKALQYLGTGFELSNIEQVVAVIDEEMCINCCKCYMTNDGSYQAIQFDPETHLPTVTDTCTGCTLCLSVCPIIDCIRMVSRTTPYEPKRGL

>d1jnr_b_ d.58.1.5 (B:) Adenylylsulfate reductase B subunit {Archaeon Archaeoglobus fulgidus} PSFVNPEKCDGCKALERACEYICPNLMLTLDKEKMKAYNREPDMCWECYSCVKMCPQGAIDVRGYVDYSPLGGACVPMRGTSIMWTVKYRNGKVLRFKFAIRTPWGSIQPFEGFPEPTEEALKSELLAGEPEIIGTSEFPQVKKA

>d1d09b1 d.58.2.1 (B:1-100) Aspartate carbamoyltransferase {Escherichia coli} MTHDNKLQVEAIKRGTVIDHIPAQIGFKLSSLFKLTETDQRITIGLNLPSEGMRKD LIKIENTFLSEDQVDQLALYAPQATVNRIDNYEVVGKSRPSL

>d2atcb1 d.58.2.1 (B:1-100) Aspartate carbamoyltransferase {Escherichia coli} MTHNDKLQVAEIKRGTVINHIPAEIGFKLSSLFKLTETQDRITIGLNLPSEGMRKD LIKIENTFLSEDEVDELALYAPQATVNRINDYEVVGKSRPSL

>d1pca_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Pig (Sus scrofa)} KEDFVGHQVLRISVDEAQVQKVKELEDLEHLQLDFWRGP ARPGFPIDVRVPFPSIQAVKV FLEAHGIRYTIMIEDVQLLDEEQEQMFASQGR

>d1pyta_ d.58.3.1 (A:) Procarboxypeptidase A {Cow (Bos taurus)} KEDFVGHQVLRITAADAEVQTVKELEDLEHLQLDFWRGP QPGSPIDVRVPFPSLQAVKV FLEAHGIRYRIMIEDVQSLLDEEQEQMFASQSR

>d1aye_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Human (Homo sapiens)} LETFVGDQVLEIVPSNEEQIKNLLQLEAQEHLQLDFWKSP TPGETAHVRVPFVNQAVKV FLESQGIAYSIMIEDVQVLLDKENEMLFNRRR

>d1nsa_2 d.58.3.1 (7A-95A) Procarboxypeptidase B {Pig (Sus scrofa)} FEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSVTQIKPHSTVDFRVKAEDILAVEDFLEQNELQYEVLINNRLSVLEAQFDSVR

>d1pba_ d.58.3.1 (-) Procarboxypeptidase B {Pig (Sus scrofa)}

HHSGEHFEKEVFRVNVEDENDISELHELASTRQIDFWKPDSTVTQIKPHSTVDFRVKAEDILAVEDFLEQNELQY
EVLIINN

>d1spbp_ d.58.3.2 (P:) Subtilisin prosegment {Bacillus amyloliquefaciens}
EKKYIVGFKQTMSAKKKDVISEKGGKVQKQFKYVDAASATLNEKAVKELKKDPSVAYVEEDHVAHY

>d1scjb_d.58.3.2 (B:) Subtilisin prosegment {Bacillus subtilis}
EKKYIVGFKQTMSAMSSAKKKDVISQKGGKVEKQFKYVNAAAATLDEKAVKELKKDPSVAYVEEDHIAHEY

>d1itpa_d.58.3.2 (A:) Proteinase A inhibitor 1, POIA1 {Oyster mushroom (Pleurotus ostreatus)}
GSAGKFIVIFKNDVSEDKIRETKDEVIAEGGTITNEYNMMPGMKGFAELTPQSLTKFQGLQGLDIDSIEEDGIVTT
Q

>d1mli_d.58.4.1 (-) Muconalactone isomerase {Pseudomonas putida}
MLFHVKMTVKLPVDMDPAKATQLKADEKELAQRQLQREGTWRHLWRIAGHYANYSVFDVPSVEALHDLMQL
PLFPYMDIEVDGLCRHPSSIHSDDR

>d2pii_d.58.5.1 (-) PII (product of glnB) {Escherichia coli}
MKKIDAIKPKLDDVREALAEVGITGMTVTEVKGFGRQKGHETLYRGAEYMVDFLPKVKIEIVVPDDIVDTCVD
TIIRTAQTGKIGDGKIFVFDVARVIRIRTGEEDDAI

>d1gnka_d.58.5.1 (A:) PII-homolog GlnK {Escherichia coli}
MKLVTVIKPKLEDVREALSSIGIQGLTVTEVKGFGRQKGHAELYRGAEYSVNFLPKVKIDVAIADDQLDEVIDIV
SKAAYTGKIGDGKIFVVAELQRVIRIRTGEADEAAL

>d1nuea_d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo sapiens)}
ANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRVLVAMKFLRASEEHLKQHYIDLKDRPFFPGLVKYMNSGPVVAM
VWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVKSAEKEISLWFKPEELVDYKSCAHDW
VYE

>d1ehwa_d.58.6.1 (A:) Nucleoside diphosphate kinases {Human (Homo sapiens), NDK4}
HMGTRERTLVAVKPDGVQRRLVGDVIQRFERRGFTLVMGKMLQAPESVLAEHYQDLRRKPFYPALIRYMSGP
VVAMVWEGYNVVRASRAMIGHTDSAEEAAPGTIRGDFSVHISRNVIHASDSVEAQREIQLWFQSSELVSW

>d1be4a_d.58.6.1 (A:) Nucleoside diphosphate kinases {Cow (Bos taurus)}
ANERTFIAIKPDGVQRGLMGEIIKRFEQKGFRVLVAMKFMRASEDLLKEHYIDLKDRPFFAGLVKYMHSVPVA
MVWEGLNVVKTGRVMLGETNPADSKPGTIRGDFCIQVGRNIIHGSDSVESAECIWLWFRPEELVNYKSCAQN
WIYE

>d1hlwa_d.58.6.1 (A:) Nucleoside diphosphate kinases {Dictyostelium discoideum}
VNKERTFLAVKPDGVARGLVGEIIARYEKKGFLVGLKQLVPTKDLAESHYAEHKERPFFGGLVSFITSGPVVAMV
FEGKGVVASARLMIGVTNPLASAPGSIRGDFGVDRGRNIIAGSDSVESANREIALWFKPEELLTEVKPNPNLYE

>d1nsqa_d.58.6.1 (A:) Nucleoside diphosphate kinases {Drosophila melanogaster}
AANKERTFIMVKPDGVQRGLVGKIIERFEQKGFKLVALKFTWASKELLEKHYADLSARPFFPGLVNYMNSGPVV
PMVWEGLNVVKTGRQMLGATNPADSLPGTIRGDFCIQVGRNIIHGSDAVESAECIWLWNEKELVTWTAAK
DWIYE

>d1nhkl_d.58.6.1 (L:) Nucleoside diphosphate kinases {Myxococcus xanthus}
AIERTLSIIKPDGLEKGVIGKIISRFEKGLPKVAIRLQHLSQAQAEFYAVHKARPFFKDLVQFMISGPVVLMVLE
GENAVLANRDIMGATNPAQAAEGTIRKDFATSIDKNTVHGSDSLENAKIEIAYFFRETEIHSPYQ

>d1ha1_1 d.58.7.1 (8-92) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
EPEQLRKLFIGGLSFETTDLSRHFEQWGLTDCVVMRDPNTKRSRGFGFVTYATVEEVDAAMNARPHKVDG
RVVEPKRAVSRE

>d1ha1_2 d.58.7.1 (99-180) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
AHLTVKKIFVGGIKEDTEEEHLDYFEQYGKIEVIEIMTDRGSGKRGFAFVTFDDHDSVDKIVIQKYHTVNGHN

CEVRKAL

>d2up1a2 d.58.7.1 (A:99-190) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
GAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFDDHDSVDKIVIQKYHTVNGH
NCEVRKALSKQEMASAS

>d1fht_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}
AVPETRPNHTIYINNLNEKIKKDELKKSLYAIFSQFGQILDILVSRSLSKMRGQAFVIFKEVSSATNALRSMQGFPFY
DKPMRIQYAKTDSDIIAKMKGTFVERDRKREKRKPQSQE

>d1nrca_ d.58.7.1 (A:) Splicesomal U1A protein {Human (Homo sapiens)}
TRPNHTIYINNLNEKIKKDELKKSLYAIFSQFGQILDILVSRSLSKMRGQAFVIFKEVSSATNALRSMQGFPFYDKPM
RICYAKTD

>d1urna_ d.58.7.1 (A:) Splicesomal U1A protein {Human (Homo sapiens)}
AVPETRPNHTIYINNLNEKIKKDELKKSLYAIFSQFGQILDILVSRSLSKMRGQAFVIFKEVSSATNALRSMQGFPFY
DKPMRIQYAKTDSDIIAKM

>d2u1a_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}
MAPAQPLSENPPNHILFLNLPEETNELMSMLFNQFPGFKEVRLVPGRHIAFVEFDNEVQAGAARDALQGF
KITQNNAMKISFAKK

>d1a9nb_ d.58.7.1 (B:) Splicing factor U2B" {Human (Homo sapiens)}
IRPNHTIYINNMNDKIKKEELKRSLYALFSQFGHVVDIVALKTMKMRGQAFVIFKELGSSTNALRQLQGFPFYGK
PMRIQYAKTDSDIIISKMRG

>d1u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}
ARRLYVGNIPFGITEAMMDFFNAQMRLGGLTQAPGNPVLAQINQDKNFALEFRSVDETTQAMAFDGIIFQ
GQSLKIRRPHDYQPLPG

>d2u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}
AHKLFIGGLPNYLNDDQVKELLTSFGPLKAFNLVKDSATGLSKGYAFCEYVDINVTDQAIAGLNGMQLGDKKLLV
QRASVGAKNA

>d1b7fa1 d.58.7.1 (A:123-204) Sex-lethal protein {Drosophila melanogaster}
SNTNLIVNYLPQDMTDRELYALFRAIGPINTCRIMRDYKTGYSYGYAFVDFTSEMDSQRAIKVLNGITVRNKRLK
VSYARPG

>d1b7fa2 d.58.7.1 (A:205-289) Sex-lethal protein {Drosophila melanogaster}
GESIKDTNLYVTNLVRTITDDQLDTIFGKYGSIVQKNILRDKLTRPRGVAFVRYNKREEAQEAISALNNVIPEGGS
QPLSVRLA

>d1sxl_ d.58.7.1 (-) Sex-lethal protein {Drosophila melanogaster}
MSYARPGGESIKDTNLYVTNLVRTITDDQLDTIFGKYGSIVQKNILRDKLTRPRGVAFVRYNKREEAQEAISALN
NVIPEGGSQPLSVRLAEEHGK

>d1d8za_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}
MDSKTNLIVNYLPQNMTQDEFKSLFGSIGDIESCKLVRDKITGQSLGYGFVNYSDPNDADKAINTNGLKLQTKT
IKVSYARPSSASIR

>d1d9aa_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}
DANLYVSLPKTMSQKEMEQLFSQYGRITSRILLDQATGVSRGVGFIRFDKRIEAEAIKGLNGQKPLGAAEPIT
VKFANNPSQ

>d1fxla1 d.58.7.1 (A:37-118) Hu antigen D (Hud) {Human (Homo sapiens)}
SKTNLIVNYLPQNMTQEEFRSLFGSIGEIESCKLVRDKITGQSLGYGFVNYYDPKDAEKAIINTNGLRLQTKT
YARPS

>d1fxla2 d.58.7.1 (A:119-203) Hu antigen D (Hud) {Human (Homo sapiens)}

SASIRDANLYVSGLPKTMTQKELEQLFSQYGRITSRILVDQVTGSRGVGFIRFDKRIEAEAIKGLNGQKPSGAT
EPITVKFA

>d1hd1a_d.58.7.1 (A:) Heterogeneous nuclear ribonucleoprotein d0 {Human (Homo sapiens)}
KMFIGGLSWDTKKDLKDYSKFGEVVDC TLKLDPITGRSRGFGVLFKESESVDKVMDOKEHKLNGKVIDPKRA

>d2msta_d.58.7.1 (A:) Neural RNA-binding protein Musashi-1 {Mouse (Mus musculus)}
KIFVGGLSVNTTVEDVKHYFEQFGKVDDAMLMFDKTTNRHRGFGFVTFESEDIVEKCEIHFHEINNKMVECKKA

>d1cvja1 d.58.7.1 (A:11-90) Poly(A)-binding protein {Human (Homo sapiens)}
ASLYVGDLHPDVTEAMLYEKFSPAGPILSIRVCRDIMITRRSLGYAYVNFPQQPADAERALDTMNF DVIKGKPVRIMWSQRD

>d1cvja2 d.58.7.1 (A:91-179) Poly(A)-binding protein {Human (Homo sapiens)}
PSLRKSGVGNIFIKNLDSIDNKALYDTFSAGNLSCKVCDENGSKGYGFVFETQEAAERAIEKMNGMLNDRKVFVGRFKSRKER

>d1qm9a1 d.58.7.1 (A:1-110) Polypyrimidine tract-binding protein {Human (Homo sapiens)}
MGNSVLLVSNLNP PERVTPQSLFILFGVYGDVQRVKILFNKKENALVQMADGNQAQLAMSHLNGHKLHGKPIRITLSKHQNVL PREGQEDQGLTKDYGN SPLHRFKKPGS

>d1qm9a2 d.58.7.1 (A:111-198) Polypyrimidine tract-binding protein {Human (Homo sapiens)}
KNFQNI FPPSATL HLSNIPPSVSEEDLKVLFSSNGGVVKGFKFQKDRKMA LIQMGSVEAVQALIDLHNHDLG ENHHLRV SFSKSTI

>d1fj7a_d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}
GSHMLED PVEGSE TTPFNLFIGNLNP NKVAELKVAI SELFAKNDLAVV DVRTGTNRKFGYVDFESAEDLEKALELTGL KVFGNEIKLEKPKGRDGTRGC

>d1fjca_d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}
SHMLED PCTS KK VRAARTLLAKNLSFNITEDELKEV FEDALEIRLV SQDGKSKGIAYIEFKSE ADAEKNLEEKQGA EIDGRSVS LYIDGRS VS LYITGEKGGTRG

>d1fjeb1 d.58.7.1 (B:1-91) Nucleolin {Golden hamster (Mesocricetus auratus)}
GSHMVEGSE TTPFNLFIGNLNP NKVAELKVAI SELFAKNDLAVV DVRTGTNRKFGYVDFESAEDLEKALELTGL KVFGNEIKLEKPKGR

>d1fjeb2 d.58.7.1 (B:92-175) Nucleolin {Golden hamster (Mesocricetus auratus)}
DSKKVRAARTLLAKNLSFNITEDELKEV FEDALEIRLV SQDGKSKGIAYIEFKSE ADAEKNLEEKQGA EIDGRSVS LYYTGEKG

>d1h6kx_d.58.7.1 (X:) CBP20, 20KDa nuclear cap-binding protein {Human (Homo sapiens)}
KSCTLYVGNL SFYTTEEQIYELFSKSGDIKKIIMGLDKMTACGFCFVEYY SRADAENAMRYINGTRLDDRI RTDW DAG

>d1fo1a2 d.58.7.2 (A:123-191) mRNA export factor tap {Human (Homo sapiens)}
TIPYGRKYDKAWL LSMIQSKCSV PFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRISIII

>d1ft8a2 d.58.7.2 (A:118-199) mRNA export factor tap {Human (Homo sapiens)}
NWFKITIPYGRKYDKAWL LSMIQSKCSV PFTPIEFHYENTRAQFFVEDASTASALKAVNYKILDRENRRISIIINSSA PPHT

>d1ft8e1 d.58.7.2 (E:) mRNA export factor tap {Human (Homo sapiens)}
WFKITIPYGRKYDKAWL LSMIQSKCSV PFTPIEFHYENTRAQFFVEDASTASALKAV

>d1koha2 d.58.7.2 (A:105-200) mRNA export factor tap {Human (Homo sapiens)}
RGGAGTSQDGTSKNWFKITIPYGRKYDKAWL LSMIQSKSSVPFTPIEFHYENTRAQFFVEDASTASALKAVNYKI

LDRENRRISIIINSSAPPHTI

>d1jmta_d.58.7.3 (A:) U2AF35 (35 KDa subunit) {Human (Homo sapiens)}

SQTIALLNIYRNPQNNSQSADGLRSAVDVEMQEHYDEFFEEVFTEMEEKYGEVEEMNVCDNLGDHLVGNVY
VKFRREEDAEEKAVIDLNNRWFNGQPIHAELSP

>d1dbda_d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}
RRTTNDGFHLLKAGGSCFALISGTANQVKCYRFRVKKNHRHRYENCTTWFTVADNGAERQGQAQILITFGSP
SQRQDFLKHVPLPPGMNISGFTASLDF

>d2bopa_d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}
SCFALISGTANQVKCYRFRVKKNHRHRYENCTTWFTVADNGAERQGQAQILITFGSPSQRQDFLKHVPLPPG
MNISGFTASLDF

>d1a7ge_d.58.8.1 (E:) Papillomavirus-1 E2 protein {Human papillomavirus type 31}
ATTPIIHLKGDANILKCLRYRLSKYKQLYEQVSSTWHWTCTDGKHKNIAVTLYISTSQRDDFLNTVVIPNTSVST
GYMTI

>d1by9_d.58.8.1 (-) Papillomavirus-1 E2 protein {Human papillomavirus type 16}
TTPIVHLKGDANTLKCLRYRFKKHCTLTAWSSTWHWTGHNVHKSAIVTLTYDSEWQRDQFLSQVKIPKTITVS
TGFMS

>d1f9fa_d.58.8.1 (A:) Papillomavirus-1 E2 protein {Human papillomavirus type 18}
HMTPIIHLKGDRNSLKCLRYRLRKHSMDHYRDISSTWHWTGAGNEKTGILTWTYHSETQRTKFLNTVAIPDSVQIL
VGYMTM

>d1b3ta_d.58.8.1 (A:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}
KGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWAGVFVYGGSKTSLYNLRRGTALAIPQCRL
TPLSLPFGMAPGPQPGPLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRTVCSFDDGVSDL

>d1vhib_d.58.8.1 (B:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}
PKFENIAEGLRALLARSHVERTTDEGTWAGVFVYGGSKTSLYNLRRGTALAIPQCRLTPLPFGMAPGP
QPGPLRESIVCYFMVFLQTHIFAEVLKDAIKDLVMTKPAPTCNIRTVCSFDDGVSDL

>d3rubi2_d.58.9.1 (L:22-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}
LTYYTPEYQTKDIDLAFAFRVTPQPGVPPEAGAAVAESSTGTWTTVWTDGLTSLDRYKGRCYRIERVVGEKD
QYIAYVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDRIPPAYVKT

>d1bura2_d.58.9.1 (A:12-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}
EFKAGVKDYKLTYTPEYETLTDILAAFRVSPQPGVPPEAGAAVAESSTGTWTTVWTDGLTNLDYKGRCY
HIEPVAGEENQYICVAYPLDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDRIPPAYVKT

>d1bwva2_d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

RIKNSRYESGVIPYAKMGYNPDYQVKDTDVLALFRVTPQPGVPDPIEAAAAGESSTATWTVVWTDLTAAD
LYRAKAYKVDQVPNNPEQYFAYIAYELDLFEEGSIANLTASIIGNVFGFKAVKALRLEDMLRPLAYLKTFQ

>d1gk8a2_d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}

TKAGAGFKAGVKDYRLTYTPDYVVRDTDILAAFRMTPQPGVPPEECGAAVAAESSTGTWTTVWTDGLTSLDR
YKGRCYDIEPVPGEDNQYIAYVAYPIDLFEEGSVTNMFTSIVGNVFGFKALRALRLEDRIPPAYVKT

>d1bxna2_d.58.9.1 (A:22-150) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}

YKMGYWDGYVPKDTDLLALFRITPQDGVDPEAAAAGESSTATWTVVWTDRLTACDMYRAKAYRVDPV
PNNPEQFFCYVAYDLSFEEGSIANLTASIIGNVFSFKPIKAARLEDMRFPVAYVKT

>d1rbla2 d.58.9.1 (A:9-147) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{*Synechococcus* sp., strain pcc 6301}

SAAGYKAGVKDYKLTYTPDYTPKDTDLLAARFRSPQPGVPADEAGAAIAAESSTGTWTTVWTDLTMDRYK
GKCYHIEPVAGEENSYFAFIAYPLDLFEEGSVTNILTSIVGNVFGFKAIRSLRLEDIRFPVALVKT

>d5ruba2 d.58.9.1 (A:2-137) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{*Rhodospirillum rubrum*}

DQSSRYVNLAKEEDLIAGGEHVLCAIMPKAGYGYVATAAHFAAESSTGTNVEVCTDDFTRGVDALVYEVD
EARELTKIAYPVALFDRNITDGKAMIASFLTMGNNQGMGDVEYAKMHDFYVPEAYRALFD

>d1geha2 d.58.9.1 (A:12-136) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Archaeon *Thermococcus kodakaraensis*}

YVDKGYEPSKKRDIIAVFRVTPAEGYTIEQAAGAVAAESSTGTWTTLYPWYEQERWADLSAKAYDFHDMGDGS
WIVRIAYPFHAFEEANLPGLLASIAGNIFGMKRVKGLRLEDLYFPEKLIREF

>d2acy_ d.58.10.1 (-) Acylphosphatase {Cow (*Bos taurus*)}

AEGDTLISVDYEIFGKVQGVFRKYTQAEGKKLGLVGWVQNTDQGTVGQLQGPASKVRHMQEWEKGSP
KSHIDRASFHNEKVIVKLDYTDFQIVK

>d1laps_ d.58.10.1 (-) Acylphosphatase {Horse (*Equus caballus*)}

STARPLKSVDYEVFGRVQGVCFRMYAEDEARKIGVVGVWVKNTSKGTGQVQGPEEKVNSMKSWLSKGSP
SSRIDRTNFSNEKTISKLEYNSFSVRY

>d1i1ga2 d.58.37.1 (A:62-141) LprA {Archaeon *Pyrococcus furiosus*}

YSLVTITGVDTKPEKLFEVAEKLKEYDFVKELYLSSGDHMIMAVIWAKDGEDLAEIISNKIGKIEGVTKVCAPAIILEKL
K

>d1dar_4 d.58.11.1 (600-689) Elongation factor G (EF-G), domains III and V {*Thermus thermophilus*}

VILEPIMRVEVTTPEEYMGDVIGDLNARRGQILGMEPRGNAQVIRAFVPLAEMFGYATDLRSKTQGRGSFVMF
FDHYQEVPKQVQEKLK

>d1fnma4 d.58.11.1 (A:404-482) Elongation factor G (EF-G), domains III and V {*Thermus thermophilus*}

VPEPVIDVAIEPKTAKDQEKLSQLALARLAEEDPTFRVSTHPETGQTISGMGELHLEIIVDRLKREFKVDANVGKP
QVA

>d1b64_ d.58.12.1 (-) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Human (*Homo sapiens*)}

MLVAKSSILLDVKPWDDETDMAKLEECVRSIQADGLVGSSKLVPGYGIKKLQIQCVVEDDKVGTDMLEEQI
TAFEDYVQSMDVAFNKI

>d1f60b_ d.58.12.1 (B:) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Baker's yeast (*Saccharomyces cerevisiae*)}

PAAKSIVTLDVKPWDDETNLEEMVANVKAIMEGLTWGAHQFIPIGFGIKKLQINCVVEDDKVSLDDLQQSIEE
DEDHQSTDIAAMQKL

>d1gh8a_ d.58.12.1 (A:) aEF-1beta {Archaeon Methanobacterium
thermoautotrophicum}

MGDVVATIKVMPESPVDLEALKKEIQERIPEGTELHKIDEEPIAGLVALNVMVVVGDAEGGTEAAEESLGIE
GVSNIEVTDVRRLM

>d1b7yb4 d.58.13.1 (B:682-775) Phenylalanyl-tRNA synthetase {*Thermus thermophilus* (*Thermus aquaticus*)}

LAFQDPSRHPAAFRDLAVVVPAAPTPYGEVEALVREAAGPYLESALFDLYQGPPPLPEGHKSIAFHRLFRHPKRTL
DEEVEEAVSRVAEALRAR

>d1jjcb4 d.58.13.1 (B:682-785) Phenylalanyl-tRNA synthetase {Thermus thermophilus (Thermus aquaticus)}

LAFQDPSRHPAAFRDLAVVVPAAPTPYGEVEALVREAAGPYLESALFDLYQGPPPLPEGHKSIAFHRLFRHPKRTL
DEEVEEAVSRVAEALRARGFGLRGLDTP

>d1loua_ d.58.14.1 (A:) Ribosomal protein S6 {Thermus thermophilus}

MRRYEVNIVLPNLDQSQLALEKEIIQRAAENY GARVEKVEELGLRLAYPIAKDPQGYFLWYQVEMPEDRVN
DLARELIRDNVRRVMVVKSQEPF

>d1qjha_ d.58.14.1 (A:) Ribosomal protein S6 {Thermus thermophilus}

MRRYEVNIVLPNLDQSQLALEKEIIQRALENY GARVEKVALGLMVLAYPIAKDPQGYFLWYQVEMPEDRVN
DLARELIRDNVRRVMVVKs

>d1fjgj_ d.58.15.1 (J:) Ribosomal protein S10 {Thermus thermophilus}

KIRIKLRGFDHKTLDSAQKIVEAARRSGAQVSGPIPLPTRVRRTFTVIRGPFKHKDSREHFELRTHNRLVDIINPNR
KTIEQLMTLDLPTGVEIEIKT

>d1fa0a1 d.58.16.1 (A:352-523) Poly(A) polymerase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

NDFFFYKFYLEITAYTRGSDEQHLKWSGLVESKVRLLVMKLEVLAGIKIAHPFTKPFESSIONYCCPTEDDYEMIQDKY
GSHKTETALNALKVTDENKEEESIKDAPKAYLSTMYIGLDFNIENKEKVDIHIPCTEFVNLCRSFNEDYGDHKVF
NLALRFVKGYDLPDEVFD

>d1f5aa1 d.58.16.1 (A:365-498) Poly(A) polymerase, C-terminal domain {Cow (Bos taurus)}

PNFFQKYKHYIVLLASAPTEKQRLEWVGLVESKIRILVGSLEKNEFITLAHVNPQSFPAPKENPDKEEFTMWVIG
LVFKKTENSENLSVDLTYDIQSFTDTVYRQAINS KMFVDMKIAAMHVKRKQLHQQLP

>d1afj_ d.58.17.1 (-) Mercuric ion binding protein MerP {Shigella flexneri}

ATQTVTLAVPGMTCAACPITVKKALSKVEGVSKVDVGFEKREAVVTFDDTKASVQKLT KATADAGYPSSVKQ

>d1fvqa_ d.58.17.1 (A:) Copper transporter domain ccc2a {Baker's yeast (Saccharomyces cerevisiae)}

AREVILAVHGMTCSACTNTINTQLRALKGVTKCDISLVTNECQVTDNEVTADSIKEIIEDCGFDCEILRDS

>d1aw0_ d.58.17.1 (-) Menkes copper-transporting ATPase {Human (Homo sapiens)}

LTQETVINIDGMTNCSCVQSIEGVISKPGVKSIRVSLANSNGTVEYDPLLTSPETLRGAIEDMGFDATLSD

>d1cc8a_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Baker's yeast (Saccharomyces cerevisiae)}

AEIKHYQFN VVMTCSGCSGAVNKVLTKLEPDVSKIDISLEKQLVDVYTTLPYDFILEKIKKTGKEVRSGKQL

>d1fe0a_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Human (Homo sapiens), HAH1}

PKHEFSVDMTCGGCAEAVSRVLNKLGGVKYDIDLPNKKVCIESEHSMDTLLATLKKTGKTVSYLGL

>d1cpza_ d.58.17.1 (A:) Copper chaperone {Enterococcus hirae}

AQEFSVKGMSCNHCVARIEEAVGRISGVKKVKVQLKKEAVVKFDEANVQATEICQAINELGYQAEVI

>d1k0va_ d.58.17.1 (A:) Copper chaperone {Bacillus subtilis, CopZ}

MEQKTLQVEGMSCQHCVKAVETSVGELDGVS A HVNLEAGKVDVSFDADKVSVKDIADAIEDQGYDVAKIEG
R

>d1qupa2 d.58.17.1 (A:2-73) Copper chaperone for superoxide dismutase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

TTNDTYEATYAIPMHCENCVNDIKACLKNVPGINSLNFDIEQQIMSVESSVAPSTIINTLRNCGKD AIRGA

>d1gmua2 d.58.38.1 (A:71-138) Urease metallochaperone UreE, C-terminal domain

{Klebsiella aerogenes}

DEEVSVRCDDPFMLAKACYALGNRHVPLQIMPGELEYHHDVLDDMLRQGLTVFGQLPFEPEAGA
>d1eara2 d.58.38.1 (A:75-142) Urease metallochaperone UreE, C-terminal domain {Bacillus pasteurii}
LEKVYVIKPQTMQEMGKMAFEIGNRHTMCIEDDEILVRYDKTLEKLIDEVGVSYEQSERRFKEPKY
>d1psda3 d.58.18.1 (A:327-410) Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain {Escherichia coli}
FPEVSLPLHGGRRLMHIHENRPGVLTALNKIFAEQGVNIAAQYLQTSQAMGYVVVIDEADEDVAEKALQAMKAI
PGTIRARLLY
>d1tdj_2 d.58.18.2 (336-423) Allosteric threonine deaminase C-terminal domain {Escherichia coli}
QREALLAVTIPEEKGSFLKFCQLLGRSVTEFNYRFADAKNACIFVGVRSLRGLEERKEILQMLNDGGYSVVDLSD
DEMAKLHVRYMV
>d1tdj_3 d.58.18.2 (424-514) Allosteric threonine deaminase C-terminal domain {Escherichia coli}
GGRPSHPLQERLYSFEFPESPGALLRFLNTLGTWNISLFHYRSHGTDYGRVLAFAELGDHEPDFETRLNELGYD
CHDETNNPAFRFFLAG
>d1phza1 d.58.18.3 (A:19-115) Phenylalanine hydroxylase N-terminal domain {Rat (Rattus norvegicus)}
GQETSYIEDNSNQNGAISLIFSLKEEVGALAKVRLFEENDINLTHIESRPSRLNKDEEFFTYLDKRTKPVLGSIIKS
LRNDIGATVHELSRDKEK
>d1cg2a2 d.58.19.1 (A:214-326) Carboxypeptidase G2, dimerisation domain {Pseudomonas sp., strain rs-16}
SGIAYQVNITGKASHAGAAPELVNALVEASDLVLRTMNIDDKAKNLRFNWTIAKAGNVSNIPASATLNADV
RYARNEDFDAAMKTLEERAQQKKLPEADVKVIVTRGRPA
>d1dqaa1 d.58.20.1 (A:587-703) NAD-binding domain of HMG-CoA reductase {Human (Homo sapiens)}
GMTRGPVVRPRACDSAEVKAWLETSEGFV р AKEAFDSTSFRARLQKLHTSIAGRNLYIRFQSRSGDAMGMNM
ISKGTEKALSKLHEYFPEMQILAVSGNYCTDKPAAINWIEGRG
>d1qaxa1 d.58.20.1 (A:111-220) NAD-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}
LMHAQVQIVGIQDPLNARLSLLRKDEIIELANRKDQLLNSLGGGCRDIEVHTFADTPRGPMVAHLIVDVRDA
MGANTVNTMAEAVAPLMEAITGGQVRLRILSNLADL
>d1ekra_d.58.21.1 (A:) Molybdenum cofactor biosynthesis protein C, MoaC {Escherichia coli}
GEAHMVDVSAKAETVREARAЕAFVTMRSETLAMIIDGRHHKGDVFATARIAGIQAAKRTWDLIPLCHPLMLSK
VEVNLQAЕPEHNVRRIETLCRLTGKTGVEMEALTAASVAALTIYDMCKAVQKDMVIGPVRLLAКSGGKSGDFK
>d1f3va_d.58.22.1 (A:) TRADD, N-terminal domain {Human (Homo sapiens)}
HEEWVGSAYLVESSLKDVKVLSDAYAHPQQKVAVYRALQAALAЕGGSPDVLQMLKIHRSDPQLIVQLRFCGR
QPCGRFLRAYREGALRAALQRSLAAALAQHSVPLQLELRAGAERLDALLADEERCLSCILAQQPDRLDEELAEL
EDALRNLKCG
>d1mla_2 d.58.23.1 (128-197) Probable ACP-binding domain of malonyl-CoA ACP
transacylase {Escherichia coli}
GTGAMAAIIGLDDASIAKACEEEAEGQVVSPVNFNSPGQVVIAGHKEAVERAGAACKAAGAKRALPLPVS
>d1ffgb_d.58.24.1 (B:) CheY-binding domain of CheA {Escherichia coli}

PRIILSRKAGEVDLLEELGHLLTLDVVKGADSLSAILPGDIAEDDITAVLCFVIEADQITFETV
>d1kp6a_d.58.25.1 (A:) Killer toxin KP6 alpha-subunit {Smut fungus (Ustilago maydis)}
NNAFAGFGSCKWECWCTAHGTGNELRYATAAGCGDHSKSYYDARAGHCLFSDDLRLRNQFYSHCSSLNNN
MSCRSLSK
>d1h72c2 d.58.26.1 (C:168-300) Homoserine kinase, C-terminal domain {Archaeon Methanococcus jannaschii}
FKLDILIAIPNISINTKEAREILPKAVGLKDLVNNVGKACGMVYALYNKDKSLFGRYMMSDKVIEPVRGKLIPNYFK
IKEEVKDKVYGITISGGPSIIAFPKEEFIDEVENILRDYYENTIRTEVGKGVEVV
>d1fi4a2 d.58.26.2 (A:191-393) Mevalonate 5-diphosphate decarboxylase {Baker's yeast (Saccharomyces cerevisiae)}
QMKA CVLVSDIKKDVSS TQGMQLTVATSELFKERIEHVV PKRFEV MRKAIVE KDFATFAKETMMDSNSFHATC
LDSF PPIFY MNDTSK RIIS WCHT INQF YGETIV AYT FDAG PNAV LYLAEN ESKL FAFI YKL FG SVP GWD KKFTTEQ
LEAF NHQF ESSN FT ARE LD L E L Q K D V A R V I L T Q V G S G P Q E T N E S L I D A K T G L
>d1regx_d.58.27.1 (X:) Translational regulator protein regA {Bacteriophage T4}
MIEITLKKPEDFLKV KETL TRMGIANNKDKVLYQSCHILQKKG LYV VHF KEM L RMD GRQ VEM TE E V R R D S I A
WLLEDWGLIEIVPGQRTFMKD L TN FRV ISFK QKHEW KL VP KY TIGN
>d1fga_d.58.28.1 (A:) Peptide methionine sulfoxide reductase {Cow (Bos taurus)}
KIVSPQE ALPGRKEPLVVA AKHHVNGNRT VEPFPE GTQMAVFGM GCFWG AERKF WT LKG VYSTQVGFAGGY
TPNPTYKEVCSGKTGHAEV V RVVFQPE HIS FEELL KVFW ENHD PTQ GM RQG NDH GSQ YRS AIY PTSAE HVG A
ALKSKEDYQKV LSEH GFG LITT DIREG QTF YYAEDYHQ QYL SKDP DG YC
>d1ff3a_d.58.28.1 (A:) Peptide methionine sulfoxide reductase {Escherichia coli}
SLFDKKHLVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMEIAIFAMGCFWGVERLFWQLPGVYSTAAG YTGGY
T PNP TYREVC SGDTGHA EAV RIVY DPSV ISYE QLLQV FWEN HDPAQGM RQG NDH GTQ YRS AIY PLT PEQ DAA AR
QDAAARASLERFQAAMLAADD DR HITTEIANATPFYYAEDDHQ QYLHKNP YGYC GIGGI G VCL PEA
>d1ff3c_d.58.28.1 (C:) Peptide methionine sulfoxide reductase {Escherichia coli}
LVSPADALPGRNTPMPVATLHAVNGHSMTNVPDGMEIAIFAMGCFWGVERLFWQLPGVYSTAAG YTGGY
T PNP TYREVC SGDTGHA EAV RIVY DPSV ISYE QLLQV FWEN HDPAQGM RQG NDH GTQ YRS AIY PLT PEQ DAA AR
ASLERFQAAMLAADD DR HITTEIANATPFYYAEDDHQ QYLHK
>d1azsa_d.58.29.1 (A:) Adenylyl cyclase VC1, domain C1a {Dog (Canis familiaris)}
DMMFHKIYIQKHDNV SILF ADIEGFTSLASQCTA QELVMTLNELFARFDK LAAENHCLRIK ILGDCYYCVSGLPEA
RADHAHCC VEMGMDMIEAISL VRE MTGV NVNMRV GIHS GRV HCGV LGLRKWQFDV WSND VT LANHMEA
GGKAGRIH ITKATLSY LNGDYEV EP CGGERNAYL KEHSIETFLI
>d1azsb_d.58.29.1 (B:) Adenylyl cyclase II C1, domain C2a {Rat (Rattus norvegicus)}
HQSYDCVCVMFASIPDFKEFYTESDVNKEGLECLRLLNEIIADF DLLS KPKFSGV EKI KTIG STY MAAT GLS AIPS
QEHAQ EPERQ YM HIG TMV EFAY ALVG KLD AIN KHSF NDF KLRV GIN HG PVI AGV IGA QKPQ YDI WGN TVN VA
SRMDSTGVLDKIQVTEETSLI LQ TLG YTCT CRGI INVKG KGDLK TYF VNT
>d1fx2a_d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma brucei), different isoform}
NNNRAPKEPTDPVT LIFT DIES STALWA AH PDL MPDA VAAH HRM VRSLIGRYK CYEV KTV GDS FMIA SKSP FAA
VQLAQELQLCFLHHDWGTN ALDD SYREFEE QRAEG ECEY TPPTA HMDP EVY SRLW NG LRV RGVI HTG LCD IR
HDEVTKG YDYY GRT PNMA ARTES VANGG QVL MTHA AYMSL SAEDRK QIDV TALGD VALRG VSDPV KM YQLN
TVPSRNFA ALRLD REYFD
>d1fx4a_d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma brucei), different isoform}

DNDsapKEPTGPVTLIFTDIESSTALWAAHPDLMPDAVATHHRLIRSLTRYECYEVKTVGDSFMIASKSPFAAVQ
LAQELQLCFLRLDWETNAVDESYREFEEQRAEGERCEYTPPTASLDPEVYSRLWNGLRVRVGIHTGLCDIRYDEVT
KGYDYYGRTSNMAARTESVANGGQVLMTHAAYMSLSGEDRNQLDVTLGATVLRGVPEPVRMYQLNAVPG
RNFAALRLDR

>d1eqoa_ d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase,
HPPK {Escherichia coli}

TVAYIAIGSNLASPLEQVNAALKALGDIPEHILTSSFYRTPPLGPQDQPDYLNAAVALETSLAPEELLNHTQRIEL
QQGRVRKAERWGPRTLDDIMLFGNEVINTERLTVPHYDMKNRGFMLWPLFEIAPELVFPDGEMLRQILHTR
AFDKLNKW

>d1cbka_ d.58.30.1 (A:) 6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase,
HPPK {Haemophilus influenzae}

MITAYIALGSNLNTPVEQLHAALKAIQLSNTHLVTTSSFYKSPLGPQDQPDYVNAVAKIETELSPKLDELQRI
ENEQGRVRLRRWGERTLDDILLYGNEIIQNERLTIPHYDMHNREFVIVPLFEIASDLVLPNSQIITELVKQFADHK
MIKLN

>d1gpja3 d.58.39.1 (A:1-143) Glutamyl tRNA-reductase catalytic, N-terminal domain
{Archaeon Methanopyrus kandleri}

MEDLVSVGITHKEAEVEELEKARFESDEAVRDIVESFGLSGSVLLQTSNRVEVYASGARDRAEELGDLIHDDAWV
KRGSEAVRHLFRVASGLESMMVGEQEILRQVKKAYDRAARLGTIDELKIVFRRAINLGKRAREETRI

>d1hbnc_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon
Methanobacterium thermoautotrophicum}

AQYYPGTTKVAQNRRNFCNPEYELEKLREISDEDVVKILGHRAPGEEYPSVHPPLEEMDEPEDAIREMVEPIDG
AKAGDRVRYIQFTDSMYFAPAQPYVRSRAYLCRYRGADAGTLSGRQIETRERDLEKISKELLETEFFDPARSGVR
GKSVHGHSRLDEDGMMFDMLRRQIYNKDTGRVEMVKNQIGDELDEPVDLGEPLDEETLMEKTTIYRVGDGE
AYRDDVEAVEIMQRHVLRSQGGFN

>d1e6vc_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanopyrus
kandleri}

FYYPGETDVAENRRKYMNPNEYELKKLREIPDEDIVRLMGHREPGEYPSVHPPLEEMEEPECPIRELVEPTEGAK
AGDRIRYIQFTDSVYFAPIHPYIRARMYMWRYRGVTGSLSGRQIIEVRERDLEKIAKELLETEIFDPARSGVRGA
TVHGHALRLDENGLMLHALRRYRLNEETGEVEYVKDQVGIELDEPIPVGAPADEDDLKERTTIYRIDGTPYREDE
ELLQVQVQRIHELRTLADYRPEE

>d1e6yc_ d.58.31.1 (C:) Methyl-coenzyme M reductase gamma chain {Archaeon Methanosaicina
barkeri}

AYERQYYPGATSVAANRRKHMSGKLEKLREISDEDLTAVLGHRAPGSDYPSTHPLAEMIGEPACSTRENVAATP
GAAAGDRVRYIQFADSMYNAPATPYFRSYFAAINFRGVDPGTLSGRQIVEARERDMEQCAVKQMECTIDHAL
AGVRGATVGHGSVRLQEDGVMFDMLDRRLLENGTHIIMDKDQVAIPLDRKVDLGKPMSSAAKRTTIYRVDN
VAFRDDAEVVEWVHRIFDQRTKFGFQPK

>d1hbna2 d.58.31.2 (A:2-269) Alpha chain {Archaeon Methanobacterium thermoautotrophicum}
ADKLFINALKKFEESPEEKTTFTLGGWKQSERKTEFVNAGKEVAAKRGIPQYNPDIGTPLGQRVLMPYQVS
TTDTYVEGDDLHFVNNAAMQQMWDDIRRTVIVGLNHAHAVIEKRLGKEVTPETITHYLETVNHAMPAAVV
QEHMVETHPALVADSYVKVFTGNDEIADEIDPAFVIDINKQFPEDQAETLKAEVGDGIWQVVRIPTVSRTCDG
ATTSRWSAMQIGMSMISAYKQAAGEAATGDFAYAAKHAEVHMGTYLPV

>d1e6va2 d.58.31.2 (A:8-272) Alpha chain {Archaeon Methanopyrus kandleri}
LFMKALKEKFEESPEEKYTKFYIFGGWKQSERKKEFWADKIVEERGVPHYNPDIGVPLGQRKLMSYQVSGTD
VFVEGDDLTFVNNAAMQQMWDDIRRTVIVGMDTAHRVLERRLGKEVTPETINEYMETLNHALPGGAVVQE

HMVEIHPGLTWDCYAKIITGDLLEADEIDDKFLIDIEKLFPEEQAEQLIAIGNRTYQVCRMPTIVGHVCDGATM
YRWAAMQIAMSIFICAYKIAAGEAAVSDFAFASKHAEVINMGEMLPA

>d1e6ya2 d.58.31.2 (A:1002-1283) Alpha chain {Archaeon Methanosaerica barkeri}

AADIFSKFKKDMEVKFAQEFGSNKQTGGDITDKTAKFLRLGPEQDPRKVEMIKAGKEIAEKRGIAFYNPMMHS
GAPLGQRAITPYTISGTDIVCEPDDLHYVNNAAMQQMWDDIRRTCIVGLDMAHETLEKRLGKEVTPETINHYL
EVLNHAMPGAAVVQEMMVETHPALVDDCYVKVFTGDDALADEIDKQFLIDINKEFSEEQAAQIKASIGKTSW
QAIHIPTIVSRTTDGAQTSRWAAMQIGMSFISAYAMCAGEAAVADLSFAAKHAALVSMIGEMLPA

>d1hbnb2 d.58.31.2 (B:2-188) Beta chain {Archaeon Methanobacterium thermoautotrophicum}

AKFEDKVDLYDDRGNLVEEQVPLEALSPLRNPAIKSIVQGIKRTVAVNLEGIENALKTAKVGGPACKIMGRELDLD
IVGNAESIAAAKEMIQVTEDDDTNVELLGGGKRALVQVPSARFDVAEYSAAPLTATAFVQAIINEFDVSMY
DANMVKAALGRYPQSVEYMGANIATMLDIPQKLEGP

>d1e6vb2 d.58.31.2 (B:7-189) Beta chain {Archaeon Methanopyrus kandleri}

DTVDLYDDRGNCAEEVPIEVLSPMRNEAIQSIVNDIKRTVAVDLEGIENALQNATVGGKGMKIPGREMDVDIV
DNAEAIADEIEKMIRVYQDDDTNVEPMYDGKRLVQLPSERVKVMADPYSGTLQAGMAVVHAIIDVCEVDM
WDANMVKAAVFGRYPQTIDYFGGNVASMLDVPMKQEGV

>d1e6yb2 d.58.31.2 (B:2002-2185) Beta chain {Archaeon Methanosaerica barkeri}

SDTVDIYDDRGKLLESNVDIMSLAPTRNAAIQSIIIMDTKRSVAVNLAGIQGALASGKMGKGKRQILGRGLNYDI
VGNADAIAENVKKLVQVDEGDDTNVIKVGGKSLLIQSPKSRIIAGADFMSATTVGAAAVTQTIMDMFGTDPY
DAPIVKS AVWGSYPQTMDLMGGQVQGILSIPQNN EGL

>d1e8ga1 d.58.32.1 (A:274-560) Vanillyl-alcohol oxidase {Fungus (Penicillium simplicissimum)}

GGYQSYLITLPKDSDLKQAVDIIRPLRLGMALQNVPTIRHILDAAVLGDKRSYSSRTEPLSDEELDKIAKQLNLGR
WNFYGALYGPPIRRVLWETIKDAFSAPIGVKFYFPEDTPENSVLVRDCKTMQGIPTYDELKWIDWLPGNGAHF
FSPIAKVSGEDAMMQYAVTKKRCQEAGLDFIGTFTVGMREMHHIVCIVFNKKDLIQKRKVQWLMRTLIDDCA
ANGWGEYRTHLAFMDQIMETYWNWNNSFLRFNEVLKNAVDPNGIAPGKSGVWPSQYSHVTWKL

>d1diqa1 d.58.32.1 (A:243-521) Flavoprotein subunit of p-cresol methylhydroxylase {Pseudomonas putida}

PVFKPFEVIFEDADIVEIVDALRPLRMSNTIPNSVVIASTLWEAGSAHLTRAQYTTEPGHTPDSVIKQMVKDTG
MGAWNLYAALYGTQEVDVNWKIVTDVFKKLKGRIVTQEEAGDTQPFKYRAQLMSGVPLQEFGLYNWRG
GGGSMWFAPVSEARGSECKKQAAMAKRVLHKYGLDYVAEFIVAPRDMHVIDVLYDRTNPEETKRADACFNE
LLDEFKEGYAVYRVNTRFQDRVAQSYGPVKRKLEHAIKRAVDPPNILAPGRSGIDLNNDF

>d1f0xa1 d.58.32.2 (A:274-567) D-lactate dehydrogenase {Escherichia coli}

KNQQVFYIGTNQPEVLTEIRRHLANFENLPVAGEYMHDIYDIAEKYGKDTFLIDKLGTDKMPFFNLKGRTD
AMLEKVKKFRPHFTDRAMQKFGHLFPSHLPPRMKNWRDKYEHLLLKMGDGVGEAKSWLVDFKQAEGD
FFVCTPEEGSKAFLHRFAAAGAAIRYQAVHSDEVEDILALDIALRRNDTEWYEHLPEIDSQVLHKLYGHFMCY
VFHQDYIVKKGVDVHALKEQMLELLQQRGAQYPAEHNVGHLYKAPETLQKFYRENTPNSMNPNGIGKTSKRK
NW

>d1i19a1 d.58.32.3 (A:274-613) Cholesterol oxidase {Brevibacterium sterolicum}

FRQRQCQSYTDIPWRELFAPKGADGRTFEKFVAESGGAEAIWYPFTEKPWMKVWTVSPTKPDSSNEVGLGSA
GSLVGKPPQAREVSGPYNIIFSDNLPEPITDMIGAINAGNPGIAPLFGPAMYEITKLGLAATNANDIWGWSKDV
QFYIKATTLRLEGGGAVVTSRANIATVINDTEWFHERIEFYRAKGEFPLNGPVEIRCCGLDQAADVVKPSVGP
PTISATRPRPDHPDWVAIWLNLGVPGTPGMFEFYREMEQWMRSHYNNDATRPEWSKGWAFGPDPY
TDNDIVTNKMRATYIEGVPTTENWDTARARYNQIDPHRVFTNGFMDKLLP

>d1ftfa1 d.58.33.1 (A:1-148)

Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon
Methanopyrus kandleri}

MEINGVEIEDTFAEAFEAKMARVLITAASHKWAMIAVKEATGFGTSVIMCPAEAGIDCGYVPPEETPDGRPGVT
IMIGHNDEDELKEQLLDRIGQCVMTAPTAASFADAMPEAEKEDEDRVGYKLSFFGDGYQEEDELDGRKVWKIPV
V

>d1ftra2 d.58.33.1 (A:149-296) Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon
Methanopyrus kandleri}

EGEFIVEDSGITTGVAGGNFYIMAESQPAGLQAAEAAVDAIKGVEGAYAPPFGGIVASASKVGSKQYDFLPAST
NDAYCPTVEDNELPEGVKCVYEIINGLNEEAVKEMARVGIEAACQQPGVVKISAGNFGGKLGQYEIHLHDLF
>d1qd1a1 d.58.34.1 (A:2-180) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}

SQLVECPNFSEGKNQEVIDAISRAVAQTPGCVLLDVDSPSTNRTVTFVRPEDVVEGALNAARAAYQLIDM
SRHHGEHPRMGALDVCPFIPVRGVTMDECVRCAQAFGQRLAELGVPVLYGEAARTAGRQSLPALRAGEYE
ALPEKLKQAEWAPDFGPSAFVPSWGATVAGARK

>d1qd1a2 d.58.34.1 (A:181-326) Formiminotransferase domain of formiminotransferase-cyclodeaminase. {Pig (Sus scrofa)}

FLLAFNINLLSTREQAHRIALDLREQGRKDQPGRLKKVQAIGWYLDEKNLAQVSTNLLDFEVTLHHTVFEETCR
EAQEELSPVVGSQLVGLVPLKALLDAAAFYCEKENLFLLQDEHRIRLVNVNRGLDSLAPFKPKERIIYLV
>d1dj0a1 d.58.35.1 (A:7-114) Pseudouridine synthase I {Escherichia coli}

PPVYKIALGIEYDGSKYYGWQRQNEVRSVQEKLEKALSQVANEPIVFCAGRTDAGVHGTGQVVFETTALRK
DAAWTLGVNANLPGDIAVRWVKTPDDFHARFSAT

>d1dj0a2 d.58.35.1 (A:115-270) Pseudouridine synthase I {Escherichia coli}

ARRYRYIYNHRLRPAVLSKGVTHFYEPIDAERMHRAAQCLLGENDFTSFRAVCQCSRTPWRNVMHINVTRHG
PYVVVDIKANAFVHHMVRNIVGSLMEVGAHNQPESWIAELLAKDRTLAAATAKAEGLYLVADYPDRYDLPK
PPMGPLFLAD

>d1k8wa1 d.58.35.2 (A:9-73) Pseudouridine synthase II TruB {Escherichia coli}

MDINGVLLDKPQGMSSNDALQKVKRIYNNRAGHTGALDPLATGMLPICLGEATKFSQYLLSD

>d1k8wa2 d.58.35.2 (A:74-312) Pseudouridine synthase II TruB {Escherichia coli}

KRYRVIARLGQRTDTSADGQIVEERPVTSAEQLAAALDTFRG DIEQIPSMYSALKYQGKKLYEYARQGIEVPRE
ARPITVYELLFIRHEGNELELEIHCSKGTYIRTIIDDLGEKLGCGAHVIYLRLAVSKYPVERMVTLEHLRELVEQAE
QQDIPAAELLDPLMPMDSPASDYPVVNLPLTSSVYFKNGNPVRTSGAPLEGIVRVTEGENGKFIGMGEIDDEG
RVAPRRLVVEY

>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}

IGWVKGIDDNWHLTLFIENGRILDYPARPLKTGLLEIAKIHKGDFRITANQNLIIAGVPESEKAKIEKIAKESGLMN
AVT

>d1bxya_d.59.1.1 (A:) Prokaryotic ribosomal protein L30 {Thermus thermophilus}

MPRLKVKLVSPIGYPKDQKAALKALGLRRLQQERVLEDTPAIRGNVEKVAHLVRVEVVE

>d1jj2v_d.59.1.1 (V:) Archaeal L30 (L30a) {Archaeon Haloarcula marismortui}

MHALVQLRGEVNMHTDIQDTLEMLNIHHVNHC TLV PETDAYRGMVAKVNDFAFGEPSQETLETVLATRAEP
LEGDADVDDEWVAEHTDYDDISGLAFALLSEETTLREQGLSPTLRLHPPRGGHGDGVKHPVKEGGQLGKHDT EG
IDDLLEAMR

>d1fw9a_d.190.1.1 (A:) Chorismate lyase {Escherichia coli}
SHPALTQLRALRYSKEIPALDPQLLDWLLEDSMTKRFEQQGKTVSVMIREGFVEQNEIPEELPLPKESRYWLR
EILLSADGEPWLAGRTVVPVSTLGPALQKLKGKPLGRYLFTSSTLTRDFIEIGRDAGLWGRRSRLLSGKPLLL
TEFLPASPLY

>d1bowa_d.60.1.1 (A:) Multidrug-binding domain of transcription activator BmrR {Bacillus subtilis}
RLGEVFVLDEEEIRIIQTEAEGIGPENVLNASYSKLKKFIESADGFTNNSYGATFSFQPYTSIDEMTYRHIFTPVLTN
KQISSITPDMEITTIPKGRYACIAYNFSPEHYFLNLQKLKYIADRQLTVVSDVYELIIPHYSPKKQEEYRVERMIRIL

>d1d5ya3 d.60.1.2 (A:122-294) Rob transcription factor, C-terminal domain {Escherichia coli}
EFTMPEHKFVTLEDTPLIGVTQSYCSLEQISDFRHFMRYQFWHDFLGNAPTPVLYGLNETRPSQDKDDEQE
VFYTTALAQDQADGYVLTGHPVMLQGGEYVMFTYEGLGTGVQEFILTIVYGTCPMLNLTRRKQGQDIERYYPAE
DAKAGDRPINLRCELLIPIRRKLAAC

>d1jh6a_d.61.1.1 (A:) tRNA splicing product Apprp cyclic nucleotide phosphodiesterase {Thale cress (Arabidopsis thaliana)}

MEEVKKDVSVAWLPDEESEPRFKLMEALRSEFTGPRFVPHVTAVSAYLTADAEAKMFESACDGLKAYTATV
DRVSTGTFFFQCVFLLQTTPEVMEAGEHCKNHFCNTTPYMPHLSLLYAELEEEKKNAQEKA YTLDSL DGL
SFRLNRLALCKTDTEDKTLETWETVAVCNLNP

>d1f32a_d.62.1.1 (A:) Pepsin inhibitor-3 {Pig roundworm (Ascaris suum)}

FLFSMSTGPFI CTVKDNQVFVANLPWTMLEGDDIQVGKEFAARVEDCTNVKHDMAPTCTKPPFCGPQDMK
MFNFVGCSVGNKLFIDQKYVRDLTAKDHAEVQTFREKIAAFEEQQENQPPSSGMHGAVPAGGLSPPPPSF
CTV

>d1d8ia_d.63.1.1 (A:) mRNA triphosphatase CET1 {Baker's yeast (Saccharomyces cerevisiae)}

HMYRNVPWAQWKPTIKALQSINVKDLKIDPSFLNIIPDDDLTKSVQDWVYATIY SIAPELRSFIELEMKFGVIID
AKGPDRVNPPVSSQCVFTELDAHLTPNIDASLFKELSKYIRGISEVTENTGKFSIIESQTRDSVYRVGLSTQRPRFLR
MSTDIKTGRVGQFIEKRHVAQLLYSPKDSYDVKISLNLELPVDPNDPPEKYKSQSPISERTKDRVSYIHNDSCTRI
DITKVENHNQNSKSRQSETTHEVELEINTPALLNAFDNITNDSKEYASLIRTFLNNGTIIRRKLSSLSY

>d2if1_d.64.1.1 (-) Eukaryotic translation initiation factor eIF-1 (SUI1) {Human (Homo sapiens)}

MRGSHHHHHHTDPMMSAIQNLHSFDPFADASKGDDLLPAGTEDYIHIRIQQRNGRKTLLTVQGIADDYDKKKLV
KAFKKKFA CNGTVIEHPEYGEVIQLQGDQRKNICQFLVEIGLAKDDQLKVHGF

>d1d1ra_d.64.1.1 (A:) YciH {Escherichia coli}

KGDGVVRIQRQTSGRKKGKVCLITGVDLDDAELTKLAAELKKKCGCGAVKDGVIEIQGDKRDLLKSLLEAKGM
KVLAGGLE

>d1lbu_2_d.65.1.1 (84-213) Zn2+ DD-carboxypeptidase, C-terminal, catalytic domain {Streptomyces albus G}

VNFTYAEURNRCNSDWGGKVSAA TARANALVTMWKLQAMRH AMGDKPITVNGGFRSVCNSNVGGASNS
RHYMGHAADLGAGSQGF CALAQ AARNHGFTEILGPYGPYHNDHTHVAGGDGRFW SAPSCGI

>d1vh__d.65.1.2 (-) Sonic hedgehog {Mouse (Mus musculus)}

KLTPPLAYKQFIPNVAEKTLGASGRYEGKITRN SERFKE LTPNYPDII FKDEENTGADRLMTQRCKDKLNAL AISV
MNQWPGVKLRVTEGWD EDGH HSEESLHYEGRAVDITTS DRDR SKYGM LARL AVEAGFDWVYYE SKAH IHC S
VKAEN SVA AK

>d1qf6a2_d.66.1.1 (A:2-62) Threonyl-tRNA synthetase (ThrRS), N-terminal 'additional' domain {Escherichia coli}

PVITLPDGSQRHYDH AVSPMDVAL DIGPLAKACIAGR VNGELVDACDLIENDAQLSIITA

>d1fjgd_d.66.1.2 (D:) Ribosomal protein S4 {Thermus thermophilus}

GRYIGPVCRLCRREGVKLYLKGERCYS PKCAMERRPYPPGQHGQKRARRPSDYAVRLREKQKLRRIGISERQFR
NLFEEASKKGVTGSVFLGLLESRLDNVVYRLGFAVSRRQARQLVRHGHITVNGRRVDLPSYRVRPGDEIAVAEK
SRNLELIRQNLEAMKGRKVGWPWLSDVEGMKGKFLRLPDREDLALPVQENLVIEFYSR
>d1c06a_ d.66.1.2 (A:) Ribosomal protein S4 {Bacillus stearothermophilus}
MKLSEYGLQLQEKKQKLRHYGVNERQFRKTFFEEAGKMPGKHGENFMILLESRLDNLVYRLGLARTRRQARQL
VTHGHILVDGSRVNIPSYRVKPGQTIAVREKSRLQVIKEALEANNYIPDYLSDPEKMEGTYTRLPERSELPAEIN
EALIVEFYSR
>d1dm9a_ d.66.1.3 (A:) Heat shock protein 15 kD {Escherichia coli}
PAVEVRLDKWLWAARFYKTRALAREMIEGGKVHYNGQRSKPSKIVELNATLRLQGNDERTVIVKAITEQRRPA
SEAALLYEETAESVEKREKMLARKLNALT
>d1qf6a3 d.67.1.1 (A:63-241) Threonyl-tRNA synthetase (ThrRS), second 'additional' domain
{Escherichia coli}
KDEEGLEIIRHSCAHLLGHAIKQLWPHTKMAIGPVIDNGFYYDVLDRTLTQEDVEALEKRMHELAEKNYDVIKK
KVSWHEARETFANRGESYKVSILDENIAHDDKPGLYFHEEYVDMCRGPHVPNMRFCHHFKLMKTAGAYWRG
DSNNKMLQRIYGTAWADKKALNAYLQRLEAAK
>d1f7ua3 d.67.2.1 (A:2-135) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional'
domain {Baker's yeast (Saccharomyces cerevisiae)}
ASTANMISQLKKLSIAEPAVAKDSHPDVNIVDLMRNYISQELSKISGVDSLIFPALEWTNTMERGDLLIPRRLI
KGANPKDLAVQWAEKFPCGDFLEKVEANGPFIQFFFNPQFLAKLVIPDILTRKEDYG
>d1iq0a3 d.67.2.1 (A:1-96) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional'
domain {Thermus thermophilus}
MLRRALEEAIAQALKEMGVPVRLKVARAPKDKPGDYGVPLFALAKELRKPPQAIQELKDRPLPEFVEEAVPV
GGYLNFRRLTEALLREALRPKA
>d1dd5a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermotoga maritima}
VNPFIKEAKEKMKTLEKIEDELRMRTGKPSPAILEEIKVDYYGVPTPVNQLATISISEERTLVIKPWDKSVLSIEK
AINASDLGLNPINDGNVIRLVFPSPTEQREKWKKAKEIVEEGKIAIRNIRREILKKIKEDQKEGLIPEDDAKRLEN
EIQKLTDEFIEKLDEVFEIKKEEIMEF
>d1eh1a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Thermus thermophilus}
MTLKELYAE TRSHMQKSLEVLEHNLAGLRTGRANPALLHLKVEYYGAHVPLNQIATVTAPDPRTL VVQSWDQ
NALKAIEKAIRDSDLGLNPNNSNKGDALYINIPPLTEERRKDLVRAVRQYAEGRVAIRNIRREALDKLKLAKELHLSE
DETKRAAEIQKITDEFIAKADQLAEKKEQEI LG
>d1ek8a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Escherichia coli}
MISDIRKDAEV RMDKCVEAFKTQISKIRTGRASPSSL D GIVVEYYGTPTPLRQLASVTVEDRTL KINV FDRSMSP
AVEKAIMASDLGLNPN SAGSDIRVPLPPLTEERRKDLT KIVGEAEQARVA VRNVR RDANDKV KALLKDKEI SED
DDRRSQDDVQKLTDAAIKKIEAALADKEAELMQF
>d1ge9a_ d.67.3.1 (A:) Ribosome recycling factor, RRF {Aequifex aeolicus}
MIKELEDIFKEAEKDMKKAVEYYKNEIAGLRTS RASTALV EEEIKVEYYGSKVPIKQLGTISVPEHNQIVIQVWDQN
AVPAIEKAIREELNLP TVQGNVIRV TLPLTEERRREL VRL LH KITEEAR VVRNVR REAKEMIEELEGISEDEKKR
ALERLQK LTD KYIDEINKLMEA KEKEIMS V
>d1j98a_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Bacillus subtilis}
VESFELDHNAVVAPYVRHCGVHKVGTG VVNKFDIRFCQPNKQAMK PDTIHTLEHLLAFTIRSHA EKYDHFDII
DISPMGCQTGYYL VVSGETTS A E IVDL LEDTM K EA VEITEIPA ANE K QCG QAKL HDLEGAKR LMR FWLS QDKEE
LLK VFG
>d1inna_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Deinococcus}

radiodurans}

NVESFDLDHTKVKAPYVRLAGVKTPKGDQISKYDLRFLQPNQGAIDPAIHTLEHLLAGYMRDHLEGVVVDVSP
MGCRTGMYMAVIGEPDEQGVMKAFAEALKDTAGHDQPIPGVSELECGNYRDHDLAAARQHARDVLDQGLK
VQETILL

>d1j6wa_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Haemophilus influenzae}

LLDSFKVDHTKMNAPAVRIAKTMLTPKGDNITVFDLRCIPNKEILSPKGIHTLEHLFAGFMRDHNGDSIEIIDIS
PMGCRTGFYMSLIGTPNEQKVSEAWLASMQDVLGVQDQASIPELNIYQCGSYTEHSLEDAHEIAKNVIARGIG
VNKNEDLSLDN

>d1j6xa_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Helicobacter pylori}
MKMNVESFNLDHTKVKAPYVRIADRKKGVNGDLIVKYDVRFKQPQRDHMDMPSLHSLEHLVAEIIRNHANYV
VDWSPMGCQTGFYLTVLNHDNYTEILEVLEKTMQDVLKAKEVPASNEKQCGWAANHTLEGAQNLARAFLDK
RAEWSEVG

>d1hr6b1 d.185.1.1 (B:24-245) Mitochondrial processing peptidase (MPP) beta chain {Baker's yeast (Saccharomyces cerevisiae)}

PGTRTSKLPNGLTIATEYIPNTSSATVGIFVADGSRAENVKNNGTAHFLEHLAFKGTQNRPQQGIELEIENIGSHL
NAYTSRENTVYYAKSLQEDIPKAVDILSDILTKSVDNSAIERERDVIRESEEVDKMYDEVVFDDHLHEITYKDQPL
GRТИLPIKNIKSITRTDLKDYITKNYKGDRMVLAGAGAVDHEKLVQYAQKYFGHVPKSESPVPLGSPR

>d1hr6b2 d.185.1.1 (B:246-462) Mitochondrial processing peptidase (MPP) beta chain {Baker's yeast (Saccharomyces cerevisiae)}

GPLPVFCRGERFIKENTLPTTHIAIALEGVSWSAPDYFVALATQAIVGNWDRAIGTGTNSPSPLAVAASQNGSLA
NSYMSFSTSYYADSGLGMYIVTDSNEHNVRLLVNEILKEWKRIKSGKISDAEVNRAKAQLKAALLSLDGSTAIV
EDIGRQVVTGKRSLPEEVFEQVDKITKDDIIMWANYRLQNKPVSMVALGNTSTPNVSYIEEKLNO

>d1hr6a1 d.185.1.1 (A:14-233) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}

ARTDNFKLSSLANGLKVATSNTPGHFSALGLYIDAGSRFEGRNLKGCTHILDRLAFKSTEHVEGRAMAETLELLG
GNYQCTSSRENLMYQASVFNQDVKGMLQLMSETVRFPKITEQELQEQQKLSAEYEIDEVWMKPELVLPELLHTA
AYSGETLGSPLICPRGLIPSISKYLLDYRNKFYTPENTVAAFVGVPHEKALELTGKYLGDWQSTHPPITKK

>d1hr6a2 d.185.1.1 (A:234-470) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}

VAQYTGGESCIAPPVFGNLPELFHIQIGFEGLPIDHPDIYALATLQTLLGGGSFSAGGPGKGMSRLYTHVLNQ
YYFVENCVAFNHSYSDSGIFGISLSCIPQAQPAVEVIAQQMYNTFANKDLRLTEDEVSRAKNQLKSSLLMNLES
KLVELEDMGRQVLMHGRKIPVNEMISKIEDLKPDDISRVAEMIFTGNVNNAGNGKGRATVVMQGDRGSFGD
VENVLKAYGLGNSSS

>d1be3a1 d.185.1.1 (A:1-233) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}

TATYAQALQSVPETQVSQLDNGLRVASEQSSQPTCTVGWIDAGSRYESEKNNNGAGYFVEHLAFKGTKNRPGN
ALEKEVESMG AHLNAYSTREHTAYYIKALSKDLPKAVELLADIVQNCSEDSQIEKERDVLQELQENDTSMRDV
VFNYLHATAFQGTPLAQSVGPSENVRKLSRADLTEYLSRHYKAPRMVLAAGGLEHRQLLDAQKHFGSGSGT
YDEDAVPTLSP

>d1be3a2 d.185.1.1 (A:234-446) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}

CRFTGSQICHREDGLPLAHVIAVEGPGWAHPDNVALQVANAIIGHDCTYGGGAHLSSPLASIAATNKLCSF
QTFNICYADTGLLGAHFVCDHMSIDDMMFVLQQWMRLCTSATESEVLRGKNNRLNALVSHLDGTPVCEDI
GRSLLTGRRRIPLAEWESRIAEVNDARVREVC SKYFYDQCPAVAGFGPIEQLPDYNRIRSGMFWLRF

>d1bcc1 d.185.1.1 (A:4-232) Cytochrome bc1 core subunit 1 {Chicken (Gallus gallus)}

YAQALQSVPETQVSQLDNGVRVASEQSSQPTCTGVWIDAGSRYESEKNNGAGYFLEHLAFGKTKNRPQNAL
EKEVESMGAHNLAYSSREHTAYYIKALSKDVPKAELLADIVQNCSEDSQIEKERDVIVRELQENDSMREVVF
NYLHATAFGQTGLAQSVEGPSENIRKLSRADLTEYLSTHYTAPRMVLAAAGGVEHQQLLEAQKHFGGPFTYD
DDAVPTLS

>d1bcc2 d.185.1.1 (A:233-445) Cytochrome bc1 core subunit 1 {Chicken (Gallus gallus)}
KCRFTGSQIRHREDGLPLAHVIAVEGPGWAHPDLVALQVANAIIGHDRYGGGLHSSPLASIAVTNKLQSF
QTFSICYSETGLFGFYFCDRMSIDDMMFVLQGQWMRLCTSISESEVLRGKNFLRNALSHLDGTPVCEDIGR
ELLTYGRRIPPLEEWEERLAEVDARMVREVC SKYIYDQCPAVAGPGPIEQLPDYNRIRSGMFWLR

>d1ezva1 d.185.1.1 (A:27-239) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}

AEVTQLSNGIVVATEHNPAHTASGVVFGSGAANENPYNNGVSNLWKNIFLSKENSAVA
AKEGLALSSNISRDF
QSYIVSSLPGSTDKSLDFLNQSFIQQQKANLLSSNFEATKKSVLKQVQDFEDNDHPNRVLEHLHSTA
FQNTPLSLP
TRGTLESLENLVADLESFANNHFLNSNAVVG TGNIKHEDLVNSIESKNLSQLTGTPV
VLKK

>d1ezva2 d.185.1.1 (A:240-456) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}

KAAFLGSEVRLRDDTLPKAWISLAVEGE PVNSPNYFVA KLAQIFGSYNAFEPASRLQGIKLLDNIQEYQLCDNF
NHFSLSYKDSGLWGFSTATR NVTMIDDLIHFTLKQWNRLTISVTDTEVERAKSLLKLQLGQLYESGNPVNDANLL
GAEVLIKGSKLSLGEAFKKIDAITVKDVKA WAGKRLWDQDIAIGTQIEGLDYMRIRS DMSMMRW

>d1be3b1 d.185.1.1 (B:21-235) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}

PQDLEFTRLP NGLVIASLE NYAPASRIGLFKIAGSRYENS NNLGTSH LRLASSLT KGASSFKITRGIEAVGGKLSVT
STREN MAYTVECL RDDV DILME FLLNVTTAPE FRRWEVA ALQPQLRIDKA VALQNPQA HVIENL HAA YRN
ANS LYCPD YRIGKV TPVELHDYV QNHFTSAR MALI GLGV SHPV LKQVA E QFLN IRGG LLSGA

>d1be3b2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Cow (Bos taurus)}

KAKYHG GEIREQNGDSL VHA ALVA E SAA IGS A EAN AF SVLQH VLGAG PHVK RGSN ATSS LYQAVAKGVH QPFD
VSA FN ASYSDS GLFG FYT ISQ AAS AGD VIK AAYN QVKTIA QGNL SNP DVQ AAKN KL KAG YL MSV ESEG FLDEV
GSQ ALAAG SYTP P STV LQQ IDA VAD ADVINA AAKF VSG RKSMA AS GNL GH TPF IDEL

>d1bccb1 d.185.1.1 (B:18-235) Cytochrome bc1 core subunit 2 {Chicken (Gallus gallus)}

PPHPQD LEITKLP NGLVIASLE NYSPG STIGV FIKAG SRYEN SS NLGT SH LRLASS LT KGASS FKITRGIEAVGGK
L SVE STREN MAYTVECL RDDV EILME FLLNVTTAPE FRPWEVADLQPQLKIDKA VAFQNPQ THVIENL HAA YRN
ALADSLYCPD YRIGKV TS VELHD FV QNHFTSAR MALV GLGV SHPV LKVN VAE QLLN IRGG LLSGA

>d1bccb2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Chicken (Gallus gallus)}

KAKYRG GEIREQNGDSL VHA A IV A E SAA IGG AE AN AF SVLQH VLGAG PHVK RGLN ATSS LYQAVAKGVH QPFD
VSA FN ASYSDS GLFG FYT ISQ AAYAG QV IK AAYN QVKTIA QGNV SN ENV QAA KN KL KAG YL MSV ESEG FLEE V
GSQ ALAAG SYNP P STV LQQ IDA VAD ADVINA AAKF VSR QKSMA AS GNL GH TPF VDEL

>d1ezvb1 d.185.1.1 (B:17-218) Cytochrome bc1 core subunit 2 {Baker's yeast (Saccharomyces cerevisiae)}

LTV SARDAP TKISTL AVK VHGG SRYATKD GV AHLL NRNF QNTN TRSALK LVRE SELL GGT FKST LDREY ITL KATF
LKDD LPYY VN ALAD VL YKTA FKPH ELTE SVLP AARY DYAVA E QCPV KSMA EDQ LYAITFRKG LGNPL LYDG VERV SL
QDI KDFAD KV YT KEN LEV SGEN VVEADLK RFV DESL LSTL PAGK SLSK

>d1ezvb2 d.185.1.1 (B:219-368) Cytochrome bc1 core subunit 2 {Baker's yeast (Saccharomyces cerevisiae)}

SEPKFFLGEENRVRFIGDSVAAIGIPVNKASLAQYEVLANLYTSALSELSGLISSAKLDKFTDGLFTLFVRDQDSA
VVSSNIKKIVADLKKGDLS PAIN YTKL NAVQNESVSSPIELNFD AVKDFKL GFNY VAVGDVSNLPYLDL

>d1tig_ d.68.1.1 (-) Translation initiation factor IF3, C-terminal domain {Bacillus}

stearothermophilus}

INVKEVRLSPTIEEHDFNTKLRNARKFLEKGDKVKATIRFKGRAITHKEIGQRVLDRLEACADIAVVETAPKMDGRNMFLVLAPKND

>d2ifea_d.68.1.1 (A:) Translation initiation factor IF3, C-terminal domain {Escherichia coli}

VIQVKIKEIKFRPGTDEGDYQVKLRSILRFLEEGDKAKITLFRGREMAHQHQIGMEVLRVKDDLQELAVVESFPTKIEGRQMIMVLAPKKQ

>d1i96v_d.68.1.1 (V:) Translation initiation factor IF3, C-terminal domain {Thermus thermophilus}

EVKSIKFRVKIDEHDYQTKLGHIKRFLQEGHKVKVTIMFRGREVAHPELGERILNRVTEDLKDLAVVEMKPEMLGRDMNMillAPVK

>d1dcja_d.68.3.1 (A:) SirA {Escherichia coli}

MTDLFSSPDHTLDALGLRCPEPVMMVRKTVRNMQPGETLLIADDPATTRDIPGFCTFMEHELVAKETDGLPYRYLIRKG

>d1jdqa_d.68.3.2 (A:) Hypothetical protein TM0983 {Thermotoga maritima}

GSSHHHHHSSGLVPRGSHMAKYQVTKTLDVRGEVCVPDVETKRALQNMKPGEILEVWIDYPMSKERIPETVKLGHEVLEIEVGPSWKEIYIKV

>d1qmha2_d.68.2.1 (A:5-184,A:280-338) RNA 3'-terminal phosphate cyclase, RPTC {Escherichia coli}

MIALDGAQGEGGGQILRSALSMTGQPFTISRAGRAKPGLLRQHLTAVKAATEICGATVEGAELGSQRLLFRPGTVRGGDYRFAIGSAGSCTLVLTQTVLPALWFADGPSRVEVSGGTDNPSAPPADFIRRVLPLAKIGIHQQTTLLRHGFYPAGGGVVATEVSPVASFNTLQLGXAVGEYLADQLVLPMALAGAGEFTVAHPSCHLLTNIAVVERFLPVRFSLIETDGTRVSI

>d1uae_d.68.2.2 (-) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT, MurA, MurZ) {Escherichia coli}

MDKFRVQGPTRKLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDVTSMKLLSQLGAKVERNGSVHIDARDVNVCAPYDLVKTMRASIWLGPLVARFGQGVSLPGGCTIGARPVDLHISGLEQLGATIKLEEGYVKASVDGRLGKGAHVMDKVSGATVTIMCAATLAEGTTIENAAREPEIVDTANFLITLGAKISGQGTDRIVIEGVERLGGGVYRVLPDRIETGTLVAAAISRGKIIICRNAQPDTLDAVLAKLRDAGADIEVGEDWISLDMHGKRPKAVNVRTAPHPAFTDMQAQFTLLNLVAEGTGFITETVFENRFMHVPELSRMGAHAEIESNTVICHGVEKLSGAQVMATDLRASSALVLAGCIAEGTTVVDRYHIDRGYERIEDKLRALGANIERVKG

>d1ejda_d.68.2.2 (A:) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT, MurA, MurZ) {Enterobacter cloacae}

MDKFRVQGPTRKLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLTQLGTKVERXGSVWIDASNVNNSFAPYDLVKTMRASIWLGPLVARFGQGVSLPGGCAIGARPVDLHIFGLEKLGAEIKLEEGYVKASVNGRLGKGAHVMDKVSGATVTIMSAATLAEGTTIENAAREPEIVDTANFLVALGAKISGQGTDRIТИEGVERLGGGVYRVLPDRIETGTLVAAAISGGKIVCRNAQPDTLDAVLAKLREAGADIEVGEDWISLDMHGKRPKAVTAPPHAFPTDMQAQFTLLNLVAEGTGFITETVFENRFMHVPELSRMGAHAEIESNTVICHGVEKLSGAQVMATDLRASSLVLAGCIAEGTTVVDRYHIDRGYERIEDKLRALGANIERVKG

>d1g6sa_d.68.2.2 (A:) 5-enol-pyruvyl shikimate-3-phosphate(EPSP) synthase {Escherichia coli}

MESLTQPIARVDTINLPGSKSVSNRALLAALAHGKTVLTNLLSDDVHRMLNALTALGVSYTLSADRTRCEIIGNGGPLHAEGALEFLGNAGTAMRPLAAALCLGSNDIVTGEPRMKERPIGHLVDALRGGAKITYLEQENYPPRLQGGFTGGNVVDGSVSSQFLTALLMTAPADETVIRIKGDLVSKPYIDITLNLMKTFGVEIENQHYQQFVVKGGQSYSPGTYLVEGDASSASYFLAAAIAKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDYISCTR GELNAIDMDMNHIPDAAMTIATAALFAKGTTLRNIYNWRVKETDRLFAMATELRKVGAEEVEEGHDYIRTPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILDPKCTAKTFPDYFEQLARISQAA

>d1imua_ d.204.1.1 (A:) Ribosome binding protein Y (HI0257, YfiA homologue) {Haemophilus influenzae}
MTLNITSKQMDITPAIREHLEERLAKLGKWQTQLISPHFVLNKVPNGFSVEASIGTPLGNLLASATSDDMYKAIN
EVEEKLERQLNKLQHKSESRRADERLKDSFEN

>d1tola2 d.69.1.1 (A:125-216) C-terminal domain of TolA {Escherichia coli}
SGADINNYAGQIKSAIESKFYDASSYAGKTCTLRIKLAPDGMLDIKPEGGDPALCQAALAAKLA
KIPKPPSQAVYEVFKNAPLDKFKA

>d1kpta_ d.70.1.1 (A:) Virally encoded KP4 toxin {Ustilago maydis, P4 strain}
LGINCRGSSQCGLSGGNLMVRIRDQACGNQGQTWCPGERRAKVCGTGN
SISAYQSTNNCISGTEACRHTN
LVNHGCRVC
GSDPLYAGNDVSRGQLTVNYVNSC

>g1kve.1 d.70.1.2 (A.;B:) SMK toxin {Halotolerant yeast (Pichia farinosa)}
WSLRWRM
QKSTTIAAIAGCSAATFGLAGGIVGCIAAGILAILQGF
EVNW
HNGGGGD
RSNPVXGEATTIWG
VGA
DEA
IDKG
TPSKNDL
QNMSADL
AKNGFKGHQGV
ACSTV
KDGNKD
DVYMIK
FSLAGGS
NDPGGSPCSDD

>d1ev0a_ d.71.1.1 (A:) Cell division protein MinE topological specificity domain {Escherichia coli}
RSDAEPHYLPQLRK
DILEVICKYV
QIDPEM
MTV
QLEQ
KDG
DISILE
LN
VTL
PEAEELK

>d1dw9a2 d.72.1.1 (A:87-156) Cyanase C-terminal domain {Escherichia coli}
RIPTDPT
MYRFY
EMLQV
YGT
TLK
ALV
HEK
FGD
GIIS
AIN
FKL
DV
KKV
AD
PEG
GER
AVIT
LDG
KYL
PTKPF

>d3rubs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Tobacco (Nicotiana tabacum), variant turkish samsun}
MQVWP
PINK
KKY
ETLS
YLP
DL
SQ
EQ
LL
SE
VE
YLL
KNG
W
VPC
CLE
FETE
HGF
V
RENN
KSP
GYY
DGRY
WTM
WKL
PMFG
CT
DAT
QV
LAE
VEE
AKK
AYP
QAW
IRI
IGFD
NVR
QC
ISFI
AYK
PEGY

>d1burs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}
MQVWP
ILGM
KKY
ETLS
YL
P
L
T
TE
QL
LA
EV
NY
LL
V
NN
W
I
P
C
LE
FE
VK
DGF
V
Y
RE
HL
KSP
GYY
DGRY
WTM
WKL
MFG
CT
DPA
QV
LNE
EE
CK
AY
P
DA
F
IRI
IGFD
NKR
QV
QC
ISFI
AYK
PAGY

>d8ruci_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Spinach (Spinacia oleracea)}
MQVWP
ILNL
KKY
ETLS
YL
P
L
T
TD
QL
ARQ
V
DY
LL
NN
K
W
V
PC
CLE
FETD
HGF
V
Y
REHH
NSP
GYY
DGRY
WTM
WK
LPMFG
CT
DPA
QV
LNE
EE
CK
KEY
PNA
F
IRI
IGFD
SN
REV
QC
ISFI
AYK
PAGY

>d1bwvs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}
VRITQ
GTFS
FLPD
LTDE
QIK
KQ
IDY
MIS
KK
LA
IG
IE
YT
NDI
H
PR
N
AY
WE
IW
GL
PL
FD
VT
DPA
AVL
FE
INAC
RK
ARS
FY
IK
VV
GF
SS
VR
GI
EST
I
IS
F
IV
NRP
K
HE
PG
F
NL
MR
QED
KS
RS
I
KY
T
HSY
SY
KP
ED
ERY

>d1gk8i_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}
MVWTP
VNN
KMF
ETFS
YL
P
PL
T
DE
QIA
AQ
V
DY
I
V
ANG
W
I
P
C
LE
FA
E
AD
K
AY
V
S
NE
A
IR
FG
SV
CL
Y
DN
RY
WT
MW
KL
PM
FG
CR
DP
MQ
V
L
R
E
I
V
ACT
KAF
P
DAY
V
RL
V
AF
DN
Q
K
Q
V
IM
G
FL
V
Q
R

>d1bxni_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Alcaligenes eutrophus}
MRITQ
GTFS
FLPE
LTDE
QIT
KQ
LEY
CL
NQ
G
WA
VG
LEY
T
DD
PH
P
R
NT
Y
WE
M
F
GL
PM
FD
LR
DA
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NAR
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FP
NHY
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>d1rbIm_ d.73.1.1 (M:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Synechococcus sp., strain pcc 6301}

SMKTLPKERRFETFSYLPPLSDRQIAAQIEYMIEQGFHPLIEFNEHSNPEEFYWTMWKLPLFACAAPQQVLDEV
RECRSEYGDCYIRVAGFDNIKECQTSSFIVHRPGR

>d1dcpa_ d.74.1.1 (A:) Pterin-4a-carbinolamine dehydratase (PCD)/dimerization cofactor of HNF1 (DCoH) {Rat (Rattus norvegicus)}

HRLSAEERDQLLPNLRAVGWNELEGRAFKQFHFKDFNRAFGFMTRVALQAEKLDHHPEWFNVYNKVHITL
STHECAGLSERDINLASFIEQVAVSMT

>d1xxaa_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Escherichia coli}
LKNLVLDIDYNDAVVIHTSPGAAQLIARLLDSLGAEGILGTIAGDDTIFTTPANGFTVKDLYEAILEFT

>d1b4ba_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Bacillus stearothermophilus}

ALVDVFIKLDGTGNLLVLRTLPGNAHAIGVLLDNLDWDEIVGTICGDDTCIICRTPKDAKKVSNQLLSML

>d1f9na2 d.74.2.1 (A:79-149) C-terminal domain of arginine repressor {Bacillus subtilis}

ALMDAFVKIDSASHMIVLKTMMPGNAQAIGALMDNLDWDEMMGTCGDDTIIICRTPEDTEGVKNRLLELL

>d1i50k_ d.74.3.2 (K:) RPB11 {Baker's yeast (Saccharomyces cerevisiae)}

MNAPDRFELFLGEGESKLKDPPDKAPNAVITFEKEDHTLGNLIRAELLNDRKVLFAAYKVEHPFFARFKLRIQT
TEGYDPKDALKNACNSIINKLGALKTNFETEWNLQTL

>d1bdfa1 d.74.3.1 (A:2-52,A:179-232) RNA polymerase alpha {Escherichia coli}
QGSVTEFLKPRLVDIEQVSSTHAKVTLEPLERGFHTGNPLRRILLSSIPXPVRRVAFQVEDTRLGQRTDLDKLT
IEMETNGTIDPEEAIRRAATILAELQLEAFV

>d1i6va1 d.74.3.1 (A:6-49,A:173-229) RNA polymerase alpha {Thermus aquaticus}

LKAPVFTATTQGDHYGEFVLEPLERGFVTGNPLRRILLSSIPXPVRRVAFQVEDTRLGQRTDLDKLT
SVTPLEALNQAVAILKEHLNYFANPE

>d1i50c1 d.74.3.1 (C:3-41,C:173-268) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

EEGPQVKIREASKDNVDFILSNVDLAMANSLRRVMIAEIXAAAIEFYDPWNKLKHTDYWYEQDSAKEWPQS
KNCEYEDPPNEGDPFDYKAQADTFYMNVESVGSIPVDQVVVRGIDTLQKKVASILLALTQMDQD

>d1c0aa2 d.74.4.1 (A:288-420) Prokaryotic AspRS, insert domain {Escherichia coli}

NPMELTDVADLLKSVEFAVFAGPANDPKGRVAALRVPGGASLTRKQIDEYGNFVKIYGAKGLAYIKVNERAKGLE
GINS PVAKFLNAEIIDILDRTAAQDGDMIFFGADNKIVADAMGALRLKVGKDLGLT

>d1g51a2 d.74.4.1 (A:295-414) Prokaryotic AspRS, insert domain {Thermus thermophilus}

FGLELKEVGPLFRQSGFRVFQEAESVKALALPKALSRKVAELEEVAKRHKAQGLAWARVEEGGFSGGVAKFLE
PVREALLQATEARPGDTLLFVAGPRKVAATALGAVRLRAADLLGLK

>d1a79a2 d.75.1.1 (A:9-82) tRNA splicing endonuclease EdnA, N-terminal domain {Archaeon Methanococcus jannaschii}

KITGLLDGDRVIVFDKNGISKLSARHYGNVEGNFLSLVEALYLINLGWLEVKYKDNKPLSFEELYARNVE

>d1ewqa4 d.75.2.1 (A:1-120) DNA repair protein MutS, domain I {Thermus aquaticus}

MEGMLKGEGPGPLPPLLQQYVELRDQYPDYLLLQVGDFYECFGEDAERLARALGLVTHKTSKDFTTPMAGIP
LRAFEAYAERLLKMGFRLAVADQVEPAEEAEGLVRREVTQLLPGT

>d1e3ma4 d.75.2.1 (A:2-116) DNA repair protein MutS, domain I {Escherichia coli}

SAIENFDAHTPMMQQYRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPIPMAGIPYHA
VENYLAKLVNQGESVAICEQIGDPATSKGPVERKVVRIVTP

>d1e3mb4 d.75.2.1 (B:14-116) DNA repair protein MutS, domain I {Escherichia coli}

MQQYLRKKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPIPMAGIPYHAVENYLAKLVNQG

ESVAICEQIGDPATSKGPVERKVVRIVTP
>d1gyfa_ d.76.1.1 (A:) GYF domain from cd2bp2 protein {Human (Homo sapiens)}
DVMWEYKWENTGDAELYGPFSAQMQTWVSEGYFPDGVYCRKLDPPGGQFYNSKRIDFDLYT
>d1jg5a_ d.205.1.1 (A:) GTP cyclohydrolase I feedback regulatory protein, GFRP {Rat (Rattus norvegicus)}
PYLLISTQIRMEVGPTMVGDEHSDPELMQQLGASKRRVLGNNFYEYYVNDPPRIVLDKLECRGFRVLSMTGVG
QTLVWCLHKE
>d1iq4a_ d.77.1.1 (A:) Ribosomal protein L5 {Bacillus stearothermophilus}
MNRLKEKYLNEVVPALMSKFNYKSIMQVPKIEKIVINMGVGDAVQNPKALDSAVEELTLIAGQRPVVTRAKKSI
AGFRLRQGMPIGAKVTLGERMYEFLDKLISVSLPRARDFRGVSKKSFDRGNYTLGIKEQLIFPEIDYDKVNKV
RGMDIVVTANTDEEARELLALLGMPFQK
>d1jj2d_ d.77.1.1 (D:) Ribosomal protein L5 {Archaeon Haloarcula marismortui}
FHEMREPRIEKVVVHMGIGHGGRDLANAEDILGEITGQMPVRTKAKRTVGEFDIREGDPIGAKVTLRDEMAEE
FLQTALPLAELATSQFDDTGNSFGVEEHTEPSQEYDPSIGIYGLDTVNLVRPGYRAKRDKASRRIPTKHRLN
PADAVAFIESTYDVE
>d1eika_ d.78.1.1 (A:) RNA polymerase subunit RPB5 (RNA polymerase subunit H) {Archaeon Methanobacterium thermoautotrophicum}
MKREILKHQLVPEHVILNESEAKRVLKELDAHPEQLPKIKTTDPVAKAIGAKRGDIVKIIRKPTAEFFVTYRLVQD
>d1hmja_ d.78.1.1 (A:) RNA polymerase subunit RPB5 (RNA polymerase subunit H) {Archaeon Methanococcus jannaschii}
PKHEIVPKEEVEEILKRYNIKIQQLPKIYEDDPVIQEIGAKEGDVVRVIRKSPTAGVSIAYRLVIKRI
>d1dzfa2 d.78.1.1 (A:144-215) Eukaryotic RPB5 C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
ITHHELVPKHIRLSSDEKRELLKRYRLKESQLPRIQRADPVALYGLKRGEVVKIIRKSETSGRYASYRICM
>d1qkla_ d.78.1.2 (A:) RPB6 {Human (Homo sapiens)}
MSDNEDNFDGDDFDDVEEDEGLDDLENAAEEGQENVEILPSGERPQANQKRITTPYMTKYERARVLGTRALQ
IAMCAPVMVELEGETDPILLIAMKELKARKIPIIIRRYPDGSYEDWGVDELIITD
>d1i50f_ d.78.1.2 (F:) RPB6 {Baker's yeast (Saccharomyces cerevisiae)}
KAIPKDQRATTPYMTKYERARILGTRALQISMNAPFVDLEGEDPARIAMKELAEKKIPLVIRRYLPDGSFEDWS
VEELIVDL
>d1qu9a_ d.79.1.1 (A:) Conserved 'hypothetical' protein Yjf {Escherichia coli}
SKTIATENAPAAIGPYVQGVDLGNMIITSGQIPVNPKTGEVPADVAQARQSLDNVKAIVEAAGLKVGDIVKTT
VFVKDLNDFATVNATYEAFFTEHNATFPARSCVEARLPKDVKIEIAIAVRR
>d1qd9a_ d.79.1.1 (A:) Purine regulatory protein YabJ {Bacillus subtilis}
TKAVHTKHAPAAIGPYSQGIIVNNMFYSSGQIPLTPSgemVNGDIKEQTHQVFSNLKAVLEEAGASFETVVKAT
VFIADMEQFAEVNEVYGQYFDTHKPARSCVEARLPKDALVEIEVIALVK
>d1jd1a_ d.79.1.1 (A:) Highdosage growth inhibitor YER057cp (YE07_YEAST)
{Baker's yeast (Saccharomyces cerevisiae)}
TTLTPVICESAPAAAASYSHAMKVNNLIFLSGQIPVTPDNKLVEGSIADKAEQVIQNIKNVLEASNSSLDRVVKVN
IFLADINHFAEFNSVYAKYFNTHKPARSCVAVAALPLGVDMEMEAIAAER
>d1dbfa_ d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}
MMIRGIRGATTVERDTEEEILQKTKQLLEIIEENHTKPEDVVQMLLSATPDLHAVFPAKAVRELSGWQYVPVTC
MQEMDVTGGLKKCIRVMMTVQTDVPQDQIRHVYLEKAVVLRPDLSLTKNTEL

>d1fnja_d.79.1.2 (A:) Chorismate mutase {Bacillus subtilis}
MIRGIRGATTVERDTEEEILQTKQLLEKIIENHTKPEDVVQMLLSATPDLHAVFPAKAVRELSGWQYVPVTCM
QEMDVVTGGLKKSIVMMTVQTDVPQDQIRHVYLEKAVVLR
>d1jy8a_d.79.5.1 (A:) 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase IspF {Escherichia coli}
MRIGHGFVDVAFGGEGPIIGGVIRPYEKLLAHSDGDVALHALTDALLGAAALGDIGKLFPTDPAFKGADSRE
LLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMRFIAEDLGCHMDDVNKAATTTEKLGFTGRGEIAC
EAVALI
>d1fsz_2 d.79.2.1 (232-356) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}
INVDFADVKAVMNNNGLAMIGIGESDSEKRAKEAVSMALNSPLLDVDIDGATGALIHVMGPEDLTLEEAREVV
ATVSSRLDPNATIIWGATIDENLENTRVVLLITGVQSRIEFTDTGLKRKKL
>d1tuba2 d.79.2.1 (A:246-440) Tubulin alpha-subunit {Pig (Sus scrofa)}
GALNVDLTFQTNLVYPYPRGHFPLATYAPVISAKEYHEQLSVAEITNACFEPANQMVKCDPRHKGKYMACCLLY
RGDVVPKDVAIAIATIKTKRTIQFVDWCPTGFVGINYEPPTVPPGGDLAKVQRAVCMLSNTTAIAEAWARLD
HKFDLMIYAKRAFVHWYVGEGMEEGFSEAREDMAALEKDYEEGVGDSV
>d1tubb2 d.79.2.1 (B:246-437) Tubulin beta-subunit {Pig (Sus scrofa)}
GQLNADLRKLAVNMVPFPRLHFFMPGFAPLTSRGSQYRALTVPELTQQMFDAKNMMMAACDPRHGRYLTV
AVFRGRMSMKEVDEQMLNVQNKNSSYFVEWIPNNVKTAVCDIPRGLKMSATFIGNSTAIQELFKRISEQFTA
MFRRKAFLHWYTGEGMDEMECTAEESNMNDLVSEYQQYQD
>d1ck9a_d.79.3.1 (A:) Eukaryotic ribosomal protein L30 (L30e) {Baker's yeast (Saccharomyces cerevisiae)}
APVKSQESINQKLAIVKSGKYTLGYKSTVKSLRQGSKLIIIAANTPVLRKSELEYYAMLSKTKVYYFQGGNNELG
TAVGKLFRVGVVSILEAGDSDLITLA
>d1jj2f_d.79.3.1 (F:) Ribosomal protein L7ae {Archaeon Haloarcula marismortui}
PVYVDFDVPADLEDDALEALEVARDTGAVKKGTNETTKSIERGSAELVFVAEDVQPEEIVMHIPELADEKGVPFIF
VEQQDDLGHAAGLEVGSAAAATDAGAAATVLEEIADKVEELR
>d1e7ka_d.79.3.1 (A:) Spliceosomal 15.5kd protein {Human (Homo sapiens)}
ADVNPKAYPLADAHLTKL禄LVQQSCNYKQLRKGANEAETKLNRGISEFIVMAADAEPLEIILHLPLLCEDKNVP
YVFVRSKQALGRACGVSRPVIACSVTIKEGSQQLQQIQQSIERLLV
>d1dt9a2 d.79.3.2 (A:277-422) C-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 {Human (Homo sapiens)}
NVKFHQEKKLIGRYFDEISQDTGKYCFGVEDTLKALEMGAVEILIVYENLDIMRYVLHCQGTEEEKILYLTPEQKD
KSHFTDKETGQEHELIESMPLLEWFANNYKKFGATLEIVTDKSQEGSQFVKGFGGIGGILRYRVDFQGM
>d1clia1 d.79.4.1 (A:5-170) Aminoimidazole ribonucleotide synthetase (PurM) N-terminal domain {Escherichia coli}
TSLSYKDAGVIDAGNALVGRIKGVVKKTRRPEVMGGLGGFGALCALPQKYREPVLVSGTDVGVTKLRLAMDL
KRHDTIGIDLVAMCVNDL禄VQGAEPLFFLDYYATGKLDVDTASAVISGIAEGCLQSGCSLVGETAEMPGMYHG
EDYDVAGFCVGVVEKSEII
>d1clib1 d.79.4.1 (B:1021-1170) Aminoimidazole ribonucleotide synthetase (PurM) N-terminal domain {Escherichia coli}
ALVGRIKGVVKKTRRPEVMGGLGGFGALCALPQKYREPVLVSGTDVGVTKLRLAMDLKRHDTIGIDLVAMCVN
DLVVQGAEPLFFLDYYATGKLDVDTASAVISGIAEGCLQSGCSLVGETAEMPGMYHGDEDYDVAGFCVGVVEKS
EII
>d1otfa_d.80.1.1 (A:) 4-oxalocrotonate tautomerase {Pseudomonas sp., Dmpl}
PIAQLYIIEGRTDEQKETLIRQVSEAMANSLDAPLERVRLITEMPKNHFGIGGEPASK

>d1bjpa_d.80.1.1 (A:) 4-oxalocrotonate tautomerase {Pseudomonas putida, XyI_H}

PIAQIHILEGRSDEQKETLIREVSEAISRSLDAPLTSVRVIITEMAKGHFGIGGELASKVRR

>d1otga_d.80.1.2 (A:) 5-carboxymethyl-2-hydroxymuconate isomerase (CHMI) {Escherichia coli}

PHFIVECSNDNIREEADLPGFLAKVNPTLAATGIFPLAGIRSRVHWVDTWQMADGQHDYAFVHMTLKIGAGRSL

ESRQQAGEMLFELIKTHFAALMESRLALSFEIEELHPTLNFKQNNVHALFK

>d1gd0a_d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Human (Homo sapiens)}

PMFIVNTNVPRASVPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGGSSEPCALCSLHSIGKIGGAQNR

SYSKLLCGLLAERLRISPDRVYINYYDMNAANVGWNNSTFALEHH

>d1fim_d.80.1.3 (-) Microphage migration inhibition factor (MIF) {Rat (Rattus norvegicus)}

PAFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTSDPCALCSLHSIGKIGGAQNR

YSKLLCGLLSDRLHISPDRVYINYYDANA

>d1mfia_d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Mouse (Mus musculus)}

PMFIVNTNVPRASVPEGFLSELTQQLAQATGKPAQYIAVHVVPDQLMTFSGTNDPCALCSLHSIGKIGGAQNR

NYSKLLCGLLSDRLHISPDRVYINYYDMNAANVGWNGSTFA

>d1hfoa_d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Trichina (Trichinella spiralis)}

PIFTLNTNIKATDVPSDFLSSTSALGNILSKPGSYVAHVINTDQQLSGFGSTNPAAFGTLMSIGGIEPSRNRDHS

AKLFDHNLNTKLGIPKNRMYIHFVNLngDDVGWNGTTF

>d1dpta_d.80.1.3 (A:) D-dopachrome tautomerase {Human (Homo sapiens)}

PFLELDTNLPANRVPAGLEKRLAAAASILGKPADRVNVTVRPGLAMALSGSTEPCAQLSISSIGVVGTAEDNRS

HSAHFFFITKELALGQDRILIRFFPLESWQIGKIGTVMTFL

>d1gado2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Escherichia coli}

CTTNCLAPLAKVINDNFGIIEGLMTTVHATTATQKTVDGPSHKDWRRGGASQNIIPSTGAAKAVGKVLPELN

GKLTGMAFRVPTPNVSVDLTVRLEKAATYEQIKAAVAAAEGEMKGVLGYTEDDVSTDFNGEVCTSVD

AGIALNDNFVKLVSWYD

>d1gd1o2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Bacillus stearothermophilus, nca 1503}

CTTNCLAPFAKVLHEQFGIVRGMMTTVHSYTNDQRLLDPLHKDLRRARAAAESIPTTGAAKAVALVLPELKGK

LNGMAMRVPTPNVSVDLVAELEKEVTVEEVNAALKAAAEGELKGILAYSEEPLVSRDYNGSTVSSTIDALSTM

VIDGKMKVKKVSWYD

>d1cero2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermus aquaticus}

CTTNSLAPVMKVLEAFGVEKALMTTVHSYTNDQRLLDPLHKDLRRARAAAENIIPTTGAAKATALVLPSLKGR

FDGMALRVPTATGSISDITALLKREVTAAEVNAALKAAAEGPLKGILAYTEDEVLQDIVMDPHSSIVDAKLT

NMVKVFAWYD

>d1hdgo2 d.81.1.1 (O:149-312) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Thermotoga maritima}

CTTNSIAPVKLHEKFGIVSGMLTTVHSYTNDQRVLDLPHKDLRRARAAAENIIPTTGAAKAVALVVPEVKGKL

DGMAIRVPTPDGSITDLTVLVEKETTVEEVNAVMKEATEGRLKGIIGYNDEPIVSSDIIGTFSGIFDATITNVIGGK

LVKVASWYD

>d1b7go2 d.81.1.1 (O:139-300) Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) {Archaeon Sulfolobus solfataricus}

CNTTALLRTICTVNKVSKVEKVRATIVRRAADQKEVKKGPINSLVPDPATVPSHHAKDVNSVRNLDIATMAVIAP

TTLMHMHFINITLKDKEKKDILSVLENTPRIVLISSKYDAEATAELVEVARDLKDRNDIPEVMIFSDSIYVKDDE

VMLMYAVHQ

>d1cf2o2 d.81.1.1 (O:139-303) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Archaeon Methanothermus fervidus}
SCNTTGLCRTLKPLHDSFGIKKVRAIVRRGADPAQVSKGPINAIIPNPPKLPSHHGPDVKTVLDINIDTMAVIP
TTLMHQHNVMVEEETPTVDDIIVFEDTPRVLISAEDGLTSTAEIMEYAKELGRSRNDLFEIPVWRESITVVDN
EIYYMQAVHQESD

>d1ggaa2 d.81.1.1 (A:165-333) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Trypanosoma brucei brucei, glyosome}
CTTNCLAPLVHVLVKEFGFISTGLMTTVHSYTATQKTVDGVSVDWRGGRAAAALNIIPSTTGAAKAVGMVIPST
QGKLTGMAFRVPTADSVVVDLTFIATRDTSIKEIDAALKRASKTYMKNILGYTDEELVSADFISDSRSSIYDSKATLQ
NNLPNERRFFKIVSWYD

>d1i32a2 d.81.1.1 (A:166-334) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Leishmania mexicana}
CTTNCLAPIVHLTKENFGIETGLMTTIHSYTATQKTVDGVSVDWRGGRAAAVNIIIPSTTGAAKAVGMVIPSTK
GKLTGMSFRVPTPDVSVDLTFRATRDTSIQEIDKAIKKAAQTYMKGILGFTDEELVSADFINDNRSSVYDSKATL
QNNLPGEKRFFKIVSWYD

>d1dssg2 d.81.1.1 (G:149-312) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Lobster (Palinurus versicolor)}
CTTNCLAPVAKVLHENFEIVEGLMTTVHAVTATQKTVDGPSAKDWRRGGAAQNIIPSTTGAAKAVGVKVIPEL
DGKLTGMAFRVPTPNVSVDLTVRLGKECSYDDIKAAMKAASEGPLQGVLYTEDDVSCDFTGDNRSSIFDA
KAGIQLSKTFVKVVSWYD

>d3gpdg2 d.81.1.1 (G:151-314) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Human (Homo sapiens)}
CTTNCLAPLAKVIHDHFGIVEGLMTTVHAITATQKTVDSPSGKLWRGGRGAAQNLIPASTGAAKAVGVKVIPELD
GKLTGMAFRVPTANVSVDLTCRLEKPAKYDDIKVVKEASEGPLKGILGYTEDEVVSDDFNGSNHSSIFDAGAGI
ELNDTFVKLVSWYD

>d1jn0a2 d.81.1.1 (A:149-312) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Spinach (Spinacia oleracea)}
CTTNCLAPFKVLDQKFGIIGTMTTHSYTGDQRLLASHRDLRRARAACLNIVPTSTGAAKAVALVLPQLKGK
LNGIALRVPTPNVSVDLVQVSKKTFAEEVNAAFRESADQELKGILSVCDEPLSIDFRCTDVSSTIDSSLTMVM
GDDMVVKVIAWYD

>d1gl3a2 d.81.1.1 (A:134-354) Aspartate beta-semialdehyde dehydrogenase
{Escherichia coli}
NCTVSLMLMSLGLFANDLWDWVSVATYQAASGGGARHMRELLTQMGHLYGHVADELATPSSAILDIERKVTT
LTRSGELPVDNFGVPLAGSLIPWIDKQLDNGQSREEWKQAE TNKILNTSSVIPDGLCVRGALRCHSQAFTI
KLKKDVSIPTEELLAAHNPWAKVVPNDREITMRELTPAAVTGTLLTPVGRLRKLNMGPEFLSAFTVGQDQLLG
>d1ebfa2 d.81.1.2 (A:151-340) Homoserine dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}
PIISFLREIIQTGDEVEKIEGIFSGTLSYIFNEFSTSQANDVKFSDVVKVAKKLGYTEPDPRDDLNGLDVARKVTIVG
RISGVESPTSFPVQSLIPKPLESVKSADEFLEKLSDYDKDLTQLKKEAATENKVLFIGKVDVATKSVSVGIEKYD
YSHPFASLKGSDNVISIKTKRYTNPVVIQGAGAG

>d1e5qa2 d.81.1.2 (A:125-391) Saccharopine reductase {Rice blast fungus (Magnaporthe grisea)}
LDPGIDHLYAIKTIEEVHAAGGKIKTFLSYCGGLPAPESSDNPLGYKFSWSSRGVLLRNAASFYKDGVTVNAG
PELMATAKPYFIYPGFAFVAYPNRDSTPYKERYQIPEADNIVRGTLRYQGFQFIKVLVDIGFLSDEEQPFLKEAIP

WKEATQKIVKASSASEQDIVSTIVSNATFESTEEQKRIVAGLKWLGIFSDKKITPRGNALDTLCATLEEKMQFEEG
ERDLVMLQHKFEIENKDGSRETRSSLCEYGAPIGSGG

>d1f06a2 d.81.1.3 (A:119-268) Diaminopimelic acid dehydrogenase (DAPDH)
{*Corynebacterium glutamicum*}

WDPGMFSINRVYAAVLAEHQQHTFWPGPLSQGHSDALRRIPGVQKAVQYTLPSADEALEKARRGEAGDLTG
KQTHKRQCFVVADAADHERIENDIRTMPDYFVGYEVEVFIDEATFDSEHTGMPHGGHVITGDTGGFNHTV
EYILKLD

>d1dih_2 d.81.1.3 (131-240) Dihydrodipicolinate reductase {*Escherichia coli*}
VGVNVMVLKLEAKVMGDTIEIIAEHHRKVDAPSGTALMGEAIAHALDKDLKDCAVSREGHTGERVP
GTIGFATVRAGDIVGEHTAMFADIGERLEITHKASSR

>d1k5ha3 d.81.1.3 (A:126-274) 1-deoxy-D-xylulose-5-phosphate reductoisomerase
{*Escherichia coli*}

ESLTCGRLFMDAVKQSKAQLLPVDSEHNAIFQSLPQPIQHNLGYADLEQNGVVSILLGSGGPRETPLRDLAT
MTPDQACRHPNWSMGRKISVDSATMMNKLEYIARWLFNASASQMEVLIHPQSVIHSMVRYQDGSVLAQ
LGEP

>d1gcua2 d.81.1.4 (A:129-246) Biliverdin reductase {*Rat (Rattus norvegicus)*}
MEEFEFLRREVLGKELLKGSLRFTASPLEERFGPAFSGISRLTWLVS LGELSISATLEERKEDQYMKMTVQLET
QNKGLLSWIEEKPGPLKRNRYNFQFTSGSLEEVPVGVN

>d1h6da2 d.81.1.5 (A:213-374) Glucose-fructose oxidoreductase {*Zymomonas mobilis*}
DPMNRAAVKLIRENQLGKLMVTTDNDVMDQNDPAQQWRLRRELAGGGSLMDIGIYGLNGTRYLLGEEPI
EVRAYTYSDPNDERFVEVEDRIIWQMRFRSGALSHGASSYSTTSRFSVQGDKA VLLMDPATGYYQNLISVQT
PGHANQSMMMPQFIMPAN

>d1dpga2 d.81.1.5 (A:182-412,A:427-485) Glucose 6-phosphate dehydrogenase
{*Leuconostoc mesenteroides*}

KEMVQNIAALRGPNPFDAAWNKDYIKNVQVTLSEVLGVEERAGYYDTAGALDMIQNHTMQIVGWLAMEK
PESFTDKDIRAAKNAAFNALKIYDEAEVNKYFVRAQY GAGDSADFKPYLEELDPADSKNNTFIAGELQFDLPR
WE GPV FV RSGKRLAAKQTRDIVFKAGTFNFGSEQEAQEAVLSIIIDPKGAI ELKLN AKSVEDAFNRTIDLGW
TVSDEDKKNTPXGSNFADWNGVSI AWFVDAISAVYTADKAPLETYKSGSMGPEASDKLLAANGDAWVFKG

>d1qkia2 d.81.1.5 (A:200-434,A:450-511) Glucose 6-phosphate dehydrogenase
{*Human (Homo sapiens)*}

DHYLGKEMVQNLMLVRFANRIFGPIWRDNIACVILTFKEPFGT EGRGGYFDEFGIIRDVMQNHLQMLCLVA
MEKPASTNSDDVRDEKVVKVLKCISEVQANNV LGQYVGPNPDGE GEATKGYLDDPTVPRGTTATFAAVVLYVE
NERWDGVPFILRCGKALNERKAEVRLQFHDVAGDIFHQCKRNELVIRVQPNEAVYTKMMTKPGMFFNP
ESELDLTGNYKNV KLPXMHFVR SDELLEAWRIFTPLLHQIELEKPKPIP YIYGSRG PTEADELMKRVGFQYEGT
YKWN

>d1oaca4 d.82.1.1 (A:5-90) Copper amine oxidase, domain N {*Escherichia coli*}
AHMVPMDKTLKEFGADVQWDDY AQLFTLIK DGAYV KV KPG A QTA IV NGQPL ALQ VP VV MKDN KAW VSDTF
INDV FQSG LDQ TFQ VE

>d1ekga_ d.82.2.1 (A:) C-terminal domain of frataxin {*Human (Homo sapiens)*}
LDETTYERLAEETLDSLAEFFEDLADKPYTFEDYDV SGSGV LTVK LGGDL GTYVINK QTPN KQIWLSSPSSGPKR
YDWTGKNWVYSHDGVSLHELLAELTKALKT KLDLSSLAYSGK

>d1ew4a_ d.82.2.1 (A:) CyaY {*Escherichia coli*}
MNDSEFHRLADQLWLTIEERLDDWDGDSDIDCEINGVLTITFENG SKII INRQEPLH QVWLATK QGGYHF DLK
GDEWICDRSGETFWDLLEQAATQQAGETVSFR

>d1ewfa1 d.83.1.1 (A:1-217) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

VNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDSFKIKHLGKGHYSFYSMDIREQLPSSQISMVPNVG
LKFSISNANIKISGKWKAQKRFLKMSGNFDSLIEGMSISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVG
WLIQLFHKKIESALRNKMNSQVCEKVTNSVSELQPYFQTLPVMTKIDSAGINYGLVAPPATTA

>d1ewfa2 d.83.1.1 (A:218-456) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

ETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRVYLGSDYFFNTAGLVYQEAGVLKMTLRDDMIPKES
KFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPAVDVQAFALPNSALASLFLIGMHTTGS
MEVSAESNRLVGELKLDRLLELKHSNIGPFPVELLQDIMNYIVPIVLPRVNEKLQKGFLPLTPARVQLYNVVLQP
HQNFLLFGADVYVYK

>d1ihra_d.191.1.1 (A:) Dimeric C-terminal domain of membrane protein TonB {Escherichia coli}

ARAQALRIEGQVKVFKFDVTPDGRVDNVQILSAKPANMFEREVKNAMRRWRYEPGKPGSGIVVNILFKINGTTE

>d2sici_d.84.1.1 (I:) Subtilisin inhibitor {Streptomyces albogriseolus, s-3253}

YAPSALVLTVGKGSATTAAPERAVTLCAPGPSGTHPAAGSACADLAvggDLNALTGEDVMCPMVYDPVL
LTVDGVVWQGKRVSYERVFNECEMNAHGSSVFAF

>d1e6ta_d.85.1.1 (A:) MS2 virus coat protein {Bacteriophage MS2}

ASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQNRKYTIKVEVPKVATQTVG
GVELPVAAWRSYLNMELTIPIFATNSDCELIVKAMQGLLKDGNPIPSAIAANSGIY

>d1unaa_d.85.1.1 (A:) GA coat protein {Bacteriophage GA}

ATLHSFVLVDNGGTGNVTVPVSNANGVAEWSNNRSRSQAYRTASYRASSGADKRKYTIKLEVPKIVTQVVNG
VELPVAWAKAYASIDLTIPIFAATDDVTVISLTLGKVNPIAEAISSQSGFYA

>d1frsa_d.85.1.1 (A:) fr coat protein {Bacteriophage FR}

ASNFEFVLVDNGGTGDVKVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSANNRKYTVKVEVPKVATQVQ
GGVELPVAAWRSYMNMELTIPIFATNDDCALIVKALQGTFKTGNPIATAIAANSGIY

>d1qbea_d.85.1.1 (A:) Qbeta coat protein {Bacteriophage Qbeta}

AKLETVTLGNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNRKNYKVQVKIQNPTA
CTANGSCDPSVTRQAYADVTFSFTQYSTDEERAFTPTELALLASPLLIDAIDQLNPAY

>d1dwna_d.85.1.1 (A:) PP7 coat protein {Bacteriophage PP7}

SKTIVLSVGEATRTLIEIQSTADRQIFEEKVGPLVGRRLTASLRQNGAKTAYRVNLKLDQADVDCSTSVCGEPLK
VRYTQVWSHDVTIVANSTEASRKSLYDLTKSLVATSQVEDLVVNLVPLGR

>d1ej1a_d.86.1.1 (A:) Translation initiation factor eIF4e {Mouse (Mus musculus)}

KHPLQNRWALWFFKNDKSKTWQANRLISKFDTVEDFWALYNHIQLSSNLMPGCDYSLFKDGIEPMWEDEK
NKRGGRWLITLNKQQRRSDLRFWLETLLCLIGESFDDYSDDVCAGAVNVRAKGDKIAIWTECENRDAVTHI
GRVYKERLGLPPKIVIGYQSHADTATKSGSTTKNRFVV

>d1ap8_d.86.1.1 (-) Translation initiation factor eIF4e {Baker's yeast (Saccharomyces cerevisiae)}

MSVEEVSKKFEENVSVDDTTATPKTVLSDSAHF DVKHP LNTKWT LWYTKPAV DKSE WSD LLR PVTS FQT VEEF
WAI IQNIPEPH EPLKSDYHVFRNDVRPEWEDEANAKGGKWSFQLRGKGADIDELWLRTLLAVIGETIDE DDSQ
INGVVL SIRKGGNKFALWTKSEDKEPLL RIGGKFQVLKLT DDGHLEFFPHSSANGRHPQPSITL

>d3grs_3_d.87.1.1 (364-478) Glutathione reductase {Human (Homo sapiens)}

YNNIPTVVFSHPPIGTVGLTEDEAIHKYGIENVKTYSTSFTP MYHAVTKRKTCKVMKMVCANKEEKVVG IHMQ
GLGCDEM LQGFAV AVKMGATKADF NTVAI HPTSSEELVTLR

>d1gesa3_d.87.1.1 (A:336-450) Glutathione reductase {Escherichia coli}

YSNIPTVVFSHPPIGTVGLTEPQAREQYGD DQVKVYKSSFTAMY TAVTTHRQPCR MKLVCVGSEEKIVGIHGIGF

GMDEMLQGFAVALKMGATKKDFDNTVAIHPTAAEEFVTMR
>d1fec a3 d.87.1.1 (A:358-485) Trypanothione reductase {Crithidia fasciculata}
HTKVACAVFSIPPMGVCGYVEEDAACKYDQVAVYESSFTPLMHNISGSTYKKFMVRIVTNHADGEVLGVHML
GDSSPEIIQSVAICLKMGAISDFYNTIGVHPTSAEELCSMRTPAYFYEKGRVEK
>d1aoga3 d.87.1.1 (A:358-487) Trypanothione reductase {Trypanosoma cruzi}
DHTRVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSFTPMLHKVSGSKYKTFVAKIITNHSDGTVLGVHLLDNA
PEIIQGIGICLKLNAKISDFYNTIGVHPTSAEELCSMRTPSYYYVKGEKMEKP
>d1h6va3 d.87.1.1 (A:367-499) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}
YDNVPTTVFTPLEYGCCGLSEEKAVEKFGEENIEVYHSFFWPLEWTVPSRDNNKCYAKVICNLKDNERVVGFB
LGPNAGEVTQGF AALKGCLTKQQLDSTIGIHPVCAEIFTTLSTVKRSGGDILQSGCCG
>d1nhp_3 d.87.1.1 (322-447) NADH peroxidase {Enterococcus faecalis}
GVQGSSGLAVFDYKFASTGINEVMAQKLGKETKAVTVVEDYLMDFNPDKQKAWFKLVYDPETTQILGAQLMS
KADLTANINAISLAIQAKMTIEDLAYADFFFQPAFDKPKWNIINTAALEAVKQER
>d1d7ya3 d.87.1.1 (A:309-405) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp., KKS102}
TAPGYAELPWYWS DQGALRIQVAGLASGDEEIVRGEVSLDAPKFTLIELQKGRIVGATCVNNARDFAPLRRLLAV
GAKPDRAALADPATDLRKLA
>d1lv1_3 d.87.1.1 (336-458) Dihydrolipoamide dehydrogenase {Pseudomonas putida}
PAAIAAVCFTDPEVVVVGKTPEQASQQGLDCIVAQFPFAANGRAMSLESKSGFVRVVARRDNHLILGWQAVG
VAVSELSTAFAQSLEMGACLEDVAGTIHAHPTLGEAVQEAALRALGHALHI
>d1lpfa3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {Pseudomonas fluorescens}
YDLIPSVIYTHPEIAWVGKTEQLKAEGVEVN VGT PFAASGRAMAANDT GLVKVIADAKTDRVLGVHVIGPS
AAELVQQGAIGMEFGTSAEDLGMMVF SHPTLSEALHEAALAVNGHAIHIA
>d3lada3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {Azotobacter vinelandii}
YDLIPAVIYTHPEIAGVGKTEQALKAEGVAINVGVF PFAASGRAMAANDTAGFVKVIADAKTDRVLGVHVIGPS
AAELVQQGAIAMEFGTSAEDLGMMVFAHPALSEALHEAALAVSGHAIHVA
>d1ebda3 d.87.1.1 (A:347-461) Dihydrolipoamide dehydrogenase {Bacillus stearothermophilus}
AIPAVVFS DPECASVGYFEQQAKDEGIDVIAAKFPFAANGRALALNDGFLKLVRKEDGVIIGAQIIGPNASD
MIAELGLAIEAGMTAEDIALTIHAHPTLGEIAMEAAEVAL
>d1ojt_3 d.87.1.1 (471-598) Dihydrolipoamide dehydrogenase {Neisseria meningitidis}
ARVIPGVAYTSPEVAWVG ETELSAKASARKITKANFPWAASGRAIANGCDK PFTKLIFDAETGRIIGGGIVGPNG
GDMIGEVCLAIEMGCDAA DIGKTIHPHPTLGE SIGMAAEVAL GTCTDLPPQKK
>d1jeha3 d.87.1.1 (A:356-478) Dihydrolipoamide dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}
YNNIPSVMYSHPEVAWVGKTEEQLKEAGIDYKIGKFPFAANSRAKTNQDTEGFVKILIDS KTERILGAHIIGPNAG
EMIAEAGLALEYGASAEDVARVCHA HPTLSEAFKEANMAAYDKAIHC
>d1dxla3 d.87.1.1 (A:348-470) Dihydrolipoamide dehydrogenase {Garden pea (Pisum sativum)}
YDKVPGVY TNPEVASVGKTEEQVKETGVEYRVGKFPFMANSRAKAI DNAEGLVKIIAEKETDKILGVHIMAPN
AGELIHEAAIALQYDASSEDIARVCHA HPTMSEA IKEAMATYDKPIHI
>d1fcda3 d.87.1.1 (A:328-401) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding subunit {Purple phototrophic bacterium (Chromatium vinosum)}

PGTPSYLNTCYSILAPAYGISVAAIYRPNADGSAIESVPDSGGVTPDAPDWVLEREVQYAYSWYNIVHDTFG
>d1qj2c1 d.87.2.1 (C:178-285) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal domain {Pseudomonas carboxydovorans}
GHGYAYEKLKRKIGDYATAAAAVLTMSGGKCVTASIGLTNVANTPLWAEEAGKVLVGTALDKPALDKAVALAEA
ITAPASDGRGPAEYRTKMAGVMLRRAVERAKAR
>d1ffvc1 d.87.2.1 (C:178-287) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal domain {Hydrogenophaga pseudoflava}
GTGWAYEKLKRKTGDWATAGCAVVMRKSGNTVSHIRIALTNVAPTA
RAEAAAALLGKAFTKEAVQAAADAA
IAICEPAEDLRGDADYKTAMAGQMVKRALNAAWARCA
>d1fo4a4 d.87.2.1 (A:415-531) Xanthine oxidase, domain 4 (?) {Cow (Bos taurus)}
DEFFSAFKQASRREDDIAKVTGMRVLFQPGSMQVKELALCYGGMADRTISALKTTQQLSKFWNEKLLQDV
AGLAEELSLSPDAPGGMIEFRRTTLSFFFKFYLTVLKKLGKDS
>d1jroa3 d.87.2.1 (A:346-462) Xanthine dehydrogenase chain A, domain 4 {Rhodobacter capsulatus}
PGLRCYKLSKRFDDQDISAVCGCLNLTGSKIETARIAFGGMAGVPKRAAAFEAALIGQDFREDTIAALPLLAQD
FTPLSDMRASAAYRMNAAQAMALRYVRELSGEAVAVLEVMP
>d1rsa_d.88.1.1 (A:) Serum response factor (SRF) core {Human (Homo sapiens)}
TRGRVKIKMEFIDNKLRRYTTFSKRKTGIMKKAYELSTLTGTQVLLVASETGHVYTFATRKLQPMITSETGKALIQ
TCLNSPD
>d1mnma_d.88.1.1 (A:) MCM1 transcriptional regulator {Baker's yeast (Saccharomyces cerevisiae)}
QKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFELSVLTGTQVLLVSETGLVYT
FSTPKFEPIVTQQEGRNLIQA
CLNAPDD
>d1egwa_d.88.1.1 (A:) Mef2a core {Human (Homo sapiens)}
GRKKIQITRIMDERNRQVTFTKRKG
LMKKAYELSVLCDCEIALIIFN
SSNKLFQYASTDM
DKVLLKYTEY
>d1tbd_d.89.1.1 (-) The origin DNA-binding domain of SV40 T-antigen {Simian virus 40}
GSKVEDPKDFPSELLSFLSHAVFSNRTLACFAIYTTKEKAALLYKKIMEKYSVT
FISRHN
SYNHNILFFLTPHRHRVS
AINNYAQKLCTFSFLICKGVNKEYLMYSALT
RDPFSVIEESLPGGLKEHDFNPESS
>d1f08a_d.89.1.2 (A:) Replication initiation protein E1 {Bovine papillomavirus}
GSRATVFKLGLFKSLFLCSFH
DIRLFKNDKTTNQQWV
LAVFGLAEVFF
EASFELLKKQCSFLQM
QKRSHEGGTC
AVY
LIC
FNTAKS
RET
VRNL
MAN
MLNV
REE
CLMLQ
PPK
IRGL
SAAL
FWF
KSSL
SPAT
LKH
GAL
PEW
IRA
QTTLN
>d1nox_d.90.1.1 (-) NADH oxidase {Thermus thermophilus, HB8}
PVLD
AKTA
LKRR
SIRR
YRK
DPV
PEG
LLR
EILE
A
ALR
PSA
WLQ
PWR
VV
VRDP
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>d1bkja_d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio harveyi}
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>d1vfra_d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio fischeri}
THPIIHDLENRYTSKKYDPSKKV
SQEDLAV
LLEALRLSASSINS
QPWK
FIVIES
DAAK
QRM
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>d1kqba_d.90.1.1 (A:) Nitroreductase {Enterobacter cloacae}
DIISVALKRHSTKAFDASKKLTAEEAEKIKTLLQYSPSSTSNSQPWHFIVASTEEGKARVAKSAAGTYVFNERKML
ASHVVVFCAKTAMDDAWLERVVDQEEADGRFNTPEAKAANHKGRTYFADMHRVLKDDDWMAKQVYL
NVGNFLLGVGAMGLDAVPIEGFDAILDEEGLKEKGFTSLVVVPVGHHSVEDFNATLPKSRLPLSTIVTEC

>d1icra_d.90.1.1 (A:) Nitroreductase {Escherichia coli, minor form}
DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTSNSQPWHFIVASTEEGKARVAKSAAGNYVFNERKML
DASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFADMRKDLHDDAEWMAKQVYL
NVGNFLLGVAALGLDAVPIEGFDAILDAEFGLEKGFTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV

>d1f5va_d.90.1.1 (A:) Nitroreductase {Escherichia coli, oxygen-insensitive form}
MTPTIELICGHRHSIRHFTDEPISEAQRERAIINSARATSSSFLQCSSIIRTDKALREELVLTGGQKHVAQAAEFWV
FCADFNRHLQICPDAQLGLAEQQLLGVVTAMMAQNALIAAESLGLGGVYIGGLRNNIEAVTKLLKLPQHVLPL
FGLCLGWPADNPDLKPRLPASILVHENSYQPLDKGALAQYDEQLAEYYLTRGSNNRRDTWSDHIRRTIIESRPFI
LDYLHKQGWATR

>d1dt9a3 d.91.1.1 (A:5-142) N-terminal domain of eukaryotic peptide chain release factor subunit 1, ERF1 {Human (Homo sapiens)}
PSAADRNVEIWKKIKLKSLEAARGNGTSMISLIIPPKDQISRVAKMLADEFGTASNIKSRVNRLSVLGAITSVQQR
LKLYNKVPPNGLVVYCGTIVTEEGKEKKVNIDFEPFKPINTSLYLCDNKFHTEALTALLSD

>d1c7ka_d.92.1.1 (A:) Zinc protease {Streptomyces caespitosus}
TVTVTYDPSNAPSQQEIANAAQIWNSSVRVNQLRAGGNADFSYYEGNDRSGYAQTDGHGRGYIFLDYQQN
QQYDSTRVTAHETGHVLGLPDHYQGPCSELMSGGPGPSCTNPYPNAQERSRVNALWANG

>d1g12a_d.92.1.12 (A:) Fungal zinc peptidase {Grifola frondosa}
TYNGCSSSEQSALAAAASAAQSYVAESLSYLQTHTAATPRYTTWFGSYISSRHSTVLQHYTDMNSNDFSSYSFDC
TCTAAGTFAYVYPNRFGTVYLCGAFWKAPTTGTDQSAGTLVHESSHFRNGGKDYAYGQAAAKSLATMDPDK
AVMNADNHEYFSENNPAQS

>d1eb6a_d.92.1.12 (A:) Fungal zinc peptidase {Aspergillus oryzae, deuterolysin}
TEVTDCKGDAESSLTALSNAAKLANQAAEAEESGDESKFEYFKTTDQQTRTTVAERLRAVAKEAGSTSGGTT
YHCNDPYGYCEPNVLAYTLPSKNEIANCDIYSELPLAQLCHAQDQATTLHEFTHAPGVYQPGTEDLGYGYD
AATQLSAQDALNNADSYALYANAIELKC

>d1ezm_d.92.1.2 (-) Elastase {Pseudomonas aeruginosa}
AEAGGGPGNNQKIGKYTYGSDYGPLIVNDRCMDDGNVITVDMNSSTDSKTPFRFACPTNTYKQVNGAYSP
LNDAHFFGGVVFKLYRDWFGTSPLTHKLYMKVHYGRSVENAYWDGTAMLFGDGATMFYPLVSLDVAHEVSH
GFTEQNSGLIYRGQSGGMNEAFSDMAGEAAEFYMRGKNDFLIGYDIKKGSALRYMDQPSRDGRSIDNASQ
YYNGIDVHHSSGVYNRAFYLLANSPGWDTRKADEVFDANRYWTATSNYNSGACGVIRSAQNRNYSADVT
RAFSTVGVTCP

>d8tlne_d.92.1.2 (E:) Thermolysin {Bacillus thermoproteolyticus}
ITGTSTVGVRGVLDQKNINTTYSTYYYLQDNTRGDGIFTYDAKYRTLPGSLWADADNQFFASYDAPAVDA
HYYAGVTYDYYKNVHNRLSYDGNNAIRSSVHYSQGYNNAFWNGSEMVGDGQTFIPLSGGIDVVAHELT
HAVTDYTAGLIYQNESGAINEAISDIFGTLVEFYANKNPDWEIGEDVYTPGISGDSLRSMSDPAKYGDPDHYSKR
YTGTQDNGGVHINSGIINKAAYLISQGGTHYGVSVVIGIRDKLKIFYRALTQYLPTSQLRAAAVQSATDLY
GSTSQEVASVKQAFDAVGVK

>d1npc_d.92.1.2 (-) Neutral protease {Bacillus cereus, strain dsm 3101}
VTGTNKVGTGKGVLGDTKSLNTTSGSSYYLQDNTRGATIFTYDAKNRSTLPGTLWADADNVFNAAYDAAAVD
AHYYAGKTYDYYKATFNRNSINDAGAPLKSTVHYGSNNNAFWNGSQMVYGDGDGVFTLSGGIDVIGHEL
THAVTENSSNLIYQNESGALNEAISDIFGTLVEFYDNRNPDWEIGEDIYTPGKAGDALRSMSDPTKYGDPDHYS

KRYTGSSDNGGVHTNSGIINKQAYLLANGGTHYGVTVTGIGKDKLGAIYYRANTQYFTQSTTFSQARAGAVQA
AADLYGANSAAVAKQSFSAVGVN

>d1bqba_d.92.1.2 (A:) Aureolysin {Staphylococcus aureus}

AAATGTGKGVLGDTKDININSIDGGFSLEDLTHQGKLSAYNFNDQTGQATLITNEDENFKDDQRAGVDANYY
AKQTYDYYKNTFGRESYDNHGSPIVSLTVNHYGGQDNRNNAAWIGDKMIIYGDGDGRFTNLGANDVVAH
EITHGVTQQTANLEYKDQSGALNESFSDVFGYFVDEDLMGEDVYTPGKEGDALRSMSNPEQFGQPSHMK
DVYVTEKDNGGVHTNSGIPNKAAYNVIAIGKSSEQIYYRALTEYLTNSNFKDLKDALYQAAKDLYEQQTAEQ
VYEAWNEVGVE

>d1hs6a3 d.92.1.13 (A:209-460) Leukotriene A4 hydrolase catalytic domain {Human (Homo sapiens)}

LESRQIGPRTLVWSEKEQVEKSAYEFSETESMLKIAEDLGGPYVWGQYDLLVPPSFYGGMENPCLTFVTPTLL
AGDKSLSNVIAHEISHSWTGNLVTNKTWDHFWLNEGHTVYLERHICRLGEKFRHFNALGGWGEQNSVK
FGETHPFTKLVVLDIDPDVAYSSVPYEKGFALLFYLEQLGGPEIFLGLKAYVEKFSYKSITTDDWKDFLYSYFK
DKVDVLNQVDWNAWLYSPGLPPIKPNY

>d1dmta_d.92.1.4 (A:) Neutral endopeptidase (neprilysin) {Human (Homo sapiens)}

GICKSSDCIKSAARLIQNMDATTEPCDTFFKYACGGWLKRNVIPETSSRYGNFDILRDELEVVLKDVLQEPKTEDI
VAVQKAKALYRSCINESAIDSRGGEPLLKLLPDIYGWPVATENWEQKYGASWTAEKAIACLNSKYGKKVLINLFV
GTDDKNVSNVHIIDQPRGLPSRDYYECTGIYKEACTAYVDFMISVARLIRQEERLPIDENQLALEMNKVMEL
KEIANATAKPEDRNDPMILLYNKMTLAQIQNNFSLEINGKPFSLNFTNEIMSTVNISITNEEDVVVYAPEYLT
KPIILTKYSARDLQNLMSWRFIMDLVSSLRTYKESRNAFRKALYGTSETATWRRCANVNGNMENAVGRLYVE
AAFAGESKHVVVEDLIAQIREVFIQTLDDLWMDAETKKRAEEKALAIKERIGYPDDIVSNDNKLNNYELENYKE
DEYFENIIQNLKFSQSKQLKLRKVDKDEWISGAAVVNAFYSSGRNQIVFPAGILQPPFFSAQQNSNLNYGGIG
MVIGHETHGFDDNGRNFNKGDLVDWWWTQQSASFKEQSQCMVYQYGNFSWDLAGGQHLNGINTLGEN
IADNGGLGQAYRAYQNYIKKNGEEKLLPGLDLNHKQLFFLNFAQVWCCTYRPEYAVNSIKTDVHSPGNFRIIGTL
QNSAEFSEAFHCRKNSYMNPEKKCRVW

>d1i1ip_d.92.1.5 (P:) Neurolysin (endopeptidase 24.16) {Rat (Rattus norvegicus)}

MSSYTAAGRNVLRWDLSP_EQIKTRTEQLIAQTKQVYDTVTIALKEVTYENCLQLADIEVTYIVERTMLDFPQH
VSSDREVRAASTEADKKLRSRDIEMSMREDVFQRIVHLQETCDLEKIKPEARRYLEKSIMGKRNGLHLSEHIRN
EIKSMKKRMSEL CIDFNKNLNEDDTSLVFSKAELGALPDDFIDSLEKTDEDKYKVTLKYPHYFPVMKKCCVPETR
RKMEMAFHTRCKQENTAILQQLPLRAQVAKLLGYNTHADFVLELNATAKSTSRAAFLDDLSQKLKPLGEAERE
FILSLKKKECEERGFYDGKINA WDLHYYM QTTEELKYSVDQESLKEYFPIEVVTEGLLSIYQELLGLSFEQVPDAH
VWNKSVLSYTVKDKATGEV LGQFYLDLYPREGKYNHAACFG LQPGCLL PDGSRMM SVAALVVNF SQPVAGR
SLLRHDEVRTYFHEFGHVMHQICAQTD FARFSGTNVETDFVEVPSQML ENWW D VDSL RKL SKHY KDG HPI
DELLEKLVASRLVNTGLL RLQIVLSKVDQSLHTNATL DAASEYAKY CT EILGVAATPGTNMPATFGHLAGGYDGG
YYGYLWSEVFSMDMFHSCFKKEGIMNPEVGMKYRNLILKPGGSLGMDMLQNLQREPNQKAFLMSRGL

>d1j7na1 d.92.1.14 (A:27-263) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}

ERNKTQEEHLKEIMKHIVKIEVKGEEAVKKEAAEKLLEKVPDVLEMYKAIGGKIYIVDGDITKHISLEALSEDKKI
KDIYGKDALLHEHYVYAKEGYEPVLVIQSSEDYVENTEKALNVYYEIGKILSRDILSKINQPYQKFLDV LNTIKNASD
SDGQDLLFTNQLKEHPTDFSVEFQNSNEVQEVFAKAFAYYIEPQH RDVLQLYAPEAFNYMDKFNEQEINLSLE
ELKDQR

>d1j7na2 d.92.1.14 (A:551-773) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}

PKSKIDTKI QEAQLNINQEWNKALGLPKYTKLITFNVHNRYASNIVESAYLILNEWKNNI QSDLIKKVTNYLVDGN

GRFVFTDITLPNIAEQYTHQDEIYEQVHSKGLYVPESRSILLHGPSKGVELRNDSEGFIEFGHAVDDYAGYLLDK
NQSDLVTNSKKFIDIFKEEGSNLTSYGRTEAEFFAEAFRLMHSTDHAERLKVKNAPKTQFINDQIKFI
>d1lml_ d.92.1.3 (-) Leishmanolysin {Leishmania major}
VVRDVNWGALRIA VSTEDLTDPAYHCA RVGQHV KD HAGA IV TCA ED ILTNE KRDILV KHLIP QAVQL HTER LKV
QVQGKWKV TDMVG DICGDFK VPQAH IT EGFS NT DFV MYV AS VP SEEGV LA WATT CQT FSDGHP AVGV NI
PAANIASRYDQLVTRVVTHEMAHALGFSGPFFEDARIVANVPNVRGKNFDV PVINS STAVAKAREQYGCDTLEY
LEVEDQGGAGSAGSHIKMRNAQDELMAPA AAAAG YYTALTMAIFQDLGFYQADFSKAEVMPWGQNAGCAFL
TNKCMEQS VTQWPAMFCNESED AIRCPTSRLSLGACGVTRH PGLPPWQYFTDPSLAGVSAFMDYCPVV PY
SDGSCTQRASEAHASLLPFNVFSDAARCIDGAFRPKATDGIVKS YAGLCANVQCDTATRTYSVQVHGSNDYTNC
TPGLRVELSTVSNAFEGGGYITCPPYVEVCQGNVQA AKD
>d1kapp2 d.92.1.6 (P:1-246) Metallo protease, catalytic (N-terminal) domain {Pseudomonas aeruginosa, alkaline protease}
GRSDAYTQVDNFLHAYARGGDELVNGHPSYTVDQAAEQLREQASWQKAPGDSVLTLSYSFLTKPNDFNTPW
KYVSDIYSLGKFSAFSAQQQAQAKLSLQSWSDTVNIHFVDAGQGDQGDLTFGNFSSVGGAAFAFLPDVPDAL
KGQSWYLINSSYSANVNPANGNYGRQTLTHEIGHTLGLSHPGDYNAGEGDPTYADATYAEDTRAYS VMSY WEE
QNTGQDFKGAYSSAPLLDIAAIQKLY
>d1sat_2 d.92.1.6 (4-246) Metallo protease, catalytic (N-terminal) domain {Serratia marcescens}
TGYDAVDDLLHYHERGNGIQINGKDSFSNEQAGLFITRENQTWNGYKVFGQPVKLTFPSFPDYKFSSTNVAGDT
GLSKFSAEQQQQAQAKLSLQSWSADVANITTEVAAGQKANITFGNYSQDRPGHYD YGTQAYAFLPNTIWQGQDL
GGQTWYNVNQSNVKH PATEDYGRQFTTHEIGHALGLSHPGDYNAGEGDPTYADVTY AEDTRQFSLMSY WSE
TNTGGDNGGHYAAAPLLDIAAIQHLY
>d3btaa3 d.92.1.7 (A:1-546) Botulinum neurotoxin {Clostridium botulinum, serotype A}
PFVNKQFN YKD PVNGV DIA YIKIP NVGQM QPV KAFK IHN KI WVIP ERDT FTNPEEGDLNPPPEAKQV PVSY DS
TYLSTDNEKDNYLKGVTKL FERIYSTD LGRMLL TSIVRG I PFWGG STIDTEL KVIDNC INVI QPDGSY RSEELNLV II
GPSADIIQFECKSF GHEV NLTR NGY G STQY IRFSPDFTFG FEES LEVD TNPLL GAGK FATD PAV TL AHE LIHAG HR
LYGIA INPN RVFK VNTN AYY EMSG LEV SFEEL RTFG GHDAK FID SLQENE FRL YYY NKF KDI AS TLN KAKSIV GTTA
SLQY MKNV FKE KYLL SEDT SGK FSV DKL FD KLY KML TEI YT EDNF VKKF KV LNR KT YL NF DKAV FK INI VP K VN YT
IYDGF NLR NTNLA ANFNG QNTE INNMNFTKLKNFTGLFEFYKLLCVRGIITS KTKSLDKG YNK ALNDLC I KVNN
WDLFFSPSEDNFTNDLNKGEEITS DTNIEAAEENISLDLIQ QYLT FNFDNE PENISIENLSSDIIGQLEL MPN IERF
PNGKKYELDK
>d1epwa3 d.92.1.7 (A:1-533) Botulinum neurotoxin {Clostridium botulinum, serotype B}
PVTINNFNYNDPIDNNIIMMEEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCEYYDPD
YLNTNDKKNIFLQTMIKLFNRI SKPLGEK LLEM IINGIPYLGDRRVPLEEFTN IASVTNKLISNPGEVERKKG IF
ANLIIFGPGPV LNENETIDIGI QNH FAS REG FGG IMQM KFCPEY VSVFNNVQENKGASIFNRRGYFSDP ALIL MH
ELIHVLHGLYGI KVDDLP IVPNEK KFMQ STDAI QAE ELYT FGG QDPSIITPSTD KSIYDKV LQN FRGIV DR LN KVL
VCISDPNININIYK NKFKD KYKF VEDSEG KYS IDV EFD KLY KSLM FGFT ETNIA ENY KIK TRAS YFSDS LPPV KIK NL
LDNEIYTI EGF NI SDK DME KEY RGQ NKAIN KQAYEE ISKEH LAVY KI QMCK SVKAPG ICID VDN E DLF FIAD KNS
FSDDL SKNERIE YNT QSN YIEND FPI NEL I LD TDLISKI LPE SSENTE SLTDFN DV P VYE KQPA IKKIFT DE
>d1f83a_ d.92.1.7 (A:) Botulinum neurotoxin {Clostridium botulinum, serotype B}
PVTINNFNYNDPIDNNIIMMEEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSSGIFNRDVCEYYDPD
YLNTNDKKNIFLQTMIKLFNRI SKPLGEK LLEM IINGIPYLGDRRVPLEEFTN IASVTNKLISNPGEVERKKG IF
ANLIIFGPGPV LNENETIDIGI QNH FAS REG FGG IMQM KFCPEY VSVFNNVQENKGASIFNRRGYFSDP ALIL MH
ELIHVLHGLYGI KVDDLP IVPNEK KFMQ STDAI QAE ELYT FGG QDPSIITPSTD KSIYDKV LQN FRGIV DR LN KVL
VCISDPNININIYK NKFKD KYKF VEDSEG KYS IDV EFD KLY KSLM FGFT ETNIA ENY KIK TRAS YFSDS LPPV KIK NL

LDNEIYTIEEGFNISDKDMEKEYRGQNKAINKQAYEEISK

>d1ast__ d.92.1.8 (-) Astacin {European fresh water crayfish (*Astacus astacus*)}

AAILGDEYLWSGGVIPYTFAGVSGADQSAILSGMQELEEKTCIRFPRTTESDYVEIFTSGSGCWSYVGRISGAQ
QVSLQANGCVYHTGIIHELMHAIGFYHEHTRMDRDNYVTINYQNVDPMSMTSNFDIDTYSRYVGEDYQYYSIM
HYGKYSFSIQWGVLETIVPLQNGIDLTDYPDKAHMLQTDANQINNLYTNECL

>d4aig__ d.92.1.9 (-) Snake venom metalloprotease {Eastern diamondback rattlesnake (*Crotalus adamanteus*), adamalysin II}

NLPQRYIELVVVADRRVFMKYNSDLNIIRTRVHEIVNIIINEFYRSLNIRVSLDLEIWSGQDFITIQSSSNTLNSFG
EWRERVLTRKRHDNAQLLTAINFEGKIIGKAYTSSMCNPRSSVGIVKDHSPINLLAVTMAHELGHNLGMEHD
GKDCLRGASLCIMRPGLTPGRSYEFSDSMGYYQKFLNQYKPQCILNKP

>d1atla__ d.92.1.9 (A:) Snake venom metalloprotease {Western diamondback rattlesnake (*Crotalus atrox*), atrolysin C}

LPQRYIELVVVADHRVFMKYNSDLNTIRTRVHEIVNFINGFYRSLNIVSLEIWSNEDQINIQSASSDTLNAF
AEWRETDLLNRKSHDNAQLLTAIELDEETLGLAPLGTMCDPKLSIGIVQDHSPINLLMGVTMAHELGHNLGME
HDGKDCLRGASLCIMRPGLTKGRSYEFSDSMHYYERFLQYKPQCILNKP

>d1buda__ d.92.1.9 (A:) Snake venom metalloprotease {Five-pace snake (*Agkistrodon acutus*), acutolysin A}

FQRYMEIVVVVDHSMVKYNGDSDSIKAWVYEMINTITESYSLKIDISLGEIWSGKDLIDVEASAGNTLKSFG
EWRAKDLIHRISHDNAQLLTATDFDGATIGLAYVASMCNPKRSVGVIQDHSSVNRLVAITLAHEMAHNLGVSHD
EGSCSCGGKSCIMSPSISDETIKYFSDCSYIQC RDYISKENPPCILN

>d1quaa__ d.92.1.9 (A:) Snake venom metalloprotease {Chinese five-pace snake (*Agkistrodon acutus*), acutolysin C}

PAPQTSEIELFLIVDHSMYAKYNSNSSKTTTLKARVNIMNAISSLNLVITLSGIEMWSAADLTVQSSRNTLKLFA
SWRETDLLKRTSNDNAQLLTATNFNGNTVGLAYLKTMCNSKYSVGLI QDHSAIPLLMAVTMAHELGHNLGMN
HDGAGCSCATCIMAPVLSGPAGSFSDCSKHDYQSFQFTIHKPQCLLN

>d1bkca__ d.92.1.10 (A:) TNF-alpha converting enzyme, TACE, catalytic domain {Human (*Homo sapiens*)}

DPMKNTCKLLVADHRFYRYMGRGEESTTNYLIELIDRVDDIYRNTAWDNAGFKGYGIQIEQIRILKSPQEVPK
GEKHYNMAKSYPNEEKDAWDVKMLLEQFSFDIAEEASKVCLAHLFTYQDFDMGTLGLAYVGSPRANSHGGVC
PKAYYSPVGKKNIYNSGLSTKNYGKTILTKEADLVTTHELGNFGAEHDPDGLAECAPNEDQGGKYVMYPIA
VSGDHENNKMFSQCSKQSIYKTIESKAQECFQER

>d1cgla__ d.92.1.11 (A:) Fibroblast collagenase (MMP-1) {Human (*Homo sapiens*)}

VLTEGNPRWEQTHLRYRIENYTPDLPRADV DHAIEKAFQLWSVTPLFTKVSEGQADIMISFVRGDHRDNSPF
DGGGNLAHAFDPGP GIGGDAHF DEDERWTNNFREYNLHRVAAHELGHSLGLSHSTDIGALMPSYTFSGDV
QLAQDDIDGIQAIYGRSQNPVQ

>d1hfc__ d.92.1.11 (-) Fibroblast collagenase (MMP-1) {Human (*Homo sapiens*)}

PRWEQTHLTYRIENYTPDLPRADV DHAIEKAFQLWSNVPLFTKVSEGQADIMISFVRGDHRDNSPF DPGGG
NLAHAFQPGPGIGGDAHF DEDERWTNNFREYNLHRVAAHELGHSLGLSHSTDIGALMPSYTFSGDV
DIDGIQAIYGRS

>d1fbl_2 d.92.1.11 (100-271) Fibroblast collagenase (MMP-1) {Pig (*Sus scrofa*)}

FVLTPGNPRWENTHLTYRIENYTPDLSREDVDRAIEKAFQLWSNVPLFTKVSEGQADIMISFVRGDHRDNSP
FDGPGGNLAHAFQPGPGIGGDAHF DEDERWTKNFRDYNLYRVAHELGHSLGLSHSTDIGALM PNYIYTGD
VQLSQDDIDGIQAIYGPSENPVQPSG

>d1hova__ d.92.1.11 (A:) MMP-2 {Human (*Homo sapiens*)}

MYNFFPRPKWDKNQITYRIIGYTPDLDPETVDDAFARAFQVVSDVTPLRFSRIHDGEADIMINFGRWEHGD
GYPFDGKDGLLAHAFAPGTGVGGDSHFDDDELWTNTSANYSLFLVAAHEFGHAMGLEHSQDPGALMAPIYT
YTKNFRLSQDDIKGIQELYG
>d1i76a_d.92.1.11 (A:) Neutrophil collagenase (MMP-8) {Human (Homo sapiens)}
MLTPGNPKWERTNLTYRIRNYTPQLSEAEVERAIKDAFELWSVASPLIFTRISQGEADINIAFYQRDHGDNSPFD
GPNGILAHAQPGQGIGGDAHFDAEETWTNTSANYNLFLVAAHEFGHSLGLAHSSDPGALMYPNYAFRETSN
YSLPQDDIDGIQAIYG
>d1qiba_d.92.1.11 (A:) Gelatinase A {Human (Homo sapiens)}
RKPKWDKNQITYRIIGYTPDLDPETVDDAFARAFQVVSDVTPLRFSRIHDGEADIMINFGRWEHGDGYPFDGK
DGLLAHAFAPGTGVGGDSHFDDDELWSLGKGVGYSFLVAAHEFGHAMGLEHSQDPGALMAPIYTAKNFRL
SQDDIKGIQELYGASP
>d1hy7a_d.92.1.11 (A:) Stromelysin-1 (MMP-3) {Human (Homo sapiens), fibroblast}
FRTPGIPKWRKTHLTYRIVNYTPDLPKDAVDSAVEKALKVVEEVPLTFSRLYEGERADIMISFAVREHGDFYPFD
GPGNVLAHAYAPPGINGDAHFDDDEQWTKDTTGTNLFLVAAHEIGHSLGLHSANTEALMYPLYHSLDLTR
FRLSQDDINGIQSLYGPPP
>d1mmq_d.92.1.11 (-) Matrilysin (MMP-9) {Human (Homo sapiens)}
YSLFPNSPKWTSKVVTYRIVSYTRDLPHITVDRLVSKALNMWGKEIPLHFRKVVWGTADIMIGFARGAHGDSYP
FDGPGNTLAHAQPGTGLGGDAHFDEDERWTDGSSLGINFLYAATHELGHSLGMGHSSDPNAVMYPTYGNG
DPQNFKLSQDDIKGIQKLYGK
>d1hv5a_d.92.1.11 (A:) Stromelysin-3 (MMP-11) {Mouse (Mus musculus)}
MFVLSGGRWEKTDLYRILRFPWQLVREQVRQTVAEALQVWSEVTPLTFTEVHEGRADIMIDFARYWHGDNL
PFDGPGGILAHAFFPKTHREGDVHFDYDETWTIGDNQGTDLLQVAHEFGHVLGLQHTTAKALMSPFYTR
YPLSLSPDDRRGIQHLYG
>d1jk3a_d.92.1.11 (A:) Macrophage elastase (MMP-12) {Human (Homo sapiens)}
GPVWRKHYITYRINNYTPDMNREDVDYAIRKAQVWSNVTPLKFSKINTGMADILVVFARGAHGDFHAFDGK
GGILAHAQPGSGIGGDAHFDEDEFWTTHSGGTNLFLAVHAIGHSLGLGHSSDPKAVMFPTYKYVDINTFRSL
ADDIRGIQSLYG
>d830ca_d.92.1.11 (A:) Collagenase-3 (MMP-13) {Human (Homo sapiens)}
YNVFPTLKWSKMNLTYRIVNYTPDMTHSEVEKAFKKAFKVWSDVTPLNFTRLHDGIADIMISFGIKEHGDFYP
FDGPSGLLAHAFFPPGPNYGGDAHFDDDETWTSSKGYNLFLVAAHEFGHSLGLHSKDPGALMFPIYTGTGS
HFMLPDDDVQGIQSLYGP
>d1cxva_d.92.1.11 (A:) Collagenase-3 (MMP-13) {Mouse (Mus musculus)}
YNVFPTLKWSQTNLTYRIVNYTPDMSHSEVEKAFRKAFKVWSDVTPLNFTRIYDGTADIMISFGTKEHGDFYP
FDGPSGLLAHAFFPPGPNYGGDAHFDDDETWTSSKGYNLFLVAAHELGHSKDPGALMFPIYTGTGS
HFMLPDDDVQGIQFLY
>d1bqqm_d.92.1.11 (M:) Membrane-type matrix metalloproteinase (CDMT1-MMP)
{Human (Homo sapiens)}
IQGLKWQHNEITFCIQNYTPKVGLEYATYEAIRKAFRVWESATPLRFREVYAYIREGHEKQADIMIFFAEGFHGDS
TPFDGEGGFLAHAYFPGPNIQGDTHFDAEPWTVRNEDLNGNDIFLVAVHELGHALGLEHSSDPSAIMAPFYQ
WMDTENFVLPDDDRGIQQLYGGES
>d1qba_4 d.92.2.1 (201-337) Bacterial chitobiase, Domain 2 {Serratia marcescens}
SNADLQLTPAGALRGKIVPTPMQVKVHAQDADLRKGVALDLSTLVKPAADVVSQRFALLGVPVQTNGYPIKTDI
QPGKFKGAMAVSGAYELKIGKKEAQVIGFDQAGVFYGLQSILSVPSDGSGKIATLDASDAPR
>d1jaka2 d.92.2.1 (A:8-150) beta-N-acetylhexosaminidase, N-terminal domain {Streptomyces}

plicatus}

DRKAPVRPTPLDRVIPAPASVDPGGAPYRITRGTHRVDSSREARRVGDYLA
RLAGGPYGDEGYRLDSGPAGVTITARKAAGLFHGVQTLRQLP
>d1cndl_d.93.1.1 (L:) p56-lck tyrosine kinase {Human (Homo sapiens)}

GSWFFKNLRSRKDAERQLLAPGNTHGSFLIRESESTAGSFSL
PGLHELVRYHTNASDGLCTRLSR
>d1lkka_d.93.1.1 (A:) p56-lck tyrosine kinase {Human (Homo sapiens)}

LEPEPWFFKNLRSRKDAERQLLAPGNTHGSFLIRESESTAGSFSL
ITFPGLHELVRYHTNASDGLCTRLSRPCQT
>d1bkl_d.93.1.1 (-) v-src tyrosine kinase {Rous sarcoma virus, Schmidt-ruppin strain a}

EEWYFGKITRRESESLLNPENPRGTFLVRESETTKGAYCLS
LQLVAYYSKHADGLCHRLTNVCPTSKEFIVTD
>d1shaa_d.93.1.1 (A:) v-src tyrosine kinase {Rous sarcoma virus, Schmidt-ruppin strain a}

AEEWYFGKITRRESERLLNPENPRGTFLVRESETTKGAYCLS
SLQQLVAYYSKHADGLCHRLTNVCPT
>d1a09a_d.93.1.1 (A:) c-src tyrosine kinase {Human (Homo sapiens)}

DSIQAEWYFGKITRRESERLLNAENPRGTFLVRESETTKGAYCLS
TQFNSLQQLVAYYSKHADGLCHRLTTVCP
>d1g83a2_d.93.1.1 (A:142-245) Tyrosine kinase Fyn {Human (Homo sapiens)}

DSIQAEWYFGKLGRKDAERQLLSFGNPRGTFLIRESETTKGAY
TTRAQFETLQQLVQHY SERAAGLSSRLVVP
>d1ayaa_d.93.1.1 (A:) Tyrosine phosphatase Syp {Mouse (Mus musculus)}

MRRWFHPNITGVEAENLLTRGV
LVQYYMEHHGQLKEKNGDVIELKYPLN
>d1fhs_d.93.1.1 (-) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo sapiens)}

GIEMKPHPWFFGKIPRAKA
FNSLNELVDYHRSTS
>d1zfpe_d.93.1.1 (E:) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo sapiens)}

KPHPWFFGKIPRAKA
NELVDYHRSTS
>d1qcf2 d.93.1.1 (A:146-248) Hemopoetic cell kinase Hck {Human (Homo sapiens)}

EEWFFKGISRKDAERQLL
HЛИYHMDNHLPIISAGSEL
>d1mil_d.93.1.1 (-) Shc adaptor protein {Human (Homo sapiens)}

GSQRLGE
HLISYHMDNHLPIISAGSEL
>d1qada_d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Cow (Bos taurus)}

EDLPHHDEKTWN
LYSSLKELVLHYQHTSLV
>d1pica_d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Human (Homo sapiens)}

GSPIPHHDEKTWN
NLYSSLKELVLHYQHTSLV

>d1fu6a_ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Rat (Rattus norvegicus)}

GMNNNMSLQDAEWYWGDISREEVNEKLRDTADGTLVRDASTKMHGDYTLTRKGNNNSIKIFHRDGKYG
FSDPLTFNSVVELINHYRNESLAQYNPKLDVKLLYPVSKY

>d1ab2_ d.93.1.1 (-) Proto-oncogen tyrosine kinase {Human (Homo sapiens)}

GSGNSLEKHSWYHGPVSRNAAEYLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLYVSSESRF
NTLAEVHHHSTVADGLITLHYPAPKRGHIRD

>d1a81a1 d.93.1.1 (A:9-137) Syk tyrosine kinase {Human (Homo sapiens)}

SANHPFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHYTIERELNGTYAIAGGRTH
ASPADLCHYHSQESDGLVCLKKPFNRQPQGVQPKTGFEDLKENLIREYVKQTWN

>d1a81a2 d.93.1.1 (A:138-262) Syk tyrosine kinase {Human (Homo sapiens)}

LQGQALEQAIISQPKPQLEKLIATTAEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKV
LHYRIDKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKI

>d1a81e1 d.93.1.1 (E:9-117) Syk tyrosine kinase {Human (Homo sapiens)}

SANHPFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHYTIERELNGTYAIAGGRTH
ASPADLCHYHSQESDGLVCLKKPFNRQPQGVQPKT

>d1a81e2 d.93.1.1 (E:152-262) Syk tyrosine kinase {Human (Homo sapiens)}

PQLEKLIATTAEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKVLHYRIDKDKTGKLSI
PEGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKI

>d1csya_ d.93.1.1 (A:) Syk tyrosine kinase {Human (Homo sapiens)}

GSRRASVGSHEKMPWFHGKISREESEQIVLIGSKTNGKFLIRARDNNGSYALCLLHEGKVLHYRIDKDKTGKLSIP
EGKKFDTLWQLVEHYSYKADGLLRVLTVPCQKIGTQ

>d2plda_ d.93.1.1 (A:) Phospholipase C-gamma-1 {Cow (Bos taurus)}

GSPGIHESKEWYHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSYAISFRAEGKIKHCRVQQEGQTVMLGNS
EFDSLVDLISYYEKHPLYRKMKLRYPINEENSS

>d1blk_ d.93.1.1 (-) P55 Bik protein tyrosine kinase {Mouse (Mus musculus)}

GSVAPVETVEKWFFRTISRKDAERQLAPMNKAGSFLIRESESNKGAFSLVKDITTQGEVVKHYKIRSLDNG
GYYISPRITFPTLQALVQHYSKKGDGLCQKLTLPVCVNLA

>d2abl_2 d.93.1.1 (140-237) Abl tyrosine kinase {Human (Homo sapiens)}

SLEKHSWYHGPVSRNAAEYLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRINTASDGKLYVSSESRFNTLAE
LVHHHSTVADGLITLHYPAP

>d1jwoa_ d.93.1.1 (A:) Csk homologous kinase Chk {Human (Homo sapiens)}

LSLMPWFHGKISGQEAVQQLQPPEDGLFLVRESARHPGDYVLCVSFGRDVHYRVLHRDGHLTIDEAVFFCNL
MDMVEHYSKDKGAICTKLVRPKRK

>d1bf5a3 d.93.1.1 (A:569-710) STAT-1 {Human (Homo sapiens)}

LLPLWNDGCIMGFISKERERALLKDQQPGTFLLRFSESSREGAITFTWVERSQNGGEPDFHAVEPYTKKELSAVT
FPDIIRNYKVMAAENIPNPLKYLYPNIDKDHAFGKYYSGYIKTELISVS

>d1bg1a3 d.93.1.1 (A:576-716) STAT3b {Mouse (Mus musculus)}

ILALWNEYIMGFISKERERAILSTKPPGTLLRFSESSKEGGVTFTWVEKDISGSTQIQSVEPYTKQQLNNMSFA
EIIMGYKIMDATNILSPLVLYPDIPKEEAFGKYCRPESQEHPADPGSAAPYLTKFICVTPF

>d2cba3 d.93.1.1 (A:264-351) Cbl {Human (Homo sapiens)}

THPGYMAFLTYDEVKARLQKFIHKPGSYIFRLSCTRLGQWAIGYVTADGNILQTIPHNKPLFQALIDGFREGFYLF
PDGRNQNPDLTG

>d2shpa2 d.93.1.1 (A:2-110) Tyrosine phosphatase shp-2 {Human (Homo sapiens)}

KSRRWFHPNITGVEAENLLTRGVDGSLARPSKSNPGLTLSVRNGAVTHIKIQNTGDYYDLYGGEKFATLAE
LVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSE
>d2shpa3 d.93.1.1 (A:111-218) Tyrosine phoshatase shp-2 {Human (Homo sapiens)}
RWFHGHLGKEAELLTEKGKHGSFLVRESQSHPGDFVLSVRTGDDKGESNDGSKVTHVMIRCQELKYDVGG
GERFDSLTDLVEHYKKNPMVETLGTVLQLKQPLNT
>d1d4ta_d.93.1.1 (A:) The Xlp protein Sap {Human (Homo sapiens)}
MDAVAVYHGKISRETGEKLLATGLDGSYLLRDSESVPGVYCLCVLYHGYIYTYRVSQTETGSWSAETAPGVHKR
YFRKIKNLISAFQKPDQGIVIPLQYPVEK
>d1spha_d.94.1.1 (A:) Histidine-containing phosphocarrier protein (HPr) {Bacillus subtilis}
AQKTFKVTADSGIHARPATLVQTASKYDADVNLLEYNGKTVNLKDIMGVMSLGIAKGAEITISASGADENDALN
ALEETMKSEGLGE
>d1ptf_d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Enterococcus faecalis}
MEKKEFHIVAETGIHARPATLLVQTASKFNSDINLEYKGKSVNLKSIMGVMSLGVGQGSVTITVDGADEAEGM
AAIVETLQKEGLA
>d1opd_d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Escherichia coli}
MFEQEVTITAPNGLHTRPAAQFVKEAKGFTSEITVTSNGKSASA
KDLFKLQTLGLTQGTVV
TISAEGEDEQKAVE
HLVKLMAELE
>d1pch_d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Mycoplasma capricolum}
AKFSAIITDKVGLHARPASVLAKEASKFSSNITIIANEKQGNLKSIMNV
MAMA
AIKTGTEITIQADGNDADQAIQAI
KQTMIDTALIQG
>d1zer_d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Staphylococcus aureus}
MEQNSYVIIDETGIHARPATMLVQTASKFDSDIQLEYNGKKVNLKSIMGVMSLGVGKDAEITIYADGSDESDAIQ
AISDVL
SKEGLT
>d1qr5a_d.94.1.1 (A:) Histidine-containing phosphocarrier protein (HPr) {Staphylococcus carnosus}
MEQQSYIIDETGIHARPATMLVQTASKFDSDIQLEYNGKKVNLKSIMGVMSLGVGKDAEITIYADGSDEADAIQ
AITDVL
SKEGLT
>d1k1ca_d.94.1.1 (A:) Crh, catabolite repression HPr-like protein {Bacillus subtilis}
VQQKVEVRLKTLQARPAALFVQEANRTSDV
FLEKDGKKVNAKSIMGLMSLAVSTGTEV
TLIAQGEDEQEAL
EKLAAYVQEEV
>d1jrma_d.206.1.1 (A:) Hypothetical protein MTH637 {Archaeon Methanobacterium
thermoautotrophicum}
VITMDCLREVGDDLLVIEVSPASGKFGIPSYNEWRKRIEV
KIHSPPQKGKANREII
KEFSETFGRDVEIVSGQKSR
QKTIRIQGMGRDLFLKLVSEKFGLEIP
>d1iba_d.95.1.1 (-) Glucose permease domain IIB {Escherichia coli}
MAPALVA
AFGGKENITNLDACITRLRV
SADVSKV
DQAGLKKLGAAGVV
VAGSGVQAIFG
TKSDNLKTEMDEY
IRNFG
>d1af5_d.95.2.1 (-) DNA endonuclease I-CreI {Chlamydomonas reinhardtii}
KYNKEFLYLAGFVDGDGSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLGKLVDEIGV
GYVRDRGSVSDY
ILS
EIKPLHNFLTQLQPFLKLQKQANLV
LKII
EQLPLEVCTW
VDQIAALNDS
>d1g9za_d.95.2.1 (A:) DNA endonuclease I-CreI {Chlamydomonas reinhardtii}
NTKYNKEFLYLAGFVDGDGSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFLD
KLVDEIGV
GYVRDRGSVSDY
ILS
EIKPLHNFLTQLQPFLKLQKQANLV
LKII
EQLPSAKESPD
KFLEV
CTW
VDQIAALNDS
KTRKT
TSETVRAVLD
>d1b24a1 d.95.2.1 (A:7-99) I-dmol {Archaeon Desulfurococcus mobilis}
VSGISAYLLGLI
GDGGLYKLKY
KGNRSEY
RVVITQ
KSEN
LIKQHIA
PLMQFL
IDE
LNVK
SKIQIV
KGDT
RYELRVSSK

KLYYYFANMLERIR

>d1b24a2 d.95.2.1 (A:100-179) I-dmol {Archaeon Desulfurococcus mobilis}

LFNMREQIAFIKGLYVAEGDKTLKRLRIWNKNKALLEIVSRWLNNLGVRNTIHLDHRHGTVVLNISLRDRIKFV
HTILS

>d1dfa2 d.95.2.2 (A:181-298) PI-Scel {Baker's yeast (Saccharomyces cerevisiae)}

PILYENDHFFDMQKSKFHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAEKLNCAEYKDRK
EPQVAKTVNLYSKVVVRGNGIRNNLNTENPLWDAIVGLGFLKD

>d1dfa3 d.95.2.2 (A:299-415) PI-Scel {Baker's yeast (Saccharomyces cerevisiae)}

GVKNIPSFLSTDNIGTRETFLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGLVSLARSLGLVSVNAEPAKVDMNG
TKHKISYAIYMSGGDVLLNVLSKCAGSKKFRPAPAAFARE

>d1dq3a3 d.95.2.2 (A:129-226) PI-Pfui intein {Archaeon Pyrococcus furiosus}

PDGEDYKFIFDYWLAGFIAGDGCDFKYHSHVKHGHEYIYDRLRIYDRIETFEIINDYLEKTFGRKYSIQKDRNIYYID
IKARNITSHYLKLLEGIDNG

>d1dq3a4 d.95.2.2 (A:227-335) PI-Pfui intein {Archaeon Pyrococcus furiosus}

IPPQILKEGKNAVLSFIAGLFDAEGHVSNKPGIELGMVNKRILEDVTHYLNALGIKARIKRELRKGIDYVLHVEEY
SSLLRFYELIGKNLQNEEKREKLEKVLNSNHKG

>d1a8ra_ d.96.1.1 (A:) GTP cyclohydrolase I {Escherichia coli}

PSLSKEAALVHEALVARGLETPLRPPVHEMDNETRKSLIAGHMTEIMQLNNLDLADDSLMETPHRIAKMYVDEI
FSGLDYANFPKITLIENKMKVDEMVTVRDITLTSTCESHFVTIDGKATVAYIPKDSVIGLSKINRIVQFFAQRPQVQ
ERLTQQILIALQTLLGTNNVAVIDAVHYCVKARGIRDATSATTTSLGGLFKSSQNTRHEFLRAVRHHN

>d1is8a_ d.96.1.1 (A:) GTP cyclohydrolase I {Rat (Rattus norvegicus)}

RPRSEEDNELNLPNLAAYSSIQLRGEDPQRQGLLKTPWRAATAMQFFTGYQETISDVLNDAIFDEDHDEMV
IVKIDIDMFSMCEHHLPVFVGRVHIGYLPNKQVLGLSKLARIVEIYSRRLQVQERLTQIAVATEALQPAGVGVVIE
ATHMCMVMRGVQKMNSKTVTSTMLGVFREDPKTREEFLLIRS

>d1b66a_ d.96.1.2 (A:) 6-pyruvoyl tetrahydropterin synthase {Rat (Rattus norvegicus)}

LRRRARLSRLVSFSASHRLHSPSLSAEENLKVFGKCNPNGHGHNYKVVVTIHGIEDPVTGMVMNLTDLKEYM
EEAIMKPLDHKNLDDVPYFADVSTTENVAVYIWENLQRLLPGALYKVKVYETDNNIVVYKGE

>d1dh_ d.96.1.3 (-) 7,8-dihidroneopterin aldolase {Staphylococcus aureus}

MQDTIFLKGMRFYGYHGALSAENEIGQIFKVDVTLKVDLSEAGRTDNVIDTVHYGEVFEEVKSIMEGKAVNLLE
HLAERIANRINSQYNRVMETKVRITKENPPPIPQHGDGVGIEIVRENK

>d1b9la_ d.96.1.3 (A:) 7,8-dihidroneopterin triphosphate epimerase {Escherichia coli}

AQPAAIIRIKNLRLRTFIGIKEEEINNRQDIVINVTHYPADKARTSEDINDALNYRTVTKNIIQHVENNRFSLLEKLT
QDVLDIAREHHWVTYAEVEIDKLHALRYADSVSMTLSWQR

>d1uox_1 d.96.1.4 (1-136) Urate oxidase (uricase) {Aspergillus flavus}

SAVKAARYGKDNRVYKVHKDEKTGVQTVYEMTCVLLEGEIETSYTKADNSVIVATDSIKNTIYITAKQNPVTPP
ELFGSILGTHFIEKYNHIHAAHVNIVCHRWRTRMDIDGKPHPHSFIRDSEEKRNQVQDVV

>d1uox_2 d.96.1.4 (137-295) Urate oxidase (uricase) {Aspergillus flavus}

GKGIDISSLGLTVLKSTNSQFWGFLRDEYTTLKETWDRILSTDV рату QWQWNFSGLQEVRSV рату PKFDATWAT
AREV рату KTFADNSASV рату QATMYKMAEQILARQQLIETVEYSLPNKHYFEIDLSWHKGLONTGKNAEVFAPQSD
PNGLIKCTVGRS

>d1puc_ d.97.1.1 (-) suc1 {Fission yeast (Schizosaccharomyces pombe)}

SKSGVPRLTASERERLEPFIDQIHYSРYADDEYEYRHVMLPKAMLKA IPTDYFNPETGTLRILQEEEWRGLGIT
QSLGWEMYEVHVPEPHILLFKREKD

>d1qb3a_ d.97.1.1 (A:) cks1 {Baker's yeast (Saccharomyces cerevisiae)}

HAFQGRKLTQERARVLEFQDSIHYSPRYSDDNYEYRHVMLPKAMLKVIPSDFNSEVGTLRILTEDEWRLGLGI
TQSLGWEHYECHAPEPHILLFKRPLNYEAELRAATAAAQ
>d1cksa_d.97.1.1 (A:) CksHs2 {Human (Homo sapiens)}
AHKQIYYSDKYFDEHYEYRHVMLPRELSKQVPKTHLMSEEEWRRLGVQQSLGVHYSIHEPEPHILLFRRPLP
K
>d1buhb_d.97.1.1 (B:) CksHs1 {Human (Homo sapiens)}
QIYYSQDKYDDEEFYRHVMLPKDIAKLPKTHLMSEEWRLGVQQSQGWVHYSIHEPEPHILLFRRPLP
>d1jtgb_d.98.1.1 (B:) beta-lactamase-inhibitor protein, BLIP {Streptomyces clavuligerus}
AGVMTGAKFTQIQFGMTRQQVLDIAGAENCETGGSGDSIHCRGHAAGDYYAYATFGTSAAADAKVDSKSQ
EKLLAPSAPTLAKFNQVTGMTRAQVLATVGQGSCTTWSEYYPAYPSTAGVTLSCFDVDGYSSTGFYRGSA
HLWFTDGVLQGKRQWDLV
>d1div_1 d.99.1.1 (56-149) Ribosomal protein L9 C-domain {Bacillus stearothermophilus}
RQAAEELANAKKLKEQLEKLTIPAKAGEGGRLFGSITSKQIAESLQAQHGLKLDKRKIELADAIRALGYTNVPV
KLHPEVTATLKVVHVTEQK
>d1div_2 d.100.1.1 (1-55) Ribosomal protein L9 N-domain {Bacillus stearothermophilus}
MKVIFLKDVKKGKKGEIKNVADGYANNFLFKQGLAIEATPANLKALEAQKQKEQ
>d1qhka_d.100.1.2 (A:) N-terminal domain of RNase HI {Baker's yeast (Saccharomyces cerevisiae)}
GNFYAVRKGRETIYNTWNECKNQVDGYGGAIYKKFNSYEQAKSFLG
>d1e3ha5 d.101.1.1 (A:152-262) Polynucleotide
phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5
{Streptomyces antibioticus}
FSGPIGGVRVALRGQWVAFPTHTELEDAVFDMVVAGRVEDGDVAIMMVEAEATEKTIQLVKDGAEAPTEEV
VAAGLDAAKPFIKVLCQAQADLAAKAAKPTGEFPVFLD
>d1e3ha6 d.101.1.1 (A:483-578) Polynucleotide
phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5
{Streptomyces antibioticus}
APVAGIAMGLISQEINGETHYVALTDILGAEDAFGDMDFKVAGTKEFVTALQLDTKLDGIPASVLAALKQARD
ARLHILDVMMEAIDTPDEMSPN
>d1efnb_d.102.1.1 (B:) Regulatory factor Nef {Human immunodeficiency virus type 1}
RPQVPLRPMTYKAADVLSHFLKEKGGLIHSQRQDILDLWIHTQGYFPDWQNYTPGPGVRYPLTFGWCY
KLVPVEPDKVEEANKGENTSLHPVSLHGMDDPEREVLEWRFDSSLAFHHVARELHPEYF
>d2nef_d.102.1.1 (-) Regulatory factor Nef {Human immunodeficiency virus type 1}
AWLEAQEEEVGFPVTPQVPLRPMTYKAADVLSHFLKEKGGLIHSQRQDILDLWIHTQGYFPDWQNYT
PGPGIRYPLTFGWCYKLVPVEPEKLEEANKDDPEREVLEWRFDSSLAFHHMARELHPEYFKNA
>d1cby_d.103.1.1 (-) Mosquitocidal delta-endotoxin CytB {Bacillus thuringiensis, strain Kyushuensis}
CSAPIIRKPFKHIVLTVPSSLDNFNTVFYVQPQYINQALHLANAQGAIDPLNLNFNFEKALQIANGIPNSAIVK
TLNQSVIQQTVEISVMVEQLKIIQEVGLVINSTSFWNSVEATIKGFTNLDQIDEAWIFWHSLSAHNTSYYYN
ILFSIQNEDTGAVMAVLPLAFEVSDVEKQKVLFITIKDSARYEVKMKALTQALHSSNAPIVDIFVN>NNNLY
>d1seta2 d.104.1.1 (A:111-421) Seryl-tRNA synthetase (SerRS) {Thermus thermophilus, strain hb27}
VGGEANREIKRVGGPPEFSFPPLDHVALMEKNGWWEPRIQSRSYALKGDLALYELALLRFAMDFMARR
GFLPMTLPSYAREKAFLGTGHFPAYRDQVWAIAETDLYLTGTAEVVLNALHSGEILPYEALPLRYAGYAPAFRSEA
GSFGKDVRLGRMLRVHQFHKEQYVLTEASLEASDRAFQELLENAAEILRLLPYRLVEATGDMGPGKWRQVDI
EVYLPSEGRYRETHSCSALLDWQARRANLRYRDPEGRVRYAYTLNNTALATPRILAMLENHQLQDGDRVVPQ

ALIPYMGKEVLEPCG

>d1e1oa2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysU}

DQEVRQRQYLDLIANDKSQTFVRSKILAAIRQFMVARGFMEVTPMMQVIPGGASARPFITHHNALDLD
MYLRIAPELYLKRLVGGFERVFEINRNFRNEGISVRHNPEFTMMELYMAYADYHDLIELTESLFRTLAQEVLGTT
KVTYGEHVDFGKPFEKLTMREAIIKKYRPETDMADLDNFDAAKALAESIGITVEKSWGLGRIVTEIFDEVAEHLI
QPTFITEYPAEVSPALARNDVNPEITDRFEFFFIGGREIGNGFSELNDAEDQAERFQEQQVNAKAAGDDEAMFYDE
DYVTALEYGLPPTAGLGIGIDRMIMLFTNSHTIRDVILFPAMRP

>d1bbua2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}

DQEARYRQRQYLDLISNDESNTFKVRSQILSGIRQFMVNRGFMEVTPMMQVIPGGAAARPFITHHNALDLD
MYLRIAPELYLKRLVGGFERVFEINRNFRNEGISVRHNPEFTMMELYMAYADYKDLIELTESLFRTLAQDILGKT
VTYGDVTLDFGKPFEKLTMREAIIKKYRPETDMADLDNFDSAKAIAESIGHVEKSWGLGRIVTEIFEEVAEHLIQ
PTFITEYPAEVSPALARNDVNPEITDRFEFFFIGGREIGNGFSELNDAEDQAQRFLDQVAKDAGDDEAMFYDED
YVTALEYHGLPPTAGLGIGIDRMIMLFTNSHTIRDVILFPAMRP

>d1kmma2 d.104.1.1 (A:4-325) Histidyl-tRNA synthetase (HisRS) {Escherichia coli}

NIQAIRGMNDYLPGETAIWQRIEGTLKNVLGSYGYSEIRLPIVEQTPLFKRAIGEVTDVVEKEMYTFEDRNGDSL
LRPEGTAGCVRAGIEHGLLYNQEQRQLWYIGPMFRHERPKGRYRQFHQLGCEVFGQLQGPIDAEIMLTARW
WRALGISEHVTLELSIGSLEARANYRDALVAFLEQHKEKLDCKRRMYTNPLRVLD SKNPEVQALLNDAPAL
GDYLDEESREHFAGLCKLLESAGIAYTVNQRLVRGLDYYNRTVFEWVTNSLSQGTVCAGGRYDGLVEQLGGR
ATPAVGFMGLERLVLLVQAVNPEFKA

>d1qe0a2 d.104.1.1 (A:1-325) Histidyl-tRNA synthetase (HisRS) {Staphylococcus aureus}

MIKIPRGQTQDILPEDSKKWR YIENQLDELMTFYNYKEIRTPIFESTDLFARGVGDSTDVVQKEMYTFDKKGDRSIT
LRPEGTAAVVRSYIEHKMQGNPNQPIKLYYNGPMFRYERKQKGRYRQFNQFGV EAIGAENPSVDAEVLMV
MHYQSFGLKHLKLVINSVGDMASRKEYNEALVKHFEPIHEFCSDCQSLHTDPMRILDCKVDRDKEAIKTAPR
ITDFLNEESKAYYEQVKAYLDDLGIPYTEDPNLVRGLDYYTHTAFELMMDNP NYDGAIITLCGGGRYNGLLELLD
GPSETGIGFALSIERLLALEEEGIELD

>d1h4vb2 d.104.1.1 (B:2-325) Histidyl-tRNA synthetase (HisRS) {Thermus thermophilus}

TARAVRGTKDLFGKELRMHQ RIVATARKVLEAGALELVTPIFEETQVFEKG V GAATDIVRKEMFTQDRGGRSL
TLRPEGTAAMVRAYLEHGMKVWPQPVR LW MAGPMFRAERPKGRYRQFH QV NYE ALGSEN PILD
SKSERDQ ALL KEL GVR
PM LD FLGEE ARAH LKEVER HLER LSV PYE LEPA LV RGL DYY V RTA FEV HHE EIGA QSA LGGG GRYD GL SELL GGP
RV PG VG FAF GVER VAL ALE AE GF GL PE

>d1atia2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}

AASSLDELVALCKRRGFIFQSSEIYGGLQGVYDYGPLGV ELKNNLQAWWRRNVYERDDMEGLDASVLTHRLVL
HYSGHEATFADPMVDNRITKKRYRLDHLLKEQPEEVLKRLYRAMEVEEENLHALVQAMM QAPERAGGAMTA
AGVLD PASGEPGDWT PPRYFNMMFQDLRGPRGG RGL LAYLRPETAQG IFVNFKNVLDAT SRKL GFGIAQIGKA
FRNEITPRNFIFRVREFEQMEIEYFVRPGEDEYWHRYWVEERLKWWQEMGLSREN LVPYQQPPESSAHYAKA
TVDILYRFPHGSLELEGIAQRTDFDLSHTKDQEALGITARVLNEHSTQRLAYRDPETGKFV PVVIEPSAGVD
RGVLALLAEAFTR EELPN GGE RIVLKLKP

>d1b76a2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}

AASSLDELVALCKRRGFIFQSSEIYGGLQGVYDYGPLGV ELKNNLQAWWRRNVYERDDMEGLDASVLTHRLVL
HYSGHEATFADPMVDNAKARYWTPPRYFNMMFQDLRGPRGG RGL LAYLRPETAQG IFVNFKNVLDAT SRKL
GFGIAQIGKA FRNEITPRNFIFRVREFEQMEIEYFVRPGEDEYWHRYWVEERLKWWQEMGLSREN LVPYQQP

PESSAHYAKATVDILYRFPHGSLELEGIAQRTDFDLGSHTKDQEALGITARVLNEHSTQRLAYRDPETGKWFVPY
VIEPSAGVDRGVALLAEEAFTREELPNEERIVLKLKP

>d1qf6a4 d.104.1.1 (A:242-532) Threonyl-tRNA synthetase (ThrRS) {Escherichia coli}
RDHRKIGKQLDLYHMQEEAPGMVFHWNDGWTIFRELEVFVRSKLKEYQYQEVKGPMMMDRVWEKTGHW
DNYKDAMFTTSENREYCIKPMNCPGHVQIFNQGLKSYRDLPLRMAEFGSCHRNEPSSLHGLMRVRGFTQD
DAHIFCTEEQIRDEVNGCIRLVYDMYSTFGFEKIVVKLSTRPEKRIGSDEMWDRAEADLAVALENNIPFEYQLG
EGAFYGPKIEFTLYDCLDRAWQCGTVQLDFSLPSRLSASYVGEDNERKVPVMIHRAILGSMERFIGILTEEFAGF

>d1eova2 d.104.1.1 (A:205-557) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}

PILLEDASRSEAAEAAGLPVVNLTRLDYRVIDLRTVTNQAIFRIQAGVCSELFREYLATKKFTEVHTPKLLGAPSE
GGSSVFEVTYFKGKAYLAQSPQFNQQLIVADFERYEIGPVFRAENSNTRHMTETGLDMEMAFEEHYHEV
LDTLSELFVFIFSELPKRFAHEIELVRKQYPVEEFKLPKDGKMRVRLTYKEGIEMLRAAGKEIGDFEDLSTENEKFGLK
LVRDKYDTDFYILDKFPLEIRPFYTMPDPANPKYSNSYDFMRGEEILSGAQRIHDHALLQERMKAHGLSPEDPG
LKDYCDGFSYGCPPHAGGGIGLERVVMFYLDLKNIRRASLFP RDPKRLRP

>d1b8aa2 d.104.1.1 (A:104-438) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus kodakaraensis}

PLPLDPTGKVKAELDTRLNNRFMDLRRPEVMAIFKIRSSVFKAVRDFFHENGFIEIHTPKIIATATEGGTELFPMKY
FEEDAFLAESPQLYKEIMMASGLDRVYEIAPIFRAEEHNTTRHLNEAWSIDSEMAFIEDEEEVMSFLERLVAHAI
NYVREHNAKELDILNFELEEPKLPFPRVSYDKALEILGDLGKEIPWGEDI DTEGERLLGKYM MENENAPLYFLYQY
PSEAKPFYIMKYDNKPEICRAFDLEYRGVEISSGGQREHRHDILVEQIKEKGLNPESFEFYLKAFRYGMPPHGGF
GLGAERLIKQMQLDLPNIREVILFPRDRRLTP

>d1c0aa3 d.104.1.1 (A:107-287,A:421-585) Aspartyl-tRNA synthetase (AspRS) {Escherichia coli}
VLPLDSNHVNTEEARLKRYLDLRRPEMAQRQLKTRAKITSVRRFMDDHGFLDIETPMLTKATPEGARDYLVPSR
VHKGFYALPQSPQLFKQLLMMMSGFDYYQIVKCFRDEDLRADRQPEFTQIDVETS FMTAPQVREVMEALVRH
LWLEVKGVDLGDFPVMTFAEAERRYGSDKPDLRXDESKWAPLWVIDFPMFEDDGEGLTAMHHPTSPKDM
TAAELKAAPENAVANAYDMVINGYEVGGGSVRIHNGDMQQTVFGILGINEEEQREKFGFLDALKYGTTPHAG
LAFLGLDLTMLLTGTNDNIRDVIAFPKTTAACLMTEAPS FANPTALAELSIQVK

>d1g51a3 d.104.1.1 (A:105-294,A:415-580) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}

TPPFPWDAGWRGEEEKEASEELRLKRYLDLRRRMQENLRLRHRVIKAIWDFLDREGFVQVETPFLTKSTPEG
ARDFLVPRHEPGLFYALPQSPQLFKQMLMVAGLDRYFQIARCFRDEDLRADRQPDFTQLDLEMSFVEVEDVL
ELNERLMAHFREALGV EPLPFPRLSYEEAMERYGSDKPDLXREGFRFLWVVDPLLEWDEEEEAWTYMH
HPFTSPHPEDPLLEKDPGRVRALAYDLVNGVEVGGGSIRIHDPRLQARVFRLLGIGEEEQREKFGFFLEALEYG
APPHGGIAWGLDRLLALMTGPSIREVIAFPKNKEGDPLTGAPSPVPEEQLRELGLMVVRP

>d1jjca_ d.104.1.1 (A:) Phenyl-tRNA synthetase (PheRS) alpha subunit, PheS {Thermus thermophilus and (Thermus aquaticus)}

RVDVSLPGASLFSGGLHPITLMERELVEIFRALGYQAVEGPEVESEFFNF DALNIPEHHPAR DMWDTFWLTGEG
FRLEGPLGEEVEGRLLLRTHTSPMQVRYMVAHTPPFRIIVPGRVFRF EQTDATHEAVHQLEG LVVGEIAMA
HLKGAIYELAQALFGPDSKVRFQPVYFPFVEPGAQFAVWWPEGGKWLELGGAGMVHPKV FQAVDAYRERLG
LPPAYRGVTGFAFGLGVERLAMLRYGIPDIRYFFGGRLKFLEQFKGVL

>d1jjcb5 d.104.1.1 (B:475-681) Phenyl-tRNA synthetase (PheRS) beta subunit, PheT, central domain {Thermus thermophilus (Thermus aquaticus)}

ALPAFFPAPDNRGVEAPYRKERRQLREVL SGLGFQEVTYSFMDPEDARRFRLDPPRLLL NPLAPEKAALRTHLF
PGLVRVLKENLDLDRPERALLFEVGRVFREREETHLAGLLFGEVGVLWAKERLSGYFLLKGYLEALFARLGLA R

VEAQAFPFLHPGVSGRVLVEGEEVGFLGALHPEIAQEELPPVHLFELRLPLPDKP
>d1hc7a2 d.104.1.1 (A:5-276) Prolyl-tRNA synthetase (ProRS) {Thermus thermophilus}
KGLTPQSQDFSEWYLEVIQKAEALADYGPVRGTIVVRPYGYAIWENIQQVLDRMFKETGHQNYFPLFIPMSFLR
KEAEHVEGFSPELAVVTHAGGELEEPLAVRPTSETVIGYMWSKWIRSWRDLQPQLNNQWGNVVRWEMRTRP
FLRTSEFLWQEGHTAHATREEAEEEVRRMILSIYARLAREYAAIPVIEGLKTEKEFKAGAVYTTIEALMKDGKALQ
AGTSHYLGENDARAFDIKFQDRDLQVKYVHTTSWGLSWRFIGAIIMTHGDD
>d1g5ha2 d.104.1.1 (A:41-330) The aaRS-like accessory subunit of mitochondrial polymerase gamma, N-terminal domain {Mouse (Mus musculus)}
EALVDLCRRRHFLSGTPQQLSTAALLSGCHARFGPLGVELRKNLASQWWSSMVVFREQVFAVDSLHQEPGS
QPRDSAFLVSPESIREILQDREPSKEQLVAFLENLLKTSGKLRTLLHGALEHYVNCLDLVNRKLPGLAQIGVCF
HPVSNNSNQTPSSVTRVGEKTEASLVWFTPTRTSSQWLDFWLRHRLWWRKFAMSPSNFSSADCQDELGRKGS
KLYYSFPWGKEPIETLWNLDQELLHTYPGNVSTIQGRDGRKNVPCVLSVSGDVDLGTLAYLYDSFQL
>d12asa_ d.104.1.1 (A:) Asparagine synthetase {Escherichia coli}
AYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGAEKAVQVKVKALPDAQFEVVHSLAKWKR
QTLGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDQWDWERVMGDGERQFSTLKSTVEAIWAGIKATEA
AVSEEFLAPFLPDQIHVFVHSQELLSRYPDLDAKGRERAIAKDLGAVFLVGIGGKLSDGHRHDVRAPDYDDWST
PSELGHAGLNGDILVWNPVLEDAFELSSMGIRVDADTLKHQLALTGDEDRLELEWHQALLRGEMPQTIGGGIG
QSRLTMILLQLPHIGQVQAGVWPAAVRESVPSLL
>d1bia_3 d.104.1.2 (64-270) Biotin repressor/biotin holoenzyme synthetase, catalytic (central) domain {Escherichia coli}
IQLLNALKQILGQLDGGSAVLPVIDSTNQYLLDRIGELKSGDACIAEYQQAGRGRGRKWFSPFGANLYLSMFW
RLEQGPAAAIGLSLVIGIVMAEVLRKLGADKVRVKWPNDLYLQDRKLAGILVELTGKTGDAAQIVIGAGINMAM
RRVEESVNQGWITLQEAGINLDRNTLAAMIRELRAALELFEQEGLAPYLSRWEKLDN
>d1qtsa2 d.105.1.1 (A:825-938) Alpa-adaptin AP2, C-terminal subdomain {Mouse (Mus musculus)}
FFQPTEMASQDFFQRWKQLSNPQQEVQNIFKAKHPMDTEITKAKIIGFGSALLEVDPNPANFVGAGIIHTKTT
QIGCLLRLEPNLQAQMYRLTLRTSKDTVSQRLCELLSEQF
>d1e42a2 d.105.1.1 (A:825-937) Beta2-adaptin AP2, C-terminal subdomain {Human (Homo sapiens)}
LFVEDGKMERQVFLATWKDIPNENEIQLQFQIKECHLNADTVSSKLQNNNVYTIAKRNVEGQDMLYQSLKLTNGI
WILAEIIRQPGNPNTLSLKCRapeVSQYIYQVYDSILKN
>d1c44a_ d.106.1.1 (A:) Sterol carrier protein 2 (SCP2) {Rabbit (Oryctolagus cuniculus)}
SSAGDGFKANLVFKIEKKLEEEGEQFVKKIGGIFAFVKVKGPGGKEATVVVDVKNGKGSVLPNSDKADCTIT
MADSDLLALMTGKMNPQS AFFQGKLKITGNMGLAMKLQNLQLQPGKA KL
>d1ikta_ d.106.1.1 (A:) SCP2-like domain of MFE-2 {Human (Homo sapiens)}
LQSTFVFEI GRRLK DIGPEV KK VNAV FEW HIT KGGNIGAKWTIDLKSGSGKVYQGPAKGAADTTIILSDEFM
EVVLGKLDPQKAFFSGRLKARGNIMLSQKLQMLKDYAKL
>d1eq6a_ d.107.1.1 (A:) Ran-binding protein mog1p {Baker's yeast (Saccharomyces cerevisiae)}
SMNNKEVELYGGAITT VVPPGFIDASTLREV PDTQEV YVNSR DEEEFEDGLATNESIIVDLLETVDKSDLKEAW
QFHVEDLT E N GTT KWE AL QED TV QQ GTK FT GLV MEV AN KW GKP DL A QT V VIG VAL I RL T QFD TDV V VIS IN VP
LTKEEASQ ASN KEL PARCH A HVY QL LQ EM VRK FHV V D TS LFA
>d1b87a_ d.108.1.1 (A:) Aminoglycoside 6'-N-acetyltransferase {Enterococcus faecium}
MIISEFDRNNPVLKDQLSDLLRTWPEEYGDSSAEEVEEMMNPERIAVAAVDQDELVGFIGAIPQYGITGWELH
PLVVESSRRKNQIGTRLVNYLEKEVASRGGITIYLGTDDLHGTTLSQTDLYEHTFDKVASIQLREHPYEFYEKLG
YKIVGVLPNANGWDKPDIMAKTIIPRPDS

>d1bo4a_ d.108.1.1 (A:) Aminoglycoside 3-N-acetyltransferase {Serratia marcescens}
GIIRTCRLGPQVKSMRAALDLGREFGDVATYSQHQPDSDYLGNLRSKTFIALAAFDQEAVVGALAAYVLPKF
EQPRSEIYIYDLAGSHERRQGIATALINLLKHEANALGAYVIYVQADYGDDPAVALYTKLG

>d1cm0a_ d.108.1.1 (A:) Histone acetyltransferase domain of P300/CBP associating factor, PCAF {Human (Homo sapiens)}
KVIEFHVVGNLSNQKPNKKILMWLVGLQNVFSHQLPRMPKEYITRLVFDPKHKTTLALIKDGRVIGGICFRMFPS
QGFTEIVFCAVTSNEQVKGYGTHLMNHLKEYHIKHDILNFTYADEYAIGYFKKQGFSKEKIPKTKYVGYIKDYEG
ATLMGCELNPRI

>d1ygha_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Baker's yeast (Saccharomyces cerevisiae)}
KIEFRVVNNNDNTKENMMVLTGLKNIFQKQLPKMPKEYIARLVYDRSHLSMAVRKPLTVVGGITYRPFDKREFAE
IVFCAISSTEQVRGYGAHLMNHLKDYVRNTSNIKYFLTYADNYAIGYFKKQGFTKEITLDKSIWMGYIKDYEGGTL
MQCSMLPRIRYLD

>d1qsta_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase {Tetrahymena thermophila}
LDFDILTNDGTHRNMKLLIDLKNIFSRQLPKMPKEYIVKLVDRLHHESMVILKNKQKVIGGICFRQYKPQRFAEVA
FLAVTANEQVRGYGTTRLMNKFDHMQKQNIEYLLTYADNFAIGYFKKQGFTKEHRMPQEKWKGYIKDYDGTT
LMECYIHYPYVDY

>d1qsma_ d.108.1.1 (A:) Histone acetyltransferase HPA2 {Baker's yeast (Saccharomyces cerevisiae)}
DNITVRVTENDKEGWQRLWKSQDFYEVSFPDDDDFNFGRFDPNIKMWA AVAVESSEKIIGMINFFNH
MTTWDFKDKIYINDLYVDENSRVKGAGGKLIQFVYDEADKLGTPSVWCTDESNHRAQLLYVKVGYKAPKILYK
RKGY

>d1bob_ d.108.1.1 (-) Histone acetyltransferase HAT1 {Baker's yeast (Saccharomyces cerevisiae)}
FKPETWTSSANEALRVSIVGENAVQFSPLFTYPIYGDSEKIYGYKDLIIHLAFDSVTFKPYVNVKYSAKLGDDNIVD
VEKKLLSFLPKDDDVIRDEAKWWDCFAERKTHNLSDVFEKVSELSNGEEFVVKSSLVDDFARRMHRRVQIFS
LLFIEAANYIDETPSWQIYWLLNKKTKEIGFVTYKYWHYLGAKSFDDEDIDKKFRAKISQFLIFPPYQNKGHGS
CLYEAIQSWELEDKSITEITVEDPNEAFDDLDRNDIQQLRKLGYDAVFQKHSDLSDEFLESSRKSLKLEERQFNRL
VEMLLLNNNS

>d1fy7a_ d.108.1.1 (A:) Histone acetyltransferase ESA1 {Baker's yeast (Saccharomyces cerevisiae)}
ARVRNLNRIMGKYEIEPWYFSPYPIELTDEDIFYIDDFTLQYFGSKQYERYRKCTLRHPPGNEIYRDDYVSFFEI
DGRKQRTWCRNLCLLSKLFLDHKTLYDVDPFLFYCMTRRDELGHHLVGYFSKEKESADGYNVACILTPQYQR
MGYKLLIEFSYELSKKENKVGSPKPLSDLGLLSYRAYWSDTLITLVEHQKEITIDEISSMTSMTTDILHTAKTL
NILRYYKGQHIIFLNEDILDYNRLKAKKRRTIDPNRLIWKPP

>d1cjwa_ d.108.1.1 (A:) Serotonin N-acetyltransferase {Sheep (Ovis aries)}
HTLPANEFRCLTPEDAAGVFEIERAFISVSGNCPLNLDEVQHFLTCPPELSLGWFVEGRLVAFIIGSLWDEERLTQ
ESLALHRPRGHS AHLHALAVHRSFRQQGKGSVLLWRYLHHVGAQPAVRAVMCEDALVPFYQRFGFHPAGP
CAIVVGSLTFTEMHCSL

>d1i12a_ d.108.1.1 (A:) Glucosamine-phosphate N-acetyltransferase GNA1 {Baker's yeast (Saccharomyces cerevisiae)}
LPDGFYIIRRMEEGDLEQVTETLKVLTTVGTITPESFCKLIKYWNEATVWNDNEDKKIMQYNPMVIVDKRTETVA
ATGNIIERKIIHELGLCGHIEDIAVNSKYQGQGLGKLLIDQLVTIGFDYGCYKIILDCDEKNVKFYEKCGFSNAGVE
MQIRK

>d1iica1 d.108.1.2 (A:34-218) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces cerevisiae)}

AMKDHKFWRTQPVKDFDEKVVEGPIDKPKTPEDISDKPLPLLSSFEWSIDVDNKKQLEDVFVLLNENYVEDR
DAGFRFNYTKEFFNWALKSPGWKKDWIGVRVKETQKLAFISAIPVTGVRGKQVPSVEINFLCVHKQLRSKR
LTPVLIKEITRRVNKCDIWHALYTGIVLPAPVSTCR

>d1iica2 d.108.1.2 (A:219-455) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces cerevisiae)}

YTHRPLNWKKLYEVDFTGLPDGHTEEDMIAENALPAKTAGLRKLKKEDIDQVFELFKRYQSRFELIQIFTKEEF
EHNFFIGEESLPLDKQVIFSYVVEQPDGKITDFFSFYSLPFTILNNTKYKDLGIGYLYYATDADFQFKDRFDPKATKA
LKTRLCELIYDACILAKNANMDVFNALTSDNTLFLDDLKGPGDGFLNFYLNYRAKPIITGGLNPDNSNDIKRR
SNVGVVML

>d1nmta1 d.108.1.2 (A:60-224) N-myristoyl transferase, NMT {Yeast (Candida albicans)}

EGPIDKLKTPEDVPNDPLPLISDFEWSTLDIDDNLQLDELYKLLYDNYVEDIDATFRFKYSHEFFQWALKPPGWR
KDWHVGVVRVKSTGKLAFIAATPVTFKLNKSNKVIDSVEINFLCIHKKLRNKRLAPVLIKEITRRVNKQNIWQALY
TGGSILPTPLTTCR

>d1nmta2 d.108.1.2 (A:225-451) N-myristoyl transferase, NMT {Yeast (Candida albicans)}

YQHRPINWSKLHDVGFSHLPPNQTKSSMVASYTLPPNPKLKGLRPMTGKDVTLSLLKYQERFDIVQLFTEE
EFKHWMLGHDENSDSNVVKSYYVEDENGIITDYFSYLLPFTVLDNAHQDELGIAYLFYYASDSFEKPNYKKRLN
ELITDALITSKKFGVDVFNCQDNFYFLKDCFGSGDGFLNYYLFNYRTFPMDGGIDKKTKEVVEDQTSGIGV
VLL

>d2vik__ d.109.1.1 (-) Villin, domain 1 (res. 1-126) {Chicken (Gallus gallus)}

VELSKKVTGKLDKTPGIQIWRIENMEMVPVPTKSYGNFYEGDCYVLLSTRKTGSGFSYNIHYWLGKNSSQDEQ
GAAAIYTTQMDEYLGSVAVQHREVQGHESETFRAYFKQGLIYKQGGVASGMK

>d1svy__ d.109.1.1 (-) Severin, domain 2 {Dictyostelium discoideum}

EYKPRLLHISGDKNAKVAEVPLATSSLNSGDCFLDAGLTIYQFNNGSKSSPQEKNKAAEVARAIDAERKGLPKVEV
FCETDSDIPAEFWKLLGGKGAIAAKH

>d1d0na2 d.109.1.1 (A:153-262) Gelsolin {Horse (Equus caballus)}

VPNEVVVQRLLQVKGRVV RATEVPVSWEFSNNGDCFILDGNNIYQWCGSKSNRFERLKATQVSKGIRDNER
SGRAQSVFEEGAPEAMLQVLGPKPTLPEATEDTVK

>d1d0na3 d.109.1.1 (A:263-383) Gelsolin {Horse (Equus caballus)}

EDAANRKLAKEYVNGAGPMVSVLADENPFAQGALARSEDCAFILDHGKDGFIFVWKGQANMEERKAALKT
ASDFISKMDYPKQTQVSVLPEGGETPLFRQFFKNWRDPDQTEGLGLAYL

>d1d0na4 d.109.1.1 (A:384-532) Gelsolin {Horse (Equus caballus)}

SSHIAHVERVPFDAATLHTSTAMAQQHGMDDGTGQKQIWRVEGSNKVPVDPATYQQFYGGDSYIILYNRH
GSRQQIIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSRVVQGKEPAHLMMSLFGGKPMIVYKGTSRE
GGQTA

>d1d0na5 d.109.1.1 (A:533-628) Gelsolin {Horse (Equus caballus)}

PASTRLFQVRASSSGATRAVEIIPKAGALNSNDAFVLKTPSAAYLWVGAGASEAEKTGAQELLRLVRAQPVQVAE
GSEPDFSWEALGGKATYRTSP

>d1d0na6 d.109.1.1 (A:629-755) Gelsolin {Horse (Equus caballus)}

RLDKKKMDAHPPRLFACSNKIGRFVIEVPGEFMQEDLATDDVMILLTDQVFVWVGKDSQDEEKTEALTSA
KRYIDTPAHRDRRTPTVVVKQGFEPSSFGWFLGWDSDYWSVDPLRALAELAA

>d1d4xg_ d.109.1.1 (G:) Gelsolin {Human (Homo sapiens)}

VEHPEFLKAGKEPGLQIWRVEKFDLVPVPTNLYGDFFTGDAYVILKTVQLRNGNLQYDLHYWLGNECSQDESG

AAAIIFTVQLDDYLNGRAVQHREVQGFESATFLGYFKSLKYKKGGVASGFK
>d1db0b1 d.109.1.1 (B:412-532) Gelsolin {Human (Homo sapiens)}
MDDDTGTGQKQIWRIEGSNKPVDPATYQFYGGDSIILYNYRHGGRQGQIYNWQGAQSTQDEVAASAILTA
QLDEELGGTPVQSRVVQGKEPAHLSLFGGKPMIYKGGTSREGGQTA
>d1db0b3 d.109.1.1 (B:629-742) Gelsolin {Human (Homo sapiens)}
RLKDKKMDAHPPLFACSNKIGRFVIEEVPGELEMQEDLATDDVMLLDTWDQVFVWVGKDSQDEEKTEALTSA
KRYIETDPANRDRRTPTIVVKQGFEPPEFVGWFLGWDDSYWS
>d1kcqa_ d.109.1.1 (A:) Gelsolin {Human (Homo sapiens)}
VVQRLFQVKGRRVVRATEVPVSWESEFNNGDCFILDLGNNIHQWCGSNSNRYERLKATQVSKGIRDNERSGRA
RVHVSEEGTEPEAMLQVLGPKPALPAGTEDTA
>d1f7sa_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Plant (Arabidopsis thaliana), ADF1}
ASGMAVHDDCKLRFELKAKRTHRFIVYKIEEKQKQVVVEKGQPIQTYEEFAACLPADECRYAIYDFDFVTAEN
CQSKSKIFFIAWCPDIAKVRSKMIYASSKDRFKRELDGIQVELQATDPTE
>d1cfya_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Baker's yeast (Saccharomyces cerevisiae)}
VAVADESLTAFNDLKLGKKYKFILGLNDAKTEIVVKETSTDPSYDAFLEKLPENDCLYAIYDFEYEINGNEGKRSKI
VFFTWSPDTAPVRSKMVYASSKDALRRALNGVSTDVQGTFSESYDSVLERVSR
>d1cnua_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {Amoeba (Acanthamoeba castellani), actophorin}
GIAVSDDCVQKFNELKLGHQHRYVTFKMNNASNTEVVVEHVGPNATYEDFKSQLPERDCRYAIFDYEFQVDG
GQRNKITFILWAPDSAPISKMMYTSTKDSIKKKLVGIQVEVQATDAAEISEDAVSERAKKD
>d1hqz1_ d.109.1.2 (1:) Cofilin-like domain of actin-binding protein abp1p {Baker's yeast (Saccharomyces cerevisiae)}
LEPIDYTTHSREIDAELYLKIVRGSDPDWTWLIISPNAKKEYEPESTGSSFHDFLQLFDETKVQYGLARVSPPGSDVE
KIIIGWCPDSAPLKTRASFAANFAAVANNLFKGYHVQVTARDEDLDELLMKISNAAGA
>d1ak7_ d.109.1.2 (-) Destrin {Human and pig (Homo sapiens) and (Sus scrofa)}
TMITPSSGNASGVQVADEVCRIFYDMKVRKCSTPEEIKRKKAVIDCLSADKKCIIVEEGKEILVGDVGVTITDPF
KHFVGMLPEKDCRYALYDASFETKESRKEELMFLWAPELAPLKSCKMIYASSKDAIKKKFQGIKHECQANGPEDL
NRACIAEKLGGSLIVAFEGCPV
>d1pne_ d.110.1.1 (-) Profilin (actin-binding protein) {Cow (Bos taurus)}
AGWNAYIDNLMADGTCQDAIVGYKDSPSVWAAVPGKTFVNITPAEVGILVGKDRSSFFVNGLTLGGQKCSV
RDSLLQDGEFTMDLRTKSTGGAPTFNITVTMTAKTLVLLMGKEGVHGGMINKKCYEMASHLRRSQY
>d1fil_ d.110.1.1 (-) Profilin (actin-binding protein) {Human (Homo sapiens), isoform I}
AGWNAYIDNLMADGTCQDAIVGYKDSPSVWAAVPGKTFVNITPAEVGVLVGKDRSSFYVNGLTLGGQKCSV
RDSLLQDGEFSMDLRTKSTGGAPTFNVTKTDLVLLMGKEGVHGGLINKKCYEMASHLRRSQY
>d1d1ja_ d.110.1.1 (A:) Profilin (actin-binding protein) {Human (Homo sapiens), isoform II}
AGWQSYVDNLMCDGCCQEAAIVGYCDAKYVWAATAGGVFQSITPIEDMIVGKDREGFFTNGLTLGAKKCSV
RDSLYVDGDCMDIRTKSQQGEPTYNVAVGRAGRALVIVMGKEGVHGGTLNKKAYELALYLRRSD
>d1acf_ d.110.1.1 (-) Profilin (actin-binding protein) {Acanthamoeba castellani}
SWQTYVDTNLVGTGAVTQAAILGLDGNTWATSAGFAVTPAQGTTLAGAFNNADAIRAGGFDLAGVHYVTLRA
DDRSIYGKKGSSGVITVKTSKAILGVGVYNEKIQPGTAANVVEKLADYLIGQGF
>d1f2ka_ d.110.1.1 (A:) Profilin (actin-binding protein) {Acanthamoeba castellani}
SWQTYVDTNLVGTGAVTQAIIIGHDGNTWATSAGFAVSPANGAALANAFKDATAIRSNGFELAGTRYVTIRAD

DRSVYGKKGSAGVITVKTSKAILIGVYNEKIQPGTAANVVEKLADYLIGQGF
>d1ypra_d.110.1.1 (A:) Profilin (actin-binding protein) {Baker's yeast (*Saccharomyces cerevisiae*)}
SWQAYTDNLIGTKVDKAVIYSRAGDAVVATSGGLSLQPNEIGEIVQGFDNPAGLQSNGLHIQGQKFMLLRA
DDRSIYGRHDAEGVVVCVRTKQTVIIAHYPPTVQAGEATKIVEQLADYLIGVQY
>d1cqa_d.110.1.1 (-) Profilin (actin-binding protein) {Birch (*Betula verrucosa*)}
SWQTYVDEHLMCIDGQGEELAASAIVGHDSVWAQSSFPQFKPQEITGIMKDFEEPGLAPTLHLGGIKY
MVIQGEAGAVIRGKKGGGITKKTGQALVFGIYEEPVTGQCNMVVERLGDYLIDQGL
>d3nul_d.110.1.1 (-) Profilin (actin-binding protein) {Mouse-ear cress (*Arabidopsis thaliana*)}
SWQSYVDDHLMCDVEGNHLTAAAILGQDGSVWAQSAKFPQLKPQEIDGIKKDFEEPGLAPTLFLGGEKYM
VIQGEQGAVIRGKKGGVTIKKTNQALVFGFYDEPMTGGQCNLVVERLGDYLIESEL
>d1g5ua_d.110.1.1 (A:) Profilin (actin-binding protein) {Para rubber tree (*Hevea brasiliensis*), hevb8}
SWQTYVDDHLMCIDGHRLTAAAIIGHDSVWAQSSFPQFKSDEVAVMKDFDEPGSLAPTLHLGGTKY
MVIQGEPGAVIRGKKGGITVKRTGQALIIGIYDEPLTPGQCNMIVERLGDYLLDQGL
>d1f5ma_d.110.2.1 (A:) Hypothetical protein ykl069wp {Baker's yeast (*Saccharomyces cerevisiae*)}
STGFHHADHVNYSSNLNKEEILEQLLSEYGLSDGQVNWVCNLSNASSLIWHAYKSLAVDINWAGFYVTQASEE
NTLILGPFQGKVACQMIQFGKGVCGTAASTKETQIVPDVNKYPGHIACDGETKSEIVVPIISNDGKTLGVIDIDCL
DYEGFDHVDKEFLEKLAKLINKSCVF
>d3pyp_d.110.3.1 (-) Photoactive yellow protein, PYP {Ectothiorhodospira halophila}
MEHVAFGSEDIENTLAKMDDGQLDGLAFGAIQLGDGNILQYNAAEGDITGRDPKQVIGKNFFKDVA
PEFYGKFKEGVASGNLNTMFETYTFDYQMTPTKVKVHMKKALSGDSYWVFVKRV
>d1ew0a_d.110.3.2 (A:) Histidine kinase FixL heme domain {Rhizobium meliloti}
GSHMLETEDVVRARD AHLRSILDTPDATVVSATDGIVSFNAAVRQFGYAEVEVIGQNLRLMPEPYRHEHD
GYLQRYMATGEKRIIGIDRVVSGQRKDGSTFPMKLA
VGEMRS GGERFFTGFIRD
>d1dp6a_d.110.3.2 (A:) Histidine kinase FixL heme domain {Bradyrhizobium japonicum}
DAMIVIDGHGIIQLFSTAERLFGWSELEAIGQNVNILMPEPDRSRHDSYISRYRTTSDPHIIGIGRIVTGKRRDGT
TFPMHLSIGEMQSGGEPYFTGFVRLTEHQQTQARLQEL
>d1bywa_d.110.3.3 (A:) Erg potassium channel, N-terminal domain {Human (*Homo sapiens*)}
SRKFIIANARVENCAVIYCNDFCELCGYSRAEVMQRPCTCDFLHG PCTQRRAAQIAQALLGAERKVEIAFYR
KDGSCFLCLVDVVPVKNEDGAVIMFILNF
EVVMEK
>d1g28a_d.110.3.4 (A:) Photoreceptor phy3 flavin-binding domain, lov2 {Maidenhair fern (*Adiantum capillus-veneris*)}
KSFVITDPRLDNPIIFASDRFLELT
EY TREEVLGN
NCRFLQGRGTDRKAVQL
RDAVKEQRD
VTQVL
NYTKGGR
AFWNLF
HLQVMR
DENGD
VQYFIGV
QQEM
>d1ifqa_d.110.4.1 (A:) Sec22b {Mouse (*Mus musculus*)}
SVLLTMIARVADGLPLAASM
MQEDEQSGRDLQQYQSQA
KQLFRKLNEQS
P
S
P
T
R
C
T
L
E
A
G
A
M
T
F
H
Y
I
I
E
Q
G
V
C
Y
L
V
L
CEAAFPKKLAFAYLEDLH
SEFDEQHGKKV
PTVSRP
YSFIE
FDT
FIQ
K
T
K
L
Y
>d1h8ma_d.110.4.1 (A:) Synaptobrevin homolog 1 ykt6 {Baker's yeast (*Saccharomyces cerevisiae*)}
MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSVGQFMTFFAETVASRTG
AGERQSIEEGNYIGHVYARSEGIC
GVLITDKQYPV
RPAYTLLNK
ILDEYLV
AHP
KEEWAD
VTETN
DAL
KM
QLDT
YISKY
QDPSQADA

>d1cfe_ d.111.1.1 (-) Pathogenesis-related protein 1 (PR1) {Tomato (Lycopersicon esculentum), P14a}
QNSPQDYLAVHNDARAQVGVGPMWDANLASRAQNYANSRAGDCNLIHSGAGENLAKGDDFTGRAAVQ
LWVSERPSNYATNQCVGGKKCRHYTQVWRNSVRLCGRARCNGWWFISCNYDPVGNWIGQRPY
>d1qnxa_ d.111.1.1 (A:) Insect allergen 5 (AG5) {Yellow jacket (Vespa vulgaris), Ves v 5}
AEAEFNNYCKIKCLKGGVHTACKYGSLSKPNCGNKVVSYGLTKQEKFQDILKEHNDFRQKIARGLETRGNPGQP
PAKNMKNLVWNDELAYAQVWWANQCQYGHDTCDVAKYQVGQNVALGSTAACYDDPVKLVKMWEDEVK
DYNPKKKFSGNDFLKTGHYTQM沃WANTKEVGCGSIKYIQEKWHKHLYCNYGPSGNFKNEELYQTK
>d1a6ja_ d.112.1.1 (A:) Nitrogen regulatory bacterial protein Ila-ntr {Escherichia coli}
LQLSSVLNRECTRSRVHCQSKKRALEIISELAAKQLSLPPQVVFAILTREKMGSTGIGNGIAIPHGKLEEDTLRAV
GVFVQLETPIAFDAIDNQPVDLLFALLVPADQTKTHLHTSLVAKRLADKTICRRLRAAQSDEELYQIITDE
>d1a3aa_ d.112.1.1 (A:) Phosphotransferase Ila-mannitol {Escherichia coli}
LFKLGAEINIFLGRKAATKEEAIRFAGEQLVKGGYVEPEYVQAMLDREKLPTYLGESIAVPHGTVEAKDRVLKTGV
VFCQYPEGVRFGEEDDIARLVIGIAARNNEHIQVITSLTNALDDESPLIERLAHTTSVDEVLELLAGRK
>d1hypn_ d.112.1.2 (P:) Erythrocyte membrane Band 3 {Human (Homo sapiens)}
KVYVELQELVMDEKNQELRWMEAARWVQLEENLGENGAWGRPHLSHLTFWSLLELRVFTKGTVLLDQETS
LAGVANQLLDRFIFEDQIRPQDREELLRALLKHSHAGELEALGGVKPAVLTRSGDPSQPLPQHSSLETQLFCEQ
GDGGTEGHSPSGILEKIPPSEATLVLVGRADFLEQPVLGFVRLQEEAELEAVELPVPIRFLFVLLGPEAPHIDYTQ
LGRAAATLMSERVFRIDAYMAQSRGELLHSLEGFLDCSLVLPPTDAPSEQALLSLVPVQRELLRRRYQ
>d1mut_ d.113.1.1 (-) Nucleoside triphosphate pyrophosphorylase (MutT) {Escherichia coli}
MKKLQIAVGIIRNENNEIFITRRAADAHMANKLEFPGGKIEGETPEQAVVRELQEEVGITPQHFSLFEKLEYEF
PDRHITLWFWLVERWEGEWGEGQPGEWMSLGLNADDFFPANEPEVIKLKRL
>d1g0sa_ d.113.1.1 (A:) ADP-ribose pyrophosphatase {Escherichia coli}
MLKPDNLPPVTFGKNDVEIIARETLYRGFFSLDLYRFRHRLFNGQMSHEVRREIFERGHAAVLLPFDPRDEVV
QIRIAAYDTSETPWLLEMVAGMIEEGESVEDVARREAIEAGLIVKRTKPVLFLASPGGTSERSSIMVGEVDATT
ASGIHGLADENEDIRVHVVSREQAYQWVEEGKIDNAASVIALQWLQLHHQALKNEWA
>d1jkna_ d.113.1.1 (A:) Diadenosine tetraphosphate hydrolase {Narrow-leaved blue lupine (Lupinus angustifolius)}
GPLGSMDSPPGYRRNVGICLMNNDKKIFAASRLDIPDAWQMPQGGIDEGEDPRNAIRELREETGVTSAEVI
AEVPYWLTYDFPPKVRKLNQWGSWDKGQAQKWFLFKFTGQDQEINLLGDGSEKPEFGEWSWVTPQLID
LTVEFKKPVYKEVLSVFAPH
>d1hx3a_ d.113.1.2 (A:) Isopentenyl diphosphate isomerase {Escherichia coli}
EHVILLNAQGVPTGTLKYAAHTADTRLHAFSSWLFNAKGQLLVTTRRALSKKAWPGVWTNSVAGHPQLGESN
EDAIVRCRYELGVEITPPESIYPDFRYRATDPSGIVENEVCPVFAARTTSALQINDEVM
DATPWAFSPWMVMQATNREARKRLSAFT
>d1hzta_ d.113.1.2 (A:) Isopentenyl diphosphate isomerase {Escherichia coli}
LHLAFSSWLFNAKGQLLVTTRRALSKKAWPGVWTNSVCGHPQLGESNEDAVIRRCRYELGVEITPPESIYPDFRY
RATDPSGIVENEVCPVFAARTTSALQINDEVM
SAFTQLKL
>d1ush_1 d.114.1.1 (363-550) 5'-nucleotidase (syn. UDP-sugar hydrolase), C-terminal domain {Escherichia coli}
KIGETNGRLEGDRDKVRFVQTNMGRILAAQMDRTGADFAVMSGGGIRDSIEAGDISYKNVLKVQPFGNVV
YADMTGKEVIDYLTAQAQMKPDSGAYPQFANVSFVAKDGKLNDLKIKGEPVDPAKTYRMATLNFNATGGDGYP
RLDNKPGYVNTGFIDAELKAYIQKSSPLDVSVYEPKGEVSWQ

>d1hrau_ d.115.1.1 (A:) Hypothetical protein YrdC {Escherichia coli}

NNLQRDAIAAAIDVLNEERVIAYPTEAVFGVGCDPSETAVMRLLEKQRPVDKGLILIAANYEQLKPYIDDMLT
DVQRETIIFSRWPGPVTFVFPAPATPRWLTGRFDLSAVRVTDHPLVVALCQAYGKPLVSTSANLSGLPPCRTVDE
VRAQFGAAFPVVPGETGGRLNPSEIRDALTGELFR

>d1g57a_ d.115.1.2 (A:) 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase,
RibB {Escherichia coli}

LLSSFGTPFERVENALAALREGRGMVLDDEDRENEGDMIFPAETMTVEQMALTRHGSGIVCLCITEDRRKQL
DLPMMPVENNTSAYGTGFTVTIEAAEGVTGVSAADRITTVRAAIADGAKPSDLNRPGVFPLRAQAGGVLTRG
GHTEATIDLMTLAGFKPAGVLCELTNDDGTMARAPCIEFANKHNMALVTIEDLVAYRQAHE

>d1dbxa_ d.116.1.1 (A:) Hypothetical protein HI1434 (YbaK homologue) {Haemophilus influenzae}
TPAIDLKKQKIPFILHTYDHDPPNNQHFGDEAAEKLGDPNRSFKTLLVAENGDKKKLACFVLATANMLNLKAA
KSIGVKKVEMADKDAAQKSTGYLVGGISPLGQKKRVKTVINSTALEFETIYVSGGKRLSVEAPIQDLAKVLGAEE
TDIVDE

>d1qqqa_ d.117.1.1 (A:) Thymidylate synthase {Escherichia coli}

MKQYLEMQKVLDQEGTQKNDRTGTGTLISFGHQMRFLNQDGFLVTTKRCHLRSHIHELLWFLQGDTNIAYLHE
NNVTIWDEWADENGDLGPVYKGKQRAWPTPDGRHIDQITVNLQLKNDPDSRIIVSAWNVGELDKMALA
PCHAFFQFYVADGKLSCQLYQRSCDVFLGLPFNIASYALLVHMMMAQQCDLEVGFVWTGGDTHLYSNHMDQ
THLQLSREPRPLPKLIKRKPESIDYRFEDFEIEGYDSHPGIKAPVAI

>d1tsy_ d.117.1.1 (-) Thymidylate synthase {Lactobacillus casei}

MLEQPYLDLAKKVLDGEHFKPDRHTGTYSIFGHQMRFDLSKGFLPLTTKKVPGLIKSELLWFLHGDTNIRFLQ
HRNHIWDEWAFEKWVKSDHEYHPDMTDGFGRHSQKDPEFAAVYHEEMAKFDDRVLHDDAFAAKYGDGLVY
GSQWRRAWHTSKGDTIDQLGDVIEQIKTHPSRKLVSAWNPEDVPTMALPPCHTLYQFYVNDGKLSLQLYQRS
ADIFLGVPFNIASYALLTHLVAHECGLEVGEIFIHTFGDAHLYVNLDQIKEQLSRTPRPAPTLQLNPDKHDIFDFD
MKDIKLLNYDPYPAIKAPVAV

>d1bkpa_ d.117.1.1 (A:) Thymidylate synthase {Bacillus subtilis}

TQFDKQYNSIIKDIINNGISDEEFDVRTKWDSDGTPAHTLSVISQMRFDNSEVPILTTKKVAWKTAIKELLWIQ
LKSNDVNDLNMMGVHIWDQWKQEDGTIGHAYGFQLGKKNRSLNGEKVDQVDYLLHQLKNPSSRRHITML
WNPDELDAMALTPCVYETQWVVKHGKLHLEVRARSNDMALGNPFNFQYNVLQRMIAQVTGYELGEYIFNI
GDCHVYTRHIDNLKIQMEREQFEAPELWINPEVKDFYDFTIDDFKLINYKHGDLLFEAV

>d1tis_ d.117.1.1 (-) Thymidylate synthase {Bacteriophage T4}

MKQYQDLIKDIFENGYETDDRTGTIALFGSKLRWDLTKGFPVTTKLAWSKACIAELIWFLSGSTNVNDLRLI
QHDSLIQGKTVWDNEYENQAKDLGYHSGELGPIYGKQWRDFGGVDQIIEVIDRIKKLPNDRRQIVSAWNPAEL
KYMALPPCHMFYQFNVRNGYLDLQWYQRSVDVFLGLPFNIASYATLVHIVAKMCNLPGLIFSGGNTHIYMN
HVEQCKEILRREPKECELCELVISGLPYKFRYLSTKEQLKYVLKLRPKDFVLNNYVSHPPIKGKMAV

>d1f28a_ d.117.1.1 (A:) Thymidylate synthase {Pneumocystis carinii}

NAEEQQYLNLVQYIINHGEDRPDRTGTLSVFAPSPLKFSLRNKTFPLTTKRVFIRGVIEELLWFIRGETDSLKL
EKNIHIWDANGSREYLDISIGLKRQEGDLGPIYGFQWRHFGAEYIDCKTNYIGQGVQLANIIQKIRTSPYDRRLI
LSAWNPADELEKMALPPCHMFQFYVHIPSNNHRPELSCQLYQRSCDMGLGVPFNIASYALLTCMIAHVCDLDP
GDFIHVMGDCHIYKDHEALQQQLTRSPPFPTLSNRSITDIEDFTLDDFNIQNYHPYETIKMKMSI

>d2tsra_ d.117.1.1 (A:) Thymidylate synthase {Rat (Rattus norvegicus)}

QHGELOQYLRQVEHIMRCGFKKEDRTGTGTLISFGMQARYSLRDEFPLLTTRVFWKGVLLELLWFIFGSTNAKE
LSSKGVRIWDANGSRDFLDLGSARQEGDLGPVYGFQWRHFGADYKDMDSYSGQGVQLQKVIDTIKT
PDDRRIIMCAWNPKDPLMALPPCHALCQFYVNGELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHITGLQ
PGDFVHTLGDIAHYLNHIEPLKIQLQREPRPFPKLRLRKVETIDDFKVEDFQIEGYNPHPTI

>d1hvya_d.117.1.1 (A:) Thymidylate synthase {Human (Homo sapiens)}

PPHGELQYLGQIQHILRCGVRKDDRTGTGTLVFGMQARYSLRDEFPLTTKRVFWKGVLLELLWFKGSTNAK
ELSSKGVKIWDANGSRDFLDLGLFSTREEGDLGPVYGFQWRHFGAEYRDMESDYSQGQVDQLQRVIDTIKTN
PDDRIIMCAWNPRDLPLMALPPCHALCQFYVNSELSCQLYQRSGDMGLGVPFNIASYALLTYMIAHTGLKP
GDFIHTLGAHIYLNHIEPLKIQLQREPRPFPKLRLRKVEKIDDFKAEDFQIEGYNPHPTIKMEMAV

>d1b5ea_d.117.1.1 (A:) dCMP hydroxymethylase {Bacteriophage T4}

MISDSMTVEEIRLHLGLALKEKDFVVDTGVKTIEIIGASFVADEPFIFGALNDEYIQRELEWYKSLSLVKDIPGE
TPKIWQQVASSKGEINSNYGWAIWSEDNYAQYDMCLAELGQNPDSSRGIMIYTRPSMQFDYNKDGMSDFM
CTNTVQYLIRDKKINAVVNMRNSNDVVFGRNDYAWQKYVLDKLVLSDLNAGDSTRQYKAGSIIWNVGSLSHVYS
RHFYLVDHWWKTGETHISKDY

>d1kq4a_d.207.1.1 (A:) Thy1 homologue {Thermotoga maritima, TM0449}

HMKIDILDKGFLVELDVMGNLDAVRAARVSFDMGLKDEERDRHLIEYLMKHGETPFEHVFTFHVKAPIFVA
RQWFRHRIASYNELSGRYSKLSYFYIPSPERLEGYKTTIPPERVTEKISEIVDKAYRTYLELIESGVPREVARIVLPLN
LYTRFFWTVNARSLMNFLNLRADSHAQWEIQQQYALAIARIFKEKCPWTFEAFLKYAYKGDL

>d1lba_d.118.1.1 (-) Bacteriophage T7 lysozyme (Zn amidase) {Bacteriophage T7}

AKQRESTDAIFVHCSATKPSQNVGVREIRQWHKEQGWLDVGYHFIIKRDGTVEAGRDEAVGSHAKGYNHN
SIGVCLVGGIDDKGKFDANFTPAQMQLRSLLVTLLAKYEGAVLRAHHEVAPKACPSFDLKRWWEKNELVTSDR
G

>d1cyo_d.120.1.1 (-) Cytochrome b5 {Cow (Bos taurus)}

SKAVKYTLEEIQKHNNSKSTWLILHYKVYDLTKFEEHPGGEELVREQAGGDATENFEDVGHSTDARELSKTFII
GELHPDDR SKIT

>d1f03a_d.120.1.1 (A:) Cytochrome b5 {Cow (Bos taurus)}

AVKYTLEEIQKHNNSKSTWLILHYKVYDLTKFEEHPGGEAVLRAQAGGDATANFEAVGHSTDARELSKTFIIGE
LHPDDR

>d1aqa_d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}

KYYTLEEIQKHDKSKSTWVILHHKVYDLTKFEEHPGGEELVREQAGGDATENFEDVGHSTDARELSKTYIIGELH
PDDR SKIAKPSETL

>d1axx_d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}

DKDVKYTLEEIQKHDKSKSTWVILHHKVYDLTKFEEHPGGEELVREQAGGDATENFEDVGHSTDARELSKTYI
IGELHPDDR SKIAKPSETL

>d1euea_d.120.1.1 (A:) Cytochrome b5 {Rat (Rattus norvegicus)}

DPAVYYRLEEVAKRNTAEETWMVIHGRVYDITRFLSEHPGEEILLEQAGADATESFEDVGHSPDAREMLKQYY
IGDVHPNDLKPK

>d1icca_d.120.1.1 (A:) Cytochrome b5 {Rat (Rattus norvegicus)}

DPAVYYRLEEVAKRNTSEETWMVIHGRVYDLTRFLSEHPGEEVLREQAGADATESFEDVGHSPDAREMLKQ
YYIGDVHPNDLKPK

>d1do9a_d.120.1.1 (A:) Cytochrome b5 {Rabbit (Oryctolagus cuniculus)}

DKDVKYTLEEIKKHNHSKSTWLILHHKVYDLTKFEEHPGGEELVREQAGGDATENFEDVGHSTDARELSKTFII
GELHPDDR SKLSKPMETL

>d1cxya_d.120.1.1 (A:) Cytochrome b558 {Ectothiorhodospira vacuolata}

TLPVFTLEQVAEHHSPPDCWMAIHGKVYDLTPYVPNHPGPAGMMLVCGQESTEAWETKSYGEPHSSLAAR
LLQRYLIGTL

>d1ltda2_d.120.1.1 (A:10-97) Flavocytochrome b2, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

KISPAEVAKHNKPDDCWVVINGYVYDLTRFLPNHPGGQDVFKFNAGKDVTIAFEPLHAPNVIDKYIAPEKKLGPL
QGSMPPELVCPPY

>d1soxa2 d.120.1.1 (A:3-93) Sulfite oxidase, N-terminal domain {Chicken (Gallus gallus)}

SYPEYTREEVGRHRSPEERVWVTHGTDVFDVTDFVELHPGGPDKILLAAGGALEPFWALYAVHGEPHVLELLQ
QYKVGEELSPDEAAPAAPDA

>d1vcc_ d.121.1.1 (-) Vaccinia DNA topoisomerase I, 9 kDa N-terminal fragment {Vaccinia virus, strain WR}

MRALFYKDGKLFTDNNFLNPVSDDNPAYEVLQHVKIPTHLTDVVYEQTWEEALTRLIFVGSDSKRRQYFYGK
MHV

>d1amw_ d.122.1.1 (-) HSP90 {Baker's yeast (Saccharomyces cerevisiae)}

ASETFEFQAEITQLMSLIINTVYSNKEIFLRELISNASDALDKIRYKSLDPKQLETEPDLFIRITPKPEQKVLEIRDGSI
GMTKAELINNLGTIAKSGTKAFMEALSAGADVSMIGQFGVGFYSLFLVADRVQVVISKSNDDEQYIWESNAGGS
FTVTLDEVNERIGRTILRLFLKDDQLEYLEEKRIKEVIKRHSEFVAYPIQLVVTKEVE

>d1byqa_ d.122.1.1 (A:) HSP90 {Human (Homo sapiens)}

PMEEEEEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIRYETLTDSKLDGKELHINLIPNKQDRTL
TIVDTGIGMTKADLINNLGTIAKSGTKAFMEALQAGADISMIGQFGVGFYSAYLVAEKVTITKHNDDEQYAWE
SSAGGSFTVRTDTGEPMGRGTVKVLHLKEDQTEYLEERRIKEIVKKHSQFIGYPITLFVE

>d1ei1a2 d.122.1.2 (A:2-220) DNA gyrase B {Escherichia coli}

SNSSDSSSIKVKGDAVRKRPGMYIGDTDDGTGLHHMVFEVVDNAIDEALAGHCKEIVTIHADNSSVQDD
GRGIPTGIHPEEGVSAAEVIMTVLHAGGKFDDNSYKVSGGLHGVGVSVVNALSQKLELVIQREGKIHRQIYEHG
VPQAPLAUTGETEKTTGTMVRFWPSLETFTNVTEFEYEILAKRLRELSFLSGVSIRLRDKRDGKEDHFHYEG

>d1b63a2 d.122.1.2 (A:-2-216) DNA mismatch repair protein MutL {Escherichia coli}

SHMPIQVLPPQLANQIAAGEVVERPASVVKELVENSLAGATRIDIDIERGGAKLIRIRDNGCGIKKDELALALAR
HATSKIASLDDLEAIISLGFRGEALASISSVSRLTLSRTAEQQEAWQAYAEGRDMNVTVKPAAHPGTTLEVLDL
FYNTPARRKFLRTEKTEFNHIDEIIRRILARFDVTINLSHNGKIVRQYRAVPEGGQKERRLGAIC

>d1bkna2 d.122.1.2 (A:20-216) DNA mismatch repair protein MutL {Escherichia coli}

VERPASVVKELVENSLAGATRIDIDIERGGAKLIRIRDNGCGIKKDELALALARHATSKIASLDDLEAIISLGFRGEA
LASISSVSRLTLSRTAEQQEAWQAYAEGRDMNVTVKPAAHPGTTLEVLDLFYNTPARRKFLRTEKTEFNHIDEI
IIRRILARFDVTINLSHNGKIVRQYRAVPEGGQKERRLGAIC

>d1h7sa2 d.122.1.2 (A:29-231) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}

GQVVLSTAVKELVENSLAGATNIDLKLKYGVLDIEVSDNGCGVEEENFEGLTLKHHTSKIQEFADELTQVETF
GFRGEALSSLCA LSDVTISTCHASAKVGTRLMFDHNGKIIQKTPYPRPRGTTVSQQLFSTLPVRHKEFQRNIKKE
YAKMVQVLHAYCIISAGIRVSCTNQLGQGKRQPVVCCTGGSPSIKENIGSVF

>d1bxda_ d.122.1.3 (A:) Histidine kinase domain of the osmosensor EnvZ {Escherichia coli}

TGQEMPMEMADLNALVGEVIAAESGYEREIETALYPGSIEVKMHPPLSIKRAVANMVVNAARYGNGWIKVSSG
TEPNRAWFQVEDDGPAPIEQRKHLFQPFVRGDSARTISGTGLGLAIVQRIVDNHNGMLELGTSERGGLSIRA
WLPVPVTRAQGTTKEG

>d1i58a_ d.122.1.3 (A:) Histidine kinase CheA {Thermotoga maritima}

GSHMVPISVFNRPRMVRDLAKKMNKEVNFMIRGEDTELDRTFVEEIGEPLLHLLRNAIDHGIEPKEERIAKG
KPIIGTLILSARHEGNVVIEVEDDGRGIDKEIIRKAIEKGLIDESKAATLSDQEILNFLVPGFSTKEVSEVSGRG
VGMDVVKNVVESLNGSISIESEKDGTKVTIRLPLT

>d1id0a_ d.122.1.3 (A:) Histidine kinase PhoQ domain {Escherichia coli}

RELHPVAPL LDNLTSALNKVYQRKGVNISLDISPEISFVGEQNDFVEVMGNVLDNACKYCLEFVEISARQTDEHLY

IVVEDDGGIPLSKREVIFDRGQRVDTLRPGQGVGLAVAREITEQYEGKIVAGESMLGGARMEVIFGRQH
>d1gkza2 d.122.1.4 (A:186-378) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK) {Rat (Rattus norvegicus)}
DFVGIICTRLSPKKIEKWVDFARRLCEHKYGNAPRVRINGHVAARFPFIPMPLDYILPELLKNAMRATMESHLDTPYNVPDVITIANNDVDLIRISDRGGGIAHKDLRVMMDYHFTTAESTQDPRIPLFGHLDMHSGGQSGPMHGFGLPLTSRAYAEYLGGSQLQLQSLQGIGTDVYVLRLRHIDGREE
>d1jm6a2 d.122.1.4 (A:1177-1366) Pyruvate dehydrogenase kinase {Rat (Rattus norvegicus), isozyme 2}
PKHIGSIDPNCVSDDVKDAYDMAKLLCDKYYMASPDLEIQEVNATNATQPIHMVVPSHLYHMLFELFKNAMRATVESHESSLTLPPIKIMVALGEEDLSIKMSDRGGVPLRKIERLFSYMYSTAPTPQPGTGGTPLAGFGYGLPISRLYAKYFQGDLQLFSMEFGTDAVIYLKALSTDVERLPVY
>d1ixma_d.123.1.1 (A:) Sporulation responce regulatory protein SpoOB {Bacillus subtilis}
SDTALTNEIHLGHSHRDWMNKQLQIKGNLQLQKYDRVEMIEEMVIDAKHESKLSNLKTPHLAFDFTFNWKTHYMTLEYVLGEIKDSLQDQKLAQKLMRKLFLFDQAVSRESENHLTVSLQTDHPDRQLILYLDFHGAFADPSAFDDIRQNGYEDVDIMRFEITSHECLIEIGL
>d1bola_d.124.1.1 (A:) Ribonuclease Rh {Rhizopus niveus}
SSCSSTALSCSNSANSDTCCSPEYGLVVLNMQWAPGYGPNAFTLHGLWPDKCSGAYAPSGGCDSNRASSIASVIKSKDSSLNSMLTYWPSNQGNNNVFWSHEWSKHGTCVSTYDPDCYDNYEEGEDIVDYFQKAMDLSRSQNVYKAFSSNGITPGGTYTATEMQSAIESYFGAKAKIDCSSGTLSDVALYFYVRGRDTYVITDALSTGSCSGDVEYPTK
>d1bk7a_d.124.1.1 (A:) Ribonuclease MC1 {Bitter gourd (Momordica charantia)}
FDSFWFVQQWPPAVCSFKSGSCPGLRTFTIHGLWPQSGSTSNTCPGSPFDITKISHLQLSQLNTLWPNVLRANNQQFWSHEWTKHGTCSESTFNQAAFKLAVDMRNNYDIIGALRPHAAGPNGRTKSROAIKGFLKAKFGKFPGLRCRTDPQTKVSYLVQVVAFCFAQDGSTLIDCTRDCGANFIF
>d1dixa_d.124.1.1 (A:) RNase LE {Tomatoes (Lycopersicon esculentum)}
ASGSKDFDFFYFVQQWPGSYCDTKQSCCYPPTGKPAADFGIHGLWPNNNDGTYPSNCDPNSPYDQSQISDLISMQQQNWP TLACPSGSGSTFW SHEWEKHGTCAESVLTNQHAYFKKALDLKNQIDLLSIQGADIHPDGE SYDLVNIRNAIKSAIGYTPWIQCNCVDQSGNSQLYQVYICVDGSGSSLIECPIFPGGKCGTSIEFPTF
>d1iqqa_d.124.1.1 (A:) S3-RNase {Japanese pear (Pyrus pyrifolia)}
YDYFQFTQQYQLAVCNSNRTLCKDPPDKLFTVHGLWPSNMVGPDPSKCIKNIRKREKLLEHQLEIIWPNVFDRTKNNLFWDKEWMKHGSCGYPTIDNENHYFETVIKMYISKKQNVSRILSKAKIEPDGKKRALLDIENAIRNGADNKKPKLKCQKKGTTTELVEITLCSDKSGEHFIDCPHPFEPISPHYCPTNNIKY
>d1g2ra_d.192.1.1 (A:) Hypothetical cytosolic protein SP0554 {Streptococcus pneumoniae}
RKIPLRKSVVSNEVIDKRDLLRIVKNKEGQVFIDPTGKANGRGAYIKLDNAEALEAKKKVFNRFSMSMEVEESFYDELIAYVDHKVKRRELGE
>d1c4ka3 d.125.1.1 (A:570-730) Ornithine decarboxylase C-terminal domain {Lactobacillus sp., strain 30a}
APLKQVLPSIYAANEERYNGTIRELCQELHDFYKNNNTFTYQKRLFLREFFPEQGMLPYEARQE FIRHNHNLVPLNKIEGIALEGALPYPPGVFCVAPGEKWSETAVKYFTILQDGINNFPGFAPEIQGVYFKQEGDKVVAYGEVYDAEVAKNDDRYNN
>d1g61a_d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Archaeon Methanococcus jannaschii}
MIIRKYFSGIPTIGVLALTTEITLLPIFLDKDDVNEVSEVLETKCLQTNIGGSSLVGSLSVANKYGLLPKIVEDEELD

RIKNFLKENNLDLNVEIJKNTALGNLILTNDKGALISPELKDFKKDIEDSLNVEVEIGTIAELPTVGSNAVVTNK
CLTHPLVEDDELEFLKSLFKVEYIGKGTANKGTTSVGACIIANSKGAVVGGDTGPELLIEDALGL

>d1g62a_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {Baker's yeast (*Saccharomyces cerevisiae*)}

MATRTQFENSNEIGVFSKLTNTYCLAVGGSENFYSAFEAEGLDAIPIVHTTIAGTRIIGRMTAGNRGLLVPTQT
TDQELQHLRNSLPDSVKIQRVEERLSALGNVICNDYVALVHPDIDRETEELISDVLGVEVFRQTISGNILVGSYCS
LSNQGGLVHPQTSVQDQEELSSLLQVPLVAGTVNRGSSVGAGMVVNDYLAUTGLDTAPELSVIESIFRL

>d1jdw_ d.126.1.2 (-) L-arginine: glycine amidinotransferase {Human (*Homo sapiens*)}

CPVSSYNEWDPLEEVIVGRAENACVPPFTIEVKANTYEKYWPFYQKQGGHYFPKDHLKKAVAEIEEMCNILKTE
GVTVRDPIDWSLKYPKTPDFESTGLYSAMPRDILIVVGNEIIAPMAWRSRFFEYRAYRSIIKDYFHRCAKWTT
APKPTMADELYNQDYPPIHSVEDRHKLAAQGKFVTFEPFCFDAADFIRAGRDIQAQRSQVTNYLGIEWMRRLH
APDYRVHIISFKDPNPMHIDATFNIIPGIVLSNPDRPCHQIDLFKKAGWTIITPPTPIPDHDPLWMSSKWLSM
NVMLDEKRMVDANEVPIQKMFEKLGITTIKVNIRNANSLGGFHCWTCVRRGTLQSYLD

>d1bwda_ d.126.1.2 (A:) L-arginine: inosamine-phosphate amidinotransferase {*Streptomyces griseus*}

RSLSVHVNEWDPLEEVIVGTAVGARVPTADRSVFAVEYAGDYESQEIQPSGAYPDRVLKETEEELHVLAELTKLG
VTVRPGPRDHSALIKTPDWETDGFHDYCPRDGLLSGQTIETPMALRSRFLESLAYKDLLLEYFASGSRWLSA
PKPRLTDDSYAPQAPAGERLTDEEPVFDAAANVLRGTDLLYVSDSGNELGAKWLQSAVGDTYTVPCKRKYAST
HVDSTIVPLRPGLVLTNPSRVNDENMPDFLRSWENITCPELVDIGFTGDKPHCSVWIGMNLLVVRPDLAVVDR
RQTALIRLLEKHGMNVLPQLQTHSRTLGGFHCATLDVRRGALETYQF

>d1h70a_ d.126.1.3 (A:) Dimethylarginine dimethylaminohydrolase DDAH {*Pseudomonas aeruginosa*}

FMFKHIIARTPARSLVDGLTSSH LGKPDYAKALEQHNAYIRALQTCVDITLLPPDERFPDSVFEDPVLCRCAII
TRPGAESRRGETEIIETVQRFPYGKVERIEAPGTVEAGDIMMVGDFHYIGESARTNAEGARQMIALEKHGLS
GSVVRLEKVLHLKTGLAYLEHNNLLAAGEFVSKPEFQDFNIIIEPEEESYAANCIWVNERVIMPAGYPRTREKIARL
GYRVIEWDTSEYRKIDGGVSSMSLRF

>d1chma2 d.127.1.1 (A:157-402) Creatinase, catalytic (C-terminal) domain {*Pseudomonas putida*}

MIKSAEEHVMIRHGARIADIGGAAVVEALGDPVPEYEVALHATQAMVRAIADTFEDVELMDTWTFQSGIN
TDGAHNPVTRKVNKGDIISLNCFPMIAGYYTALERTLFLDHCSDDHLRLWQVNVEVHEAGLKLICKPGARCSDI
ARELNEIFLKHDLQYRTFGYGHSGFTLSHYYGREAGLELRREDITVLEPGMVVSMEPMIMLPEGLPAGGYRE
HDILIVNENGAENITKFPYGPEKNIR

>d1c22a_ d.127.1.1 (A:) Methionine aminopeptidase {*Escherichia coli*}

AISIKTPDIEKMRVAGRLAAEVLEMIEPYVKPGVSTGELDRICNDYIVNEQHAVSACLGYHGPKSVCISINEVV
CHGIPDDAKLLKGDIVNIDVTIKDGFHGDTSKMFIVGKPTIMERLCRITQESLYLALRMVKPGINLREIGAAI
QKFVEAEGFSVREYCGHGIGQGFHEEPQLHYDSRETNVVLKPGMTFTIEPMVNAGKKEIRTMKDGTWVKT
KDRSLSAQYEHTIVTDNGCEILTRKDDTIPAIISHD

>d1xgsa2 d.127.1.1 (A:1-194,A:272-295) Methionine aminopeptidase {Archaeon *Pyrococcus furiosus*}

MDTEKLMKAGEIAKKVREKAIKLARPGMILLLEAESIEKMIMELGGKPAFPVNLSINEIAAHYTPYKGDTTVLKE
GDYLKIDVGVHIDGFIADTAUTVRVGMEEDELMEAACEALNAAISVARAGVEIKELGKAIENEIRKRGFKPIVNL
GHKIERYKLHAGISIPNIYRPHDNYVLKEGDVFAIEPFATIGAXRNGIVAQFEHTIIVEKDSIVTTE

>d1b6a_2 d.127.1.1 (110-374,449-478) Methionine aminopeptidase {Human (*Homo sapiens*)}

KVQTDPSPVPCDLYPNGVFPKGQECEYPPTDGRTAAWRTTSEEKKALDQASEEIWNDFREAAEAHRQVRKY

VMSWIKGPMTMIEICEKLEDCSRKLICKENGLNAGLAFPTGCSLNNAAHYTPNAGDTTVLQYDDICKIDFGTHI
SGRIIDCAFTVTNPKYDTLLKAVKDATNTGIKCAGIDVRLCDVGEAIQEVMESYEVEIDGKTYQVKPIRNLNGHS
IGQYRIHAGKTVPIVKGEATRMEEGEVAIETFGSTGKGVXDIKGSYTAQFEHTILLRPTCKEVVSRGDDY
>d1az9_2 d.127.1.1 (177-440) Aminopeptidase P, C-terminal domain {Escherichia coli}
SPEIAVLRRAGEITAMAHTRAMEKCRPGMFEYHLEGEIHHEFNRHGARYPSYNTIVGSGENGCLHYTENECE
MRDGDLVLIDAGCEYKGYAGDITRTFPVNGKFTQAQREIYDIVLESLETSLRLYRPGTSILEVTGEVVRIMVGLVK
LGILKGDVDDELIAQNAHRPFFMHGLSHWLGLDVHDVGVYQQDRSRILEPGMVLTVEPGLIAPDAEVPEQYRG
GIRIEDDIVITETGNENLTASVVKPEEIEALMVAARKQ
>d1f52a2 d.128.1.1 (A:101-468) Glutamine synthetase, C-terminal domain {Salmonella typhimurium}
DRDPRTSIKRAEDYL RATGIADTVLFGPEPEFFLFDDIRFGASISGSHVAIDDIEGAWNSSTKYEGGNKGHRPGV
KGGYFPVPPVDSAQDIRSEMCLVMEQMGLVVEAHHEVATAGQNEVATRFNTMTKKADEIQIYKVVHNVA
HRFGKTATFMPKPMFGDNGSGMHCHMSLAKNGTNLFGDKYAGLSEQALYYIGGVIKHAKAINALANPTTNS
YKRLVPGYEAPVMLAYSARNRSASIRIPVVASPKARRIEVRFPDPAANPYLCFAALLMAGLDGIKNKIHPGEPMD
KNLYDLPPEAKEIIPQVAGSLEEALNALDLDREFLKAGGVFTDEAIDAYIALRREEDDRVRMTPHPVEFELYSV
>d1crka2 d.128.1.2 (A:99-380) Creatine kinase, C-terminal domain {Chicken (Gallus gallus), mitochondria}
TMKHHTDLDASKITHGQFDERYVLSSRVRTGRSIRGLSLPPACRSAERREVENVVTLAGLKGDLGGKYYSLTN
MSERDQQQLIDDHFLFDKPVSPLLTCAGMARDWPDARGIWHNNDKTFLVWINEEDHTRVISMEKGGMNMKR
VFERFCRGLKEVERLIKERGWEMWNERLGYVLTCPNSLGTGLRAGVHVKLPLRSKDPFPKILENRLQKRG
GGVDTAAVADVYDISNLRMGRSEVELVQVIDGVNYLVDCCEKKLEKGQDIKVPPLPQFGRK
>d1qh4a2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Chicken (Gallus gallus), brain-type}
TDEHKTDLNADNLQGGDDLDPNYVLSSRVRTGRSIRGFCLPPHCSRGERRAIEKLSVEALGSLGGDLKGKYALR
NMTDAEQQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKTFLVWINEEDHLRVISMKGGMNMK
EVFTRCTGLTQIETLFKSKNYEFMWNPHLGYILTCPSNLGTGLRAGVHIKLPLNLKHEKFGEVLKRLRLQKRG
GVDTAAVGGVFDVSNADRLGFSEVELVQMVVDGVKLLIMEKRLKGQSIDDLMPAQK
>d1qk1a2 d.128.1.2 (A:103-379) Creatine kinase, C-terminal domain {Human (Homo sapiens), mitochondria}
TTDLDASKIRSGYFDERYVLSSRVRTGRSIRGLSLPPACTRAERREVERVVVDALSGLKGDLAGRYYRLSEMTEAE
QQQLIDDHFLFDKPVSPLLTAAGMARDWPDARGIWHHNNEKSFLIWVWNEEDHTRVISMEKGGMNMKRVFERFC
RGLKEVERLIQERGWEMWNERLGYILTCPSNLGTGLRAGVHIKLPLLSKDSRFPKILENRLQKRG
TGGVFDISNLDRLGKSEVELVQLVIDGVNYLIDCERRLERGQDIRIPTVVIHTKH
>d2crka2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Rabbit (Oryctolagus cuniculus)}
TDHKHTDLHENLKGDDLDPHYVLSSRVRTGRSIRGFCLPPHCSRGERRAVEKLSVEALNSLTGEFKGKYPLKS
MTEQEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKSFLWVWNEEDHLRVISMKGGMNMKE
VFRRFCVGLQKIEEFKKAGHPFMWNEHLGYVLTCPNSLGTGLRGGVHVLAHLSKHPFEEILTRLRLQKRG
VFDTAAVGSVFDISNADRLGSSEVEQVQLVVDGVKLMVEMEKLEKGQSIDDMIPAQK
>d1g0wa2 d.128.1.2 (A:103-381) Creatine kinase, C-terminal domain {Cow (Bos taurus), retinal isoform}
TDEHKTDLNPDNLQGGDDLDPNYVLSSRVRTGRSIRGFCLPPHCSRGERRAIEKLA
VEALSSLDGLAGRYYALK
SMTEAEQQQLIDDHFLFDKPVSPLLLASGMARDWPDARGIWHNDNKTFLVW
INEEDHLRVISMKGGMNMK
EVFTRFCNGLTQIETLFKSKNYEFMWNPHLGYILTCPSNLGTGLRAGVH
IKLPHLGKHEKFS
EVLKRLRLQKRG
TG

GVDAAVGGVFDVSNADRLGFSEVELVQMVVGVKLLIEMEQRLEQGQAIDDLMPAQK
>d1bg0_2 d.128.1.2 (96-357) Arginine kinase {Horseshoe crab (*Limulus polyphemus*)}
TDKHPPKQWGDINTLVGLDPAGQFIISTRVRCGRSLQGYPFNPCLTAEQYKEMEEKVSSTLSSMEDELKGTYPL
TGMSKATQQQLIDDHFLFKEGDRFLQTANACRYWPTGRGIFHNDAKTFLVVWVNEEDHLRIISMQKGGDLKTV
YKRILVTAVDNIESKLPFSHDDRGFLTCPNLGTTMRASVHQLPKLAKDRKVLEDIAKFNQLQVRGTRGEHTES
EGGVYDISNKRRGLTEYQAVREMQDGILEMIKMEKAAA
>d1cdwa1 d.129.1.1 (A:155-252) TATA-box binding protein (TBP), C-terminal domain
{Human (*Homo sapiens*)}
SGIVPQLQNIVSTVNLGCKLDLKIALRARNAEYNPKRFAAVIMRIREPRTTALIFSSGKMWCTGAKSEENSLAA
RKYARVVQKLGFPACKFLDFKIQ
>d1cdwa2 d.129.1.1 (A:253-333) TATA-box binding protein (TBP), C-terminal domain
{Human (*Homo sapiens*)}
NMVGSCDVKFPIRLEGVLTHQQFSSYEPELFPGLIYRMKPRIVLLIFVSGKVVLTGAKVRAEIYEAFENIYPILKGF
RK
>d1qnaa1 d.129.1.1 (A:17-115) TATA-box binding protein (TBP), C-terminal domain
{*Arabidopsis thaliana*}
HPSGIVPTLQNIVSTVNLDCKLDLKIALQARNAEYNPKRFAAVIMRIREPPTTALIFASGKMWCTGAKSEDFSK
MAARKYARIVQKLGFPACKFKDFKI
>d1qnaa2 d.129.1.1 (A:116-198) TATA-box binding protein (TBP), C-terminal domain
{*Arabidopsis thaliana*}
QNIVGSCDVKFPIRLEGLAYSHAAFSSYEPELFPGLIYRMKVPKIVLLIFVSGKIVITGAKMRDETYKAFENIYPVLS
EFRKI
>d1ytba1 d.129.1.1 (A:61-155) TATA-box binding protein (TBP), C-terminal domain
{Baker's yeast (*Saccharomyces cerevisiae*)}
SGIVPTLQNIVATVTLGCRDLKTVLHARNAEYNPKRFAAVIMRIREPPTTALIFASGKMWVTGAKSEDDSKLAS
RKYARIIQKIGFAAKFTDF
>d1ytba2 d.129.1.1 (A:156-240) TATA-box binding protein (TBP), C-terminal domain
{Baker's yeast (*Saccharomyces cerevisiae*)}
KIQNIVGSCDVKFPIRLEGTFSSYEPELFPGLIYRMVKPKIVLLIFVSGKIVLTGAKQREEIYQAFEAIYPVLS
EFRKM
>d1aisa1 d.129.1.1 (A:1-92) TATA-box binding protein (TBP), C-terminal domain
{Archaeon *Pyrococcus woesei*}
MVDMISKVLRRIENIVASVDLFAQLDLEKVLDCPNSKYNPEEFPGIICHLDDPKVALLIFSSGKLVTGAKSVQDIE
RAVAKLAQKLKSIGV
>d1aisa2 d.129.1.1 (A:93-181) TATA-box binding protein (TBP), C-terminal domain
{Archaeon *Pyrococcus woesei*}
KFKRAPQIDVQNMVFSGDIGREFNLDVVALTPNCEYEPEQFPGVIYRVKEPKSVILLFSSGKIVCSGAKSEADA
WEAVRKLLRELDKY
>d1mpga2 d.129.1.2 (A:1-99) 3-Methyladenine DNA glycosylase II (gene alkA or aidA) {*Escherichia coli*}
MYTLNWQPPYDWWSMLGFLAARAVSSVETVADSYYARSLAVGEYRGVVTAPIRHTLHINLSAGLEPVAAE
CLAKMSRLFDLQCNPQIVNGALGRLG
>d1ko9a2 d.129.1.2 (A:12-135) 8-oxoguanine glycosylase {Human (*Homo sapiens*)}
GHRTLASTPALWASIPCPRSELRLDLVLPQGSFRWREQSPAHWSGVLADQVWTLTQTEEQLHCTVYRGDKSQ

ASRPTPDELEAVRKYFQLDVTLAQLYHHWGSVDSHFQEVAQKFQGVRLLRQ
>d1f46a_d.129.4.1 (A:) Cell-division protein ZipA, C-terminal domain {Escherichia coli}
RKEAVIIMNVAAHGSELNGEELLNSIQQAGIFGDMNIYHRHLSPDGSGPALFSANMVKPGTFDPEMKDFT
TPGVТИFMQVPSYGDELQLFKLMLQSAQHIADEVGGVLLDDQRRMMTPQKLREYQDIIREVKDANA
>d3pmga4 d.129.2.1 (A:421-561) Phosphoglucomutase {Rabbit (Oryctolagus cuniculus)}
RNFFTRYDYEEVEAEGATKMMKDLEALMFDRSFVGKQFSANDKVYTVEKADNFYHDPVDGSVSKNQGLRI
FADGSRIIFRLSGTGSAGATIRLYIDSYEKDNAKINQDPQVMLAPLISIALKVSQQLQERTGRTAPTVIT
>d1kfia4 d.129.2.1 (A:444-572) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}
RNYYSSRYDYEQVDSAGANKMMEHLTKFQYFEQLKQGNKADIYDYVDPVDQSVSKNQGVRFVFGDGSRIIFR
LSGTGSVGATIRIYFEQFEQQQIQHETATALANIILGLEISDIAQFTGRNEPTVIT
>d1bv1_d.129.3.1 (-) Major tree pollen allergen {White birch (Betula verrucosa), Bet v 1}
GVFNYETETTSV рАARLFKAFLDGDNLFPKVAPQAISSVENIEGNGGPGTIKKISFPEGLPFKYVKDRVDEVDHT
NFKYNYSVIEGGPIGDTLEKISNEIKIVATPDGGSILKISNKYHTKGДHEVKAEQVKASKEMGETLLRAVESYLLAH
SDAYN
>d1e09a_d.129.3.1 (A:) Major tree pollen allergen {Sweet cherry (Prunus avium), pru av 1}
GVFTYESEFTSEIPPPRLFKAFVLDADNLVPKIAPQAIIKHSEILEGDGGPGTIKKITFGEGSQYGYVKHKIDSIDKEN
YSYSYTLIEDALGDTLEKISYETKLVASPSGGSIKSTSHYHTKGNVEIKEEHVKAGKEKASNLKLIETYLKHPDA
YN
>d1em2a_d.129.3.2 (A:) Lipid transport domain of Mln64 {Human (Homo sapiens)}
SFSAQEREYIRQGKEATAVVDQILAQEENWKFEKNNEYGDTVYTIEVPFHGKTFILKFLPCPAELVYQEVLQPE
RMVLWNKTVTACQILQRVEDNTLISYDVSAAGGVSPRDFVNRRRIERRDRYLSSIATSHSAKPPTHKYV
RGENGPGGMIVLKSASNPRVCTFWILNTDLKGRPLPRYLIHQSLAATMFEFAFHLRQRISELGA
>d1fvza_d.129.3.4 (A:) Phoshatidylinositol transfer protein, PITP {Rat (Rattus norvegicus)}
VLLKEYRVILPVSDEYQVGQLYSVAEASKNETGGGEGVEVLVNEPYEKDDGEKGQYTHKIYHLQSKVPTFVRM
LAPEGALNIHEKAWNAYPYCRTVITNEYMKEDFLIKIETWHKPDLGTQENVHKEPEAWKHVEVIYIDIADRSQV
LSKDYKAEDPAKFKSITKGRGPLGPWNKQELVNQKDCPYMCAYKLTVKFKWWGLQNQKVENFIHKQEKRIFT
NFHRQLFCWLDKWVDLTMDDIRRMEEETKRQLDEMQRKDPVKGMTAD
>d1eg9a2 d.129.3.3 (A:155-447) Naphthalene 1,2-dioxygenase alpha subunit, C-domain {Pseudomonas putida}
EAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVKANWKAPENFVGDAYHVGWTHASSLRSGESIFSS
LAGNAALPPEGAGLQMITSKYGSGMGVLWDGYSGVHSADLVPЕLMAGGGAKQERLNKEIGDVRARIYRSHLN
CTVFPNNMSLTCGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSQRTFGPAGFWESDDNDNMET
ASQNGKKYQSRDSLNLGFGEDVYGDAYPGVVGKSAIGETSYRGFYRAYQAHVSSNWAEFEHASSTWH
TELTKTT
>d1mxa_1 d.130.1.1 (1-102) S-adenosylmethionine synthetase {Escherichia coli}
AKHLFTSEVSEGHPDKIADQISDAVLDAILEQDPKARVACETYVKTGMVLVGGEITTSAWVDIEEITRNTVREIG
YVHSDMGFDANSACAVLSAIGKQSPDI
>d1mxa_2 d.130.1.1 (108-231) S-adenosylmethionine synthetase {Escherichia coli}
RADPLEQGAGDQGLMFGYATNETDVLMPAPIYAHLRVQRQAEVRKNGTLPWLRPDAKSQVTFQYDDGKIV
GIDAVV рLSTQHSEEIDQKSLQEAVMEEIIPILPAEWLTSATKFFINPTGRFV
>d1mxa_3 d.130.1.1 (232-383) S-adenosylmethionine synthetase {Escherichia coli}
IGGPMGDCGLTGRKIIVDTYGGMARHGGAFSGKDPSKVDRSAAYAARYVAKNIVAAGLADRCEIQVSYAIGV

AEPTSIMVETFGTEKVPSEQLTLLVREFFDLRPYGLIQMILDLLHPIYKETAAYGHFGREHFPWEKTDKAQLLRDAA
GLK

>d1qm4a1 d.130.1.1 (A:17-116) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}
GAFMFTSEVGEGHPDKICDQISDAVLD AHLKQDPNAKVACETVCKTGMVLLCGEITSMAMIDYQRVVRDTIK
HIGYDDSAKGFDFTCNVLVALEQQSP

>d1qm4a2 d.130.1.1 (A:129-252) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}
EDVGAGDQGLMFGYATDETECMLTIVLAHKLNTRMADLRRSGVLPWLRPDSKTQVTQYVQDNGAVIPVR
VHTIVISVQHNEDITLEAMREALKEQVIKAVVPAKYLDEDTIYHLQPSGRFV

>d1qm4a3 d.130.1.1 (A:253-396) S-adenosylmethionine synthetase {Rat (Rattus norvegicus)}
IGGPQGDAGVTGRKIIVDTYGGWGAHGGGAFSGKD YTKVDRSAAYAARWVAKSLVKAGLCRRVLVQVSYAIG
VAEPLSISIFTYGTSSKKTERELLEVVNKNFDLRPGVIVRDLKKPIYQKTACYGHFGRSEFPWEVPKKLVF

>d2pola1 d.131.1.1 (A:1-122) DNA polymerase III, beta subunit {Escherichia coli}
MKFTVEREHLKPLQQVSGPLGGRPTLPILG NLLLQADGTLSTGTDLEMEMVARVALVQPHEPGATTVPARK
FFDICRGLPEGAEIAVQLEGERMLVRSGRSRFLSTLPAADFPNLDDW

>d2pola2 d.131.1.1 (A:123-244) DNA polymerase III, beta subunit {Escherichia coli}
QSEVEFTLPQATMKRLIEATQFSMAHQDVRYYLNGMLFETEGEELRTVATDGHRLAVCSMPIGQSLPSHSVIVP
RKGVIELMRMLDGGDNPLRVQIGSNNIRAHVGDFIFTSKLVDGRFPDY

>d2pola3 d.131.1.1 (A:245-366) DNA polymerase III, beta subunit {Escherichia coli}
RRVLPKNPDKHLEAGCDLLKQAFARAIALSNEKFRGVRLYVSENQLKITANNPEQEEAEI LDVTYSGAEMEIGF
NVSYVLDVLNALKCENVRMMILTDSSVSVQIEDAASQSAAYVVMPMRL

>d1b77a1 d.131.1.2 (A:1-110) gp45 sliding clamp {Bacteriophage RB69}
MKLSKDTIAILKNFASINSGILLSQGKFIMTRAVNGTTYAEANISDEIDFDVALYDLNSFLSILSVSDDAEISMHTD
GNIKIADTRSTVYWPAA DKSTIVFPNKPIQFP

>d1b77a2 d.131.1.2 (A:111-228) gp45 sliding clamp {Bacteriophage RB69}
VASVITEIKAEDLQQQLRVSRGQLQIDTIAITNKDGKIVINGYNKVEDSGLTRPKYSLTLDYDGSNNNFVINMAN
MKIQPGNYKVMLWGAGDKVA AKFESSQVSYVIA MEADSTHDF

>d1czda1 d.131.1.2 (A:1001-1110) gp45 sliding clamp {Bacteriophage T4}
MKLSKDTTALLKNFATINS GIMLKSGQFIMTRAVNGTTYAEANISDVIDFDV AYDLNGFLGILSLVND AEISQSE
DGNIKIADARSTIFWPAADPSTVVAPNKPIPFP

>d1czda2 d.131.1.2 (A:1111-1228) gp45 sliding clamp {Bacteriophage T4}
VASAVTEIKAEDLQQQLRVSRGQLQIDTIAITVKEGKIVINGFNKVEDS ALTRVKYSLTLDYD GENTFNFIIINMAN
MKMQPGNYKLLLWAKGKQGA AKFEGEHANYVVA LEADSTHDF

>d1dmla1 d.131.1.2 (A:29-169) UL42 {Human herpes virus type 1}
APCQVVLQGAELNGILQAFAPLRTSLLSLLVMGDRGILIHNTIFGEQVFLPLEHSQFSRYWRGPTAAFLSLD
QKRSLLSVFRANQYPDLRRVELAITGQAPFRTL VQRIWTTSDGEA VELASETLMKRELTSFVVLV

>d1dmla2 d.131.1.2 (A:170-319) UL42 {Human herpes virus type 1}
PQGTPDVQLRLTRPQLTKVLNATGADSATPTT FELGVNGKFSVTTSTCVTAFAAREEGVSSSTTQVQILSNALT
KAGQAAANAKTVYGENTHRTFSVVVDDCSMRAVLRLQVGGTLKFFLTPVPSLCVTATGPNAVSAVFL KPKQ
K

>d1plq_1 d.131.1.2 (1-126) Proliferating cell nuclear antigen (PCNA) {Baker's yeast (Saccharomyces cerevisiae)}

MLEAKFEEASLFKRIIDGF KDCVQLVNFQCKEDGIIAQAVDDSRVLLSLEIGVEAFQEYRC DHPVT LGMDL TSLS
KILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIA EYSLKLMIDADFL

>d1plq_2 d.131.1.2 (127-258) Proliferating cell nuclear antigen (PCNA) {Baker's yeast}

(*Saccharomyces cerevisiae*)}

KIEELQYDSTLSLPSSEFSKIVRDLSQLSDSINIMITKETIKFADGDIGSGSVIICPFVDMEHPESTIKLEMDQPVDLTFGAKYLLDIKGSSLSDRVGVIRLSSEAPALFQFDLKSGFLQFFLAPKFNDEE

>d1axca1 d.131.1.2 (A:1-126) Proliferating cell nuclear antigen (PCNA) {Human (Homo sapiens)}

MFEARLVQGSILKKVLEALKDLINEACWDISSGVNLQSMDSHVSLVQLTRSEGFDTYRCDRNLAMGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEVSODYEMKLMULDVEQL

>d1axca2 d.131.1.2 (A:127-255) Proliferating cell nuclear antigen (PCNA) {Human (Homo sapiens)} GIPEQEYSCVVKMPSGEFARICRDLSHIGDAVVISCAKDGVKFSASGELGNIGNIKLSQTNSVDKEEEAVTIEMNEPVQLTFALRYLNFFTAKTPLSMSADVPLVVEYKIADMGHLKYLAPKI

>d1ge8a1 d.131.1.2 (A:2-117) Proliferating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}

PFEIVFEGAKEFAQLIDTAKLIDEAAFKVTEDGISMRAAMDPSRVVLIDLNLPSSIFSKYEVVEPETIGVNLDHLKKILKRGKAKDTLILKKGEENFLEITIQGTATRTFRVPLID

>d1ge8a2 d.131.1.2 (A:126-247) Proliferating cell nuclear antigen (PCNA) {Archaeon Pyrococcus furiosus}

PELPFTAKVVVLGEVLKDAVKDASLVSDFIARENEFIMKAEGETQEVEIKLTLEDEGLLDIEVQEETKSAYGVSYLSDMVKGLGKADEVTIKFGNEMPMQMEYYIRDEGRLTFLAPRV

>d1hlra4 d.133.1.1 (A:311-907) Aldehyde oxidoreductase {Desulfovibrio gigas}

MSGPAAAAEDAIEIHPGTPNVYFEQPIVKGEDTGPIFASADVTVEGDFYVGRQPHMPIEPDVAFAYMGDDGKCYIHSKSIGVHLHLYMIAPGVGLEPDQLVLVANPMGGTGYKFSPTSEALVAVAAMATGRPVHLRNYQQQQQYTGKRSPWEMNVKFAAKKDGTLLAMESDWLVDHGPYSEFGDLLTRGAQFIGAGYNIPNIRGLGRTVATNHVWGSAFRGYGAPQSMFASECLMDMLAEKLGMDFPLERLRYKNAYRPGDTNPTGQEPEVFSLPDMIDQLRPKYQAALEKAQKESTATHKKVGVisGVYGSGLDPASEAWAELNADGTTVHTAWEDHGQGADIGCVGTAHEALRPMGVAPEKIKFTWPNTATTPNSGPSGSREQVMTGNAIRVACENLLKACEKPGGGYYTYDELKAADKPTKITGNWTASGATHCDAVTGLKPFVVMYGVMAEVTVDVATGQTTDGMTLADLGLSCNQLATDGQIYGGLAQGIGLALSEDDEFEDIKKHATLGAGFPFIKQIPDKLDIVYVNHPRPDGPGFASGVGELPLTSPHAAIINAISATGVRIYRPPAYPEKVLEALKA

>d1dgja4 d.133.1.1 (A:311-906) Aldehyde oxidoreductase {Desulfovibrio desulfuricans}

MSAPEAMAPDAIEIHPGTPNVYDQLEEKGEDTVPFNDPANVVAEGSYYTQRQPHLPIEPDVGYGYINEQQQVVIHSKSVAIHLHALMIAPGLGLEFPKDLVLVQNTTGGTGYKFSPTMEALGVAVMATGRPCHLRNYEQQQNYTGKRSPFWTTMRYAADRQGKILAMETDWSVDHGPYSEFGDLLTRGAQYIGAGYGIANIRGTGRTVATNHCWGAARFRGYGAPSEFPSEVLMDELAEKLGMDPFEALNCYREGDTTSSGQIPEVMSLPEMFDMRKPYYEE SKKRVKERSTAEIKRGVGVALGVYAGLDGPDTSEAWVELNDDGSVTLGNNSWEDHGQGADAGSLGTAHEALRPLGITPENIHLVMNTSKTPNSGPAGGSRSQVVTGNAIRVACEMILEGMRKPGGGFTPAEMKAEGRPMRYDGKWTAPAKDCDAKGQGSPFACMYGLFLTEVAVEVATGKATVEKMVCVADIGKICNKLVVDGQIYGGLAQGVGLALSEDYEDLKKHSTMGGAGIPSIMIPDDIEIVYVETPRKDGPFGASGVGEMPLTAPHAAIINGIYNACGARVRHLPARPEKVLEAMP

>d1fo4a5 d.133.1.1 (A:695-1332) Xanthine oxidase, C-terminal domain {Cow (Bos taurus)}

IITIEDAIKNNSFYGSELKIEKGDLKKGFSEADNVVSGELYIGGQDHFYLETHCTIAIPKGEEGEMELFVSTQNAMKTQSFVAKMLGVNVNRILVRVKRMGGGGKETRSTLVSVALAAAYKTGHPVRCMLDRNEDMLITGGRHPFLARYKVGFMKTGTIVALEVDHYSAGNSRDLHSIMERALFHMDCYKIPNIRGTGRLCKTNLSSNTAFRGFGGPQALFIAENWMSEVAVTCGLPAEEVRWKNMYKEGDLTHFNQRLEGFSVPRCWDECLKSSQYYARKSEVDKFNK

ENCWKKRGLCIPTKFGISFTVFLNQAGALIHVTGDSVLVSHGGTEMGQLHTKMQVASKALKIPIISKIYISE
TSTNTVPNSSPTAAVSTDIFYGQAVYEACQTILKRLEPFKKNPDGSWEDWVMAAYQDRVSLTTGFYRTPNLG
YSFETNSGNAFHYFTYGVACSEVEIDCLTDHKNLRTDIVMDVGSSLNPADIGQVEGAFVQGLGLFTLEELHYS
PEGSLHTRGPSTYKIPAFGSIPTEFRVSLLRDCPNKKAIYASKAVGEPLFLGASVFFAIKDAIRAARAQHTNNNTK
ELFLRDSPATPEKIRNACVDKFTLCVTGAPGNCPWSLRV

>d1jrob2 d.133.1.1 (B:124-777) Xanthine dehydrogenase chain B, C-terminal domain
{Rhodobacter capsulatus}

PAILTLDQALAADSRFEGGPVIWARGDVETALAGAAHLAEGCFEIGGQEHFYLEGQAALALPAEGGVVIHCSSQ
HPSEIQHKVAHALGLAFHDVRVEMRRMGGFGGKESQGNHLAIACAVAARATGRPCMKRYDRDDDMVITG
KRHDFRIRYRIGADASGKLLGADFVHLARCGWSADSLPVCDRAMLHADGSYFVPALRIESHRLRTNTQSNTAF
RGFGGPQGALGMERAIEHLARGMGRDPAELRALNFYDPPERGGLSAPPSPPEIATKKTQTHYGQEADCVL
GELVTRLQKSANFTTRRAEIAAWNNSTNRTLARGIALSPVKFGISFTLHLNQAGALVQIYTDGSVALNHGGTEM
GQGLHAKMVQVAAAVLGIDPVQVRITATDTSKVNTSATAASSGADMNGMAVKDACETLRGRLAGFVAARE
GCAARDVIFDAGQVQASGKSWRFAEIVAAAYMARISLSATGYATPKLSWDRLRGQGRPFLFYFAYGAAITEVVID
RLTGENRILRTDILHDAGASLNPALEGQIEGAVYQGAGWLTEELVWDHCGRLMTHAPSTYKIPAFSDRPRIFN
VALWDQPNREETIFRSKAVGEPPFLLGISAFLALHDACAACGPHWPDLQAPATPEAVLAavrRAEGRA

>d1qj2b2 d.133.1.1 (B:147-809) Carbon monoxide (CO) dehydrogenase molybdoprotein
{Pseudomonas carboxydovorans}

VDPFKAMEPDAPLLREDIKDKMTGAHGARKHHNHIFRWEIGDKEGTDATFAKAEVVSKDMFTYHRVHPSLE
TCQCVASMDKIKGELTLWGTQAPHVIRTVSLISGLPEHKIHIAPDIGGGFGNKVGAYSGYVCVVASIVLG
PVKWVEDRMENLSTS FARDYHMTTELAATKDGIKLMRCHVLADHGAFDACADPSKWPAGFMNICTGSYD
MPVAHLAVDGVYTNAKASGGVAYRXSFRVTEAVYAIERAIETLAQRLEMDSADLRIKNFQPEQFPYMAPLGWEY
DSGNYPLAMKKAMDTVGYHQLRAEQKAKQEAFKRGETREIMGIGISFFTEIVGAGPSKNCDILGVSMFDSEI
RIHPTGSIARMGTSQGQGHETTYAQIIATELGIPADDIMIEEGNTDTAPYGLGTYGSRSTPTAGAATAVAARKI
KAKAQMIAAHMLEVHEGDLEWDVDRFRVKGLPEKFKTMKELAWASYNSSPPNLEPGLEAVNYDPPNMV
FGAYFCIMIDIDTGVAKTRRFYALDDCGTRINPMIIEGQVHGLTEAFAVAMGQEIRYDEQGNVLGASFMDFF
LPTAVETPKWETDYTVTPSPHHPIGAKGVGESPHVGVGGPCFSNAVNDAYAFLNAGHIQMPHDAWRLWKVGE
QLGLHV

>d1ffvb2 d.133.1.1 (B:147-803) Carbon monoxide (CO) dehydrogenase molybdoprotein
{Hydrogenophaga pseudoflava}

IDALKPDAPVLREDLAGKTSGAHGPREHHNHIFTWGAGDKAATDAVFANAPVTVSQHMYYPRVHPCPLETCG
CVASFDPIKGDLTTYSQAPHVVRTVMSLGSIPESKVRIVSPIDGGFGNKVGYIYPGYVCAIVASIVLGRP
VEDRVENISTTAFARDYHMDGELAATPDGKILGLRVNVVADHGAFDACADPTKFPAGLFHICSGSYDIPRAHCS
VKGVYTNAKPGGVAYRCSFRVTEAVYLIERMVDVLAQKLNDKAEIRAKNFIRKEQFPYTTQFGFEYDSDYHT
ALKKVLDADVDPALRAEQARRADPNSPTLMGIGLVTTEVGAGPSKMCDILGVGMFDSCIEIHPGSAIAR
MGITQGQGHQTTYAQIIATELGIPSEVIQVEEGDTSTAPYGLGTYGSRSTPVAGAAIALAARKIHAKARKIAAH
MLEVNENDLDWEVDRFKVKGDDSKFTMADIAWQAYHQPPAGLEPGLEAVHYYDPPNFTYPFGIYLCVVDID
RATGETKVRRFYALDDCGTRINPMIIEGQIHGGLTEGYAVAMGQQQMPFDAQGNLLGNTLMDYFLPTAVETPH
WETDHTVTPSPHHPIGAKGVAESPHVGSIPTFTA VVDAFAHVGVTLDMPHTSYRVWKSLEHNLAL

>d1aop_3 d.134.1.1 (149-345) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4
{Escherichia coli}

NDMNRNVLCSTSNPYESQLHAEAYEWAKKISEHLLPRTRAYAEIWLDQEKVATTDEEPILGQTYLPRKFKTTVVIP
PQNDIDLHANDMNFAIAENGKLVGFNLLGGGLSIEHGNKKTARTASEFGYPLEHTLAVAEEAVTTQRDW
GNRTDRKNAKTKYTLERVGVETFKAEVERRAGIKFEPIRPYEFTGRGDR

>d1aop_4 d.134.1.1 (426-570) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4 {Escherichia coli}
PQRЕНSMACVSPTCPLAMAЕAERFLPSIDNIDNLMAKHGVСDEHIVMRVTGCPNGCGRAMLAEVGLVGK
APGRYNLHLGGNRIGTRIPRMYKENITEPEILASLDELIGRWAKERЕAGEGFГDFTVRAGIIRPVLDPARDLWD

>d1klqa_d.135.1.1 (A:) The spindle assembly checkpoint protein mad2 {Human (Homo sapiens)}
GSITLRGSAEIVAEFFSGINSILYQRGIYРSETFTRVQKYGLTLLTTDLELIKYLNNVVEQLKDWLЫKCSVQKLVV
ISNIESGEVLERWQFDIECDKTAKDDSPREKSQKAIQDEIRSVIRQITATVTFPLLEVSCSFДLIYTДKDLVVPEK
WEESGPQFITNSEEVRLRSFTTIHKVNSMVAYKIPVND

>d1byra_d.136.1.1 (A:) Nuclease Nuc {Salmonella typhimurium}
EPSVQVGYSPEGSARVLVLSAIDSАКTSIRMМAYSFADPMKALVAАKKRGVDVKIVIDERGNTGRASIAAMNY
IANSGIPLRTDSNFPIQHDKVIVDNVTETGSFNFTKAAETKNSENAVVИWNMPKLAESFLEHWQDRWNQGR
DYRS

>d1f0ia1 d.136.1.2 (A:6-263) Phospholipase D {Streptomyces sp.}
AATPHLDAVEQTLRQVSPGLEGDVWERTSGNKLGSAADPSDWLLQTPGCWGDDKCADRVGTKRLLAKMTE
NIGNATRTVDISTLAPFPNGAFQDAIVAGLKESAАKGNSLKVRILVGAAPVYHMNGIPSKYRDКLTAKLGKAAEN
ITLNVASMTTSKTAFSWNHSKILVVDGQSALTGGINSWKDDYLTTHPVSDV рALT GPAAGSAGRYLDTLWT
WTCKNKSNIASVWFAASGNAGCMPTMHKDTNPKASPATG

>d1f0ia2 d.136.1.2 (A:264-514) Phospholipase D {Streptomyces sp.}
NVPVIAVGGLVGИKDVDPKSTFRPDLPTASDTKCVVGLHDNTNADRDYDTVNPEESALRALVASAKGHIEISQ
QDLNATCPPLPRYDIRLYDALAAKMAAGVKVRIIVSDPANRGAVGSGGYSQIKSLSEISDTLRNRLANITGGQQ
AAKTAMCSNLQLATFRSSPNGKWADGHPYAQHHKLVSVDSTSFYIGSKNLYPSWLQDFGYIVESPEAKQLDA
KLLDPQWKYSQETATVDYARGICGA

>d1jy1a1 d.136.1.3 (A:145-350) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}
LEDPGEGQDIWDMLDKGНPQFYЛTRVSGVKPKYNSGALHКDILSPЛFGTLVSSAQFNYCFDВDVLVQYPPE
FRKKPILLVHGDKREAKAHLHAQAKPYENISLCQAKLIAFGTHHTKMMLLYEЕGLRVVIHTSNLIADWHHQK
TQGIWLSPLYPRIADGTHKSGESPTHFKANLISYLТАNAPSLKEWIDVIHKHDЛSET

>d1jy1a2 d.136.1.3 (A:351-608) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}
NVYЛIGSTPGRFQGSQKDNWGHFRLLKDHASSMPNAESWПVVGQFSSVGLADESKWLCEFKESMLT
LGKESKTPGKSSVPLYLIYPSVENVRTSLEGYPAGGSLPSIQTAEKQNWLHSYFHKWSAETSGRSNAMPHIKTY
MRPSPDFSКIAWFLVTSANLSKAАWGALEKNGTQLMIRSYELGVLFPSALGLDSFKVKQKFFAGSQEPMATFP
VPYDLPPELYGSKDRPWIWNIPYVKAPDTHGNMWVPS

>d1ckv_d.137.1.1 (-) Soluble methane monooxygenase regulatory protein B {Escherichia coli}
MSVNSNAYDAGIMGLKGKDFADQFFADENQVVHESDTVVLV рLKSDEINTFIEILLTDYKKNVNPTVNVEDRA
GYWWIKANGKIEVDCDEISELLGRQFNVYDFLVDVSSTIGRAYTLGNKFTITSELМGLDRKLEDYHA

>d2moba_d.137.1.1 (A:) Soluble methane monooxygenase regulatory protein B {Methylosinus trichosporium}
SNAVVLVLMKSDEIDAIIEDIVLKGKAKNPSIVVEDKAGFWWIKADGAIEIDAAEAGELLGKPFСVYDLLINVSS
TVGRAYTLGТKFTITSEL

>d1g10a_d.137.1.1 (A:) Toluene-4-monooxygenase catalytic effector protein {Pseudomonas mendocina}
STLADQALHNNNVGPIIRAGDLVEPVIETAЕIDNPGKEITVEDRRAYVRIAЕEGELILTRKTLEEQLGRPFNMQEL
EINLASFAGQIQADEDQIRFYFDKTM

>d1hqj_d.137.1.1 (-) Phenol hydroxylase P2 protein {Pseudomonas sp., CF600}
MSSLVYIAFQDNDNARYVVEAIIQDNPHAVVQHHPAMIRIEAKRLEIRRETVEENLGRAWDVQEMLVDVITIG

GNVDEDDDRFVLEWKN

>d1jjcb6 d.138.1.1 (B:191-399) B3/B4 domain of PheRS, PheT {Thermus thermophilus (Thermus aquaticus)}

LKAELPLPFALKVEDPEGAPHFTLGYAFGLRVAPSPLWMQRALFAAGMRPINNVDVTNYVMLERAQPMHA
FDLRFVGEGIAVRRAREGERLKTLGVERTLHPEDLVIAGWRGEESFPLGLAGVMGGAESEVREDTEAIALEVA
CFDPVSIRKTARRHGLRTEASHRFERGVDPGLQVPAQRRLSLLQALAGARVAEALLEAGSPK

>d1clia2 d.139.1.1 (A:171-345) Aminoimidazole ribonucleotide synthetase (PurM) C-terminal domain {Escherichia coli}

DGSKVSDGDVLIALGSSGPHNSNGYSLRKILEVSGCDPQTTELGDGPLADHLLAPTRIYVKSYLEIEKVDVHAIA
HTGGGFIVENIPRVLPDNTQAVIDESSWQWPEVFNLQTAGNVEHHEMYRTFNCVGMIIALPAPEVDKAL
ALLNANGENAWAKIGIIKASDSEQRVIE

>d1hw7a_d.193.1.1 (A:) Heat shock protein 33, Hsp33 {Escherichia coli}

HDQLHRYLFENFAVRGELTVSETLQQILENHDPQPVKNVLAELLVATSLLTATLKFQDGDITVQLQGDGPMNLA
VINGNNNQQMRGVARVQGEIPENADLKTLVGNGYVITIPSEGERYQGVVGLEGDTAACLEDYFMRSEQLP
TRLFIRTGDVDGKPAAGGMILLQVMPAQNAQQDDFDHLATLTETIKTEELLTPANEVLWRLYHEEEVTYDPQ
DVEFKCTC

>d1jw3a_d.208.1.1 (A:) Hypothetical protein MTH1598 {Archaeon Methanobacterium thermoautotrophicum}

MKGFEFFDVTADAGFWAYGHDLLEVFENAALAMFEVMTDSLVEAAEERRVEITSEDRVSLLYDWLDELLFIHD
TEFILFSKFKVKIDEKDDGLHLTGTAMGEEIKEGHERRDEVKAVTFHMMEILDDEDGLIKARVILD

>d1dl5a2 d.197.1.1 (A:214-317) Protein-L-isoaspartyl O-methyltransferase, C-terminal domain {Thermotoga maritima}

NLLERNRKLLREFPFNREILLVRSHIFVELV DLLTRRLTEIDGTFYYAGPNGVVEFLDDRMRIYGDAPEIENLLTQW
ESCGYRSFEYLMLHVGYNAFSHISCSI

>d1seia_d.140.1.1 (A:) Ribosomal protein S8 {Bacillus stearothermophilus}
VMTDPIADMFTAIRNANMVRHEKLEVPAKIKREIAEILKREGFIRDYEYIEDNKQGILRIFLKYGPNERVITGLKRI
SKPGLRVVKAHEVPRVLNGLGIAILSTSQGVTDKEARQKGTGGEIAYVI

>d1an7a_d.140.1.1 (A:) Ribosomal protein S8 {Thermus thermophilus}

TDPIADMTRIRNATRVYKESTDVPASRFKEEILRILAREGFIKYERVDGKPYLRVLYKGPRRQGPDRPEQ
VIHHIRISKPGRRVYVGVKEIPRVRRGLGIAILSTSKGVLTDREARKLGVGGEICEVW

>d1i94h_d.140.1.1 (H:) Ribosomal protein S8 {Thermus thermophilus}

MLTDPIADMTRIRNATRVYKESTEVPASRFKEEILKILAREGFIKYERVEVDGKPYLRVLYKGPRRQGPDRPE
QVIKHIRRISRPGRRVYVGVKEIPRVRRGLGIAILSTPKGVLDREARKLGVGGEICEVW

>d1i6ua_d.140.1.1 (A:) Ribosomal protein S8 {Archaeon Methanococcus jannaschii}

SLMDPLANALNHISNCERVGKKVYIKPASKLIGRVLKVMQDNGYIGEFEFIEDGRAGIFKVELIGKINKCGAIKP
RFPVKKFGYEKFCKYLPARDGFILIVSTTQGVMSHEEAKRGLGGRLLAYVY

>d1rl6a1 d.141.1.1 (A:7-81) Ribosomal protein L6 {Bacillus stearothermophilus}
PIEPAGVTVTNGNTVTKGPKGELTRFHPDMTITVEGNVITVTRPSDEKHHRALHGTTSSLANMVEGVSK
G

>d1rl6a2 d.141.1.1 (A:82-170) Ribosomal protein L6 {Bacillus stearothermophilus}
YEKALELVGVGYRASKQGKKLVLGVYSHPVEIEPEEGLEIEVPSQTKIIVKGADKQRVGELAANIRAVRPPEPYKG
KGIRYEGELVRL

>d1jj2e1 d.141.1.1 (E:1-79) Ribosomal protein L6 {Archaeon Haloarcula marismortui}

PRVELEIPEDVDAEQDHLDITVEGDNGSVTRRLWYPIDVSVDGDTVIESDEDNAKTMSTIGTFQSHIENMFH

GVTEG

>d1jj2e2 d.141.1.1 (E:80-172) Ribosomal protein L6 {Archaeon Haloarcula marismortui}

WEYGMEVFYSHFPMQVNVEGDEVVIENFLGEKAPRRTTIHGDTDVEIDGEELTVSGPDIEAVGQTAADIEQLTR
INDKDVRVFDQDGVYITRK

>d1gsa_2 d.142.1.1 (123-314) Glutathione synthetase {Escherichia coli}

NEKLFTAWFSDLTPETLVTRNKAQLKAFWEKHSDIILKPLDMGGASIFRVKEGDPNLGVIAETLTEHGTRYCMA
QNYLPAIKDGDKRVLVVDGEPPVYCLARIPQGGETRGNLAAAGGRGEPRPLTESDWKIARQIGPTLKEKGLIFVGL
DIIGDRLTEINVTSPCIREIEAEFPVSITGMILMDAIEARLQ

>d1iow_2 d.142.1.1 (97-306) D-ala-D-ala ligase {Escherichia coli, gene ddIB}

KLRSKLLWQGAGLPVAPWVALTRAEEFKGLSDKQLAEISALGLPIVVKPSREGSSVGMSKVVAENALQDALRLAF
QHDEEVVIEKWLSGPPEFTVAILGEEILPSIRIQPSGTFYDYEAKFSLDETQYFCPAGEASQEANLQALVLKAWTTL
GCKGWGRIDVMLDSGDQFYILLEANTSPGMTSHSLVPMAARQAGMSFSQLVVRILEAD

>d1ehia2 d.142.1.1 (A:135-362) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}

DKALTKELLTVNGIRNTKYIVVDPESANNWSWDKIVAELGNIVFVKAANQGSSVGISRVTNAEYTEALSDSFQY
DYKVLIEAVNGARELEVGVIGNDQPLVSEIGAHTVPNQGSGDGWYDYNNKFDNSAVHFQIPAQLSPEVTKE
VKQMALDAYKVLNLRGEARMDFLLDENNPVYLGEPNLPGFTNMSLFKRLWDYSDINNAKLVDMLIDYGFED
FAQNKKLS

>d1e4ea2 d.142.1.1 (A:132-342) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}

DKSLTYIVAKNAGIATPAFWVINKDDRPVAATFTYPVFKPARSGSSFGVKKVNSADELDYAIIESARQYDSKILIEQ
AVSGCEVGCAVLGNSAALVVGEVDQIRLQYQFRHQEVPEKGSENAVITVPADLSAEERGRIQETVKKIYKTLG
CRGLARVDMFLQDNNGRIVLNEVNTLPGFTSYSRYPRMMAAAGISLPELIDRLIVLALK

>d1dv1a3 d.142.1.2 (A:115-330) Biotin carboxylase subunit of acetyl-CoA carboxylase {Escherichia coli}

DKVSAIAAMKKAGVPCVPGSDGPLGDDMDKNRAIAKRIGYPVIKASGGGGGRGMRRVVRGDAELAQSIMT
RAEAKAAFSNDMVYMEKYLENPRHVEIQVLADGQGNAYLAERDCSMQRHHQKVVEEAPAPGITPELRRYIG
ERCAKACVDIGYRGAGTFEFLENGEFYFIEMNTRIQLQEVHPVTEMITGVVDLKEQLRIAAGQPLSIKQEEVHV

>d1gsoa3 d.142.1.2 (A:104-327) Glycinamide ribonucleotide synthetase (GAR-syn) {Escherichia coli}
SKAFTKDFLARHKIPTAEYQNFTEVEPALAYLREKGAPIVIKADGLAAGKGVIVAMTLEEAAVHDMLAGNAFG
DAGHRIVIEEFLDGEASFIVMDGEHVLPMTSQDHKRVGDKDTGPNTGGMGAYSPAPVVTDDVHQRTME
RIIWPTVKGMAAEGNTYTGFLYAGLMIDKQGNPKVIEFNCRGDLETQPIMLRMKSDLVELCLAACESKLDEKT
SEWD

>d1b6ra3 d.142.1.2 (A:79-276) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

DRLTKQLFDKLHLPTAPWQLLAERSEWPAPFDRLGELAIVKRRTGGYDGRGQWRLRANETEQLPAECYGEI
VEQGINFSGEVSLVGARGFDGSTVFYPLTHNLHQDGILRTSVAFPQANAQQQARAEEMLSAIMQELGYVGVM
AMECFVTPQGLLINELAPRVHNSGHWTQNGASISQFELHLRAITDLPLPQPVV

>d1eyza3 d.142.1.2 (A:113-318) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

NREGIRRLAAEELQLPTSTYRFADSESLFREAVADIGYPCIVKPVMSSSGKGQTFIRSAEQLAQAWKYAQQQGGA
GAGRIVVEGVVKDFEITLLTVASDGVHFCAPVGHRQEDGYRESWPQQMSPLALERAQEIAKVVLAG
GYLFGVELFVCGDEVIFSEVSPRPHDTGMVTLISQDLSEFALHVRAFLGLPVGGIRQY

>d1a9xa5 d.142.1.2 (A:128-402) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia

coli}

DRRRFDVAMKKIGLETARSGIAHTMEEALAVAADVGFPCIIRPSFTMGSGGGIAYNREEFEEICARGLDLSPTK
ELLIDESLIGWKEYEMEVVRDKNDNCIIVCSIENFDAMGIHTGDSITVAPAQLTDKEYQIMRNASMAVLREIGV
ETGGSNVQFAVNPKNGRLIVIEMNPRVSRSSALASKATGFPIAKVAALKAVGYTLELMNDITGGRTPASFEPSI
DYVVTKIPRFNFEKFAGANDRLLTQMKSVEVMAIGRTQQESLQKALRGL

>d1a9xa6 d.142.1.2 (A:677-935) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

RFQHAVERLKLKQPANATVTAIEMAVEKAKEIGYPLVRAAMEIVYDEADLRRYFQTAVLLDHFLDDAVEVDVD
AICDGEMVLIGGIMEHIEQAGVHSGDSACSLPAYTLSQEIQDVMRQQVQKLAFLQVRGLMNQFAVKNNEV
YLIEVNPRARTVPFVSKATGVPLAKVAARVMAGKSLAEQGVTKEVIPPYYSVKEVVLPFNKFPGVDPLLGPEM
RSTGEVMVGVRTFAEAFAKAQLGS

>d1auva2 d.142.1.3 (A:214-417) Synapsin Ia, C-terminal domain {Cow (Bos taurus)}

NSLHSVYNFCDKPWVFAQMVRHLKKLGTEEFPLINQTFYPNHKEMLSSTTPVVVKMGHAHSGMGKVVDN
QHDFQDIASVVALTKTYATTEPFIDAKYDVRIQKIGQNYKAYMRTSVSGNWKTNTGSAMLEQIAMSdryKLWV
DTCSEIFGGLDICAVEALHGKDGRDHIIEVGSSMPLIGDHQDEDKQLIVEVNVKMAQA

>d1jkjb2 d.142.1.4 (B:1-238) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Escherichia coli}

MNLHEYQAKQLFARYGLPAPVGYACTTPREAAAASKIGAGPWWVKCQVHAGGRGKAGGVKVVNSKEDIRAF
AENWLGKRLVTYQTDANGQPVNQILVEAATDIAKELYLGAVVDRSSRRVVFMASTEggVEIEKVAEETPHLIHK
VALDPLTGMPYQGRELAFKLGLEGKLVQQFTKIFMGLATIFLERDLALIEINPLVITKQGDLCLDGKLGADGNAL
FRQPDLREMRDQSQE

>d1eucb2 d.142.1.4 (B:0-245) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Pig (Sus scrofa)}

MVNLQEYQSKKMSDNGVKVQRFFVADTANEALEAAKRNLNAKEIVLKAQILAGGRGKGVFSSGLKGGVHLT
PEVVGQLAKQMIGYNLATKQTPKEGVVKVNKMVAEALDISRETYLAILMDRSCNGPVLVGSPQGGVDIEEVAA
SNPELIFKEQIDIIEGIKDSQAQRMAENLGLGPLQNQAADQIKKLYNLFLKIDATQEVNPFGTPEGQVVCFD
AKINFDDNAEFRQKDIFAMDDKSEN

>d1kbla3 d.142.1.5 (A:2-376) Pyruvate phosphate dikinase, N-terminal domain {Clostridium symbiosum}

AKWVYKFEEGNASMRNLLGGKGCLAEMLTILGMPIPQGFTVTEACTEYYNSGKQITQEIQDQIFEAITWLEEL
NGKKFGDTEDPLLVSVRSGARASMPGMMDTILNLGLNDVAEGFAKKTGNPRFAYDSYRFIQMYSDFVVMEV
PKSHFEKIIDAMKEEKGVHFDTDLTADDLKELAEKFKA
VYKEAMNGEEFPQEPKDQLMGAVKAVFRSWDNPR
AIVYRRMNDIPGDWGTAVNVQTMVFGNKGETSGTVA
FTRNPSTGEKGIYGEYLINAQGEDVVAGVRTPQPI
TQLENDMPDCYKQFMDLAMKLEKHFRDMQDMEFTIEEGKLYFLQTRNGKRT
TAPAALQIACDLVDEGMITEEE
AVVRIEAKSLDQL

>d2hgaa2 d.142.1.6 (A:304-474) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

TKKVQQELSRPGMILEMLLPQPEAVRLRATFAGLYSLDVGEEGDQIAEA
LAAPSRFVLKPQREGGGNNLYG
EEMVQALKQLKDSEERASYILMEKIEPEPFENCLLRPGSPARVVQC
ISELGINFGVYVRQEKT
LVMNKHVGHLLRT
KAI
EHADGGVAAGVA
LDNPYPV

>d2hgaa3 d.142.1.6 (A:3-201) Eukaryotic glutathione synthetase {Human (Homo sapiens)}

TNWGSLLQDKQQLEELARQAVDRA
LAEGVLLRTSQE
PTSSEVVSYAPFTL
FPLVPSALLEQAYAVQMDFNLLV
DAVSQNAAFLEQTLSSTIKQDDFTARLF
DIHKQLKEGIA
QTVFLGLNRSDYM
FQRSADGSPALKQIE
INTISASF
GGLASRTPAVHRHVLSVLSKT
KEAGKILSNNPSKGLALGI
AKAWELYGS

>d1a0i_2 d.142.2.1 (2-240) ATP-dependent DNA ligase, N-terminal domain {Bacteriophage T7}

VNIKTNPKAVSFVESAIIKKALDNAGYLIAEIKYDGVRGNICVDNTANSYWSRVSKTIPALEHLNGFDVRWKRL
NDDRCFYKDGFMIDGELMVKGDFNTGSLLRTKWTDTKNQEFHEELFVEPIRKDKVPFKLHTGHLHIKLYAI
LPLHIVESGEDCDVMTLLMQUEHVKNMLPLLQEYFPEIEWQAAESYEVYDMVELQQLYEQKRAEGHEGLIVKDP
MCIYKRGKKSGWWKMK

>d1fvia2 d.142.2.1 (A:2-189) ATP-dependent DNA ligase, N-terminal domain {Chlorella virus, PBCV-1}

AITKPLLAATLENIEDVQFPCLATPKIAGIRSVKQTQMLSRTFKPIRNSVMNRLTELLPEGSDGEISIEGATFQDTT
SAVMTGHKMYNAKFSYYWFDYVTDDPLKKYIDRVEDMKNYITVPHILEHAQVKIPLIPVEINNITELLQYERD
VLSKGFEVGVMIRKPDKYKFGRTLKEGILLKMKQ

>d1b04a_ d.142.2.2 (A:) Adenylation domain of NAD⁺-dependent DNA ligase {Bacillus stearothermophilus}

DRQQAERRAELRELLNRYGYEYYVLDRPSVPDAEYDRLMQELIAIEEQYPELKTSDSPTQRIGGPPLEAFRKVA
HRVPMMSLANAFGEGDLRDFDRVRQEVGEAAYVCELAIDGLAVSVRYEDGYFVQGATRGDGTTGEDITENL
KTIRSLPLRLKEPVSLARGEAFMPKASFLRNNEERKARGEELFANPRNAAAGSLRQLDPKVAASRQLDLFVYGL
ADAEALGIASHSEALDYLQALGFKVNPERRCANIDEVIAFVSEWHDKRPQLPYIDGIVIKVDSFAQQRALGAT
AKSPRWAIAYKFPAE

>d1dgsa3 d.142.2.2 (A:1-314) Adenylation domain of NAD⁺-dependent DNA ligase {Thermus filiformis}

MTREEARRRINELRDLIRYHNRYYYVLADPEISDAEYDRLRELKELEERFPEFKSPDSPTEQVGARPLEPTFRPVR
HPTRMYSLDNAFTYEEVLAFFERLEREAEAPSPLYTVEHKVDGLSVLYEEGVWSTGSGDGEVGEEVTQNLLTIPTI
PRRLKGVPDRLEVRGEVYMPIEAFLRLNEELEERGEKVFKNPRNAAAGSLRQLDPRVTAKRGLRATFYALGLGLG
LEESGLKSQYELLWLKEKGFPVEHCYEKALGAEGVEEVYRRGLAQRHALPFEADGVVLKLDLTLWGEGLYTAR
APRFALAYKFP

>d1ckma2 d.142.2.3 (A:11-238) RNA guanylyltransferase (mRNA capping enzyme), N-terminal domain {Chlorella virus, PBCV-1}

NITTERAVLTNLGLQIKLHKVVGESRDDIVAKMKDLAMDDHKFPRLPGPNPVSIERKDFEKLQKQNVVSEKTD
GIRFMFFTRVFGFKVCTIIDRAMTVYLLPFKNIPRVLFQGSIFDGECLVDIVEKKFAFVLFDAVVSGVTVSQM
DLASRFFAMKRSLEKFKNVPEDPAILRYKEWIPLHEPTIICKDHLKKANAIYHTDGLIIMSDEPVIYGRNFNLFKL
PG

>d1a48_ d.143.1.1 (-) SAICAR synthase {Baker's yeast (Saccharomyces cerevisiae)}

SITKTELGDILPLVARGKVRDIYEVADAGTLLVATDRISAYDVIMENSipeKGILLTKLSEFWFKFLSNDVRNHLDIA
PGKTIFDYLPAKLSEPKYKTQLEDRSLLVHKHKLIPLEVIVRGYITGSAWKEYVKTGTVHGLQPQGLKESQFPEP
IFTPSTKAEQGEHDENISPAQAAELVGEDLSRRVAELAVKLYSKCKDYAKEKGIIIADTKFEFGIDEKTNEIIIVDEV
TPDSSRFWNGASYKVGESQDSYDKQFLRDWLTANKLNGVNGVKMPQDIVDRTRAKYIEAYETLTGSKWSH

>d1bo1a_ d.143.1.2 (A:) Phosphatidylinositol phosphate kinase IIbeta, PIPK IIbeta {Human (Homo sapiens)}

KLFRASEPILSVLMWGVNHTINELSVPVPVMLMPDDFKAYSIKVDNHLFNKENLPSRFKFKEYCPMVFRNL
RERFGIDDQDYQNSVTRSAPINSQSGRCGTRFLTYDRRFVIKTVSSEDVAEMHNILKKYHQFIVECHGNTLLP
QFLGMYRLTVGVETYMVVTRNVFSHRLTVHRKYDLKGSTVAREASDKEAKDLPTFKDNDLNEGQKLHVGE
ESKKNFLEKLKRDVEFLAQKLIMDYSLLVGIHDVDRAEQQEMEVEERAEDEECENDGVGGNLLCSYGTPPDSPG
NLLSFPRFFGPGEFDPSVDVYAMKSHESSPKKEVYFMAIIDILTPYDTKKAAHAAKTVKHGAGAEISTVNPEQY
SKRFNEFMSNILT

>d1blxa_ d.144.1.1 (A:) Cyclin-dependent PK (CDK, different isoforms) {Human (Homo sapiens)}

GLCRADQQYECVAEIGEGAYGKVKARDLNGGRFVALKRVRVQTGEEGMLSTIREVAVLRHLETFEHPNVVR

LFDVCTSVRTDRETKLTLVFEHVDQDLTTYLDKVEPGVPTETIKDMMFQLLRLGDFLHSHRVVHRDLKPQNILV
TSSGQIKLADFGLARIYSFQMALTSSVVTLWYRAPEVLLQSSYATPVDLWSVCIFAEMFRRKPLFRGSSDVDQL
GKILDVIGLPGEEDWPRDVALPRQAFHSKAQPIEKFTVTDIDELGKDLLLCLTFNPAKRISAYSALSHPYFQDLER
CKEN

>d1jvpp_d.144.1.1 (P:) Cyclin-dependent PK (CDK, different isoforms) {Human (Homo sapiens)}
MENFKVEKIGEGTYGVVYKARNKLTGEVVALKKIRLDTEGVPSTAIREISLLKELNHPNIVKLLDIHTENKLYL
VFEFLHQDLKKFMDASALTGIPLPLIKSYLFQLQGLAFCHSHRVLHRDLKPQNLLINTEGAIKLADFGLARAFGV
PVRTYTHEVVTLWYRAPEILLGCKYYSTAVDIWSLGIFAEMVTRRALFPGDSEIDQLFRIFRTLGTGTPDEVVWPG
VTSMPDYKPSFPKWQRQDFSKVVPPLDEDGRSLLSQMLHYDPNKRISAKAALAHPFFQDVTKPVPHRL

>d1apme_d.144.1.1 (E:) cAMP-dependent PK, catalytic subunit {Mouse (Mus musculus)}
SEQESVKEFLAKAKEDFLKKWETPSQNTAQLQFDRIKTLGTGSFGRVMLVKHKESGNHYAMKILDQKVVKLK
QIEHTLNEKRILQAVNFPFLVKLEFSFKDNSNLVMVMEYVAGGEMFSHLRIGRFAEPHARFYAAQIVLTFEYLHS
LDLIYRDLKPENLLIDQQGYIQVTDFGFAKRVKGRTWLCGTPPEYLAPEIILSKGYNKAVDWALGVLIYEMAAG
YPPFFADQPIQIYEKIVSGKVRFPSHFSSDLKDLLRNLLQVDLTKRGNLKNGVNDIKNHWFATTDWIAIYQRK
VEAPFIPFKKGPGDTSNFDDYEEEIRVSINEKCGKEFTEF

>d1fota_d.144.1.1 (A:) cAMP-dependent PK, catalytic subunit {Baker's yeast (Saccharomyces cerevisiae)}

YSLQDFQILRTLGTGSFGRVHLRSRHNGRYYAMKVLKEIVVRLKQVEHTNDERLMLSIVTHPFIIRMWGTQD
AQQIFMIMDYIEGGELFSLLRKSQRFPNPVAKFYAAEVCLALEYLSKDKIYRDLKPENILDKNGHKITDFGFAKY
VPDVTTLCGTPDYIAPEVVSTKPYNKSIDWWSGFILYEMLAGYTPFYDSNTMKTYEKILNAELRFPPFFNEDVK
DLSRLITRDLSQRQLGNLQNGTEDVKNHPWFKEVVWEKLLSRNIETPYEPPIQQGQGDTSQFDKYPEEDINYGV
QGEDPYADLFRDF

>d1a06_d.144.1.1 (-) Calmodulin-dependent protein kinase {Rat (Rattus norvegicus)}
WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAVLHKIKHPNIVALDDIYE
SGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDALKYLHDLGIVHRDLKPENLLYSLDEDSKIMISDF
GLSKMEDPGSVLSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILCGYPFYDENDAKLFEQILKAEEFDS
PYWDDISDSAKDIFRHLMEKDPEKRTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKSKWKQAFNATAV
VRHM

>d1ia8a_d.144.1.1 (A:) Cell cycle checkpoint kinase chk1 {Human (Homo sapiens)}
AVPFVEDWDLVTLGEGAYGEVQLAVNRVTEEAVALKIVDMKRAVDCPENIKKECINKMLNHENVVKFYGHR
REGNIQYLLEYCSGGELFDRIEPDGMPEPDARQFFFQQLMAGVVYLHGIGITHRDIKPENLLDERDNLKISDF
GLATVFRYNNRERLLNKMCGTLPYVAPELLKRREFHAEPVDVWSCGIVLTAMILAGELPWDQPSDSCQEYSDW
KEKKTYLNPWKKIDSAPALLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRP

>d1phk_d.144.1.1 (-) gamma-subunit of glycogen phosphorylase kinase (Phk) {Rabbit (Oryctolagus cuniculus)}

FYENYEPKEILGRGVSSVRRCIHKPTCKEYAVKIIDVTGGGSFSAEEVQELREATLKEVDILRKVSGHPNIIQLKDT
YETNTFFFLVFDMKKGEFLDYLTEKVTLSKETRKIMRALLEVICALHKLNVHRDLKPENILDDDMNIKLTDFG
FSCQLDPGEKLRREVCGTPSYLAPEIIECSMNDNHPGYKEVDMWSTGVIMYTLAGSPPFWHRKQMLMLRMI
MSGNYQFGSPEWDDYSDTVKDLVSRFLVVQPQKRYTAEEALAHPFFQQYV

>d1h8fa_d.144.1.1 (A:) Glycogen synthase kinase-3 beta (Gsk3b) {Human (Homo sapiens)}
SKVTTVVATPGQGPDRPQEVSYTDTKVGNGSFGVVYQAKLCDGELVAIKKVLQGKAFKNRELQIMRKLDHC
NIVRLRYFFYSSGEKDEVYLNLDYVPEVYRVARHYSRAKQTLPVIYVKLYMYQLFRSLAYIHSFGICHARDIKPQ
NLLDPDTAVLKLCDFGSAKQLVRGEPNVSYICSRYYRAPELIFGATDYTSSIDVWSAGCVAELLGQPIFPGDSG
VDQLVEIIKVLGTPREQIREMNPNTFTEFAFPQIKAHWPWTKVFRPRTPPEAIALCSRLEYPTARLPLEACAHSF

FDELRDPNVKLPNGRDTPALFNFTTQELESSNPLATILIPPHARIQA

>d1tkia_d.144.1.1 (A:) Titin, kinase domain {Human (Homo sapiens)}

KELYEKYMAIAEDLGRGEFGIVHRCVETSSKKTYMAKFVKVKGTDQVLVKKEISILNIARHRNILHLHESFESMEELV
MIFEFISGLDIFERINTSAFELNEREIVSYVHQVCEALQFLHSNIGHFDIRPENIYQTRRSSTIKIIEFGQARQLKP
GDNFRLLFTAPEYYAPEVHQHDVVSTATDMWSLGTLYVLLSGINPFLAETNQQIENIMNAEYTFDEEAFCHEISI
EAMDFVDRLLVKERKSRTASEALQHPWLQKIERVSTKVIRTLKHRRYYHTLIKDLNMVVSAARISCGGAIRS
QKGVSVAKVKVASI

>d1koba_d.144.1.1 (A:) Twitchin, kinase domain {California sea hare (Aplysia californica), twk43}
INDYDKFYEDIWKYVVPQPVEVKQGSVYDYYDILEELGSGAFGVVHRCVEKATGRVFVAKFINTPYPLDKYTVKN
EISIMNQLHHPKLINLHDAFEDKYEMVLILEFLSGGELFDRIAEDYKMSEAEVINYMROACEGLKHMHEHSIV
HLDIKPENIMCETKKASSVKIIDGLATKLNPDIEVKTATAEFAAPEIVDREPVGFYTDMWAIAGVGLGVLLSGLS
PFAGEDDLETQNWKRCDWFFEDAFSSVSPEAKDFIKNLQKEPRKRLTVHDALEHPWLKDHSNLTSRIPSSR
YNKIRQKIKEKYADWPAPQPAIGRIANFSSLRKHRPQEYQIYDSYFDRKEAV

>d1koa_2 d.144.1.1 (5915-6264) Twitchin, kinase domain {Caenorhabditis elegans, pjk4}

YDNYVFDIWKQYYPQPVEIKHDHVLDHYDIHEELGTGAFGVVHRVTERATGNNFAAKFVMTPHESDKETVRKE
IQTMSVLRHPTLVNLHDAFEDDNEMVMYEFMSGGELFEKVADEHNKMSDEAVEYMRQVCKGLCHMHEN
NYVHLDLKPEINMFTTKRSNELKLIDFGTAHLDPKQSVKVTGTAEFAAPEVAEGKPVGYYTDMWSVGVLSYIL
LSGLSPFGGENDETTRNVKSCDWNMDDSAFSGISEDGKDFIRKLLLADPNTRMTIHQALEHPWLTPGNAPG
RDSQIPSSRYTKIRDSIKTKYDAWPEPLPPLGRISNYSSLRKHRPQEYQIYDSYFDRSEA

>d1p38_d.144.1.1 (-) MAP kinase p38 {Mouse (Mus musculus)}

ERPTFYRQELENKTIWEVPERYQNLSPVGSGAYGSVCAAFDTKTGHRVAVKKLSRPFQSIIHAKRTYRELRLKHM
KHENVIGLLDVFTPARSLEEFNDVYLVTHLMGADLNNIVKCQKLDDHVQFLYQILRGLKYIHSADIHRDLKPSN
LAVNEDCELKILDGLARHTDDEMGTGVATRWYRAPEIMLNWMHYNQTVDIWSVGCIMAELLTGRTLFPGTD
HIDQLKLILRLVGTPGAELLKKISSESARNYIQSLAQMPKMFANVFIGANPLAVDLLEKMLVLDSDKRITAAQAL
AHAYFAQYHDPDDEPVADPYDQSFESRDLLIDEWKSLSITYDEVISFVPPPLD

>d1cm8a_d.144.1.1 (A:) MAP kinase p38-gamma {Human (Homo sapiens)}

RSGFYRQEVTKTAWEVRAVYRDLQPVGSGAYGAVCSAVDGRGAKVAIKKLYRPFQSELFAKRAYRELRLKHM
RHENVIGLLDVFTPDETLDFTDFYLVMPFMGTDLGKLMKHEKLGEDRIQFLVYQMLKGLRYIHAAGIIHRDLK
PGNLAVNEDCELKILDGLARQADSEMTGYVVTRWYRAPEVILNWMRVTQVDIWSVGCIMAEMITGKTLFK
GSDHLDQLKEIMKVTGTPPAEFVQRLQSDEAKNYMKGLPELEKKDFASILTNASPLAVNLLEKMLVLDAEQRVT
AGEALAHPYFESLHDTEDEPQVQKYDDSFDDVDRTLDEWKRTVYKEVLSFKP

>d1pme_d.144.1.1 (-) MAP kinase Erk2 {Human (Homo sapiens)}

GQVFDVGPRTNTLSIYIGEGAYGMVCSAYDNVNKVRVAIKKISPFEHQTYCQRTLREIKILLRFRHENIIGINDIIRA
PTIEQMKDVYLVTHLMGADLYKLLKTQHLSNDHICYFLYQILRGLKYIHSANVLHRDLKPSNLLNTCDLKICDF
GLARVADPDHDHTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMSNSRPIFPGKHYLDQLNHILGI
LGSPSQEDLNCIINLKARNYLLSLPHKNKVPWNRLFPNADSKALDLLDKMLTFNPHKRIEVEQALAHPYLEQYYD
PSDEPIAEAPFKFDME CDDLPKKEKLKELIFEETARFQPGYRS

>d1jnk_d.144.1.1 (-) c-jun N-terminal kinase (jnk3s) {Human (Homo sapiens)}

DNQFYSVEVG DSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDRNVAIKKLSRPFQNQTHAKRAYRELVLMKCV
NHKNIISLLNVFTPQKTLEEFQDVYLMELMDANLCQVIQMELDHERMSYLLYQMLCGIKHLHSAGIIHRDLKP
SNIVVKS DCTLKILDGLARTAGTSFMMTPYVVTRYRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGR
DYIDQWNKVIQLGTPCPEFMKKLQPTVRNYVENRPKYAGLTFPKLFPSLFPADSEHNKLKASQARDLLSKML
VIDPAKRISVDDALQHPYINVWYDPAEVEAPPQIYDKQLDEREHTIEEWKELIYKEVMN

>d1ckia_d.144.1.1 (A:) Casein kinase-1, CK1 {Rat (Rattus norvegicus)}

MELRVGNRYRLGRKIGSGSGFIDYLGTIDAAGEEEVAIKLECVKTCKHPQLHIESKIYKMMQGGVGIPTIRWCGAE
GDYNVMVMELLGPSLEDLFNFCSRKFSLTVLЛАDQMISRIEYIHSKNFIHRDVKPDNFLMGLGKKGNLVYIIDF
GLAKKYRDARTHQHIPYRENKNLTGARYASINTHLGIEQSRRDDLES LGYVLMYFNLGSLPWQGLKAATKRQK
YERISEKKMSTPIEVLCKGYPSEFATYLNFCRSLRFDKPDYSYLRQLFRNLFRQGFSYDYVFDWNMLKFGASR

>d1csn_d.144.1.1 (-) Casein kinase-1, CK1 {Fission yeast (Schizosaccharomyces pombe)}

NVVGVHYKVGRIGEGSGFVIFEGTNLLNNQQVAIKFEPRRSDAPQLRDEYRTYKLLAGCTGIPNVYYFGQEGL
HNVLVIDLLGPSLEDLLDCGRKFSVKTVAMA AKQMLARVQSIHEKSLVYRDIKP DNFLIGRPN SKNANMIYVV
DFGMVKFYRDPVTQHIPYREKKNLSGTARYMSINTL GREQSRRDDLEALGHVF MYFLRGSLPWQGLKAAT

NKQKYERIGEKKQSTPLRELCA GFPEEFYKYMHYARNLAF DATPDYDYLQGLFSKVLERLNTTEDENFDWNLL

>d1a6o_d.144.1.1 (-) Protein kinase CK2, alpha subunit {Maize (Zea mays)}

SKARVYADVNVL RKEYWDYEALTQWGEQDDYEV VRKVGR GK YSEV FEGIN VNNNEKCI KILKPV KKKKIKR
EIKILQNL CGGP NIVK L DIV RDQHS KTPS LIFE YVN NTDF KVLY PT LT D YDIR YYI YELL KAL DYCH SQG IMH RDVK
PHNVMIDHEL RKL RL DWGL AEFYHPGKEYNRV ASRYFKG PELL VDL QD YD SLD MWSLG CMFAGM IFR KEP
FFY GH D NH DQLV KIA KV LG TD GL NVY LN KYRI ELPQ LE ALV GR HSR KP WL KFM NADN QH LV SPEA IDFL DK LL
RYDH QERL TALE AMTH PYF QQV RAAENS

>d1b6cb_d.144.1.1 (B:) Type I TGF-beta receptor R4 {Human (Homo sapiens)}

TTLKDLIYDMTTSGSGGLPLLVQRTIARTIVLQESIGKGRFGEVWRGKWRGEEAVKIFSSREERSWFRAEAIYQ
TVMLRHENILG FIAADNKDNGTWTQLWLVSDYHEHGS LF DYL NRYTVT VEG MIK L STAS GLAH L HMEIV GT
QGKPAIAHRDLKSKN ILV KKNGT CCIADL GLA VRH DSAT DTIDIA PNHRV GTKRYMAPEV L D S IN MKH FES FKR
ADIYAMGLVFW EIARRCSIGGIHEDYQLPYYDLVPSDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIM
REC WYANGAARL TALRIKK TLSQLSQ QEG

>d1f3mc_d.144.1.1 (C:) pak1 {Human (Homo sapiens)}

SDEEILEKLRSIVSGDPKKYTRFEKIGQGASGTVYTAMD VATGQEV AIRQMNLQQQPKKELIINEILVMRENK
NPNIVNYLDSYLV GDELWV VMEYLAGGS LTDV VTETCM DEGQIAV CRECL QALEFLHSNQVIH RD IKSDNILL
GMDGSVKLTDGFCAQITPEQSKRSTMVGTPYWMAPEV VTRKAYGP KVDI WSLGIMA EMI EGEPP YLNENP
LRLYLIATNGTPELQNPEKLSAIFRDFLNRCLMDV EKRGSAKE LLQHQFLKIAKPLSSLTPLIAAAKEATK

>d1howa_d.144.1.1 (A:) Sky1p {Baker's yeast (Saccharomyces cerevisiae)}

FH PAFKGE PYKDARYILVRKLGWGHFSTVWLAKDMVNN THVAMKIVRGDKV YTTEAAEDEIKL LQRVN DADNT
KEDSMGANHILKLLDHFNHKPNGVHV VMVFEV LGENLL ALIKK YEHR GIPLIYVKQISKQLL GLD YMHR RCGI
IHTDIKPENVLMEIVD SPENL IQK IADL GNACW YDEH YTSI QTRE YRSPEV LLGAPWG CGAD IWSTA CLF ELI
TGDFLFEPDEGH SYTK DDDHIAQII ELLGELPSY LLR NGKYTRT FFNSR GLLRN ISKL KFWPLE DVLT EKYK FSKDE
AKEISDFLSPMLQLDPRK RADAGGL VNHPWL KDTLG MEEIRV PDRELYGSGSDIPGW FEEVR

>d1qcfa3 d.144.1.2 (A:249-531) Haemopoetic cell kinase Hck {Human (Homo sapiens)}

KPQKPWEKDAWEIPRESLKLEKKLGAGQFGEVWMATYNKHTKVA V KTM PGSMS VEAFLAEANVMKTLQH
DKLVKLHAVVTKEPIYIITEFMAKGSLLDFLKSDEGSKQPLPKLIDFSAQIAEGMAFIEQRNYIHRDLRAANILVSAS
LVCKIADFLGLARVIEDNEY TAREGAKFPIKWTAP EA INF GSF TIKSDV WSFG ILL MEIV TYGRIP YPG MSNPEVIRA
LERGYRM PRPEN CPEELY NIMMRCW KNRPEERPT FEYIQSVLDDFTATESQYEEIP

>d1qpca_d.144.1.2 (A:) Lymphocyte kinase (lck) {Human (Homo sapiens)}

KPWWEDEWEVPRE TLK LVERLGAGQFGEVWMGYYNGHTKVA V KSL QGSMSP DAFLAEANLMKQLQHQR
LVRLYAVTQEPIYIITEY MENGS LVDFL KTPSGIKLTINKL DMAAQIAEGMAFIEERNYIHRDLRAANILVSDTLS
CKIADFLGLARLIEDNEY TAREGAKFPIKWTAP EA INF GSF TIKSDV WSFG ILL MEIV TYGRIP YPG MTNPEV IQNLE
RGYRMVRPDNCPEELY QLMR LCW KER PEDRPT FDYLSV LED FFTATE

>d1fmk_3 d.144.1.2 (249-533) c-src tyrosine kinase {Human (Homo sapiens)}

KPQTQGLAKDAWEIPRESLRLEVKGQGCFGEWMGTWNGTTRVAIKTLKPGTMSPEAFLQEAQVMKKLRHEKLVQLYAVVSEPIYIVTEYMSKGSLDFLKGETGKYLRLPQLVDMAAQIASGMAYVERMNYVHRDLRAANILVGENLVCKVADFGALARLIEDNEYTARQGAKFPIKWTAPEAALYGRFTIKSDVWSFGILLTELTKGRVPYPGMVNREVLQVERGYRMPCCPPECPSLHDLMCQCWRKEPEERPTFEYLQAFLEDYFTSTEPQYQPGENL

>d1fgka_d.144.1.2 (A:) Fibroblast growth factor receptor 1 {Human (Homo sapiens)}

ELPEDPRWELPRDRRLVKGKPLGEGAFGQVVLAEAIGLDKDKPNRVTKVAVKMLKSDATEKDLSDLISEMEMMKMIGKHKNIIINLLGACTQDGPLYVIVEYASKGNLREYLQARRPPGLEYSYNPSHNPEEQLSSKDLVSCAYQVARGMEYLASKKCIHRDLAARNVLVTEDNVMKIADFGLARDIHHIDYYKKTTNGRLPVKWMAPPEALFDRIYHQSDVWSFGVLLWEIFLGGSPYPGPVVEELFKLLKEGHRMKDPSNCTNELYMMMRDCWHAVPSQRPTFKQLVEDLDRIVALTS

>d1vr2a_d.144.1.2 (A:) Vascular endothelial growth factor receptor 2 (kdr) {Human (Homo sapiens)}

LPYDASKWEFPRDRRLKGKPLGKGAFGQVIEADAFGIDKTATCRTAVKMLKEGATHSEHRALMSELKILIHIGHHNVNVNLGACTKPGGPLMVIVEFCFKFGNLSTYLSKRNEFVPKVAPEDLYKDFLTLEHLICYSFQVAKGMEFLASRKCIHRDLAARNILLSEKNNVKICDFGLARDIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASPYPGVKIDEFCRRLKEGTRMRAPDYTTPEMYQTMLDCWHGEPSQRPTFSELVEHGNLQANA

>d1ir3a_d.144.1.2 (A:) Insulin receptor {Human (Homo sapiens)}

SSVFVPDEWEVSREKITLLRELQGSFGMVYEGNARDIIGEAETRVAVKTVNESASLRERIEFLNEASVMKGFTCHHVVRLLGVVSKGQPTLVVMELOMAHGLDKSYLRSRPEAENNPGRPPTLQEMIQMAAEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYETDYYRKGGKGLLPVRWMAPESLKDGVFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQVLFVMDGGYLDQPDNCPERVTLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSSFHSEENK

>d1k3aa_d.144.1.2 (A:) Insulin-like growth factor 1 receptor {Human (Homo sapiens)}

VPDEWEVAREKITMSRELQGSFGMVYEGVAKGVVKDEPETRVAIKTVNEAASMRERIEFLNEASVMKEFNCCHHVVRLLGVVSKGQPTLVIMELMTRGDLKSYLRSLRPEMENNPNLAPPSSKMIQMAGEIADGMAYLNANKFVHRDLAARNCMVAEDFTVKIGDFGMTRDIYETDYYRKGGKGLLPVRWMSPESLKDGVFTTSDVWSFGVVLWEIATLAEQPYQGLSNEQVLFVMEGGLDKPDNCPDMILLELMRMCWQYNPKMRPSFLEIISSIKEEMEPGRREVSFYYSEENK

>d1byga_d.144.1.2 (A:) C-terminal src kinase (csk) {Human (Homo sapiens)}

GWALNMKELKLLQTIGKGEFGDVMLGDYRGNKVAVKCIKNDATAQAFLAEASVMTQLRHSNLVQLGVIVEEKGGLYIVTEYMAKGSVLDYLRSGRSVLLGGDCLLKFSLDVCEAMEYLEGNNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALREKKFSTKSDVWSFGILLWEIYSFGRVPYPRIPLKDVVPRVEKGYKMDAPDGCPPAVYEVMKNCWHLDAAMRPSFLQLREQLEHIKTHEL

>d1iepa_d.144.1.2 (A:) Abelson tyrosine kinase (abl) {Mouse (Mus musculus)}

MDPSSPNYDKWEMERTDITMKHKLGQQYGEVYEGVWKYSLTAVKTLKEDTMEEFLKEAAVMKEIKHPNLVQLGVCTREPPFYIITEFMTYGNLLDYLRRECNRQEVSADVLLYMATQISSAMEYLEKKNFIHRDLAARNCLVGENHLVKVADFGSRLMTGDTYTAHAGAKFPIKWTAPESLAYNFSIKSDVWA FGVLLWEIATYGMSPYPGIDL SQVYELLEKDYRMERPEGCPEKVKYELMRACWQWNPSDRPSFAEIHQAFETMFQ

>d1jpaa_d.144.1.2 (A:) ephb2 receptor tyrosine kinase {Mouse (Mus musculus)}

KIFIDPFTFEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKGKREIFVAIKTLKSGYTEKQRRDFLSEASI MGQFDHPNVIHLEGVVTKSTPMIITEFMENGSDSFLRQNDGQFTVIQLVGMLRGIAAGMKYLA DMNYVH RDLAARNILVNSNLVCKVSDFGLSRFLEDDTSDFPTYSALGGKIPIRWTAPEAIQYRKFTSASDVWSYGIVMWEMSYGERPYWDMTNQDVINAIEQDYRLPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMIRNP

SLKA

>d1fvra_d.144.1.2 (A:) Tie2 kinase {Human (Homo sapiens)}

PTIYPVLDNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAGELEVCLKLGHHPNII
NLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTASTLSSQQLLHFADVARGMDYLSQKQFIH
RDLAARNILVGENYVAKIADFGLSRGQEYVVKTMGRLPVRWMAIESLNYSVTTNSDVSYGVLLWEIVSLG
GTPYCGMTCAELYEKLPGYRLEKPLNCDDDEVYDLMRQCWRKPYERPSFAQILVSLNRMLEERKTYVNNTLYE
KFTYAGIDCSAE

>d1cjaa_d.144.1.3 (A:) Actin-fragmin kinase, catalytic domain {Slime mold (Physarum polycephalum)}

AGALWEIEKEFLTKLPAPSSAINSHLQPAKPKVPQKKPSKWDPPAEFKVDSLAVSYNDIDINWKNLQQFKGIE
RSEKGTEGLFFVETESGVFIVKRSTNIESETFCSSLCMRLGLHAPKVRVSSNSEEATNMLECLAAIDKSFRVITL
ANQANILLMELVRGITLNKLTTSAPEVLTKSTMQQLGSLMALDVIVNNSDRLPIAWTNEGNLDNIMLSERGAT
VVPIDSKIIPLDASHPHGERVRELLRTLIAHPGHESSQFHISIRDIITLYTGYDVGTEGSISMQEGFLATVRECASFDL
DAFERELLSWQESLQKCHNLSISPQAIPFILRMLRIFH

>d1ia9a_d.144.1.5 (A:) Trp Ca-channel kinase domain {Mouse (Mus musculus)}

YYYSVERNNLMRLSQSIPFPVPPRGEPVTVRLEESSPSILNNNSMSSWSQLGLCAKIEFLSKEEMGGGLRRAV
KVLCTWSEHDILKGHLYIISFLPEVINTWSSIYKEDTVLHLCLREIQQQRAAQKLTFAFNQMKPKSIPYSPRFLE
VFLLYCHSAGQWFAVEECMTGEFRKYNNNNNGDEIIPNTLEEIMAFSHWTYEYTRGELLVLDLQGVGENLTD
SVIKAEKRSCDMVFGPANLGEDAIAKNFRACKHCNSCCRKLKLPPDLKRNDYT

>d1e8xa4 d.144.1.4 (A:726-1092) Phosphoinositide 3-kinase (PI3K), catalytic domain {Pig (Sus scrofa)}

TAMLHDFTQQVQVIDMLQKVTDIKSLSAEKYDVSSQVISQLQKLENLQNLNLPQSFRVPYDPGLKAGALVIEK
CKVMASKKKPLWLEFKCADPTALSNETIGIIFKHGDDLQRQDMLILQILRIMESIWETESLDLCLPYGCISTGDKIG
MIEIVKDATTIAKIQQSTVGNTGAFKDEVLSHWLKEKCPIEEKFQAAVERFVYSCAGYCVATFVLGIGDRHNDNI
MISETGNLFHIDFGHILGNYKSFLGINKERVPFLPDFLVMGTSGKTSLHFQKFQDVVCVKAYLALRHHTNLLII
LFSMMMLMTGMPQLTSKEDIEYIRDALTGVKSEEDAKKYFLDQIEVCRDKGWTQFNWFLHLVL

>d1j7la_d.144.1.6 (A:) Type IIIa 3',5"-aminoglycoside phosphotransferase {Enterococcus faecalis}

AKMRISPELKLIKYRCVKDTEGMSPAKVYKLVGENENLYLKMTDSRYKGTTDVEREKDMMLWLEGKLPVP
KVLHFERHDGWSNLLMSEADGVLCESEYEDEQSPEKIIELYACIRLFHSIDISDCPYTNSDLRRAELDYLLNNNDL
ADVDCENWEEDTPFKDPRELYDFLKTEKPEEEVFSGHDLGDSNIFVKDGKVSGFIDLGRSGRADKWYDIAFCV
RSIREDIGEEQYVELFFDLLGIKPDWEKIKYYILLDEF

>d1e8ga2 d.145.1.1 (A:6-273) Vanillyl-alcohol oxidase {Fungus (Penicillium simplicissimum)}

EFRPLTLPKLSLSDFNEFIQDIIRIVGSENVEVISSKDQIVDGSYMKPHTHDPTHVMDQDYFLASAIVAPRNVA
DVQSIVGLANKFSFPLWPISIGRNNSGYGGAAPRVSGBVLLDMGKNMNRVLENVSEGAYCVVEPGVTYHDLHN
YLEANNLRDKLWLDVPDLGGGSVLGNAVERGVGYTPYGDHWMMHSGMEVLANGELLRTGMGALPDPKR
PETMGLKPEDQPWSKIAHLFPYGFGPYIDGLFSQSNSMGIVTKIGIWLMPNP

>d1diqa2 d.145.1.1 (A:7-242) Flavoprotein subunit of p-cresol methylhydroxylase {Pseudomonas putida}

AVLPKGVTQGEFNKAVQKFRALLGDDNVLVESDQLVPYNKIMMPVENAAHAPSAAVTATTVEQVQGVVKICN
EHKIPIWISTGRNFGYGSAAVPQRGQVILDLKKMNIKIDPEMICYALVEPGVTFGQMYDYIQENNLPVMLSF
SAPSAIAGPVGNTMDRGVGTYTPYGEHFMMQCGMEVLANGDVYRTGMGGVPGSNTWQIFKWGYGPTLD
GMFTQANYGICTKMGFWLMPKP

>d1f0xa2 d.145.1.1 (A:9-273) D-lactate dehydrogenase {Escherichia coli}
NKAFLNELARLVGSSHLLTDPAKTARYRKGFRSGQGDALAVVFPGLLELWRVLACVTADKIIQMANTGLTE
GSTPNGNDYDRDVIISTRLDKLHLVGKGEQVLAYPGTTLSLEKALKPLGREPHSIVGSSCIGASVIGGCNNSG
GSLVQRGPAYTEMMSLFARINEDGKLTNVHLGIDLGETPEQILSKLDDRIKDDDVRHDGRHAHDYDYVHRVRDI
EADTPARYNADPDRLFESSGCAGKLAFAVRLDTFEAE

>d1i19a2 d.145.1.1 (A:57-273) Cholesterol oxidase {Brevibacterium sterolicum}
VAPLPTPPNFPNDIALFQQAYQNWSKEIMLDATWVCSPKTPQDVRLANWAHEHDYKIRPRGAMHGWTPLT
VEKGANVEKVILADTMTHLNGITVNTGGPVATVTAGAGASIEAVTELQKHDLGWANLPAPGVLSIGGALAVNA
HGAALPAVGQTTLPGHTYGSLSNLVTELVAVVWNGTTYALETYQRNDPRITPLTLNLGRCFLTSVTMQAGPN

>d1uxy_1 d.145.1.2 (3-200) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Escherichia coli}
HSLKPWNTFGIDHNAQHIVCAEDEQQLNAWQYATAEGQPVLILGEGSNVLFLEDYRGTVINRIKGIEIHDEPD
AWYLHVGENWHRLVKYTLQEGMPGLENLALIPCGVGSSPIQNIGAYGVELQRVCAYVDSVELATGKQVRLT
AKECRFGYRDSIFKHEYQDRFAIVAVGLRLPKEWQPVLTYGDLTRLDPTT

>d1hska1 d.145.1.2 (A:15-208) Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Staphylococcus aureus}
NKDIYQALQQLIPNEKIKVDEPLKRYTYKTGGNADFYTPTKNEEVQAVVKYAYQNEIPVTYLGNGSIIIREGGI
RGIVISLLSLDHIEVSDDAIAGSGAAIIDVSRVARDYALTGLEFACGIPGSIGGAVVMNAGAYGGEVKDCIDYALCV
NEQGSLIKLTTKELELDYRNIIQKEHLVVLEAAFTLAP

>d1qj2c2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal domain {Pseudomonas carboxydovorans}
MIPGSFDYHRPKSIADAVALTKGEDARPLAGGHSLIPIMKTRLATPEHLVLDLRDIGDLVGIREEGTDVVIGAMT
TQHALIGSDFLAAKLPIIRETSLLIADPQIRYMGTTGGNAANGDPGNDMPALMQCLGAAYELTGPEGARIVAARDYYQGAYFTAIEPGELLTAIRIPVPP

>d1ffvc2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal domain {Hydrogenophaga pseudoflava}
MIPPRFEYHAPKSVGAEVALLGQLGSDAKLLAGGHSLPMMKLRFAQPEHLIDINRIPELRGIREEGSTVVIGAM
TVENDLISSPIVQARLPLAEEAKLIADPQVRNRGTIGGDIAHGDPGNDHPALSIAVEAHFVLEGPNRRTVPAD
GFFLGYMTLLEENEVMVEIRVPAFAQ

>d1fiqb2 d.145.1.3 (B:224-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}
PKQLRFEGERVTWIQASTLKEELDLKAQHPEAKLVGNTEIGIEMKFKNQLFPMIICPAWIPELNAVEHGPEGISFGAACALSSVEKTLLEAVAKLPTQKTEVFRGVLEQLRWFAGKQSRGTRRTVMDHTFFPSYRKTLGPEEILLSIEIPYSRE

>d1fo4a6 d.145.1.3 (A:192-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}
SPSLFNPEEFMPLDPTQEPIFPPPELLRKDVPPKQLRFEGERVTWIQASTLKEELDLKAQHPEAKLVGNTEIGIEMKFKNQLFPMIICPAWIPELNAVEHGPEGISFGAACALSSVEKTLLEAVAKLPTQKTEVFRGVLEQLRWFAGKQVKSVASLGGNIITASPISDLNPVFMASGTLIV

>d1jroa4 d.145.1.3 (A:179-345) Xanthine dehydrogenase chain A, domain 3 {Rhodobacter capsulatus}
PAFLPETSDALADWYLAHPEATLIAGGTDVSLWVTKALRDLPEVAFLSHCKDLAQIRETPDGYGIGAGVTIAALRAFAEGPHPALAGLRRFASEQVRQVATIGGNIANGSPIDGPPALIAMGASLTLLRGQERRRMPLEDFFLERYKQDRRPGEFVESVTPKSA

>d1uxy_2 d.146.1.1 (201-342) Uridine diphospho-N-

Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Escherichia coli}
VTPQQVFNAVCHMRTTKLPDPKVNGNAGAFFKNPVSAETAKALLSQFPTAPNYPQADGSVKLAAGWLIDQ
CQLKGMQIGGAAVHRQQALVLINEDNAKSEDVVQLAHVRQKVGEKFNVWLEPEVRFIGASGEVSAETIS
>d1hska2 d.146.1.1 (A:209-317) Uridine diphospho-N-
Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain {Staphylococcus aureus}
GKMTEIQAKMDDLTERRESKQPLEYPSCGSVQRPPGHFAGKLIQDSNLQGHRIGGVEVSTKHAGFMVNVDN
GTATDYENLIHYVQKTVKEKFGIELNREVRIIGEHPK
>d1qlma_ d.147.1.1 (A:) Methenyltetrahydromethanopterin cyclohydrolase
{Archaeon Methanopyrus kandleri}
MVSVNENALPLVERMIERAELLNVEVQELENTTVIDCGVEAAGGFEEAGLLFSEVMGGLATVELTEFEHDGLC
LPAVQVTTDHPAVSTLAAQKAGWQVQVGDYFAMGSGPARALALKPKETYEEIDYEDDAVAILCLESelpded
VAEHVADECVDVPENLYLLVAPTASIVGSVQVSARVETGLYKLLEVLEYDVTRVKYATGTAPIAPVADDGEAM
GRTNDCLYGGTVYLYVEGDDELPEVVEELPSEASEDYKPFMkIFEEADYDFYKIDPGVFAPARVVVNDLSTGKT
YTAGEINV DVLKESFL
>d1c4za_ d.148.1.1 (A:) Ubiquitin-protein ligase E3a, Hect catalytic domain (E6ap) {Human (Homo sapiens)}
NPYLRLKVR RDHIIDDALVRLEMIA MENPADLKKQLYVEFE GEQGVDEGGVSK EFFQLV VEEIFNP DigmFTYDE
STKLFWFNPSSFETEGQFTLIGIVLGLAIYNNCILDVHFPMVVYR KLMGKKGTFRDLGDSHPVLYQSLKDLLEYEG
NVEDDDMMITFQISQTDLFGNPMMYDLKENGDKIPITNENRKEFVNLYSDYILNKSVEKQFKAFRRGFHMVTNE
SPLKYLFRPEEIELLICGSRNLDLQALEETTEYDGGYTRDSVLIREFW EIVHSFTDEQKRLFLQFTTGTDRAPVGGL
GKLK MIIAKNGPDTERLPTSHTCFNVLLPEYSSKEKLKERLLKAITYA
>d2ahja_ d.149.1.1 (A:) Nitrile hydratase alpha chain {Rhodococcus erythropolis}
IDHTTENAAPAQAPVSDRAWALFRALDGKGLVPDG YVEGW KKT FEEDFS PRRGAELVAR AWT DPEFR QLLTD
GTAAVAQYGYLGPQGEYIVAVEDPTLKNVIVCSLASCTAWPILGPPTWYKSFEYRARV VREPRKV LSEM GTEI
ASDIEIRVYDTTAETRYMVL PQR PAGTEGWSQEQLQEIVTKD CLIGVAIPQV
>d1f7la_ d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS {Bacillus subtilis}
GIYGIGLDITELKRIASMAGRQKRFAERILTRSELDQYYELSEKRKNEFLAGRFAAKEAFSKAFGTGIGRQLSFQDIE
IRKDQNGKPYIICKLSPAAVHVSITHKEYAAAQVVIER
>d1ftha_ d.150.1.2 (A:) Holo-(acyl carrier protein) synthase ACPS {Streptococcus pneumoniae}
MIVGHGIDIEELASIESAVTRHEGFAKRVLT ALEMERTS LKGRRQIEYLAGRW SAKEAFSKAMGTGISKLG FQDL
EVLN NERGAPYFSQAPFSGKIWLSISHTDQFVTASVILEEN
>d1qr0a1 d.150.1.1 (A:1-101) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}
MKIYGIYMDRPLSQEENERFMTFISPEKREK CRRFYHKEDA HRTLLGDVL VRSV ISRQYQLDKSDIRF STQ EY GKP
CIPDLPAHFNISHSGRWVIGAFDS
>d1qr0a2 d.150.1.1 (A:102-228) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}
QPIGIDIEKTPISLEIAKRFFSKTEYSDLLAKDKDEQTDYFYHLWSMKESFIKQEGKGLSPLDSFSVRLHQDGQV
SIELPDSHSPCYIKTYEVDPGYKMAVCAAHPDFPEDITM VS YEELL RAAA
>d1ako_ d.151.1.1 (-) DNA-repair enzyme exonuclease III {Escherichia coli}
MKFV SFN INGLRAPHQLEAIVEKHQPDVIGLQETKVHDDMFPLEEVAKLGYNVYHGQKGHYGV ALLT KETPI
AVRRGFP GDDEAQ RRIIMA EIPS LLGN VT VINGYFPQ GESRDHP IKFPAKAQFYQNLQ NYLET ELK RDNPV LIM
GDMN ISPT DLDI GIGE ENR KRW LRTG KCSFL PEERE WMDR LMSW GLV DT FRH ANP QTADR FSW FDYRS KGF
DDNR GLR IDLL ASQPLA EC CVETG IDYEIRSM EKPS DHAPV WATF RR

>d1hd7a_d.151.1.1 (A:) DNA repair endonuclease Hap1 {Human (Homo sapiens)}
LYEDPPDQKTSPSGKPATLKICSWNVGGLRAWIKKGLDWVKEEAPDILCLQETKSENKLPAELQELPGLSHQY
WSAPSDKEGYSGVGLLSRQCPLKVSYGIGDEEHQEGRIVVAEFDSFLVTAYVPNAGRGLVRLEYRQRWDEAF
RKFLKGLASRKPLVLCGDLNVAHEEIDLNPKGNNAGFTPQERQGFELLQAVPLADSRHLYPNTPYAYTF
WTYMMNARSKNVGWRLDYFLLSHSLLPALCDSKIRSKALGSDHCPITLYLAL

>d2dnja_d.151.1.1 (A:) Deoxyribonuclease I {Cow (Bos taurus)}
LKIAAFNIRTGETKMSNATLASIYIVRIVRRYDIVLIQEVRDSDLVAVGKLLDYLNQDDPNTYHYVVSEPLGRNSYK
ERYLFRLFRPNKVSLDTYQYDDGCESCNGNDSFSREPAVVKFSSHSTKVKEFAIVALHSAPSDAVAIEINSLYDVYLDV
QQKWHLNDVMLMGDFNADCSYVTSSQWSSIRLRTSSTFQWLIPDSADTTATSTNCAYDRIVVAGSLLQSSVVP
GSAAPPDFQAAYGLSNEMALAISDHYPVEVTLT

>d1i9za_d.151.1.2 (A:) Synaptojanin, IPP5C domain {Yeast (Schizosaccharomyces pombe)}

YDPIHEYVNHELRKRENEFSEHKNVKIFVASYNLNGCSATTKLENWLPENTPLADIYVVGQEIQLTPQQVISA
DPAKRREWESCVKRLNGKCTSGPGYVQLRGQLVGTLAMIFCKESCLPSIKNVEGTVKKTGLGGVSGNKGAVA
IRFDYEDTGLCFITSHLAAGYTNYDERDHDYRTIASGLRFRRGRSFNHDYVVWFGDFNYRISLTYEVVPCIAQG
KLSYLFYDQLNKQMLTGKVFPPFSELPITFPPTYKFDIGTDIYDTSKHRVPAWTDRILYRGEVPHSYQSVPLYY
DHRPIYATYEANIVKVDREKKKILFEELYNQRKQEVRDASQ

>d1aora2_d.152.1.1 (A:1-210) Aldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

MYGNWGRFIRVNLTGDIKVEEYDEELAKKWLGSRGLAIYLLLKEMDPTVDPLSPENKLIIAGPLTGTSAAPTGG
RYNVVTKSPLTGIFTMANSGGYFGAELKFAGYDAIVVEGKAEPVYIYIKDEHIEIRDASHIWGKKVSETEATIRKE
VGSEKVKIASIGPAGENLVKFAAIMNDGHRAAGRGGVGAVMGSKNLKAIAVEGSKTVP

>d1b25a2_d.152.1.1 (A:1-210) Formaldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus furiosus}

MYGWWGRILRVNLTTGEVKVQEYYPEEVAKFIGGRGLAAWILWNEARGVEPLSPENKLIFAAGPFNGLPTPSG
GKLVVAKSPLTGGYGDGNLGTMASVHLRRAGYDALVVEGKAKKPVYIYIEDDNVSILSAEGLWGKTTFETEREL
KEIHGKNVGVLTIGPAGENLVKYAVVISQEGRAAGRPGMGAVMGSKKLKAIVIRGTKEIPVA

>d1gdoa_d.153.1.1 (A:) Glucosamine 6-phosphate synthase, N-terminal domain {Escherichia coli}

CGIVGAIAQRDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTRLRLGVQMLAQAAEEHPLHGGTIAHTR
WATHGEPEVNAHPHVSEHIVVHNGIIHENHEPLREELKARGYTFVSETDTEVIAHLVNWELKQGGTLREAVLR
AIPQLRGAYGTVIMDSRHPDTLLAARSGSPLIVLGMGENFIASDQLALLPVTRRFIFLEEGDIAEITRRSVNIFDK
TGAEVKRQDIESNL

>d1gph12_d.153.1.1 (1:1-234) Glutamine PRPP amidotransferase, N-terminal domain {Bacillus subtilis}

CGVFGIWGHEEAPQITYGLHSLQHRGQEGAGIVATDGEKLTAKHGQGLITEVFQNGELESVKKGKAIGHVRYA
TAGGGGYENVQPLLFRSQNNGLALAHNGNVLNATQLKQQLENQGSIFQTSSDTEVLAHLIKRSGHFTLKDQIK
NSLSMLKGAYAFLIMTETEMIVALDPNGLRPLSIGMMGDAYVVASETCAFVVGATYLREVEPGEMLIINDEG
MKSERFSMNIINRS

>d1ecfa2_d.153.1.1 (A:1-249) Glutamine PRPP amidotransferase, N-terminal domain {Escherichia coli}

CGIVGIAGVMPVNQSIYDALTVLQHRGQDAAGIITIDANNCFRLRKANGLVSDVFEARHMQLQGNMGIGHV
RYPTAGSSASEAQPFYVNSPYGITLAHNGNLTNAHELRKKLFEKRRHINTTSDEILLNIFASELDNFRHYPLEA
DNIFAAIAATNRLIRGAYACVAMIIGHGMVAFRDPNGIRPLVLGKRDIDENRTEYMVASESVALDTLGFDFLRDV
APGEAIYITEEGQLFTRQCADNPVS

>d1ct9a2 d.153.1.1 (A:1-192) Asparagine synthetase B, N-terminal domain {Escherichia coli}
ASIFGVFDIKTDAVELRKKALESRLMRHGPDSGIYASDNAILAHERLSIVDVNAGAQPLYNQQKTHVLAVN
GEIYNHQALRAEYGDRYQFQTGSDCEVILALYQEKGPEFLDDLQGMFAFALYDSEKDAYLIGRDHLGIIPLYMGY
DEHGQLYVASEMKALPVVCRTIKEFPAGSYLWSQDGIEIRSYH

>d1jgta2 d.153.1.1 (A:4-209) beta-Lactam synthetase {Streptomyces clavuligerus}
PVLPAAFGLASARTGGGRAPGPVFATRGSHTIDTPQGERSLAATLVHAPSVAPDRAVARSLTGAPTTAVLAGE
IYNRDELLSVLPAGPAPEGDAELVRLLERYLHAFRLVNGRFATVVRTGDRVLLATDHAGSVPLYTCVAPGEVRA
STEAKALAAHRDPKGFLADARRVAGLTGVYQVPAGAVMDIDLGSGTAVTHRTWT

>d1ea0a3 d.153.1.1 (A:1-422) Alpha subunit of glutamate synthase, N-terminal domain {Azospirillum brasilense}
CGVGFIIDGKPRRSVVEKGIEALKAVWHRGAVDADGKTGDGAGIHVAVPQKFFKDHVVKVIGHRAPDNKLA
VGQVFLPRISLDAQEACRCIVETEILAFGYYIYGWRQVPINVDIIGEKANATRPEIEQIIVGNNGVSDEQFELDLYI
IRRRIEKAVKGEQINDFYICSLSARSIIYKGMFLAEQLTTFYPDLLDERFESDFAIYHQRYSTNTFPTWPLAQPFML
AHNGEINTVKGNVNWMKAHETRMEHPAFTGTHMQDLKPVIGVGLSDSGSLDTVFEVMVRAGRTAPMVKM
MLVPQALTSSQTPDNHKALIQYCNSVMEPWDPGAALAMTDGRVVGGMDRNRPMRYTITTDGLIIGG
SETGMVKIDETQVIEKGRGPGEIMIAVDLQSGKLYRDRELKDHLATLKPWDKWVQN

>g1gk9.1 d.153.1.2 (A:,B:) Penicillin acylase {Escherichia coli}
QSSSEIKIVRDEYGMMPHIYANDTWHLFYGYGYVVAQDRLFQMEMARRSTQGTVAEVLGKDFVKFDKDIRNY
WPDAIRAQIAALSPEDMSILQGYADGMNAWIDKVNTNPETLLPKQFNTFGFTPKRWEFPDVAMIFVGTMAN
RFS DSTSEIDNLALLTALKDKYGVSQGMAVFNLKWLNVNPSAPTTIAVQESNYPLKFNFNQQNSQTAXSNMWVIG
KSKAQDAKAIMVNGPQFGWYAPAYTYIGLHGAGYDVTGNTPFAYPGLVFGHNGVISWGSTAGFGDDVDIFA
ERLSAEKPGYYLHNGKWKVMLSREETITVKNGQAETFTVWRTVHGNILQTDQTTQTAKSRAWDGKEVASLL
AWTHQMKAKNWQEWWTQQAQKALTINWYYADVNGNIGYVHTGAYPDRQSGHDPLPVGTVKWDWKG
LLPFEMNPVKVYNPQSGYIANWNNSPQKDYPASDLFAFLWGGADRVEIDRLLEQKPRLTADQAWDVIRQTSR
QDLNLRFLPTLQAATSGLTQSDPRRQLVETLTRWDGINLLNDDGKTWQQPGSAILNVWLTSMLKRTVVAAP
MPFDWKYSASGYETTQDGPTGSLNISVGAKILYEAVQGDKSPIPQAVDLFAGKPKQQEVVLALEDTWETLSKRY
GNNVSNWKTPAMALTFRANNFFGPQAAAETRHQAELYQNRTENDMIVFSPTTSDRPVLAWDVVAPGQS
GFIAPDGTVDKHEDQLKMYENFGRKSLWLTQDVEAHKESQEVLVHQR

>g1cp9.1 d.153.1.2 (A:,B:) Penicillin acylase {Providencia rettgeri}
ESTQIKIERDNYGVPHIYANDTYSFYGYGYAVAQDRLFQMEMAKRSTQGTVSEVFGKDYISFDKEIRNNYWPD
SIHKQINQLPSQEQQDILRGYADGMNAWIKQINTKPDDLMPKQFIDYDFLPSQWTSFDVAMIMVGTLANRFSD
MNSEIDNLALLTALKDKYGEQLGEFFNQINWLNNPNAPTTISSEEFTYSDXSNVWLVGKTKASGAKAILLNGP
QFGWFNPAYTYIGLHGAGFNIVGNTPFAYPAILFGHNGHVSWGSTAGFGDGVDIFAEQVSPEDPNSYLHQG
QWKKMILSRQETLNVKGEQPITFEIYRTVHGNVVKRDKTTHTAYSKARAWDGKELTLSMAWVKQGQAQNWQ
QWLDQAQNQALTINWYYADKDGNIGYVHTGHYPDRQINHDPLPVGSGTGEWDWKGIQPFANNPKVYNPKS
GYIANWNNSPAKNYPASDLFAFLWGSADRVEIDNRIEAYDKLTADDMWAILQQTDRVLDNHRLFTPFLTQATQ
GLPSNDNSVKLVSMLQQWDGINQLSSDGKHYIHPGSAILDIWLKEMLKATLGQTVPAPFDKWYLASGYETTQE
GPTGSLNISTGAKLLEYSLLEDKSPISQSIDLFSGQPQNDVIRKTLNTTYQKMIKEYGDN PANWQTPATALTREN
NFFGIPQALPQENFHQNEYHNRGTENDLIVFTEEGVSAWDVVA PGQSGFISPQGKPSPHYQDQLSLYQQFGK
KPLWLNSEDVAPYIESTETLIER

>g1fm2.1 d.153.1.2 (A:,B:) Cephalosporin acylase {Brevundimonas diminuta}
QAPIAAYKPRSNEILWDGYGVPHIYGV DAPS AFYGYGWAQARSHGDNILRLYGEARGKGA EYWGPDY EQTTV
WLLTNGVPERAQHQWYAQQS PDRANLDAFAAGINAYAQQNPDDISPEVRQVLPVSGADVV AHAHRLMNFLY
VASPGRTLGXSNSWA VAPGKTANGN ALLQNPHLSWTTDYFTYYEAHLVTPDFEIY GATQIGLPVIRFAFNQRM

GITNTVNGMVGATNYRLTLQDGGLYDGGVQRFERRQASYRLRQADGSTVDKPLEIRSSVHGPVFERADGTA
AVRVAGLDRPGMLEQYFDMITAHSFDDYEAMARMQVPTFNIVYADREGTINYSFNGVAPKRAEGDIAFWQ
GNVPGDSSRYLTETPLDDLPRVTNPPGGVQNSNDPPWTPWPVTCANHPSYLAPQTPHSLRAQQSV
RLMSENDDLTLERFMALQFSHRAVMADRTLPDLIPAAALIDPDPEVQAAARLLAAWDRDFTSDSRAALLFEWA
RLFAGQNFGAQAAFATPWSLDKPVSTPYGRDPKAADVQLRTAIANTKRKYGAIDRPGDASRMILNDVNPG
AAGYGNLGSFRVFTWSDPDENGIRTPVHGETWVAMIEFSTPVRAYGLMSYGNRSQPGTTHYSDQIERVSRAD
FRELLLRREQVEAAVQERTPFNF

>d2pvaa_ d.153.1.3 (A:) Penicillin V acylase {Bacillus sphaericus}

CSSLSIRTDDKSLFARTMDFTMEPSKVIVPRNYGIRLLEKENVVINNSYAFVGMGSTDITSPVLYDGVNEKTY
ADEPKKGTGLMGAMLYYATFATYADEPKKGTGINPVYVISQVLNCVTVDVIEKLTSYLLNEANIIIGFAPPL
HYTFTDASGESIVIEPDKTGITIHRKTIVMTNSPGYEWHTQNLRAYIVGTPNPPQDIMMGDLDTFGQGAG
GLGLPGDFTPSARFLRVAYWKYTEAKNETEGVTNLFHILSSVNIPKGVVLTNEGKTDYIITSAMCAQSKNYY
FKLYDNSRISAVSLMAENLNSQDLITFEWDRKQDIKQLNQVN

>d1pma1_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Archaeon Thermoplasma acidophilum}

TTTVGITLKDAVIMATERRVTMENFIMHKNGKKLFQIDTYGMIAGLVGDAQVLVRYMKAELELYRLQRRVN
MPIEAVATLLSNMLNQVKYMPYMVQLVGGIDTAPHFSIDAAGGSVEDIYASTGSGSPFVYGVLESQYSEKMT
VDEGVDLVIRAISAAKQRDSASGGMIDVAVITRKDGYVQLPTDQIESRIRKLGIL

>d1ryp1_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

QFNPYGDNGGTILGIAGEDFAVLAGDTRNITDYSINSRYEPKVFDCGDNIVMSANGFAADGDALVKRFKNSVK
WYHFDHNDKKLSINSAARNIQHLLYGRKFFPYVHTIIAGLDEDGKGAVYSFDPVGSYEREQCRAAGAAASLIM
PFLDNQVNFKNQYEPGTNGVKKPLKYLSEEVIKLVRDSFTSATRHIQVGDGLEILIVTKDGVRFYELKRD
>d1ryp2_ d.153.1.4 (2:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TQQPIVTGTSVISMKYDNGVIAADNLGSYGSLLRFNGVERLIPVGDNVVGISINGDISDMQHIERLLKDLVTENAY
DNPLADAEEALEPSYIFEYLATVMYQRRSKMNPLWNAAIVAGVQSNGDQFLRYVNLLGVTYSSPLATGFGAH
MANPLLRKVVDRESDIPKTTVQVAEEAIVNAMRVLYYRDARSSRNFLAIIDKNTGLTFKKNLQVENMKWDFAK
DIKGYGTQKI

>d1ryph_ d.153.1.4 (H:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

LKKGEVSLGASIMAVTFKDGVILGADSRTTGAYIANRVTDKLTRVHDKIWCRCRSGSAADTQAIADIVQYHLEYT
SQYGTPSTETAASVFKELCYENKDNLTAGIIVAGYDDKNKGEVYTIPLGGSVHLPYAIAGSGSTFIYGYCDKNFRE
NMSKEETVDFIKHLSQAIKWDGSSGGVIRMVVLTAAGVERLIFYPDEYEQL

>d1rypi_ d.153.1.4 (I:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTIVGVFNNGVVIADTRSTQGPIVADKNCAKLHRISPCKIWCAGAGTAADTEAVTQLIGSNIELHSLYTSREPRV
VSALQMLKQHLFYQGHIGAYLIVAGVDPGTGSHLFSIHAGSTDVGGYLSGGSLAAMAVLESHWKQDLTKEE
AIKLASDAIQAGIWNDLGSNSNDVCVMEIGKDAEYLRYLTPNVREEKQKSYKFPRGTTAVLKESIVNICD

>d1rypj_ d.153.1.4 (J:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

SDPSSINGGIVVAMTGKDCVIAACDLRLGSQSLGVSNKFEKIFHYGHVFLGITGLATDVTLNEMFRYKTNLYKLK
EERAIEPETFTQLVSSSLYERRFGPYFVGPVAGINSKSGKPFIAGFDLIGCIDEAKDFIVSGTASDQLFGMCESLYE
PNLEPEDLFETISQALLNAADRDALSGWGAVVYIICKDEVVKRYLKMQRQD

>d1rypk_ d.153.1.4 (K:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MDIILGIRVQDSVILASSKAVTRGISVLKDSDDKTRQLSPHTLMSFAGEAGDTVQFAEYIQANIQLYSIREDYELSP
QAVSSFVRQELAKSIRSRRPYQVNVLIGGYDKKKNKPELYQIDYLGTKVELPYGAHGYSGFYTFSLDDHHYRPDM
TTEGLDLLKLCVQELEKRMPMDFKGIVIKIVDKDGRQVDDFQAQ

>d1rypl_ d.153.1.4 (L:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

TTTLAFRFQGGIIVAVDSRATAGNWVASQTVKRVIEINPFLGTMAGGAADCQFWETWLGSQCRLHELREKER
ISVAAASKILSNLVYQYKGAGLSMGTMICGYTRKEGPTIYVVDSDGTRLKGDFCVGSGQTFAYGVLDNSNYKWDL
SVEDALYLGKRSILAAAHRDAYSGGSVNLYHVTEDGWYHGNHDVGELFWKVKEEEGSFNNVIG

>d1pmaa_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Archaeon Thermoplasma acidophilum}

TVFSPDGRLFQVEYAREAVKGSTALGMKFANGVLLISDKVKRSRLIEQNSIEKIQLIDDYVAVTSGLVADARVLV
DFARISAQQEKVTY GSLVNIENLVKRVADQM QQYTQYGGVRPYGVSLIFAGIDQIGPRLFDCDPAGTINEYKATAI
GSGKDAVVSFLEREYKENLPEKEAVTLGIKALKSSLEEGERKAPEIASITVGNKYRIYDQEEVKKFL

>d1rypa_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

AGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVPDKLLDPTTVSYIFCISRTIGMVNGP
IPDARNAALRAKAEAAEFRYKYGYDMPCDVLAKRMANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDP
GYYVGYKATATGPQQEITTNLENHFKKSKIDHINEESWEKVEFAITHMIDALGTEFSKNDELGVATDKFFT
SAENIEERLVAIAEQD

>d1rypb_ d.153.1.4 (B:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MTDRYSFLTTFSPSGKLGQIDYALTAVKQGVTSLGKATNGVVIATEKKSSPLAMSETLSKVSLLTPDIGAVYSG
MGPDYRVLVDKSRKVAHTSYKRIYGEYPPTKLLVSEVAKIMQEATQSGGVRPFGVSLLIAGHDEFNGFSLYQVDP
SGSYFPWKATAIGKGSVAAKTFLEKRWNDELEDAIHIALTLKESVEGEFNGDTIELAIIGDENPDLLGYTIPTD
KGPRFRKLTSQEINDRREAL

>d1rypc_ d.153.1.4 (C:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GSRRYDSRTTIFSPEGRLYQVEYALEISHAGTAIGIMASDGIVLAAERKVSTLLEQDTSTEKLYKLNDKIAVAVAG
LTADAEILINTARIHAQNYLKTYNEDIPVEILVRRLSDIKQGYTQHGLRPGVSFIAGYDDRYGYQLYTSNSPGN
YTGWKAISVGANTSAAQTLQMDYKDDMKVDDAIELALKTLSKTTDSSALTYDRLEFATIRKGANDGEVYQKIF
KPQEIKDILVKTGIT

>d1rypd_ d.153.1.4 (D:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GYDRALSIFSPDGHIFQVEYALEAVKRGTCAVGVKGKNCVVLGCERRSTLKLQDTRITPSKVKIDS HVVLSFGL
NADSRLIEKARVEAQSHRLTLEDPTVTEYLTRYAGVQQRYTQSGGVRPFGVSTLIAGFDPRDDEPKLYQTEPS
GIYSSWSAQQTIGRNSKTVREFLEKNYDRKEPPATVEECVKLTVRSILLEVQQTGAKNIEITVVKPDSDIVALSSEEIN
QYVTQIEQEKKQEQ

>d1rype_ d.153.1.4 (E:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

DRGVSTFSPEGRLFQVEYSLEAIKGSTAIGIATKEGVVLGVEKRATSPLLESIEKIVEIDRHIGCAMSLTADARS
MIEHARTAAVTHNLYYDEDINVESLTQSVCSDLALRFGE GASGEERLMSRPGVALLIAGHDADDGYQLFHAEPS
GTFYRYNAKAIGSGSEGAQAELLNEWHSSLTLKEAELLVLKILKQVMEEKLDENNAQLSCITKQDGFKIYDNEKTA

ELIKELKEKEAAE

>d1rypf_d.153.1.4 (F:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

FRNNYDGDVTFSPTGRLFQVEYALEAIKQGSVTVGLRSNTHAVLVALKRNADELSSYQKKIIKCDEHMGLSLAG
LAPDARVLSNYLRQQCNYSSLVFNRKLAVERAGHLLCDKAQKNTQSYGGRPYVGGLIIGYDKSGAHLLEFQPS
GNVTELYGTAIGARSQGAKTYLERLDTFIKIDGNPDELIKAGVEAISQLRDESLTVDNLSIAIVGKDTPFTIYDGE
AVAKYI

>d1rypg_d.153.1.4 (G:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GTGYDLSNSVFSPDGRNFQVEYAVKAVENGTTSIGIKCNDGVFAVEKLITSKLLVPQKNVKIQVVDRHIGCVYS
GLIPDGRHLVNRGREEASFKKLYKTPIPAFADRLGQYVQAHTLYNSVRPGVSTIFGGVDKNGAHLYMLEPS
GSYWGYKGAATGKGRQSAKAELEKLVDDHHPEGLSAREAVQAAKIIYLAHEDNKEKDFELEISWCSLSETNGLH
KFVKGDLLQEAIDFAQKEIN

>d1ht1a_d.153.1.4 (A:) HslV (ClpQ) protease {Escherichia coli}

TTIVSVRRNGHVIAGDGQATLGNTVMKGNVKKVRLYNDKVIAGFAGGTADAFTLFELFERKLEMHQGHLVK
AAVELAKDWRTDRMLRKLEALLAVADETASLIITNGNDVVQPENDLIAIGSGGPYAQAAARALLENTELSAREIA
EKALDIAGDICIYTNHFHTIEELSYK

>d1jjwa_d.153.1.4 (A:) HslV (ClpQ) protease {Haemophilus influenzae}

TTIVSVRRNGQVVVGGDGQVSLGNTVMKGNAKVRRLYNGKVLAGFAGGTADAFTLFELFERKLEMHQGHLL
KSAVELAKDWRTDRALRKLEAMLIVADEKELESIIITGIGDVVQPEEDQILAIGSGGNYALSAARALVENTELSAHEI
VEKSLRIAGDICVFTNTNFTIEELP

>g1apy.1 d.153.1.5 (A:,B:) Glycosylasparaginase
(aspartylglucosaminidase, AGA) {Human (Homo sapiens)}

SPLPLVVNTWPFKNATEAAWRALASGGSALESGCAMPEREQCDGSVFGGGSPDELGETTLDAMIMDGT
TMDVGAVGDLRRIKNAIGVARKVLEHTHTLLGESATTFAQSMGFINEDLSTSASQALHSDWLARNCQPNY
WRNVIPDPSKYCGPKPPXTIGMVIHKTGHIAAGTSTNGIKFKIHGRVGDSPIPGAGAYADDTAGAAAATGNG
DILMRFLPSYQAVEYMRRGEDPTIACQKVISRIQKHFPEFFGAVICANVTGSYGAACNLSTFTQFSFMVYNSEK
NQPTEEKVDCI

>g2gac.1 d.153.1.5 (A:,B:) Glycosylasparaginase
(aspartylglucosaminidase, AGA) {Flavobacterium meningosepticum}

NKPIVLSTWNFGLHANVEAWKVLSKGKALDAVEKGVRLEDPTERSVGYGGRPDRGRVTLDACIMDENY
NIGSVACMEHIKNPISVARAVMEKTPHVMLVGDGALEFALSQGFKKENLLTAESEKEWKEWLKTXCIGMIALDA
QGNLSGACTTSGMAYKMHGRVGDSPIIGAGLFVDNEIGAATATGHGEEVIRTGTHLVVELMNQGRTPQQAC
KEAVERIVKIVNRRGKNLKDIQVGFIALNKKGEYGAYCIQDGFNFVAVHDQKGNRLETP

>d1b65a_d.154.1.1 (A:) L-aminopeptidase D-Ala-esterase/amidase {Ochrobactrum anthropi}

KPRARDLGLPFTGTVGPYNAITDVGVGFGQTIIENEPRPGRKRPARSGVTAILPHMQSETPVYPVYAGVHRFN
GNGETMTGTHWIEDGGYFLGPVITNTHGIGMAHHATVRWMVDRYASTYQTDDFLWIMPVVAETYDGALND
INGFPVTEADVRKALDNVASGPVQEGNCGGTGMITYGFKGGTGTASRVVEFGGRSFTIGALVQANHGQRD
WLTIAGVPVGQHMRDGTPSQLQERGSIIVVLATDPLMPHQLKRLARRASIGIRNGTPGGNNSGDIFIAFST
ANQRPMQHRSAPFLDVEMVNDEPLDTVYLAAVDSVEAVVNAMIAAEDMGTPFDRLVQAIDHERLRAVL
RQYGRLA

>g1pya.1 d.155.1.1 (A:,B:) Histidine decarboxylase {Lactobacillus sp., strain 30a}

SELDAKLNKLGVDRDIAISPYKQWTRGYMEPGNIGNGYVTGLKVAGVRDKSDDDVLGIVSYDRAETKNAYIG

QINMTTASXFTGVQGRVIGYDILRSPEVDKAKPLFTETQWDGSELPIYDAKPLQDALVEYFGTEQDRRHYPAPG
SFIVCANKGVTAPERKNDADMKGQGYGVWSAIAISFAKDPTKDSSMFVEDAGVWETPNEDELLEYLEGRRK
AMAKSIAECGQDAHASFESSWIGFAYTMMEPGQIGNAITVAPYVSLPIDSIPGGSILTPDKMEIMENLTMPE
WLEKMGYKSLSANNALKY

>d1jl0a_d.156.1.1 (A:) S-adenosylmethionine decarboxylase {Human (Homo sapiens)}
HFFEGTEKLLEVWFSRQQPDANQSGSDLRTIPRSEWDILLKDVQCSIISVTKTDKQEAYVLESSMFVSKRRFILK
TCGTTLLKALVPLLKARDYSGFDIQSFFYSRKNFMKPSHQGYPHRFQEEIEFLNAIFPNGAGYCMGRMNS
DCWYLYTLDLFPESRVISQPDQTLEILMSELDPAVMDQFYMKDGVAKDVTRESGIRDLIPGSVIDATMFNPCGY
SMNGMKSDGTYWTIAITPEPEFSYVSFETNLSQTSYDDLIRKVVEVFKPGKFVTLFVNQSSKCRTVLASPQKIE
GFKRLDCQSAMFNDYNFVFTSFAKKQ

>d2bc2a_d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacillus cereus}
TVKNETGTISISQLNKNVVHTELGSFNGEAVPSNLVNTSKGLVLVDSSWDDKLTKELIEMVEKKFQKRVTD
VIITHAHADRGIGIKTLKERGIKAHSTALTAELAKNGYEEPLGLDLQTVTNLKFGNMVKETFYPGKGHTEDNIVV
WLPQYNILVGGALVKSTSAKDGNVADAYVNEWTSIENVLKRYRNINAVVPGHGEVGDKGLLLHTLDLLK
>d1a7ta_d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacteroides fragilis}
SVKISDDISITQLSDKVYTYSLAEIEGWGMVPSNGMIVINNHQAALLDTPINDAQTEMILVNWVTDSLHAKVT
TFIPNHWHGDCIGGLGYLQRKGVQSYANQMTIDLAKEKGKPVPEHGFDSLTVDGMPLQCYYLGGGHATD
NIVVWLPTENILFGGCMLKDNQTTSIGNISDADVTAWPKTLKVKAKFPSARYVPGHGNYGGTELIEHTKQIV
NQYIESTS

>d1smla_d.157.1.1 (A:) Zn metallo-beta-lactamase {Xanthomonas maltophilia}
EVPLPQLRAYTVDASWLQPMAPLQIADHTWQIGTEDLTALLVQTPDGAVLLDGGMPQMASHLLDNMKARG
VTPRDLRLILLSHAHADHAGPVAELKRRTGAKVAANAESA VLLARGGSDDLHF GDTYPPANADRIVMDGEVI
TVGGIVFTA HFMAGHTPGSTA WTDT RNGKPVRIAYADSL SAPGYQLQGNPRY PHLIEDYRRSFATVRALPC
DVLLTPHPGASNWDYAA GARAGAKALTCKAYADAAE QKFDGQ LAKETAG

>d1jjea_d.157.1.1 (A:) Zn metallo-beta-lactamase {Pseudomonas aeruginosa, IMP-1}
SLPDLKIEKLDEGVYVHTSFEEVNGWGVVKHGLVVLVNAEAYLIDTPFTAKDTEKLVTWFVERGYKIKGSISSHF
HSDSTGGIEWLNSRSIPTYASELTNELLKDGKVQATNSFGVNYLVKNKIEVFYPGPHTPDNVVVWLPERK
ILFGGC FIKPYGLGNLGDANIEAWPKSAKLLKSKYGA KLVVPSHSEVG DASLLKL TLEQAVKGLNESKK

>d1qh5a_d.157.1.2 (A:) Glyoxalase II (hydroxyacylglutathione hydrolase) {Human (Homo sapiens)}

MKVEVLPALTDNYMYLVIDDETKEAAIVDPVQPQKVVD AARKHGVKLTVLTTHHHWDHAGGNEKLVKLESG
LK VYGGDDRIGALTHKITHLSTLQVGSLNVKCLATPCHTSGHIC YFVSKPGGSEPPAVFTGDTLFVAGCGKFYEGT
ADEMCKALLEVLGRLPPDTRVYCGHEYTI NNLFARHVEPGNAIREKLAWAKEKYSIGEPTV P STLAEEFTYNP
FMRVREKTVQQHAGETDPVTTMRAVRREKDFKMPRD

>d1e5da2_d.157.1.3 (A:2-250) Rubredoxin oxygen:oxidoreductase (ROO), N-terminal domain {Desulfovibrio gigas}

QATKIIDGFHLVGAIDWNSRDFHGYTLSMGTTYNAYLVEDEKTLFDTVKA EYKGELLCGIASVIDPKKIDYLVIQ
HLELDHAGALPALIEACQPEKIFTSSLGQKAMESHFHYKDW PVQVVKHGETLSLGKRTVTFYETRMLHWPDS
MVS WFADEKVLISNDIFGQNI AASERFSDQIPVHTLERAMREYYANIVNPYAPQTLKAIETLVGAGVAPEFICPD
HGVIFRGADQCTFAVQKYVEYAEQK

>d1a6q_d.158.1.1 (-) Protein serine/threonine phosphatase 2C {Human (Homo sapiens)}
GAFLDKPKMEKHNAQGQGNGLRYGLSSMQGWRVEMEDAHTAVIGLPSGLESWSFFAVYDGHAGSQVAKYC
CEHLLDHITNNQDFKGSAGAPS VENVKNGIRTGFLEIDEHM RVMSEKKHGADRGSTAVGVLISPQHTYFINCG
DSRGLLCRNRKVHFFTQDHKPSNPLEKERIQNAGGSVM IQRVNGSLAVSRALGDFDYKCVHGKGPTEQLVSP

PEVHDIERSEEDDQFIILACDGIVDVMGNEELCDFVRSRLEVTDDLEKVCNEVVDTCLYKGSRDNMSVILICFPN
APKVSPEAVKKEAELDKYLECRVEEIKKQGEGVPDLVHVMRTLASENIPSLPPGGELASKRNVIEAVYNRLNPY
>d4kbpa2 d.159.1.1 (A:121-432) Plant purple acid phosphatase, catalytic domain
{Kidney bean (*Phaseolus vulgaris*)}
QTGLDPYTFGLIDLGQSFDNTLHYELSPKKGQTVLFVGDLSYADYPNHDNVRWDTWGRFTERSVAYQ
PWIWTAGNHEIEFAPEINETEPFKPFSYRYHVPYEASQSTSPFWYSIKRASAHIIVLSSYSAYGRGTPQYTWLKEL
RKVKRSETPWLVLMHSPLYNNSYNHHFMEGEAMRTKFEAWFVKYKVDDVVAGHVFHAYERSERVSNIAYKITDG
LCTPVKDQSAPVYITIGDAGNYGVIDSNMIQPQPEYSAFREASFHGMFDIKNRTHAHFSWNRNQDGVAVEA
DSVWFFNRHWYWPVDDST
>d1qhwa_d.159.1.1 (A:) Mammalian purple acid phosphatase {Rat (*Rattus norvegicus*)}
STLRFVAVGDWGGVPNAPFHTAREMANAKEIARTVQIMGADFIMSLGDNFYFTGVHDANDKRFQETFEDVF
SDRALRNIPWYVLAGNHDLGNVSAQIAYSKISKRWNPSPYYRLRFKVRPSNITVAIFMLDTVMLCGNSDDFV
SQQPEMPRDLGVARTQLSWLKKQLAAAKEDYVLVAGHPIWSIAEHGPTRCLVKNLRPLLAAYGVTAYLCGHD
HNLQYLQDENGVGYVLSGAGNFMDPSVRHQRKVPNGYLRFHYGSEDSLGGFTYVEIGSKEMSITYVEASGKSL
FKTSLPRRP
>d1utea_d.159.1.1 (A:) Mammalian purple acid phosphatase {Pig (*Sus scrofa*)}
PTPILRFVAVGDWGGVPNAPFHTAREMANAKAIATTVKTLGADFLSLGDNFYFTGVHDAKDKRFQETFEDVFS
DPSLRNVPWHVLAGNHDLGNVSAQIAYSKISKRWNPSPYYRLRFKIPRSNVSAIFMLDTVLCGNSDDFVS
QQPERPRNLALARTQLAWIKKQLAAAKEDYVLVAGHYPVWSIAEHGPTHCLVKQLLPLTTHKVTAYLCGHDHN
LQYLQDENGLGFVLSGAGNFMDPSKKHLRKVPNGYLRFHFGAENSLGGFAYVEITPKEMSVTYIEASGKSLFKT
KLPRRA
>d1ii7a_d.159.1.4 (A:) Mre11 {Archaeon *Pyrococcus furiosus*}
MKFAHLADIHLGYEQFKPQREEEAEAFKNALEIAVQENVDFILAGDLFHSSRPSPGTLLKAIALLQIPKEHSIP
VFAIEGNHDRTQRGPSVNLLEDNFLVYVIGMRKEKVENEYLTSERLGNGEYLVKGVYKDLEIHGMKYMSSAWF
EANKEILKRLFRPTDNAIMLHQGVREVSEARGEDYFEIGLSDLPEGYLYALGHIHKRYETSGSPVVPGSLER
WDFGDYEVRYEWTDGIKFKERYGVNKGFYIVEDFKPRFVEIKVRFIDVKIKGSEEEIRKAIRKLIPLIPKNAYVRLNI
GWRKPFDLTEIKELLNVEYLKIDTWRI
>d1ush_2 d.159.1.2 (26-362) 5'-nucleotidase (syn. UDP-sugar hydrolase), N-terminal
domain {Escherichia coli}
YEQDKTYKITVLHTNDHHGHFWRNEYGEYGLAAQKTLVDGIRKEVAEEGGSVLLSGGDINTGPESDLQDAE
PDFRGMNLVGYDAMAIGNHEFDNPLTVLRQQEKWAKFPLLSANIYQKSTGERLFKPWALFKRQDLKIAVIGLTT
DDTAKIGNPEYFTDIEFRKPADEAKLVIQELQQTEKPDIIAATHMGHYDNGEHSNAPGDVEMARALPAGSLA
MIVGGHSQDPVCMAAENKKQVDYVPGTPCKPDQQNGIWIVQAHEWGKYVGRADFEFRNGEMKMVNQYQL
IPVNLKKKVTWEDGKSERVLYTPEIAENQQMISLLSPFQNKGKAQLEV
>d1jk7a_d.159.1.3 (A:) Protein phosphatase-1 (PP-1) {Human (*Homo sapiens*)}
KLNIDSIIQLLEVRGSKPGKVNQLQENEIRGLCLKSREIFLSQPILELEAPLKICGDIHGQYYDLLRLFEYGGFPPE
SNYLFGLDYVDRGKQSLETICLLAYKIKYPENFFLLRGNHECASINRIYGFYDECKRRYNIKLWKTFTDCFNCLPIA
AIVDEKIFCCCHGGLSPDLQSMEQIRRIMRPTDVPDQGLCDLLWSDPDKDVLGWGENDRGVTSFTFGAEVVAK
FLHKHDDLICRAHQVVEDGYEFFAKRQLTFSAPNYCGEFDNAGAMMSVDETLMCSFQILKPA
>d1tcoa_d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Cow (*Bos taurus*)}
VPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEETVALRIITEGASILRQEKNLLIDAPVTVCVDIHGQFF
DLMKLFEVGGSPANTRYLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLLRGNHECRHLTEYFTFKQECKIKYSERV
YDACMDAFCDFCLPLAALMNQQFLCVHGLSPEINTLDDIRKLDKFKEPPAYGPMCDILWSDPLEDFGNEKTQEH
FTHNTVRGCSYFYSYPAVCEFLQHNNLLSILRAHEAQDAGYRMYRKSQTTGFPSSLITIFSPNYLDVYNNKAABL

KYENNVMNIRQFNCSHPYWLPNFMDVFTWSLPFVGEKVTEmLVNVNLNIC

>d1auia_ d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Human (Homo sapiens)}

TDRVVKAVPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALRIATEGASILRQEKNLLIDAPVTVC
DIHGQFFDLMKLFEVGGSPANTRYLFLGDYVDRGYFSIECVLYLWALKILYPKTLFLRGHNHECRHLTEYFTFKQEC
KIKYSERVYDACMDAFCPLAALMNQQFLCVHGGSPEINTLDDIRKLDRFKEPPAYGPMCDILWSDPLEDFG
NEKTQEHTHNTVRGCSYFYSYPAVCEFLQHNNLLSILRAHEAQDAGYRMYRKSQTTGPSLITIFsapnyldv
NNKAALVLYENNVMNIRQFNCSHPYWLPNFMDVFTWSLPFVGEKVTEmLVNVNLICSDDELGSEEDGFDG
ATAAAARKEVIRNKIRAIKGMARVFSVLREESESVLTKGTLPTGMLPSGVLSGGKQLQSATVEAIEADEAIKGFP
QHKITSFEEAKGLDRINERMPPR

>d1g5ba_ d.159.1.3 (A:) lambda ser/thr protein phosphatase {Bacteriophage lambda}
MRYYEKIDGSKYRNIVVVGDLHGCYTLMNKLDTIGFDNKKDLLISVGDLVDRGAENVECLETIPFWFRAVR
GNHEQMMIDGLSERGNVNHWLLNGGGWFFNLDYDKEILAKALAHKADELPLIILVSKDVKYVICHADYPFDE
YEFGKPVDHQQVIWNRERISNSQNGIVKEIKGADTFIFGHTPAVKPLKFANQMYIDTGAFCGNLTLIQVQGA

>d1emsa2 d.160.1.1 (A:10-280) NIT-FHIT fusion protein, N-terminal domain {Nematode (Caenorhabditis elegans)}

MATGRHFIAVCQMTSDNDLEKNFQAANMIERAGEKKCEMVFLPECFDFIGLNKNEQIDLAMATDCEYMEKY
RELARKHNIWLSLGGLHHKDPDAAHPWNTLHIIIDSGVTRAEYNKLHLFDLEIPGKVRLMESEFSKAGTEMIP
PVDTPIGRLGLSICYDVRFPELSLWRKRGQAQLLSFPSAFTLNTGLAHWETLLRARAIENQCYVAAAQTGAHN
PKRQSYGHSMVVDPWGA VVAQCSERVDMCFAEIDL SYVDTLREMQPVFSHR

>d1f89a_ d.160.1.1 (A:) hypothetical protein yl85 {Baker's yeast (Saccharomyces cerevisiae)}
SASKILSQKIKVALVQLGSSPDKMANLQRAATFIERAMKEQPDTKLVLPECFNSPYSTDQFRKYSEVINPKEPS
TSVQFLSNLANKFKIILVGGTIPELDPKTDKIYNTSIIFNEDGKLIDKHRKVHLFDVDIPNGISFHESETLSPGEKSTTI
DTKYKGKFGVGICYDMRFP EAML SARKGAFAMIYPSAFNTVTGPLHWILLARSRAVDNQVYVMLCSPARNLQ
SSYHAYGHSIVVDPRGKIVAEAGEGEEIIYAELDPEVIESFRQAVPLTKQRFF

>d1erza_ d.160.1.2 (A:) N-carbamoyl-D-aminoacid amidohydrolase {Agrobacterium sp.}
TRQMILAVGQQGPIARAETREQVVVRLLMLTKAASRGANFIVFPEALTTFFPRWHFTDEAEELDSFYETEMP
PVVRPLFEKAAELGIGFNLGYAELVVEGGVKRRFNTSILVDKSGKIVGKYRKIHLPGHKEYEAYRPFQHLEKRYFEP
GDLGFPVYDVDAAKMGMFICNDRWPEAWRVMGLRGAIIICGGYNTPTHNPPVPQHDHLSFHLLSMQA
GSYQNGAWSAAAGKVGMEENCMLLGHSCIVAPTGEIVALTTLEDEVITA AVDLDRCRELREHIFNFQKQHRQP
QHYGLIAEL

>d1hq0a_ d.194.1.1 (A:) Type 1 cytotoxic necrotizing factor, catalytic domain {Escherichia coli}
SIESTSKSNFQKLSRGNIDVLKGRGSISSTRQRAIYPYFEAANADEQQPLFFYIKKDRFDNHGYDQFYDNTVGP
NGIPTLNTYTGIEIPS DSSSLGSTYWKKYNLNTNETSIIRV SNSARGANGIKIALEE VQEGKPVII TSGNL SGCTTIVAR
KEGYIYKVHTGTTKSLAGFTSTTVKKA VEVLELLTKEPIPRVEGIMSNDLV DYLSEN FEDSLITYSSSEKKPDSQIT
IIRDNVSVFPYFLDNPIEHGF GTSATV LRV DGNVV RSLSESY SLNADASE ISV LKV FSKKF

>d1qdla_ d.161.1.1 (A:) Anthranilate synthase
aminodeoxyisochorismate synthase/lyase subunit, TrpE {Archaeon Sulfolobus solfataricus}
AMEVHPISEFASPFEVFKCIERDFKVAGLLESIGGPQYKARYS VIAWSTNGYLIHDDPVNILNGYLKDLKLADIPG
LFKGGMIGYISYDAVRFWEKIRDLKPAAEDWPYAEFFTDPNIIYDHNEGKV YVNADLSSVGGCGD IGEFKV SFY
DESLNKNSYERIVSESLEYIRSGYIFQVVL SRFYRYIFSGDPLRIYYNLLRINPS PYMFYLK FDE KYLIGSSPELLFRVQ
DNIVETYPIAGTRPRGADQEE DLKLELMNSEKD KAEHMLV DLA RNDLGKVCVPGTVK VPEL MYVEK YSHV
QHIVSKVIGTLKKKNALNVLSATFPAGTVSGAPKPMAMNII ETLEEYKRGPYAGAVGFISADGNAEFAIAIRTA
LNKE LLRIHAGAGIVYDSNPESEYFETEHKLKALKTAIGVR

>d1i1qa_ d.161.1.1 (A:) Anthranilate synthase
aminodeoxyisochorismate synthase/lyase subunit, TrpE {Salmonella typhimurium}
KPTLELLTCDAAYRENPTALFHQVCGDRPATLLESADIDSKDDLKSLLLVD SALRITALGDTVTIQALSDNGASLLP
LLDTALPAGVENDVLPA GRVLRFPPVSP LLDENARLC SLSV FDAF RLLQGV VNIPTQEREAMFFGGLFAYDLVAG
FEALPHLEAGNNCPD YCFYLAETLMVIDH QKKSTRIQASLTASDREKQLRNARLAYLSQQLTQPAPPLPVTPV
DMRCECNQSDDA FGAVVRQLQKAIRAGEIFQVVP SRRFLPCPSPLA AYYV LKKS NPS PYMFFMQDNDFTLFG
ASPESS LYDAASRQIEIYPIAGR PRGR RADGTLDRLDSRIELDMRTDH KELSEH LMLV DLA RNDLARIC TPGS
RYVADLT KVD RYSY VMHL VSRV VGE LRHD LDA HAY RAC MNM GTLS GAK VRAM QLIA DAEG QRRG SYGG
VGYFTA HG DLD TCIVIR SAL VEN GIAT VQAG AGIV LD SV P QSEAD ETRN KAR A VL RAIATA HHA
>d1i7qa_ d.161.1.1 (A:) Anthranilate synthase
aminodeoxyisochorismate synthase/lyase subunit, TrpE {Serratia marcescens}
TKPQLTLLKVQASYRGDP TTLFHQLCGARPATLLES A EINDKQNLQSLLV D SALRITALGHTV SVQALTANGPAL
LPLLDE ALPPE VRNQARPNGRELTFPAIDAVQDEDARLRSLSVFDALRTILTLDSPADEREAVMLGGLFAYDLVA
GFENLPALRQDQRCDFCFYLAETLLVLDHQ RGSARLQASVFSEQASEAQRLQHRLEQLQAELOQQPPQPIPHQ
KLENMQLSCNQSDEEYGA VVSELQEAIRQGEIFQVVP SRRFLPCPAP LGPYQTLKDNNP SP YMFFMQ DDDFT
LFGASPESALKYDAGNRQIEIYPIAGR PRGR RADGS LLDL DSD RIELEM RTDH KELAEH LMLV DLA RNDLARIC
QAGSRYVADLT KVD RYSFVMH LVS RVVG TLRAD L DV HAY QAC MNM GTLS GAK VRAM QLIA ALR STR RGSY
GGRVGYFTAVRNLDTCIVIRSAVVEDGHRTVQAGAGVVQDSIPEREA DETRN KAR A VL RAIATA HHAKEVF
>d1k0ga_ d.161.1.1 (A:) P-aminobenzoate synthase component I {Escherichia coli}
MKTLS PAVITLLWRQDAAEFYFSRSLSHLPWAMLLHSYADHPYSRF DIVVAEPICTLTFGKETV VSESEKRTTTT
DDPLQVLQQVLDRADIRPTHNEDLPFQGGALGLFGYDLGRRFESLPEIAEQDIVLPDMAVGIYDWALIVDHQR
HTVSLSHNDVNARRAWLESQQFSPQEDFTLTS DWQSNTMREQYGEKFRQVQEYLHSGDCYQVNLAQRFHA
TYSGDEWQAFLQLNQANRAPFSAFLRLEQGAILSLSPERFILCDNSEIQT RPIKGTLP RLPPQEDSKQAVKLANS
AKDRAENLMI DLMRNDIGRVAVAGSVK VP ELFVVEPFPAVHLV STITAQLPEQLHAS DLLRAAFPGGSITGAP
KVRAMEI IDELEPQRRNAWC SIGYLSFCGNMDTSITIRLTAINGQIFCSAGGGIVADSQEEA YQETFD KVNR
LKQLEK
>d1m1da2 d.162.1.1 (A:145-313) Malate dehydrogenase {Pig (Sus scrofa)}
VTTLDIVRANAFVAELKG LD PARVSPVIGGHAGKTIPLSQ CTPK VDFPQDQLST LTGRIQEAGTEVVKAKAGA
GSATLSMAYAGARFVFS LV DAMNGKEGV VECSFVKSQETDCPYFSTPLLGKKIEKNL GIGKISPFEK MIAEAI
PELK ASIKKGE EFVK NM
>d5mdha2 d.162.1.1 (A:155-333) Malate dehydrogenase {Pig (Sus scrofa)}
TRL DHNRAKAQIALKLG VTSDDV KNVII WGNHSSTQYPDV NHAKV KLQAKEV GVYAEV KDD SWLKG E FITTVQ
QRGA AVIKARKLSSA MSAKAICDH VRDIWF GTPE GE FVSMG IISDG NSYGV PDD LLYSFP VTIKDKT WKIVEGL
PIN DFSREKMDLTAKELA EEKETAF EFLSSA
>d7mdha2 d.162.1.1 (A:198-385) Malate dehydrogenase {Sorghum (Sorghum vulgare), chloroplast}
TRL DENRAK CQLALKAGV FYDKV SNTI WGNH STTQV PDFLNA KIDGR PVKEV KRTK WLEE FTITVQ KRGGA
LIQ KWGRSSA AASTAV SIADA KSLV TP TPEGD WFSTGV YTTGN PYGIA EDIVF SMC RSKGD GDY ELATD VS NDD
FLW ERIK KSEA ELLA EKKC VAH LTGE GNAY CDV PEDTML PGEM
>d1civa2 d.162.1.1 (A:194-385) Malate dehydrogenase {Flaveria bidentis, chloroplast}
TRL DENRAK CQLALKAGV FYDKV SNTI WGNH STTQV PDFLNA KIDGR PVKEV KRTK WLEE FTITVQ KRGGA
GVL IKK WGRSSA AASTAV SIVDAIRSLV TP TPEGD WFSTGV YTN GNP YGIA EDIVF SMC RSKGD GDY EFV KDV IF
DDYLSKKIKKSE DELLA EKKC VAH LTGE GIAV CDL PEDTML PGEM
>d2cmd_2 d.162.1.1 (146-312) Malate dehydrogenase {Escherichia coli}
VTTLDIIRSNTFVAELKGKQPG E VEV P VIGGHSGV TILPLLSQVPGVS FTEQEVADLT KRIQNAGTEV VEA KAGGG

SATLSMGQAAARFGLSLVRALQGEQGVVECAYVEGDGQYARFFSQPLLGKNGVEERKSIGTLSAFEQNALEG
MLDTLKKDIALGQEfvNK
>d1bdma2 d.162.1.1 (A:155-332) Malate dehydrogenase {Thermus flavus}
TRLDHNRAKAQLAKKTGTGVDRIRRMWGNHSSIMFPDLFHAEVDRPALELVDMEWYEKVFPTVAQRGA
AAIIQARGASSAASAANAAIEHIRDWALGTPEGDWVSMAVPSQGEYGIPEGIVYSFPVTAKDGAYRVVEGLEIN
EFARKRMEITAQELLDEMEQVKALGLI
>d2hlpA2 d.162.1.1 (A:163-330) Malate dehydrogenase {Archaeon Haloarcula
marismortui}
FGGRLDSARFRYVLSEEFDAPVQNVEGTILGEHGDAQVPVFSKVRVDGTDPEFSGDEKEQLLGDQESAMDVI
ERKGATEWGPARGVAHMVEAILHDTGRVLPASVKLEGEGHEDTAFGVPVRLGSNGVEEIVEWDLDDYEQDL
MADAAEKLSQYDKIS
>d1b8pa2 d.162.1.1 (A:159-329) Malate dehydrogenase {Aquaspirillum arcticum}
LRLDHNRLSQIAAKTGPVSSIEKLFVWGNHSPTMYADYRYAQIDGASVKDMINDDAWNRTFLPTVGKRG
AAIIDARGVSSAASAANAAIDHIHDWVLGTAGKWTMGI PSDGSYGIPEGVIFGFPVTENGEYKIVQGLSIDAF
SQRERINVTLNELEEQNGVQHLLG
>d1guya2 d.162.1.1 (A:144-306) Malate dehydrogenase {Chloroflexus aurantiacus}
AGVLDAARYRTFIAMEAGVSVEDVQAMLMGGHGDEMVPPLRFSTISGIPVSEFIAPDRLAQIVERTRKGGGEI
VNLLKTGSAYYAPAAAATAQMVEAVLKDKKRVMPVAAYLTGQYGLNDIYFGVPVILGAGGVKEKILELPLNEEMAL
LNASAKAVRATLDTL
>d1gyoA2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium tepidum}
AGVLDsarfrsfiamelgvsmqdtacvlggghdamvpvvkyttvagipvalisaeriaelvertrtggaeiv
NHLKQGSAFYSPATSVVEMVESIVLDRKRVLTCAVSLDGQYQIDGTFVGVVPVKGKNGVEHIYEIKLDQSDL DLL
QKSAKIVDENCKML
>d1guza2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium vibrioforme}
AGVLDAARFRSFIAAMELGVSMQDINACVLGGHGDAMVPVVKYTTVAGIPISDLLPAETIDKLVERTRNGGAEIV
EHLKQGSAFYAPASSVEMVESIVLDRKRVLPACVGLEGQYQIDKTFVGVVPVKGKNGVEHIYEIKLDQSDL DLL
QKSAKIVDENCKML
>d1hyha2 d.162.1.1 (A:167-329) L-2-hydroxyisocapronate dehydrogenase, L-HICDH {Lactobacillus
confusus}
GTLLDTARMQRAGEAFDLDPRSVSGYNLGEHGNSQFWAWSTVRVMGQPIVTLADAGDIDLAAIEEARKGG
FTVLNGKGYTSYGVATSAIRIAKAVMADAHAELVSNRRDDMGMYLSYPAIIGRDGVLAETTLDLT DEQEKL
QSRDYIQQRFDEIVDTL
>d9ldta2 d.162.1.1 (A:163-331) Lactate dehydrogenase {Pig (Sus scrofa)}
SGCNLDsarfrylmgerlgvhplschgwlgehgdsavwsgvnagvslknlhpegtadkehkavh
KEVVDSAYEVIKLKGYTSAIGLSVADLAESIMKNLRRVHPISTMIKGLYGIKENVFLSVPCLGQNGISDVVKVTL
TPEEE AHLKKSADTLWGIQKELQF
>d1i0za2 d.162.1.1 (A:161-332) Lactate dehydrogenase {Human (Homo sapiens), heart isoform (H
chain)}
SGCNLDsarfrylmgerlgvhplschgwlgehgdsavwsgvnagvslknlhpegtadkehkavh
KMVVESAYEVIKLKGYTNAIGLSVADLIESMLKNLSRIHPVSTMVKGMYGIENEVFLSLPCILGQNGISDVVKVTL
LKDDEVAQLKKSADTLWDIQKDLKD
>d1i10a2 d.162.1.1 (A:160-331) Lactate dehydrogenase {Human (Homo sapiens), muscle isoform
(M chain)}
SGCNLDsarfrylmgerlgvhplschgwlgehgdsavwsgmnagvslktlhpdlgtdkdkeqwkev

HKQVVESAYEVIKLKGYTSAIGLSADLAESIMKNLRRVHPVSTMIKGLYGIKDDVFLSVCILGQNGISDLVKV
TLTSEEARLKKSAIDLWGIQKELQF

>d2Idx_2 d.162.1.1 (160-331) Lactate dehydrogenase {Mouse (*Mus musculus*)}
SGCNLD SARFRYLIGEKLGVNPTSCHGVVLGEHGDSVPIWSGVNVAGVTLKSLNPAIGTDKNQHWKNVHK
QVVEGGYEVLDMKGYTSAIGLSVTDLARSILKLNKRVHPVTTLVKGFGHGIKEEVFLSIPCVLGESGITDFVKVN
MTAEEEGLLKKSAIDLWNMQKNLEL

>d1ldm_2 d.162.1.1 (161-329) Lactate dehydrogenase {Dogfish (*Squalus acanthias*)}
SGCNLD SARFRYLMGERLGVHSCSCHGVVIGEHGDSVPSVWSGMNVASIKLHPLDGTNKDKQDWKKLHKD
VVDSAYEVIKLKGYTSAIGLSADLAETIMKNLCRVHPVSTMVKDFYGIKDNDVFLSLPCVLNDHGISNIVKMKL
KPNEEQQLQKSATTLWDIQQKDLKF

>d1ceqa2 d.162.1.1 (A:164-329) Lactate dehydrogenase {Malaria parasite (*Plasmodium falciparum*)}
GGVLDTSRLKYYISQKLNVCPRDVNAHIVGAHGNKMVLLKRYITVGGIPLQEFINNKLISSDAELEAIFDRTVNTAL
EIVNLHASPYVAPAAIIEMAESYLKDLKKVLCSTLLEGQYGHSDIFGGTPVVLGANGVEQVIELQLNSEEKAKFD
EAIAETKRMKALA

>d1ldna2 d.162.1.1 (A:163-330) Lactate dehydrogenase {Bacillus stearothermophilus}
TILD TARFRFLLGEYFSVAPQN VHAYIIGEHDTELPVWSQAYIGVMPIRKLVESKGEEAQKDLERIFVNVRDAAY
QIIEKKGATYYG IAMGLARVTRAILHNENAILTVSAYLDGLYGERDVYIGVPAVINRNGIREVIEELNDDEKNRFH
HSAATLKVSLRAFT

>d1llc_2 d.162.1.1 (165-334) Lactate dehydrogenase {Lactobacillus casei}
TSLDTARFRQSIAEMVNVDAR SVHAYIMGEHGDTEFPVWSHANIGGV TIAEWVKAHPEIKEDKLVKMFEDVR
DAAYEIIKLKGATFYGIATALARISKAILNDENAVLPLSVYMDGQYGLNDIYIGTPAVINRNGIQNILEIPLTDHEEES
MQKSASQLKKVLTDAFAKNDI

>d1ez4a2 d.162.1.1 (A:163-334) Lactate dehydrogenase {Lactobacillus pentosus}
TSLDSSRLRVALGKQFNVDPRSVDAYIMGEHGDSEFAAYSTATIGTRPV RDVAKEQGVSSDDLAKLEDGVRNKA
YDIINLKATFYGIGTALMRISKAILRDENAVLPVGAYMDGQYGLNDIYIGTPAIIGGTGLKQII ESPLSADELKKMQ
DSAATLKKVNDGLAELEN

>d1llda2 d.162.1.1 (A:150-319) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}
TNLDSARLRFLIAQQTGVNVKNVHAYIAGEHGDSEVPLWESATIGGVPMSDWTPLPGHDPLDADKREEHQEV
KNAAYKII NGKGATNYAIGMSGVDIIEAVLHDTNRILPVSSMLKDFHG ISDICMSVPTLNRQGVNNNTINTPVSD
KELAALKRSAETLKETA AQFGF

>d1a5z_2 d.162.1.1 (164-333) Lactate dehydrogenase {Thermotoga maritima}
GTVLDTARLRTLIAQHCGFSPRSVHVYVIGEHGDSEPVWSGAMIGGIPLQNCVCQKCD SKILENFAEKTK
RAAYEIIERKGATHYAI ALAVADIVESIFFDEKRVLTLSVYLEDYLGVKDLCISVPVTLGKHGVERILELNNEEELEAF
RKSASILKNAINEITAEN

>d1hyea2 d.162.1.1 (A:146-313) MJ0490, lactate/malate dehydrogenase {Archaeon *Methanococcus jannaschii*}

LGTHLDSLRFKVAIAKFFGVHIDEVRTRIIGEHGDSMVPLLSATSIGGIPIQKFERFKELP IDEIIEDVKT KGEQIIRLK
GGSEFGPAAIILNVVRCIVNNEKRLLTLSAYDGEFDGIRDVCIGVPVKIGRDGIEEVVSIELDKDEIIAFRKSAEIIK
KYCEEVKNL

>d1aiha_ d.163.1.1 (A:) Integrase {Bacteriophage HP1}
ETELAFLYERDIYRLLAECDNSRNPDGLIVRICLATGARWSEAETLTQSQVMPYKITFTNTSKKNRTV PISDELF
DMLPKKRGRLFN DAYESFENAVLRAEIELPKGQLTHVLRHTFASHFMMNGGNILVLKEILGHSTIEMTMRYAHF

APSHLESAVKFNPLSNPAQ

>d1ae9a_d.163.1.1 (A:) Integrase (Int) {Bacteriophage lambda}

RSRLTADEYLKIYQAAESSPCWLRLAMELAVVTGQRVGDLCMKWSDIVDGYLYVEQSKTGVKIAIPTALHIDAL
GISMKETLDKCKEILGETIIASTRREPLSSGTVSRYFMRARKASGLSFEGDPPTFHELRSL SARLYEKQISDKFAQH
LLGHKSDTMASQFRDDRGREWDKIEI

>d1f44a2 d.163.1.1 (A:130-343) Cre recombinase {Bacteriophage P1}

RAKQALAFERTDFDQVRSLMENS DRCQDIRNLAFLGIAYNTLL RIAE IARIRVKDISRTDGGRMLIHIGRTKTLVST
AGVEKALSLGVTKLVERWISVSGVADDPNNYLFCRVRKNGVAAPSATSQLSTRALEGIFEATHRLIYGAKDDSGQ
RYLAWSGHSARVGAARDMARAGVSIPEIMQAGGWTVNVNIVMN FIRNLSETGAMVRLLEDGD

>d5crxb2 d.163.1.1 (B:130-314) Cre recombinase {Bacteriophage P1}

RAKQALAFERTDFDQVRSLMENS DRCQDIRNLAFLGIAYNTLL RIAE IARIRVKDISRTDGGRMLIHIGRTKTLVST
AGVEKALSLGVTKLVERWISVSGVADDPNNYLFCRVRKNGVAAPSATSQLSTRALEGIFEATHRLIYGAKDDSGQ
RYLAWSGHSARVGAARDMARAGVSIPEIMQAGG

>d1a0p_2 d.163.1.1 (111-292) Recombinase XerD {Escherichia coli}

KDLSEAQVERLLQAPLIDQPLELRDKAMLEVLYATGLRVSELVGLTMSD ISLRQGVVRVIGKGNKERLVPLGEEAV
YWLETYLEHGRPWLNGVSIDVLFPSQRAQQMTRQTFWHRIKYAVLAGIDSEKLSPHVLRHAFATHLLNHGA
DLRVVQM LLGHSDLSTTQIYTHVATERLRQLHQ

>d1floa2 d.163.1.1 (A:135-423) Flp recombinase {Baker's yeast (Saccharomyces cerevisiae)}

KGNSHKSKMLKALLSEGESIWEITEKILNSFEYTSRFTKTLYQFLFLATFINCGRFS DIKNVDPKSF KLVQNKYLGV
VIIQCLVTETKTSVSRHIYFFSARGRIDPLVYLD EFLRN SEPVLKRVNRTGNSSSNKQEYQLLKDNLVR SYNKALK
NAPYSIFA KNGPKSHIGRHLMTSFLSMKG LTEL TNVVG NWSDKRASA VARTTYTHQ ITAIPDH YFAL VS RYYAYD
PISKEMIALKDETNP IEEE WQHIEQLKG SAEGSIRYP AWNGIISQE VL DYLSSY INRR

>d1a31a1 d.163.1.2 (A:431-626,A:720-765) Eukaryotic DNA topoisomerase I, catalytic core {Human (Homo sapiens)}

PSSRIKGEKD WQKYETARRLKKCVDKIRNQYREDWKS KEMKV RQRAVALYFIDKL ALRAGNEKEEGETADTVGC
CSLRVEHINLHP ELDGQ EYV VEFDFLGKDSIRYYNKVP VEKRVFKNLQLFMENKQP EDDLFD RLNTGILNKHLQ
DLMEGLTAKVFR TYNASITLQQQLKELTAPDENI PAKILSYN RANRAVXKL NYLD PRITV AWCK KWGVPIEKIYNK
TQREKFAWAIDMADEDYEF

>d1a41_d.163.1.2 (-) Eukaryotic DNA topoisomerase I, catalytic core {Vaccinia virus}

NAKRDRIFVRV NVVMKRINCFINKNIKKSSTD SNYQLAVFMLMETMFFIRFGKMKYLKENETVGLLTKNKHIEI
SPDEIVIKFVGKDKVSHFVVHKSNR LYKPLLKL TDSSPEEFL FNKL SERK VYE CIKQFGIRIKDL RTYGV NYTF LY
FWTNVKSISPLPSPKLIALTIKQTAEVVGHTPSISKRAYMATTILEMV KDKNFLDV VS KTTFDEF LSIVVDHV KS

>d1mhda_d.164.1.1 (A:) SMAD MH1 domain {Human (Homo sapiens)}

PIVKRLLGWKKGEQNGQEEKWCEKAVKSLVKKLKTGQLDELEKA ITT QNVNTKCITIPRS LDGRLQVSHRKGLP
HVIYCRLWRWPDLHSHEL RAMELCEF AFNM KKDEV CVNP YHY QRV ET

>d1hufa_d.195.1.1 (A:) YopH tyrosine phosphatase N-terminal domain {Yersinia pestis}

LSLS D LHRQV SRLVQQ QES GDCTG KLR GNVAANKETTF QGL TIAS GARE SEK VFA QT VLS H V ANV VLT QED TAK LL
QSTV KHN LN NYDL RSV GNG NSV L VSL RDQ MTL QDA KV LLE AAL RQ ES

>d1mrj_d.165.1.1 (-) alpha-Trichosanthin {Mongolian snake gourd (Trichosanthes kirilowii maxim)}

DVSFR LSGATSSYGV FISNL RKA LPNERK LYDI PLLR SS LPGS QRYALI HLT NYADET ISVA IDV TNV YIM GY RAGD
TSYFF NEASATEAA KYV FK DAMR KVTLP YSG NYERL QTA AGKIRE NIPL GLP ALD SAI TT LF YYN ANSA ASAL MVL
IQST SEA ARYK FIE QQI GK RV DK TFL PSL AIIS LENS WSAL SKQI QIA STN NGQ FESP VV LINA QN QR V IT NV DAG

VVTSNIALLNRNNMA

>d1bryy_d.165.1.1 (Y:) Bryodin {Red briony (*Bryonia dioica*)}

DVSFRLSGATTTSYGVFIKNLREALPYERKVYNIPLLRSSISGSGRYLLHLTNYADETISVAVDVTNVYIMGYLAGD
VSYFFNEASATEAAKFVFKAKKVTLPPSGNYERLQTAAGKIRENIPLGLPALDSAITTLYYTASSAASALLVLIQS
TAESARYKFIEQQIGKRVDKTFLPSLATISLENNWSALSKQIQUIASTNNGQFESPVLIDGNQNRVSITNASARVV
TSNIALLNRNNIA

>d1mrg_d.165.1.1 (-) alpha-Momorcharin (momordin) {Bitter gourd (*Momordica charantia*)}

DVSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLPSVSGAGRYLLMHLFNRDGKTITVAVDVTNIYIMGYL
ADTTSYFFNEPAEELASQYVFRDARRKITLPYSGDYERLQIAAGKPREKIPIGLPALDSAISTLLHYDSTAAGALL
LIQTTAEARFKYIEQQIQERAYRDEVPSLATISLENSWSGLSKQIQLAQGNNGIFRTPIVLVDNKGNRQVQITNV
SKVVTSMNIQLLNTRNI

>d1cf5a_d.165.1.1 (A:) Beta-momorcharin {Bitter gourd (*Momordica charantia*)}

DVNFDLSTATAKTYKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLNTSYAYETISVAIDVTNVYVVAYRTRDVSY
FFKESPPEAYNILFKGTRKITLPYTGNYENLQTAAHKIRENIDLGLPALSSAITTLFYNAQSAPSALLVLIQTTAEAA
RFKYIERHVAKYVATNFKNLAIISLENQWSALSKQIFLAQNQGGKFRNPVDLIKPTGQRFQVTNVDSVVKGNI
KLLLNSRASTADEN

>d1ce7a_d.165.1.1 (A:) Mistletoe lectin I A-chain {European mistletoe (*Viscum album*)}

YERGDLVTQAQTTGAGYFSITLLRDYVSSGSFSNAIPLLSQSGGGGEAGRFLVELTNSGGDGITVAIDVTNLYV
VAYQAGSQSYFLSGPGGRHGFTGTRSSLFPNGSYPDLEQYGGQRKQIPLGIDQLIQSVTALKFPGSTRTGARSIL
ILIQMISEAARFNPILWRARQYINSGASFLPDVYMLEETSWGQQSTQVQHSTDGVFNNPIALADPGGGVTLT
NVRDVIASLAIMLFVC

>d1abra_d.165.1.1 (A:) Abrin A-chain {Abrus precatorius}

EDRPIKFSTEGATSQSYKQFIEALRERLRGGIHDIPVLPDPTTLQERNRYITVELNSNSDTESIEVGIDVTNAYVVAY
RAGTQSYFLRDAAPSSASDYLFTGTDQHSLPFYGTGDLERWAHQSRQQIPLGLQALTHGISFRSGGNDNEEK
RTLIVIIQMVAEAARFRYISNRVRVSIQTGTAQPDAAAMISLENNWDNLSRGVQESVQDTFPNQVTLTNIRNEP
VIVDSLSHPTVAVLALMLFVCNPPN

>d1apa_d.165.1.1 (-) Pokeweed antiviral protein alpha {Pokeweed (*Phytolacca americana*)}

INTITFDVGATNINKYATFMKSIHNQAKDPTLKCYGIPMLPNTNLTKYLLVTLQDSSLKTITLMLKRNNLYVMGY
ADTYNGKCRYHIFKDINSNTTERNDVMTTLCNPSSRVGKNINYDSSYPALEKKVGRPRSQVQLGIQILNSGIGKIY
GVDSFTEKTEAEFLVIAIQMVSEAARFKYIENQVKTNFNRAFPNAKVLNLEESWGKISTAIHNAKNGALTSPEL
KNANGSKWIVLRVDDIEPDVGLLKYVNGTCQAT

>d1d6aa_d.165.1.1 (A:) Pokeweed antiviral protein alpha {Pokeweed (*Phytolacca americana*)}

VNTIIYNGSTTISKYATFLNDLNEAKDPSLKCYGIPMLPNTNTPKYVLVELQGSNKKTITLMLRRNNLYVMGY
SDPFETNKCRYHIFNDISGTERQDVETTLCNPANSRSVSKNINFDSRPTLESKAGVKSRSQVQLGIQILDSNIGKIS
GVMSFTEKTEAEFLVIAIQMVSEAARFKYIENQVKTNFNRAFPNAKVLNLEESWGKISTAIHDAKNGVLPKPL
ELVDASGAKWIVLRVDEIKPDVALLNYVGGSCQTT

>d1qi7a_d.165.1.1 (A:) Saporin So6 {Common soapwort (*Saponaria officinalis*)}

VTSITLDVNPTAGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGPPSKEKFLRINFQSSRGTVSLGLKRDNLVYVAYL
AMDNTNVNRAYYFKSEITSALTEPEATTANQKALEYTEDYQSIEKNAQITQGDKSRSRKEGLGIDLLTFMEAV
NKKARVVKNEARFLIAIQMTAEVARFRYIQNLVTKNFPNKFDSDNKVIQFEWSRKISTAIYGDAKNGVFNKDY
DFGFGKVRQVKDLQMGLLMLGKPK

>d1ift_d.165.1.1 (-) Ricin A-chain {Castor bean (*Ricinus communis*)}

YPIINFTTAGATVQSYTNFIRAVRGRLLTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVV
GYRAGNSAYFFHPDNQEDAIAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYSTG

GTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGLSTAIQESNQGAFASPIQLQR
RNGSKFSVYDVSLIPIALMVYRCAPPP

>d1hwma_d.165.1.1 (A:) Ebulin A-chain {Sambucus ebulus}

IDYPSVSFNLAGAKSTTYRDFLKLNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLVRLTNYNGDTVTSAVDVTN
LYLVAFSANGNSYFFKDATELQKSNLFLGTTQHTLSFTGNYDNLETAAGTRRESIELGPNPPLDGAITSLWYDGGVA
RSLLVLIQMVPPEAARFRYIEQEVRSLQQLTSFTPNALMSMENNWSMSLEVQLSGDNVSPFSGTVQLQNYD
HTPRLVDNFEELYKITGIAILLFRCVA

>d1dm0a_d.165.1.2 (A:) Shiga toxin, A-chain {Shigella dysenteriae}

KEFTLDFSTAKTYVDSLNVIRSAIGTPLQTISGGTSLLMDSGTGDNLFADVGRGIDPEEGRFNNRLIVERNNLY
VTGFVNRTNNVFYRFADFSHVTFPGTTAVTSGDSSYTLQRVAGISRTGMQINRHSLLTSDLMHSHTSLTQ
SVARAMILRFVTVTAEALRFRQIQRGFRLLDDLSGRSYVMTAEDVDLTNWGRLLSVLPDYHGQDSRVGRISF
GSINAILGSVALILNCHHHASRVARMASDEFPSMCPADGRVRGITHNKILWDSSTLGAIM

>g1lts.1 d.166.1.1 (A:,C:) Heat-labile toxin, A-chain {Escherichia coli, type IB}

RLYRADSRPPDEIKRGGLMPRGHNEYFDRGTQMNINLYDHARGTQTGFVRYDDGYVSTSLSRSAHLAGQSIL
SGYSTYYIYVIATPNMFNVNDVLGVYSPHPYEQEVSALGGIPYSQIYGWYRVNFGVIDERLHRNREYRDRYYRN
LNIAPAEDGYRLAGFPPDHQAWAREEPWIHHAPQGCGXGDTNEETQNLSTIYLREYQSKVKRQIFSDYQSEVDI
YNRI

>g1tii.1 d.166.1.1 (A:,C:) Heat-labile toxin, A-chain {Escherichia coli, type IIB}

NDYFRADSRTPDEVRRSGGLIPRGQDEAYERGTPININLYDHARGTATGNTRYNDGYVSTTTLRQAHLLGQN
MLGGYNEYIYVVAAPNLFDVNGVLGRYSPYPSENeyaALGGIPLSQIIGWYRVSFGAIEGGMHRNRDYRRDL
FRGLSAAPNEDGYRIAGFPDGFPAWEWPWREFAPNSCLPXTTCASLTNKLSQHDLADFKKYIKRKFTLMTLLSI
NN

>d1f0la2 d.166.1.1 (A:1-187) Diphtheria toxin, N-terminal domain {Corynebacterium diphtheriae}
GADDVVDSKSFVMENFSSYHGTKGPGVDSIQKGIQKPKSGTQGNYDDDWKGFYSTDNKYDAAGYSVDNEN
PLSGKAGGVVKVTPGLTKVLALKVDNAETIKKELGLSLTEPLMEQVGTEEFIKRGDGASRVVLSLPFAEGSSSV
EYINNWEQAKALSVELEINFETRGKRGQDAMYEYMAQACA

>d1ikpa2 d.166.1.1 (A:395-606) Exotoxin A, C-terminal domain {Pseudomonas aeruginosa}

PTGAEFLGDGGDVSFSTRGTQNWTVERLLQAHRQLEERGYVFVGYHGTLEAAQSIVFGGVRARSQDLDIAW
RGFYIAGDPALAYGYAQDQEPDARGRIRNGALLRVYVPRSSLPGFYRTSLTAAPEAAGEVERLIGHPLPLRLDAI
TGPxEEGGRLLETILGWPLAERTVVIPTSAIPTDPRNVGGDLDPSSIPDKEQAIASALPDYASQPGK

>d1prta_d.166.1.1 (A:) Pertussis toxin, S1 subunit {Bordetella pertussis}

DPPATVYRYDSRPEDVFQNGFTA WGNNNDNVLEHTGRSCQVGSSNSAFVSTSSRRYTEVYLEHRMQEAVEA
ERAGRGTGHFIGIYIYEVRA DNNFYGAASSYF EYVDTYGDNAGRILAGALATYQSEYLAHRRIP PENIRR VTRVH
NGITGETTT EYSNARYVSQQTRANPNPYTSRRSVAIVGTLVRMAPVVGACMARQAESSEAMA AW SERAGE
AMVLVYYESIAYSF

>g1xtc.1 d.166.1.1 (A:,C:) Cholera toxin {Vibrio cholerae}

NDDKLYRADSRPPDEIKRGGLMPRGQSEYFDRGTQMNINLYDHARGTQTGFVRHDDGYVSTSLSRSAHLVG
QTILSGHSTYYLYVLATAPNMFNVNDVLGAYSPHPDEQEVSALGGIPYSQIYGWYRVHFGVLDEQLHRNRGYRD
RYYSNLDIAPAADGYGLAGFPPEHRAWREEPWIHHAPP CGNAPRXSNTCDEKTQSLGVKFLDEYQSKVKRQI
FSGYQSDIDTHNRIKDEL

>d1qs1a1 d.166.1.1 (A:60-264) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}

TDKVEDFKEDKEAKEWGKEKEWKL TATEKGKMN NFDN KNDIKT NYKEITFS MAGSF EDEIK DLKE IDKMF
DKTNL SNSI ITYKN VEPTTIGFN KSLTEG NTINS DAMA QFKE QFL RD IKF DS YLD THL TA QQV SS KER VIL KV TVP

SGKGSTTPKAGVILNNSEYKMLIDNGYMVHVDKVKVVKKGVECLQIEGTLKK
>d1qs1a2 d.166.1.1 (A:265-461) Vegetative insecticidal protein 2 (VIP2) {Bacillus cereus}
SLDFKNDINAEAHSGMKNYEEWAKDLTDSQREALDGYARQDYKEINNYLRNQGGSGNEKLDQIKNISDAL
GKKPIPEINTVYRWCGMPEFGYQISDPLPSLKDFEEQFLNTIKEDKGYMSTSLSERLAAGFSRKIILRLQVPKGST
GAYLSAIGGFASEKEILDKDSKYHIDKVTEVIIGVKRYVVDATLLT
>d1g24a_d.166.1.1 (A:) Exoenzyme c3 {Clostridium botulinum}
AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVINGFPSNLIKQVELLDKSF
NKMKTPEINMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAKAKFLNKDRLEYGYISTSLMNVSQFAGRPIIT
KFKVAKGSKAGYIDPISAFAGQLEMLLPRHSTYHIDDMRLSSDGKQIITATMMGTAINPK
>d1j7na3 d.166.1.1 (A:264-550) Anthrax toxin lethal factor, middle domain {Bacillus anthracis}
MLSRYEKWEKIKQHYQHWSDSLSEERGRLKKLQIPIEPKKDDIIHSLSQEEKELLKRIQIDSSDFLSTEEKEFLKKL
QIDIRDSLSEEKELLNRIQVDSSNPLSEKEKEFLKKLKKLQIPIEQKQIITATMMGTAINPK
DALLHQSIGSTLYNKIYLYENMNINNLATLGADLVSTDNTKINRGIFNEFKKNFKYSISSNYMIVDINERPALDN
ERLKWRQLSPDTRAGYLENGKLILQRNIGLEIKDVQIIKQSEKEYIRIDAKVV
>d1a26_2 d.166.1.2 (797-1012) Poly(ADP-ribose) polymerase, C-terminal domain
{Chicken (Gallus gallus)}
LRTDIKVVDKDSEEAKIHKQYVKNTHAATHNAYDLKVVEIFRIEREGESQRYKPFKQLHNRQLLWHGSRTTNFAGI
LSQGLRIAPPEAPVTGYMFGKGIYFADMVSKSANYCHTSQADPIGLILLGEVALGNMYELKNASHITKLPKGKHS
VKGLGKTAPDPTATTLGVEVPLNGNGISTGINDTCLLYNEYIVYDVAQVNLKYLLKLKFNYKTS
>d1g2aa_d.167.1.1 (A:) Peptide deformylase {Escherichia coli}
SVLQLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSENRDERLVLINPEL
LEKSGETGIEEGCLSIPEQRALVPRAEKVKIRALDRDGKPFELEADGLLAICIQHEMDHLVGKLFMDYLSPLKQQR
IRQKVEKLDRL
>d2def_d.167.1.1 (-) Peptide deformylase {Escherichia coli}
VLQVLHIPDERLRKVAKPVEEVNAEIQRIVDDMFETMYAEEGIGLAATQVDIHQRIIVIDVSENRDERLVLINPELL
EKSGETGIEEGCLSIPEQRALVPRAEKVKIRALDRDGKPFELEADGLLAICIQHEMDHLVGKLFMDYLS
>d1jbia_d.209.1.1 (A:) Cochlin {Human (Homo sapiens)}
TAPIAITCFTRGLDIRKEKADVLCPGGCPLEEFSVYGNIVYASVSSICGAHAVRGVISNSGGPVRVYSLPGRENYSS
VDANGIQSQMLSRSASFTVTLE
>d1chua3 d.168.1.1 (A:238-353) L-aspartate oxidase {Escherichia coli}
LEFNQFHPTALYHPQARNFLTEALRGEGAYLKRPDGTRMPDFDERGELAPRDIVARAIDHEMKRLGADCMF
LDISHKPADFIRQHFPMIYEKLLGLGIDLTCQEPVPIVPAAHYT
>d1fuma3 d.168.1.1 (A:226-357) Fumarate reductase flavoprotein subunit {Escherichia coli}
MEFVQYHPTGLPGSGILMTEGCRGEGGILVNKNGYRYLQDYGMGPETPLGEPKNKYMELGPRDKVSQAFWH
EWRKGNTISTPRGDVYLDRLHLGEKKLHERLPFICEAKAYGVDPVKEPIPVRPTAHYT
>d1qlaa3 d.168.1.1 (A:251-371) Fumarate reductase flavoprotein subunit {Wolinella succinogenes}
MEAVQFHPTPLFPGILLTEGCRGEGGILRDVGDHRFMPDYEPEKKELASRDVVSRRMIEHIRKGKGVQSPYG
QHLWLDISILGRKHETNLRDVQEICEYFAGIDPAEKWAPVLPMQHYS
>d1e39a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase)
{Shewanella frigidimarina}
QYIQAAPTLSVKGGVMVTEAVRGNGAILVNREGKRFVNEITRDKASAAILAQTGKSAYLIFDDSVRKSLSKIDKY
IGLGVAPTADSLVKLGKMEGIDGKALTETVARYNSLVSSGKDTFERPNLPRALNEGNYIAEVTPGVHH

>d1qo8a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase)
{*Shewanella frigidimarina*}

HPTVGKDSRILSETVRGVGAVMVNKDGNRFISELTRDKASDAILKQPGQFAWIIFDNQLYKKAKMVRGYDHL
EMLYKGDTVEQLAKSTGMKVADLAKTVDYNGYVASGKDRAFTGRADMLNMTQSPYYAVKVAPGIHHTMGG
V

>d1d4ca3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase)
{*Shewanella putrefaciens*}

YIQAHPTYSPAGGV MITEAVRGNGAIVVNREGNRFMNEITTRDKASAAILQQKGESAYLVFDD SIRKSLKAIEGY
VHLNIVKEGKTI EELAKQIDVPAAE LAKTVTAYNGFVKSGKDAQFERPDLPREL VVAPFYALEIAPAVHHT

>d1jnra3 d.168.1.1 (A:257-401) Adenylylsulfate reductase A subunit {Archaeon *Archaeoglobus fulgidus*}

FEHRFIPFRFKDG YGPVGAWFLFFKCKAKNAYGE EYIKTRA ELE KYKPYGA AQP ITP L RNHQV MLEIMDG NQ
PIYMHTEEE ALAELAGGD KKKLKHIYE AFEDFLDMT VSQ ALLWAC QNIDPQE QPSEA APAEPYIMGSHS GE

>d1lit__ d.169.1.1 (-) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}

CPEGTNAYRSYCY FNEDRET WVDADLYCQNMNSGNL VSLTQAEGAFVASLIKESGT DDFNVWIGLHD PKKN
RRWHWSSGSLV SYKSWGIGAPSSVNP GYC VSL TSSTGFQKWKD VPCEDKFSF VCK FKN

>d1qdda_ d.169.1.1 (A:) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}

QEAQTELPQARISC PEGTNAYRSYCY FNEDRET WVDADLYCQNMNSGNL VSLTQAEGAFVASLIKESGT DDF
NVWIGLHD PKKN RAWHWSSGSLV SYKSWGIGAPSSVNP GYC VSL TSSTGFQKWKD VPCEDKFSF VCK FKN

>d1b6e__ d.169.1.1 (-) CD94 {Human (Homo sapiens)}

CSCQE KWVG YRCNC YFISSE QKTWNESRHL CASQKSS LLQLQNT DELDFMSSSQFYWIGLSYSEEHTAWLWE
NGSALSQYLFPSFET FNTKNCIAYNPNGNAL DESCED KNRYICKQQLI

>d1e87a_ d.169.1.1 (A:) CD69 {Human (Homo sapiens)}

SSCSEDWVG YQRK CYFISTV KRWSW TSQAQN ACSEH GATL AVIDSE KDMN FLKRYAGREE HWV GLKKE PGH PWK
WSNGKEFNNWFN VTGSDK CVFLK NT EVSS MECE KNL YWICN KPYK

>d1hq8a_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Mouse (Mus musculus)}

GYCGPCPNWICH RNN CYQFFNEEK TWNQS QASCLS QNSSLKI YSKEEQDFLKL VSYH WMGLV QIPANGS
WQWEDGSSLSYNQL TLVEIPKGSCAVYGSF KAYTEDC ANLNTYICMKRAV

>d1hyra_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Human (Homo sapiens)}

ESYCGPCPKNWIC YKNN CYQFFDE SKN WYESQASCMSQ NASLLK VSYK SKEDQ DLLK LVSYH W/MGLV H IPTNG
SWQWEDGSI LSPN LLIEMQ KGDCAL YASS FKGYIENC STP NTYIC MQRTV

>d1egia_ d.169.1.1 (A:) Macrophage mannose receptor, CRD4 {Human (Homo sapiens)}

CPEDWGASSRTSLCFK LYAKG KHEK KTWFESRDFC RALGGDL ASINNKEE QQTI WRLITASGSYH KLF WL GLTYG
SPSEGFTWSDGSPV SYENWAYGE PN NYQN VEY C GELK GDPT MSW NDIN CEH LNN WIC QI Q

>d1bj3a_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (*Trimeresurus flavoviridis*)}

DCPSGWSSYEGH CYKPF KLYKT WDDAER FCTEQAKG GAHL V SIESAGE AD FVA QLV TENI QNT KSYV WIGLRV Q
GKEKQCSSEWSDGSSV SYENWIEAESK T CLGLEKETGFRK WVN IYCGQQNP FV CEA

>d1ixxa_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (*Trimeresurus flavoviridis*)}

DCLSGWSSYEGH CYKAF EKYKT WEDAER VCTEQAKG AHL V SIESGE AD FVA QLV TQNM KRL DFYI WIGLRV Q
GKVQCNSEWSDGSSV SYENWIEAESK T CLGLEKETD FRK WVN IYCGQQNP FV CEA

>d1ixxb_ d.169.1.1 (B:) Snake coagglutinin {Habu snake (*Trimeresurus flavoviridis*)}

DCPSDWSSYEGH CYKPF SEPKN WADAEN FCTQ QHAGGHLV SFQS SEEAD FVV KLA F QT FGH SIFWM GLSN V
WNQCNWQWSNAAM LRYKAWAEESYCVYFKSTNNK WRSRACRMMAQF VCEFQA

>d1c3aa_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (*Trimeresurus flavoviridis*), flavocetin-A}

DFDCIPGWSAYDRYCYQAFSKPKNWEDAESFCEEGVKTSHLVSIESSGEGDFVAQLVAEKIKTSFQYVWIGLRIQ
NKEQQCRSEWSDASSVNYENLVKQFSKKCYALKKGTELRTWFNVYCGTENPEVCKYTPEC
>d1c3ab_d.169.1.1 (B:) Snake coagglutinin {Habu snake (*Trimeresurus flavoviridis*), flavocetin-A}
GFCCPLGWSSYDEHCYQVFQQKMNWEDAECFKCTQQHKGSHLFSHSEEVDFTSKTFPILKYDFVWIGLSN
VWNNECTKEWSDGTLDYKAWSGGSDCIVSKTTDNQWLSMDCSSKYYVCKFQA
>d1fvua_d.169.1.1 (A:) Snake coagglutinin {Snake (*Bothrops jararaca*), botrocetin}
DCPSGWSSYEGNCYKFFQQKMNWADAERFCSEQAKGGHLVSIKIYSKEKDFVGDLVTKNIQSSDLYAWIGLRV
ENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEKDLGFVLWINLYCAQKNPFVCKSPPP
>d1fvub_d.169.1.1 (B:) Snake coagglutinin {Snake (*Bothrops jararaca*), botrocetin}
DCPPDWSSYEGHCYRFFKEWMHWDDAEEFCTEQQTGAHLVSFQSKEEADFVRSLTSEMLKGDVVWIGLSDV
WNKCRFEWTDMIEFDYDDYLLAEYECVASKPTNNKWWIIPCTRKFNFVCEFQA
>d1ioda_d.169.1.1 (A:) Snake coagglutinin {Sharp-nosed viper (*Deinagkistrodon acutus*)}
DCSSGWSSYEGHCYKVFQSKTWADAESFCTKVNGGHLVSIESSGEADFGQLIAQKIKSAKIHVWIGLRAQ
NKEKQCSIEWSDGSSISYENWIEEESKKCLGVHIETGFHKWENFYCEQQDPFVCEA
>d1iodb_d.169.1.1 (B:) Snake coagglutinin {Sharp-nosed viper (*Deinagkistrodon acutus*)}
DCPSDWSSYEGHCYKPFNEPKNWADAENFCTQQHTGSHLVSFQSTEEADFVVKLAQFTFDYGFWMGLSKIW
NQCNWQWSNAAMLKYTDWAEESYCVYFKSTNNKWRSLTCRMIANFVCEFQA
>d1jwia_d.169.1.1 (A:) Snake coagglutinin {Puff adder (*Bitis arietans*), bitiscetin}
CLPDWSSYKGHCYKVFKKVGTWEDAECFKCVENSGHLASIDSKEEADFVTKLASQTLTKFVYDAWIGLRDESKTQ
QCSPQWTDGSSVYENVDEPTKCFGLDVHTEYRTWDLPCGEKNPFICKS
>d1jwib_d.169.1.1 (B:) Snake coagglutinin {Puff adder (*Bitis arietans*), bitiscetin}
GCLPDWSSYKGHCYKVFKEVTWADAECFKCKELVNGGHLMSVNSREEGEFISKLALEKMRIVLVWIGLSHFWR
ICPLRWTDGARLDYRALSDEPICFVAESFHNIQWTCNRKKSFVCKYRV
>d2afpa_d.169.1.1 (A:) Type II antifreeze protein {Sea raven (*Hemitripterus americanus*)}
QRAGPNCPAGWQPLGDRCIYYETTAMTWALAETNCMKLGGHLASIHSQEEHSFIQTLNAGVVWIGGSACLQ
AGAWTWSDGTPMNFRSWCSTKPDDVLAACCMQMTAAADQCWDDLPCPASHKSVCAMTF
>d1h8ua_d.169.1.1 (A:) Eosinophil major basic protein {Human (*Homo sapiens*)}
RYLLVRSLOQTSQAWFTCRRCYRGNLVSIHNFNINYRIQCSVASLNQGQVWIGGRITGSGRCRRFQWVDGSRW
NFAYWAAHQPSRGGHCVALCTRGGYWRRAHCLRLPFICSY
>d1qo3c_d.169.1.1 (C:) NK cell receptor ly49a {Mouse (*Mus musculus*)}
STVLDLSLQHTGRGDKVYWCYGMKCYFVMDRKTSQCKTCQSSLSLLKIDDEDELKFLQLVVPSDSCWV
GLSYDNKKKDWAVIDNRPSKLALNTRKYNIRDGGCMLLSKTRLNGNCQVFICICGKRLD
>d1qo3d_d.169.1.1 (D:) NK cell receptor ly49a {Mouse (*Mus musculus*)}
DKVYWCYGMKCYFVMDRKTSQCKTCQSSLSLLKIDDEDELKFLQLVVPSDSCWVGLSYDNKKKDWA
WIDNRPSKLALNTRKYNIRDGGCMLLSKTRLNGNCQVFICICGKRLDK
>d1dv8a_d.169.1.1 (A:) H1 subunit of the asialoglycoprotein receptor {Human (*Homo sapiens*)}
CPVNWVEHERSCYWFSRSGKAWADADNYCRLEDAHLVVTSWEEQKFVQHHIGPVNTWMGLHDQNGPW
KWVDGTDYETGFKNWRPEQPDDWYGHGLGGGEDCAHFTDDGRWNDDVCQRPYRWVCETEL
>d1k9ia_d.169.1.1 (A:) DC-SIGN (dendritic cell-specific ICAM-3 grabbing nonintegrin) {Human (*Homo sapiens*)}
PCPWEWTFFQGNCYFMSNSQRNWHDSETACKEVGAQLVVIKSAEEQNFLQLQSSRSNRTWMGLSDLNQE

GTWQWVDGSPLPSFKQYWNRGEPPNNVGEEDCAEFGNGWNDDCNLAKFWICKSAA
>d1k9ja_d.169.1.1 (A:) DC-SIGNR (DC-SIGN related receptor) {Human (Homo sapiens)}
CRHCPKDWTFFQGNCYFMSNSQRNWHD SVTACQEVR ALVVIKTAEEQNFLQLQT SRNSR FSWMGLSDLN
QE GTWQWVDGSPLSPSFQRYWNSGEPPNNSGNEDCAEFGSGWNDNRCDVDNYWICKKPAA
>d1g1sa1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}
WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVL PYSSYYWIGIRKNNKTWTVG TKKALTNEAE
NWADNEPNKRNNE DCEIYIKSPSAPGKW NDEHCLKKHALCY
>d1g1ta1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}
WSYNTSTEAMTYDEASAYCQQRYTHLVAIQNKKEEIEYLN SILSYSPSYYWIGIRKVNNVVWVGTQKPLTEEAK
NWAPGE PNNRQKDED CVEIYIKREKDVG MWN DERS KKKLALCY
>d1hup_1 d.169.1.1 (112-228) Mannose-binding protein A, lectin domain {Human (Homo sapiens)}
KQVGNKFFLTNGEIMTFEKVKALCVKFQASVATPRNA AENGAIQN LIKEAFL GITDEKTEGQFVDLTGNRLTYT
NWNEGE PNNAGS DEDC VLLL KNGQW NDVPC STSH LAVCEFPI
>d1fifa1 d.169.1.1 (A:105-226) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}
KKSGKKFFVTNHERMPFSKVKALCSEL RGTV AIPRNAEENKAIQE VAKT SAFL GITDEVTEGQF MYVTGG RLTY
NWKKDQPDDWYH GLGG EDCV HIVD NGLW NDDSC QRP YAVCE FPA
>d1rdl1_d.169.1.1 (1:) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}
KYFMSSVRRMPLNRAKALCSELQGT VATPRNAEENRAIQNVAKDVAFL GITDEVTEGQF MYVTGG RLTY
NEGE PNNVGSGENC VLLTNGK WNDV PCSDSFLV CEFS
>d2msba_d.169.1.1 (A:) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}
KKFFVTNHERMPFSKVKALCSEL RGTV AIPRNAEENKAIQE VAKT SAFL GITDEVTEGQF MYVTGG RLTY
KDEPNDHGSGED C VTDNGLW NDISC QASHTA VCEFP
>d1b08a1 d.169.1.1 (A:235-355) Surfactant protein, lectin domain {Human (Homo sapiens), SP-D}
PNGQSVGEKFKTAGFVKPFTEAQ LLCTQAGGQLAS PRSA AENA ALQQLV VAKNEA AFLSMTDSKTEGKFTYPT
GESLV YSNWAPGE PNDGG SEDC VEIFT NGK WND RAC GEK RL VCEF
>d1byfa_d.169.1.1 (A:) Lectin TC14 {Tunicate (Polyandrocarpa misakiensis)}
DYEILFSDETM NYADAG TYCQS RGM ALVSSA MRD STMV KAILA FTEVKG HDY WVGADNLQDGAYN FLWND
GVSLPTDSDLWSPNEPSNPQ SWQLCVQIWSKYNLL DDVG CGGARR VICEKELD
>d1tn3_d.169.1.1 (-) Tetranectin {Human (Homo sapiens)}
ALQTVCLKGTKVHM KCFLAFT QT KTFHEASE D C ISR GGTL STP QT GSE NDA LY EYL RQ S VGN EA EIWL GLND MA
AEGTWVDMTGARIAYKNWETEITA QPDGGKT ENCAV LSGAANGKWF D KRC RDQLPYICQFGIV
>d1prt b2_d.169.1.2 (B:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain
{Bordetella pertussis}
GIVIPPQE QITQ HGSPY GRCANK TRAL TVAELRGSGDLQ EYLR HVTRG WSIF ALYDG TYLG GEYGGV IKDGTPG
GAFDLKTTFCIM
>d1prtc2_d.169.1.2 (C:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain
{Bordetella pertussis}
GIVIPP KALFTQQGGAY GRCPNG TRAL TVAELRGNAELQTYLRQITPGW SIYGLYDG TYLG QAYGGI IKDAPPGA
GFIY RETFCIT
>d1prea1_d.169.1.2 (A:2-84) Proaerolysin, N-terminal domain {Aeromonas hydrophila}
EPVYPDQLRLFSLGQGVC GD KYRP VNRE AQSV KS NIVGMMGQWQISGLANGWV IMGP GYNG EIKPGT AS
NTWCYPTNP VTGE
>d1f00i3 d.169.1.3 (I:842-939) Intimin {Escherichia coli}
LIVPNMSKR VTYND AVNTCKNFGGKL PSSQ NELEN VFKA WGAANKY EYYK SSQ TIISW VQQTAQDAK SGVAST

YDLVKQNPLNNIKASESNAYATCVK

>d1cwva5 d.169.1.3 (A:887-986) Invasin {Yersinia pseudotuberculosis}

NRWIYDGGRSLVSSLEASRQCQGSDMSAVLESSRATNGTRAPDGLWGEWGSLTAYSSDWQSGEYWVKKTS
TDFETMNMDTGALQPGPAYLAFPLCALSI

>d1tsg_ d.169.1.4 (-) TSG-6, Link module {Human (Homo sapiens)}

GVYHREARSGKYKLTYAEAKAVCEFEGGHLATYKQLEAARKIGFHCAAGWMAKGRVGYPIVKPGPNCFGKT
GIIDYGIRLNRSERWDAYCYNPHAK

>d1bnla_ d.169.1.5 (A:) Endostatin {Human (Homo sapiens)}

HSHRDFQPVLHLVALNAPLSGGMRGBIRGADFQCFQQARAVGLAGTFRAFLSSRLQDLYSIVRRADRAAVPIVNL
KDELLFPSWEALFGSEGPKPGARIFSFDGKDVLHPTWPQKSVWHGSDPNGRRLESYCETWRTEAPSATG
QASSLLGGRLLGQSAASCHAYIVLCIENSF

>d1koe_ d.169.1.5 (-) Endostatin {Mouse (Mus musculus)}

QPVLHLVALNTPLSGGMRGBIRGADFQCFQQARAVGLSGTFRAFLSSRLQDLYSIVRRADRGSPVIVNLKDEVLSP
SWDSLFSGSQGQLQPGARIFSFDGRDVLRHPAWPQKSVWHGSDPSGRRLMESYCETWRTETTGATGQASSL
LSGRLLEQKAASCHNSYIVLCIENSF

>d1dy2a_ d.169.1.5 (A:) Endostatin domain of collagen alpha1(xv) {Mouse (Mus musculus)}

RPVLHLVALNTPVAGDIRADFQCFQQARAAGLLSTFRAFLSSHLDLSTVVRKAERFGLPIVNLKGQVLFNNWD
SIFSGDGGQFNTHIPIYSFDGRDVMTDPSWPQKVWHGSNPHGVRVDKYCEAWRTDMAVTGFASPLSTG
KILDQKAYSCANRLIVLCIENSF

>d1by2_ d.170.1.1 (-) M2BP {Human (Homo sapiens)}

AVNDGDMRLADGGATNQGRVEIFYRGQWGTVCNDLWDLTDASVVCRALGFENATQALGRAAFGQGSGPI
MLDEVQCTGTEASLADCKSLGWLKSNCRHERDAGVVCTNETRSTHTL

>d1mwp_ d.170.2.1 (A:) N-terminal domain of the amyloid precursor protein {Human (Homo sapiens)}

LLAEPQIAMFCGRLNMHMNVQNGKWDSDPGTTCIDTKEGILQYCQEYVPELQITNVVEANQPVTIQNW
KRGRKQCKTHPHFVIPYRCLVGEFV

>d1fid_ d.171.1.1 (-) Fibrinogen C-terminal domains {Human (Homo sapiens), gamma}

QIHDTGKDCQDIANKGAKQSGLYFIKPLKANQQFLVYCEIDGSGNGWTVFQKRLGSVDFKKNWIQYKEGFG
HLSPTGTTEFWLGNEKIHLISTQSAIPYALRVELEDWNGRTSTADYAMFKVGPEADKYRLTYAYFAGGDAGDAFD
GFDFGDDPSDKFFTSHNGMFSTWDNDNDKFEGNCAEQDGSGWWMNKCHAGHLNGVYYQGGTYSKAST
PNGYDNGIIWATWKTRWYSMKTTMKIIPFNRLTIGEGQQHH

>d1fzcb1 d.171.1.1 (B:200-458) Fibrinogen C-terminal domains {Human (Homo sapiens), beta}

SCNIPVVGKECEEIRKGGETSEMYLIQPDSSVKPYRVYCDMNTENGWTVIQRQDGSVDFGRKWDPPYKQ
GFGNVATNTDGKNYCGLPGEYLGNNDKISQLTRMGPTELIEMEDWKGDVKAHYGGFTVQNEANKYQISV
NKYRGTAGNALMDGASQLMGENRTMTIHNGMFFSTYDRDNDGWLTSDPRKQCSKEDGGGWYNRCHAA
NPNGRYYWGGQYTWDMAKHGTDDGVVWMNWKGSWYSMRKMSMIRPFF

>d1fzda_ d.171.1.1 (A:) Fibrinogen C-terminal domains {Human (Homo sapiens), fibrinogen-420, alpha-E}

GGWLLIQQRMDGSLNFNRTWQDYKRGFGSLNDEGEGEFWLGNDYLHLLTQRGSVLRVELEDWAGNEAYA
HFRVGSEAEGYALQVSSYEGTAGDALIEGSVEEGAETYSHNNMQFSTFDRDADQWEENCAEVYGGGWWYN
NCQAANLNGIYYPGGSYDPRNNSPYEIENGVVWVSFRGADYSLRAVRMKIRPLVTQ

>d1jfec1 d.171.1.1 (C:142-393) Fibrinogen C-terminal domains {Chicken (Gallus gallus), gamma}

TAEIQETTGRDCQDIANKGARKSGLYFIKPQKAKQSFLVYCEIDTYGNGWTVLQRRLDGSEDFRRNWVQYKEG
GHLSPDDTEFWLGNEKIHLITTQSTLPYALRIELEDWSGKKGTA
DYAVFKVGTEEDKYRLTYAYFIGGEAGDAFD

GFNFGDDPSDKSYTYHNGMRFSTFDNDNDNFEGNCAEQDGSGWWMNRCAGHLNGPYYIGGVYSRDTGT
NSYDNGIIWATWRDRWYSMKTTMKIIPFNRLS

>d1jf61 d.171.1.1 (B:200-464) Fibrinogen C-terminal domains {Chicken (Gallus gallus), beta}
SPCVASCNIPVVGRECEDIYRKGGTSEMYIIQPDPTTPYRVYCDMETDNGGWTLIQNRQDGSVNFRAW
DEYKRGFGNIAKSGGKKYCDTPGEYWLGNKDQLSQLTKIGPTKVLIEDWNGDKVSALYGGFTIHNEGNKYQLS
VSNYKGNAZNALMEGASQLYGENRTMTIHNGMYFSTYDRDNDGWLTTPRKQCSKEDGGGWYNRCHA
ANPNGRYYWGGBTWSDMAKHGTDDGIVWMNWKGSWYSMKMSMKIKPYFPD

>d1jc9a_d.171.1.1 (A:) Tachylectin 5a {Japanese horseshoe crab (Tachylepus tridentatus)}
DPTDCADILLNGYRSSGGYRIWPKSWMVTGTLNVYCDMETDGGGWTVIQRGNYGNPSDYFYKPWKNYKL
GFGNIEKDFWLGNDRIFALTNRNMYIRFDLKDKEKDTRYAIYQDFWIENEDYLYCLHIGNYSGDAGNSFGRH
NGHNFSTIDKDHDTHETHCAQTYKGGWWYDRCHESNLNGLYLNGEHNSYADGIEWRAWKGYHSLPVEM
KIRPVEF

>d1g9mg_d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type 1}
EVVLVNVTENFNMWKNDMVEQMHEIDIISLWDQSLKPCVKLPLCVGAGSCNTSVITQACPKVSFEPIPIHYCA
PAGFAILKCNNKTFGNTGPCTNVSTVQCTHGIRPVVSTQLLNGSLAEEEVIRSVNFTDNAKTIIVQLNTSVEIN
CTGAGHCNISRACKWNNTLKQIAKLRQFGNNKTIIFKQSSGGDPEIVTHSFNCGGEFFYCNSTQLFNSTWFNS
TWSTEGLNNTEGSDTITLPCRICKQIINMWQKVKGAMYAPPISGQIRCSSNITGLLTRDGGNSNNESEIFRPGGG
DMRDNWRSELYKYKVVKIE

>d1g9ng_d.172.1.1 (G:) gp120 core {Human immunodeficiency virus type 1}
LENVTENFNMWKNNMVEQMHEIDIISLWDQSLKPCVKLPLCVGAGSCNTSVITQACPKVSFEPIPIHYCAPAG
FAILKCNDKFNGTGPCTNVSTVQCTHGIRPVVSTQLLNGSLAEEEVIRSENFTNNAKTIIVQLNESVVINCTGA
GHCNLSKTQWENTLEQIAIKLKEQFGNNKTIIFNPSSGGDPEIVTHSFNCGGEFFYCNSTQLFTWNDTRKLNNNT
GRNITLPCRICKQIINMWQEVGKAMYAPPIRGQIRCSSNITGLLTRDGGKDTNGTEIFRPGGGDMRDNWRSEL
YKYKVVKIE

>d1msk_d.173.1.1 (-) Methionine synthase (activation domain) {Escherichia coli}
TPPVTLAARDNDFAFDWQAYTPPVVAHRLGVQEVEASIETLRNYIDWTPFFMTWSLAGKYPRILEDEVVGVEA
QRLFKDANDMLDKLSAEKTLNPRGVVGLFPANRVGDDIEIYRDETRTHVINVSHHLRQQTEKTGFANYCLADFV
APKLSGKADYIGAFAVTGGLEEDALADAFEAQHDDYNKIMVKALADRLAEAAFAEYLHERVRKVYWGYPNENL
SNEELIRENYQGIRPAPGPACPEHTEKATIWELLEVEKHTGMKTESFAMWPGASVSGWYFSPDSKYYAVAQ
IQRDQVEDYARRKGMSVTEVERWLAPNLGYDAD

>d1jwka_d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Mouse (Mus musculus)}
QYVRIKNWGSGEILHDTLHHKATSCDFTCKSKSCLGSIIMNPKSLRGPRDKPTPLELLPHAIIFINQQYGSFKEA
KIEEHLARLEAVTKEIETTGTYQLTDELIFATKMAWRNAPRCIGRIQWSNLQVFDARNCTAQEMFQHICRHILY
ATNNGNIRSAITVFPQRSDGKHDFRLWNSQLIRYAGYQMPDGTIRGDAATLEFTQLCIDLGWKPRTYGRFDVLPL
VLQADGQDPFVFEIPPDLVLEVTMEHPKYEWFWQELGLKWLPAVANMLLEVGGLEFPACPFNGWYMGTEIG
VRDFCDTQRYNILEEVGRRMGLEHTLASLWKDRAVTEINVAVLHSFQKQNVTIMDHHTASESFMKHMQNEY
RARGGCPADWIALVPPVSGSITPVFHQEMLNVLSPFYYYQIEPWKTHIWQN

>d1nos_d.174.1.1 (-) Nitric oxide (NO) synthase oxygenase domain {Mouse (Mus musculus)}
NPKSLTRGPRDKPTPLELLPHAIIFINQQYGSFKEAKIEEHLARLEAVTKEIETTGTYQLTDELIFATKMAWRNAP
RCIGRIQWSNLQVFDARNCTAQEMFQHICRHILYATNNGNIRSAITVFPQRSDGKHDFRLWNSQLIRYAGYQ
MPDGTIRGDAATLEFTQLCIDLGWKPRTYGRFDVLPLQADGQDPFVFEIPPDLVLEVTMEHPKYEWFWQELGLK
WLPAVANMLLEVGGLEFPACPFNGWYMGTEIGVRDFCDTQRYNILEEVGRRMGLEHTLASLWKDRAVTE
INVAVLHSFQKQNVTIMDHHTASESFMKHMQNEYRARGGCPADWIWLVPPVSGSITPVFHQEMLNVLSPF
YYQIEPWKTHIWQNEHHHH

>d3nosa_d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Human (Homo sapiens)}

KFPRVKNWEVGSITYDTLSAQAAQGDGPCTPRRCLGSLVPRKLQGRSPGPPAPEQLSQARDFINQYYSSIKRS
GSQAHEQLQEVEAEVAATGYQLRESELVFGAKQAWRNAPRCVGRIQWGKLQVFDARDCRSAQEMFTYIC
NHIKYATNRGNLRSAITVFPQRCPGRGFRIWNSQLVRYAGYRQQDGSVRGDPANVEITELCIQHGWTPGNG
RFDVLPLLLQAPDEPELFLPPELVLEVPLEHPTLEWFAALGLRWYALPAVSNMILLEIGGLEFPAAPFSGWYMS
TEIGTRNLCDPHRYNILEDVAVCMDLDTRTSSLWKDKAAVEINAVLHSYQLAKVTIVDHHAATASFMKHLEN
EQKARGGCPADWAIVPPISGLTPVFHQEMVNLYLSPAFRYQPDPW

>d4nosa_d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Human (Homo sapiens)}

RHVRIKNWGSGMTFQDTLHHKAKGILTCSRKSCLGSIMTPKSLTRGPRDKPTPPDELLPQAIEFVNQYYGSFKEA
KIEEHLARVEAVTKEIETTGTYQLTGDELIFATKQAWRNAPRCIGRIQWSNLQVFDARSCSTAREMFHICRHVR
YSTNNNGNIRSAITVFPQRSDGHDFRVWNAQLIRYAGYQMPDGSIRGDPANVEFTQLCIDLGWKPQYGRFDVV
PLVLQANGRDPELFEPPLDLVLEVAMEHPKYEWFREREELKWYALPAVANMLLEVGGLEFPGCPFNGWYMGTEI
GVRDFCDVQRYNILEEVGRRMGLETHKLASLWKDQAVVEINIAVIHSFKQKQNVTIMDHHSAAESFMKYMQNE
YRSRGGCPADWIWLVPPMSGISITPVFHQEMLNLYLSPFYYYQVEAWKTHVWQD

>d1d0ca_d.174.1.1 (A:) Nitric oxide (NO) synthase oxygenase domain {Cow (Bos taurus)}

GPKFPRVKNWEVGSITYDTLCAQSQQDGPCPRRCLGSLVPRKLQTRPSPGPPPAEQLSQARDFINQYYSSIK
RSGSQAHEERLQEVEAEVASTGYHLRESELVFGAKQAWRNAPRCVGRIQWGKLQVFDARDCSSAQEMFTYI
CNHIKYATNRGNLRSAITVFPQRAPGRGFRIWNSQLVRYAGYRQQDGSVRGDPANVEITELCIQHGWTPGNG
GRFDVLPLLLQAPDEAPELFVLPPELVLEVPLEHPTLEWFAALGLRWYALPAVSNMILLEIGGLEFSAAPFSGWYMS
STEIGTRNLCDPHRYNILEDVAVCMDLDTRTSSLWKDKAAVEINLAFLHSFQLAKVTIVDHHAATVSFMKHLD
NEQKARGGCPADWAIVPPISGLTPVFHQEMVNLYLSPAFRYQPDPW

>d1k25a3 d.175.1.1 (A:67-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}

QITRTVPAKRTIYDRNGVPIAEDATSYNVAVIDKKYKSATGKILYVEDAQFNKVAEVFKYLDMEESYVREQLS
QPNLKQVSFGSKGNITYANMMMAIKKELETAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTS
GMESSLNSILAGTDGIITYEKDRVGNIVPGTELVSQQTVDGKDVTY

>d1qmea3 d.175.1.1 (A:71-263) Penicillin-binding protein 2x (pbp-2x), N-terminal domain {Streptococcus pneumoniae}

TVPAKRTIYDRNGVPIAEDATSYNVAVIDENYKSATGKILYVEKTQFNKVAEVFKYLDMEESYVREQLSQPNL
KQVSFGAKGNITYANMMSIKKELEAAEVKGIDFTTSPNRSPNGQFASSFIGLAQLHENEDGSKSLLGTSGME
SSLNSILAGTDGIITYEKDRGNIVPGTEQVSQRTMDGKDVTY

>d1soxa3 d.176.1.1 (A:94-343) Sulfite oxidase, middle catalytic domain {Chicken (Gallus gallus)}

QDPFAGDPPRHGGLRVNSQKPFNAEPPAELLAERFLTPNELFFTRNHLPVPAVEPSSYRLRVDPGGGTLSLSA
ELRSRFKHEVTATLQCAGNRSEMSRVRPVKGKLPWDIGAISTARWGGARLRDVLLHAGFPEELQGEWHVCFE
GLDADPGGAPYGASIPYGRALSPAADVLLAYEMNGTELPRDHGFPVRVVPGVVGARSVKWLRRAVSPDES
PSHWQQNDYKGFSPCVWDVDYRTAPAIQ

>d1hyoa2 d.177.1.1 (A:119-416) Fumarylacetoacetate hydrolase, FAH, C-terminal domain {Mouse (Mus musculus)}

ATIGDYTFYSSRQHATNVGIMFRGKENALLPNWLHLPVGYHGRASSIVSGTPIRRPMGQMRRPDNSKPPVY
GACRLLDMELEMAFFVGPGNRFGEPPIPISKAHEHIFGMVLMNDWSARDIQQWEYVPLGPFLGKSFGTISPW
VVPMDALMPFVVNPKQDPKPLPYLCHSQPYTFDINLSVSLKGEGMSQAATICRSNFKHMWTMLQLTHH
SVNGCNLRPGDILLASGTISGSDPESFGSMILESWKGTKAIDVGQQQTRFLLDGDEVIITGHCQGDGYRVGFG
QCAGKVLPA

>d1i7oa1 d.177.1.1 (A:1-213) 4-hydroxyphenylacetate degradation bifunctional

isomerase/decarboxylase HpcE {Escherichia coli}
MKGTTIFAVALNHRSQLDAWQEAFQQSPYKAPPKAVWFIFPRNTVIGCGEPFPQGEVKLSGATVALIVGKTA
TKVREEDAAEYIAGYALANDVSLPEESFYRPAIKAKCRDGFCPIGETVALSNVDNLITYTEINGRPADHWNTADLQ
RNAAQLLSALSEFATLNPGDAILLGTPQARVEIQPGDRVRVLAEGFPPLENPVVDEREVTRK
>d1i7oa2 d.177.1.1 (A:214-429) 4-hydroxyphenylacetate degradation bifunctional
isomerase/decarboxylase HpcE {Escherichia coli}
SFPTLPHPHGTLFALGLNYADHASELEFKPPEEPLVFLKAPNLTGDNQTSVRPNNIEYMHYAEELVVVIGKQAR
NVSEADAMDYVAGYTCNDYAIRDYLENYYRPNLRVKSRDGLTPMLSTIVPKAIPDPHNLTRTFVNNGELRQQ
GTTADLIFSVPFLIAYLSEFMTLNPGDMIATGTPKGLSDVVPGDEVVVEVEVGVRVLNRIVSEETAK
>d1toh_ d.178.1.1 (-) Tyrosine hydroxylase {Rat (Rattus norvegicus)}
KVPWFPRKVSELDKCHHLVTKFDPDLDLDPFGSDQVYRQRRKIAEIAFQYKHGEPIPHVEYTAEEIATWKEVY
VTLKGLYATHACREHLEGFQLLERGYREDSIPQLEDVSRLKERTGFQLRPVAGLLSARDFLASLAFRVFQCTQY
IRHASSPMHSPEPDCCHELLGHVPMЛАДРТFAQFSQDIGLASLGASDEEIEKLSTVWFTVEFGLKQNGELKA
YGAGLLSSYGEЛHSLSEEPEVRAFDPTAAVQPYQDQTYQPVYFVSESFNDAKDKLRYNAYASRIQRPFVKFDPY
TЛAIDVLDSPHTIQRSLEGVQDELHTLAHALSAIS
>d3pah_ d.178.1.1 (-) Phenylalanine hydroxylase {Human (Homo sapiens)}
TVPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYMEEEKTWGT
VFKTLKSLYKTHACYEYNHIFPLLEKYCGFHEDNIPQLEDVSQFLQCTGFRRLPVAGLLSSRDFLGGLAFRVFHCT
QYIRHGSKPMYTPEDPICHLLGHVPLFSDRSFAQFSQEIGLASLGAPDEYIEKLATIYWFTVEFGLKQGDSIKAY
GAGLLSSFGEЛQYCLSEKPKLPLELEKTAIQNYTVTEFQPLYVVAESFNDAKEKVRNFAATIPRPFVRYDPYTQRI
EVL
>d1phza2 d.178.1.1 (A:116-427) Phenylalanine hydroxylase {Rat (Rattus norvegicus)}
NTVPWFPRTIQELDRFANQILSYGAELDADHPGFKDPVYRARRKQFADIAYNYRHGQPIPRVEYTEEKQTWGT
VFRTLKALYKTHACYEHNHIFPLLEKYCGFREDNIPQLEDVSQFLQCTGFRRLPVAGLLSSRDFLGGLAFRVFHCT
TQYIRHGSKPMYTPEDPICHLLGHVPLFSDRSFAQFSQEIGLASLGAPDEYIEKLATIYWFTVEFGLKQGDSIKAY
YGAGLLSSFGEЛQYCLSDKPKLPLELEKTACQEYSVTEFQPLYVVAESFSDAKEKVRTFAATIPRPFVRYDPYTQR
VEVLDNT
>d1dqa4 d.179.1.1 (A:462-586,A:704-870) Substrate-binding domain of HMG-CoA reductase
{Human (Homo sapiens)}
LSDAEIIQLVNAKHIPAYKLETLIETHERGVSI RRQLLSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVG
VAGPLCLDEKEFQVPMATTEGCLVASTNRGCRAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIE
VNINKNLVGSAMAGSIGGYNAAHAAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTV
GGGTNLLPQQACLQMLGVQGACKDNPGENARQLARI CGTVMAGELSLMAALAAGHLVKSHMIHN
>d1hw8a2 d.179.1.1 (A:441-586,A:704-861) Substrate-binding domain of HMG-CoA reductase
{Human (Homo sapiens)}
EPRPNEECLQILGNAEKGAFLSDAEIIQLVNAKHIPAYKLETLIETHERGVSI RRQLLSKKLSEPSSLQYLPYRDYNYS
SLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLVASTNRGCRAIGLGGGASSRVLADXKSVVC
EAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNAAHAAANIVTAIYIACGQDAAQNVGSSNCITLME
ASGPTNEDLYISCTMPSIEIGTVGGTNLLPQQACLQMLGVQGACKDNPGENARQLARI CGTVMAGELSLM
AALAAGH
>d1hw8c2 d.179.1.1 (C:488-586,C:704-860) Substrate-binding domain of HMG-CoA reductase
{Human (Homo sapiens)}
HERGVSI RRQLLSKKLSEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCL
VASTNRGCRAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVGSAMAGSIGGYNAA

AANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMPSIEIGTVGGGTNLLPQQACLQMLGVQGA
CKDNPGENARQLARIVCGTVMAGELSLMAALAAG

>d1qaxa2 d.179.1.1 (A:4-110,A:221-428) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLGLSHDDVSLLANAGALPMIDIANGMIENVIGTFELPYAVASNFCQINGRDVLVP
LVVEEPSIVAAASYMAKLARANGFTTSSSAPXRLARAQVRITPQQLETAEFSGEAVIEGILDAYAFAAVDPYRAA
THNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGSLLTWEKDNNNGHLVGTLEMPMPVGLVGGATKT
HPLAQLSLRILGVKTAQALAEIAVAVGLAQNLGAMRALATEGIQRGHMALHARNIAVVAGARGDEVDWVARQ
LVEYHDVRADRAVALLQKRGQ

>d1qaxb2 d.179.1.1 (B:504-610,B:721-875) Substrate-binding domain of HMG-CoA reductase {Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLGLSHDDVSLLANAGALPMIDIANGMIENVIGTFELPYAVASNFCQINGRDVLVP
LVVEEPSIVAAASYMAKLARANGFTTSSSAPXRLARAQVRITPQQLETAEFSGEAVIEGILDAYAFAAVDPYRAA
THNKGIMNGIDPLIVATGNDWRAVEAGAHAYACRSGHYGSLLTWEKDNNNGHLVGTLEMPMPVGLVGGATKT
HPLAQLSLRILGVKTAQALAEIAVAVGLAQNLGAMRALATE

>d1k92a2 d.210.1.1 (A:189-444) Argininosuccinate synthetase, C-terminal domain {Escherichia coli}

AYSTDNSMLGATHEAKDLEYLNSSVKIVNPIMGVKFWDENVKIPAAEVTVRFEQGHPVALNGKTFSSDDVEMML
EANRIGGRHGLGMSDQIENRIIEAKSRGIYEAPGMALLHIAYERLLTGHHNEDTIEQYHAHGRQLGRLLYQGRWF
DSQALMLRDSLQRWWASQITGEVTLELRGNDYSILNTVSENLYKPERLTMEKGDSVSPDDRIGQLTMRNLD
ITDTREKLFGYAKTGLSSAASGVPQVENLENK

>d16vpa_d.180.1.1 (A:) Conserved core of transcriptional regulatory protein vp16 {Herpes simplex virus type 1}

SRMPSPMPVPPAALFNRLDDLGSAGPALCTMLDTWNEDLFSALPTNADLYRECKFLSTLPSDVVEWDAY
VPERTQIDIRAHGDVAFPTLPATRDGLGLYYEALSRRFFHAELRAREESYRTVLANFCSALYRYLRAVRQLHRQAH
MRGRDRDLGEMLRATIADRYYRETARLARVLFLHLYLFLTREILWAAYAEQMMRPDLFDCLCCDLESWRQLAGL
FQPFMFVNGALTVRGVPIEARRLRELNHIREHNLPLVRSAATEEPGAPLTTPTLHGNQARASGYFMVLIRAKL
DSYSSFTTSPSEAVMREHAYSRAPTKNNYGSTIEGLLDPDDAPEEAGLAAPRLSFL

>d1bdfa2 d.181.1.1 (A:53-178) RNA polymerase alpha subunit {Escherichia coli}

GCAVTEVIDGVHLHEYSTKEGVQEDILEILLNLKGLAVRVQGKDEVILTNKSGIGPVTAADITHGDVEIVKPQH
VICHLTDENASISMRIKVQRGRGYVPASTRIHSEEDERPIGRLLVDACYS

>d1i6va2 d.181.1.1 (A:50-172) RNA polymerase alpha subunit {Thermus aquaticus}

GTAVTSVYIEDVLHEFSTIPGVKEDVVEIIINLKELVVRFLDPKMASTTLRAEGPKEVRAVDFTPSADVEIMNPDL
LHIATLEGGKLYMEVRVDRGVGYVPAERHGIKDRINAIPVDAIFS

>d1i50c2 d.181.1.1 (C:42-172) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

PTLAIDSVEVETNTTVADEFIAHRLGLIPLQSMDIEQLEYSRDCFCEDHCDKCSVVLTQAFGESESTTNVYSKDL
VIVSNLMGRNIGHPIIQDKEGNGVLICKLRKGQELKLTCVAKKGIAKEHAKWGP

>d1el6a_ d.182.1.1 (A:) Baseplate structural protein gp11 {Bacteriophage T4}

SRLADFLGFRPKTGIDVMNRQSVGSVTISQLAKGFYEPNIESAINDVHNFSIKDVTIITNKTGVSPEGVSQTDY
WAFSGTVTDDSLPPGSPITVLVFGLPVSATTGMTAIEFVAKVRVALQEAIASFTAISYKDHTDGSKLEVTYLDN
QKHVLSTYSTYGITISQEIISESKPGYGTWNLLGAQTVLDNQQTPTVFYHFERTA

>d1fh6a_ d.183.1.1 (A:) Major capsid protein gp5 {Bacteriophage HK97}

SLGSDADSAGSLIQPMQIPGIIMPGLRRLTIRDLLAQGRTSSNALEYVREEVFTNNADVVAEKALKPESDITFSKQ
TANVKTIAHWVQASRQVMDDAPMLQSYINNRLMYGLALKEGQLLNGDTGDNLEGLNKVATAYDTSLNAT

GDTRADIIAHAIYQVTESEFSASGIVLNPRDWHNIALLKDNEGRYIFGGPQAFTSNIMWGLPVVPTKAQAAAGTF
TVGGFDMASQVWDRMDATVEVSREDRDNFVKNMLTILCEERLALAHYRPTAIKGTSS
>d1fn9a_ d.196.1.1 (A:) Outer capsid protein sigma 3 {Reovirus}
MEVCLPNGHQVVDLINNAFGRVSIYSAQEGWDKTISAQPDMMVCGGAVVCMHCLGVVGSLQRKLKHLPH
HRCNQQIRHQDYVDVQFADRVTAHWKRGMLSVAQMHEMMNDVSPDLDVRTEGGSLVELNWLVDP
NSMFRSIHSSWTDPLQVVDLDTKLDQYWTALNLMDSSDLIPNFMMRDPSHAFNGVKLGGDARQTQFSRT
FDSRSSLEWGVMVYDYSELEHDPSKGRAYRKELVTPARDFGHFGFLSHYSRATTPILGKMPAVFSGMLTGNCKM
YPFIKGTAKLKTVRKLVAVNHAWGVEKIRYALGPGBTGWYNRTMQQAPIVLTAAALTMFPTIKFGDLNYP
VMIGDPAMILG
>d1qgwa_ d.184.1.1 (A:) Phycoerythrin 545 alpha-subunits {Cryptophyte (Rhodomonas sp.),
cs24}
AMDKSAKPQTIFDHRCRAPKESTGGKAGGQDDEMMVKVASTKVTVSESDAAKKLQEFTFEKGIDGPFT
SKN
>d1qgwb_ d.184.1.1 (B:) Phycoerythrin 545 alpha-subunits {Cryptophyte (Rhodomonas sp.),
cs24}
AMDKSAKPVTIFDHRCRAPKEYTGAKAGGKDDEMMVKAQSVKIEVSTGTAEGVLATSLAKMTK
>d1jyoe_ d.184.1.2 (E:) Virulence effector SptP domain {Salmonella typhimurium}
DKAYVAPEKFSSKVLTWLGMPLFKNTEVVQKHTENIRVQDQKILQTLHALTEKYGETAVNDALLMSRINMNK
PLTQRLAVQITECVKAADEGFINLIKS
>g1hle.1 e.1.1.1 (A:,B:) Elastase inhibitor {Horse (Equus caballus)}
MEQLSTANTHFAVDLFRALNESDPTGNIFISPLSISSALAMIFLGTRGNTAAQVSKALYFDTVEDIHSRFQSLNADI
NKPGAPYILKLANRLYGEKTYNFLADFLASTQKMYGAELASVDFQQAPEDARKEINEWWKGQTEGKIPPELLVKG
MVDNMTKLVNVNAIFKGNWQQKFMKEATRDAPFRLNKKDTKTVKMMYQKKKFPVNYIEDLKCRVLELPYQ
GKELSMIILLPDDIEDESTGLEKIEKQLTLKREWTKPENLYLAEVNVHLPRFKLEESYDLTSHLARLGVQDLFNR
GKADLSGMSGARDLFVSKIIHKSFDLNEEGTEAAAATAGTILLAXEENFNADHPFIFFIRHNPSANILFLGRFSSP
>d1ovaa_ e.1.1.1 (A:) Ovalbumin {Hen (Gallus gallus)}
GSIGAASMEFCFDVFKELKVHHANENIFYCPIAIMSALAMVYLGAKDSTRTQINKVVRFDKLPFGFDSIEAQCG
TSVN VHSSLRDILNQITKPNDVYSFLASRLYAEEYRPILEYQCVKELYRGGLEPINFQTAADQARELINSWVES
QTNGIIRNVLQPSSVDSQTAMVLNAIVFKGLWEAKFDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMA
SEKMKILELPFASGTMSMLVLLPDEVSGLEQLESIINFEKLTETSSNVMEERKIKVYLPRMKMEEKYNLTSVLM
AMGITDVSSSANLSGISSAESLKISQAVHAAHAEINEAGREVVGSAEAGVDAASVSEEFRADHPFLFCIKHIATN
AVLFFGRCVSP
>g1as4.1 e.1.1.1 (A:,B:) Antichymotrypsin, alpha-1 {Human (Homo sapiens)}
GLASANVDFAFSLYKQLVLKAPDKNVIFSPLSISTALAFLSLGAHNTTLEILKGLKFNLTEI
NQSSDELQLSMGNAMFVKEQLSLLDRFTEDAKRLYGSEAFATDFQDSAAKKLINDYVNGTRGKITDLIKDLD
SQTMMVLVNYIFFKAKWEMPFDPQDTHQSRFYLSKKWVMPMMSLHHLTIPYFRDEELSCTVVELKYTG
ASALFILPDQDKMEEVEAMLLPETLKRWRDSLEFREIGELYLPKFSISRDYNLNDILLQLGIEEAFTSKADLSGITGA
RNLA VSVVHKAVLVDVFEEGTEASRATAVKITLLXGTIVRFNRPFLMIIVPTDTQNIFMSKVTNPQK
>d1qlpa_ e.1.1.1 (A:) Antitrypsin, alpha-1 {Human (Homo sapiens)}
FNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMILSLGTkadthdeileglnfnlteipeaqihegfqell
RTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKE
DRDTVFAVNYIFFKGKWERPFEVKDTEEEDFHVDQTTVKVPMKRLGMFNIQHCKLSSWVLLMKYLG
ATAIFFLPDEGKLQHLENELTHDIITKFLNEDRRSASLHLPKLSITGYDLKSVLGQLGITKVFSNGADLSGVTEEA
PLKLSKAHVKA VLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNP
TQK

>d1atta_e.1.1.1 (A:) Antithrombin {Cow (Bos taurus)}

VEDVCTAKPRDIPVNPMCIYRATEGQGSEQKIPGATNRRWELSKANSHATAFYQHLADSKNNNDNIFLSPLSI
STAFAMTKLGACNNTLQLMEVFKFDTISEKTSDQIHFFAKLNCRLYRKANKSSELVSANRLFGDKSITFNETYQ
DISEVVGAKLQPLDFKGNAEQSRLTINQWISNKTEGRITDVIPPQAINETVLVLVNTIYFKGLWKSFKSPENTRK
ELFYKADGESCSVLMIMYQESKFYRRAESTQVLELPFKGDDITMVLILPKLETLAKVEQELTPDMIQEWLDEL
TETLLVVHMPRFRIEDSFVKEQLQDMGLEDFSPEKSLPGIVAEGRSIDLVDASFHKAFLEVNEEGSEAAAST
VISIAGRSLRVTFKANRPFLVLIRESVALNTIIFMGRVANPCV

>d1e05i_e.1.1.1 (I:) Antithrombin {Human (Homo sapiens)}

SPVDICTAKPRDIPMNPMCIYRSPEKKATEDEGSEQKYPEATNRRWELSKANSRFATTFYQHLADSKNDNDNIF
LSPLSISTAFAMTKLGACNDTLQQLMEVFKFDTISEKTSDQIHFFAKLNCRLYRKANKSCLVSANRLFGDKSLTF
NETYQDISLEVVGAKLQPLDFKENAEQSRAAINKWVSNKTEGRITDVIPSEAINELTVLVLVNTIYFKGLWKSFKSP
ENTRKELFYKADGESCSASMMYQEGKFYRRAEGTQVLELPFKGDDITMVLILPKPEKSLAKVEKELTPEVLQE
WLDELEEMMLVHMPRFRIEDGFSLKEQLQDMGLVLDLSPEKSKLPGIVAEGRDDLYVDAFHKAFLLEVNEEG
SEAAASTAVVIAGRSLNPNRVTFKANRPFLVIREVPLNTIIFMGRVANPCV

>d1a7ca_e.1.1.1 (A:) Plasminogen activator inhibitor-1 {Human (Homo sapiens)}

HHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSPYGVASVLAMILQLTTGGETQQQIQAAMGFKIDDKGMA
PALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMHFFRLFRSTVKQVDFSEVERARFIINDWVKHTKG
MISNLGKAVDQLTRLVNVNALYFNGQWKTPFDSSTHRRLFHKSDGSTSVPMMAQTNKFNYTEFTTPDG
HYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLG
MTDMFRQFQADFTSLSDQEPHLVAQALQKVIEVNESGTVESSTAVIVSARMAPEEIIMDRPFLVVRHNPT
GTVLFMGQVMEP

>d1by7a_e.1.1.1 (A:) Plasminogen activator inhibitor-2 {Human (Homo sapiens)}

EDLCVANTLFALNLKHLAKASPTQNLFLSPWSISSTMAMVYMGSRGSTEDQMAKVLQFNEVGAAADKIHSFF
RSLSSAINASTGNYLLESVNKLFGEKSASFREYIRLCQKYYSEPPQAVDFLECAEEARKKINSWVKTQTKGKIPNL
LPEGSVGDTRMVLVNAVYFKGKWKPFEKKLNGLYPFRVNSAQRTPVQMMYLREKLNIGYIEDLKAQILELPY
AGDVSMFLLPDEIADVSTGLELESEITYDKLNKWTSDKMAEDEVEVYIPQFKLEEHYELRSILRSMGMEDAF
NKGRANFSGMSERNDLFLSEVFHQAMVDVNEEGTEAAAGTGGMTGRTGHGGPQFVADHPFLFLIMHKIT
NCILFFGRFSSP

>g1jjo.1_e.1.1.1 (A.;C.;E;) Neuroserpin {Mouse (Mus musculus)}

TITEWSVNMYNHLRGTEDENILFPLSIALAMGMMELGAXENQYVMKLANSLFVQNGFHVNEEFLQMLKM
YFNAEVNHVDFSQNVAVANSINKVENYNTNSLLKDLVSPEDFDGVTNLALINAVYFKGNWKSQFRPENTRTFS
FTKDDSEVQIPMMYQQGEFYGEFSDGSNEAGGIYQVLEIPYEGDEISMMILALSQEVPLATEPLLKAQLIEE
WANSVKKQKVEVYLPRFTVEQEIDLKDILKALGVTEIFIKDANLTAMSDKKELFLSKAVHKSCIEVNEEGSEAAA
SGMIAISXPQVIVDHPFLYLIRNRKSGIILFMGRVMNPHH

>d1sek_e.1.1.1 (-) Serpin K {Tobacco hawkmoth (Manduca sexta)}

GETDLQKILRESNDQFTAQMSEVVKANPGQNVLSAFSVLPLGQLALASVGESHDELLRALALPNDNVTKD
VFADLNREGVRAVKGVDLKMASKIYVAKGLELNDFAAVSRDVGSEVQNVDFVKSVEAAGAINKWVEDQTNN
RIKNLVDPDALDETTRSVLVNAIFKGSKDKFNKERTMDRDFHVSKDKTIKVPTMIGKKDVRYADPDAK
MIEMSYEGDQASMMIILPNQVDGITALEQKLKDPKALSRAEERLYNTEVEIYLPFKIETTDLKEVLSNMNIKKLF
TPGAARLENLLKTKESLYVDAAIQKAFIEVNEEGAEAAAANAFKITTYSFHFVPKVEINKPFFSLKYNRNSMFSG
VCVQP

>d1k9oi_e.1.1.1 (I:) Alaserpin (serpin 1) {Tobacco hornworm (Manduca sexta)}

GETDLQKILRESNDQFTAQMSEVVKANPGQNVLSAFSVLPLGQLALASVGESHDELLRALALPNDNVTKD
VFADLNREGVRAVKGVDLKMASKIYVAKGLELNDFAAVSRDVGSEVQNVDFVKSVEAAGAINKWVEDQTNN

RIKNLVDPDALDETTRSVLVNAIYFKGSWKDKFVKERTMDRDFHVSNDKTIKVPTMIGKKDVRYADVPELDAK
MIEMS YEGDQASMIILPNQVDGITALEQKLKDPKALSRAEERLYNTEVEITLPKFKIETTDLKEVLSNMNIKKLF
TPGAARLENLLKTKESTVDAAIQKAFIEVNEEGAEAAAANAFGIVPKSLILYPEVHIDRPFYFELKIDGIPMFNGK
VIEP

>g1f0c.1 e.1.1.1 (A;B:) Viral serpin crmA (cytokine response modifier protein) {Cowpox virus}
MDIFREIASSMKGENVFISPPSISSVLTILYYGANGSTAEQLSKYVEKEADKNKDDISFKSMNKVYGRYSAVFKDSF
LRKIGDNFQTVDFDCRTVDAINCKVDIFTEGKINPLLDEPLSPDTCLLAISAVYFKAKWLMPFEKEFTSDYPFYVS
PTEMVDVSMMSMYGEAFNHASVKEFGNFSIILPYVGDTSMVILPDNIDGLESIEQNLTDNFKKWCDSM
DAMFIDVHIPFKVTGSYNLVDALVKGLTEVFGSTGDYSNCNSDVSVDAMIHKTYIDVNEEYTEAAAATCAL
VADCAXSTVTEFCADHPFIYVIRHVDGKILFVGRYCSPTTN

>d1imva_ e.1.1.1 (A:) Rignment epithelium-derived factor, PEDF {Human (Homo sapiens)}
TGALVEEDPFFKVPVNKLAIAVSNFYDLYRVRSSMSPTNVLLSPLSVATALSALSGADERTESIIHALYYDLI
SSPDIHGTYKELLDVTAPQKNLKSASRIVFEKKLRIKSSFVAPLEKSYGTRPRVLTGNPRLDLQEINNWVQAQMKG
GKLARSTKEIPDEISILLGVAHFKGQWVTKFDSRKTSLDEFYLDEERTVRVPMMSDPKAVLRYGLSDLSCKIAQ
LPLTGSMSIIFFLPLKVTQNLTIEESLTSEFIHDIDRELKTVQAVLTVPKLKSYEGERVTKSQLEMKLQSLFDSPDFSK
ITGKPIKLTQVEHRAGFEWNEDGAGTTSPGLQPAHLTFPLDYHLNQPFIFVRLDTDTGALLFIGKILDPRGP

>d1ecra_ e.2.1.1 (A:) Replication terminator protein (Tus) {Escherichia coli}
DLVDRLNTTFRQMEQELAIFAAHLEQHKLLVARVFSLPEVKKEDEHNPLNRIEVQHQLGNDQSLALRHFRHLFI
QQQSENRSSKAAVRLPGVLCYQVDNLSQAALVSHIQHINKLKTTFEHIVTVESELPTAARFEWVHRHLPGLITLN
AYRTLTVLHDPATLRFGWANKHIIKNLHRDEVLAQLEKSLKSPRSVAPWTREEWQRKLEREYQDIAALPQNAKL
KIKRPVKVQPIARVWYKGDQKQVQHACPTPLIALINRDNGAGVPDVGELLNYDADNVQHRYKPQAQPLRLIIP
RLHLYVAD

>d1es5a_ e.3.1.1 (A:) D-alanine carboxypeptidase/transpeptidase {Streptomyces sp., K15}
KPTIAAVGGYAMNNNGTGTLYTKAADTRRSTGTTKIMTAKVLAQSNLNLDAKVTIQKAYS DYVVANNASQA
HLIVGDKVTVRQLYGLMLPSGCDAAYALADKYGSGSTRAARVKSFIGKMNTAATNLGLHNTHFDSFDGIGNG
ANYSTPRDLTKIASSAMKNSTFRVVKTKEYTAKTVTKTSIRTMDTWKNTNGLSSYSGAIGVKTGAGPEAKYC
LVFAATRGGKTVIGTVLASTSIPARESDATKIMNYGFAL

>d1hvba_ e.3.1.1 (A:) D-alanine carboxypeptidase/transpeptidase {Streptomyces sp., R61}
DLPAPDDTGLQAVLHTALSQGAPGAMVRDDNGTIHQLSEGVAD RATGRAITTD RFRVGSVTKFSAVVLLQ
LVDEGKLDLDAVNTYLPGLPDDRITVRQVM SHRS GLYD YTNDMFAQT VPGFESVRNKVFSYQDLITLSLKHG
VTNAPGAAYSNTNFVAGMLIEKLTGH SVATEYQNRIFTPLNITDTFVHPDTVIPGTHANGYLT PDEAGGAL
VDSTEQTWSAQASAGAVISSTDLDTFFSALMSGQLMSAAQLAQM QQWTTVN STQGYGLR RRDLS CGIS
VYGHGTQGYYTYAFASKDGKRSVTALANTSNNVNLNTMARTLES AFCGK P

>d1ci9a_ e.3.1.1 (A:) Esterase EstB {Burkholderia gladioli}

AASLAARLDAVFDQALRERRLVGAVAIVARHGEILYRRAQGLADREAGRPMREDTLFRLASVTKPIVALAVLRLV
ARGELALDAPVTRWLPEFRPRLADGSEPLVTIHHLLTHTSGLGYWLLEGAGS VYDRLGISD GIDL RDFD LDEN RL
RLASAPLSFAPGSGWQYSLALDV LGAVVERATGQPLAAV DALVAQPLGM RD CGFVSAE PERFA VPYHDGQP
EPVRMRDGIEVPLPEGHGA VRFAPS RVFEPGAYPSGGAGM GSADDV LRALEAIRANPGFLPETLADAARRD
QAGVGAETRGPGWGFGYLSA VLD DPAAAGTPQHAGTLQWGGVYGH SWFVD RAL GLS VLL NTAYEGMSG
PLTIALRDAVYA

>d1bt1_ e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TEM-1}

HPETLVKVDAEDQLGARVGYIELDNSGKILESRPPEERFPM MSTKVLLCGAVLSRIDAGQEQLGRRIHYSQN
DLVEYSPVTEKHLTDGMTVRELCSAITMSDNTAANLLTIGGP KELTAFLHNMGDHVTRLDRWEPELNEAIP
NDERTTMPVAMATT LRKLLT GELLTLASRQQLIDWMEADK VAGPLLRSALPAGWFIAKSGAGERGSRGIIA

ALGPDGKPSRIVVIYTGSQATMDERNRQIAEIGASLIKHW

>d1bza__ e.3.1.1 (-) beta-Lactamase, class A {Escherichia coli, TOHO-1}

SVQQQLEALEKSSGGRLVALINTADNSQILYRADERFAMCSTSKVMAAAAVLKQSES DKHLLNQRVEIKKSDL
VN YNPIAEKHVN GNTMTLAELGAAALQYS DNTAMNK LIAHLGGPDKVTA FARSLGDETFR LDRTAPLNTAIPGD
PRDTTPLAMAQT KNLTLGKALAETQRAQLVTWLKGNTTG SASIRAGLPKS WVGDKTSGD YGTTNDIAVI
WPENHAPLVLVTYFTQPEQKAERRRDILAAA AKIVT

>d1g56a_ e.3.1.1 (A:) beta-Lactamase, class A {Klebsiella pneumoniae, SHV-1}

SPQPLEQIKLSESQLSGRVGMIE MDLASGR TLAW RADERFP MMSTFKV VLCAVL RVDAGDE QLERKIHYR
QQDLVDYSPVSEKHLADG MTVGELCAA ITMSD NSAAN LLA T VGGPAGLTAFLRQIGDNVTRLD RWETELNE
ALPGDARDTTTPASMAATLRKLLTSQRLSARSQRQLQWMVDDRVAGPLR SVLPAGWFIA DKTGAGERGAR
GIVALLGPNNKAERIVVIYL RDTPASMAERNQQIAGIGA ALIEHWQR

>d1g6aa_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PSE-4 carbenicillinase}
SKF QQV E QDV KAIEV SLSARIGV S VLD TQN G EYWDY NGN QRF PLT FKT IACAK LYDAE QG KVNP N STVEIKK
ADLV TYSPVIEKQV GQAITL DDACF ATMT SDNT AAN II SAVGGPKGVDF LRQIGD KETR LDRIEPD LNEG KLG
DL RD TTPKAI A STLN KFLFGS ALSEM NQ KLESW MVNN QVTG NLLRSV LPAGW NIADK SGAGG FGARSIT AV
VWSEHQAPIVSIYLA QTQ ASMEER NDIAV KIGH SIFDV YTS

>d1alq__ e.3.1.1 (-) beta-Lactamase, class A {Staphylococcus aureus}

SEPIVLVIFTNKDNKSDKPNDKLISETAKS VMKEAAGSKNAAKELND LEKKYNAHIGVYALDTKSGKEVKF NSDK
RFAYASTSKAINSAILLEQVPYNKLNKKVHINKDDIVASPILEK YVGKD ITLK ALIEASMTYSDNTANNKIIKEIGGI
KKVQRLKELGDKVTPN P VRYE IELNYYSPSKSKKD TSTPAAFGK TLN KLIANGK LSKENKKFL DLMLNNKSGDTL
KDGVPKDYKVADKSGQAITYASRNDVAFVYPK

>d1ghpa_ e.3.1.1 (A:) beta-Lactamase, class A {Staphylococcus aureus}

KELND LEKKYNAHIGVYALDTKSGKEVKF NSDK RFAYASTSKAINSAILLEQVPYNKLNKKVHINKDDIVASPILEK
YVGKD ITLK ALIEASMTYSDNTANNKIIKEIGGI KKVKQRLKELGDKVTPN P VRYDIELQYYSPSKSKKD TSTPAAFGK
TLN KLIANGK LSKENKKFL DLMLNNKSGDTL IKDGVPKDYKVADKSGQAITYASRNDVAFVYPKGQSEPIVLVIF
TNKDNKSDKPNDKLISETAKS VMKEF

>d4blma_ e.3.1.1 (A:) beta-Lactamase, class A {Bacillus licheniformis}

DDFAKLEE QFD A KLG IFAL DTGT NRTV AYRP DERFA FASTIKALT VGVL LQQKSIE DLN QRTY TRDD LVN YN PITE
KH VDTG MTL KELADAS LRY SDNA A QN LILK QIGGPESLK KELRK IGD EVTN PERF EPEL NEVNP GET QDT STARA
LV TSL RFA LED KLP SEKRELL IDW MKR NTG DALI RAGV PDG WEVAD KTGA ASY GTRNDIA II WPPKG DPV VL
AVLSS RD KKD AKY DD K LIAEAT KVVM KAL N

>d1buea_ e.3.1.1 (A:) beta-Lactamase, class A {Enterobacter cloaceae, NMC-A carbapenemase}

NTKGIDEIKNLETDFNGRIGVYALDTGSGKFSYRANERFPLCSSFKGFLAAVLKGSQDNRLNLNQIVNYNTRSL
EFHSPITTKYKDNGMSLGDAAA ALQYSDNGATNI LERYIGGPEGMTKF MRSIGDED FRLDRWE LDLN TAIP
GDERDTSTPAAVAKSLKTLALGNILSEHEKETYQTWLKGNTTGAARI RASVPSDWVVGDKTGSCGAYGTANDYA
VVWPKNR API LIISVYTTKNEKEAKHEDK VIAEASRIAIDNLK

>d1bsg__ e.3.1.1 (-) beta-Lactamase, class A {Streptomyces albus G}

SDAERRLAGLERASGARLG VYADT GSGRTV AYRA DEL FPMCSV FKTLSSA VLR DLD RNGEFLSRR ILYT QDDV
EQADGAP ETGKPQNL ANG M TVEEL CEVSITAS DNCA ANLMLREL GGPA AVTRFVRSLGDRVTRLD RWEPE LN
SAEPGRVTD TTS PRAIT RTY GRLV LGDALN PRDR LL SWL LANT SGDR FRAGL PDDW TLGDKT GAG RY GTN
NDAGV TWPPGR API VLT VLTAKTEQDA ARDD GLVADA ARV LAET LG

>d1mfoa_ e.3.1.1 (A:) beta-Lactamase, class A {Mycobacterium fortuitum}

APIDDQ LAELERRDNV LIGLYA ANLQSGR RITHRP DEMFAMCSTFKGYVAARV LQMAE HGE ISLDN RVF VDAD
ALVPNSPV TEARAGAEM TLAELC QAA LQRSDNTA ANLLK TIGGPA AVTA FAR SVG DERTRLD RWE VELNSA IP

GDPRDTSPAALAVGYRAILAGDALSPPQRGLLEDWMRANQTSSMRAGLPEGWTTADKTGSGDYGSTNDAG
IAFGPDGQRLLLVMTRSQAHDPKAENLRPLIGELTALVLPSSL

>d1e25a_e.3.1.1 (A:) beta-Lactamase, class A {*Pseudomonas aeruginosa*, PER-1}

SPLLKEQIESIVIGKKATGVAVWGPDDLEPLLINPFEKPMQSFKLHLAMVLHQVDQGKLDLNQTVIVNRAK
VLQNTWAPIMKAYQGDEFSPVQQQLQYSVSHSDNVACDLLFELVGGPAALHDYIQSMGIKETAVVANEAM
HADDQVQYQNWTSMKGAAEILKKFEQKTLQSETSQALLKWMVETTGPERLKGLPAGTVVAHKTGTSQIK
AGKTAATNDLGIIIPDGRPLLAVFKDSAESSRTNEAIIAQVAQTYQFELKKLSAL

>d1dy6a_e.3.1.1 (A:) beta-Lactamase, class A {*Serratia marcescens*, Sme-1}

NKSDAAAKQIKKLEEDFDGRIGVFAIDTGSNTFGYRSDERFPLCSSFKGFLAAAVERVQQKLDINQKVYESR
DLEYHSPITTKYKGSGMTLGDMAAAALQYSDNGATNIIMERFLGGPEGMTKFMRSIGDNEFRLDRWELENNTA
IPGDKRDTSTPKAVANSLNKLALGNVLNAVKAIYQNWLGNTTGDARIRASVPADWVGDKTGSCGAYGTA
NDYAVIWPKNRAPLIVSIYTRSKDDKHSOKTIAEASRIAIAQAI

>d1fr1a_e.3.1.1 (A:) AMPC beta-Lactamase, class C {*Citrobacter freundii*}

AAKTEQQIADIVNRTITPLMQUEQAPIGMAVAAIYQGKPYYFTWGKADIANNRPVTQQLFELGSVSFTNGVLG
GDAIARGEIKLSDPVTQYWPETGKQWQGISLLHLATYTAGGLPLQVPDDVTDKAALLRFYQNWQPQWAPGA
KRLYANSIGLFGALAVKPSGMSYEEAMSRLVHPLKLAHTTWITVPQSEQKDYAWGYREGKPVHSPGQLDAE
AYGVKSSVIDMTRWVQANMDASQVQEKTLLQQGIELAQSRYWRIGDMYQGLGWEMLNWPVKADSIISGDS
KVALAAALPAVEVNPPAPAVKASWVHKTGSTGGFGSYAFVPEKNLGIVMLANKSYPNPRVVEAAWRILEKLQ

>d1ga0a_e.3.1.1 (A:) AMPC beta-Lactamase, class C {*Enterobacter cloacae*, P99, cephalosporinase}

PVSEKQLAEVVANTVTPLMKAQSVPGMMAVAVIYQGKPYYTFGKADIAANKPVTQTLFELGSISKFTGVLLGG
DAIARGEISLDDPVTRYWPQLTGKQWQGIRMLDLATYTAGGLPLQVPDEVTDNASLLRFYQNWQPQWKPGT
TRLYANASIGLFGALAVKPSGMPYEQAMTTRVLKPLKLDHTWINVPKAEEAHYAWGYRDGKAVRAVRVSPGM
LDAQAYGVKTNVQDMANWVMANMAPENVADASLKGIALAQSRYWRIGSMYQGLGWEMLNWPVEANT
VVEGSDSKVALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYAFIPEKQIGIVMLANTSYPNPARVEAAYHIL
EALQ

>d1i5qa_e.3.1.1 (A:) AMPC beta-Lactamase, class C {*Escherichia coli*, cephalosporinase}

APQQINDIVHRTITPLIEQQKIPGMAVAVIYQGKPYYFTWGYADIACKQPVTQQLFELGSVSFTGVLLGDAI
ARGEIKLSDPTTKWPELTAKQWNGITLLHLATYTAGGLPLQVPDEVKSSDLLRFYQNWQPAWAPGTQRLYAA
SSIGLFGALAVKPSGLSFEQAMQTRVFQPLKLNHTWINVPPAEKNYAWGYREGKAVHVSPGALDAEAYGVKS
TIEDMARWVQSNLKLPLDINEKTLQQGIQLAQSRYWQTGDMYQGLGWEMLDWPVNPDSSIINGSDNKIALAA
RPVKAITPPPTPAVRASWVHKTGATGGFGSYAFIPEKELGIVMLANKNYPNPARNDAAWQILNALQ

>d1k55a_e.3.1.1 (A:) Class D beta-lactamase {*Pseudomonas aeruginosa*, OXA-10}

SITENTSWNKEFSAEAVNGVFVLCKSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVIKNEHQVFKWDGKP
RAMKQWERDLTLRGAIQVSAPVFQQIAREVGEVRMQKYLKKFSYGNQNQNSGGIDKFVWLEGQLRISAVNQVE
FLESLYLNKLSASKENQLIVKEALVTEAAPELYVHSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNMDID
NESKLPLRKSIPTKIMESEGIIG

>d1k25a4_e.3.1.1 (A:264-631) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain {*Streptococcus pneumoniae*}

TLSSPLQSFMETQMDAFLEKVKGYMTATLVAKTGEILATTQRPTFNADTKEGITEDFWWRDILYQSNYEPGSA
MKVMTASSIDNNTPSGEYFNNSSELKIADATTRDWDVNEGTTGGMMTFLQGFAHSSNVGMSLLEQKMGD
ATWLDFLKRKFGVPTRFGLTDEYAGQLPADNIVSIAQSSFGQGISVTQMLRAFTAIANDGVMLEPKFISAIY
DTNNQSVRKSQKEIVGNPVSKEAATTRNHMILVGTDPYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEK
NGGYLVGSTNYIFSAVTMNPAENPDFILYVTVQQPEHSGIQLGEFATPIERASAMKESLNQSPAKNLDKVT

>d1qmea4_e.3.1.1 (A:264-620) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain

{Streptococcus pneumoniae}

TISSPLQSFMETQMADFQEVKKGKYMATLVSAGTGEILATTQRPTFDADTKEGITEDFVWRDILYQSNYEPGST
MKVMMMLAAIDNNTPFGGEVFNSSELKIADATIRDWDVNEGILTGGRMMTFSQGFAHSSNVGMTLLEQKMG
DATWLDYLNRFKFGVPTRFLDEYAGQLPADNIVNIAQSSFGQQGISVTQTQMIRAFTAIANDGVMLEPKFISAI
YDPNDQTARKSQKEIVGNPVSQDAASLRTNMVLGVTDVYGTMYNHSTGKPTVTVPGQNVALKSGTAQIAD
EKNGGYLVGLTDYIFSAVSMSPAENPDFILYVTVQQPEHYSIGIQLGEFANPILERASAMKDSLNL

>d1hd8a2 e.3.1.1 (A:3-262) Penicillin-binding protein 5, N-terminal domain {Escherichia coli}

LNIKTMIPGPQIDAESYILIDYNSGKVLAEQNADVRRDPASLTKMMTSYVIGQAMKAGKFETDLVTIGNDAW
ATGNPVFKGSSLMFLKPGMQPVSQIIRDINLQSGNDACVAMADFAAGSQDAFVGLMNSYVNALGLKNTHF
QTVHGLDADGQYSSARDMALIGQALIRDVPNEYSIYKEKEFTFNGIRQLRNGLLWDNSLNVDGIKTGHTDKA
GYNLVASATEGQMRLLISAVMGGRTFKGREAESKKLTWGFRF

>d1ei5a3 e.3.1.1 (A:3-335) D-aminopeptidase, N-terminal domain {Ochrobactrum anthropi}

KFDTSALEAFVRHIPQNYKGPGGVAVVKGEVVLQHAWGFADLRTRPMTLDRMPICSVKQFTCAVLLDA
VGEPELDDALEAYLDKFEDERPAVRDLCNNQSGLRDYWALSVCAGADPEGVFLPAQAQSLLRRLKTTHFEPGS
HYSYCNGNFRILADLIEAHTGRTLVDILSERIFAPAGMKRAELISDTALFDECTGYEGDTVRGFLPATNRIQWMGD
AGICASLNDMIAWEQFIDATRDESGLYRRLSGPQTFKDGVAAAPYGFGLNLHETGGKRLTGHHGALRGWRQCQ
RWHCADERLSTIAMFNFE GGASEVAFKLMNIALGVSSS

>d1lbea_ e.4.1.1 (A:) ADP ribosyl cyclase {Sea hare (Aplysia californica)}

IVPTRELENVFLGRCKDYEITRYLDILPRVRSDCSALWKDFFKAFFSKNPKCDLDLGSYKDFFTSAQQQLPKNKVMF
WSGVYDEAHDYANTGRKYITLEDTLPGYMLNSLVCGQRANPGFNEKVCPDFKTCPVQARESFWMASSYY
AHSAEGERVTYMDGSNPKVPAYRPDSFFGKYELPNLTNKVTRVKVIVLHRLGEKIIKGAGSLLDLEKLVKAKHF
AFDCVENPRAVLFLCSNDNPNAECRL

>d4blca_ e.5.1.1 (A:) Catalase I {Cow (Bos taurus)}

NRDPASDQMHWKEQRAAQKPDVLTTGGGNPVGDKLNSLTVGPRGPLLQDVVFTEMAHFDRERIPERVV
HAKGAGAFGYFEVTHDITRYSKAKVFEHIGKRTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDLVGN
NTPIIFFIRDALLFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLSDRGIPDGHRHMNGYGSHTFK
LVNADGEAVYCKFHKTQDGKIKNLSEDAARLAHEDPDYGLRDLFNATGNYPSWTLYIQVMTFSEAEIFPFNP
FDLTKVWPHDYPLIPVGKLVLRNPVNYFAEVEQLAFPSNMPPGIEPSPDFKMLQGRLFAYPDTHRHLGP
YLQIPVNCPYRARVANYQRDGPMMCMDNQGGAPNYPNSFAPEHQPSALEHRTHFSGDVQRFNSANDD
NVTQVRTFYLKVLNEEQRKRCENIAGHLKDAQLFIQKKAVKNFSDVHPEYGSRIQALLDKYNE

>d1dgfa_ e.5.1.1 (A:) Catalase I {Human (Homo sapiens)}

RDPASDQMHWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLQDVVFTEMAHFDRERIPERVV
HAKGAGAFGYFEVTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDLVGN
NTPIIFFIRDPLFPSFIHSQKRNPQTHLKDPDMVWDFWSLRPESLHQVSFLSDRGIPDGHRHMNGYGSHTFKL
VNANGEAVYCKFHKTQDGKIKNLSEDAARLSQEDPDYGLRDLFNATGKYPSTFYIQVMTFNQAETFPFN
PFDLTKVWPHDYPLIPVGKLVLRNPVNYFAEVEQIAFDPSNMPPGIEASPDFKMLQGRLFAYPDTHRHLGP
NYLHIPVNCPYRARVANYQRDGPMMCMDNQGGAPNYPNSFAPEHQPSALEHSIQYSGEVRRFNTANDD
NVTQVRAFYVNVLNEEQRKRCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALLDKYNE

>d1a4ea_ e.5.1.1 (A:) Catalase I {Baker's yeast (Saccharomyces cerevisiae)}

DVREDRVVTNSTGNPINEPFVTQRIGEHGPLLQDYNLIDS LAHFNRNIPQRNPHAHGSGAFGYFEVTDDITDI
CGSAMFSKIGKRTKCLTRFSTVGGDKGSADTVRDPRGFATKFYTEEGNLDWVNNTPVFFIRDPSKFPFIHTQ
KRNPQTNLRDADMFWDFLTTPENQVAIHQVMILFSDRGTPANYRSRMHGYSGHTYKWSNKNGDWHYVQVHI
KTDQGKIKNLTIEEATKIAGSNPDYCQQDLFEAIQNGNYPSTVYIQTMTTERDAKKLPFSVFDLTKVWPQGQFPL

RRVGKIVLNENPLNFFAQVEQAAFAPSTTVPYQEASADPVLQARLFYADAHRYRLGPNFHQIPVNCPYASKFF
NPAIRDGMNVNGNFGSEPTYLANDKSYTIQQQDRPIQQHQEVWNGPAIPYHWATSPGDVDFVQARNLYRV
LGKQPGQQKQNLAYNIGIHLVEGACPCIQQRVYDMFARVDKGLSEAIKKVAE

>d1e93a_e.5.1.1 (A:) Catalase I {Proteus mirabilis}

KKLTAAAGAVVDDNNNITAGPRGPMLLQDVWFLEKLAHFDREVIPERRMHAKGSGAFGTFTVHDITKYTRA
KIFSEVGKKTEMFARFSTVAGERGAADAERDIRGFALKFYTEEGNWDMVGNNTPVFYLDPKFPDLNHIVKR
DPRTNMNRNMYKWDFSHLPESHLQLTIDMSDRGLPLSYRFVHFGSHTYSFINKDNERFWVKFHFCQQGI
KNLMDEAEALVGKDRESSQRDLFEAIKRGDYPRWKLQIQIMPEKEASTVPYNPFDLTKVWPHADYPLMDVG
YFELNRNPNDYFSDVEQAAFSANIVPGISFSPDKMLQGRLFSYGDYRGLVNHQIPVNAPKCPFHNYHR
DGAMRVGDGSNGNITYEPNSGGVFQECPDFKEPPLSIEGAADHWNHREDEDYFSQPRALYELLSDEHQRM
FARIAGELSQASKETQQRQIDLFTKVHPEYGAGVEKAIVLE

>d1hbza_e.5.1.1 (A:) Catalase I {Micrococcus lysodeikticus}

TTPHATGSTRQNGAPAVSDRQSLTVGSEGPIVLHDTHLLETHQHFNRMNIPIERRPHAKGSGAFGEFEVTEDVS
KYTKALVFQPGTKTETLLRFSTVAGELGSPDTWRDVRGFALRFYTEEGNYDLVGNNTPIFFLRDPMKFTHFIRSQ
KRLPDGLRDATMQWDFWTNNPESAHQVTYLMGRGLPRTWREMNGYGSHTYLWVNAQGEKHVVKYHF
ISQQGVHNLSNDEATKIAGENADFHRQDLFESIAKGDHPKWDLYIQAIPYEEGKTYRFNPFDLTKTISQKDYPRIK
VGTTLRNRPKNHFAQIESAAFSPSNTVPGIGLSPDRMLLGRAFAYHDAQLYRVGAHVNLQPVNRPKNAVHNY
AFEGQMWMYDHTGDRSTVPNNSGDSWSDETGPVDDGWEADGTLTREAQALRADDFFGQAGTLVREVFS
DQERDDFVETVAGALKGVRQDVQARAFYWKVNDATIGQRIEDEVKRHEGDGIPGVEAGGEARI

>d1cf9a2 e.5.1.1 (A:27-597) Catalase II {Escherichia coli, HPII}

DSLAPEDGSHRPAEPTPPGAQPTAPGSLKAPDTRNEKLSLEDVRKGSENYALTTNQGVRIADDQNSLRAGS
RGPTLLEDIFLREKITHFDHERIPERIVHARGSAAHGYFQPYKSLSDITKADFLSDPNKITPVFVRFSTCQGGAGSA
DTVDIRGFATKFYTEEGIFDLVGNNTPIFFIQDAHKFPDFVHAVKPEPHWAIPQGQSAHDTFWDYYSLQPETL
HNVMWAMSDRGIPRSYRTMEFGIHTFRLINAEGKATFVRFHWKPLAGKASLVWDEAQKLTGRDPDFHRRE
LWEAIEAGDFPEYELGFQLIPEEDEFKFDFLLDPTKLIPEELVPVQRVGKMVLNRNPDNFFAENEQAAFHPGHI
VPGLDFTNDPLLQGRLFSYDTQISRLGGPNFHEIPINRPTCPYHNFQRDMHRMGIDTNPANYEPNSINDNW
PRETPPGPKRGGFESYQERVEGNKVRERSPSFGEYYSHPRLFWSQTPFEQRHIVDGFSELSKVVRPYIRERVV
DQLAHIDLTLAQAVAKNLGIELTDDQLNITPPDVNGLKKDPSLSSYAIPDGD

>d1buca2 e.6.1.1 (A:1-232) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}

MDFNLTDIQQDFLKLAHDFGEKKLAPTVTERDHKGIDKELIDELLSLGITGAYFEEKYGGSGDDGGDVLSYILAV
EELAKYDAGVAITLSATVSLCANPIWQFGTEAQKEKFVPLVEGTKLGAFLTEPNAGTDASGQQTIATKNDDGT
YTLNGSKIFITNGGAADIYIVFAMTDKSKGNHGITAFILEDGTGFTYGKKEDKMGIIHTSQTMELVFQDVKPAE
NMLGEE

>d1jqia2 e.6.1.1 (A:4-234) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus)}

VYQSVELPETHQMLRQTCRDFAEKELVPIAAQLDKEHLFPTSQVKKMGEGLLAMDVPEELSGAGLDYLAYSIAL
EEISRGCASTGVIMSVNNNSLYLGPLIKFGSSQQKQQWITPFTNGDKIGCFALSEPGNGSDAGAASTTAREEGDS
WVLNGTKAWITNSWEASATVVFASDTRSQRQNKGISAFLVPMPTPGLTLGKKEDKLGIRASSTANLIFEDCRIPKE
NLLGEPG

>d3mdda2 e.6.1.1 (A:11-241) Medium chain acyl-CoA dehydrogenase {Pig (Sus scrofa)}

GFSFELTEQQKEFQATARKFAREEIIPVAAEYDRTGEYPVPLLKRAWELGLMNTHIPESFGLGLGIIDSCLITEELA
YGCTGVQTAIEANTLGQVPLIIGGNYQQQKYLGRMTEEPLMCAYCVTEPGAGSDVAGIKTKAEKKGDEYIING
QKMWITNGGKANWYFLLARSDPDPKAPASKAFTGFIVEADTPGVQIGRKEINMGQRCSDTRGIVFEDVRVPK
ENVLTGE

>d1legda2 e.6.1.1 (A:10-241) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens)}

LGFSFEFTEQQKEFQATARKFAREEIIPVAAEYDKTGEYPVPLIRRAWELGLMNTHIPENCGGLGLGTFDACLISEE
LAYGCTGVQTAIEGNLSGQMIIAGNDQQKKYLGRMTEEPLMCAYCVTEPGAGSDVAGIKTKAEKKGDEYII
NGQKMWITNGGKANWYFLLARSDPDPKAPANKAFTGFIVEADTPGIQIGRKELNMGQRCSDTRGIVFEDVKV
PKENVLIGD

>d1ivha2 e.6.1.1 (A:6-241) Isovaleryl-coa dehydrogenase {Human (Homo sapiens)}

VDDAINGLSEEQRQLRQTMKAFLQEHLAPKAQEIDRSNEFKNLREFWKQLGNLGVLGITAPVQYGGSGLGYLE
HVLVMEISRASGAVGVLGSYGAHSNLCINQLVRNGNEAQKEKYLPLKISGEYIGALAMSEPNAGSDVVSMKLKAE
KKGNHYILNGNKFWITNGPDADVLIVAKTDLAAPASRGITAIVEKGMPGSTSKLDKLGMRGNSNTCELIFE
DCKIPAANILGHEN

>d1frpa_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Pig (Sus scrofa)}

NIVTLTRFVMEQGRKARGTGEWTQLLNSLCTAVKAISTAVRKAGIAHYGIAGATNVTGDQVKKLDVLSNDLVIN
VLKSSFATCVLVEEDKNAIIVEPEKRGKYVVCDFPLDGSSNIDCLVSIGTIFGIYRKNSTDEPSEKDALQPGRNLVA
AGYALYGSATMLVLAMVNGVNCFMLDPAIGEFILVDRNVKIKKKGSIYSINEGYAKEFDPAITEYIQRKKFPPD
APYGARYVGSMVADVHRTLVYGGIFMYPANKSPKGKLRLLYECNPMAVVMEKAGGLATTGKEAVLDIVPTDI
HQRAPIILGSPEDVTELLEIYQKHA

>d1ftaa_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Human (Homo sapiens)}

DVVTLTRFVMEEGRKARGTGETQLLNSLCTAVKAISSAVRKAGIAHYGIAGSTNVTGDQVKKLDVLSNDLV
NMLKSSFATCVLSEEDKHAIIVEPEKRGKYVVCDFPLDGSSNIDCLVSIGTIFGIYRKKSTDEPSEKDALQPGRNL
VAAGYALYGSATMLVLAMDCGVNCFMLDPAIGEFILVDKDVKIKKKGKIYSLNEAYAKDFDPAVTEYIQRKKFPPD
NSAPYGARYVGSMVADVHRTLVYGGIFLYPANKSPNGKLRLLYECNPMAVVMEKAGGMATTGKEAVLDVIPT
DIHQRAPIILGSPDDVLEFLKVYEKHS

>d1bk4a_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Rabbit (Oryctolagus cuniculus)}

FDTDISTMTRFVMEEGRKAGGTGEWTQLLNSLCTAVKAISTAVRKAGIAHYGIAGSTNVTGDQVKKLDVLSND
LVMNMLKSSFATCVLSEEDKHAIIVEPEKRGKYVVCDFPLDGSSNIDCLVSIGTIFGIYRKKSTDEPSTKDALQPG
RNLVAAGYALYGSATMLVLAGGSGVNSFMLDPAIGEFILVDKNVKIKKKGNIYSLNEGYAKDFDPAVTEYIQRKKF
PPDNSSPYGARYVGSMVADVHRTLVYGGIFLYPANKSPDGKLRLLYECNPMAFIMEKAGGMATTGKEAILEDIV
PTDIHQRAPVILGSPDDVQEFLYEKKHAVK

>d1spia_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Spinach (Spinacia oleracea)}

AATQTKARTRSKYEITLTGWLLKQPMAGVIDAELTIVLSSISLACKQIASLVRQAGISNLTIQGAVNIQGEDQKK
LDVVSNEVFSSCLRSSGRTGIASEEEEDVPVAVEESYSGNYIVVFDPLDGSSNIDAAVSTGSIFGIYSPNDECIVDSD
HDDESQLSAEEQRCVNVQCQPGDNLLAAGYCMYSSSVIFVLTIGKGVYAFTLDPMYGEFVLTSEKIQIPKAGKIYS
FNEGNYKMWPDKLKKYMDDLKEPGESQKPYSSRYIGSLVGFHRTLLYGGIYGYPRDAKSNGKLRLLYECAPM
SFIVEQAGGKGSDGHQRILDIQPTIEHQRPVLYIGSVEEVEKLEYLA

>d1dcua_e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Garden pea (Pisum sativum)}

KRSGYEIITLTSWLLQQEQKGIIIDAELTIVLSSISMACKQIASLVRQANISNLTGAVNIQGEDQKKLDVISNEVF
SNCLRSSGRTGIASEEEEDVPVAVEESYSGNYIVVFDPLDGSSNLDAAVSTGSIFGIYSPNDECIPDFGDDSDNTL
GTEEQRCIVNCQPGSNLLAAGYCMYSSSVIFVLTIGKGVFVFTLDPLYGEFVLTQENLQIPKSGKIYSFNEGNYKL
WDENLKKYIDDLKEPGPSGKPYSSRYIGSLVGFHRTLLYGGIYGYPRDKKSNGKLRLLYECAPMSFIVEQAGG
KGSDGHQRVLDIQPTIEHQRPVLYIGSTEEEVEKLEYLA

>d2hhma_e.7.1.1 (A:) Inositol monophosphatase {Human (Homo sapiens)}

WQECDMDYAVTLARQAGEVVCEAIKNEMNVMLKSSPVDLVTADQKVEKMLISSIKEKYPHSFIGEESVAAGEK
SILTDNPTWIIDPIDGTTNFHRFPFVAWSIGFAVNKKIEFGVVYSCVEGKMYTARKGKGAFCNGQKLQVSQQED
ITKSLLVTELGSSRTPETVRMVLNSMEKLF CIPVHGIRSVGTAANMCLVATGGADAYYEMGIHCWDVAGAGIIV

TEAGGVLMVTGGPFDLMSRRVIAANNRILAERIAKEIQVIPLQRDDE

>d1g0ha_ e.7.1.1 (A:) Archaeal inositol
monophosphatase/fructose-1,6-bisphosphatase {Archaeon Methanococcus jannaschii, MJ0109}
MKWDEIGKNAKEIEKEILPYFGRKDKSYVVGTSPSGDETEIFDKISEDIALKYLKSLNVNIVSEELGVIDNSSEWTV
VIDPIDGSFNFINGIPFFAFCFGVKNNEPYYGLTYEFLTKSFYEAYKGKGAYLNGRKIKVKDFNPNNIVISYPSKKI
DLEKLRNKVKRVIRFGAFGLEMCYAKGTLDAVFDRVPKVRAVDIASSYIICKEAGALITDENGDELKFDLNATDR
LNIIVANSKEMLDIIDL

>d1inp_ e.7.1.1 (-) Inositol polyphosphate 1-phosphatase {Cow (Bos taurus), brain}
MSDILQELLRVSEKAANIARACRQQETLFQLLIEEKKEGEKNKKFAVDFKTLADVLVQEVIKENMENKFPGLGKKI
FGEESNELTNDLGEKIIMRLGPTEETVALLSKVLNGNKLASEALAKVHVQDVFFSDPALDSVEINIPQDILGIWV
DPIDSTYQYIKGSADITPNQGIFPSGLQCCTVLIGVYDIQTGVPLMGVINQPFVSQLHTRRWKGQCYWGLSYL
GTNIHSSLPPVSTRSNSEAQSQGTQNPSSEGCRFSVVISTSEKETIKGALSHVCGERIFRAAGAGYKSLCVILGLA
DIYIFSEDTTFKWDSCAAHILRAMGGGMVDLKECLERNPDTGLDLPQLVYHVGNEAGVDQWANKGLIA
YRSEKQLETFLSRLLQHLAPVATH

>d1ka1a_ e.7.1.1 (A:) 3';5'-adenosine bisphosphatase, PAP phosphatase {Baker's yeast (Saccharomyces cerevisiae)}

ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTGDYAAQTIINAISNFPDDKVVGEESSSGLS
DAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDVRQIIDFGNYEGGRKGRFWCLDPIDGPKGFLRG
QFAVCLALIVDGVVQLGCIGCPNLVSSYGAQDLKGHESFGYIFRAVRLGAFYSPSSDAESWTIHRHLKDTK
DMITLEGVEKGHSSHDEQTAIKNKNISKSLHLDSQAKYCLALGLADVYLRLPIKLSYQEKIWDHAAGNVIVHEA
GGIHTDAMEDVPLDFGNRGLATKGVIASSGPRELHDVVSTCDVIQSR

>d1jp4a_ e.7.1.1 (A:) PiPase {Rat (Rattus norvegicus)}

HNVLMLRVASAYSIAQKAGTIVRCVIAEGDLGIVQKTSATDLQTKADRMVQMSICSSLSRKFPKLTIIGEEDLPPG
EVHQELIEDGQSEEILKQPCPSQYSAIKEEDLVVWVDPVDTKEYTEGLLDNNTVLIQYEGKAIAGIINQPYNNY
QAGPDAVLGRTIWGVGLGAFGFQLKEAPAGKHIITTRHSNKLVTDCIAAMNPDNVLVGGAGNKIIQLIEG
KASAYVFASPGCKWDTCAPEVILHAVGGKLTDIHGNPLQYDKEVKHMNSAGVLAALRNYYASRPESVKSA
LIP

>d1kfsa2 e.8.1.1 (A:519-928) DNA polymerase I (Klenow fragment) {Escherichia coli}

HKGPLNVFENIEMPLVPVLSRIERNGVKIDPKVLHNHSEELTRLAELEKKAHEIAGEEFNLSSTKQLQTLFEKQGI
KPLKKTPGGAPSTSEEVLEELALDYPLPKVILEYRGLAKLKSTYTDKPLMINPKTGRVHTSYHQAVTATGRLSTD
PNLQNIPVRNEEGRRIQAFIAPEDYVIVSADYSQIELRIMAHLSRDKGLLTAFEGKDIHRATAAEVFLPLETVT
SEQRRSAKAINFGLIYGMASFGLARQLNIPRKEAQKYMDFYERYPGVLEYMERTRAQAKEQGYVETLDGRRLY
LPDIKSSNGARRAAAERAACINAPMQGTAADIKRAMIAVDAWLQAEQPRVRMIMQVHDELVFEVHKDDVDA
VAKQIHQLMENCTRLVPLLEVGSSENWDQAH

>d1qtma2 e.8.1.1 (A:423-831) DNA polymerase I (Klenow fragment) {Thermus aquaticus}

EERLLWLYREVERPLSAVLMEATGVLDVAYLALSLEVAEEIARLEAEVFRLAGHPFNLSRDQLERVLFDEL
GLPAIGKTEKTGKRSTSAAVLEALREAHPIVEKILQYRELTKLKSTYIDPLPDLIHPRTGRLHTRFNQTATGRLSS
DPNLQNIPVRTPLGQRIRRAFIAEEGWLLVALDYSQIELRVL AHLSGDENLIRVFQEGRDIHTETASWMFGVPRE
AVDPLMRRAAKTINFVLYGMSAHLRSQELAIPYEEAQAFIERYFQSFPKVRAWIEKTLEEGRRRGYVETLFGR
RYVPDLEARVKSvreerMAFNMPVQGTAADLMKLAMVKLPRLEEMGARMILLQVHDELVLEAPKERA
VARLAKEVMEGVYPLAVPLEVEVGIGEDWLSAK

>d1xwl_2 e.8.1.1 (469-876) DNA polymerase I (Klenow fragment) {Bacillus stearothermophilus, newly identified strain as yet unnamed}

EQDRLLVELEQPLSSILAEMEFAGVKVDTKRLEQMGKELAEQLGTVQEYIYELAGQEFNINSPKQLGVILFEKLQL

PVLKKTGTGSTSADVLEKLAPYHEIVENILHYRQLGKLQSTYIEGLLKVVRPDTKKVHTIFNQALTQTGRLSSTEP
NLQNIPIRLEEGRKIRQAFVPSEDWLIFAADYSQIELRVLAHIAEDDNLMEAFRRLDIHTKTAMDIFQVSEDEV
TPNMRRQAKAVNFGIVYGISDYGLAQNLNISRKEAAEFLYFESFPGVKRYMENIVQEAKQGYVTLLHRRRY
LPDITSRNFNVRSAFAERMAMNTPIQGSADIKKAMIDLNLARLKEERLQAHLLQVHDELEAPKEEMERLCRL
VPEVMEQAVTLRPLKVDYHYGSTWYDAK

>d1t7pa2 e.8.1.1 (A:211-704) T7 phage DNA polymerase {Bacteriophage T7}
LEAVDIEHRAAWLLAKQERNGFPFDKAIEELYVELAARRSELLRKLTFGWSYQPKGGTEMFCHPRTGKPLPK
YPRIKTPKGIFKKPKNAQREGREPCELDTREYVAGAPYTPVEHVFNPSSRDHIQKKLQEAGWVPTKYTDK
GAPVVDDEVLEGVRVDDPEKQAAIDLKEYLMIQKRIGQSAEGDKAWLRYVAEDGKIHGHSVNPNGAVTGRATH
AFPNLAQIPGVRSPYGEQCRAAFGAEEHLDGITGKPWVQAGIDASGLELRCLAHFMARFDNGEYAHEILNGDI
HTKNQIAAEELPTRDNAKTFIYGLYFAGDEKIGQIVGAGKRGKELKKKFLENTPAIAALRESIQQLVESSQWVA
GEQQVKWKRRWIKGKDGRKVHVRSPHAALNTLQSAGALICKLWIIKTEEMLVEKGLKHGWDGDFAYMAWV
HDEIQVGCRTTEEIAQVIETAQEAMRWVGHDHNFRCLLDTEGKMGPNWAICH

>d1ih7a2 e.8.1.1 (A:376-903) T4-like DNA polymerase {Bacteriophage RB69}
QNKVIPQGRSHPVQPYPGAFVKEPIPNEYVMSFDLTSLYPSIIRQVNISPETIAGTFKVAPLHDYINAVAERPSD
VYSCSPNGMMYYKDRDGVPTEITKVNQRKEHKGYMLAAQRNGEIKEALHNPNLSVDEPLDVDYRFDFSD
EIKEKIKLSAKSLNEMLFRAQRTEVAGMTAQINRKLLINSYGALGNWFRRYDLRNATAITTFGQMLQWIER
KVNEYLNEVCCTEGEAFVLYGDTDSDIYVSADKIIDKVGESKFRDTNHWDFLDKFARERMEPAIDRGFREMCEY
MNNKQHLMFMDREAIAGPPLGSKGIGGFWTGKKRYALNVWDMEGTRYAEPKLKIMGLETQKSSTPKAVQKA
LKECIRRMILQEGEESLQEYFKEFEKEFRQLNYISIASVSSANNIAKYDVGGFPGPCKPFHIRGILTYNRAIKGNIDAP
QVVEGEKVVVLPLREGNPFGDKCIAWPSGTEITDLIKDDVLHWMDYTVLLEKTFIKPLEGFTSAAKLDYEKKASL
FDMFDF

>d1tgao2 e.8.1.1 (A:348-773) T4-like DNA polymerase {Archaeon Thermococcus gorgonarius}

STGNLVEWFLLRKAYERNELAPNKPDERELARRRESYAGGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLN
REGCEEYDVAPQVGHFKCKDFPGFIPSLLGDLLEERQKVKKMKATIDPIEKLLDYRQRAIKLANSFYGYGYAK
ARWYCKECAESVTAWGRQYIETTIREIEEKFGFKVLYADTDGFFATIPGADAETVKKAKEFLDYINAKLPGLELE
YEGFYKRGFFVTKKYAVIDEEDKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEV
PPEKLVIYEQITRDLKDYKATGPHVAVAKRLAARGIKIRPGTVISYIVLKGSGRIGDRAIPFDEFDPKAHKYDAEYYIE
NQVLPVERILRAFGYRKEDLRYQKTRQVGLGAWLKPCT

>d1qhta2 e.8.1.1 (A:348-750) T4-like DNA polymerase {Archaeon Thermococcus sp., 9on-7}

STGNLVEWFLLRKAYKRNE LAPNKPDERELARRGGYAGGYVKEPERGLWDNIVYLDFRSLYPSIIITHNVSPDTL
NREGCKEYDVAPQVGHFKCKDFPGFIPSLLGDLLEERQKVKKMKATVDPLEKKLLDYRQRAIKLANSFYGYGY
AKARWYCKECAESVTAWGREYIEMVIRELEEKFGFKVLYADTDGLHATIPGADAETVKKAKEFLKYINPKLPG
ELEYEGFYVRGFFVTKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSKYEV
EVPPEKLVIHEQITRDLRDYKATGPHVAVAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPADEFDPTKHRYDAE
YYIENQVLPVERILKAFGY

>d1d5aa2 e.8.1.1 (A:348-756) T4-like DNA polymerase {Archaeon Desulfurococcus tok} STGNLVEWFLLRKAYERNDVAPNKPDERELARRTESYAGGYVKEPEKGLWENIVYLDYKSLYPSIIITHNVSPDTL
NREGCREYDVAPQVGHRFCKDFPGFIPSLLGDLLEERQKVKKMKATVDPIERKLLDYRQRAIKLANSYYGYAY
ANARWYCRECAESVTAWGRQYIETTMREIEEKFGFKVLYADTDGFFATIPGADAETVKNKAKEFLNYINPRLPGL
LELEYEGFYRRGFFVTKKYAVIDEEDKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSR
HEVPPEKLVIYEAGPHVAAAATVISYIVLKGPGRVGDRDRAIPFDEFDPKAHKYDAEYYIENQVLPVERILRAFGYRK

EDLR

>d1gcxa2 e.8.1.1 (A:348-758) T4-like DNA polymerase {Archaeon Pyrococcus kodakaraensis}

STGNLVEWFLLKAYERNELAPNPKDEKELARRQSYEGGYVKEPERGLWENIVYLDFRSLYPSIIITHNVSPDTLNREGCKEYDVAPQVGHRFCKDFPGFIPSLLGDLERQKIKKKMKATIDPIERKLLDYRQRAIKILANSYYGGYYGA
RARWYCKECAESVTAWGREYITMTIKEIEEKYGFKVIYSDTDGFFATIPGADAETVKKKAMEFLKYINA
LEYPYKRGFFVTKKKYAVIDEEGKITTRGLEIVRRDWSEIAKETQARVLEALLKGDGV
EVPPEKLVIHEQITRDLKDYKATGPHVAVAKRLAARGVKIRPGTVISYIVLKGSGRIGDRAIPFDEF
DPTKHKYDAE
YYIENQVLP
PAVERILRAFGYRKEDLRYQ

>d1jx4a_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus, DNA polymerase IV}

MIVLFVDFDYAQVEEVNPSLKGKPVVVCVFSGRFEDSGAVATANYEARFKFGVKAGIPIVEAKKILPNAVYLP
MRKEVYQQVSSRIMLLREYSEKIEIASIDEAYLDISDKVRDYREAYNLGLEIKNKILEKEKITVTVGISKNKVFAKIA
ADMAKPNGIKVIDDEEVKRLIRELDIADVPIGNITAEKLKKLGINKLVDTLSIEFDKLKGMIKEAKAKYLI
SLARDE
YNEPIRTVRKSIGRIVTMKRNSRNLEEIKPYLFRAIEESYYKLDKRIPKAIHVVA
VATEDLDIVSRGRTFPHGISKETA
YESVKLLOKILEEDERKIRRIGVRFSKFI

>d1im4a e.8.1.5 (A:) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}

HHHHHVIFVDFDYFFAQVEEVLPQYKGKPLVVCVYSGRTKTSGAVATANYEARLGVKAGMPIIKAMQIAPS
AIYVPMRKPIYEAFSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGNFENGIELARKIKQEILEKEKITVTGVAP
NKIIAKIIADSKSPNGIGVIRPTEVODEINFLDIDEIPGIGSVIARRIINFGLQOKLRD

>d1k1sa e-8.1.5 (A) DinB homolog (DBH) {Archaeon Sulfolobus solfataricus}

MIVIFVDFDYFFAQVEEVLPQYKGKPLVSVYSGRTKTSGAVATANYEARLGVKAGMPIIKAMQIAPSAIYVP
MRKPIYEAFSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGFENGIELARKIKQEILEKEKITVTGVAPNILA
KIIADKSCKPNGLGVIRPTEVQDFNLNELDIDEIPGIGSVLARRLNELGIQKLRDILSKNYNELEKITGAKALYLLKLAQ
NKYSEPVENKSCHIPHGRYLTLPYNTRDVKVILPYLKKAINEAYNKVNIGPMRITVIAIMEDLDILSKGKKFKHGISID
NAYKVAFDLIRELIYRDKRRNVBRIGVKIDNIIIN

>d1jih - e 8 1.5 (A:) DNA polymerase eta {Baker's yeast (*Saccharomyces cerevisiae*)}

MSKFTWKELIQLGSPSKAYESSLACIAHIDMNAFFAQVEQMRCGLSKEDPVVCVQWNSIIAVSYAARKYGISRM
DTIQEALKKCSNLIPIHTAVFKGEDFWQYHDGCGSWVQDPAKQISVEDHKVSLEPYRRESRKALKIFKSACDLV
ERASIDEVFSDLGRICFNMLMFNDNEYLTGDLKLKDALSNIREAFIGGNYDINSHLPLIKEKIKSLKFEGDVFNPEG
RDLITDWDDVIALGSQVCKGIRDSIKDILGYTTSCGLSSTKNVCKLASNYKKPDAQTIVKNDCLDFLDCGKFEIT
SFWTLGGVLGKELIDVLDLPHENSIKHIRETWPDNAGQLKEFLDAVKQSDYDRSTSNIPLKTADLAEKLFKLSR
GRYGLPLSSRPVVKSMMSNKNLRGKSCNSIVDCISWLEVFCALTSRIQDLEQEYNKIVIPRTVSISLTKSYEVYR
KSGPVAYKGINFOSHFIJVKVGIFKVTDIJKGKNKSYYPITKISMITNFIDII

>d1mmI e.8.1.2 (-) MMLV reverse transcriptase {Moloney murine leukemia virus}

TWLSDFPQAWAETGGMGLAVRQAPLIPLKATSTPVSIKQYPMSQEARLGKPHIQRLLDQGILVPCQSPWNTP
LLPVKKPGTNDYRPVQDLREVNKRVEDIHPVPNPNYLSSGLPPSHQWYTVDLKD AFFCLRHPTSQLFAFE
WRDPEMGISGQLTWTRLPQGFKNSPTLFDEALHRDLADFRIQHPDLILLQYVDDLLAATSELDCCQQGTRALLQ
TLGNLGYRASAKKAQICOKOVKYLGYLLK

>d1c9ra2 e.8.1.2 (A:1-429) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PISPIETVPVKLAPGMDGPKVQWP LTAEIAALVAICTAMEAEGKISKIGPENPYNTPVFAIKKAAAAAAAALVD
FRELNKRTQDFWEVQLGIPHAGLKKKS VTVLDVGDAYFSVPLDEDFRKYTAFTIPSIANATPGIRYQYNVLPQ
GWKGSPAIFOSSMTKII FPFKKONPDIVIYQYIDDIYVGSDI FIGOHA TKAIFIROHII AWGITTPD KKHA AFPPF

LWMGYELHPDAWTVAPAALAAAASA AVNDIQKLVGKLNWASQIYPGIAVRALSAAAAGTKAAAEEAAAATAAA
ALALAAAREALAAPVHGYYDPSKDLIAEIQAQGQQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEA
VQKITTESIVIWGKTPFKLPIQKETWETWWTEYWQATWIPEWEFVNTPPLVKLWYQL
>d1c9rb1 e.8.1.2 (B:) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}
PISPIETPVKLAPGMDGPVKQWPPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKDSTKWRKLVD
FRELNKRTQDFWEALGIPHPAGLKKKSVTLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLQP
GWKGSPAIFQSSMTKILEPFKAQNPDIVIYQYIDDLYVGSDELIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPPF
LWMGYELHPDKWAAAAAAAAAAATVDIQLVKGKLNWAAQIYPGIAAAALSAALAGTKALTAAAPLTAAA
ALELAANRAAAAAAAAGVYYDPSKDLIAEIQKQGQQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEA
VQKITTESIVIWGKTPFKLPIQKETWETWWTEYWQATWIPEWEFVNTPPLVALWYALE
>d1har_ e.8.1.2 (-) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}
PISPIETPVKLKPGMDGPVQAQWPPLAAKIAALVAICTEMEKEGKISKIGPENPYNTPVFAIKKDSTKWAKLVD
FRELNKRTQDFWEVQLGIPHPAGLKKKSVTLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLQP
GWKGSPAIFQSSMTKILAPFKAANPDIVIYQYMDDLYVGSDELAIGAHRTKIEELRQHLLRWGLTT
>d1vrta2 e.8.1.2 (A:4-429) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}
PIETPVKLKPGMDGPVKQWPPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAIKKDSTKWRKLVD
LNKRTQDFWEVQLGIPHPAGLKKKSVTLDVGDAYFSVPLDEDFRKYTAFTIPSINNETPGIRYQYNVLQP
KGSPAIFQSSMTKILEPFRKQNPDIVIYQYMDDLYVGSDELIGQHRTKIEELRQHLLRWGLTTPDKKHQKEPPFL
WMGYELHPDKWTVQPIVLPEKDSWTVDIQLVKGKLNWASQIYPGIKVRQLCKLLRGTKALTEVPLTEEA
LAENREILKEPVHGYYDPSKDLIAEIQKQGQQWTYQIYQEPFKNLKTGKYARMRGAHTNDVKQLTEAVQKIT
TESIVIWGKTPFKLPIQKETWETWWTEYWQATWIPEWEFVNTPPLVKLWYQL
>d1ceza_ e.8.1.3 (A:) T7 RNA polymerase {Bacteriophage T7}
IAKNDFSDELAAIPFNTLADHYGERLAREQLALEHESYEMGEARFRKMFERQLKAGEVADNAAKPLITLLPK
MIARINDWFEEVAKRGKRPTAFQFLQEIKPEAVAYITIKTTLACLTSADNTTVQAVASAIGRAIEDEARFGRIRDL
EAKHFKKNVEEQLNKRKGHVVYKAFMVMQVEADMLSKGLGGAEWSSWHKEDSIHGVRCIEMLIESTGMVSL
HRQNAGVVGQDSETIELAPEYAEAIATRAGALAGISPMFQPCVPPKPWTGITGGYWANGRRPLALVRTHSK
KALMRYEDVYMPEVYKAINIAQNTAWKINKVLAVANVITWKHCPVEDIPAIEREELPMKPEDIDMNPEALTA
WKRAAAAVYRKDKARKSRRISLEFMLEQANKFANHKAIWFYNMDWRGRVYAVSMFNPQGNDMTKGLTL
AKGKPIKEGYYWLKIHGANCAGVDKVPFPERIKFIEENHENIMACAKSPLENTWWAEQDSPFCFLAFCEYAG
VQHHGLSYNCNSLPLAFDGSCSGIQHFSAMLDEVGGRAVNLLPSETVQDIYGIVAKVNEILQADAINGTDNEV
VTVDENTGEISEVKVLGTTKALAGQWLAGVTRSVTKRSVMTLAGSKFGFRQQVLEDTIQPAIDSGKGLMFT
QPNQAAGYMAKLIWESVSVTVAAVEAMNWLKSAAKLAAEVKDKKTGEILRKRCAVHWVTPDGFPVWQE
YKKPIQTRLNLMFLGQFRLQPTINTNKDSEIDAHKQESGIAPNFVHSQDGSHLRKTVWAHEKYGIESFALIHDS
FGTIPADAANLFKAVRETMVDTYESCDVLADFYDQFADQLHESQLDKMPALPAKGNLNRDILESDFAFA
>d1rdr_ e.8.1.4 (-) Viral RNA-dependent RNA-polymerase {Poliovirus type 1, strain Mahoney}
VGYPPIINAPS GTKLEPSAFHYVFEVGKEPAVLTKNDPRLKTDFFEAIFSKYVGNKITEVDEYMKEAVDHYAGQLMS
LDINTEQMCLEDAMYGTDGLEALDLSTSAGYPVAMGKKKRDILNKQTRDTKEMQKLLDTYGINLPLVTYVKD
ELRSKTKVEQGKSRLIEASSLNDSVAMRMAFGNLYAAFHKNPGVITGSAVGCDPDLFWSKIPVLMEEKLFADF
TGYDASLSPAWFEALKMVLEKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGMPGCSGTSIFNSMINNLIIRTLL
KTYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMPADKSATFETVTWENVTLKRFFRADEKYP
FLIHPVMPMKEIHEISRWTKDPRTNTQDHVRSLCLLAWHNNGEEEYNKFLAKIRSVPGRALLPEYSTLYRRWLDS

F

>d1c2pa_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Hepatitis C virus}
HHSYWTGALITPCAAEESKLPINALSNSLLRHHNMVYATTSRSAGLRQQKVFDRQLVQDDHYRDVLKEMKAK
ASTVKAKLLSVEEACKLTPPHSAKSFKGYGAKDVRNLSSKAVNHIHSVWKLLEDTVTPIDTTIMAKNEVFCVQP
EKGGRKPARLIVFPDLGVRVCEKMALYDVSTLPQVMGSSYGFQYSPGQRVEFLVNTWSKKNPMGFSYDT
RCFDSTVTENDIRVEESIYQCCLAPEARQAISLTERLYIGGPLTNKGQNCGYRRCRASGVLTSCGNTLCYLK
ASAACRAAKLQDCTMLVNGDDLVVICESAGVQEDAASLRAFTEAMTRYSAPPGDPPQPEYDLEITSCSSNVSV
AHDASGKRVYYLTRDPTTPLARAAYETARHTPVNSWLGNIIYAPTLWARMILMTHFFSILLAQEQLKEKALDC
QIYGACYSIEPLDLPQIIERLHGLSAFLSHSYSPGEINRVASCLRKLGVPPRLVRHRARSVRARLLSQGGRAATC
GKYLFNWAVKTKLKLTPIPAASQLDLSGWVFAGYSGGDIYHS
>d1khva_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Rabbit hemorrhagic disease virus}
FCGEPIDYRGITAHLVGAEPRRPPVSGTRYAKVPGVPDEYKTGYRPANLGRSDPDSKSLMNIAVKNLQVYQQE
PKLDKVDEFIERAAADVGLYLRFLTGERQANLNFKAAFNTLDSLSCGPVPGKKIDHVKGMDQVLAKHLY
KCWSVANSGKALHHIYACGLKDELRPLDKVKEGKKRLLWGCDVGAVCAAASFHNICYKLKMVARFGPIAVGV
DMTSRDVDVIINNLTKASDFLCLDYSKWDSTMSPCVVRLAIDILADCQTELTKSVVLTKSHPMTILDAMIV
QTKRGLPSGMPTFTSVINSICHWLLWSAAVYKSCAEIGLHCSNLYEDAPFYTYGDDGVYAMTPMMVSLLPAIIEN
LRDYGLSPTAADKTEFIDVCPLNKISFLKRTFELTDIGWVSKLDKSSLRQLEWSKTTSRHMVIEETYDLAKEERGV
QLEELQVAAAAGQEFFNFVCRELERRQAYTQFSVSYDAARKILADRKR
>d1hhsa_ e.8.1.6 (A:) dsRNA phage RNA-dependent RNA-polymerase {Bacteriophage PHI-6}
PRRAPAFPLSDIKAQMLFANNIKAQQASKRSFKEGAIETYEGLLSVDPRFLSFKNELSRYLTDHF PANVDEYGRVY
GNGVRTNFFGMRHMNGFPMIPATWPLASNLLKKRADADLADGPVSE RDNL FRAAVRLMFSDLEPVPLKIRKG
SSTCIPYFSNDMGTKIEIAERA LEKAEEAGN LMLQGKFDDAYQLHQ MGGAYVYRAQSTD AITLDPKTGKFVS
KDRMVA DFEYAVTGGEQGS LFAASKDAS RLKEQY GIDV P DGF CERR RTAMGGP FALNAPIMA V AQP VRN KIY
SKYAYTFHHTTRLNKEEKVKEW SLCVATD VSDHDTFW PGWLRD LICDELL NMGYAPWWV KLFETSLKLPV YVG
APAPEQGH TLLGDP SNP DLEV GLSSG QGAT DLM GTLL MSITY LMQL DHTAP HNS RIKD MPSAC RFL DSY W
QGHEEIRQISKSDA MLGWT KGR ALVGGHRLF EMLKEG KVNP SP YM KIS YEH GGAFL GDIL YDSR REPG SAIF
VGNINSM LNNQFSPEYGVQSG VDRS KRKP FPGLAW ASMKD TYGAC PIY SDV L AIE RCW WNA FGE SYRAY
REDMLK RD TLELS RYVAS MARQAGLA ELTP IDLE VLA DP NKLQ YK WT EAD VSANI HEV L MH GVS EKTER FLRS
VMP R
>d1i50a_ e.29.1.1 (A:) RBP1 {Baker's yeast (Saccharomyces cerevisiae)}
VGQQYSSAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMDETQTRAKIGLNDPRLGSIDRNLCQTCQEGMN
EC PGHFGHIDLAKPVFHVGFI AKIKK VCEC VCMHCGKLLDEH NELMRQALAIKDSKKRFAAIWTLCKTMVCE
TDVPS EDDPTQLV SRGGCG NTQPTIRKD GLKLVGSW KKDRATG DADEPEL RVLSTEE I NIFKHISVKDFTSLGF N
EVFSRPEW MILT CLPV PPPP VRPS ISFN EQRGE DDLTFKLADILKANISLETLEHNGA PHHAIEEAESL LQFHVAT
YMDNDIAGQPQALQKSGR PVKSIRARLKKGKEGRIRG NL MGK RVDF SARTVIS GDPN L ELDQV GPV KSI A KTLTY
PEVVTPYNIDRLTQLVRNGPNEHPGAKYVIRD SGDRIDL RYSK RAGD IQLQ YGW KVERHIMDNDPVL FNRQPS
LHKMSMMAHRV KVIPYSTFRNL NSVTSPYNA FDGDEM NLH VPQSEET RAELSQLCAVPLQIVSPQSNKPCM
GIVQDTLCGIRKLTLRDTFIELDQVLNMLYWWPDW DGVIPTPAI KPKPLWSGKQILSVAIPNGIHLQRFDEGTTL
LSPKDNGMLIIDGQIIFGVVEKKT VGSSN GGLI HVV T REKGPQVCAK LFGNIQKVVNFWLLHNGFSTGDTIA
DGPTMREITETIAEAKKVL DVTK EAQANLLTA HGMLTRESFEDNV VRFN EARDKAGRLAEVN LKDLNNVK
QMVMAGSKGSFINIAQMSACVGQQSVEGKRIA FGFDRTLPHFSKDDYSPESKG FVENSYLRGLTPQEFFFA
MGGREGLIDTAVKTAETGYIQRRLVKALEDIMVHYDNTTRNSLG NVI QF IYGEDGM DAHIEKQSLDTIGGSDA
AFEKRYRVDLLNTDHTLDP SLES GSEI LGDLKLQVLL DEEY KQLV KDRKFL REV FVDGE ANWPLPVNIRRIQNA

QQTFHIDHTKPSDLTIKDIVLGVKDLQENLLVLRGKNEIIQNAQRDAVTLFCCLLRSRLATRRVLQEYRLTKQAFD
WVLSNIEAQFLRSVVHPGEMVGVLAAQSIGEPATQMTLNTFHAGVASKVTPRLKEILNVAKNMKTPSL
TVYLEPGHAADQEQAQLIRSAIEHTTLKSVTIASEIYYDPDPRSTVPIEDEEIQLHFSLLDEAEQSFDQQSPWLLR
LELDRAAMNDKDLTMGQVGERIKQTFKNDLFVIWSEDNDEKLIIRCRVVRPKSLDAETEAEDHMLKKIENTM
LENITLRGVENIERVVMMKYDRKVPSPTEGYVKEPEWVLETGVNLSEVMTPGIDPRTIYTNSFIDIMEVLGIE
AGRAALYKEVYNVIASDGSYVNYRHMAALLVDVMTTQGGLTSVTRHGFNRSNTGALMRCSEETVEILFEAGAS
AELDDCRGVSENVILGQMAPIGTGAFDVMIDEESL

>d1i6vc_e.29.1.1 (C:) RNA-polymerase beta {Thermus aquaticus}

KIKRGRIREVIPLPPLTEIQVESYKKALQADVPPEKRENVGIQAAFKETFPIEEEGDKGKGGLVLDLEYRIGDPPFS
QDECREKDLTYQAPLYARLQLIHKDTGLIKEDEVFLGHPLMTEDGSFIINGADRIVVSQIHRSPGVYFTPDPARP
GRYIASIPLPKRGWPWIDLEVEASGVVTMKVNKRKFPLVLLRLVGLYDQETLVRELSAYGDLVQGLLDEAVLAMRP
EEAMVRLFTLLRPGDPPKKDKALAYLFGLADPKRYDLGEAGRYKAEEKLGVGGLSGRTLVRFEDGEFKDEVFLPT
LRYLFALTAGVPGHEVDDIDHLGNRRIRTVGELMADQFRVGLARLARGVRERMVMGSPDTLTPAKLVNSRPLE
AALREFFSRSQSQFKDETNPSSLRHKRRISSALGPGLTRERAGFDVVDVHRTHYGRICPVETPEGANIGLITS
AAVARVDALGFIRTPYRRVKNGVVTEEVVYMTASEEDRYTIAQANTPLEGDRITDRVVARRGEPVIVAPEEVE
FMDVSPKQVFSLNTNLIPFLEHDDANRALMGNSNMQTQAVPLIRAQAPVVMTGLEERVVRDSLAALEYAEDGE
VVKVDGTRIAVRYEDGRLVHPLRRYARSNQGTAFDQRPRVRVGQRVKKGDLLADGPASEEGFLALGQNVLVAI
MPFDGYNFEDAIVISEELLKDFYTSIHIERYIEARDTKLGPERITRDIPHLSEAALRDLDEEGIVRIGAEVKPGDIL
VGRTSFKGEQEPSPEERLLRSIFGEKARDVKDTSLRVPPGEGGIVVGRRLRRGDPGVELKPGVREVVRVFVAQK
RKLQVGDKLANRHNKGVVAKILPVEDMPHLPDGTVDVILNPLGVPSRMNLGQILETHLGLAGYFLGQRYISP
VFDGATEPEIKELLAEAFNLYFGKRQGEGFGVDKREKEVLARAEKGLVSPGKSPEEQLKELFDLGKVVLYDGR
EPFEGPIVVGQMFIMKLYHMVEDKMHARSTGPYSLITQQPLGGKAQFGQQRFGEIMEVWALEAYGAAHTLQE
MLTIKSDDIEGRNAAYQAIKGEDVPEPSVPESFRVLVKELOQALALDVQLDEKDNPVDVFEGL

>d1i50b_e.29.1.2 (B:) RBP2 {Baker's yeast (Saccharomyces cerevisiae)}

FEDESAPITAEDSWAVISAFFREKGLVSQQLDSFNQFDYTLQDIICEDSTLILEQLAQHTTESDNISRKYEISFGKIY
VTKPMVNEDGVTHALYPQEARNLNLYSSGLFVDVKKRTYEIDVPGRELKYELIAEESEDDSES GKVFIGRLPI
MLRSKNCYLSEATESDLYKLKECPDMGGYFIINGSEKVLIAQRSAGNIVQVFKAAPSPISHVAEIRSALEKGSR
FISTLQVKLYGREGSSARTIKATLPYIKQDIPIVIIFRALGIIPDGEILEHICYDVNDWQMLEMLKPCVEDGFVIQDR
ETALDFIGRRGTALGIKEKRIQYAKDILQKEFLPHITQLEGFESRKAFFLGYMINRLLL CALDRKDQDDRDFGKK
RLDLAGPLLAQLFKLKLTDIFRYMQRTVEEAHDNFNMKLAINAKTISGLKYALATGNWGEQKKAMSSRAG
VSQVLNRNTYSSTLSHLRRNTPIGRDGKLAKPRQLHNTHWGLVCPAETPEGQACGLVKNLSLMSCISVGTD
MPIITFLSEWGMEPLEDYVPHQSPDATRVFNGVWHGVHRNPALMETLRTLRRKGDIINPEVSMIRDIREKEL
KIFTDAGRVRVYRPLFIVEDDESLGHKELKVRKGHIAKLMATEYQDIEGGFEDVEEYTWSLLNEGLVEYIDAEEE
LIAMQPEDLEPAEANEENDLVDPAKIRVSHHATTFTHCEIHPSMILGVAASIIPFDHNQSPRNTYQSAMGK
QAMGVFLTNYNVRMDTMANILYYPQKPLGTTRAMEYLKFRELPAGQNAIVAIACYSGYNQEDSMIMNQSSID
RGLFRSLFFRSYMDQEKKYGMISITETFEKPQRTNLRMKHGTYDKLDDGLIAPGVRVSGEDVIIGKTTISPDE
EELGQRTAYHSKRDASTPLRSTENGIVDQVLTTNQDGLKFVVRVRTTKIPQIGDKFASRHGQKGTTIGITYRRE
DMPFTAEGIVPDLIINPAPSRMTVAHLIECLLSKVAALSGNEGADSPFTDITVEGISKLLREHYQSRGFEVMY
NGHTGKKLMAQIFFGPTYYQRLRHMVDDKIHARARGPMQVLRQPVEGRSRDGLRGEMERDCMIAHGA
ASFLKERLMEASDAFRVHICGICGLMTVIAKLNHNQFECKGCDNKIDIYQIHIPYAAKLLFQELMAMNITPRLYTD
RSRDF

>d1i6vd_e.29.1.2 (D:) RNA-polymerase beta-prime {Thermus aquaticus}

KEVRKVRIALASPEKIRWSYGEVEKPETINYRTLKPERDGLFDERIFGPIKDYECACGKYKRQRFEAKVCERCAVE
VTRSIVRRYRMAHIELATPAAHIFWFVKDVPSKIATLLDSATELEQVLYFNKYIVLDPKAAVLDAVPVEKRQLLTDX

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXIDARMGAEAIQELLKELDLEKLERELLEEMKHPSRARAK
ARKRLEVVRALDSGNRPEWMILEAVPVLPDLRPMVQVDGGRFATSDLNDLYRRLINRNNRLKKLLAQGAPE
IIIRNEKRMLQEAVDAVIDNGRRGSPVTNPGRPLRSLTDILSGKQGRFRQNLLGKRVDYSGRSVIVGPQLKL
HQCGLPKRMALELFKPFLKKMEEKAFAPNVKAARRMLERORDIKDEVWDALEEVIGHKVVLNRAPTLHRLG
IQAFQPVLVEGQSIQLHPLVCEAFNADFDDGDMQMAHVPLSSFAQAERIQLMSAHNLLSPASGEPLAKPSRDIIL
GLYYITQVRKEKKGAGMAFATPEEALAAYERGEVALNAPIVVAGRETSVGRLKVFANPDEALLAVAHGLLDLQD
TVTTRYLGRRLETSPGRILFARIVGEAVGDEKVAQELIQMDVPQEKNSLKDLYQAFLRLGMEKTARLLDALKY
GFTLSTTSGITIGIDDAVIPEEKQRYLEEADRKLQRQEIQAYEMGFLDRERYDQVIQLWTETTEKVTQAVFNNFEE
NYPFNPLYVMAQSGARGNPQQIRQLCGMRGLMQKPSGETFEVPRSSFREGLTVEYFISSHGARKGGADTA
RTADSGYLTRKLVDVAHEIVVREADCGTTNYISVPLFQMDEVTRTLRLRKRSIESGLYGRVLAREVEALGRRLEE
GRYLSLEDVHFLIAAEAGEVREVPVRSPLCQCTRYVCQKCYGYDLSMARPVSIGEAVGVVAAESIGEPGTQLT
MRTFHGGAVGTDTQGLPVIELFEARRPKAKAVISIEIDGVVRIEEGEDRLS VFVESEGSKEYKLPKDARLLVK
DGDYVEAGQPLTRGAIDPHQLEAKGPEAVERYLVDEIQKVYRAQGVKLHDKHIEIVVRQMLKYEVTDPGDS
RLEGQVLEKWDVEALNERLIAEGKVPVAWKPLMGVTKSALSTKSWLSAASFQNTTHVLTEAAIAGKKDELIG
LKENVILGRLIPAGTGSDFVRFTQVVDQRTLKAIE

>d1bpya2 e.9.1.1 (A:92-335) DNA polymerase beta, catalytic (31 kD) fragment {Human (Homo sapiens)}

DTSSSINFLTRVGIGPSAARKFVDEGIKTLedLRKNEDKLNHHQRIGLKYFGDFEKRIPREEMLQMQLDIVLNEV
KKVDSEYIATVCGSFRRGAESSGDMDVLLTHPSFTSESTKQPKLLHQVVEQLQKVHFITTLSKGETKFMGVCQL
PSKNDEKEYPHRRRIDIRLIPKDQYYCGVLYFTGSDIFNKNMRAHALEKGFTINEYTIRPLGVTGVAGEPLPVDS
EKFIDYIQWKYREPKDRSE

>d1jn3a_e.9.1.1 (A:) DNA polymerase beta, catalytic (31 kD) fragment {Rat (Rattus norvegicus)}

DDTSSSINFLTRVTGIGPSAARKLVDEGIKTLedLRKNEDKLNHHQRIGLKYFEDFEKRIPREEMLQMQLDIVLNEV
KKLDPEYIATVCGSFRRGAESSGDMDVLLHPNFTSESSKQPKLLHRVVEQLQKVRFITTLSKGETKFMGVCQL
PSENDENEYPHRRRIDIRLIPKDQYYCGVLYFTGSDIFNKNLRAHALEKGFTINEYTIRPLGVTGVAGEPLPVDS
EKFIDYIQWKYREPKDRSE

>d1jmsa2 e.9.1.1 (A:243-510) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}

DERYKSFKLFTSVFGVGLKTAEKWFRMFGRTLSKIQSDKSLRFTQMOKAGFLYYEDLVSCVRPEAEAVSMLVK
EAVVTFLPDALVTMTGGFRRGKMTGHDVDFLITSPEATEDEEQQLHKVTDFWKQQQLLYCDILESTFEFKFQ
PSRKVDALDHFKCFLILKLDHGRVHSEKSGQQEGKGKWAIRVLDVMCPYDRRAFALLGWTGSRQFERDLRY
ATHERKMMMLDNHALYDRTKRVFLEAESEEIFAHLGLDYIEPWERNA

>d1jaja_e.9.1.1 (A:) DNA polymerase X {African swine fever virus}

MLTLIQGKKIVNHLRSRLAFYEYNGQLIKILSKNIVAVGSLRREEMLNDVLLIVPEKKLLKHVLPNIRIKGLFSVK
VCGERKCVLFIEWEKTYQLDLFTALAEEKPYAIFHFTGPVSYLIRIRAALKKKNYKLNQYGLFKNQTLVPLKITTEK
ELIKELGFTYRIPKKRL

>d1fa0a2 e.9.1.2 (A:3-351) Poly(A) polymerase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

SQKVFGITGPVSTVGATAAENKLNDLSLIQELKKEGSFETEQETANRVQVLKILQELAQRFYEVSKKNMSDGM
ARDAGGKIFTYGSYRLGVHGPBSDIDLTVVVKHVTREDFFTVDSSLRERKELDEIAPVPAFVPIIKIKFSGISID
LICARLDQPVPLSLLSDKNLLRNLDKDLRALNGTRTDEILELVPKPNVFRIALRAIKLWAQRRAVYANIFGFP
GGVAWAMLVARICQLYPNACSAVILNRFFIILSEWNWPQPVILKPIEDGPLQVRVWNPKIYAQDRSHRMPVITP
AYPSMCATHNITESTKKVILQEFVRGVQITNDIFSNKKSCHANLFEK

>d1f5aa2 e.9.1.2 (A:20-364) Poly(A) polymerase, catalytic domain {Cow (Bos taurus)}

YGITSPISLAAPKETDCLLTQKLVELKPFGVFEEEEELQRRILILGKLNLLVKEWIREISESKNLPQSVIENVGGKIFT

FGSYRLGVHTKGADIDALCVAPRHVDRSDFFTSFYDKLKLQEEVKDLRAVEEAFVPVIKLCFDGIEIDILFARLALQTIPEDDLRDDSLLKNLDIRCIRSLNGCRVTDEILHLPVNIDNFRTLRAIKLWAKRHNIIYSNILGFLGGVSWAMLVARTCQLYPNAIASTLVHKFFLVFSKWEWPNPVLLKQPEECNLNLPWDPRVNPSDRYHLMPIITPAYPQQNSTYNVSSTRMVMVEEFKQGLAITDEILLSKAIEWSKLFEA

>d1knya_ e.9.1.3 (A:) Kanamycin nucleotidyltransferase (KNTase) {Staphylococcus aureus}

MNGPIIMTREERMKIVHEIKERILDKYGDDVKAIGVYGSGLRQTDGPYSDIEMMCMVSTEEAEFSHEWTTGE
WKVEVNFYSEEILLYDASQVESDWPLTHGQFFSILPIYDGGYLEKVYQTAKSVEAQTFHDAICALIVEELFYEAGK
WRNIRVQGPTTFLPSLTVQVAMAGAMIGLHHRICYTSASVLTEAVKQSDLPSGYDHLCQFVMSGQLSDSEKL
LESLENFWNGIQEWTERHGYIVDVSKRIPF

>d1k8ta_ e.9.1.4 (A:) Adenylylcyclase toxin (the edema factor) {Bacillus anthracis}
DRIDVLKGEALKASGLVPEHADAFKKIARELNTYILFRPVNKLATNLNIKGKVATKGLNVHGKSSDWGPVAGYIPF
DQDLSKKHGQQLAVEKGNLENKKSITEHEGEIGKIPLKLDHLRIEELKENGIIKGKKEIDNGKKYYLLESNNQVYE
FRISDENNEVQYKTKEGKITVLGEKFNWRNIEVMAKNVEGLVKPLTADYDLFALAPSLEIKKQIPQKEWDKVNN
TPNSLEKQKGVTNLLIKYGIERKPDSTKGTLSNWQKQMLDRLNEAVKYTGTYGGDVVNHGTEQDNEEFPEKDN
EIFIINPEGEFILTGNWEMTGRFIEKNITGKDLYYFNRSYNKIAPGNKAYIEWTDPITAKINTIPTSAEFIKNLSSIR
RSSNVGVYKDSGDKDEFAKKESVKKIAGYLSDYNSANHIFSQEKKRKISIFRGIQAYNEIENVLKSKQIAPEYKNY
FQYLKERITNQVQLLLTHQKSNIEFKKLLYKQLNFTENETDNFEVFQKIIDE

>d1cy9a_e.10.1.1 (A:) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}
FVPEEFWEVDASTTPSGEALALQVTHQNDKPFRPVNKEQTQAASLLEKARYSVLEREDKPTTSKPGAPFITST
LQQAASTRLGFGVKTMMMAQRLYEAGYITYMRTDSTNLSQLDAVNMRGVIISDNFGKKLPESPQYASKEN
SQEAHEAIRPSDVNVMAESLKDMEADAQKLYQLIWRQFVACQMTPAKYDSTTLTVGAGDFRLKARGRILRFD
GWTKVMPALRKGDEDRILPAVNKGDAITLVEITPAQHFTKP

>d1ecl__ e.10.1.1 (-) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}
GKALVIVESPAKAKTINKYLGSDYVVKSSVGHIRDLTSGSAAKKSADSTSTKAKPKKPDERGALVNRMGVDPW
HNWEAHYEVLPGKEKVSELQLAEKADHIYLATDLDREGEAIAWHLREVIGGDDARYSRVFNEITKNAIRQA
FNKPGELNIDRVNAQQQARRFMDRVVGYMSPLLWKKIARGLSAGRVSQSVAVRLVVEREREIKAFVPEEFWEV
DASTTPSGEALALQVTHQNDKPFRPVNKEQTQAAVSLLKARYSVLEREDKPTTSKPGAPFITLQQAASTRL
GFGVKKTMMMAQRLYEAGYITYMRTDSTNLSDAVNMVRGYISDNFGKKLPESPNQYASKGNSQEAHEAIR
PSDVNVMAESLKDMEADAQKLYQLIWRQFVACQMTPAKYDSTTLTVAGDFRLKARGRILRFDGWTKVMPA
LRKGDEDRILPAVNKGDAITLVELTPAQHFTKPPARFSEASLVKELEKRGIGRPSTYASIISTIQDRGYVRVENRRFY
AEKMGEIVTDRLEENFRELNYDFTAQMENSLDQVANHEAEWKAVLDHFFSDFTQQLDKAEKDPEEGGMR
PN

>d1i7da_e.10.1.1 (A:) DNA topoisomerase III {Escherichia coli}
MRLFIAEKPSLARAIADVLKPHRKGDGFIECGNGQVVTWCIGHLEQAQPDAYDSRYARWNLADLPIVPEKW
QLQPRPSVTKQLNVIKRFLHEASEIVHAGDPDREGQLLVDEVLDYLQLAPEKRQQVQRCLINDLNPQAVERAID
RLRSNSEFVPLCVSALARARADWLYGINMTRAYTILGRNAGYQGVLSGRVQTPVGLVVRRDEEINFVAKDF
FEVKAHIVTPADERFTAIWQPSEACEPYQDEEGRLLHRPLAEHVVNRIISGQPAIVTSYNDKRESESAPLPFSLAL
QIEAAKRGFLSAQNVLDCQKLYETHKLITFPRSDCRYLPEEHFAGRHAMNAISVHAPDLLPQPVVDDPDIRNRC
WDDKKVDAHHAIPTARSSAINLTENEAKVYNLIARQYLMQFCPDAVFRKCVIELDIAGKGFVAKARFLAEAGW
RTLLGSKERDEENDGTPLPVVAKGDELLCEKGEVVERQTQPPRHFTDATLLSAMTGIARFVQDKDLKKILRATDG
LGTEATRAGIIELLFKRGFLTGGRYIHSTDAGKALFHSLPEMATRPDMTAHWESVLTQISEKQCryQDFMQPLV
GTLYQLIDQAKRTPVRQFRGIVAP

>d1gkub3 e.10.1.1 (B:499-1054) Topoisomerase "domain" of reverse gyrase {Archaeon}

Archaeoglobus fulgidus}

QEFDLIKPALFIVESPTKARQISRFFGKPSVKLDGAVVYEIPMQKYVLMVTASIGHVVDLITNRGFHGVLVNGRF
VPVYASIKRCRDCGYQFTEDRESCPCKGSENVDNSRSRIEALRKLADAEFVIVGTDPTDEGEKIAWDLKNLLSG
CGAVKRAEFHEVTRRAILEALESLRVDENLVKAQVVRRIEDRWIGFVLSQLWERFNNRNLSAGRAQTLVGL
WIIDRFQESRERRKIAIVRDFDLVLEHDEEEFDLTIKVVEERELRTPLPPYTETMLSDANRILKFVQKTMQIAQE
LFENGLITYHRTDSTRVSDVGQRIAKEYLGDDFVGREWGESGAHECIRPTRPLTRDDVQRLIQEGVLVVEGLRW
EHFALYDLIFRRFMASQCQCRPKVVKKYSIEFDGKTAEEERIVRAEGRAYELYRAVWVKNELPTGTFRVKAEVKSV
PKVLPFTQSEIIQMMKERGIGRPSTYATIVDRLFMRNYVVEKYGRMIPTKLGIDVFRFLVRRYAKFVSEDRTDLE
SRMDAIERGELDYLKALEDMYAEIKSID

>d1bjt__ e.11.1.1 (-) DNA topoisomerase II, C-terminal fragment (residues 410-1202) {Baker's yeast (Saccharomyces cerevisiae)}

RKSRTNYPKLEDANKAGTKEGYKCTLVTEGDSALSLAVAGLAVVGRDYYGCYPLRGKMLNVREASADQILKNA
EIQAIIKKIMGLQHRKKYEDTKSLRYGHLMIMTDQDHGSIIKGIIINFLESSFLGLLDIQGFLLEFITPIIKVSITKPT
KNTIAFYNMMPDYEKWREEESHKFTWKQKYYKGLGTSIQAQEVREYFSNLDRLKIFHSLQGNDKDYIDLAFSKKK
ADDRKEWLRQYEPGTVDPLTLKEIPISDFINKELILFSLADNIRSIPNVLDGFKPGQRKVLYGCFKKNLKSELKVAQ
LAPYVSECTAYHHGEQSLAQTIIGLAQNFGVSNNIYLLPNGAFGTRATGGKAAAARYIYTELNKLTRKIFHPAD
DPLYKYIQEDEKTVEPEWYLPIPMILVNGAEGIGTGWSTYIPPFNPLEIKNIRHLMNDEELEQMHPFWRGWT
GTIEEIEPLRYMYGRIEQIGDNVLEITELPARTWTSTIKEYLLLGSNDKIKPWIKDMEQHDDNIKFIITLSPEE
MAKTRKIGFYERFKLISPISLMNMVAFDPHGKIKKYNNSVNEILSEFYYVRLEYQQKRKDHSERLQWEVEKYSFQ
VKFIKMIIEKELTVTNKPRAIIQLENLGFPFNKEGKPYYGSPNDEIAEQINDVKGATSDEEDEESSHEDTENV
NGPEELYGTYEYLLGMRIWSLTKERYQKLLQKQEKELENLKLSAKDIWNTDLKAFEVGYQEFLQRDAEARG

>d1ab4__ e.11.1.1 (-) DNA Gyrase A {Escherichia coli}

VGRALPDVRDGLKPVHRRVLYAMNVLGNDWNKAYKKSARVVGDVIGKYHPHGSAYVDTIVRMAQPFSRLY
MLVDGQGNFGSIDGDSAAAMRYTEIRLAKIAHELMADEKETVDFVDNYDGTEKIPDVMPTKIPNLLVNGSSG
IAVGMATNIPPHNLTEVINGCLAYIDDEDISIEGLMEHIPGPDFPTAAIINGRRGIEEAYRTGRGKVYIRARAEEVE
ETIIVHEIPYQVNKARLIEKIAELVKEKRVEGISALRDESDKDMRIVIEGEVVLNNLYSQTQLQVSFGINMVALHH
GQPKIMNLKDIIAAFVRHRREVTRRTIFELRKARDRAHILEALAVALANIDPIIELIRHAPTPAEAKTALVANPWQ
LGNVAAMLEDAARPEWLEPEFGVRDGLYYLTEQQAQAILDLRLQKLTGLEHEKLLDEYKELLDQIAELLRILGSAD
RLMEVIREEELVREQFGDKRREIT

>d1d3ya__ e.12.1.1 (A:) DNA topoisomerase IV, alpha subunit {Archaeon Methanococcus jannaschii}
QAKIFAQTTKMLEFAKQLLETDDFSTLREAYYVSKNWGEARFDDQQASNNVIEDLEAALGVLRHHLGFIPEEDG
SSVGPLKIIETPEGELVVDCTKLGTYGAINIPNDVTKLNLETDADFLAIETSGMFARLNAERFWDKHNCILVSLK
GVPARATRRFIKRLHEEHDPVLVFTDGDYGYLNIYRTLKVSGKAIHLADKLSIPAARLIGVTPQDIIDYDLPTH
LKEQDIKRIKDGKNDDFVRSFPEWQKALKQMIDMGVRAEQQSLAKYGLKVVNTYLPKIKDESTWLP

>d1dd9a__ e.13.1.1 (A:) DNA primase DnaG catalytic core {Escherichia coli}

TLYQLMDGLNTFYQQSQLQQPVATSARQYLEKRLSHEVIARFAIGFAPPWDNVLKRGFGNPENRQLIDAGM
LVTNDQGRSYDRFRERVMFPIRDKGRVIGFGRVLGNDTPKYLNSPETDIFHKGRQLYGLYEAQQDNAEPNR
LLVVEGYMDVVALAQYGINYAVASLGTTADHIQLLFRATNNVICCYDGDRAGRDAAWRALEATALPYMTDGR
QLRFMFLPDGEDPDTLVRKEGKEAFEARMEQAMPLSAFLNSLMPQVDLSTPDGRARLSTLALPLISQVPGTEL
RIYLRQELGNKLGILDDSQLE

>d1ee8a__ e.14.1.1 (A:) DNA repair protein MutM (Fpg) {Thermus thermophilus}

PELPEVETRRRLRPLVQVHDPARYRNTALAEGRRILEVDRRGKFLLFALEGGVVELVHLGMTGGFR
LEPTPHTRAALVLEGRTLYFHDPRRGRLFGVRRG DYREIPLLRLGP EPLSEAFAFPGFFRGLKESARPLKALLD
QR LAAGVGNIYADEALFRARLSPFRPARSLTEEARRLYRALREVLA EAVELGGSTLSDQS YRQPDGLPGGFQTR

HAVYGREGGLPCPACGRPVERRVAGRGTHFCPTCQGEGP

>d1i3ja_e.30.1.1 (A:) DNA-binding domain of intron endonuclease I-TevI {Bacteriophage T4}
KFCKCGVRIQTSAUTCSKCRNRSGENNSFFNHKHSITKSKEKMKGKKPSNIKKISCDGVIFDCAADAARHFKIS
SGLVTYRVKSDKWNWFYIN

>d1a31a2 e.15.1.1 (A:215-430) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment {Human (Homo sapiens)}

IKWKFLEHKGPVFAPPYEPLPENVKFYDGKVMKSPKAEEVATFFAKMLDHEYTTKEIFRKNFFKDWRKEMTN
EEKNIITNLSCDFTQMSQYFKAQTEARKQMSKEEKLKIKEENEKLLKEYGFCIMDNHKERIANFIEPPGLFRGR
GNHPKMGMKLRRIMPEDIIINCSKDAKVPSSPGHKWKEVRHDNKVTWLWSWTENIQGSIKYIMLN

>d1ois_e.15.1.1 (-) Eukaryotic DNA topoisomerase I, N-terminal DNA-binding fragment {Baker's yeast (Saccharomyces cerevisiae)}

DTIKWVTLKHNGVIFPPPYQPLPSHIKLYDGKPVLDPPQAEEVAGFFAALLESDHAKNPVFQKNFFNDFLQVLK
ESGGPLNGIEIKEFSRCDFTKMFDYFQLQKEQQKQLTSQEKKQIRLEREKFEEDYKFCELDGRREQVGNFKVEPP
DLFRGRGAHPKTGKLKRRVNPDIVNLSKDAPVPPAEGHKWGEIRHDNTVQWLAMWRENIFNSFKYVRLA
A

>d1g71a_e.16.1.1 (A:) DNA primase {Archaeon Pyrococcus furiosus}

MLMREVTKEERSEFYSKEWSAKKIPKFIVDTLESREFGFDHNNEGPSDRKNQYSDIRDLEDYIRATSPYAVYSSVA
FYENPREMEGWRAELVFDIDAKDPLKRCNHEPGTVCPICTEDAKELAKDTLILREELGFENIHVVYSGRGYHI
RILDEWALQLDSKSRSRERILAFISASEIENVEEPRFLLEKRGWFVLKHGYPRVFRLRLGYFILRVNVPHLLSIGIRRNI
AKKILDHKEEYEGFVRKAILASFPEGVGIESMAKLFALSTRFSKAYFDGRVTVDIKRILRLPSTLHSKVGLIATYVGT
KEREVMKFNPFHRAVPKFRKKEVREAYKLWRESL

>d1jeya_e.31.1.1 (A:) Ku70 subunit {Human (Homo sapiens)}

GRDSLIFLVASKAMFESQSEDELTPFDMSIQCISVYISKIISSDRDLLAVVFGTEKDKNVSNFKNIYVLQELDN
PGAKRILELDQFKGQQGQKRFQDMMGHGSDYLSLEVWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDS
AKASRARTKAGDLRDTGIFLDLMHLKKPGFDISLFYRDIISIAEDEDLRVHFESSKLEDLLRKVRAKETRKRAL
RLKLKLNKDIVISVGIVNLVQKALKPPPICKLYRETNEPVKTKRTFNTSTGGLLPSDTKRSQIYGSRQIILEKEETEEL
KRFDDPGMLMGFKPLVLLKKHYLRPSLFVYPEESLVGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPFVALVP
QEEELDDQKIQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIIVEKLRTYRSDSFENPVLQQHFRN
LEALALDLMEPEQAVDLTPKVEAMNKRLGSLVDEFKELVYPPDY

>d1jeyb_e.31.1.2 (B:) Ku80 subunit {Human (Homo sapiens)}

NKAAVVLCMDVGFTMSNSIPGIESPFEQAKKVTMFVQRQVFAENKDEIALVFGTDGTNDNPLSGGDQYQNIT
VHRHMLMPDFDLLEDIESKIQPGSQQADFLDALIVSMVDIQHETIGKKFEKRHIEIFTDLSSRFSKSQLDIIIHSLKK
CDISLQFFLPFSLGKEDGSGDRGDGPFRGGHGPSPLKGITEQQKEGLEIVKMVMISLEGEDGLDEIYSFSESLR
KLCVFKKIERHSIHWPCLRTIGSNSLIRIAAYKSILQERVKKTWVDAKTLKKEDIQKETVYCLNDDDETEVLKEDI
IQGFRYGSIDVPFSKVDDEQMKYKSEGKCFVLGFCKSSQVQRRFFMGNQVLKVFAARDDEAAVALSSLIHAL
DDLDMAIVRYAYDKRANPQVGVAFPHIKHNYECLVVQLPFMEDLRQYMFSSLKNSKKYAPTEAQLNAVDAL
IDSMSLAKKDEKTDTLEDLFPPTKIPNPRFQRLFQCLLHRALHPREPLPPIQQHIWNMLNPPAEVTTKSQIPLSKI
KTLFPLIEAKKK

>d1daaa_e.17.1.1 (A:) D-amino acid aminotransferase {Bacillus sp., strain YM-1}

GYTLWNDQIVKDEEVKIDKEDRGYQFGDGVYEVVKVYNGEMFTVNEHIDRLYASAECIRITIPYTKDKFHQLLHE
LVEKNELNTGHIYFQVTRGTSPRAHQFPENTVKPVIIGYTKENPRPLEKGVKATFVEDIRWLRCDIKSLNLLG
AVLAKQEAHEKGCYEAAILHRNNTVTEGSSSNVFGIKDGLYTHPANNMILKGITRDVVIACANEINMPVKEIPFTT
HEALKMDELFVTSTTSEITPVIEIDGKLIRDGKVGEWTRKLQKQFETKIP

>d1i1ka_e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Escherichia coli}

KADYIWNGEMVRWEDAKVHVMshalHYGTSVFEGIRCYDSHKGPVFRHREHMQLHDSAKIYRFPVSQSI
DELMEACRDVIRKNNLTSAYIRPLIFVGDMGVNPPAGYSTDVIAAFPGAYLGAEALEQGIDAMVSSWNR
AAPNTIPTAAKAGGNYLSSLVGSEARRHGYQEGLDVNGYISEGAGENLFEVKGVLFTPFTSALPGITRDA
IIKLAKELGIEVREQVLSRESLYLADEVFMMSGTAAEITPVRSDGIQVGEGRCPVTKRIQQAFFGLFTGETEDKW
GWLDQVNQ

>d1ekfa_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Human (Homo sapiens), mitochondrial}

ASSSFKAADLQLEMTQKPHKKPGPGEPLVFGKTFTDHMLMVEWNDKGWQPRIQPFQNLTHPASSLHYSL
QLFEGMIKAFKGKDQQVQLFRPWLNMDRMLRSAMRLCLPSFDKLELLECIRRLIEVDKDWPDAAGTSLYVRP
VLIGNEPSLGVSQPRRALFVILCPVGAYFPGGSVTPVSLADPAFIRAWVGGVGNYKLGGNYGPTVLVQQEALK
RGCEQVWLWYGPDHQLTEVGMNIFVYWTEDGVLELVTPLNGVILPGVVRQSLLDMAQTWGEFRVVERTI
TMKQLLRAEEGRVREVFGSGTACQVCVHRILYKDRNLHIPTMENGPELIRFQKELKEIQYGIRAHEWMFPV

>d1et0a_ e.17.1.1 (A:) Aminodeoxychorismate lyase {Escherichia coli}

MFLINGHKQESLA VSDRATQFGDGCFTTARVIDGKVSLSAHIQLQDACQRLMISCDFWPQLEQEMKTLAAE
QQNGVLVVISRSGGRRGYSTLNSGPATRILSVTAYPAHYDRLRNEGITALSPVRLGRNPHLAGIKHLNRLEQVL
IRSHLEQTNADEALVLDSEGWVTECCAANLFWRKGNVVTPLDQAGVNGIMRQFCIRLLAQSSYQLVEQAS
LEESLQADEMVICNALMPVMPVACGDVSFSATLYEYLAPLCE

>d2frvb_ e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit {Desulfovibrio gigas}
NKIVVDPITRIEGHLRIEVEVEGGKIKNAWSMSTLFRGLEMILKGRDPRDAQHFTQRACGVCTVHALASRAV
DNCVGVKIPENATLMRNLTMGAQYMHDLVHFYHLHALDWVNANALNADPAKAARLANDLSPKKTTTESI
KAVQAKVKALVESGQLGIFTNAYFLGGHPAYVLPAEVDLIATAHYLEALRVQVKAARAMAIFGAKNPHTQFTVV
GGCTNYDSLRPERIAEFRKLYKEVREFIEQVYITDLLAVAGFYKNWAGIGKTSNFLTCGEFPTEYDLNSRYTPQG
VIWGNDLSKVDDFNPDLIIEHVKSWSYEGAGAHHPYKGVTPKWTEFHGEDRYSWMKAPRYKGEAFEVGPL
ASVLVAYAKKHEPTVKAVDLVLTKLGVGPEALFSTLGRTAARGIQCLAAQEVEVWLDKLEANVKAGKDDLYTD
WQYPTESQGVGFVNAPRGMLSHTMLVQRGGKIENFQLVVPSTWNLGPRCAEGKLSAVEQALIGTPIADPKRPV
EILRTVHSYDPCIACGVH

>d1h2rl_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio vulgaris}
SSYSGPIVVDPVTRIEGHLRIEVEENGKVKNAYSSSTLFRGLEIILKGRDPRDAQHFTQRACGVCTVTHALASTRC
VDNAVGVHIPKNATYIRNLVLGAQYLHDHVHFYHLHALDFVDVTAALKADPAKAAKVASSISPRKTTAADLKAV
QDKLKTFTVETGQLGPTNAYFLGGHPAYYLDPETNLIATAHYLEALRLQVKAARAMAVFGAKNPHTQFTVVG
VTCYDALTPQRIAEEALWKETKAFVDEVYIPDLLVVAAYKDWTQYGGTDNFITFGEFPKDEYDLNSRFFKPGV
VFKRDFKNIKPFDMQIEEHVRHSWYEGAEARHPWKGQTQPKYTLHGDDDRYSWMKAPRYMGEPMETGP
LAQVLIAYSQGHPVKAVTDAVLAKLGVGPEALFSTLGRTAARGIETAVIAEYVGVMLQEYKDNIAKGDNVICAP
WEMPKQAEGVGFVNAPRGGLSHWIRIEDGKIGNFQLVVPSTWTLGPRCDKNNVSPVEASLIGTPVADAKRPV
EILRTVHSFDPICIACGVH

>d1frf1_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio fructosovorans}

TPQSTFTGPIVVDPITRIEGHLRIMVEENGKVDAWSSSQLFRGLEIILKGRDPRDAQHFTQRACGVCTVHAL
ASSRCVDDAVKVSIPANARMMRNLVMASQYLHDHVHFYHLHALDWVDVTAALKADPNKAALKAAISIDTART
GNSEKALKAVQDKLKAFVESGQLGIFTNAYFLGGHKAYYLPPENVLIATAHYLEALHMQVKAASAMAILGGKNP
HTQFTVGGCSNYQGLTKDPLANYLALSKEVCQFVNECYIPDLLAVAGFYKDWWGGIGGTSNYLAFGEFATDDSS
PEKHLATSQFPGVITGRDLGKVDNVLGAIYEDVKYSWYAPGGDGKHPYDGVTDPKYTKLDDKDHYWMKA
PRYKGKAMEVGPLARTFIAYAKGQPDKVVDMVLGKLSVPATALHSTLGRTAARGIETAIVCANMEKWIKEMA
DSGAKDNTLCAKWEPEESKGVGLADAPRGSLSHWIRIKGKKIDNFQLVVPSTWNLGPRGPQGDKSPVEEALI

GTPIADPKRPVEILRTVHAFDPCIACGVH

>d1cc1l_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfomicrobium baculatum}

VKISIDPLTRVEGHLKIEVEVKDGKVVDAKCSGGMFRGFEQILRGDRDPRDSSQIVQRICGVCPТАHCTASVMAQ
DDAFGVKVTTNGRIRTRNLIFGANYLQSHILHFYHLAALDYVKGPDVSPFVPRYANADLLTDRIKGAKADATNTY
GLNQYLKALEIRRICHEMVAMFGGRMPHVQGMVVGGATEIPTADKVAEYAARFKEVQKFVIEEYLPLIYTLGSV
YTDLFETGIGWKNVIAFGVPEDDDYKTFLKPGVYIDGKDEEFDSKLVKEYVGHSSFDHSAPGGLHYSVGETNP
NPDKPGAYSFVKAPRYKDKPCEVGPLARMWVQNPELSPVGQKLLKELYGIEAKKFRDLGDKAFSIMGRLVLA
EETWLTAVAVEKWLKVQVQGAETYVKSEIPDAAEGTGFTEAPRGALLHYLKIKDKKIENYQIVSATLWNANPRD
DMGQRGPIEEALIGVPVPDIKNPVNVGRVLRSYDPXLGCAVH

>d1e3db_ e.18.1.1 (B:) Nickel-iron hydrogenase, large subunit {Desulfovibrio desulfuricans}

TPRSNYTGPVVDPDPLTRIEGHLRIEVEVEGGVIKEARSCATLFRGIETILKGRDPRDAQHFTQRTCGVCTYTHALAS
TRCLEDAINKPIPANATYIRNLVLGNQFMHDHLVFYHLHALDFVDVTSALLADPAKAAKLANSISPRKATTEEFA
AVQAKLKTFSAGQQLPFTNAYFLGGHEGYMDPEANLVCTAHYLQALRAQVEVAKGMAVFGAKNPHTQFTV
AGGVTCYEALTPERIKQFRELYVKARAFIEEVYIPDLLVASYYKDWGKIGGTNNFMAFGEFPAPGGERDLNSRW
YKPGVIYDRKVGSVQPFDP SKIEEHVRHSWYEGKARAPFEGETNPHFTFMGDTDKYSWNKAPRYDGHAVETG
PLAQMLVAYGHNHKTIKPTIDAVLGKLN LGPEALFSTLGRTAARGIQLTVIAQQMENWLNEYENNIVDKQIVE
DYAVPTSARGVGFADVSRGGLSHWM TIEDGKIDNFQLVPTTWNLGPRDDKGVP SAAEAALVGTPVADPKRP
VEILRTIHSFDPCIACSTH

>d2frva_ e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio gigas}

KKRPSVVLHNAECTGCSESVLRTVDPYVDELILDVISMDYHETLMAGAGHAVEEALHEAIKGDFVCVIEGGIP
MGDGGYWGKVGGGRNMYDICAEVAPKAKAVIAIGTCATYGGVQA AKPNPTGTVGVNEALGKLGVKAINIAGC
PPNPMNFVGTVVHLLTKGMPELDKQGRPVMF GETVHDNCPRLKHF EAGEFATSFGSPEAKKGYCLYELGCKG
PDTYNNCPKQLFNQVNWPVQAGHPCIACSEPNFWDLYSPFYSA

>d1h2rs_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfovibrio vulgaris}

LMGPRRPSVVLHNAECTGCSESVLRAFEPYIDLTLIDTLS DYHETIMAAAGDAAEALEQAVNSPHGFI AVVE
GGIPTAANGIYGKVANHTMDICSRLPKAQAVIAYGTCATFGGVQA AKPNPTGAKGVNDALKHLGVKAINIAG
CPPNPYNLVGTIVYYLKNKAPELDSLNRPTMFFQTVHEQCPRLP HDAGEFAPSFESEEARKGWCLYELGCK
GPVTMNNCPKIKFNQTNWPDAGHPCIGCSEPDFWDAMTPFYQN

>d1frfs_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfovibrio fructosovorans}

KHRPSVVLHNAECTGCTEAIRTIKPYIDALILD TISLDYQETIMAAAGETSEAALHEALEGKDGYYLVEGGIP
TIDGGQWGMVAGHPMIETCKKAAAKAKGIIICGTCSPYGGVQAKPNPSQAKGVSEALGVKTINIPGCPPNPI
NFVGAVVHVLTKGIPDLDENG RPKLFY GELVHDNCPRLP HFEASEFAPSFDSEEAKKGFC LYELGCKGPV TYN NC
PKVLFNQVNWPVQAGHPCIGCSEPDFWDAMTPFYEQG

>d1cc1s_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfomicrobium baculatum}

KKAPVIWVQGQGCTGCSVLLNAVHPRIKEI LLDV ISLEFHPTVMASEGEMALAHMYEIAEKFNGNFFLLVEGAI
PTAKEGRYCI VGETLDAKHHHEVTMMELIRDLAPKSLATVAVGTC SAYGGIPAAEGNVTGSKSRDFFADEKIE
KLLNVPGCPPHPDW MVGTLVAAWSHVLPNTEHPLPELDDDRPLFFGDNIHENCPYLDKYDNSEFAETFTK
PGCKAELGCKGPSTYADCAKRRWNNGINWCVENAVCIGC VEPDFPDGKSPFYVAE

>d1e3da_ e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio desulfuricans}

SRPSVVLHAAECTGCSEALLRTYQPFIDLTLILDTISLDYHETIMAAAGEAAEALQAAVNGPDGFICLVEGAIPGMDNKYGYIAGHTMYDICKNILPKAKAVSIGTCACYGGIQAACKNPTAAKGINDCYADLGVKAINVPGCPPNPLNMVGTLVAFLKGQKIELDEVGRPVMFQGSVHDLCKHFAGEFAPSFNSEEARKGWCLYDVGCKGPETYNNCPKVLNETNWVPAAGHPCIGCSEPNFWDDMTPFYQN

>d1dg4a_e.20.1.1 (A:) DnaK {Escherichia coli}

LSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKSLGQFNLDGINPAPRGM
PQIEVTFDIDADGILHVSADKDKNSGEQKITIKASSGL

>d1dkza_e.20.1.1 (A:) DnaK {Escherichia coli}

VLLLDVTPLSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVIHVLQGERKRAADNKSLGQFNLDGIN
PAPRGMPQIEVTFDIDADGILHVSADKDKNSGEQKITIKASSGLNEDEIQKMRDAEANAEADRKFELVQTRN
QGDHLLHSTRKQVEEAGDKLPADDKTAIESALTALETALKGEDKAAIEAKMQELAQVSQKLMEIAQ

>d2bpr_e.20.1.1 (-) DnaK {Escherichia coli}

SIEGRVKDVLLDVTPSLGIETMGGVMTTLIAKNTTIPTKHSQVFSTAEDNQSAVTIHVLQGERKRAADNKSLG
QFNLDGINPAPRGMPQIEVTFDIDADGILHVSADKDKNSGEQKITIKASSGLNEDEIQKMRDAEANAEADRKF
EELVQTRNQGDHLLHSTRKQVEEA

>d1ckra_e.20.1.1 (A:) DnaK {Rat (Rattus norvegicus)}

SENVQDLLLDVTPLSLGIETAGGVMTVLIKRNNTIPTKQTQFTTYSDNQPGVLIQVYEGERAMTKDNNLLGKF
ELTGIPPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKENKITITNDKGRSKEDIERMVQEAEKYKAEDEKQRDK
VSSKNSLE

>d1dqsa_e.22.1.1 (A:) Dehydroquinate synthase, DHQS {Aspergillus nidulans}

PTKISILGRESIIADFGLWRNYVAKDLISDCSSTTYVLVTDTNIGSIYTPSFEEAFRKRAAEITPSPRLLIYNRPPGEVS
KSRQTAKADIEDWMLSQNPPCGRDTVIALGGGVIGDLTFVASTYMRGVRYVQVPTTLLAMVDSSIGGKTAID
TPLGKNLIGAIWQPTKIYIDLEFLETLPVREFINGMAEVIKTAASSEEFTALEENAETILKAVRREVTPEHRFEG
TEEILKARILASARHKAYVVSADEREGGLRNLLNWGHSGIGHAIEALTPQILHGECVAIGMVKEAELARHLGILKG
VAVSRIVKCLAAYGLPTSLKDARIRKLTAGKHCSVDDQLMFNMALDKNDGPKKKIVLLSAIGTPYETRASVVANE
DIRVVL

>d1jq5a_e.22.1.2 (A:) Glycerol dehydrogenase {Bacillus stearothermophilus}
AAERVFISPACYVQGKVNITKIANYLEGIGNKTVVIADEIVWKIAGHTIVNELKGNIAAEVVFSGEASRNEVERI
ANIARKAEAAIVGVGGKTLDTAKAVADELDAYIVIVPTAASTDAPTSALSVIYSDDGVFESYRFYKKNPDLVLVD
TKIIANAPPRLLASGIADALATWVEARSVIKSGGKTMAGGIPTAAEAIAEKCEQTLFKYGLAYESVKAKVVTPAL
EAVVEANTLLSGLGFESEGGLAAAHAIHNGFTALEGIEIHLTHGEKVAFTLVQLALEEHSQQEIERYIELYLCLDLP
VTLEDIKLDASREDILKVAKATAAEGETIHNAFNTADDVADAIFAADQYAKAYKEK

>d1kq3a_e.22.1.2 (A:) Glycerol dehydrogenase {Thermotoga maritima, TM0423}

HMITTTIFPGRYVQGAGAINILEEELSRFGERAFVVIDDFVDKNVLGENFFSSFTKVRVNQKIFGGECSDDEIERLS
GLVEEETDVGIGGGKTLDTAKAVAYKLKKPVIVPTIASTDAPCSALSVIYTPNGEFKRYLFLPRNPDVVLVDTE
IVAKAPARFLVAGMGDALATWFEAESCKQKYAPNMTGRLGSMTAYALARLCYTLLEYGVLAQRSVEEKSVTPAL
EKIVEANTLLSGLGFESEGGLAAAHAIHNGLTVELENTHKLHGKVAIGVLASLFLTDKPRKMIEEVYSFCEEGLPT
TЛАЕИGLGVSDEDLMKVAEKACDKNETIHNEPQPVTSKDVFFALKAADRYGRMRKNL

>d1lci_e.23.1.1 (-) Luciferase {Firefly (Photinus pyralis)}

AKNIKKGPAPFYPLEDTAGEQLHKAMKRYALVPGTIAFTDAHIEVNITYAEYFEMSVRLAEAMKRYGLNTNHRI
VVCENSLQFFMPVLGALFIGVAVAPANDIYNERELLNSMNISQPTVVFVSKKGLQKILNVQKKLPIIQKIIIMDSK
TDYQGFQSMYTFVTSHLPPGFNEYDFVPEFDRDKTIALIMNSSGSTGLPKGVALPHRTACVRFSHARDPIFGN
QIIPDTAILSVPFHHFGFMFTLGYLICGFRVVLMYRFEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSN
LHEIASGGAPLSKEVGEAVAKRFHLPGIRQGYGLTETTSAILITPEGDDKPGAVGKVVPFFEAJVVDLDTGKTLGV

NQRGELCVRGPMIMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFFIVDRLKSLIKYKGYQVAPAELESIL
LQHPNIFDAGVAGLPDDDAHELPAAVVLEHGKTMEKEIVDYVASQVTAKLRGGVVFVDEVPKGLTGKLD
ARKIREILIKAKK

>d1amua_e.23.1.1 (A:) Phenylalanine activating domain of gramicidin synthetase 1 {Bacillus brevis}
GTHEEEQYLFAVNNTKAEPYPRDKTIHQLFEEQVSKRPNNAIVCENEQLTYHELNVKANQLARIEKGIGKDTLV
GIMMEKSIDLFIGILAVLKAGGAYVPIDIEYPKERIQYILDDSQARMLLTQKHLVHLIHNIQFNGQVEIFEEDTIKIR
EGTNLHVPSKSTDLAYVIYTSGGTGNPKGTMLEHKGISNLKVFFENSLNTEKDRIGQFASISFDASVWEMFMA
LLTGASLYIILKDTINDFKFEQYINQKEITVITLPPTYVVHLDPERILSIQLTAGSATSPSLVWKKEVTVYINAYGP
TETTICATTWVATKETIGHSPVPIGAPIQNTQIYIVDENIQLKSVGEAGELCIGGEGLARGYWKRELTSQLKFVDNP
FVPGEKLYKTGDQARWLSDGNIEYLGRIDNQVKIRGHRVELEEVESILLKHMVYISETAVSVHKDHQECPYLCAYF
VSEKHIPLEQLRQFSSEELPTYMIPSYFIQLDKMPLTSNGKIDRKQLPEPDLT

>d1ad2_e.24.1.1 (-) Ribosomal protein L1 {Thermus thermophilus}
KRYRALLEKVDPNKIYTIDEAAHLVKELATAKFDDETVEVHAKLGIDPRRSQNVRGTVSLPHGLGKQVRVLIAIKG
EKIKEAEEAGADYVGEEIIQKILDGWMDFDAVVATPDVMGAVGSKLGRILGPRGLLPNPKAGTVGFNIGEIIRE
IKAGRIEFRNDKTGAIHAPVGKACFPPEKLAQNRAFIRALEAHKPEGAKGTFRSVYVTTMGPSVRINPHS

>d1cjsa_e.24.1.1 (A:) Ribosomal protein L1 {Archaeon Methanococcus jannaschii}
MDREALLQAVKEARELAKPRNFTQSFEFIATLKEIDMRKPENRIKTEVVLPHGRGKEAKIAVIGTGDLAKQAEL
GLTVIRKEEIEELGKNKRKLRKIAKAHDFFIAQADLMPLIGRYMGVILGPRGKMPKPVPANANIKPLVERLKKTVV
INTRDKPYFQVLVGNEMKMTDEQIVDNIEAVLNVVAKYEKGLYHIKDAYVKLTMGPAVKVKK

>d1dwua_e.24.1.1 (A:) Ribosomal protein L1 {Archaeon Methanococcus thermolithotrophicus}
MDRENILKAVKEARSLAKPRNFTQSLDLIINLKELDLRPENRLKEQVVLPGNGRKEPKIAVIKGDLAAQAEEM
GLTVIRQDEEELGKNKKMAKKIANEHdffIAQADMMPLVGKTLGPVLGPRGKMPQPVPANANLTPLVERLKK
TVLINTRDKPLFHVLVGNEMKMSDEELAENIEAILNTVSRKYEKGLYHVKSAYTKLTMGPPAQIEK

>d1dn1a_e.25.1.1 (A:) Neuronal Sec1, NSec1 {Rat (Rattus norvegicus)}
IGLKAVVGEKIMHDVIKKVKKGEWKVLVVDQLSMRMLSSCCKMTDIMTEGITIVEDINKRREPLPSLEAVYLIT
PSEKSVHSLISDFKDPPATAKYRAAHVFTDSCPDALFNELVKSRAAKVIKLTENIAFLPYESQVYSLSDASFQSF
YSPHKAQMKNPLIERLAEQIATLCATLKEYPAVRYRGEYKDNLALLAQLIQDKLDAYKADDPTMGEGPDKARSQL
LILDRGFDPSSPVHLHETFQAMSYDLLPIENDVYKYETSGIGEARVKEVLLDEDLLWIALRHKHIAEVSQEVTRS
LKDFSSSKRMNTGEKTTMRDLSQMLKKMPQYQKELSKYSTHLHLAEDCMKHYQGTVDKLCRVEQDLAMGTD
AEGEKIKDPMRAIVPILLDANVSTYDKIRIILLYIFLKNGITEENLNKLIQHAQIPPDEIITNMAHLGPIVTDSTLR
RRSKPERKERISEQTYQLSRWTPIKDIIMEDTIEDKLDTKHYPYISTRSSASFSTTAVSARYGHWHKNKAPGEYRS
GPRLIIFLGGVSLNEMRCAYEVQTANGKWEVLIGSTHILTPQKLLDTLKKLNKTDEEI

>d1epua_e.25.1.1 (A:) Neuronal Sec1, NSec1 {Longfin inshore squid (Loligo pealei)}
ALKTAVHEKIMNDVVLAVKKNAEWKVLIVDQLSMRMRVSACCKMHEIMSEGITLVEDINRRREPLPLEAVYLIT
PTEESVKCLMADFQNPDPNPQYRGAHIFFTEACPEELFKELCKSTTARFIKTLKEINIAFLPYESQIFSLDSPDTFQVY
YNPSRAQGGIPNKERCAEQIATLCATLGEYPSVRYRSDFDENASFAQLQQKLDAYRADDPMTGEGPQKDRSQ
LILDRGFDPISPLLHETFQAMAYDLLPIENDVYKYVNTGGNEVPEKEVLLDEKDDLWEMRHQHIAVVSQNV
TKKLKQFADEKRMGTAADKAGIKDLSQMLKKMPQYQKELSKYSTHLHLAEDCMKQYQQHVDKLCVSEQDLA
MGTDADGEKIRDHMRNIVPILLDQKISAYDKIRIILLYIHKGIGISEENLAKLVQHAHIPAEEKWIINDMQNLGVPII
QDGGRRKIPQPYHTHNRKERQADHTYQMSRWTPYMKDIMEAAVEDKLDRHYPFLNGGPRPSCQQPVSV
RYGHWHKDKGQASYKSGPRLIIFVVGGSYSEMRSAYEVTTAKNNWEVILGSTHILTPGLLRDLRKISNP

>d1e2ua_e.26.1.1 (A:) Hybrid cluster protein (prismane protein) {Desulfovibrio vulgaris}
MFCFQCQETAKNTGCTVKGMCGKPEETANLQDLLIFVLRGIAIYGEKLKELGQPDRSNDDFVLQGLFATITNAN
WDDARFEAMISEGLARRDKLRNAFLAVYKAKNGKDFSEPLPEAATWTGDSTAFAEKAKSVGILATESEDVRSR

ELLIIGLKGVAAYAEHAAVLGFRKTEIDEFMLEALASTKDLVDEMVALVMKAGGMATTMALLDEANTTYG
NPEITQVNIGVGKNPGILISGHDLKDMAELLKQTEGTGVYTHGEMLPANYPAFKKYPHFGNYGGSWWQ
QNPEFESFNGPILLTNCLVPLKKENTYLDRLYTTGVVGYEGAKHIADRPAGGAOKDFSALIAQAKKCPPPVEIETG
SIVGGFAHHQVLALADKVVEAVKSGAIKRFFVMAGCDGRQKSRSYYTEVAENLPKDTVILTAGCAKYRYNKLNL
GDIGGIPRVLADAGQCNDSYSLAVIALKLKEVFLGDDINDLPVSYDIAWYEQKAVAVLLALLFLGVKGIRLGPTLAF
LSPNVAKVLVENFNPIGTVQDDIAAMMAGK

>d1jjya_ e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase {Carboxydothermus hydrogenoformans}

QLNKSTDRAVQQMLDKAKREGIQTVWDRYEAMKPQCGFGETGLCCRHCLQGPCRINPFGDEPKVGICGATAE
VIVARGLDRSIAAGAAGHSGHAKHLAHTLKKAVQGKAASYMIKDRKLHSIAKRLGIPTEGQKDEDIALEVAKAA
LADFHEKDTPVLWTTVLPPSRVKVLSAHGLIPAGIDHEIAEIMHRTSMGCDADAQNLLGGRLRCSLADLAGCY
MGTDLADILFGTPAPVVTESNLGVLKADAVNVAVGHNPVLSDIIVSVKEMENEARAAGATGINVVGICCTG
NEVLMRHGIPACTHSVSQEMAMITGALDAMILDYQCIQPSVATIAECTGTTVITMEMSKITGATHVNFAEEAA
VENAKQILRLAIDTFKRRKGKPVEIPNIKTVVAGFSTEAIINALSKLNANDPLKPLIDNVVNGNIRGVCLFAGCNN
VKVPQDQNFTTIARKLLQNVLVATGCGAGALMRHGFMDPANVDELCGDGLKAVLTAIGEANGLGGPLPPV
LHMGSVDNSRSVALVAALANRLGVDMDRPVVASAAQAMHEKAVAIGTWAVTIGLPTHIGVFPPITGSLPVT
QILTSSVKDITGGYFIVELDPQVAADKLLAINERRAGLGLPR

>d1jqka_ e.26.1.2 (A:) Ni-containing carbon monoxide dehydrogenase {Rhodospirillum rubrum}
ETAWHRYEKQQPQCGFGSAGLCCRICLKGPCRIDPFGECPKYGVCAGARDTIVARHLVRMIAAGTAAHSEHGR
HIALAMQHISQGEIHDYSIRDEAKLYIAIKTLGVATEGRGLLAIVGDLAAITLGDFQNQDYDKPCAHLAASLTPR
RVKRLGDLGLLPHNIDASVAQTMSRTHVGCDADPTNLILGGLRVAMADLDGSMLATELSDALFGTPQPVSAA
NLGVMKRGAVNIAVNGHNPMSDLIIDCVAADLRDEAIAAGAAEGINIIGCCTGHEVMMRHGVPALTNYLSQE
LPILTGALEAMVVVDVQCIMPSLPRIAECFHTQIITTDKHNKISGATHVPFDEHKAVETAKTIIRMAIAAFGRDPN
RVAIPAFKQKSIVGSAEAVVAALAKVNADDPLKPLVDNVVNGNIQGIVLFVGCNTTKVQQDSAYVDAKSLAK
RNVLVLATGCAAGAFAKAGLMTSEATTQYAGEGLKGVLSAIGTAAGLGGPLPLVMHMGSVDNSRAVALATAL
ANKLGVDLSDLPLVASAECMSEKALAIGSWAVTIGLPTHVGSPVPIGSQIVTKLTETAKDLVGGYFIVDTDPK
SAGDKLYAAIQERRAGL

>d1h5wa_ e.27.1.1 (A:) Upper collar protein gp10 (connector protein) {Bacteriophage PHI29}
RQKRNRFIHYLNLYQLFEWENLPPINPSFLEKSIHQFGYVGFYKDPVISYIACNGALSGQRDVYNQAT
VFRAASPVYQKEFKLYNYRDMKEEDMGVVIYNNDMAFPPTPTLELFAELKEIISVNQNAQKTPVLRAND
NNQLSLKQVYNQYEGNAPVIFAHEALDSDSIEVFKDAPYVVDKLNQNAQKNAVWNEMMTFLGIKNANLEKKER
MVTDEVSSNDEQIESSGTFLKSREEACEKINELYGLNVKVKFRYDI

>d1io1a_ e.32.1.1 (A:) F41 fragment of flagellin {Salmonella typhimurium}
NIKGLTQASRNANDGISAQTTEGALNEINNNLQRVRELAVQSANSTNSQSDLSDIQAETQRLNEIDRVSGQTQ
FNGVKVLAQDNTLTIQVGANDGETIDIDLQINSQTLGLDTLNQQKVKVSDTAATVTGYADTTIALDNSTFKAS
ATGLGGTDQKIDGDLKFDDTTGKYYAKVTGVTGGTGKDGYYEVSDKTNGEVTAGGATPLTGGPATATEDVK
NVQVANADLTEAKAALTAAGVTGTASVVKMSYTDNNNGKTIDGGLAVKVGDDYYSATQNKGDSISINTTKYTAD
DGTSKTAJNKGADGKTEVVSIGGKTYAASKAEGHNFKAQPDLAEEAATTENPLQKIDAALAQVDTLRSDEA
AVQNRFNSAITNLGNTVNNLTSAR

>d1htya_ e.33.1.1 (A:) Golgi alpha-mannosidase II {Fruit fly (Drosophila melanogaster)}

CQDVVQDVPNVDQMLEYDRMSFKDIDGGVWKQGWNIKYDPLKYNAAHHKLKVFPVPHSHNDPGWIQTF
EEYYQHDTKHILSNALRHLHDNPEMKFIWAIESYFARFYHDLGENKKLQMKSIKNGQLEFVTGGWVMPDEA
NSHWRNVLLQLTEGQTWLKQFMNVTPPTASWAIDPFGHSPTMPYILQKSGFKNMLIQRTHYSVKKELAQQRQ

LEFLWRQIWWDNKGD TALFTHMMPFYSYDIPHTCGPPDKVCCQFDKRMGSFGLSCPWKVPPRTISDQNVAARSDLLVDQWKKKAELYRTNVLLIPLGDDFRFKQNTEWDVQRVNYERLFEHINSQAHFNVQAQFGTLQEYFDAVHQAERAGQAEFTLSGDFFTYADRSNDYWGGYTSRPYHKRMDRVLHYVRAAEMLSAWHSWDGMARIEERLEQARRELSLFQHHDGITGTAKTHVVVDYEQRQMQUEALKACQMVMQQSVYRLTKPSIYSPDFSF SYFTLDDS RWP GSGVEDSRTTILGEDILPSKH VVMHNTLPHREQLVDFYVSSPFVSVTDLANNPVEAQVSPVWSWHDTLT KTIHPQGSTTKYRIIFKARVPPMGLATYVLTISDSKPEHTSYASNLLRK NPTSLPLGQYPEDVKFGDPREISLRVGNGPTLAFSEQGLLKS IQL TDSPHVPVHF KFLKYGVRS HGDRSGAYLF LPNGPASPVELGQPVVLTKGKLES SVSVGLPSV VHQTIMRGGAPEIRNL DIGSLDNTEIVMRLETHIDSGDIFYDLNGLQFIKRRRLDKPLQANYYP IPSGMFIEDANTRLLTGQPLGGSSLASGELEIMQD RRLAS DDERGLGQGVLDNKPVLHIYRLVLEKVN NCVRPSKLHPAGYLTSAAHKASQSLLDPLDKFIFAENEWIGAQGQFGGDHPSAREDLDVSMRRLTKSSAKTQRVGYVHLRTNLMQCGTPEEHTQKLDVCHLPNVARCERTTLTFLQNLEHLDGMVAPEVCPMETAAYVSSHS

>d1knza_e.34.1.1 (A:) NSP3 homodimer {Simian 11 rotavirus}

TQQMAVSIINSSFEAAVVAATSALENMGIEYDYQDIYSRVKNKFDFVMDDSGVKNNPIGKAITIDQALNNKFGSAIRNRNWLA DTSRPAKLD EDVNKL RMM LSSKG IDQKMRVLNACFSVKRIPGKSSIIKCTKLMRD KLERGEVEV DDSFVDEKM

>g1jmu.1 e.35.1.1 (A;B:) Membrane penetration protein mu1 {Reovirus}

TINVTDGDNVFKPSAETSS TAVPSL SLPGMLNXPGGPWIAIGDETSVTSPGALRRMTSKDIPETAIINTD NSSGAVPSESALVPYNEPLVVVTEHAIANFTKAEMALEFNREFL DKL RVL SVSPK YSD LLTVDCYVGVSARQALNN FQKQVPVITPTRQTMVVD SIQ AALKALEKWEIDL RVAQ TL PTN VPIGEVSCPMQSVV KL DDQLP DDSL RRYPK EAAVALAKRNGGIQWMDVSEGTVMNEAVNAVASALAPSASAPPLEKS KLT EQAMDLVTAAEPEIIASLVP VPAPVFAIPPKPADYNVRTLKIDEATWLRMIPKTMGTLFQIQVTDNTGTNWHFNLRGGRV VNLDQIAPMRF VLDLGGKSYKETSWDPNGKKVGFIVFQSKIPFELWTAASQIGQATVNVYVQLYAEDSSFTAQSIIATTSLAYNYEP EQLNKT DPEM NY YLLATFDSA ITPTN M T QPDV W D ALLT M S PLS A G E VTVKGAVVSEV PAELIGSYTPESLN ASLPNDAARCMIDRASKIAEA KIDDDAGPDEYSPNSVPIQGQLAISQLETGYGVRIFNPKGILSKIASRAMQAFI GDPSTIITQAAPVLSDKNNWIALAQGVKTS LRTK SLSAGVKTAVSKLSS SESI QNWTQGFLDKVSTHFPAP

>d2btva_e.28.1.1 (A:) BTV inner layer core protein vp3 {Bluetongue virus, strain 1}

VDFTVPDVQQIQLDIKALAAEQVYKIVKVPSTSFRHIVTQSRDRVL RVDTYYEEMSQVGDVITEDEPEKFYSTI I KK VR FIRGKGSFILHDIPARDHRGMEVAEPEVLGV EFKNVL PVLA EH RAMI QNAL DGS IIENG NVAT RDV D VFIGA CSEPIYR IYNRLQGYIEAVQLQELRNSIGWLERLGQRKRITYSQEV LTD FRR QDM I WVL ALQLPVNPQV VWDVP RSSIANLIMNIATCLPTGEYIAPNPRISSITLTQ RIT TGPF ALT G SPTA QQLNDVRK IYLA LMFP GQI IL DLK IDPG ERMDPAVRMVAGVVGHLLTAGGRFTNL TQN MARQL DIALNDYLLYMYNTRVQVNYGPTGEPLDFQIGRNQ YDCNVFRADFTGTGNGWATIDVEYRDPAPVHAQRYIRYCIDSRE INPTTYGIGMTYHCYNEMLRLMVA AGKDSEAAYFRSMLPFHMVR FARINQI INEDLHSVFSLPDDMFNALLPDLIAGAHQNA DPV VLDV SWISLWFA FNRSFEPTHR NEMLEIAPILESVYASELSVMK VDMRHLSLMQRRFPDVL IQARPSHFWKAVL ND SPEAKAVM NLSHSHNFINIRDMMRWVLLPSLQPSLKVLEEEAWAAANDFEDML LTDQV YMHRDMLPEP RL DIERFRQE GFYYTNM LEAPPEIDRVVQYT EYIARLQANMGQFRAALRRIMDDDDWVRFGGV LRTV RKFFDARPPD DILQ GLPFSYDTNEKGGLSYATIKYATETTIFYLIYNVEFSNTPDSLVLINPTYTMTKV FINKRIVERVRVGQILA VLN RRFV AYKGKMRIMDITQSLKMGTKLAAPTV

>d1cola_f.1.1.1 (A:) Colicin A {Escherichia coli}

AKDERELLEKTS ELIAGMGDKIGEHLGD KYKAIK DIADNIK NFQGK TIRS FDDA MASLN KITANPAMKINKADR DALVNAWKHVDAQDMANKLGNL SKAF KVADV VMK VEK VREKSIEGYETGNWG PLM LEVESWVLSGIASSVALGIFSATLGAYALSLGVPAIAVGIAGILLAAVVGALIDDKFADALNNEIIR

>d1a87_f.1.1.1 (-) Colicin N {Escherichia coli}

SAKVGEITITPDNSKPGRYISSNPEY SLLAKLIDAESIKGTEVYTFHTRKGQYVKTVPDSNIDKMRV DYV NWKGP

KYNNKLVKRFVSQFLLFRKEEKEKNEKEALLKASELVMGDKLGEYLGVKYKNVAKEVANDIKNFHGRNIRSYN
EAMASLNKVLANPKMKVNKSDKDAIVNAWKQVNAKDMANKIGNLGKAFKVADLAIKVEKIREKSIEGYNTGN
WGPLLVEVESIIGGVVAGVAISLFGAVLSFLPISGLAVTALGVIGIMTISYLSSFIDANRVSNIINNISSVIR
>d1cii_1 f.1.1.1 (451-624) Colicin Ia {Escherichia coli}
DAINFTEFLKSVEKYGAKAEQLAREMAGQAKGKKIRNVEEALKTYEKYRADINKKINAKDRAAIAAALESVKLS
DISSNLNRFSRGLGYAGKFTSLADWITEFGKAVRTENWRPLFVKTETIIAGNAATALVALVFSILTGSALGIIGYGLL
MAVTGALIDESLVEKANKFW
>d1f0la3 f.1.2.1 (A:201-380) Diphtheria toxin, middle domain {Corynebacterium diphtheriae}
CINLDWDVIRDKTCKIESLKEHGPIKNKMSESPNKTSEEKAKQYLEEFHQTALEHPSELKTVGTNPVFAGA
NYAAWAVNVAQVIDSETADNLEKTTAALSILPGIGSVMGIADGAVHHNTEEIVAQSIALSSLMVAQAIPLVGELV
DIGFAAYNFVESIINLFQVVHNSYNRPAY
>d1dlc_3 f.1.3.1 (61-289) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis tenebrionis, CRYIIIA (BT13)}
TTKDVIQKGISVVGDLGVGFPFGALVSFYTNFLNTIWPSEDPWKAFCMEQVEALMDQKIADYAKNKALAE
QGLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFRNSMPSFAISGYEVFLTTYAQAAANTHLFL
LKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYTDHCVKWNVGLDKLRGSSYESWVNFRREMTLTVLDLIA
LFPLYDVR
>d1ji6a3 f.1.3.1 (A:64-290) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis, CRY3bb1}
DAVGTGISVVGQILGVVGVPFAGALTSFYQSFLNTIWP\$ADPWKAFCMAQVEVLIDKKIEEYAKSKALAEQGL
QNNFEDYVNALNSWKTPSLRSKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLKDA
QVFGEEWGYSSEDVAEFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNFRREMTLTVLDLIVL
PFYDIR
>d1ciy_3 f.1.3.1 (33-255) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis, CRYIA (A)}
YTPIDISLTLQFLLSEFVPGAGFVLVDIIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYA
ESFREWEADPTNPALREEMRIQFNMDMSNALTATPLAVQNYQVPLLSVYVQAANLHSVLRDVSFGQRWGF
DAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELTDTVLDIVALFSNYDSRRY
>d1i5pa3 f.1.3.1 (A:1-263) delta-Endotoxin (insecticide), N-terminal domain {Bacillus thuringiensis subsp. kurstaki, CRY2AA}
MNNVLNSGRTTICDAYNVVAHDPSFEHKSLDTIQKEWMEMWKRTDHSLYAPVVGTVSSFLKKVGSLIGKRIL
SELWGIIFPSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELIGLQANIREFNQQVDNFLNPTQNPVPLSITSS
VNTMQLFLNRLPQFQIQGYQLLLPLFAQANMHLSFIRDVILNADEWGISAATLRTYRDYLRYTRDYSNYCI
NTYQTAFRGLNTRLHDMILEFRTYMFLNVFEYVSIWSLFK
>d1g5ma_ f.1.4.1 (A:) Bcl-2 {Human (Homo sapiens)}
HAGRTGYDNREIVMKYIHYKLSQRGYEW DAGDDVEENRTAPEGTESEVHLALRQAGDDFSRRYRGDFAE
SSQLHLPTFTARGFATVVEELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRLH
WIQDNGGWDAFVELYGPSMR
>d1bxla_ f.1.4.1 (A:) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}
MSMAMSQSNRELVVDFLSYKLSQKGYSWSQFSDVEENRTAPEGTESEAVKQALREAGDEFELRYRRAFSDLT
SQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFEFGGVMCVESVNREMSPLVDNIALWMTEYLNRLH
QENGGWDTFVELYGNAAAESRKQERLEHHHHHH
>d1lxl_ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSMAMSNRELVDFLSYKLSQKGYSWSQFSDEENRTEAPEGTESEMTPSAINGNPSWHLADSPAVNG
ATGHSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIV
AFFSGGALCVESVDKEMQVLVSRIAAMATYLNDHLEPWIQENGWDTFVELYGNAAAESRKGQERLEH
HHHHH

>d1maz_ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSQSNRELVDFLSYKLSQKGYSWSQFSDEENRTEAPEGTESEMTPSAINGNPSWHLADSPAVNGATGHSS
SLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVVNELFRDGVNWGRIVAFFSFG
GALCVESVDKEMQVLVSRIAAMATYLNDHLEPWIQENGWDTFVELY

>d2bida_ f.1.4.1 (A:) Proapoptotic molecule Bid {Human (Homo sapiens)}

GSMDCEVNNGSSLRDECITNLLVFGFLQSCSDNSFRRELDALGHELPVLAPQWEGYDELQTDGNRSSHSRLGRI
EADSESQEDIIRNIARHLAQVGDSMDRSIPPGLVNGLALQLRNTSRSEEDRNRLATALEQLLQAYPRDMEKEKT
MLVLALLLAKKVASHTPSLLRDVFHTTVNFINQNLRTYVRSLARNGMD

>d1ddba_ f.1.4.1 (A:) Proapoptotic molecule Bid {Mouse (Mus musculus)}

MDSEVSNGSGLGAKHTDLLVFGFLQSSGCTRQELEVGLGRELPVQAYWEADLEDELQTDGSQASRSFNQGRIEP
DSSEQEEIHNIARHQAQIGDEMHDHNIQPTLVRQLAAQFMNGSLSSEEDKRNCALAKALDEVKTAFPRDMENDKA
MLIMTMALLAKKVASHAPSLLRDVFHTTVNFINQNLFSYVRNLVRNEMD

>d1f16a_ f.1.4.1 (A:) Proapoptotic molecule Bax {Human (Homo sapiens)}

MDGSGEQPRGGGPTSSEQIMKTGALLLQGFIQDRAGRMGGEAPELALDPVPQDASTKLSECLKRIGDELDS
NMELQRMIAAVDTDSPREVFFRVAADMFSDDGNFNWGRVVALFYFASKLVLKALCTKVPTELRTIMGWTLDL
ERLLGWIQDQGGWDGLLSYFGPTWQVTIFVAGVLTASLTIKKMG

>d1ikpa3 f.1.5.1 (A:252-394) Exotoxin A, middle domain {Pseudomonas aeruginosa}

EGGSLAALTAAHQACHLPLETFTRHRQPRGAEQLEQCQGPVQRLVALYLAARLSWNQVDQVIRNALASPGSGGD
LGEAIREQPEQARLALTAAAESERFVRQGTGNDEAGAANADVSLTCPVAAGECAGPADSGDALLERNY

>d1c3wa_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIWLALGTALMGLTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLGYGLTMVPFGGEQNPI
YWARYADWLFTPLLLDLALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYRFVWWAISTAAMLYILYVLFF
GFSMRPEVASTFKVLRNVTVVLWSAYPVWLGSEGAGIVPLNIETLLFMVLDVSAKVGFLILLRSRAIFG

>d1c8sa_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIWLALGTALMGLTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLGYGLTMVPFGGEQNPI
YWARYADWLFTPLLLNLALLVDADQGTILALVGADGIMIGTGLVGALTKVYSYRFVWWAISTAAMLYILYVLFF
NVTVVLWSAYPVWLGSEGAGIVPLNIETLLFMVLDVSAKVGFL

>d1e12a_ f.2.1.1 (A:) Halorhodopsin {Halobacterium salinarum}

RENALLSSSLWVNVALAGIAILVFVYMGRTIRPGRPRIWGATLMIPVSISYLGLLSGLTGMIEMPAGHALAG
EMVRSQWGRYLTWALSTPMILLALGLLADVDLGLSLFTVIAADIGMCVTGLAAAMTTSALLFRWAFYAISCAFFV
VVLSALVTDWAASASSAGTAEIFTLRVLTVVLWLGYPIVWAVGVEGLALVQSGATSWAYSVLDVFAKYVFAFI
LLRWVANNERTVAV

>d1h68a_ f.2.1.1 (A:) Sensory rhodopsin II {Natronobacterium pharaonis}

VGLTTLFWLGAIGMLVGTLAGFAWAGR DAGSGERRYYVTLVGISGIAAVAYVVMALGVGVWPVAERTVFAPRYI
DWILTTPLIVYFLGLLAGLDSREFGIVITLNTVVMLAGFAGAMVPGIERYALFGMGAVALGLVYYLVPMTESA
SQRSSGIKSLYVRLRNLTVLWAIYPFIWLLGPPGVALLPTVDVALIVYLDLTVKGFGFIALDAAATL

>d1hzxa_ f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}

MNGTEGPNFYVPSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLLIMLGFPINFLTYVTQHKKLRTPLNY
ILLNLAVADLFMVFGGFTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSVLAIERYVVCKPMSNFRFGE
NHAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCGIDYYTPHEETNNESFVIYMFVVHFIIPLIVIFFCYG

QLVFTVKEAAAQQQESATTQKAKEKEVTRMVIIMVIAFLICWLWYAGVAFYIFTHQGSDFGPIFMTPAFFAKTSAY
YNPVIYIMMNKQFRNCMVTLCCGKNPLGDDEASTTVSKTETSQVAPA

>d1jfpa_f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}

LAAYMFLLIMLGFPINFLTLVTVQHKKLRPLNYILLNLAVALDMVFGGFTTLYTSLHGYFVFGPTGCNLEGFF
ATLGGEIALWSVVLAIERYVVVCKPMNSNRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIPEGMQCSCG
IDYYTPHEETNNESFVIYMFVVHFIPLIVIFFCYGQLVFTVKEAAAQQQESATTQKAKEKEVTRMVIIMVIAFLICW
LPYAGVAFYIFTHQGSDFGPIFMTPAFFAKTSAVYNPVIYIMMNKQFRNCMVTLCCGKNPLGDDEASTTVSK
TETSQVAPA

>d1dxrh2 f.2.1.2 (H:1-36) Photosynthetic reaction centre, L-, M- and H-chains
{Rhodopseudomonas viridis}

MYHGALAQHLDIAQLVWYAQWLVIWTVVLLYLRRRED

>d1dxrl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

ALLSFERKYVRGGTLIGGDLFDFWVGPYFVGFFGVSAIFFIFLGVSILGYAASQGPTWDPFAISINPPDLKYGLGA
APLLEGGFWQAITVCALGAFISWMLREVEISRKLIGIGWHVPLACVPIMFCVLQVFRPLLLGSWGHAFPYGILS
HLDWVNNGYQYLNWFYNPGHMSSVSFLFVNAMALGLHGGLILSVANPGDGDVKVTAEHENQYFRDVVGY
SIGALSIHRLGLFLASNIFLTGAFGTIASGPFWTRGWPEWWGWWLDIPFWS

>d1dxrm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodopseudomonas viridis}

ADYQTIYTQIQARGPHITVSGEWGDNDRVGKPFYSYWLKIGDAQIGPIYLGASGIAAAFAFGSTAILIILFNMAAE
VHFDPQLQFRQFFWLGLYPPKAQYGMGIPPLHDGGWWLMAGLFMTLSGSWWIRVYSRARALGLGTHIAW
NFAAAIFVFVLCIGCIHPTLVGSWSEGVPFGIWPHIDWLTAFSIRYGNFYCPWHGFSIGFAYGCGLLFAAHGATIL
AVARFGGDREIEQITDRGTAVERAALFWRWTIGFNATIESVHRWGWFSLMVMVSASVGILLTGTVDNWYL
WCVKHGAAPDYPAYLPATPDPASLPGAPK

>d1qovh2 f.2.1.2 (H:11-35) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

DLASLAIYSFWIFLAGLIYYLQTN
>d1qovl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}
ALLSFERKYRPGGTIVGGNLDFWVGPFYVGFFGVATFFAALGIILIAWSAVLQGTWNPQLISVYPPALEYGL
GGAPIAKGGWLQIITCATGAFVSWALREVEICRKLIGIGYHIPFAFAFAILAYLTFLRPVMMGAWGYAFPYGIW
THLDWVSNNTGYTYGNFHYNPAHMIAISFFTNALALALHGALVLSAANPEKGKEMRTPDHEDTFRDLVGYSIG
TLGIHRLGLLSLSAVFFSALCMIIGTIWFDQWVDDWWQWWVKLPWWANIPGGING

>d1qovm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

AEYQNIFSQVVRGPADLGMTEDVNLANRSGVGPSTLLGWFGNAQLGPIYLGSLGVLFSGLMWFFTIGIW
FWYQAGWNPAVFLRDLFFFSEPPAPEYGLSFAAPLKEGGLWLIASFFMFVAVWSWWGRTYLRAQALGMGK
HTAWAFLSAIWLWMVLGFIRPLMGWSSEAVPYGIFSHLDWTNNFLVHGNLFYNPFHGLSIAFLYGSALLFAM
HGATILAVSRFGGERELEQIADRGTAERAALFWRWTMGFNWTMEGIHRWAIWMAVLVLTGGIGLLSGTV
VDNWYVWGQNHG

>d2rcrh2 f.2.1.2 (H:1-35) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter sphaeroides}

MVGVTAGNFDLASLAIYSFWIFLAGLIYYLQTN

>d1eysh2 f.2.1.2 (H:7-43) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

HYIDAAQITIWAFWLFFFGLIYLRREDKREGYPLDS

>d1eysl1 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

AMLSFEKKYVRGGTLIGGDLDFWVGPFYVGFFGVGFCFTLLGVLLIVWGATIGPTGPTSDLQTYNLWRISIA
PPDLSYGLRMAPLEGGWLQIITICAAGAFISWALREVEICRKLGIFHVPFAFSFAIGAYLVLVFRPLLGMAGW
HGFPYGILSHLDWVSNVGYQFLHFHYNPAHMLAISFFTNCALSMHGSILSVNPQRGEPVKTSEHENFFR
DIVGYSIGALAIHRLGLFLASAAFWSAVCILISGPFWTRGWPEWWNWWLELPLW

>d1eysm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Thermochromatium tepidum}

PEYQNIIFTAVQVRAPAYPGVPLPKGNLPRIGRPIFSYWLKGIGDAQIGPIYGLGTLSIFFGLVAISIIGFNMLASV
HWDFVFQFLKHFFWLGLEPPPQYGLRIPPLSEGWWLIAGLFLTLSILLWWVRTYKRAEALGMSQHLSWAFA
AAIFFYLVLFIRPVMMGSWAKAVPFGIFPHLDWTAAFSIRYGNLYNPFHMLSIAFLYGSALLFAMHGATILSVS
RFGGDREIDQITHRGTAEEGAALFWRWMTMGFNATMESIHRWAWWCAVLTITAGIGILLSGTVVNDNWYLWA
VKHGMAPAYPEVVTAVNPYET

>d1ocra1 f.2.1.3 (A:) Cytochrome c oxidase {Cow (Bos taurus)}

MFINRWLFSTNHKDITLYLLFGAWAGMVGVTALSLLRAELGQPGTLLGDDQIYNVVVTAHAFVMIFFMVMP
MIGGFGNWLVPLMIGAPDMAFPRMNNMSFWLLPPSFLLLASSMVEAGAGTGWTVYPLAGNLAHAGAS
VDLTIFSLHLAGVSSILGAINFTTIINMKPPAMSQYQTPLFVWSVMITAVLLLLSLPVLAAIGITMLTDRLNLNTFF
DPAGGGDPILYQHLFWFFGHPEVYILILPGFGMISHIVYYSGKKEPFGYGMGVWAMMSIGFLGFIVWAHHM
FTVGMDVDTRAYFTSATMIIAIPGVKVFSWLATLHGGNIKWSPAMMWALGFIFLFTVGGLTGIVLANSSL DIVI
HDTYYVVAHFHYVLSMGAVFAIMGGFVHWFPLFSGYTLNDTWAKIHFAIMFVGVNMTFPQHFLGLSGMP
RYSYPDAYTMWNTISSMGSFISLTAVMLMVIIWEAFASKREVLTVDLTTNLEWLNGCPPPYHTFEEPTYVN
LK

>d1ocrb2 f.2.1.3 (B:1-90) Cytochrome c oxidase {Cow (Bos taurus)}

MAYPMQLGFQDATSPIMEELLHFHDHTLMIVFLISSLVLYIISLMLTTKLHTSTMADAQEVTIWTLPAILIALP
SLRILYMMDEI

>d1ocrcl1 f.2.1.3 (C:) Cytochrome c oxidase {Cow (Bos taurus)}

MTHQTHAYHMVNPSWPWTGALSALLMTSGLTMWHFNSMTLLMIGLTNMLTMYQWWRDVIRESTFQG
HHTPAVQKGLRYGMILFIISEVLLFTGFFWAFYHSSLAPTPELGGCWPPGTIHPLNPLEVPLLNTSVLLASGV
WAHHSLMEGDRKHMLQALFITITLGVYFTLLQASEYYEAPFTISDGVYGSTFFVATGFHGLHVIGSTFLIVCF
LKFHTSNHHFGFEAGAWYWHFDVWWFLYVSIYWWGS

>d1ocrd1 f.2.1.3 (D:) Cytochrome c oxidase {Cow (Bos taurus)}

SVVKSEDYALPSYDERRDYLPLDVAHVKNLNASQKALKEKEKASWSSLSIDEKVELYRLKFESFAEMNRSTNEW
KTVVGAAMFFFIGFTALLIWEKHYVYGPPIHTFEEEWVAKQTKRMLDMKVAPIQGFSAKWDYDKNEWKK

>d1ocrg1 f.2.1.3 (G:) Cytochrome c oxidase {Cow (Bos taurus)}

ASAAKGDHGGT GARTWRFLTFGLALPSVALCTLNSWLHSGHRERPAFIPYHHLIRTKPFSWGDGNHTFFHNP
RVNPLPTGYEK

>d1ocri1 f.2.1.3 (I:) Cytochrome c oxidase {Cow (Bos taurus)}

STALAKPQM RGLLARRRFHIVGAFM VSLGFATFYKFAVAEKRKKAYADFYRNYDSMKDFEEMRKAGIFQS
AK

>d1ocrj1 f.2.1.3 (J:) Cytochrome c oxidase {Cow (Bos taurus)}

FENRVAEKQKLFQEDNGLPVHLGGATDNILYRVTMTCLGGTLYSLYCLG WASFPHK

>d1ocrk1 f.2.1.3 (K:) Cytochrome c oxidase {Cow (Bos taurus)}

APDFHDKYGN AVLASGATFCVAVWVYMATQIGIEWNPSPVGRVTPKEWR

>d1ocrl1 f.2.1.3 (L:) Cytochrome c oxidase {Cow (Bos taurus)}

SHYEEGPGKNIPFSVENKWRLAMMTLFFSGFAAPFFIVRHQLKK
>d1ocrm1 f.2.1.3 (M:) Cytochrome c oxidase {Cow (Bos taurus)}
ITAKPAKTPSPKEQAIGLSVTFLSFLPAGWVLYHLDNYKKS
>d1ar1a1 f.2.1.3 (A:) Cytochrome c oxidase {Paracoccus denitrificans}
GFFTRWMSTNHKDIGILYLTAGIVGLISCVFTVYMRMELQHPGVQYMCLEGARLIADASAECTPNGHLWNV
MITYHGVLMMFFVVIPALFGGFGNYFMPLHIGAPDMAFPRLNNLSYWMYVCVALGVASLLAPGGNDQMG
SGVGWVLYPPSLTEAGYSMDLAIFAVHVSGASSILGAINIITFLNMRAPGMTLFKVPLFAWSVFITAWLILLSLP
VLAGAITMLLMDRNFGTQFFDPAGGGDPVLYQHILWFFGHPEVYIIILPGFGIISHVISTFAKKPIFGYLPMLVAM
AAIGILGFVVVAHHMYTAGMSLTQQAYFMLATMTIAVPTGIKVFSWIATMWGGSIEFKTPMLWAFGLFLFT
VGGVTGVVLSQAPLDRVYHDTYYVAHFHYVMSLGAVGIFAGVYYWIGKMSGRQYPEWAGQLHFWMMF
GSNLIFFPQHQFLGRQGMRRYIDYPVEFAYWNNISSIGAYISFASFLLFIGIVFYTLFLAGKRVNVPNEYNEHADTL
EWTLPSPPPEHTFET
>d1ar1b2 f.2.1.3 (B:1-107) Cytochrome c oxidase {Paracoccus denitrificans}
QDVLGDLPVIGKPVNNGMNFQPASSPLAHDQQWLDFVLYIITAVTIFVCLLLICIVRFNRRANPVPARFHNT
PIEVIWTLPVVLILVAIGAFSLPILFRSQEMP
>d1qlec1 f.2.1.3 (C:) Cytochrome c oxidase {Paracoccus denitrificans}
AHVKNHDYQILPPSIWPFFGAIGAFVMLTGAVAWMKGITFFGLPVEGPWMFLIGLVGVLYVMFGWWADVNN
EGETGEHTPVVRIGLQYGFILFIMSEVMFFVAWFWAFAIKNALYPMGPDSPIKDGWPPEGIVTFDPWHLPLINT
LILLLSGVAVTWAHHAFVLEGDRKTTINGLIVAVILGVCFGLQAYEYSHAAGLADTVYAGAFYMATGFHGAHV
IIGTIFLFVCLIRLLKGQMKTQKHVGFEAAAWYWHFVDVWLFVVIYIWGR
>d1qled1 f.2.1.3 (D:) Cytochrome c oxidase {Paracoccus denitrificans}
TDHKHGEMDIRHQQTAFAGFIKGATWVSILSIAVLFLALANS
>d1ehka1 f.2.1.3 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}
AYPEKKATLYFLVLGFLALIVGSLFGPFQALNYGNVDAYPLLKRLLPFVQSYYQGLTLHGVLNAAIVFTQLFAQAIMV
YLPARELNMRPNMGLMWLSWWMAFIGLVVAALPLANEATVLYTFYPLKGHWAFYLGASVFLSTWVSIYI
VLDLWRRWKAANPGKVPLVTYMAVVFWLMWFLASLGLVLEAVLFLLPSFGLVEGVDPVARTLFWWWTGH
PIVFWLLPAYAIYTILPKQAGGKLVSDPMARLAFLFLSTPVGFHHQFADPGIDPTWKMIHSVLTFLVAVPSL
MTAFTVAASLEFAGRRLRGGRGLFGWIRALPWDNPAPVAPVLGLLGIPGGAGGIVNASFTLDYVVHNTAWPV
GHFHLQVASLVTLTAMGSLYWLLPNLTGPISDAQRRLGLAVVWLWFLGMMIMAVGLHWAGLLNVPRRAYIA
QVPDAYPHAAVPMVFNVLAGIVLVALLLFYGLFSVLLSRERKPELAEAPLFAEVISGPEDRRLVLAMDRI
FAVAAILVVLAYGPTLVQLFGHLPVPGWRLW
>d1ehkb2 f.2.1.3 (B:3-40) Cytochrome c oxidase {Thermus thermophilus, ba3 type}
DEHKAHKAILAYEKGWLAFLSAMLVFIALIAYTLATH
>d1ehkc1 f.2.1.3 (C:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}
EEKPKGALAVILVLTILVFWLGVYAVFFARG
>d1ffta1 f.2.1.3 (A:) Ubiquinol oxidase {Escherichia coli}
VDHKRLGIMYIIVAIVMLLRGFADAIMMRSQQALASAGEAGFLPPHYDQIFTAHGVIMIFFVAMPFVIGLMN
LKVPLQIGARDVAFPFLNNLSFWFTVVGVLVNVSLGVGEFAQTGWLAYPPLSGIEYSPGVGVDYWIWSQLSGI
GTTLTGINFFVTILKMRAPGMTMFKMPVFTWASLCANVLIIASFPILTWTALLTLDRLGTHFFTNDGGNM
MMYINLIWAUGHPEVYLILPVFGFSEIAATFSRKRLFGYTSLVWATVCITVLSFIVWLHFFTMGAGANVNAF
FGITTMIIAIPGVKIFNWLFMYQGRIVFHSAMLWTIGFIVTFSVGGMTGVLLAVPGADFVLHNSLFLIAHFHN
VIIGGVVFGCFAGMTYWWPKAFGFKLNETWGKRAFWFIIGFFVAFMPLYALGFMGMTRRLSQQIDPQFHT
MLMIAASGAVLIALGILCLVIQMYVSIRDRDQNRLTGDWPGGRTLEWATSSPPPFYNF
>d1fftb2 f.2.1.3 (B:27-117) Ubiquinol oxidase {Escherichia coli}

SALLDPKGQIGLEQRSLILTAFGLMLIVVIPAILMAVGFAWKYRASNKDAKYSPNWSHSNKVEAVVWTVPIIIIFL
AVLTWKTTTHALEPS

>d1fftc1 f.2.1.3 (C:) Ubiquinol oxidase {Escherichia coli}

HDAGGT KIFGF WIYLM SDCLFSILFATYAVLVNGTAGGPTGKDIFELPFVLVETFLLLFSITYGMAAIAMYKNNK
SQVISWLALT WLF GAG FIGMEI YEFHHLIVNGMGPDRSGFLSAFFALVGTHGLHVTSGLIWMAVL MVQIARRG
LTSTNRTRIMCLSLFWHFLDVVWICVFTVVYLMGA

>d1c0va_ f.2.1.4 (A:) Subunit C {Escherichia coli}

MENLNMDLLYMAAAVMMGLAAIGAAIGIGILGGKFLEGAARQPDLIPLLRTQFFIVMGLVDAIPMIAVGLGLY
VMFAVA

>d1c17m_ f.2.1.4 (M:) Subunit A {Escherichia coli}

HGKS KLIAPLA LTIFVVVF LMNL MDLL PIDLL PYIA EHVL GLP ALRV VPSADVN VTLS MALGV F I L F Y SIK MKGI
GGFT KELT L QPFN HWAF I PVNL ILEG V SLLSKPV SGLRLFGN MYA GELI F ILIAG L LPW W SQWILN VPWA IFHILI
ITLQAFIFMVLTIVYLS

>d1h6ia_ f.2.1.5 (A:) Aquaporin-1 {Human (Homo sapiens)}

LFWRAVVAEFLATTLFV FISIGS ALGF KYPV GNQTA VQDN KVSLA FGLSIAT LAQSVGHIS GAHLNPAV TLG LL
LSCQISIFRALMYIIACVGAIVATA ILSGITSSLTGNSLGRNDLADGVNSQGLGIEIIGTLQLVLCV LATTDR RRRD
LGGSAPLAIGLSVALGHLLAIDYTGCINPARSGSAVITHNFSNHWIFWVGPFIGGALAVLIYDFILAP

>d1fx8a_ f.2.1.5 (A:) Glycerol uptake facilitator protein GIpF {Escherichia coli}

TLKGQCIAEFLGTGLI FFVG VGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAHLNPAV TIALWLFAC
FDKRKVPIFIVSQVAGAFCAA ALVYGLYYN LFFDFEQTHHIVRGVESVDLAGTFSTYPNPHINFVQAF AVE MVIT
AILMGLL ALTD DNGV P RGPLAPL LIGL LIAVIGASMGPLTG FAMNPARD FGPKVFAWLAGWGNV AFTG GRD
IPYFLVPLFGPIVGAIVGAFAYRK LIGRHL

>d1kpka_ f.2.1.13 (A:) Clc chloride channel {Escherichia coli}

QAARLRRRQLIRQLLERDKTPLA ILFMAAVV GTL VGLAAV AFDKGV AWLQNQRM GALVHTAD NYPL LLTV AFL
CSAVLAMFGYFLVR KYA P EAGG SGIP EIEGA LEDQRP VRWW RVL PVKFFG GLT LGG GMV LGREG PTVQ IGG
NIGRMVLDIFRLKGDEARHTLL ATGAAAGLAA AFNAPLAGILF II EEMRPQFRY NLISIKA VFIGVIM STI MYR IFN
HEVALIDVGK LSDAPL NTLW LYLILG IIFG PIF NKW VLGMQ DLLH RVH GGN IT KWVLM GG AIGG LC LL GFV
APATSGGGFN LIP IATAGNF SMG M L VFIF VARV ITLL CFSSG APGG I FAPM L ALGTVL GTAF GMV AVEL FPQY HL
EAGTFAIAG MGALLA ASIRAP LTG IILV LEM TDNY QLIP MIIT GLGAT LLAQFTGGKPLYSAIL ARTLAK QEA EQL

>d1kpla_ f.2.1.13 (A:) Clc chloride channel {Salmonella typhimurium}

TPLA ILFMAAVV GTL VGF AFEKA VSWV QNM RIGA LVQV ADH A FLLWPLA F ILS ALLA MVGYFL VRK F APEA
GGSGIPEIEGA LEEL RPVRWWRVLPVK FIGGM GTL GAGM VLGREGPTVQIGGNLGRM VLDVFRM RSAE ARH
TLL ATGAAAGL SAA FNAPLAGILF II EEMRPQFRY NLISIKA VFTG VIM SSIV FRIF NG EAPII EVG KLS DAPV NTLW
LYLILG IIFG VV GPV FNSL VLR TQDMF QR FH GGEIKK WVL MGGAIGG LCG IGL LIEPAA AGGG FN LIP IAAG NF
VG LLLF IFIT RVV TLL CFSSG APGG I FAPM L ALG TLL GTAF GM AA AVL FPQY HLEAGTFAIAG MGAL MAAS VR
PLT GIVL VLEM TDNY QLIP MIIT CLGAT LLAQFL GGKPL YSTI LARTL AKQ DAEQ

>d1f6ga_ f.2.1.11 (A:) Potassium chanel protein {Streptomyces lividans}

MPPMLSGLLARLVKLLGRHGSALHWAAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLITYPAALWW SVETAT
TVGYGDLYPVTLWGRCVAVV VMVAGITSFGLVTAALATWFVGREQERRGHFVRHSEKAAEEAYTRTTRALHER
FDRLERMLDDNRR

>d1jq2a_ f.2.1.11 (A:) Potassium chanel protein {Streptomyces lividans}

LWGRCVAVV VMVAGITSFGLVTAALATWFVGREQ

>d1k4cc_ f.2.1.11 (C:) Potassium chanel protein {Streptomyces lividans}

SALHWRAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLITYPRALWW SVETATT VGYGDLYPVTLWGRCVAVV

MVAGITSFGLVTAALATWFVGREQERRGH

>d1g4yb_f.2.1.11 (B:) Small conductance potassium channel {Rat (Rattus norvegicus)}

DTQLTKRVNAANVLRETWLIYKNTKLVKIDHAKVRKHQRKFLQAIHQLRSVKMEQRKLNDQANTLVDLAK
TQLEHHHHH

>d1kkda_f.2.1.11 (A:) Small conductance potassium channel {Rat (Rattus norvegicus)}

RKLELTKAEKHVHNFMMDTQLTKRVNAANVLRETWLIYKNTKLVKIDHAKVRKHQRKFLQAIHQLRSVKM
EQRKLNDQANTLVDLAKTQ

>d1msla_f.2.1.11 (A:) Gated mechanosensitive channel {Mycobacterium tuberculosis}

ARGNIVDLAVAVVIGTAFTALVTKFTDSIITPLINRIGVNAQSDVGILRIGIGGGQTIDLNVLLSAAINFFLIAFAVYFL
VVLPYNTLRKKGEVEQPGDTQVVLTEIR

>d1be3c1_f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

MTNIRKSHPLMKIVNNAFIDLAPSNISSWWNFGSLLGICLILQILTGLFLAMHYTSDDTTAFSSVTHICRDVNYG
WIIRYMHANGASMFVICLYMHVGRGLYYGSYTLETWNIGVILLTVMATAFMGYVLPWGQMSFWGATVITN
LLSAIPYIGTNLVEWIWGGFSVDKATLTFRAFHFIPLFIIIMAIAMVHLLFLHETGSNNPTGISSDVKIPFHPYYTI
KDILGALLLILALMLLVLFAPDLLGDPDNYPANPLNTPPHIKPEWYFLFAYAILRSIPNLGGVLALAFSILALIPLL
HTSKQRSMMFRPLSQCLFWALVADLLTWIGGQPVEHPYITIGQLASVLYFLLILVLMPTAGTIENKLLKW

>d1be3e2_f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

SHTDIKVPDFSDYRRPEVLDSTKSSKEARKGFSYLVLTATTVGVAYAAKNVVSQFVSSMSASADVL

>d1be3f1_f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

AVSASSRWLEGIRKWWYNAAGFNKLGMRDDTIHENDDVKEAIRRLPENLYDDRVFRIKRALDLSMRQQILPKF
QWTKYEEDKSYLEPYLKEVIRERKEREEWAKK

>d1be3g1_f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRTRACILRVAPPVAFYLVYTWTGTQEFEKSKRKNPAA
YENDR

>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)}

GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRTRACILRVAPPVAFYLVYTWTGTQEFEKSK

>d1qcrh1_f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

TTVREQCEQLEKCVKARERLELCERVSSRSQTEEDCTEELDFLHARDHCVAHKLFNSL

>d1qcrk1_f.2.1.8 (K:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

MLTRFLGPRYRQLARNWVPTAQLWGAVGAVGLVSATDSRLILDWV

>d1bccc1_f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

APNIRKSHPLKMINNSLIDLPAPSNIASAWNFGSLLAVCLMTQILTGLLLAMHYTADTSLAFSSVAHTCRNVQY
GWLIRNLHANGASFFFICIFLHIGRGLYYGSYLYKETWNTGVILLTMATAFVGYVLPWGQMSFWGATVITNLF
SAIPYIGHTLVEWAWGGSVDNPTLTFALHFLLPFAIAGITIIHLTLHESGSNNPLGISSSDKIPFHPYYSFKDIL
GLTLMITPFLTLALFSPNLLGDOPENFTPANPLVTPPHIKPEWYFLFAYAILRSIPNLGGVLALAASVLILFLPFLHKS
KQRTMTFRPLSQLFWLLVANLLTWIGSQPVIEHPFIIGQMASLSYFTILLFLPTIGTLENKMLNY

>d1bccd3_f.2.1.8 (D:196-241) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

PEHDHRKRMGLKMLMMGLLVPLVYYMKRHKWSVLKSRKLAYRPPK

>d1bcce2_f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

SHTDIKVPNFSDYRRPDDYSTKSSRESDPSRKGF SYLVLTAVTTLGVAYAAKNVVTQFVSSMSASADVL

>d1bccf1_f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

SRWLEGIRKWWYNAAGFNKYGLMRDDTIYENDDVKEAIRRLPENLYDDRMFRIKRALDNLNRQQILPKEQWT

KYEEDVPYLEPYLKEVIRERKEREERWDK

>d1bccg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

RQFGHLTRVRHLITYSLSPFEQRPFPHYFSKGVPNVWRRLRACILRVAPPFLAFYLLYTWTGTQEFEKSKRKNPAAVN

>d1bcch1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

LVDPLTTVREQCEQLEKCVKARERLELCERVSSRSQTEEDCTEELDFLHARDHCVAHKLFNSLK

>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)}

MAFRKSNVYLSVNSIIDSPQPSSINYWWNMGSLLGLCLVIQIVTGIFMAMHYSSNIELAFSSVEHIMRDVHN
GYILRYLHANGASFFFMVFMFHMAKGLYYGSYRSPRVTLNNGVIIITLTIAFLGYCCVYQMSHWGATVIT
NLFSAIFFVGNDIVSWLWGGFSVSNPTIQRFFALHYLVPIIAAMVIMHLMALHIHGSSNPLGITGNLDIPMHS
YFIFKDLTVFLFMLILALFVFYSPNTLGHPDNYIPGNPLVTTPASIVPEWYLLPFYAILRSIPDKLLGVITMFAAILVLL
VLPTDRSVVRGNTFKVLSKFFFFIFVFNFVLLGQIGACHVEVPYVLMQIATFIYFAYFLIVPVISTIENVLFYIGRNK

>d1ezvd2 f.2.1.8 (D:261-306) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

PEHDERKRLGLKTVIILSSLYLLSIWVKFKWAGIKTRKFVNPPK

>d1ezve2 f.2.1.8 (E:31-86) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

KSTYRTPNFDDVLKENNDADKGRSYAYFMVGAMGLSSAGAKSTVETFISSMTATA

>d1ezvf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

QSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRRLPEDESYARAYRIRAHQ
TELTHHLLPRNEWIKAQEDVPYLLPYILEAAAAKEKDELDNIEVSK

>d1ezvg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

GPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGIFHNAVFNSFRRFKSQFLYVLIPAGIYWYWWKN
GNEYNEFLYSKAGREELERVNV

>d1ezvh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

VTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQQPGYADLEHKEDCVEEFFHLQHYLDTATAPRLFDKLK

>d1ezvi1 f.2.1.8 (I:) Cytochrome bc1 transmembrane subunits {Baker's yeast (Saccharomyces cerevisiae)}

SSLYKTFFKRNAVFGTIFAGAFVFQTVFDTAITSWYENHNKGKLWVDVKARIAA

>d1fumc_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {Escherichia coli}

TTKRKPYVRPMTSTWWKKLPFYRFYMLREGTAVPAWFSIELIFGLFALKNGPEAWAGFVDFLQNPVIVIINLIT
LAAALLHTKTFELAPKAANIIVKDEKMGPEPIKSLWAVTVVATIVLVALYW

>d1fumd_ f.2.1.9 (D:) Fumarate reductase respiratory complex transmembrane subunits {Escherichia coli}

INPNPKRSDEPVFWGLFGAGGMWSAIIAPVMILLVGILLPLGLFPGDALSYERVLAFQAQSFIGRVFLFLMIVLPLW
CGLHRMHHAMHDLKIHVPGKWWFYGLAAILTVTLLGVVTI

>d1qlac_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {Wolinella succinogenes}

MNTESILESYSGVTPERKKSRMPAKLDWWQSATGLFLGLFMIGHMFFVSTILLGDNVMLWVTKKFELDFIFEG
GKPIVVSFLAAFVFAVFIAHAFLAMRKFPINYRQYLTFKTHKDLMRHGDLLWWIQAQMTGFAMFFLGSVHLIY
MMTQPQTIGPVSSSFRMVSEWMWPLYLVLFAVELHGSVGLYRLAVKWGWFDGETPDKTRANLKKLKTLM
AFLIVLGLLTFGAYVKKLEQTDPNIDYKYFDYKRTH

>d1jb0a_ f.2.1.12 (A:) Photosystem I {Synechococcus elongatus}

RVVVNDNPVPTSFEKWAKPGHFRTLARGPQTTWIWNLHALAHDFDHTSDLEDISRKIFSAHFGLAVVFI
WLSGMYFHGAKFSNYEAWLADPTGIKPSAQVWPIVGQGILNGDVGGGFHGIQITSGFLQLWRASGITNEFQ
LYCTAIGGLVMAGLMLFAGWFHYHKRAPKLEWFQNVESMLNHHLAGLLGLSLAWAGHQIHVSPLINKLLDA
GVAAKDIPLPHEFILNPSLMAELYPKDWGFFSGVIPFFTNAWASYSDFTFNGGLNPVTGGLWLSDTAHHHLA
IAVLFIAGHMYRTNWGIGHSLKEILEAHKGPFAGHKGLYEVLTSWHAQLAINLAMMGSLSIIVAQHMYAM
PPYPYLATDYPTQLSLFTHHMWIGGLVVGAAHGAIFMVRDYDPAMNQNNVDRVLHRDAAISHLNWCVI
FLGFHSFGLYVHNDTMRAFGRPQDMFSDTGIQLQPVFAQWVQNLHTLAPGGTAPNAATASVAFGGDVVAV
GGKVAMMPIVLGTADFMVHHIHAFTIHVTVLILLKGVLFARSSRLPDKANLGFRFCDGPGRGGTCQVSGWD
HVFLGLFWMYNCISVVFHFWSWMQSDVWGTVAPDGTVSHITGGNFAQSAITINGWLRDFLWAQASQVIGS
YGSALSAYGLLFLGAHFIWAFLMFLSGRGYWQELIESIVWAHNLKVAPAIQPRALSIIQGRAVGVAHYLLGGI
ATTWAFFLARIISVG

>d1jb0b_ f.2.1.12 (B:) Photosystem I {Synechococcus elongatus}

ATKFPKFSQDLAQDPTRRIWYAIAMAHDFESHDMTEENLYQKIFASHFGHLAIIFLWVSGSLFHVAWQGNF
EQWVQDPVNTRPIAHAIWDPQFGKAADVDAFTQAGASNPVDIAYSGVYHWWYTIGMRTNGDLYQGAIFLLIL
ASLALFAGWLHLQPKFRPSLSWFKNAESRLNHHLAGLFGVSSLAWAGHLIHVAIPESRGQHVGWDNFLSTMP
HPAGLAPFFTGNWGVAQNPDTASHVFGTAQGAGTAILTFLGGFHPQTESLWLTDMAHHHLAIAVLFIVAGH
MYRTQFGIGHSIKEMMDAKDFFGTKEGPNMPHQGIYETYNNSLHFQLGWHLACLVITSVAQHMYSLPP
YAFIAQDHHTMAALYTHHQYIAGFLMVGAFAHGAIFLVRDYDPAQNKGNVLDRLVLQHKEAIISHLSWVSLFLGF
HTLGLYVHNDVVVAFGTPEKQILIEPVFAQFIQAAHGKLLYGFDTLLSNPSIASTAWPNYGNVWLPGWLDAIN
SGTNSLFLTIGPGDFLVHHIALGLHTTLILVKGALDARGSKLMPDKDFGYAFPCDGPGRGGTCDISAWDAFY
LAMFWMLNTIGWTFYWHWKHLGVWEGNVAQFNESSTYLMGWLRYLWLNSSQLINGYNPFGTNNSV
WAWMFLFGHLWATGFMFLISWRGYWQELIELTVWAERTPLANLVRWKDKPVALSIVQARLVGLAHFSVG
YILTYAAFLIASTAAKF

>d1jb0f_ f.2.1.12 (F:) Photosystem I {Synechococcus elongatus}

DVAGLVPCKDSPAFKRAAAAVNTTADPASGQKRFERYSQALCGEDGLPHLVVDGRSLRAGDFLIPSVLFYIAG
WIGWVGRAYLIAVRNSGEANEKEIIDVPLAIKCMLTGFAWPLAALKELASGELTAKDNEITVSPR

>d1jb0i_ f.2.1.12 (I:) Photosystem I {Synechococcus elongatus}

MMGSYAAFLPWIFIPVVCWLMPVVMGLLFLYIEGEA

>d1jb0j_ f.2.1.12 (J:) Photosystem I {Synechococcus elongatus}

MKHFLTYLSTAPVLAIIWMTITAGILIEFNRFYPDLLFHPL

>d1jb0k_ f.2.1.12 (K:) Photosystem I {Synechococcus elongatus}

ILCNLFAIALGRYAIQSRGKGPGPLIALPALFEGFGLPELLATTSGHLLAAGVVSGL

>d1jb0l_ f.2.1.12 (L:) Photosystem I {Synechococcus elongatus}

LVKPYNGDPFVGHLSPISDGLVKTFIGNLPAYRQGLSPIRGLEVGMAGHYFLIGPWVKGPLRDSDVANLGG
LISGIALILVATACLAAYGLVSFQKGSSSDPLKTSEGWSQFTAGFFVGAMGSAFVAFFLLENFLVVDGIMTGLFN

>d1jb0m_ f.2.1.12 (M:) Photosystem I {Synechococcus elongatus}

MALTDTQVYVALVIALPAVLAFRLSTELYK

>d1jb0x_ f.2.1.12 (X:) Photosystem I {Synechococcus elongatus}

PTYAFRTFWAVLLAINFLVAAYYFAAAA

>d1eula_ f.2.1.10 (A:) Calcium ATPase {Rabbit (Oryctolagus cuniculus)}

MEAAHSKSTEECLAYFGVSETTGLTPDQVKRHEKYGHNELPAEEGKSLWEVIEQFEDLLVRILLAAACISFVLAW
FEEGEETITAFVEPFVILLILIANAIVGVWQERNAENAENAEALKEYPEMGMKVYRADRKSVQRRIKARDIVPGDIVEVA
VGDKVPADIRILSIKSTTLVDQSILTGESVSKVHTEPVDPRAVNQDKKNMLSGTNIAAGKALGIVATTGVSTE
IGKIRDQMAATEQDKTPLQQKLDEFGEQLSKVISLICVAVWLINIGHFNDPVHGGSWIRGAIYYFKIAVALAVAII
PEGLPAVITTCLALGTRRMAKKNAIVRSLPSVETLGCTSVICSDKTGTLTTNQMSVCKMFIIDKVDGDFCSLNEFSI
TGSTYAPEGEVLKNDKPIRGQFDGLVELATICALCNDSSLFNETKGVYEVGEATETALTLVEKMNVFNTEVR
NLSKVERANACNSVIRQLMKKEFTLEFSRDRKSMSVYCSPAKSSRAAVGNKMFVKGAPEGVIDRCNYVRVGTT
RVPMTGPVKEKILSVIKEWGTGRDTLRLALATRDTPPKREEMVLDSSRFMEYETDLTFVGVVGMLDPPRKE
VMGSIQLCRDAGIRVIMITGDNKGTAIAICRRIGIFGENEEVADRAYTGREFDDLPLAEQREACRRACC FARVEPS
HKS KIVEYLQSYDEITAMTDGVDNDPALKKAEIGIAMI GSGTAVAKTASEMV LADDNFSTIVAAVEEGRAIYNN
MKQFIRYLISSNVGEVVCIFLTAALGLPEALIPVQLLWVNLT DGLPATALGFNPPDLDIMDRPPRSPKEPLISGW
FFRYMAIGGYVGAATVGAAWWFMYAEDPGVTYHQLTHFMQCTEDHPFEGLDCEIFEAPEPMTMALS
LVTIEMCNALNSLENQSLMRMPPWVNWLGSICLMSLHFLLYVDPLPMIFKLKALDLTQWLMVLKISLPVI
GLDEILKFIARNYLEG

>d1kzua_ f.3.1.1 (A:) Light-harvesting complex subunits {Purple bacterium (Rhodopseudomonas acidophila)}

MNQGKIWTVVNPAGIPALLGSVTVIAILVHLAILSHTTWFPAYWQGGV

>d1kzub_ f.3.1.1 (B:) Light-harvesting complex subunits {Purple bacterium (Rhodopseudomonas acidophila)}

ATLTAEQSEELHKYVIDGTRVFLGLALVAHFLAFSATPWLH

>d1lgha_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodospirillum molischianum}

SNPKDDYKIWLVINPSTWLPVIWIVATVVAIAVHAALVAAAPGFNWIALGAAKSAAK

>d1lghb_ f.3.1.1 (B:) Light-harvesting complex subunits {Rhodospirillum molischianum}

RSLSGLTEEEIAVHDQFKTTSAFIILAAVAHVVLVWWKPWF

>d1jo5a_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodobacter sphaeroides}

ADKSDLGTYGLTDEQAQELHSVYMSGWLFSAVAIVAHLAYIWRPWF

>d1ijda_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodopseudomonas acidophila}

MNQGKIWTVVPPAFLPLMLGAVAITALLVHAALHTTWYAAFLQ

>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}

APKDNTWYTGAKLGFSQYHDTGFINNNGPTHENQLGAGAFGGYQVNPyVGFEMGYDFLGRMPYKGSVEN
AYKAQGVQLTAKLGYPITDDDIYTRLGGMVFRADTKSNVYGNHDTGVSPVFAGGVEYAITPEIATRLEYQFTN
NIGDAHTIGTRPDNGMLS LGVSYRFGQQGEAA

>d1qjpa_ f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}

APKDNTWYTGAKLGWSQYHDTGLINNNGPTHENKLGAGAFGGYQVNPyVGFEMGYDWLGRMPYKGSVEN
GAYKAQGVQLTAKLGYPITDDDIYTRLGGMVWRADTSNVYGNHDTGVSPVFAGGVEYAITPEIATRLEYQ

WTNNIGDAHTIGTRPDNGMILSLGVSYRFG

>d1qj8a_f.4.1.1 (A:) Outer membrane protein X (OMPX) {Escherichia coli}

ATSTVTGGYAQSDAQGQMNKMGGFNLKYRYEEDNSPLGVIGSFTYTEKSRTASSGDYNKNQYYGITAGPAYRI
NDWASIYGVVGVGYGKFQTTEYPTYKNDTSYGF SYGAGLQFNP MENVALDFSYEQSRIRSV DVG TWIAGVGY
RF

>d1i78a_f.4.4.1 (A:) Outer membrane protease OMPT {Escherichia coli}

STETLSFTPDNINADISLGTSGTKERVYLAEEGGRKVSQLDWKFNFNAAIIKGAINWDLMPQISIGAAGWTTL
GSRGGNMVDQDWMDSSNPGTWTDEARHPDTQLNYANEFDLNIKGWLNEPNYRLGLMAGYQESRYSFTA
RGGSYIYISSEEGFRDDIGSF PN GERAIGYKQRFKMPYIGLTGSYRYEDFELGGTFK YSGW VESSDNDEHYDPKGR
ITYRSKVKDQNYYSVAVNAGYYVTPNAKVYVEGA WNR VT NKGNT SLYDHNNNTSDYSKNGAGIENYN FITTA
GLKYTF

>g1qd6.1 f.4.2.1 (A;C:) Outer membrane phospholipase A (OMPLA) {Escherichia coli}

AVRGSIIANMLQEXFTLPYDTNYLIYTQTS DLNKEAIASYDWAENARKDEVKFQLSLAFFPLWRGILGPNSVLGAS
YTQKSWWQLSNSEESSPFRETNYEPQLFLGFATDYRFAGWTLRDVEMGYNHDSNGRSDPTSRSWNRLYTRL
MAENGNWLV EVKPWYVVGN TDDNP DITK YM GYYQLKIGYHLGDAVLSAKGQY NWNTGYGGAELGLSYPITK
HVR LYT QVYSGYGE S LIDY NF NQ TRVG VG VM LNDLF

>d1hxxa_f.4.3.1 (A:) Porin {Escherichia coli, different sequences}

AEIYNKDGNKVDLYGKAVGLHYFSKGNGENSYGGNGDMTYARLGKGETQINS DLTG YGQWEYNFQGN NS
GADA QTGNKTRLA FAGL KYADVGSFDYGRNYGV F DALG YT DMLPEFGG DT ASDD FFV GRV GG VATY RNSN
FFGLVDGLNFAVQYLGKNERDTARRSNGDG VGG SISYEYEGFGIVGAYGAADRTNLQEAQPLGNGKKAEQWA
TGLYDANNIYL A ANYGETRNATP ITNKFTNTSGFANKTQDVLLVAQYQFD FGLRPSIAYTKSKAKDVEGIGD VD
LV NYF EVG AT YY FN K NM STY VD YI IN QIDS DNKL GV GS DDT V AVGIVYQF

>d1pho_f.4.3.1 (-) Porin {Escherichia coli, different sequences}

AEIYNKDGNKLDVYVGKVKAMHYMSDNASKDGDQSYIRFGFKGETQINDQLTG YGRWEAEFAGNKAESDTAQ
QKTRLA FAGL KYKDLGSFDYGRNLGALYDVEAWTDMFPEFGG DSSA QTDNFMTKRASGLATYRNTDFG VID
GLNLTQYQGKNE NR DV KKQNGDG FGT SLTYDFGG SDFA ISGAYTNSDRTNEQNLQSRGTGKRAEAWATGLK
YDANNIYLATFYSETRK MTPITGGFANKTQNFEAVAQYQFD FGLRPSLGYVLSKGKDIEGIGDEDLV NYIDVGATY
YFNKNMSAFV D YKINQLSDNKL NIINN DDIVAVG MTYQF

>d2por_f.4.3.1 (-) Porin {Rhodobacter capsulatus}

EVKLSGDARMGV MYNGDDWNFSSRSRV LFTMS GTTD SGLEFGASFKAHESVGAETGEDGT VFLSGA FGKIE
MGDALGASEALFGDLYEVGYTDLDDRG GNDIPYLTGDERLTAEDNPVLLY TSAGAFSVAASMSDG KVGETSED
DAQEMA VAAAYTFGN YTVGLGYEKIDSPDT ALMADMEQLEAAIAKFGATNVKAYYADGEL RDFA RA VF DLT
PVAAAATAVDHKAYGLSVDSTFGATT VGGYVQVLDIDTIDDVTYY LGAS YDLGGASIVGGIADNDLPNSDM
VADLGVKFKF

>d3prn_f.4.3.1 (-) Porin {Rhodopseudomonas blastica, strain DSM2131}

MISLNGYGRFGLQYVEDRGVGLEDTISSRLRINIVGTTETDQGVTFGAKLRMQWDDGDAFAGTAGNAAQFW
TSYNGVTVSGNVDTAFDSVALTYDSEMGYEWSSFGDAQSSFFAYNSKYDASGALDNYNGIAVTYSISGVNLYL
SYVDPDQTVDSL VTEFGIAADWSNDMISLAAAYTTDAGGIVNDIAFVGAA YKFNDAGTVGLNWYDNGLS
TAGDQVTLYGNYAFGATT VRAYVSDIDRAGADTAYGIGADYQFAEGVKVSGSVQSGFANETVADGVRFDF

>d1osma_f.4.3.1 (A:) Porin {Klebsiella pneumoniae}

AEIYNKDGNKLDLYGKIDGLHYFSDDKDVG DQTYMRLGVKGETQINDQLTG YGQWEYNVQANNT ESSSDQ
AWTRLA FAGL KFGDAGSF DYGRNYGVYDVT SWTD VLPEFGG DT YGSDN FLQSRANGVATYRNSDFF GLV DG
LN FALQYQGKNGSVS GEGATNNRGALKQNGDGFGT SVTYDIFDG ISAGFAYANSKRTDDQNQLLL GE GDHA
ETYTGGLKYDANNIYLATQYTQTYNATRAGSLGFANKAQNFEVAQYQFD FGLRPSVAYLQSKGKD LNGYGDQ

DILKYVDVGATYYFNKNMSTYVDYKINLLDDNSFRSAGISTDDVVALGLVYQF

>d1e54a_ f.4.3.1 (A:) Porin {Comamonas acidovorans}

ESSVTLFGIVDTNVAYVNKDAAGDSRYGLTSGASTSRLGLRGTEDLGGGLKAGFWLEGEIFGDDGNASGFNF
RRSTVSLSGNFGEVRLGRDLVPTSQKLTSYDLFSATGIGPFMGFRNWAAGQGADDNGIRANNLISYYTPNFGGF
NAGFGYAFDEKQTIGTADSVGRYIGGYVAYDNGPLSASLGLAQQQKTAvgGLATDRDEITLGASYNFGVAKLSLL
QQTGFKRDIGGDIKTNSYMLGASAPVGGVGEVKLQYALYDQKAIDSKAHQITLGYVHNLSKRTALYGNLAFLKN
KDASTLGLQAKGVYAGGVQAGESQTGVQVGIRHAF

>d1af6a_ f.4.3.2 (A:) Maltoporin (also LamB protein) {Escherichia coli}

VDFHGYARSGIGWTGSERGEQQCFQTTGAQSKYRLGNECETYAEELKLGQE伟WKEGDKSFYFDTNVAYSVAQQN
DWEATDPAFREANVQGKNLIEWLPGSTIWAGKRFYQRHDVHMIDFYWDISGPGAGLENIDVGFGLSLAAT
RSSEAGGSSSFASNNIYDYTNETANDVFDVRLAQMEINPGTLELGVDYGRANLRDNYRLVDGASKDGWLFTA
EHTQSVLKGFNKVVQYATDSMTSQGKGLSQGSGVAFDNEKFAYNINNNNGHMLRILDHGAISMGDNWDM
YVGMYQDINWDNDNGTKWWTVGIRPMYKWTPISTMVEIGYDNVESQRTGDKNNQYKITLAQQWQAG
DSIWSRPAIRVFATYAKWDEKWGYDYTGNADNNANFGKAVPADFNGGSFGRGDSDEWTFGAQMEIWW

>d2mpa_ f.4.3.2 (A:) Maltoporin (also LamB protein) {Salmonella typhimurium}

VDFHGYARSGIGWTGSERGEQQCFQATGAQSKYRLGNECETYAEELKLGQE伟WKEGDKSFYFDTNVAYSVNQQ
NDWESTDPAFREANVQGKNLIEWLPGSTIWAGKRFYQRHDVHMIDFYWDISGPGAGIENIDLGFGLSLAAT
RSTEAGGSYTFSQNIYDEVKDTANDVFDVRLAGLQTNPDGVLELGVDYGRANTTDGYKLADGASKDGMFT
AEHTQSMILKGYNFKVVQYATDAMTTQGKGQARGSDGSSSTEKINYANKVINNNNGMWRILDHGAISLGDK
WDLMYVGMYQNIWDNNLGTTEWWTVGVVRPMYKWTPISTMILLEVGYDNVKSQQTGDRNNQYKITLAQQ
WQAGDSIWSRPAIRFATYAKWDEKWGYIKDGDNISRYAAATNSGISTNSRGDSDEWTFGAQMEIWW

>d1a0tp_ f.4.3.2 (P:) Sucrose-specific porin {Enterobacterium (Salmonella typhimurium)}
SGFEFHGYARSGVIMNDSGASTKSGAYITPAGEΤGGΑΙGRLGNQADTYVEMNLEHKQTLNGATTRFKVMVA
DGQTSYNDWTASTSDLNVRQAFVELGNLPTFAGPKGSTLWAGKRFDRNFDIHVIDSDVVFLAGTGGIYD
VKWNDGLRSNFSLYGRNFGDIDDSSNSVQNYILTMNHFAGPLQMMVSGLRAKDNDERKDSNGNLAKGDA
NTGVHALLGLHNDSFYGLRDGSSKTALLYHGLGAEVKIGSDGALRPGADTWRIASYTTPLSENWSVAPAM
LAQRSKDRYADGDSYQWATFNLRLIQAINQNFALEYEGSYQYMDLKPEGYNDRQAVNGSFYKLTAPTFKVGS
GDFFSRPEIRFYTSWMDWSKKLNNYASDDALGSDGFNSGGEWWSFGVQMETWF

>d1by5a_ f.4.3.3 (A:) Ferric hydroxamate uptake receptor FhuA {Escherichia coli}
QESAWGPAATIAARQSATGTKTDTPIQKVPSISVTAEEMALHQPKSVKEALSYTPGVSVGTRGASNTYDHII
RGFAAEQSQNNYLNGLKLQGNFYNDAVIDPYMLERAЕIMRGPVSVLYGKSSPGLLNMVSKRPTTEPLKEVQ
FKAGTDSLFTQGFDSDSLEDDGVSYRLTGLARSANAQQKGSEEQRYAIAPAFTWRPDDKTNFTFLSYFQNEP
ETGYYGWLPEGTVEPLPNGKRLPTDFNEGAKNNTYSRNEKMVGYSFDHEFNDTFTVRQNLRAENKTSQNS
VYGYGVCSDPANAYSQCAALAPADKGHYLARKYVVDEKLQNFSDTQLQSKFATGDIIDHTLLGVDFMRMR
NDINAWFYDDSVPLLNLYNPVNTDFDFNAKDPANSGPYRILNKQKQTGVYVQDQAQWDKVLVTLGGRYDW
ADQESLRVAGTTDKRDDKQFTWRGGVNYLFDNGVTPYFSYSESFEPSSQVGKDGNIFAPSKGKQYEVGVKYY
PEDRPIVVTGAVYNLTKTNLMADPEGSFFSVEGGEIRARGVEIEAKRPLSASVNVSYTYDAEYTTDTTYKG
NTPAQVPKHMASLWADYTFDGPLSGTLGTGGRTGSSYGDPANSFKVGSYTVDALVRYDLARVGMAGSN
VALHVNNLFDREYVASCFNTYGCFWGAERQVVAATFRF

>d1fepa_ f.4.3.3 (A:) Ferric enterobactin receptor FepA {Escherichia coli}

DDTIVVTAAEQNLQAPGVSTITADEIRKNPVARVSKIIRTMPGVNLGNSTSGQRGNRQDIRGMGPENTLIL
IDGKPVSSRNSVRQGWRGERDTRGDTSWVPPEMIERIEVLRGPAAARYGNGAAGGVVNIITKKGSGEWHGS
WDAYFNAPEHKEEGATKRTNFSLTGPLGDEFSFRLYGNLDKTQADAWDINQGHQSARAGTYATLPGREGVI
NKDINGVVRWDFAPLQSLLEAGYSRQGNLYAGDTQNTNSDSYTRS SKYGD ETNR LYRQNYALT WNGGWWDNG

VTTSNWVQYEHTRNSRIPEGLAGGTEGFNEKATQDFVDIDLDDVMLHSEVNLPIDFLVNQTLTGLEWNQQ
RMKDLSNTQALTGTNTGGAIDGVSTTDRSPYSKAEIFSLFAENNMELETDSTIVTPGLRFDHHSIVGNNSPAL
NISQGLGDDFTLKMGIARAYKAPSLYQTNPNYILYSKGQGCYASAGGCYLQGNDDLKAETSINKEIGLEFKRDG
WLAGVTWFRNDYRNKIEAGYVAVGQNAVGTDLQWDNVPKAVVEGLEGSLNVPVSETVMWTNNITYMLKS
ENKTTGDRLSIPEYTLNSTLWQAREDLSMQTTFTWYGKQQPKKYNKGQPAVGPETKEISPYSIVGLSATWD
VTKNVSLTGGVDNLFDKRLWRAGNAQTTGDLAGANYIAGAGAYTYNEPGRTWYMSVNTHF
>d1ek9a_f.5.1.1 (A:) Integral outer membrane protein TolC, efflux pump component {Escherichia coli}
ENLMQVYQQARLSNPELRKSAADRDAAFEKINEARSPLLPQLGLGADYTYSNGYRDANGINSNATASLQLTQS
IFDMMSKWRALTLQEKAAGIQDVYTQTDQQLILNTATAYFNVLNAIDVLSYTQAQKEAIYRQLDQTTQRFNVGL
VAITDVQNARAQYDVTLANELTARNNLNAVEQLRQITGNYYPELAALNVENFKTDKPQPVNALLKEAEKRNL
SLLQARLSQDLDAREQIRQAQDGHLPTLDLTASTGISDTSYSGSKTRGAAGTQYDDSNMGQNKGQVGLSFLPIYQG
GMVNSQVKQAQYNFVGASEQLESahrsvvQTVRSSFNNINASISSINAYKQAVVSAQSSLAMEAGYSGVTRT
IVDVLDATTLYNAKQELANARYNLYNQLNIKSLGTLNEQDLLALNNALSKPVSTNPE
>d7ahla_f.6.1.1 (A:) Alpha-hemolysin {Staphylococcus aureus}
ADSDINIKTGTTDIGSNTTVKTGDLVTYDKENGMHKKVFYSFIDDKNHNKLLVIRTKGTIAQGYRVYSEEGANK
SGLAWPSAFKVQLQLPDNEVAQISDYYPRNSIDTKEYMSTLTGFGNGNVTGDDTGKIGGLIGANVSIGHTLKYY
QPDKTILESPTDKKVGVWKVIFNNMVQNQWGPYDRDSWNPVYGNQLFMKTRNGSMKAADNFLDPNKASS
LLSSGFSPDFATVITMDRKASKQQTNIDVIYERVRDDYQLHWTSTNWKGNTDKWTDRSSERYKIDWEKEE
MTN
>d1pvl_f.6.1.1 (-) Leucocidin K component LukF-PV {Staphylococcus aureus}
AQHITPVSEKKVDDKITLYKTTATSDSDKLKISQILTFFNIKDKSYDKDTLILKAAGNIYSGYTKPNPKDTISSQFYW
GSKYNISINSDSNDSVVVYAPKNQNEEFQVQQTVGYSYGGDINISNGLGGGNGSKFSETINYKQESYRTSL
DKRTNFKKIGWDVEAHKIMNNNGWGPYGRDSYHSTYGNEMFLGSRQSNLNAGQNFLEYHKMPVLSRGNFNP
EFIGVLSRKQNAAKSKITVTYQREMDRYTNFWNQLHWIGNNYKDENRATHTSIYEVDWENHTVKLIDTQSKE
KNPMS
>d3lkfa_f.6.1.1 (A:) Leukocidin F (HlgB) {Staphylococcus aureus}
EGKITPVSKVDDKVTLYKTTATADSDKFKISQILTFFNIKDKSYDKDTLVLKATGNINSGFVKPNPNDYDFSKLY
WGAKYNVSISSQSNDSVVVYAPKNQNEEFQVQNTLGYTFGGDISISNGLGGLNGNTAFSETINYKQESYRT
TLSRNTNYKNVGVWVGEAHKIMNNNGWGPYGRDSFHPTYGNELFLAGRQSSAYAGQNFIAQHQMPLLSRSNF
NPEFLSVLSHRQDGAKKSITVTYQREMDLYQIRWNGFYWAGANYKNFKTRTFKSTYEIDWENHKVKLLDTKE
TENN
>d1prea2_f.8.1.1 (A:85-470) (Pro)aerolysin, pore-forming lobe {Aeromonas hydrophila}
IPTLSALDIPDGDEVDVQWRLVHDSANFIKPTSYLAHYLGYAWVGGNHSQYVGEDMDVTRDGDGVIRGN
DGGCDGYRCGDKTAIKVSNFAYNLDPSFKHGDVTQSDRQLVTVGVAVNDSDTPQSGYDVTLYDTATN
WSKTNTYGLSEKTTKNKFKWPLVGETELSIEIAANQSWASQNGGTTTSLQSVRPTVPARSKIPVKIELYKADI
SYPYEFKADVSYDLTSGFLRWGGNAWYTHPDNRPNWNHTFVIGPYKDKASSIRYQWDKRYIPGEVKWW
WNWTIQQNGLSTMQNNLARLRLPVRAGITGDFSAESQFAGNIEIGAPVPLAADSKVRRARSVDGAGQGLRLE
IPLDAQELSGLGFNNVSLSVTPAANQ
>d1pfo_f.9.1.1 (-) Perfringolysin {Clostridium perfringens}
DITDKNQSIDSGISSLSSYRNEVLASNGDKIESFVPKEGKKAGNKFIVVERQKRSLLTSPVDISIIDSVDNDRYPGA
LQLADKALVENRPTILMVKRKPININIDLPGPLKGSENSIKVDDPTYGVSGAIDELVSKWNEKYSSTHTLPARTQYS
ESMVYSKSQISSALNVNAKVLNSLGVDNAVANNEKKVMILAYKQIFYTVSADLPKNPSDLFDDSVTFNDLKQ
KGVSNEAPPLMVSNVAYGRTIYVKLETTSSKDQAAFKALIKNTDIKNSQQYKDIYENSSFTAVVLGGDAQEHN

KVVTKDFDEIRKVIKDNATFSTKNPAYPISYTSVFLKDNSVAAVHNKTDIETTSTEYSKGKINLDHSGAYVAQFEV
AWDEVSYDKEGNEVLTHKTWDGNYQDKTAHYSTVILEANARNIRIKARECTGLAWEWWRDVISEYDVPLTN
NINVIWGTTLYPGSSITYN
>d1svb_2 f.10.1.1 (1-302) Envelope glycoprotein, central and dimerisation domains
{Tick-borne encephalitis virus}
SRCTHLENRDFVTGTQGTTRTLVELEGGCVITAEGKPSMDVWLDAIQENPAKTREYCLHAKLSDTKVAARC
PTMGPATLAEEHQGGTVCKRDQS DRGWGNHCGLFGKGSIVACVKAACEAKKKATGHVYDANKIVYTAKVEP
HTGDYVAANETHSGRKTA SFTISSEK TILT MGEYGDVSLLCRVASGV DLAQTV IELDKT VEHLP TAWQVH RDW
FN DLAL PWKHEGAQNWNNAERLVEFGA PHAVKMDV YNLGDQTGV LLKALAGVPVA HIEG TKYHLKSGHVTC
EV GLEKLKMKG L
>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}
DGRPLAAAGIVVTGDKAVNIYTSSQTGSIIKKLXQITSPALTQLTIQALYNLAGGNMDYLLTKLGVGNNQLSSLISS
GLITGNPILYDSQTQLLG IQVTLPSVGNLNNMRATYLETSLVSTTKGFASALVPKVVTQGVSVIEELDTSYCIETDL
DLYCTRIVTFPMSPGIYSCLSGNTSACMYSKTEGALTPYMTLKGSVIANCKMTTCRCADPPGIISQNYGEAVSLI
DRQSCNILSLDGITLRLSGEF DATYQKNISI QDSQ
>d1acc_ f.11.1.1 (-) Anthrax protective antigen {Anthrax bacillus (Bacillus anthracis)}
SSSQGLLGYYFSDLNFQAPMVVTSS TGDL SIPSSELENIPSENQYFQS A IWSGF IKV KKSDEY TFAT SAD NHVT
MWVDDQE VINKA SNSNKIR LEKGR LYQIKI QYQREN PTEKGLDFKLYW TDSQ NKVEI SS DN LQLPELKQKSSN
SRKKRSTSAGPTV PDRNDGIPDSLEVEGYTVDVKNKR TLSPW ISNI HEKK GLT KYKSSPEK W STAS DPY SD F EK
VTGRIDKNV SPEARHPLV AAYPIVHVDMENI ILSKNEDQSTQNTDSETRTISKNTSTS RHT SEVHGNAEVHAS F
FDIGGSV SAGFSNSNSSTVAIDHSLSLAGERTWAETMGLNTADTARLNANIRYVNTGTAPIYNVLP TSLV LGKN
QTLATIKA KENQLSQ I LAPNNY YPSK NLAPI ALNAQDDFS STPITM NYNQF LEKTKQLR LTDQV YGNIATY NF
ENGR VRV DTGS NWSEV LPQI QETTARI IFNGKDLN LVERRIA AVNP SDPLETTKPD MTLKEALKIAFGF NEPNG
NLQYQGKDITEFDFNFDQQTSQNIKNQ LAELNAT NIYTV LDKIKLNAKM NI LIRD KRFHYDRNNIAVG ADES VV
KEAHREVINSSTEGLLNIDKDIRKILSGYI VEIEDTEGLKEVINDRYDMLN ISSLRQDGKTFIDFKKYNDKPL YISN
PNYKVNVYAVTKENTIINPSENGDTSTNGIKKILIFS KKG YEIG
>g1cph.1 g.1.1.1 (B:,A:) Insulin {Cow (Bos taurus)}
FVNQHLCGSHLVEALYLVCGERGFFYTPKAXGIVEQC CASVCSLYQLEN YCN
>g1pid.1 g.1.1.1 (B:,A:) Insulin {Cow (Bos taurus)}
FVNQHLCGSHLVEALYLVCGERGFFXGIVEQC CASVCSLYQLEN YCN
>d1fea_g.1.1.1 (A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSHLVEALYLVCGERGFFYTPKTRYPGDV KRGIVEQCCTSICSLYQLEN YCN
>g1a7f.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}
FVNQHLCGSHLVEALELVCGERGGFYTPKXGIVEQCCTSICSLYQLEN 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)}
FVNQHLCGSDLV EALYLVCGERGFFYTDKXGIVEQCCTSICSLYQLEN YCN
>g1vks.1 g.1.1.1 (B:,A:) Insulin {Human (Homo sapiens)}

FVNQHLCGSDLVEALYLVCGERGFYTAKPTXGIVEQCCTSICSLYQLENYCN
>d1zeia_g.1.1.1 (A:) Insulin {Pig (Sus scrofa)}
FVNQHLCGSHLVEALYLVCGERGFYTAKPTXGIVEQCCTSICSLYQLENYCN
>g1dei.1 g.1.1.1 (B;,A;) Insulin {Pig (Sus scrofa)}
FVNQHLCGSHLVEALYLVCGERGXGIVEQCCTSICSLYQLENYCN
>g1sdb.1 g.1.1.1 (B;,A;) Insulin {Pig (Sus scrofa)}
NQHLCGSHLVEALYLVCGERFFXGIVEQCCTSICSLYQLENYCN
>g6rlx.1 g.1.1.1 (B;,A;) Relaxin {Human (Homo sapiens)}
SWMEEVIKLCGRELVRAQIAICGMSTWXELYSALANKCCHVGCTKRSALARFC
>d1b9ga_g.1.1.1 (A;) Insulin-like growth factor {Human (Homo sapiens)}
GPETLCGAELVDALQFVCGDRGFYFNKPGIVDECCFRSCDLRRLEMYCAPLPAKSA
>d1igl_g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}
AYRPSETLCGGELVDTLQFVCGDRGFYFSRPASRVSSRGIVEECCFRSCDLALLETYCATPAKSE
>d1imxa_g.1.1.1 (A;) Insulin-like growth factor {Human (Homo sapiens)}
ETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIVDECCFRSCDLRRLEMYCAPL
>d2gf1_g.1.1.1 (-) Insulin-like growth factor {Human (Homo sapiens)}
GPETLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRAPQTGIVDECCFRSCDLRRLEMYCAPLPAKSA
>d3lria_g.1.1.1 (A;) Insulin-like growth factor {Human (Homo sapiens)}
MFPAAMPLSSLFVNGPRTLCGAELVDALQFVCGDRGFYFNKPTGYGSSSRACQTGIVDECCFRSCDLRRLEMYCAPLPAKSA
>g1bom.1 g.1.1.1 (B;,A;) Bombyxin-II {Silkworm (Bombyx mori)}
EQPQAVHTYCGRHLARTLADLCWEAGVDXGIVDECCRLRPCSVDVLLSYC
>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)}
ASATWGAAYPACENNCRKKYDLCIRCQKGWAGKRGKCAAHCIIQKNNCKGKCKKE
>d1wgta3_g.3.1.1 (A:87-129) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}
IKCGSQAGGKLCPPNNLCCSQWGYCGLGSEFCGEGCQNGACSTD
>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)}
ERCGEQGSNMECPNNLCCSQYGYCGMGGDYCGKGCGQNGACWTSKRCGSQAGG
>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)}
IKCGSQGGKLCPPNNLCCSQWFGCGLGSEFCGGGCQSGACSTD
>d9wgaa4_g.3.1.1 (A:130-171) Wheat germ agglutinin (WGA) {Wheat (Triticum vulgaris)}
KPCGKDAGGRVCTNNYCCSKWGSCGIGPGYCGAGCQSGGCDA
>d1ehda1_g.3.1.1 (A:1-45) Isolectin VI {Stinging nettle (Urtica dioica), UDA}
ERCGSQGGGATCPGLRCCSIWGWCGDSEPYCGRTCENKCWSGERS

>d1ehda2 g.3.1.1 (A:46-89) Isolectin VI {Stinging nettle (*Urtica dioica*), UDA}
DHRCGAAVGNPPCGQDRCCSVHGWCGGGNDYCSGGKCQYRCSSS

>d1en2a1 g.3.1.1 (A:1-45) Isolectin VI {Stinging nettle (*Urtica dioica*), UDA}
ERCGSQGGGGTCPALWCCSIWGWCGDSEPYCGRTCENKCWSGERS

>d1en2a2 g.3.1.1 (A:46-86) Isolectin VI {Stinging nettle (*Urtica dioica*), UDA}
DHRCGAAVGNPPCGQDRCCSVHGWCGGGNDYCSGSKCQYRC

>d1hev__ g.3.1.1 (-) Hevein {Hevea brasiliensis}
EQCGRQAGGKLCPPNNLCCSQWGWCGSTDEYCSPDHNCQSNCKD

>d1mmc__ g.3.1.2 (-) Antimicrobial peptide 2, AC-AMP2 {Tassel (*Amaranthus caudatus*)}
VGECVRGRCPSGMCCSQFGYCGKGPKYCGR

>d1f2si_ g.3.2.1 (I:) Trypsin inhibitor {Bitter gourd (*Momordica charantia*), linn. Cucurbitaceae, seed}
RICPRIWMECKRDSDCMaecicVMGHCG

>d1mcti_ g.3.2.1 (I:) Trypsin inhibitor {Bitter gourd (*Momordica charantia*), linn. Cucurbitaceae, seed}
RICPRIWMECTRDSDCMAKCICVAGHCG

>d2stai_ g.3.2.1 (I:) Trypsin inhibitor {Squash (*Cucurbita maxima*)}
RVCPRILMECKKDSDCLAEVCVLEHGYCG

>d1ha9a_ g.3.2.1 (A:) Trypsin inhibitor {Spiny bitter cucumber (*Momordica cochinchinensis*), MCOTI-II}
SGSDGGVCPKILKKRRCSDCPGACICRGNGYCG

>d2btci_ g.3.2.1 (I:) Trypsin inhibitor {Vegetable marrow (*Cucurbita pepo*)}
RVCVKILMECKKDSDCLAEVCICLEHGYCG

>d2let__ g.3.2.1 (-) Trypsin inhibitor {Jumping cucumber (*Ecballium elaterium*)}
GCPRLLMRCKQDSCLAGCVCGPNGFCG

>d4cpai_ g.3.2.1 (I:) Carboxypeptidase A inhibitor {Potato}
ZHADPICNKPCCKTHDDCSGAWFCQACWNSARTCGPYV

>d1clvi_ g.3.2.1 (I:) alpha-amylase inhibitor (AAI) {Prince's feather (*Amaranthus hypochondriacus*)}
CIPKWNRCPKMDGVPCCEPYTCTSDYYGNCS

>d1kal__ g.3.3.1 (-) Kalata B1 {African plant (*Oldenlandia affinis dc*)}
SWPVCTRNLGPVCGETCVGGTCNTPGCTC

>d1df6a_ g.3.3.2 (A:) Cycloviolacin O1 {Plant (*Viola odorata*)}
SCVYIPCTVTALLGCSCSNRVCYNGIPCAE

>d1bh4__ g.3.3.3 (-) Circulin A {Chassalia parviflora}
CGESCVWIPCISAALGCSCKNKCYRNGIP

>d1c4ea_ g.3.4.1 (A:) Gurmarin, a sweet taste-suppressing polypeptide {Gymnema sylvestre}
EQCVKKDELCPYYLDCEPLECKKVNWWDHKCIG

>d1dkca_ g.3.4.2 (A:) Antifungal peptide PAFP-S {Pokeweed (*Phytolacca americana*)}
AGCIKNGGRCNASAGPPYCCSSYCFQIAGQSYGVCKNR

>d1hyka_ g.3.5.1 (A:) Agouti-related protein {Synthetic, based on *Homo sapiens* sequence}
CVRLHESCLGQQVPCCDPATCYCRFFNAFCYCRKLGTAMNPCSRT

>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}
ACSGRGSRCPQCCMGLRCGRGNPQKCIGAHEDV
>d1cnna_ g.3.6.1 (A:) Conotoxin {Sea snail (Conus magus), M VIIc}
CKKGKAPCRKTMYDCCSGSGCRGKCK
>d1omg__ g.3.6.1 (-) Conotoxin {Sea snail (Conus magus), M VIIa}
CKKGKAKCSSLMYDCCSGSGCRGKCK
>d1mvj__ g.3.6.1 (-) Conotoxin {Conus striatus, S VIb}
CKLKGQSCRKTSYDCCSGSGCRGKCK
>d1fyga_ g.3.6.1 (A:) Conotoxin {Conus striatus, SO3}
CKAAGKPCSRIAYNCCTGSCRSRGKCK
>d1kcp__ g.3.6.1 (-) Conotoxin {Conus purpurascens, kappa-pVIIa}
CRIPNQKCFQHLDCCSRKCNRFNKCV
>d1eyoa_ g.3.6.1 (A:) Conotoxin {Conus tulipa, T VIIa}
SCSGRDRCPPVCCMGLMCSRKGKCVSIYGE
>d1g1za_ g.3.6.1 (A:) Conotoxin {Conus ermineus, E VIa}
DDCIKPYGFCSLPIKNGLCCSGACVGVCADL
>d1f3ka_ g.3.6.1 (A:) Conotoxin {Conus textile, Tx VII}
CKQADEPCDVFSLDCCGTICLGVCMW
>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)}
ECVPENGHCRDWYDECCEGFYCSCRQPPKICRNNNN
>d1kqha_ g.3.6.2 (A:) ACTX-HI:OB4219 {Funnel-web spider (Hadronyche infensa)}
KCLAEAADCSPWSGDSCCKPYLCSCIFFYPCSCRPKG
>d1axh__ g.3.6.2 (-) Atracotoxin-hvl (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}
SPTCIPSGQPCPYNENCCSQSCTFKENENGNTVKRCD
>d1hvwa_ g.3.6.2 (A:) Atracotoxin-hvl (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}
CIPSGQPCPYNENCCSQSCTGGRCD
>d1vtx__ g.3.6.2 (-) Atracotoxin-hvl (versutoxin) {Australian funnel-web spider (Hadronyche versuta)}
CAKKRNWCGKTEDCCPMKCVYAWYNEQGSCQSTISALWK
>d1dl0a_ g.3.6.2 (A:) J-atracotoxin-hv1c {Australian funnel-web spider (Hadronyche versuta)}
AICTGADRCAACCPCCPGTSCKAESNGVSYCRKDEP
>d1g9pa_ g.3.6.2 (A:) Atracotoxin-hv2a {Funnel-web spider (Hadronyche versuta)}
LLACLFNGNRCSSNRDCCELTPVCKRGSCVSSGPGLVGGILGGIL
>d1qdp__ g.3.6.2 (-) Robustoxin {Funnel-web spider (Atrax robustus)}

CAKKRNWCGKNEDCCCPMKCIYAWYNQQGSCQTTITGLFKKC
>d1qk6a_g.3.6.2 (A:) Huwentoxin-I {Chinese bird spider (Selenocosmia huwena)}
ACKGVFDACTPGKNECCPNRVCSDKHKWCKWKL
>d1i25a_g.3.6.2 (A:) Huwentoxin-II {Chinese bird spider (Selenocosmia huwena)}
LFECFSCEIEKEGDKPCKKKCKGGWKCKFNMVCVKV
>d1qk7a_g.3.6.2 (A:) Lectin SHL-I {Chinese bird spider (Selenocosmia huwena)}
GCLGDKCDYNNNGCCSGYVCSRTWKWCVLAGPW
>d1d1ha_g.3.6.2 (A:) Hanatoxin 1 {Tarantula (Grammostola spatulata)}
ECRYLFGGCKTSDCCHLGCKFRDKYCAWDFTS
>d1emxa_g.3.6.2 (A:) Heteropdatoxin 2, hptx2 {Spider (Heteropodidae venatoria)}
DDCGKLFGCDTNADCCEGYVCRLWCKLDW
>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}
KEGYLVNKSTGCKYGLKLGENEGCDKECKAKNQGGSYGACYAFACWCEGLPESTPTYPLPNKSCS
>d2sn3_g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing, variant 3}
KEGYLVKKSDGCKYGLKLGENEGCDTECKAKNQGGSYGACYAFACWCEGLPESTPTYPLPNKSC
>d1b3ca_g.3.7.1 (A:) Scorpion toxin {Centruroides sculpturatus ewing, beta}
KDGYLVEKTGCKKTCYKLGENDFCNRECKWKHIGGSYGYCYGFGCYCEGLPDSTQTWPLPNKTC
>d1vnb_g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing, variant 1}
KEGYLVKKSDGCKYDCFWLGKNEHCNTECKAKNQGGSYGACYAFACWCEGLPESTPTYPLPNKSC
>d1nrb_g.3.7.1 (-) Scorpion toxin {Centruroides sculpturatus ewing, variant V}
KKDGYPVDGNCYCLKDDYCNDLCLERKADKGYCYWGVKSCYGLPDNSPTKSGKCNPA
>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}
KEGYLVDKNTGCKYECCLKLGNDYCLRECKQQYGKGAGGYCYAFACWCTHLYEQAIWPLPNKRC
>d1bcg_g.3.7.1 (-) Scorpion toxin {Scorpion (Buthotus judaicus), BXTR-IT}
MKKNGYPLDRNGKTTECSGVNAIAPHYCNECTKVYYAESGYCCWGACYCFGLEDDKPIGPMKDITKKYCDVQ
I
>d1snb_g.3.7.1 (-) Scorpion toxin {Scorpion (Buthus martensii), toxin m8}
GRDAYIADSENCTYFCGSNPYCNDVCTENGAKSGYQWAGRYGNACYCIDLPASERIKEGGRCG
>d1djta_g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus martensii), toxin m1}
VRDAYIAKPHNCVYECARNEYCNDLCTKNGAKSGYQWVGKYNGNCWCIELPDNVPIRPGKCH
>d1sn4a_g.3.7.1 (A:) Scorpion toxin {Chinese scorpion (Buthus martensii), toxin m4}
VRDAYIAKPENCYHAGNEGCKLCTDNAESGYCQWGGGRYGNACWCICLPPDVPIRPGKCH
>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)}
KEGYLMDHEGCKLSCFIRPSGYCGRECGIKKGSSGYCAWPACYCYGLPNWVKVWDRATNKC
>d1i6fa_g.3.7.1 (A:) Scorpion toxin {Bark scorpion (Centruroides sculpturatus), cse-v5}

KDGYPVDSKGCKLSCVANNYCDNQCKMKKASGGHCYAMSCYCEGLPENAKVSDSATNICG
>d1lqq__ g.3.7.1 (-) alpha toxin {Leiurus quinquestriatus quinquestriatus, LQQIII}
VRDAYIAKNYNCVYECFRDSYCNDLCTKNGASSGYCQWAGKYGNACWCYALPDNVPIRVPGKCH
>d1lqi__ g.3.7.1 (-) alpha toxin {Scorpion (Leiurus quinquestriatus hebraeus)}
MVRDAYIAKNYNCVYECFRDAYCNELETCKNGASSGYCQWAGKYGNACWCYALPDNVPIRVPGKCR
>d1bmr__ g.3.7.1 (-) LQH III alpha-like toxin, LQH {Hebraei scorpion (Leiurus quinquestriatus hebraeus)}
VRDGYIAQPENCVYHCFPGSSGCDTLCKEKGTSGHCGFKVGHGLACWCNALPDNVGIIVEGEKCHS
>d1big__ g.3.7.2 (-) Bmtx1 {Buthus martensii}
EFTDVVKCTGSKQCWPVCKQMFGKPNGKCMNGKCRCYS
>d1bkt__ g.3.7.2 (-) Bmctx {Buthus martensii}
VGINVKCKHSGQCLPKCKDAGMRFGKCINGKCDCTPK
>d2bmt__ g.3.7.2 (-) Bmtx2 {Buthus martensii}
EFTNVSCSASSQCWPVCKLFGTYRGKCMNSKRCYS
>d1du9a_g.3.7.2 (A:) Bmp02 neurotoxin {Chinese scorpion (Buthus martensii)}
VGCEECPMHCKGKNAKPTCDDGVCNCNV
>d1hp2a_ g.3.7.2 (A:) alpha-KTX, K+-channel blocker {Brazilian scorpion (Tityus serrulatus), Tstx-k alpha}
VFINAKCRGSPECLPKCKEAIGKAAGKCMNGKCKCYP
>d1jlza_g.3.7.2 (A:) alpha-KTX, K+-channel blocker {Scorpion (Tityus cambridgei)}
ACGSCRKKCKGSGKCINGRCKY
>d1mtx__ g.3.7.2 (-) Margatoxin {Scorpion (Centruroides margaritatus)}
TIINVKCTSPKQCLPPCKAQFGQSAGAKCMNGKCKCYPH
>d1sxm__ g.3.7.2 (-) Noxiustoxin {Scorpion (Centruroides noxius hoffmann)}
TIINVKCTSPKQCSKPCKELYGSSAGAKCMNGKCKCYNN
>d1txm__ g.3.7.2 (-) Maurotoxin {Scorpion (Scorpio maurus)}
VSCTGSKDCYAPCRKQTGCPNAKCINKSCKCYGC
>d1cmr__ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
CTTSKECWVCQRLHNTSKGWCDHRGCICES
>d2crd__ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
EFTNVSCTSKECWVCQRLHNTSRGKCMNNKKCRCYS
>d1scy__ g.3.7.2 (-) Scyllatoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
AFCNLRMQQLSCRSLGLGKCI GDKCECVKH
>d1agt__ g.3.7.2 (-) Agitoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
GVPINVSGSPQCIKPCDKAGMRFGKCMNRKCHCTPK
>d1chl__ g.3.7.2 (-) Chlorotoxin {Scorpion (Leiurus quinquestriatus), venom}
MCMPCTTDHQMARKCDDCCGGKGRGKCYGPQCLCR
>d1c55a__ g.3.7.2 (A:) Butantoxin {Brazilian scorpion (Tityus serrulatus)}
WCSTCLDLACGASRECYDPCFKAFGRAHGKCMNNKRCYT
>d1tsk__ g.3.7.2 (-) Toxin ts kappa {Scorpion (Tityus serrulatus)}
VVIGQRCYRSPDCYSACKLVLGKATGKCTNGRCDC
>d1sis__ g.3.7.2 (-) Toxin I5a {Scorpion (Buthus eupeus)}
MCMPCTTDPNMAKKCRDCCGGNGKCFGQPQCLCNR
>d1pnh__ g.3.7.2 (-) Toxin analog {Scorpion (Androctonus mauretanicus mauretanicus)}

TVCNLRCQLSCRSLGLGKCIGVKCECVKH
>d1acw_ g.3.7.2 (-) Toxin analog P01 {Scorpion (Androctonus mauretanicus mauretanicus)}
VSCEDCPEHCSTQKAQAKCDNDKCVCEPI
>d1sco_ g.3.7.2 (-) OSK1 TOXIN {Central asian scorpion (Orthochirus scrobiculosus)}
GVIINVKCKISRQCLEPCKKAGMRFGKCMNGKCHCTPK
>d2ktx_ g.3.7.2 (-) Kaliotoxin (KTX) {Scorpion (Androctonus mauretanicus mauretanicus)}
GVEINVKCSGSPQCLPKCKDAGMRFGKCMNRKCHCTPK
>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
>d1qkya_ g.3.7.2 (A:) PI7 {Scorpion (Pandinus imperator)}
DEAIRCTGTKDCYIPCRYITGCFNSRCINKSCKCYGCT
>d1fjna_ g.3.7.3 (A:) Defensin MGD-1 {Mediterranean mussel (Mytilus galloprovincialis)}
GFGCPNNYQCHRHKSIPIGRGGYCGGWHLRCTCYRCG
>d1i2ua_ g.3.7.4 (A:) Heliomycin {Tobacco budworm (Heliothis virescens)}
DKLIGSCVWGAVNYTSDCNAGECKRRGYKGGHCGSFANVNCWCET
>d1myn_ g.3.7.4 (-) Drosomycin {Fruit fly (Drosophila melanogaster)}
DCLSGRYKGPCAVWDNETCRVCKEEGRSSGHCSPLKCWCEGC
>d1ica_ g.3.7.4 (-) Defensin A {Flesh fly (Phormia terranova), larva}
ATCDLLSGTGINHSACAHCLLRGNRGGYCNGKGVCVCRN
>d1gpt_ g.3.7.5 (-) gamma-Thionin {Barley (Hordeum vulgare)}
RICRRRSAGFKGPCVSNKCAQVCMQEGWGGNCGPLRRCKCMRRC
>d1gps_ g.3.7.5 (-) gamma-Thionin {Wheat (Triticum turgidum)}
KICRRRSAGFKGPCMSNKCAQVCQQEGWGGNCGPFRRKCIROQC
>d1ayj_ g.3.7.5 (-) Antifungal protein 1 (RS-AFP1) {Radish (Raphanus sativus)}
EKLCERPSGTWSGVCGNNACKNQCINLEKARHGSCNYVFPAHKCICYFPC
>d1bk8_ g.3.7.5 (-) Antimicrobial protein 1 (AH-AMP1) {Horse chestnut (Aesculus hippocastanum)}
LCNERPSQTWSGNCGNTAHCDKQCQDWKEASHGACHKRENHWKCFCYFNC
>d1jkza_ g.3.7.5 (A:) Defensin 1 (PSD1) {Pea (Pisum sativum)}
KTCEHLADTYRGVCFTNASCDHCKNKAHLISGTCHNWKCFCTQNC
>d1brz_ g.3.7.5 (-) Brazzein {J'oublie (Pentadiplandra brazzeana)}
EDKCKVYENYPVSKCQLANQCNYDCKLDKHARSGEFYDEKRNLQCIDYCEY
>d2cbh_ g.3.8.1 (-) Cellobiohydrolase I {Trichoderma reesei, ct-cbh I}
TQSHYGQCGGIGYSGPTVCASGTTCQVLNPYYSQCL
>d1boea_ g.3.9.1 (A:) Insulin-like growth factor-binding protein-5 (IGFBP-5) {Human (Homo sapiens)}
ALAEGQSCGVYTERCAQGLRCLPRQDEEKPLHALLHGRGVCLNEKS
>d1igra3 g.3.9.1 (A:150-299) Cys-rich domain of the type 1 insulin-like growth factor receptor {Human (Homo sapiens)}
DLCPGTMEEKPMCEKTTINNEYNYRCWTTNRCQKMCPCSTCGKRACTENNECCHPECLGSCSAPDNDTACVA

CRHYYYAGVCVPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVIHDGECMQECPSGFIRNGSQSMYCIP
CEGPCP
>d1lpba1 g.3.10.1 (A:6-44) (Pro)colipase {Pig (Sus scrofa)}
GIIINLDEGECLNSAQCKSNCCQHDTILSLSRALKAR
>d1lpba2 g.3.10.1 (A:45-90) (Pro)colipase {Pig (Sus scrofa)}
ENSECSAFTLYGVYYKPCERGLTCEGDKSLSVGSIINTNFGICHNV
>d1pco_1 g.3.10.1 (1-44) (Pro)colipase {Pig (Sus scrofa)}
VPDPRGIIINLDEGECLNSAQCKSNCCQHDTILSLSRALKAR
>d1imt_1 g.3.10.1 (1-36) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}
AVITGACERDLQCGKGTCNAVSLWIKSVRVCTPVGT
>d1imt_2 g.3.10.1 (37-80) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}
SGEDCHPASHKIPFSGQRMHHTCPACPNLACVQTSPKKFKCLSK
>d1edmb_ g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}
VDGDQCESNPCLNGGSCKDDINSYECWCPEGFKNCEL
>d1rfnb_ g.3.11.1 (B:) Factor IX (IXa) {Human (Homo sapiens)}
MTCNIKNGRCEQFCKNSADNKVVCSCTEGYRLAENQKSCPAVPFPCGRVSQSQTSK
>d1pxl1 g.3.11.1 (L:47-86) Factor IX (IXa) {Pig (Sus scrofa)}
DGDQCEPNPCLNGGLCKXDINSYECWCQVGFEKGKCELDA
>d1pxl2 g.3.11.1 (L:87-146) Factor IX (IXa) {Pig (Sus scrofa)}
TCNIKNGRCKQFCKTGADSKVLCSCTTYRLAPDQKSCPKPAVPFPCGRVSVHSPTTLTR
>d1danl1 g.3.11.1 (L:49-86) Coagulation factor VIIa {Human (Homo sapiens)}
QCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKD
>d1danl2 g.3.11.1 (L:87-142) Coagulation factor VIIa {Human (Homo sapiens)}
DQLICVNENGCEQYCSHTGTKRSCRCHEGYSLADGVSCTPTVEYPCGKIPILE
>d1dval1 g.3.11.1 (L:42-86) Coagulation factor VIIa {Human (Homo sapiens)}
ISYSDGDQCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKD
>d1f7ea_ g.3.11.1 (A:) Coagulation factor VIIa {Human (Homo sapiens)}
SDGDQCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCETHKD
>d1g1sa2 g.3.11.1 (A:119-158) E-selectin, EGF-domain {Human (Homo sapiens)}
TASCDMMSCSKQGECLETIGNYTCSCYPGFYGPCEYVRD
>d1g1ta2 g.3.11.1 (A:119-157) E-selectin, EGF-domain {Human (Homo sapiens)}
TAACNTSCSGHGEVCETINNYTCKCDPGFSGLKCEQIV
>d1fjsl_ g.3.11.1 (L:) Factor X, N-terminal module {Human (Homo sapiens)}
KLCSDLNGDCDQFCHEEQNSVVCSCARGYTLADNGKACIPTGPYPCGKQTL
>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)}
KGDGDQCEGHPCLNQGHCKDGIGDYTCTCAEGFEGKNCEFSTR
>d1kigl_ 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)}
QCLVLPLEHPCASLCCGHGTCIDGIGSFSCDCRGWEGRFCQREVSFL
>d1autl2 g.3.11.1 (L:97-146) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}
NCSDLNGGCTHYCLEEVGWRRSCAPGYKLGDDLLQCHPAVKFPCGRPWK

>d1eqga2 g.3.11.1 (A:33-73) Prostaglandin H2 synthase-1, EGF-like module {Sheep (Ovis aries)}
VNPCCYPCQHQGICVRGLDRYQCDCTRTGYSGPNCTIPE

>d1cvua2 g.3.11.1 (A:33-73) Prostaglandin H2 synthase-1, EGF-like module {Mouse (Mus musculus)}
ANPCCSNPCQRGECMSTGFDQYKCDCTRTGFYGENCTTPE

>d1a3p__ g.3.11.1 (-) Epidermal growth factor, EGF {Mouse (Mus musculus)}
PGXPSSYDGYCLNGGVXMHIESLDSYTCNCVIGYSGDRCQTRDLR

>d3egf__ g.3.11.1 (-) Epidermal growth factor, EGF {Mouse (Mus musculus)}
NSYPGCPSSYDGYCLNGGVCMHIESLDSYTCNCVIGYSGDRCQTRDLRWELR

>d1jl9a_g.3.11.1 (A:) Epidermal growth factor, EGF {Human (Homo sapiens)}
CPLSHDGYCLHDGVCMYIEALDKYACNCVVGYIGERCQYRDL

>d3tgf__ g.3.11.1 (-) Transforming growth factor alpha {Human (Homo sapiens)}
VVSHFNDCPDSDHTQFCFHGTCRFLVQEDKPACVCHSGYVGARCEHADLLA

>d1xdtr_g.3.11.1 (R:) Heparin-binding epidermal growth factor, HBEGF {Human (Homo sapiens)}
PCLRKYKDFCIHGEKYVKELRAPSCICHPGYHGERCHGLS

>d1urk_1 g.3.11.1 (6-49) Plasminogen activator (urokinase-type) {Human (Homo sapiens)}
QVPSNCDCLNNGTCVSNKYFSNIHWCPNPKFGQQHCEIDKSKT

>d1hae__ g.3.11.1 (-) Heregulin-alpha, EGF-like domain {Human (Homo sapiens)}
SHLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTENVPMKVQNQEKAEELY

>d1adx__ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
QMFCNQTACPADCDPNTQASCECPEGYILDDGFICTDIDE

>d1dx5i1 g.3.11.1 (I:345-387) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
VEPVDPFRANCEYQCQPLDQTSYLCVCAEGFAPIPHEPHRCQ

>d1dx5i2 g.3.11.1 (I:388-422) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
MFCNQTACPADCDPNTQASCECPEGYILDDGFICT

>d1dx5i3 g.3.11.1 (I:423-462) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
DIDECENGGFCGVCHNPGTFECICGPDSALAGQIGTDC

>d1zaq__ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
EPVDPFRANCEYQCQPLNQTSYLCVCAEGFAPIPHEPHRCQMF

>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)}
TDECSPGNPCGNGTCKNVIGGFECTCEEGFEPGPMMTCE

>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)}
CSEPRCFNNGTCQQALYFSDFVCQCPEGFAGKSCEIDTRAT

>d1hz8a1 g.3.11.1 (A:1-41) Low density lipoprotein (LDL) receptor, different EGF domains {Human

{Homo sapiens}}

GTNECLDNNGGCSHVCNDLKIGYECLCPDFQLVAQRRCED

>d1hz8a2 g.3.11.1 (A:42-82) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}

IDEAQDPDTCSQLCVNLEGGYKCQCEEGFQLDPHTKACKAV

>d1ijqa2 g.3.11.1 (A:643-692) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}

VNWCERTTLSNGGCQYLCLPAPQINPHSPKFTACPDGMILLARDMRSCLT

>d1jv2b4 g.3.11.6 (B:532-562) Integrin beta EGF-like domains {Human (Homo sapiens)}

KGEMCSGHGQCSCGDCLCDSDWTGYYCNCTT

>d1jv2b5 g.3.11.6 (B:563-605) Integrin beta EGF-like domains {Human (Homo sapiens)}

RTDTCMISSNLLCSRHKCECGSCVCIQPGSYGDTCEKCPTCP

>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)}

CPCPGGSSCAIVPKTKEVVCTHCPTGTAGKRCELDDGYFGDPLGSNGPVRLCRP

>d1klo_2 g.3.11.2 (66-121) Laminin gamma1 chain {Mouse (Mus musculus)}

CQCNDNIDPNAVGNCNRLTGECLKCIYNTAGFYCDRCKEGFFGNPLAPNPADKCKA

>d1klo_3 g.3.11.2 (122-172) Laminin gamma1 chain {Mouse (Mus musculus)}

CACNPYGTVQQQSSCNPVTGQCQCLPHSGRDCGTCDPGYYNLQSGQGCER

>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}

NISQHQCVKKQCPQNSGCFRHLDEREECKCLNYKQEGDKCVENP

>d1ceja2 g.3.11.4 (A:46-96) Merozoite surface protein 1 (MSP-1) {Plasmodium falciparum}

NPTCNENNGGCDADAKTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSSN

>d2bi6h1 g.3.12.1 (H:8-31) Bromelain inhibitor VI (cysteine protease inhibitor) {Pineapple (Ananas comosus)}

TDTYSDCPGFCKTCAEFGKYICL

>g2bi6.2 g.3.12.1 (L:,H:1-7,H:32-41) Bromelain inhibitor VI (cysteine protease inhibitor) {Pineapple (Ananas comosus)}

TACSECVCPLRXEYKCYCXDLISPNDCK

>d1pi2__ g.3.13.1 (-) Bowman-Birk inhibitor, BBI {Soybean (Glycine max), PI-II}

YSKPCCDLCMCTRSMPPQCSCEDRINSCHSDCKSCMCTRSQPGQCRLDTNDFCYKPCRSR

>d1d6ri_g.3.13.1 (I:) Bowman-Birk inhibitor, BBI {Soybean (Glycine max)}

KPCCDQCACTKSNPPQCRCSDMRLNSCHSACKSCICALSYPAQCFCVDITDFCYEPCK

>d2bbi__g.3.13.1 (-) Bowman-Birk inhibitor, BBI {Soybean (Glycine max)}

DDESSKPCCDQCACTKSNPPQCRCSDMRLNSCHSACKSCICALSYPAQCFCVDITDFCYEPCKPSEDDKEN

>d1pbia_g.3.13.1 (A:) Bowman-Birk inhibitor, BBI {Winter pea (Pisum sativum)}

KSACCDTCLCTKSNPPTCRCDVGETCHSACLSCICAYSNPPKCQCFDTQKFCYKQCHNSELEEVIKN

>d1df9c_g.3.13.1 (C:) Bowman-Birk inhibitor, BBI {Mung bean (Vigna radiata)}

SHDEPSESSEPCCDSCDCTKSIPPQCHCANIRLNSCHSACKSCICTRSMPGKRCRCLDDFCYKPCESMDKD

>d1c2aa1 g.3.13.1 (A:4-64) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}

KRPWKCCDEAVCTRSIPPICTCMDEVFECPKTCKSCGPGMDPSRRICQDQYVGDPGPICR

>d1c2aa2 g.3.13.1 (A:65-123) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}

PWECCDKAICTRSNPPTCRCDEVKKCAPTCKTCLPSRSRPSRRVCIDSYFGPVPPRCT

>d1tabi_ g.3.13.1 (I:) Bowman-Birk inhibitor, BBI {Adzuki bean (Phaseolus angularis)}

SESSKPCCDQCSCTKSMPPKRCSDIRLNSCHSACKSCACTYSIPAKCFCTDINDFCYEPCK

>d1flei_g.3.14.1 (I:) Elafin, elastase-specific inhibitor {Human (Homo sapiens)}

TKPGSCPPIILRCAMLNPPNRCLKDTDCPGIKKCCEGSGMACFVPQ

>d2rel_ g.3.14.1 (-) Elafin, elastase-specific inhibitor {Human (Homo sapiens)}

AQEPVKGPVSTKPGSCPPIILRCAMLNPPNRCLKDTDCPGIKKCCEGSGMACFVPQ

>d1bx7_ g.3.15.1 (-) Hirustasin {Medicinal leech (Hirudo medicinalis)}

GNTCGGETCSAAQVCLKGKCVNEVHCRIRCKYGLKKDENGEYPCSCAKA

>d1ejab_ g.3.15.1 (B:) Bdellastasin {Medicinal leech (Hirudo medicinalis)}

TPPCGPVTCSCGAQMCEVDKCVSDLHCKVKCEHGFKDDNGCEYACICADAPQ

>d1skz_1 g.3.15.1 (7-58) Factor Xa inhibitor antistasin {Mexican leech (Haementeria officinalis)}

GCEEAGCPEGSACNIITDRCTSGVRCRVHCPHGFQRSRYGCEFCKCRLEPM

>d1skz_2 g.3.15.1 (59-110) Factor Xa inhibitor antistasin {Mexican leech (Haementeria officinalis)}

KATCDISECPGMMCSRLTNKCDCKIDINCRKTCPNGLKRDKLGEYCECRP

>d1hic_ g.3.15.2 (-) Hirudin {Leech (Hirudo medicinalis)}

VVYTDCTESGQNLCLEGSNVCGQGNKCLGSDGEKNQCVTGEGTPKPQSHNDGDFEEIPEEYLQ

>d1hrti_ g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}

VVYTDCTESGQNLCLEGSNVCGQGNKCLGSDGEKNQCVTGEGTPKPQSHNDGDFEEIPEEYLQ

>d4htci_ g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}

ITYTDCTESGQNLCLEGSNVCGKGNKCLGNGKGNQCVTGEGTPKPESHNNGDFEEIPEEYLQ

>d1dec_ g.3.15.2 (-) Decorsin {North american leech (Macrobdella decora)}

APRLPQCQGDDQEKCCLNKDECPPGQCRFPRGDADPYCE

>d1e0fi_ g.3.15.2 (I:) Haemadin {Indian leech (Haemadipsa sylvestris)}

IRFGMGKVPCPDGEVGYTDCGEKICLYQQSCNDGQCSGDPKPSSEFFEIIDEEEK

>d1qgma_ g.3.16.1 (A:) N-terminal domain of granulin-1 {Carp (Cyprinus carpio)}

VIHCDAATICPDGTTCSLSPYGVWYCSPFS

>d1g26a_ g.3.16.1 (A:) N-terminal domain of granulin-1 {Human (Homo sapiens)}

VVHCDMEVICPDGYTCCRLPSGAWGCCPFTQ

>d1fwoa_ g.3.16.1 (A:) Oryzain beta chain {Rice (Oryza sativa)}

DHVCDDNFSCPAGSTCSSAFGFRNLSLVWGSPVE

>d1hy9a_ g.3.17.1 (A:) Satiety factor CART (cocaine and amphetamine regulated transcript) {Human (Homo sapiens)}

YGQVPMCDAGEQCAVRKGARIGKLCDPRGTSCNSFLKCL

>d1gl1i_g.4.1.1 (I:) Protease inhibitor PMP-C {Migratory locust (Locusta migratoria)}
ISCEPGKTFDKCNCRCGADGKSAACTLKACPN

>d1gl0i_g.4.1.1 (I:) Protease inhibitor PMP-D2V {Migratory locust (Locusta migratoria)}
KCTPGQVKQQDCNTCTPTGVWGCTLMGCP

>d1kgma_g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}
EVTCEPGTTFKDKCNCRCGSDGKSAACTLKACPQ

>d1kioa_g.4.1.1 (A:) Protease inhibitor SGCI {Desert locust (Schistocerca gregaria)}
EVTCEPGTTFKDKCNCRCGSDGKSAACTRMACPQ

>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}
KKDKVKKGPGSECAEWAWGPCTPSSKDCGVGFREGTCGAQTQRIRCRVPCNWKEFG

>d1mkca_g.5.1.2 (A:) Midkine, a heparin-binding growth factor, C-terminal domain {Synthetic}
CKYKFENWGACDGGTGTKVQRQGTLKKARYNAQCQETIRVTKPC

>d2bbg_g.6.1.1 (-) Amb V allergen {Giant ragweed (Ambrosia trifida), pollen}
DDGLCYEGTNCGKVGKYCCSPIGKYCVCYDSKAICNKNCT

>d3ebx_g.7.1.1 (-) Erabutoxin B (also neurotoxin B) {Sea snake (Laticauda semifasciata)}
RICFNHQSSQPQTTKTCSPGESSCYHKQWSDFRGTIERGCGCPTVKPGIKLSCCEVCNN

>d1tgxa_g.7.1.1 (A:) gamma-Cardiotoxin {Snake (Naja nigriceps)}
LKCNQLIPPFWKTCPKGKNLCYKMTMRAAPMVPVKRGCIDVCPKSSLIKYMCCNDKCN

>d1fas_g.7.1.1 (-) Fasciculin {Green mamba (Dendroaspis angusticeps)}
TMCYSHHTTSRAILTNCGENSCYRKSRRHPPKMVLGRGCGCPCGDDYLEVKCCTSPDKCNY

>d1qm7a_g.7.1.1 (A:) Fasciculin {Green mamba (Dendroaspis angusticeps)}
TMCYSHHTTSRAILTNCPGETNCYKKSRRHPPKMVLGRGCGCPTVAPGIKLNCCTTDKCNY

>d1ntn_g.7.1.1 (-) Neurotoxin I {Snake (Naja naja oxiana)}
ITCYKTPIISETCAPGQNLCYKTWCDAWCGSRGKIELGCAATCPTVESYQDIKCCSTDNCNPHPKQKRP

>d1cdta_g.7.1.1 (A:) Cardiotoxin V4II (Toxin III) {Naja mossambica mossambica}
LKCNKLIPIAYKTCPEGKNLCYKMMMLASKKMVPVKRGCINVCPKNSALVKYVCCSTDRCN

>d1kxia_g.7.1.1 (A:) Cardiotoxin V {Taiwan cobra (Naja naja atra)}
LKCHNTQLPFIYKTCPEGKNLCFKATLKKPLKFPVKRGCADNCPKNSALLKYVCCSTDKCN

>d2ctx_g.7.1.1 (-) alpha-Cobratoxin {Cobra (Naja naja siamensis)}
IRCFITPDITSKDCPNHGVCYTWTCDAFCSIRGKRVDLGCAATCPTVKTGVDIQCCSTDNCNPFPTRKRP

>d1lsi_g.7.1.1 (-) Long neurotoxin 1 (component LSIII) {Sea snake (Laticauda semifasciata)}
RECYLNPHDTQTCPSGQEICYVKSWCNAWCSSRGKVLEFGCAATCPSVNTGTEIKCCSADKCNTYP

>d1tfs_g.7.1.1 (-) FS2 toxin {Black mamba (Dendroaspis polylepis polylepis)}
RICYSHKASLPRATKTCVENTCYKMFIRTHREYISERGCGCPTAMWPYQTECCKGDRCNK

>d1hc9a_g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), Alpha-bungarotoxin}
IVCHTTATSPISAVTCPPGENLCYRKMWCDVFCSSRGKVVELGCAATCPSKKPYEEVTCCSTDKNPHPKQPG

>d2abxa_g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), Alpha-bungarotoxin}
IVCHTTATIPSSAVTCPPGENLCYRKMWCDAFCSSRGKVVELGCAATCPSKKPYEEVTCCSTDKNHPPKRQPG

>d1kbaa_g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), kappa-

bungarotoxin}

RTCLISPSSTPQTCPNGQDICFLKAQCDKFCISIRGPVIEQGCVATCPQFRSNYRSLLCCTTDNCNH
>d1f94a_g.7.1.1 (A:) Bucandin {Malayan krait (Bungarus candidus)}
MECYRCGVSGCHLKITCSAEETFCYKWLNKISNERWLGAKTCTEIDTNVYNKCCTTLCNT
>d2cdx_g.7.1.1 (-) Cardiotoxin CTXI {Taiwan cobra (Naja naja atra)}
LKCNKLIPIASKTCPAGKNLCYKMFMMSDLTIPVKRGCIDVCPKNSLLVKYVCCNTDRCN
>d1chvs_g.7.1.1 (S:) Cardiotoxin II {Taiwan cobra (Naja naja atra)}
LKCNKLVLPLFYKTCAGKNLCYKMFMVSNKMPVKRGCIDVCPKSSLLVKYVCCNTDRCN
>d1cb9a_g.7.1.1 (A:) Cardiotoxin II {Central asian cobra (Naja naja oxiana)}
LKCKKLVLPLFSKTCPAGKNLCYKMFMVAAHPVPVKRGCIDVCPKSSLLVKYVCCNTDRCN
>d1i02a_g.7.1.1 (A:) Cardiotoxin III {Taiwan cobra (Naja naja atra)}
LKCNKLVLPLFYKTCAGKNLCYKMFMVATPKVPVKRGCIDVCPKSSLLVKYVCCNTDRCN
>d1kbs_g.7.1.1 (-) Cardiotoxin IV {Taiwan cobra (Naja naja atra)}
RKCNKLVLPLFYKTCAGKNLCYKMFMVSNLTVVKRGCIDVCPKNSALVKYVCCNTDRCN
>d1cod_g.7.1.1 (-) Cobrotoxin II (ct2) {Taiwan cobra (Naja naja atra)}
LECHNQQSSQTPTTGCSGGETNCYKKRWRDHRGYRTERGCGCPSVKNGIEINCCTTDRCNN
>d1g6ma_g.7.1.1 (A:) Cobrotoxin II (ct2) {Monocled cobra (Naja kaouthia)}
LECHNQQSSQTPTTGCSGGENNCYKKEWRDNRGYRTERGCGCPSVKKGIGINCCTTDRCNN
>d1nea_g.7.1.1 (-) alpha-Toxin {Snake (Naja nigricollis)}
LECHNQQSSQPPTTKTCPGETNCYKKVWRDHRGTIIERGCGCPTVKPGIKLNCCTTDRCNN
>d1ntx_g.7.1.1 (-) alpha-Toxin {Black mamba (Dendroaspis polylepis polylepis)}
RICYNHQSTTRATTKSCEENSCYKKYWRDHRGTIIERGCGCPVKPGVGIHCCQSDKCNY
>d1nor_g.7.1.1 (-) Neurotoxin II (Nt2) {Central asian cobra (Naja naja oxiana)}
LECHNQQSSQPPTTKTCGETNCYKKWSDHRGTIIERGCGCPVKPGVNLNCCRTDRCNN
>d1txb_g.7.1.1 (-) Toxin B (long neurotoxin) {King cobra (Ophiophagus hannah)}
TKCYVTPDATSQTCPDGQDICYTWTCDGFCSSRGKRIDLGAATCPKVPGVDIKCCSTDNCNPFTWKRKH
>d1jgka_g.7.1.1 (A:) Candoxin {Malayan krait (Bungarus candidus)}
MKCKICNFDTCRAGELKVCASGEKYCFKESWREARGTRIERGCAATCPKGSVYGLYVLCCCTDDCN
>d1drs_g.7.1.2 (-) Dendroaspin {Dendroaspis jamesoni kaimosae}
RICYNHLGTPPTTETCQEDSCYKNIWTFDNIIRRGCGCFTPRGDMPGPYCCESDKCNL
>d1erh_g.7.1.3 (-) CD59 {Human (Homo sapiens)}
LQCYNCPNPTADCKTAVNCSSDFDACLITKAGLQVYNKCKWFHCFNNDVTRLRENELYYCCKKDLGN
>d1btea_g.7.1.3 (A:) Type II activin receptor {Mouse (Mus musculus)}
ETQECLFFNANWERDRTNQTGVEPCYGDKDCKRRHCFATWKNISGSIEIVKQGCWLDDINCYDRTDCIEKKDSP
EVYFCCCEGNMCNEKFSYFPEME
>d1es7b_g.7.1.3 (B:) BMP receptor Ia ectodomain {Human (Homo sapiens)}
TLPFLKCYCSGHCPDDAINNTCITNGHCFAIEEDDQGETTLASGCMKYEGSDFQCKDSPKAQLRRTIECCRTNL
CNQYLQPTLPP
>d1ktzb_g.7.1.3 (B:) TGF-beta type II receptor extracellular domain {Human (Homo sapiens)}
PQLCKFCDFVRSTCDNQKSCMSNCITSICEKPQEVCVAVWRKNDENITLETVCHDPKLPYHDFILEDAAASPCKI
MKEKKKPGETFFMCSCSSDECNDNIIIFSEEEY
>d1brbi_g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
AGEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTA
>d1ejmb_g.8.1.1 (B:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}

RPDFCLEPPYTGPCRLRIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>d1faki_g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
APDFCLEPPYDGPCRALHLRYFYNAKAGLCQTFYGGCRAKRNNFKSAEDCMRTC
>d1g6xa_g.8.1.1 (A:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
RPDFCLEPPYAGACRARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCLRTCGGA
>d3bthi_g.8.1.1 (I:) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
DFCLEPPYTGPCHARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTC
>d5pti__g.8.1.1 (-) Pancreatic trypsin inhibitor, BPTI {Cow (Bos taurus)}
RPDFCLEPPYTGPCKARIIRYFYNAKAGLCQTFVYGGCRAKRNNFKSAEDCMRTC
>d1ktha_g.8.1.1 (A:) Collagen type VI (domain C5 from alpha 3 chain) {Human (Homo sapiens)}
ETDICKLPKDEGTCRDFILWYYDPNTKSCARFWYGGCGGNENKFGSQKECEKVCAPV
>d1adz__g.8.1.1 (-) Tissue factor pathway inhibitor {Human (Homo sapiens)}
DYKDDDDKLKPDCFLLEEDPGICRGYITRYFYNQTKQCERFKYGGCLGNMNNFETLEECKNICEGPNGF
>d1irha_g.8.1.1 (A:) Tissue factor pathway inhibitor {Human (Homo sapiens)}
EFHGSPSWCLTPADRGLCRANEFRYYNSIGKCRPFKYSAGCGGNENNFTSKQECLRACKKG
>d1tfxc_g.8.1.1 (C:) Tissue factor pathway inhibitor {Human (Homo sapiens)}
KPDFCFLEEDPGICRGYITRYFYNQTKQCERFKYGGCLGNMNNFETLEECKNICEG
>d1aapa_g.8.1.1 (A:) Alzheimer's amyloid B-protein precursor, APPI {Human (Homo sapiens)}
VREVCSEQAETGPCRAMISRWFVDVTEGKCAPFFYGGCGGNRNNFDTEEYCMAVCG
>d1bik_1_g.8.1.1 (25-78) Bikunin from inter-alpha-inhibitor complex {Human (Homo sapiens)}
SCQLGYSAGPCMGMSTSRYFYNGTSMACETFQYGGCMGNGNNFVTEKECLQTCRT
>d1bik_2_g.8.1.1 (79-134) Bikunin from inter-alpha-inhibitor complex {Human (Homo sapiens)}
VAACNLPIVRGPCRAFIQLWAFDAVKGKCVLFPYGGCQGNGNKFYSEKECREYCGV
>d1dtx__g.8.1.1 (-) alpha-Dendrotoxin {Green mamba (Dendroaspis angusticeps)}
EPRRKLCILHRNPGRCYDKIPAFYYNQKKQCERFDWSGCGGNSNRFKTIEECRRTCIG
>d1bunb_g.8.1.1 (B:) beta2-bungarotoxin, neurotoxin chain {Many-banded krait (elapid) (Bungarus multicinctus)}
RKRPDCDKPPDTKICQTVVRAFYKPSAKRCVQFRYGGCNGNGNHFKSDHLCRCECLEYR
>d1shp__g.8.1.1 (-) Trypsin inhibitor {Sea anemone (Stichodactyla helianthus)}
SICSEPKKVGRCKGYFPRFYFDSETGKCTPIYGGCGGNNFETLHQCRACRA
>d1dtk__g.8.1.1 (-) Dendrotoxin K {Black mamba (Dendroaspis polylepis polylepis)}
AAKYCKLPLRIGPCKRKIPSFYWKAKQCLPDFYSGCGGNANRFKTIEECRRTCVG
>d1den__g.8.1.1 (-) Dendrotoxin I {African elapid snake (Dendroaspis polylepis polylepis)}
QPLRKLCILHRNPGRCYQKIPAFYYNQKKQCEGFTWSGCGGNSNRFKTIEECRRTCIRK
>d1bf0__g.8.1.1 (-) Calciclidine (cac) {Green mamba (Dendroaspis angusticeps)}
WQPPWYCKEPVIRGSCKKFSSFYFKWTAKKCLPFLSGCGGNANRFQTIGECRKCLGK
>d1tocr1_g.8.1.2 (R:1A-56) Ornithodorin {Soft tick (Ornithodoros moubata)}
SLNVLCNPHTADCNNDAQVDRYFREGTTCLMSPACTSEGYASQHECQQACFVGGED
>d1tocr2_g.8.1.2 (R:57-119) Ornithodorin {Soft tick (Ornithodoros moubata)}
HSSEMHSCLGDPPTSCAEGTDITYYDSDSKTCKVLAASCPSGENTFESEVECQVACGAPIEG
>d1d0da_g.8.1.2 (A:) Anticoagulant protein, factor Xa inhibitor {Soft tick (Ornithodoros moubata)}
YNRLCIKPRDWIDECDSNEGGERAYFRNGKGGCDSFWICPEDHTGADYYSSYRDCFNACI
>d1dfna_g.9.1.1 (A:) Defensin HNP-3 {Human (Homo sapiens)}
DCYCRIPACIAGERRYGTCIYQGRLWAFCC

>d1ijva_g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD1}
DHYNCVSSGGQCLYSACPIFTKIQGTCYRGAKCCK
>d1e4qa_g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}
PVTCCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKP
>d1fd3a_g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}
GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKP
>d1e4ta_g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD5}
NSKRACYREGGECLQRCIGLFHKIGTCNFRFKCCKFQ
>d1e4ra_g.9.1.1 (A:) Beta-defensin, BD {Mouse (Mus musculus), MBD6}
NEPVSCIRNGGICQYRCIGLRHKIGTCGSPFKCCK
>d1bnb_g.9.1.1 (-) Beta-defensin, BD {Cow (Bos taurus), BD12}
APLSCRNGGVCIPIRCVPVMRQIGTCFGRPVKCCRSW
>d1ewsa_g.9.1.1 (A:) Alpha-defensin rk-1 {Rabbit (Oryctolagus cuniculus)}
MPCSCKKYCDPWEVIDGSCGLFNSKYICCREEK
>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)}
AACCKCDDEGPDIRTAPLTGTVDLGSCNAGWEKCASYTIIADCCRKKK
>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)}
GVSCLCDSDGPSVRGNTLSGTLWLYPSGCPGWHNCKAHGPTIGWCCKQ
>d1apf_g.9.1.1 (-) Anthopleurin-B {Giant green sea anemone (Anthopleura xanthogrammica)}
GVPCLCDSDGPRPRGNTLSGILWFYPSGCPGWHNCKAHGPNIGWCKK
>d1bhta1 g.10.1.1 (A:35-126) Hepatocyte growth factor {Human (Homo sapiens)}
RRNTIHEFKKSAKTTLIKIDPALIKTKVNTADQCADRCTRNKGLPFTCAVFVDKARKQCLWFPFNSMSSGVK
KEFGHEFDLYENKDYIR
>d1gmnb1 g.10.1.1 (B:42-125) Hepatocyte growth factor {Human (Homo sapiens)}
FKKSAKTTLIKIDPALIKTKVNTADQCADRCTRNKGLPFTCAVFVDKARKQCLWFPFNSMSSGVKKEFGHEF
DLYENKDYI
>d1i8na_g.10.1.2 (A:) Anti-platelet protein {Leech (Haementeria officinalis)}
ETITAGNEDCWSKRPWKLPDNLLTKEFTSVDECRLMCEESAVEPSCYILQINTETNECYRNNEGDTWSSLQ
YDQPNNVQWHLHACS
>d1ans_g.11.1.1 (-) Neurotoxin III (ATX III) {Sea anemone (Anemonia sulcata)}
RSCCPWCYWGCPWGQNCYPEGCSGPKV

>d1ajj_ g.12.1.1 (-) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

PCSAFEFHLSGECHSSWRCDGGPDCKDKSDEENCA

>d1cr8a_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

PGGCHTDEFQCRLGLCIPLRWRCGDGTDCMDSSDEKSCEGV

>d1d2la_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

GSPPQCQPGEFACANSRCIQERWKCDGDNDCLDNSDEAPALCHQH

>d1f5ya1 g.12.1.1 (A:1-44) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

GSAVGDRCERNEFQCQDGK CISYKWVCDGSAECQDGSDSQETC

>d1f5ya2 g.12.1.1 (A:45-85) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

LSVTCKSGDFSCGGRVNRCIPQFWRCDGQVDCDNGSDEQGC

>d1f8za_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

ATCRPDEFQCSDGNCIHGSRQCDREYDCKDMSDEVGCVN

>d1j8ea_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

GSHSCSSTQFKCNSGRCIPEHWTCGDNDGDSDETHANCTNQ

>d1ldl_ g.12.1.1 (-) Ligand-binding domain of low-density lipoprotein receptor {Human (Homo sapiens)}

AVGDRCERNEFQCQDGK CISYKWVCDGSAECQDGSDSQETCLSVT

>d1k7ba_ g.12.1.1 (A:) soluble Tva ectodomain, sTva47 {Quail (Coturnix coturnix)}

SCPPGQFRCEPPGAHGECYPQDWLCDGHPCDDGRDEWGCG

>d1ejga_ g.13.1.1 (A:) Crambin {Abyssinian cabbage (Crambe abyssinica)}

TTCCPSIVARSNFNVCRLPGTPEALCATYTGCIIIPGATCPGDYAN

>d1bhp_ g.13.1.1 (-) beta-Purothionin {Wheat (Triticum aestivum)}

KSCCKSTLGRNCYNLCRARGAQKLCANVCRKLTSGLSCP KDFPK

>d2plh_ g.13.1.1 (-) alpha-1-Purothionin {Wheat (Triticum aestivum)}

KSCCRSTLGRNCYNLCRARGAQKLCAGVCRKCISSGLSCP KGF PK

>d1ed0a_ g.13.1.1 (A:) Viscotoxin a3 {European mistletoe (Viscum album)}

KSCCPNTTGRNIYNACRTGAPRPTCAKLSGCKIISGSTCP SDYPK

>d1i5ka_ g.14.1.1 (A:) Plasminogen kringle {Human (Homo sapiens)}

ECMHGSGENYDGKISKTMSGLECAWDSQSPHAHYI PSKFPNKNLKKNYCRNPDRDLRPWCFTTDPNKR

WEYCDIPRC

>d1krn_ g.14.1.1 (-) Plasminogen kringle {Human (Homo sapiens)}

DCYHGDGQS YRGTSSTTTGKKCQSWSMTPHRHQKTPENYPNAGLT MNYCRNP DADKGPWCFTTDPSVR

WEYCNLKKC

>d1pmla_ g.14.1.1 (A:) Plasminogen kringle {Human (Homo sapiens)}

SDCYFGNGSAYRGTHSLTESGASCLPWNSMILIGKVYTAQNPSAQ ALGLGKHNYCRNP DGDAKPWCHVLKNR

RLTWEYCDVPSCST

>d1ceaa_ g.14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}

ECKTGNGKNYRGTM SKNGITCQKWSSTSPHRPRFSPATHPSEGLEENYCRNPDNDPQGPWCYTTDPEKRY
DYCDILEC
>d5hpg_a_14.1.1 (A:) Plasminogen kringle domains {Human (Homo sapiens)}
DCMFNGKGYRGKRVTTVTGTPCQDWAAQEPRHSIFTPETNPRAGLEKNYCRNPDGDVGGWCYTTNPR
KLYDYCDVPQCAAP
>d2pf1_1 g.14.1.1 (66-156) Prothrombin kringle domain {Cow (Bos taurus)}
CAEGVGMNYRGNVSVTRSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSI TGWCYTTSPTRLREE
CSVPVCGQDRVTVEVIPR
>d2pf2_1 g.14.1.1 (66-146) Prothrombin kringle domain {Cow (Bos taurus)}
CAEGVGMNYRGNVSVTRSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNPDGSI TGWCYTTSPTRLREE
CSVPVCGQ
>d1a0ha1 g.14.1.1 (A:164-270) Meizothrombin kringle domain {Cow (Bos taurus)}
SPLLETCPDRGREYRGRLAVTTHGSRCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVAD
QPGDFEYCDLN YCEEPVDGLGDRLGEDPD PDAI EG
>d2hпп_14.1.1 (P:) Meizothrombin kringle domain {Cow (Bos taurus)}
CVPDRGREYRGRLAVTTS GS RCLAWSSEQAKALSKDQDFNPAVPLAENFCRNPDGDEEGAWCYVAD QPGDF
EYCNLNYC
>d2hpqp_14.1.1 (P:) Meizothrombin kringle domain {Human (Homo sapiens)}
CVPDRGQQYQGRLAVTTHGLPCA WASAQAKALSKHQDFNSA VQLVENFCRNPDGDEEGVWCYVAGKPGD
FGYCDLN YC
>d1kdu_14.1.1 (-) Urokinase-type plasminogen activator kringle domain {Human (Homo sapiens)}
TCYEGNGHFYRGKASTDTMGRPCLPWNSATVLQQTYHAHRS DALQLGLGKHNYCRNPDNRRPWCYVQVG
LKPLVQECMVHDCAD
>d3kiv_14.1.1 (-) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-10/M66 variant}
QCYHNGNGQSYRGTSTTVGRT CQS WSSMTPHRHQ RTPENY PNDGLTMNYCRNP DADTGPWCFTTDPSIR
WEYCNLTRC
>d1i71a_g.14.1.1 (A:) Apolipoprotein A kringle domain {Human (Homo sapiens), IV-7 variant}
DCYHGDGQSYRGSFSTTVGRT CQS WSSMTPHW HQRTTEYYPNGGLTRNYCRNPDAEIRPWCYTMDPSVR
WEYCNLTQCPVME
>d1bhta2 g.14.1.1 (A:127-210) NK1 fragment of hepatocyte growth factor {Human (Homo sapiens)}
NCIIGKGRSYKGTVSITKSGIKCQPWSSMIPHEHSFLPSSYRGKDLQENYCRNPRGE EGGPWCFTSNPEVRYEV
DIPQCSEVE
>d1pdc_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)}
AVTQTYGGNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTS NYEQDQKYS FCTDHT
>d1e88a2 g.14.1.2 (A:102-160) Fibronectin {Human (Homo sapiens)}
VLVQTRGGNSNGALCHFPFLYNNHNYT DCTSEGRRDNMKWC GTTQNYDADQKFGFCPMA
>d1ck7a3 g.14.1.2 (A:217-277) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}
EGQVVRVKYGNADGEYCKFPFLNGKEYNSCTDTGRSDGFLWCSTT NFEKD GKYGFCPHE
>d1ck7a4 g.14.1.2 (A:278-335) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}
ALFTMGGNAEGQPCKFPFRFQGTSYDSCTTEGR TDGYRWCGTTEDYDRD KKYGFCPET
>d1ck7a5 g.14.1.2 (A:336-393) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}

AMSTVGGNSEGAPCVFPFTLGNKYESCTSAGRSDGKMW CATTANYDDDRKGFCPDQ
>d1j7ma_g.14.1.2 (A:) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}
SWMSTVGGNSGGAPCVFPFTLGNKYESCTSAGRSDGKMW CATTANYDDDRKGFCPDQG
>d1ks0a_g.14.1.2 (A:) Gelatinase A (MMP-2) type II modules {Human (Homo sapiens)}
RIPVKYGNADGEYCKFPFLFNGKEYNSCTDGRSDGFLWCSTTYNFEKDGYGFCPHEA
>d1sgpi_g.15.1.1 (I:) Ovomucoid III domain {Turkey (Meleagris gallopavo)}
VDCSEYPKPACTAEYRPLCGSDNKTYGNKCNFCNAVVESNGTTLSHFGKC
>d3ovo_g.15.1.1 (-) Ovomucoid III domain {Japanese quail (Coturnix coturnix japonica)}
LAAVSVDCEYPKPACPKDYRPVCSDNKTYSNKCNFCNAVVESNGTTLNHFGKC
>d2ovo_g.15.1.1 (-) Ovomucoid III domain {Silver pheasant (Lophura nycthemera)}
LAAVSVDCEYPKPACTMEYRPLCGSDNKTYGNKCNFCNAVVESNGTTLSHFGKC
>d1hpt_g.15.1.1 (-) Secretory trypsin inhibitor {Human (Homo sapiens)}
DSLREAKCYNELNGCTYEYRPVC GTDGDTYPNECVLCFENRK RQTSILIQKSGPC
>d1tgsi_g.15.1.1 (I:) Secretory trypsin inhibitor {Pig (Sus scrofa)}
TSPQREATCTSEVSGCPKIYNPVC GTDGITYSNECVLCSENKRQTPVLIQKSGPC
>d1tbrr1 g.15.1.1 (R:1-51) Rhodniin {Bug (Rhodnius prolixus)}
EGGEPCACPHALHRVCGSDGETYSNPCTLNCNAKFNGKPELVKVHDGPCEPD
>d1tbrr2 g.15.1.1 (R:52-103) Rhodniin {Bug (Rhodnius prolixus)}
EDEDVCQECDGDEYKPVC GSDDITYDNNCRLECASISSPGVELKHEGPCRT
>d1nuba3 g.15.1.1 (A:78-135) Domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}
CQDP TSCPAPIGEFEEKVCSNDNKTFDSSCHFFATKCTLEGTKKGHKLHLDYIGPCKYI
>d2bus_g.15.1.1 (-) Seminal plasma inhibitor Iia {Cow (Bos taurus)}
EGAQVDCAEFKDPKVYCTRESNPHC GSNGETYGNKCAFCKAVMKSGGKINLKHRGKC
>d1pce_g.15.1.1 (-) PEC-60 peptide {Pig (Sus scrofa)}
EKQVFSRMPICEHMTESPDCSRIYDPVC GTDGVTESECKLCLARIENKQDIQIVKDGE
>d1an1i_g.15.1.1 (I:) Leech derived tryptase inhibitor (LDI-C) {Medicinal leech (Hirudo medicinalis)}
KVCACPKILKPVCGSDGRTYANSCIARCNGVSIKSEGSCP
>d1ldtl_g.15.1.1 (L:) Leech derived tryptase inhibitor (LDI-C) {Medicinal leech (Hirudo medicinalis)}
KKVCACPKILKPVCGSDGRTYANSCIARCNGVSIKSEGSCPTGILN
>d4sgbi_g.15.1.2 (I:) Plant chymotrypsin inhibitor {Potato tuber (Solanum tuberosum)}
PICTNCCAGYKGNCYYSANGAFICEGQSDPKPKACPLNCDPHIAYS KCP
>d1ce3a_g.15.1.2 (A:) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}
MKA CLNCDPRIAYGVC PRSEEKKNDRICTNCCAGTKGCKYFSDDGTFVCEGES
>d1fyba1 g.15.1.2 (A:1-55) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}
DRIC TNCCAGTKGCKYFSDDGTFVCEGESDPRNP KACTLNCDPRIAYGVC PRSEE
>d1tih_g.15.1.2 (-) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}
DRIC TNCCAGTKGCKYFSDDGTFVCEGESDPRNP KACPRNCDPRIAYGICPLA
>g1qh2.1 g.15.1.2 (B:,A:) Multidomain proteinase inhibitor {Winged tobacco (Nicotiana alata)}
RIC TNCCAGKKGCKYFSDDGTFICEGESXKACTLNCDPRIAYGVC PR
>d2pspa1 g.16.1.1 (A:1-53) Pancreatic spasmolytic polypeptide {Pig (Sus scrofa)}
EKPAACRCSRQDPKNRVNCGFPGITSDQCFTSGCCFDSQVPGVPWCFKPLPAQ

>d2pspa2 g.16.1.1 (A:54-106) Pancreatic spasmolytic polypeptide {Pig (Sus scrofa)}
ESEECVMQVSARKNCGYPGISPEDCAARNCCFSDTIPEVPWCFFPMSSVEDCHY

>d1hi7a_g.16.1.1 (A:) PNR-2/PS2, TFF1 {Human (Homo sapiens)}
EAQTECTVAPRERQNCGFPGVTPSQCANKGCCFDDTVRGVPWCFYPNTIDVPPEEECEF

>d1e9ta_g.16.1.1 (A:) Intestinal trefoil factor {Human (Homo sapiens)}
EEYVGLSANQCAVPAKDRVDCGYPHVTPKECNNRGCCFDSRIPGVWCFKPLQEAEACTF

>d1pdga_g.17.1.1 (A:) Platelet-derived growth factor BB {Human (Homo sapiens)}
EPAMIAECKTRTEVFEISRRLIDRTNANFLVWPPCDEVQRCSGCCNNRVQCRPTQVQLRPVQVRKIEIVRKPI
FKKATVTLLEDHLACKCETVAA

>d1fltv_g.17.1.1 (V:) Vascular endothelial growth factor, VEGF {Human (Homo sapiens)}
EVVKFMDVYQRSYCHPIETLVDIFQEYDIEYIFKPSCVPLMRCGGCNDEGLECVPTESNITMQIMRIKPHQ
GQHIGEMSFLQHNKCECRPK

>d1fzva_g.17.1.1 (A:) Placenta growth factor-1, PLGF-1 {Human (Homo sapiens)}
SSEVEVVPFQEWWGRSYCRALERLVDVVSEYPSEVEHMFPSCVSLRCTGCCDENLHCPVETANVTMQLL
KIRSGDRPSYVELTSQHVRCECRPLR

>d1ktza_g.17.1.2 (A:) TGF-beta3 {Human (Homo sapiens)}
ENCCVRPLYIDFRQDLGWKVVHEPKGYYANFCSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPL
TILYYVGRTPKVEQLSNMVVKSCCKCS

>d1tgj_g.17.1.2 (-) TGF-beta3 {Human (Homo sapiens)}
ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKVVHEPKGYYANFCAGACPYLWSSDTQHSRVLSLYNTINPEASA
SPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVKSCCKCS

>d2tgi_g.17.1.2 (-) TGF-beta2 {Human (Homo sapiens)}
ALDAAYCFRNVQDNCCRLRPLYIDFKRDLGWKWIHEPKGYNANFCAGACPYLWSSDTQHSRVLSLYNTINPEASA
SPCCVSQDLEPLTILYYIGKTPKIEQLSNMIVRSCKCS

>d1klaa_g.17.1.2 (A:) TGF-beta1 {Human (Homo sapiens)}
ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPAGASA
APCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS

>d1bmp_g.17.1.2 (-) Bone morphogenetic protein-7 (BMP-7) {Human (Homo sapiens)}
QACKKHELYVSFRDLGWQDWIIAPEGYAAYYCEGECAFPLNSYMNATNHAIVQTLVHFINPETVPKPCCAPTQL
NAISVLYFDDSSNVILKKYRNMVVRACGCH

>d1es7a_g.17.1.2 (A:) Bone morphogenetic protein-2 (BMP-2) {Human (Homo sapiens)}
KSSCKRHPLYVDFSDVGWNDWIVAPPGYHAFYCHGECPFPLADHLNSTNHAIVQTLVNSVNSKPKACCVPTEL
SAISMLYLDENEKVVLKNYQDMVVEGCGCR

>d1agqa_g.17.1.2 (A:) Glial cell-derived neurotrophic factor, GDNF {Rat (Rattus norvegicus)}
NRGCVLTIAHLNVTDLGLGYETKEELIFRYCSGSCEAAETMYDKILKNLRSRRLTSDKVGQACCRPVAFDDDSLF
LDDSLVYHILRKHSAKRCGCI

>d1bnnda_g.17.1.3 (A:) Brain-derived neurotrophic factor/neurotrophin 3 heterodimer, BDNF/NT3 {Human (Homo sapiens)}
GQLSVCDISIEWVTAADKKTAVDMSGGTVTLEKVPVSKGQLQFYETKCNPMGYTKEGCRGIDKRHWNSQ
CRTTQSYYVRAUTMDSKKRIGWRFIRIDTSCVCTLIK

>d1bndb_g.17.1.3 (B:) Brain-derived neurotrophic factor/neurotrophin 3 heterodimer, BDNF/NT3 {Human (Homo sapiens)}
RGEVSVCDSSESLWVTDKSSAIDIRGHQVTVLGEIKTQNSPVKQFYETRCKEARPVKNGCRGIDDKHWNSQL
TSQTYVRAUTSENNKLGVWRWIRIDTSCVCALSRK

>d1b8mb_g.17.1.3 (B:) Neurotrophin 4 {Human (Homo sapiens)}
GELAVCDAVSGWVTDRRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADNAEEGGPGAGGGGCRGVD
RRHWVSECKAKQSYVRALTADAQGRVGWRWIRIDTACVCTLLSRTGRA

>d1hcfa_g.17.1.3 (A:) Neurotrophin 4 {Human (Homo sapiens)}
GVSETAPASRRGELAVCDAVSGWVTDRRTAVDLRGREVEVLGEVPAAGGSPLRQYFFETRCKADNAEEGGPGA
GGGGCRGVDRRHWWVSECKAKQSYVRALTADAQGRVGWRWIRIDTACVCTLLSRT

>d1bet_g.17.1.3 (-) beta-Nerve growth factor {Mouse (Mus musculus)}
GEFSVCDSVSVVGDKTTATDIKGKEVTVAEVNIINNSVFRQYFFETKCRASNPVESGCRGIDSKHWN SYCTTT
HTFVKALTTEKQAAWRFIRIDTACVCVLSRK

>d1www_g.17.1.3 (V:) beta-Nerve growth factor {Human (Homo sapiens)}
SSHPIFHGEFSVCDSVSVVGDKTTATDIKGKEVMVLGEVNIINNSVFKQYFFETKCRDPNPVDSGCRGIDSKH
WNSYCTTHTFVKALTMDGKQAAWRFIRIDTACVCVLSRK

>d1hcna_g.17.1.4 (A:) Glycoprotein hormones alpha chain (Gonadotropin A,
Follitropin alpha) {Human (Homo sapiens)}
QDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSYNRVTVMGGFKVE
NHTACHCSTCYY

>d1hcnb_g.17.1.4 (B:) Gonadotropin B chain {Human (Homo sapiens)}
KEPLRPRCRPINATLAVEKEGCPVCITVNNTICAGYCPTMTRVLQGVLPALPVVCNYRDVRFESIRLPGCPRGV
NPVVSYAVALSCQCALCRRSTTDCGGPKDHPLCD

>d1fl7b_g.17.1.4 (B:) Follicle stimulating hormone, follitropin, beta chain {Human (Homo sapiens)}
CELTNITIAIEKEECRFCISINTAWCAGCYCTRDLVYKDPARPKIQKTCTFKELVYETVRVPGCAHHADSLYTPVAT
QCHCGKCDSDSTDCTVRGLGPSYCSFGEM

>d1jpya_g.17.1.6 (A:) Interleukin 17F, IL-17F {Human (Homo sapiens)}
HTFFQKPESCVPVPGGSMKLDIGIINENQRVMSRSNIESRSTSPWNYTVTWDPNRYPSEVVQAQCRLNLGCINA
QGKEDISMNSVPIQQETLVVRRKHQGCSVSFQLEKVLTVGCTCVTPV

>d1aoca_g.17.1.5 (A:) Coagulogen {Japanese horseshoe crab (Tachyleus
tridentatus)}
ADTNAPICLCDEPGVLGRTQIVTTEIKDKIEKAVEAVAQESGVSGRGFSIFSHHPVFRECGKYECRTVRPEHSRCY
NFPPFTHKSECPVSTRDCEPVFGYTVAEFRVIVQAPRAGFRQCVWQHKCRFGNSCGYNGRCTQQRSVVR
LVTYNLEKDGFLCESFRTCCGCPCRSF

>d1hcc_g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}
EGLPCKSPPEISHGVVAHMSDSYQYGEETYKCFEGFGIDGPAlAKCLGEKWShPPSCI

>d1hfi_g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}
EKIPCSQPPQIEHGTINSSRSSQESYAHGTLSYTCEGGFRISEENETTCYMGKWSSPPQCE

>d1g40a1 g.18.1.1 (A:1-64) Complement control protein {Vaccinia virus}
CCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCLPGYRKQKMGPPIYAKCTGTGWTLFNQCIK

>d1g40a2 g.18.1.1 (A:65-126) Complement control protein {Vaccinia virus}
RRCPSPRIDNGQLDIGGVDFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICES

>d1g40a3 g.18.1.1 (A:127-184) Complement control protein {Vaccinia virus}
VKCQSPPSISNGRHNGYEDFYTDGSVVTYSCNSGYSLIGNSGVLCGGEWSDPPTCQI

>d1g40a4 g.18.1.1 (A:185-243) Complement control protein {Vaccinia virus}
VKCPHPTISNGYLSGGFKRSYSYNDNVDFKCKYGYKLSSSTCSPGNTWKPELPKCV

>d1ckla1 g.18.1.1 (A:1-62) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}
CEEPPTFEAMELIGKPKPYYEIGERVVDYKCKGYFYIPPLATHTICDRNHTWLPSDDACYR

>d1ckla2 g.18.1.1 (A:63-126) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}
ETCPYIRDPLNGQAVPANGTYEFGYQMHCICNEGYYLIGEEILYCELGSVAIWSGKPPICEKV

>d1c1za5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}
SCKLPVKKATVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFKEHSSLAFWKT
DASDVKPC

>d1quba1 g.18.1.1 (A:1-62) beta2-glycoprotein I {Human (Homo sapiens)}
GRTCPKPDDLPFSTVPLKTFYEPGEEITYSCKPGYVSRGGMRKFCPLTGLWPINTLKCTP

>d1quba2 g.18.1.1 (A:63-120) beta2-glycoprotein I {Human (Homo sapiens)}
RVCDFAGILENGAVRYTTFEYPNTISFCNTGFYNGADSAKCTEEGKWSPELPVCAP

>d1quba3 g.18.1.1 (A:121-183) beta2-glycoprotein I {Human (Homo sapiens)}
IICPPPSIPTFATLRVYKPSAGNNSLYRDTAVFECLPQHAMFGNDITCTTHGNWTKLPECRE

>d1quba4 g.18.1.1 (A:184-243) beta2-glycoprotein I {Human (Homo sapiens)}
VKCPFPSRPDNGFVNYPAKPTLYYDKATFGCHDGYSLDGPEEIECTKLGNSAMPSCKA

>d1quba5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}
SCKVPVKKATVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIEVPKCFKEHTDASDVK
PC

>d1ghqb1 g.18.1.1 (B:1-66) Complement receptor 2, cr2 {Human (Homo sapiens)}
AISCGSPPPILNGRISYYSTPIAVGTVIRYSCSGTFRLLGEKSLLCITDKVDGTWDKPKCEYF

>d1ghqb2 g.18.1.1 (B:67-129) Complement receptor 2, cr2 {Human (Homo sapiens)}
NKYSSCPEPIVPGGYKIRGSTPYRHGDSVTFAKTNFSMNGNKSVCQANNMWGPTRLPTCVS

>d1elva2 g.18.1.1 (A:342-409) Complement C1S protease domain {Human (Homo sapiens)}
LDCGIPESIENGKVEDPESTLFGSVIRYTCEPYMMENGGGEYHCAGNGSWVNEVLGPELPKCVPV

>d1bgk_ g.19.1.1 (-) Sea anemone toxin k {Sea anemone (Bunodosoma granulifera), BGK}
VCRDWFKETACRHAKSLGNCRTSQKYRANCACAKTCELC

>d1c2ua_ g.19.1.1 (A:) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}
RSXIDTIPKSRCTAFQCKHSACKYRLSFCRKTCGTX

>d1roo_ g.19.1.1 (-) Sea anemone toxin k {Sun anemone (Stichodactyla helianthus), SHK}
RSCIDTIPKSRCTAFQCKHSCKYRLSFCRKTCGTC

>d2ech_ g.20.1.1 (-) Echistatin {Echis carinatus}
ECESGPCCRNCFLKEGTICKRARGDDMDDYCNGKTCDCPRNPHKGPAT

>d1fvl_ g.20.1.1 (-) Flavoridin {Snake (Trimeresurus flavoviridis)}
GEECDCGSPSNPCCDAATCKLRPGAAQCAGLCCDQCRFKKRTICRIARGDFPDDRCTGLSNDPRWNDL

>d1kst_ g.20.1.1 (-) Kistrin {Agkistrodon rhodostoma}
GKECDCSSPENPCCDAATCKLRPGAAQCAGLCCDQCRFKKRTICRIARGDFPDDRCTGLSNDPRWNDL

>d1mdal_ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}
VDPRAKWPQPDNDIQACDYWRHCSIAGNICDCSAGSLTSCPPGTLVASGSVGSCYNPPDPNKYITAYRDCC
GYNVSGRCACLNTEGELPVYNKDANDIIWCFFGEDGMTYHCSISPVSGA

>d2bbkl_ g.21.1.1 (L:) Methylamine dehydrogenase {Paracoccus denitrificans}
TDPRAKWPQPDNDIQACDYWRHCSIAGNICDCSAGSLTSCPPGTLVASGSVGSCYNPTDGQSYLIAYRDCC
GYNVSGRCPLNTEGELPVYRPEFANDIIWCFFGAEDDAMTYHCTISPIVGKAS

>d1atb_ g.22.1.1 (-) Ascaris trypsin inhibitor, ATI {Pig roundworm (Ascaris Lumbricoides), variant suum}
EAEKCTKPNEQWTKGCGCEGTCAQKIVPCTRECKPPRCECIASAGFVRDAQGNCIKFEDCPK

>d1eaic_ g.22.1.1 (C:) Ascaris elastase inhibitor {Pig roundworm (Ascaris suum)}

GQESCGPNEVWTECTGCEMIKCGPDENTPCPLMCRRPSCESPGRGMRTNDGKIPASQCP
>d1coua_ g.22.1.1 (A:) Anticoagulant protein {Dog hookworm (*Ancylostoma caninum*)}
KATMQCGENEKYDSCGSKECDKKCKYDGVEEDDEEPNVPCRVCHQDCVCEEGFYRNKDDKCVSAEDCEL
DNMDFIYPGTRNP
>d1ccva_g.22.1.1 (A:) Chymotrypsin inhibitor AMCI {Honeybee (*Apis mellifera*)}
EECGPNEVFNTCGSACAPTCAQPKTRICTMQCRIGCQCQEGFLRNNEGACVLPENC
>d1hx2a_g.22.1.2 (A:) BSTI {Fire-bellied toad (*Bombina bombina*)}
NFVCPPGQTFCASSCPKTCTRNKLVLCDKKCNQRCGCISGTVLKS KDSSECVHPSKC
>d1apj_g.23.1.1 (-) Fibrillin {Human (*Homo sapiens*)}
SAQDLRMSYCYAKFEGGKCSSPKSRNHSKQECCALKGEGWGDPCELCPTEPDEAFRQICPYGSGIIVGPDDSA
>d1exta1 g.24.1.1 (A:13-71) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}
SVCVPQGKYIHPQNNNSICCTKCHKTYLYNDCPGPGQDTDCRECESGSFTASENHLRHCL
>d1exta2 g.24.1.1 (A:72-115) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}
SCSKCRKEMGQVEISSCTVDRDTVCGRKNQYRHYWSENLFQCF
>d1exta3 g.24.1.1 (A:116-172) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}
NCSLCLNGTVHLSCQEKKQNTVCTCHAGFFLRENECVSCSNCKSLECTKLCLPQIEN
>d1ncfa3 g.24.1.1 (A:116-150) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}
NCSLCLNGTVHLSCQEKKQNTVCTCHAGFFLRENEC
>d1ncfb3 g.24.1.1 (B:116-155) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}
NCSLCLNGTVHLSCQEKKQNTVCTCHAGFFLRENECVSCSN
>d1d0gr1 g.24.1.1 (R:21-61) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}
SSPSEGGLCPPGHHISEDGRDCISCKYQGDYSTHWNDLLFCL
>d1d0gr3 g.24.1.1 (R:102-128) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}
KCRTGCP RGMVKVG DCTPWS DIECVHK
>d1d4va1 g.24.1.1 (A:69-114) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}
PQQKRSSPSEGGLCPPGHHISEDGRDCISCKYQGDYSTHWNDLLFCL
>d1d4va2 g.24.1.1 (A:115-154) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}
RCTRCDSGEVELSPCTTRNTVCQCEEGTFREEDSPEMCR
>d1d4va3 g.24.1.1 (A:155-185) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}
KCRTGCP RGMVKVG DCTPWS DIECVHKESGD
>d1du3a3 g.24.1.1 (A:102-123) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}
KCRTGCP RGMVKVG DCTPWSDI
>d1jmab1 g.24.1.1 (B:4-59) Cellular receptor HveA {Human (*Homo sapiens*)}
CKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQ
>d1jmab2 g.24.1.1 (B:60-105) Cellular receptor HveA {Human (*Homo sapiens*)}
MCDPAMGLRASRNCSR TENAVCGCSPGHFCIVQDGDHCAACRAYAT
>d1vgh_g.25.1.1 (-) Heparin-binding domain from vascular endothelial growth factor {Human (*Homo sapiens*)}
ARQENPCGPCSERRKHLVQDPQTCKCSCKNTDSRCKARQLELNERTCRCDKP RR
>d1afp_g.26.1.1 (-) Antifungal protein (AGAFP) {Mold (*Aspergillus giganteus*)}
ATYNGKCYKKDNICKYKAQSGKTAICKCYVKKCP RDGA KCEFDSYKGKCYC
>d1e88a3 g.27.1.1 (A:1-41) Fibronectin {Human (*Homo sapiens*)}
YGHCVTDSGVVYSVGMQWLKTQGNKQMLCTLGNGVSCQET
>d1fbr_1 g.27.1.1 (1-46) Fibronectin {Human (*Homo sapiens*)}

AEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGRITCSR
>d1fbr_2 g.27.1.1 (47-93) Fibronectin {Human (Homo sapiens)}
NRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNNGRGEWKERHTS
>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)}
EAEETCFDKYTGNTRYVGDTYERPKDSMIWDCTCIGAGRGRISCTIANR
>d1tpg_2 g.27.1.1 (1-50) Tissue-type plasminogen activator, t-PA {Human (Homo sapiens)}
SYQVICRDEKTQMIFYQQHQSWLRPVLRSNRVEYCWCNSGRAQCHSVPVKS
>d1icfi_g.28.1.1 (I:) MHC class II associated p41 invariant chain fragment {Human (Homo sapiens)}
LTKCQEEVSHIPAVHPGSFRPKCDENGNYLPLQCYSIGYCWCVFPNGTEVPNTRSRRGHHCSES
>d1e8ra_g.29.1.1 (A:) Endo-1,4-beta-xylanase A CBDX {Pseudomonas fluorescens, subsp. cellulosa}
MGNQQCNWYGTLYPLCVTTTNGWGVEDQRSCIARSTCAAQPAPFGIVGSG
>d1e8qa_g.55.1.1 (A:) Cellulose docking domain, dockering {Piromyces equi}
ASCWAQSQGYNCCNNPSSTKVEYTDASGQWGVQNGQWCGIDYSYGQ
>d1dtb_g.30.1.1 (B:) Carboxypeptidase inhibitor {Medicinal leech (Hirudo medicinalis)}
DESFLCYQPDQVCCFICRGAAPLPSEGECNPHTAPWCREGAVEWVPYSTGQCRTTCIPYV
>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)}
YLAFCRGYSPCLDDGPVNLYSCCSFYNCNKCLARLENCPKGLHYNAYLKVCDWPSKAGCTSVNKECHLWKT
>d1ha8a_g.58.1.1 (A:) Pheromone ER-23 {Euploites raikovi}
GECEQCFSDGGDCTTCFNNGTGPCANCLAGYPAGCSNSDCTAFLSQCYGGC
>d1danl3 g.32.1.1 (L:1-48) Coagulation factor VIIa {Human (Homo sapiens)}
ANAFLEELRPGSLERECKEEQCSFEEAREIFKDAERTKLFWISYSDGD
>d2pf1_2 g.32.1.1 (36-65) Prothrombin {Cow (Bos taurus)}
SATDAFWAKYTACESARNPREKLNECLEGN
>d2pf2_2 g.32.1.1 (1-65) Prothrombin {Cow (Bos taurus)}
ANKGFLEEVRKGNLREECLEEPSREEAFEALESLSATDAFWAKYTACESARNPREKLNECLEGN
>d1cfi_g.32.1.1 (-) Coagulation factor IX (IXa) {Human (Homo sapiens)}
YNSGKLEEFVQGNLERECKEEKCSFEEAREVFENTERTEFWKQYVD
>d1pxl3 g.32.1.1 (L:1-46) Coagulation factor IX (IXa) {Pig (Sus scrofa)}
YNSGKLEEFVRGNLERECKEEKCSFEEAREVFENTERTEFWKQYV
>d1iodg_g.32.1.1 (G:) Coagulation factor X {Cow (Bos taurus)}
ANSFLEEVKQGNLERECLLEEACSLEEAREVFEDAEQTDEFWSKY
>d1d6ga_g.33.1.1 (A:) Cholecystokinin A receptor, N-domain {Human (Homo sapiens)}
MDVVDSLLVNGSNITPPCELGLENELFCLDQPRPSKEWQPAQVILL
>d1vpu_g.34.1.1 (-) HIV-1 VPU cytoplasmic domain {Human immunodeficiency virus type 1}
LQIDRLRIDRITERAEDSGNESEGDQEELSAVERGHLAPWDVDDL
>d1isua_g.35.1.1 (A:) HIPIP (high potential iron protein) {Rhodococcus tenuis}
GTNAAMRKAFNYQDTAKNGKKCSGCAQFVPGASPTAAGGCKVIPGDNQIAPGGYCAFIVKK
>d1b0ya_g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochromatium vinosum, (formerly Chromatium vinosum)}

SAPANAVAADNATAIALKYNQDATKSERVAAARPGLPPEEQQCANCQFMQADAAGATDEWKGCQLFPGKLI
NVNGWCASWTLKAG

>d1js2a_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Allochromatium vinosum,
(formerly Chromatium vinosum)}

MEFMSAPANAVAADDATAIALKYNQDATKSERVAAARPGLPPEEQHCANCQFMQADAAGATDEWKGCQLF
PGKLINVNGWSASWTLKAG

>d3hipa_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Chromatium purpuratum}

VPANAVTESDPAAVALKYHRDAASSERVAAARPGLPPEEQHCENCQFMNPDAAA DWKGCLFPGKLINLSG
WCASWTLRAG

>d2hipa_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Ectothiorhodospira
halophila}

EPRAEDGHAHDYVNEAADASGHPRYQEGQLCENCAFGEAVQDGWGRCTHPDFDEVLVKAEGWCSVYAP
AS

>d1hpi_ g.35.1.1 (-) HIPIP (high potential iron protein) {Ectothiorhodospira
vacuolata}

MERLSEDDPAAQALEYRHDASSVQHPAYEGQTCLNCLLYTDASAQDWGPCSVFPGKLV SANGWCTAWVAR

>d1eyta_ g.35.1.1 (A:) HIPIP (high potential iron protein) {Thermochromatium
tepidum}

AAPANAVTADDPTAIALKYNQDATKSERVAAARPGLPPEEQHCANCQFMQANVGEGDWKGCLFPGKLINV
NGWCASWTLKAG

>d1dj7a_ g.36.1.1 (A:) Ferredoxin thioredoxin reductase (FTR), catalytic beta chain
{Synechocystis sp.}

NNKT LAAMKNFAEQYAKRTDTYFCSDL SVT AVVIEGLARHKEELGSPLCP CRHYEDKEAEVKNTFWNCPCVPM
RERKECHCMLFLTPND FAGDAQDIPMETLEEVKAS

>d1a1ga1 g.37.1.1 (A:103-131) ZIF268 {Mouse (Mus musculus)}

RPYACPVESCDRRFS DSSNLTRHIRIHTG

>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)}

QKPFQCRCMRNFSRS DHLTTIRTHHTG

>d1a1ia3 g.37.1.1 (A:160-187) ZIF268 {Mouse (Mus musculus)}

EKPFACDICGRKFARS DERKRHTKIHLR

>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)}

NLLNYVVPKMRPYACP VESCDRRFSRSDELTRHIRIHTG

>d1rmd_1 g.37.1.1 (87-116) V(D)J recombination activating protein 1 (RAG1), dimerization
domain {Mouse (Mus musculus)}

LMVKCPAQDCNEEV SLEKYNHHVSSH KESK

>d2drpa1 g.37.1.1 (A:103-139) Tramtrack protein (two zinc-finger peptide) {Drosophila
melanogaster}

FTKEGEHTYRCKCSR VY THISNFCRHYVTSHKRNVK

>d2drpa2 g.37.1.1 (A:140-165) Tramtrack protein (two zinc-finger peptide) {Drosophila melanogaster}
VYPCPFCFKEFTRKDNMTAHVKIIHK

>d1paa_ g.37.1.1 (-) ADR1 {Synthetic, based on Saccharomyces cerevisiae sequence}
KAYACGLCNRAFTRRDLLIRHAQKIHSGNL

>d2adr_1 g.37.1.1 (102-130) ADR1 {Synthetic, based on Saccharomyces cerevisiae sequence}
RSFVCEVCTRAFARQEHLKRHYRSHTNEK

>d2adr_2 g.37.1.1 (131-161) ADR1 {Synthetic, based on Saccharomyces cerevisiae sequence}
PYPCGLCNRAFTRRDLLIRHAQKIHSGNLGE

>d1znf_ g.37.1.1 (-) XFIN, third domain {Xenopus laevis}
YKCGLCERSFVEKSALSRRHQRVHKN

>d5znf_ g.37.1.1 (-) ZFY {Human (Homo sapiens)}
KTYQCQYCEYRSADSSNLKTHIKTSHSKEK

>d7znf_ g.37.1.1 (-) ZFY {Human (Homo sapiens)}
KTYQCQYCEKRFADSSNLKTHIKTSHSKEK

>d1ncs_ g.37.1.1 (-) SWI5 zinc-finger domains {Baker's yeast (Saccharomyces cerevisiae)}
TLPRGSIDKYVKEMPDKTFECLFPGCTKTFKRRYNIRSHIQTHLEDR

>d1zfd_ g.37.1.1 (-) SWI5 zinc-finger domains {Baker's yeast (Saccharomyces cerevisiae)}
DRPYSCDHPGCDKAFFVRNHDLIRHKKSHQEKA

>d2glia1 g.37.1.1 (A:103-134) Five-finger GLI1 {Human (Homo sapiens)}
ETDCRWGCSQEFDSQEQLVHHINSEHIHGER

>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)}
KPYMCEHEGCSKAFAFSNASDRAKHQNRTHSNE

>d2glia5 g.37.1.1 (A:229-257) Five-finger GLI1 {Human (Homo sapiens)}
KPYVCKLPGCTKRYTDPSLRLHVKTVHG

>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)}
PYHCTYCNSFKTKGNLTGHMKSKAHSKK

>d4znf_ g.37.1.1 (-) Enhancer binding protein {Human (Homo sapiens)}
RPYHCSYCNFSFKTKGNLTGHMKSKAHSKK

>d1sp1_ g.37.1.1 (-) Transcription factor sp1 {Human (Homo sapiens)}
KKFACPECPKRFMRSDHLSKHIKTHQNKK

>d1sp2_ g.37.1.1 (-) Transcription factor sp1 {Human (Homo sapiens)}
RPFMCTWSYCGKRFTRSDELQRHKRTHTGEK

>d1bhi_ g.37.1.1 (-) Transactivation domain of cre-bp1/atf-2 {Human (Homo sapiens)}
MSDDKPFLCTAPGCGQRFTNEDHLAVHKHHEMTLKFG

>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)}
RVHVCAECGKAFV ESSKLKRHQLVHTGE

>d1ubdc3 g.37.1.1 (C:351-380) Ying-yang 1 (yy1, zinc finger domain) {Human (Homo sapiens)}
KPFQCTFEGCGKRFSLDFNL RTHVRIHTGD

>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}
MKRYICSFADC GAAYNKNWKLQAHLSKHTGE

>d1tf3a2 g.37.1.1 (A:41-70) Transcription factor IIIA, TFIIIA {Xenopus laevis}
KPFPCKEEGCEKGFTSLHHLTRHSLTHTGE

>d1tf3a3 g.37.1.1 (A:71-101) Transcription factor IIIA, TFIIIA {Xenopus laevis}
KNFTCDSDGCDLRFTTKANM KKHFNRFHNIK

>d1tf6a1 g.37.1.1 (A:10-40) Transcription factor IIIA, TFIIIA {Xenopus laevis}
YKRYICSFADC GAAYNKNWKLQAHLC KHTGE

>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}
PKAKRAKHPPGTEKPRSR SQSEQPATCPIC YAVIRQSRNLRRHLELRHFAKPGV

>d1fu9a_ g.37.1.2 (A:) U-shaped transcription factor, different fingers {Fruit fly (Drosophila melanogaster)}

GSAAEV MKKYCSTCDISFNYVK TYLAHKQFYCKNKP

>d1fv5a_ g.37.1.2 (A:) U-shaped transcription factor, different fingers {Fruit fly (Drosophila melanogaster)}

GSLLKPARFMCLPCGIAFSSP STLEAHQAYYCSHRI

>d1aw6_ g.38.1.1 (-) Gal4 {Baker's yeast (Saccharomyces cerevisiae)}

MKLLSSIEQACDICR LKKLKC SKEKPKCAKCLKNNWECRYSPK

>d1d66a1 g.38.1.1 (A:8-48) Gal4 {Baker's yeast (Saccharomyces cerevisiae)}

EQACDICR LKKLKC SKEKPKCAKCLKNNWECRYSPK

>d1pyia1 g.38.1.1 (A:30-71) PPR1 {Baker's yeast (Saccharomyces cerevisiae)}

SRTACKRCRLKKI KCDQEFPSCKRCAKLEVPCVSLDPATGKD

>d1zme c1 g.38.1.1 (C:31-66) PUT3 {Baker's yeast (Saccharomyces cerevisiae)}

SVACLS CRKRHI KCPGGN PCQKCVTSNAICEYLEPS

>d1hwtc1 g.38.1.1 (C:59-97) Hap1 (Cyp1) {Baker's yeast (Saccharomyces cerevisiae)}

RIPLSCTICRKRKV KCDKLRPHCQQCTKTGVAHLCHYME

>d2hapc1 g.38.1.1 (C:55-97) Hap1 (Cyp1) {Baker's yeast (Saccharomyces cerevisiae)}

RKRNRIPLRCTICRKRKV KCDKLRPHCQQCTKTGVAHLCHYME

>d1cld_ g.38.1.1 (-) CD2-Lac9 {Milk yeast (Kluyveromyces lactis)}

QACD ACRKKW KCSKT VPTCTNCL KYNLDCVYS

>d2alca_g.38.1.1 (A:) Ethanol regulon transcriptional activator ALCR DNA-binding domain {Aspergillus nidulans and Emericella nidulans}

GSMADRRRNQHCDPCRKGKRRCDAPENRNEANENGWVSCSNCKRWNKDCTFNWLSSQRSKNSS

>d3gata_g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}

KRAGTVCNSNCQTSTTLWRRSPMGDPVCNACGLYYKLHQVNRLPTMRKDGIQTRNRKVSSKGKKRR

>d7gata_g.39.1.1 (A:) Erythroid transcription factor GATA-1 {Chicken (Gallus gallus)}

MKNQEQNPGTTCTNCFTQTPVWRRNPEGQPLCNACGLFLKLHGVRPLSLKTDVICKRNRNSANS

>d1gnf_g.39.1.1 (-) Erythroid transcription factor GATA-1 {Mouse (Mus musculus)}

GSEARECVNGATATPLWRRDRTGHYLCACGLYHKMNGQNRPLIR

>d1dszb_g.39.1.2 (B:) Retinoid X receptor (RXR-alpha) DNA-binding domain {Human (Homo sapiens)}

GSFTKHICAICGDRSSGKHYGVYCEGCKGFFKRTVRKDLTYCRDNKDCLIDKRQRNRCQYCRYQKCLAMGM
KREAVQEERQR

>d2nlla_g.39.1.2 (A:) Retinoid X receptor (RXR-alpha) DNA-binding domain {Human (Homo sapiens)}

CAICGDRSSGKHYGVYCEGCKGFFKRTVRKDLTYCRDNKDCLIDKRQRNRCQYCRYQKCLAMGM

>d2nllb_g.39.1.2 (B:) Thyroid hormone receptor (TR-beta) DNA-binding domain {Human (Homo sapiens)}

DELCVVCGDKATGYHYRCITCEGCKGFFRTIQKNLHPSYSCKYEGKCVIDKVTRNQCQECKFKCIVYGMATDL
VLDDSKRLAKRKLIIFENREKRRREELEK

>d1cita_g.39.1.2 (A:) Orphan nuclear receptor NGFI-B {Rat (Rattus norvegicus)}

GRCAVCGDNASCQHYGVRTCEGCKGFFKRTVQKSAKYICLANKDCPVDKRRRNRCQFCRFQKCLAVGMVKEV
VRTDSLKGRRGRLPSKP

>d1hcqa_g.39.1.2 (A:) Estrogen receptor DNA-binding domain {Human and chicken (Homo sapiens) and (Gallus gallus)}

MKETRYCAVCNDYASGYHYGVWSCEGCKAFFKRSIQGHNDYMCPATNQCTIDKNRRKSCQACRLRKCYEVG
MMK

>d1glua_g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain {Rat (Rattus norvegicus)}

MKPARPCLVCSDEASGCHYGVLTGSCKVFFKRAVEGQHNYLCAGRNDIIDKIRRKNCPACRYRKCLQAGMN
LEARKTKK

>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)}

LCLVCSDEASGCHYGVLTGSCKVFFKRAVEGQHNYLCAGRNDIIDKIRRKNCPACRYRKCLQAGMNLEAR

>d1dsza_g.39.1.2 (A:) Retinoic acid receptor DNA-binding domain {Human (Homo sapiens)}

PCFVCQDKSSGYHYGVSACEGCKGFFRSIQKNMVYTCHRDKNCIINKVTRNRCQYCRLQKCFEVGMSKESVR
ND

>d1hra_g.39.1.2 (-) Retinoic acid receptor DNA-binding domain {Human (Homo sapiens)}

PPRVYKPCFVCQDKSSGYHYGVSACEGCKGFFRSIQKNMIYTCHRDKNCVINKVTRNRCQYCRLQKCFEVGM
SKESVRN

>d1a6ya_g.39.1.2 (A:) Orphan nuclear receptor reverb {Human (Homo sapiens)}

LLCKVCGDVASFHYGVHACEGCKGFFRSIQQQNIQYKRCLENCSIVRINRNRCQQCRFKKCLSVGMSRDAV
RFGR

>d1b8ta1_g.39.1.3 (A:1-35) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}

MPNWGGGKKCGVCQKAVYFAEEVQCEGSSFKSCF
>d1b8ta2 g.39.1.3 (A:36-100) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (Gallus gallus)}
LCMVCKNLDSTTVAVHGDIEYCKSCYGKKYGPKGKGKGMAGTLSTDKGESLGIKYEEGQSHRP
>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)}
RCAKCGKSLESTTLADKDGEIYCKGYAKNFGPKGFGQGQAGALIHSQ
>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}
LCMVRKNLDSTTVAIHDAEVYCKSCYGKKYG
>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}
FRCAKCGKSLESTTLTEKEGEIYCKGYAKN
>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)}
KCEKCGKLTSGGHAEHEGKPYCNHPCYSAMFGPKGFGRRGAESHTFK
>d1g47a1 g.39.1.3 (A:1-35) Pinch (particularly interesting new Cys-His) protein {Human (Homo sapiens)}
MANALASATCERCKGGFAPAAEKIVNSNGELYHEQC
>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)}
MEFDYVICEECGKEFMDSYLMNHFDLPTCDNCRDAD
>d1xpa_2 g.39.1.5 (98-133) DNA repair factor XPA DNA- and RPA-binding domain, N-terminal subdomain {Human (Homo sapiens)}
MEFDYVICEECGKEFMDSYLMNHFDLPTCDNCRDAD
>d1jj2t_g.39.1.6 (T:) Ribosomal protein L24e {Archaeon Haloarcula marismortui}
RECDYCGTDIEPGTGTMFVHKDGATTHFCSSKCENNADLGREARNLEWTDTAR
>d1fjgn_g.39.1.7 (N:) Ribosomal protein S14 {Thermus thermophilus}
ARKALIEKAKRTPKFVRAYTRVRCGRARSVYRFFGLRICLRELAKGQLPGVRKASW
>d1aaf__g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}

MQRGNFRNQRKIIKCFNCGKEGHIAKNCRAPRKRCWKGKEGHQMKDCTERQAN
>d1eska_g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
NVKCFNCGKEGHTARNCRAPRKKGCGKEGHQMKDCTERQ
>d1f6ua_g.40.1.1 (A:) HIV nucleocapsid {Human immunodeficiency virus type 1, different isolates}
MQKGNFRNQRKTVKCFNCGKEGHIAKNCRAPRKKGCGKEGHQMKDCTERQAN
>d1nc8_g.40.1.1 (-) HIV nucleocapsid {Human immunodeficiency virus type 2}
AQQRKVIRCWNCGKEGHHSARQCRAPIRQG
>d1cl4a_g.40.1.1 (A:) Nucleocapsid protein from mason-pfizer monkey virus (MPMV) {Mason-pfizer monkey virus}
VPGLCPCKRGKHWAENECKSDTNQGNPIPPH
>d1a6bb_g.40.1.1 (B:) Zinc finger protein ncp10 {Moloney murine leukemia virus}
GERRRSQLDRDQCAYCKEKGHWAKDCPKPRGPRGPRPQT
>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}
PPGLCPCKKGYHWKSECKSKFDKDGNPLPP
>d1f4la3_g.41.1.1 (A:141-175) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}
VKGTCPKCKSPDQYGDNCVCGATYSPTELIEPKS
>d1mea_g.41.1.1 (-) Methionyl-tRNA synthetase (MetRS), Zn-domain {Escherichia coli}
GSDRFVKGTCPKCKSPDQYGDNCVCGA
>d1zin_2_g.41.2.1 (126-160) Microbial and mitochondrial ADK, insert "zinc finger" domain {Bacillus stearothermophilus}
GRRICRNCGATYHLIFHPPAKPGVCDKGCGELYQR
>d1e4ya2_g.41.2.1 (A:122-156) Microbial and mitochondrial ADK, insert "zinc finger" domain {Escherichia coli}
GRRVHAPSGRVYHVFNPPKVEGKDDVTGEELTR
>d2ak3a2_g.41.2.1 (A:125-161) Microbial and mitochondrial ADK, insert "zinc finger" domain {Cow (Bos taurus), mitochondrial izozyme-3}
ARWIHPGSGRVYNIEFNPPKTMGIDDLTGEPLVQRED
>d1ak2_2_g.41.2.1 (147-176) Microbial and mitochondrial ADK, insert "zinc finger" domain {Cow (Bos taurus), mitochondrial izozyme-2}
PQSGRSYHEEFNPPKEPMKDDITGEPLIRR
>d1aky_2_g.41.2.1 (131-168) Microbial and mitochondrial ADK, insert "zinc finger" domain {Baker's yeast (Saccharomyces cerevisiae)}
GRLIHPASGRSYHKIFNPPKEDMKDDVTGEALVQRSDD
>d1zaka2_g.41.2.1 (A:128-158) Microbial and mitochondrial ADK, insert "zinc finger" domain {Maize (Zea mays)}
GRRLLDPVTGKIYHLKYSPPEEIASRLTQR
>d1tfi_g.41.3.1 (-) Transcriptional factor SII, C-terminal domain {Human (Homo sapiens)}
KTGGTQTDLFTCGKCKKNCTYTQVQTRSADEPMTTFVVCNECGNRWKFC
>d1pft_g.41.3.1 (-) Transcription initiation factor TFIIB, N-terminal domain {Archaeon Pyrococcus furiosus}
MVNKQKVC PACESAELIYDPERGEIVCAKCGYVIEENIIDMGPEWRAFDA
>d1dl6a_g.41.3.1 (A:) Transcription initiation factor TFIIB, N-terminal domain {Human (Homo sapiens)}

sapiens})

ASTSRLDALPRVTCPNHPDAILVEDYRAGDMICPECGLVVGDRVIDVGSEWRTFSNDK

>d1d0qa_g.41.3.2 (A:) Zinc-binding domain of DNA primase {Bacillus stearothermophilus}

GHRIPPEETIEAIRRGVDIVDVIGEYVQLKRQGRNYFGLCPFHGEKTPSFVSPEKQIFHCFGCGAGGNAFTFLMDI
EGIPFVEAAKRLAAKAGVDSLKYELD

>d1yua_1 g.41.3.3 (1-65) Prokaryotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}
MNGEVAPPKEDPVPLPELPCEKSDAYFVLRDGAAGVFLAANTFPKSRETRAPLVEELYRFRDRLP

>d1yua_2 g.41.3.3 (66-122) Prokaryotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}

EKLRYLADAPQQDPEGNKTMRFSRKTQQYVSSEKDKGATGWSAFYVDGKWVEGKK

>d1qf8a_g.41.4.1 (A:) Casein kinase II beta subunit {Human (Homo sapiens)}

VSWISWFCGLRGNEFFCEVDEDYIQDKFNLTGLNEQVPHYRQALDMILDLEPDEELEDNPNQSDLIEQAAEMI
YGLIHARYILTNRGIAQMILEKYQQGDFGYCPRVYCENQPMPLIGLSDIPGEAMVKLYCPKCMDVYTPKSSRHHH
TDGAYFGTGFPHMLFMVHPEYRPKRP

>d1rb9_g.41.5.1 (-) Rubredoxin {Desulfovibrio vulgaris}

MKKYVCTVCGYEYDPAEGDPDNGVKPGTSFDDLPADWVCVCPVCGAPKSEFEAA

>d2rdva_g.41.5.1 (A:) Rubredoxin {Desulfovibrio vulgaris}

MKKYVCTVCGYEYDPAEGDPDNGVKPGTAFEDVPADWVCVCPVCGAPKSEFEPA

>d1rdg_g.41.5.1 (-) Rubredoxin {Desulfovibrio gigas}

MDIYVCTVCGYEYDPAKGDPDSGIKPGTKFEDLPDDWACPVCVGASKDAFEKQ

>d6rxn_g.41.5.1 (-) Rubredoxin {Desulfovibrio desulfuricans, strain 27774}

MQKYVCNVCGYEYDPAEHDNVPFDQLPDDWCCPVCVGSKDQFSPA

>d1iro_g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}

MKKYTCTVCGYIYNPEDGDPDNGVNPGTDFKIDPDDWVCPLCGVGKDQFEEVE

>d5rxn_g.41.5.1 (-) Rubredoxin {Clostridium pasteurianum}

MKKYTCTVCGYIYDPEDGDPDDGVNPGBTDFKIDPDDWVCPLCGVGKDQFEEVE

>d1brfa_g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}

AKWVCKICGYIYDEDAGDPDNGISP GTKFEE LPDDWVC PICGAPKSEFEKLED

>d1qcva_g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}

AKWVLKITGYIYDEDAGDPDNGISP GTKFEE LPDDWVAPI GAPKSEFEKLED

>d1dx8a_g.41.5.1 (A:) Rubredoxin {Guillardia theta}

MEIDEKYCEACGYIYEPEKGGDKFAGIPPGTPFVDSLDSFMCPACRSPKNQFKSIKKVIAGFAENQKYG

>d1h7va_g.41.5.1 (A:) Rubredoxin {Guillardia theta}

MEIDEKYCEACGYIYEPEKGGDKFAGIPPGTPFVDSLDSFMCPACRSPKNQFKSIKKVI

>d1dvba2_g.41.5.1 (A:148-191) Rubrerythrin, C-terminal domain {Desulfovibrio vulgaris}

FLREQATKWRCRNCGYVHEGTGAPELCPACAHPKAHFELLGINW

>d1dxga_g.41.5.2 (A:) Desulforedoxin {Desulfovibrio gigas}

ANEGDVYKCELCGQQVKVLEEGGGTLVCCGEDMVKQ

>d1dfx_2_g.41.5.2 (1-36) Desulfoferrodoxin N-terminal domain {Desulfovibrio desulfuricans}

PKHLEVYKCTHGNIVEVLHGGGAELVCCGEPMKHM

>d1ocrf_g.41.5.3 (F:) Cytochrome c oxidase Subunit F {Cow (Bos taurus)}

ASGGGVPTDEEQATGLEREVMLAARKGQDPYNILAPKATSGTKEDPNLVPSITNKRIVGCICEEDNSTVIWFWL

HKGEAQRCPS CGTHYKLVPHQLAH

>d1gh9a_ g.41.6.1 (A:) Hypothetical protein MTH1184 {Archaeon Methanobacterium thermoautotrophicum}
MYIIFRDCGRALYSREGAKTRKCVCGRTVNVKDRRIFGRAADDFEEASELVRKLQEEKYGSCHFTNPSKRE

>d1d09b2 g.41.7.1 (B:101-153) Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain {Escherichia coli}
ERIDNVLVCPNSNCISHAEPVSSSFAVRKRANDIALKCKYCEKEFSHNVVLAN

>d2atcb2 g.41.7.1 (B:101-152) Aspartate carbamoyltransferase, Regulatory-chain, C-terminal domain {Escherichia coli}
ERNIDVLVCPDSNCISHAEPVSSSFAVRRADDIALKCKYCEKEFSHNVVLAN

>d1ffkw_g.41.8.1 (W:) Ribosomal protein L37ae {Archaeon Haloarcula marismortui}
PTGRGFPYGLKIRVRVDVEIKHKKKYKCPVCGFPKLKRASTSIWVCGHCGYKIAGGAYTPETVAGKAVMKA

>d1jj2y_g.41.8.1 (Y:) Ribosomal protein L37ae {Archaeon Haloarcula marismortui}
RTGRGFPYGLKIRVRVADVEIKHKKHKCPVCGFKLKRAFTGIWMCGHCGYKIAGGCYQPETVAGKAVMKA

>d1jj2z_g.41.8.2 (Z:) Ribosomal protein L37e {Archaeon Haloarcula marismortui}
TGAGTPSQGKKNNTTHTCRRCGEKSYHTKKVCSSCGFGKSAKRRDYEWQSKAGE

>d1jj22_g.41.8.3 (2:) Ribosomal protein L44e {Archaeon Haloarcula marismortui}
MQMPRRFNTYCPHCNEHQEHEVEKVRSGRQTGMWIDRQRERNSGIGNDGKFSKVPGGDKPTKKTDLKYS
CGECGKAHLREGWRAGRLEFQE

>d1qyp_g.41.9.1 (-) RBP9 subunit of RNA polymerase II {Archaeon Thermococcus celer}
GSHMEQDLKTLPTTKITCPKCGNDTAYWWEMQTRAGDEPSTIFYKCTKCGHTWRSYE

>d1i50i1 g.41.9.1 (I:1-49) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}

MTTFRCRDCNNMLYPREDKENNRLFECRTCSYVEAGSPLVYRHELI

>d1i50i2 g.41.9.1 (I:50-122) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}

TNIGETAGVVQDIGSDPTLPRSDRECPKCHSRENFFQSQQRRKDTSMVLFFCLSCSHIFTSDQKNKRTQFS

>d1i50i_ g.41.9.2 (L:) RBP12 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}

ATLKYICAECSSKLSLSRTDAVRCKDCGHRILLKARTKRLVQFEAR

>d1dfa_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)}

TPQDHIKVTQEQQYELYCEMGSTFQLCKICAENDKDVIEPCGHLMCTSCLTSWQESEGQGCPFCRCEIKGTEPIV
VDPF

>d1rmd_2 g.44.1.1 (1-86) V(D)J recombination activating protein 1 (RAG1), dimerization domain {Mouse (Mus musculus)}

NCSKIHLSKLLAVDFPAHFVKSISQCICEHILADPVETSCKHLFCRICILRCLKVMGSYCPSCRYPFCPTDLESPVKS
FLNILNS

>d1chc_g.44.1.1 (-) Immediate early protein, IEEHV {Equine herpes virus type 1}
MATVAERCPICLEDPSNYSMALPCLHAFCYVCITRWIRQNPTCPLCKVPVESVHTIESDSEFGDQLI

>d1bor_g.44.1.1 (-) Acute promyelocytic leukaemia proto-oncoprotein PML {Human (Homo sapiens)}

EEEFQFLRCQQCQAEAKCPKLLPCLHTLCGCLEASGMQCPCIQAPWPLGADTPAL
>d1g25a_g.44.1.1 (A:) TFIIH Mat1 subunit {Human (Homo sapiens)}
MDDQGCPCKTTKRYNPSLKLMLNVNCGHTLCESCVDLLFVRGAGNCPECGTPLRKSNFRVQLFED
>d1e4ua_g.44.1.1 (A:) Not-4 N-terminal RING finger domain {Human (Homo sapiens)}
MSRSPDAKEPVECPLCMEPLEIDDINFFPCTCGYQICRFCWHRIRTDENGLCPACRKPYPEDPAVYKPLSQEEL
QRI
>d1jm7a_g.44.1.1 (A:) brca1 RING domain {Human (Homo sapiens)}
MDLSALRVEEVQNINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQCPLCKNDITKRSLQES
TRFSQLVEELLKIICAFQLDTGLEYAN
>d1jm7b_g.44.1.1 (B:) bard1 RING domain {Human (Homo sapiens)}
MEPDGRGAWAHSRAALDRLEKLLRCSRCTNILREPVCVLLGCEHIFCSNCVSDCIGTGCPVCYTPAWIQLDKINR
QLDSMIQLCSKLRNLLHDNELD
>d1dcqa2_g.45.1.1 (A:247-368) Pyk2-associated protein beta ARF-GAP domain {Mouse (Mus musculus)}
LTKEIISEVQRMTGNDVCCDCGAPDPTWLSTNLGILTCIECGSIHRELGVHYSRMQSLTDVLGTSELLLAKNIGN
AGFNEIMECCLPSEDPVKPNPGSDMIARKDYITAKYMERRYARKKH
>d1mhu_g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}
KSCCSCCPVGCAKCAQGCICKGASDKCSCCA
>d2mhu_g.46.1.1 (-) Metallothionein {Human (Homo sapiens)}
MDPNCSCAAAGDSCTCANSCTCKACKCTSCK
>d2mrb_g.46.1.1 (-) Metallothionein {Rabbit (Oryctolagus cuniculus)}
MDPNCSCAAAGDSCTCANSCTCKACKCTSCK
>d1mrt_g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
KSCCSCCPVGCAKCSQGCICKEASDKCSCCA
>d2mrt_g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
MDPNCSCATDGSCSCAGSCKQCKCTSCK
>d4mt2_g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}
MDPNCSCATDGSCSCAGSCKQCKCTSCK
>d1dfa_g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
KSCCSCCPVGCSKCAQGCVCKGAADKCTCCA
>d1dfa_g.46.1.1 (A:) Metallothionein {Mouse (Mus musculus)}
MDPNCSCTGGSCTCTSSCACKNCKCTSCK
>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}
PGPCCNDKVCVCQEGGCKAGCQCTSCRC
>d1fmya_g.46.1.1 (A:) Metallothionein {Baker's yeast (Saccharomyces cerevisiae)}
QNEGHECQCQCGSCKNNEQCQKSCSCPTGCNSDDKPCPGN
>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}

TLVKCACEPCLCNVDP SKAIDRNGLYYCSEACADGHTGGSKGC GHTGCNCHG

>d1co4a_ g.47.1.1 (A:) Zinc domain conserved in yeast copper-regulated transcription factors {Synthetic}

MVVINGVKYACDSCI KSHKAAQCEHNDRPLKILKPRGRPPTT

>d1adn_ g.48.1.1 (-) Ada DNA repair protein, N-terminal domain (N-Ada 10) {Escherichia coli}

MKKATCLTDDQRWQS VLARDPNADGEFVFAVRTTGIFCRPSCRARHALRENV SFYANASEAL AAGFRPKRCQ PDKANPRQHRLDKITHACR

>d1ptq_ g.49.1.1 (-) Protein kinase C-delta (PKCdelta) {Mouse (Mus musculus)}

HRFKV VNYMSPTFC DHC GSLLWGLVKQGLKCEDCG MNVHHKCREKVANLC

>d1faq_ g.49.1.1 (-) RAF-1 {Human (Homo sapiens)}

LTTHNFARKTFLKLA FDCICQKFLLNGFRC QTCGYK FHEHC STKVPTMCVDW

>d1tbo_ g.49.1.1 (-) Protein kinase c-gamma {Rat (Rattus rattus)}

QTDDPRNKH KFRLHSYSSPTFC DHC GSLLYGLVHQGMK CSCCE MNVH RRC VR SVPSL CGV DHTERR

>d1kbea_ g.49.1.1 (A:) Kinase suppressor of Ras, Ksr {Mouse (Mus musculus)}

GSVTHR FSTK SWLSQVCNVCQ KSMIFGVKCKH CRLK CHNK CTKEAPACR

>d1e53a_ g.49.1.2 (A:) TFI IH p44 subunit cysteine-rich domain {Human (Homo sapiens)}

LDAFQEIP LEYNG ERF CYGC QGELKDQH VYVCAV CQNV FCV DCDV FVHD SLH CCP GCI

>d1vfy a_ g.50.1.1 (A:) vps27p protein {Baker's yeast (Saccharomyces cerevisiae)}

DWIDSDACMICS KKF SLLNRK HH CRSC GGVFC QEH SSNSIPLPD LGIYEPV RV CDSC FED YEFIV TD

>d1joca1 g.50.1.1 (A:1348-1411) Eea1 {Human (Homo sapiens)}

KWAEDNEVQNC MACGKG FS TVRR HCRQ CGN IFCAECSAKN ALTPSSKK PV RV CDAC FND LQG

>d1dvpa2 g.50.1.1 (A:149-220) Hrs {Fruit fly (Drosophila melanogaster)}

MFTADTAP NWAD GRV CHRC RVE FTFT NRK HH CRNC GQVFC GQCTAKQC PLPK YGIE KEVR VCD GCF AAL QR

G

>d1zbdb_ g.50.1.1 (B:) Effector domain of rabphilin-3a {Rat (Rattus norvegicus)}

EELTDEE KEIINR VIARA EK METME QERIG RL VDR LETMR KNVAGD GVNR CILCG EQLGML GSAS VV CED CKKN VCT KCGV ET SNNR PHPV WL KICLE QREV WKR SGAW FF KGFP KQVLP QPM

>d1f62a_ g.50.1.2 (A:) Williams-Beuren syndrome transcription factor, WSTF {Human (Homo sapiens)}

ARCKVCRKKGEDDKL IL CDEC NKAFHL FCLRP ALYE VP DGEW QCPAC QPAT

>d1fp0a1 g.50.1.2 (A:19-88) Nuclear corepressor KAP-1 (TIF-1beta) {Human (Homo sapiens)}

GTL DDSAT ICRC VQ KPGD LV MCN QCE FCF HLD CLP ALQ DV PGEE WSCS LCHV LPDL KEED VDL QACK LN

>d1adt_2 g.51.1.1 (266-385) First Zn-domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}

TG CALWLH RCAEIE GELK CLH GSIM INKE HVIEMD VTSE NGQ RALKE QSS KAKIV KNRW GRNV VQIS NT DARC CVH DAACP ANQ FSGK SC GMFF SEGA KQ VAFK QIK AFM QAL YPNA QT

>d1adt_3 g.51.1.1 (386-529) Second Zn-domain of early E2A DNA-binding protein, ADDBP {Human adenovirus type 5}

GH GHILL MPLR CE CNS KPGH APFL GRQL PKL TP FALS NAED LDAD L ISDK SV LASV HHPAL I VFQCCNP VY RNS R AQGGGP NCDF KISAP DLLN ALVM VRSLW SENFT ELP RMV VPQ FKW STK HQY RN VS LPVA HSD ARQ NP PDF

>d1qbha_g.52.1.1 (A:) 2MIHB/C-IAP-1 {Human (Homo sapiens)}

GSHMQTHAARMRTFMYWPSSVPVQPEQLASAGFYYGRNDDVKCFCDCGGLRCWESGDDPWEHAKWF
PRCEFLIRMKGQEFVDEIQGRYPHLLEQLLSTS

>d1f9xa_g.52.1.1 (A:) BIR domains of XIAP {Human (Homo sapiens)}

MSDAVSSDRNFPNSTLPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWK
PSEDPWEQHAKWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTT

>d1g73c_g.52.1.1 (C:) BIR domains of XIAP {Human (Homo sapiens)}

LPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPG
CKYLLEQKGQEYINNIHLTHSLEECLVRTT

>d1g73d_g.52.1.1 (D:) BIR domains of XIAP {Human (Homo sapiens)}

LPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVKCFHCGGGLTDWKPSEDPWEQHAKWYPG
CKYLLEQKGQEYINNIHLTHSLEECLVRTT

>d1i3oe_g.52.1.1 (E:) BIR domains of XIAP {Human (Homo sapiens)}

FALDRPSETHADYLRTGQVVDISDTIYPRNPAMYSEEARLKSFQNWPDYAHLPRELASAGLYYTGIGDQVQCF
ACGGKLKNWEPGDRAWSEHRRHFPNCFFVLGRNLNI

>d1jd5a_g.52.1.1 (A:) BIR2 domain of DIAP1 {Fruit fly (Drosophila melanogaster)}

GNYFPQYPEYAIETARLRTFEAWPRNLKQKPHQLAEAGFFYTGVGDRVRCFSCGGGLMDWNDNDEPWEQHA
LWLSQCRFVKLMKGQLYIDTVAAKPVLAAEKEES

>d1e31a_g.52.1.1 (A:) Anti-apoptotic protein survivin {Human (Homo sapiens)}

TLPPAWQPFLKDHRISTFKNWPFLLEGCACTPERMAEAGFIHCPTENEPLAQCCFCFKELEGWEPDDDPFEEHK
KHSSGCAFLSVKKQFEELTLGEFLKLDRERAKNKIAKETNNKKKEFEETAKKVRAIEQLAA

>d1f81a_g.53.1.1 (A:) CREB-binding transcriptional adaptor protein CBP {Mouse (Mus musculus)}

SPQESRRLSIQRCIQSLVHACQCRNANCSLPSCQKMKRVVQHTKGCKRKTNNGCPVCKQLIALCCYHAKHCQE
NKCPVPCFLNIKHK

>d1hc7a3_g.56.1.1 (A:404-477) C-terminal domain of ProRS {Thermus thermophilus}

TRKVDTYEAFKEAVQEGFALAFHCGDKACERLIQEETTATTRCPFEEAPEEGFCVRCGRPSAYGKRVVFAKAY

>d1exka_g.54.1.1 (A:) Cysteine-rich domain of the chaperone protein DnaJ. {Escherichia coli}

GVTKEIRIPTLEECDVCHGSGAKPGTQPQTCPTCHGSGQVQMRQGFFAVQQTCPHCQGRRTLKDPCNKCHG
HGRVERS