

Online Supporting Information S2. The benchmark dataset S2 includes 3,187 proteins from 540 super-families and 777 families.

>d1dlwa_ a.1.1.1 (A:) Truncated hemoglobin {Ciliate (Paramecium caudatum)}
SLFEQLGGQAAVQAVTAQFYANIQADATVATFFNGIDMPNQTNKTAAFLCAALGGPNAWT
GRNLKEVHANMGVSNAQFTTVIGHLRSALTGAGVAAALVEQTVAVAETVRGDVVTV

>d1dlya_ a.1.1.1 (A:) Truncated hemoglobin {Green alga (Chlamydomonas eugametos)}
SLFAKLGGREAVEAAVDKFYNKIVADPTVSTYFSNTDMKVQRSKQFAFLAYALGGASEWK
GKDMRTAHKDLVPHLSDVHFQAVARHLSDTLTTELGVPPEDITDAMAVVASTRTEVLNMPQ
Q

>d1idra_ a.1.1.1 (A:) Truncated hemoglobin {Mycobacterium tuberculosis}
GLLSRLRKREPISYDKIGGHEAIEVVVEDFYVRVLADDQLSAFFSGTNMSRLKGKQVEFF
AAALGGPEPYTGAPMKQVHQGRGITMHHFSLVAGHLADALTAAGVPSETITEILGVIAPLA
VDVTS

>d1sctb_ a.1.1.2 (B:) Hemoglobin I {Ark clam (Scapharca inaequalis)}
KVAELANAVVSNAQDKLLRMSWGVLSVDMEGTGLMLMANLFKTSPSAKKGKFARLGD
VSAGKDNSKLRGHSITLMYALQNFVDALDDVERLKC VVEKFAVNHINRQISADEFG EIVG
PLRQTLKARMGNYFDEDTVAAWASLVAVVQASL

>d1b0b_ a.1.1.2 (-) Hemoglobin I {Clam (Lucina pectinata)}
SLSAAQKDNVKSSWAKASAAWGTAGPEFFMALFDAHDDVFAKFSGLFSGAAKGTVKNT
PEMAAQASQFKGLVSNWVDNLDNAGALEGQCKTFAANH KARGISAGQLEAAFKVLAF
MKS YGGDEGAWTAVAGALMGMIRPDM

>d1h97a_ a.1.1.2 (A:) Trematode hemoglobin/myoglobin {Paramphistomum epiclitum}
TLTKHEQDILLKELGPHVDTPAHIVETGLGAYHALFTAHPQYISHFSRLEGHTIENVMQSEG
IKHYARTLTEAIVHMLKEISNDAEVKKIAAQY GKDHTSRKVTKDEFMSG EPIFTKYFQNLV
KDAEGKAAVEKFLKHVFPMMAAEI

>d1vrea_ a.1.1.2 (A:) Glycera globin {Marine bloodworm (Glycera dibranchiata)}
GLSAAQRQVVASTWKDIAGSDNGAGVGKECFTKFLSAHHDMAAVFGFSGASDPGVADL
GAKVLAQIGVAVSHLGDEGKMVAEMKAVGVRHKG YGNKHIKAEYFEPLGASLLSAMEH
RIGGKMNA AAKDAWAAAYADISGALISGLQS

>d1mba_ a.1.1.2 (-) Myoglobin {Sea hare (Aplysia limacina)}
SLSAAEADLAGKSWAPVFANKNANGLDFLVALFEKFPDSANFFADFKGKSVADIKASPKL
RDVSSRIFTRLNEFVNNAANAGKMSAMLSQFAKEHVGFGVGS AQFENVRSMPG FVASV
AAPPAGADA AAWTKLFGLIIDALKAAGA

>d1mbs_ a.1.1.2 (-) Myoglobin {Common seal (Phoca vitulina)}
GLSDGEWHLVLNVWGKVETDLAGHGQEV LIRLFKSHPETLEKFDKFKHLKSEDDMRSE
DLRKHGNTVLTALGGILKKKGHHEAELKPLAQSHATKH KIPKYLEFISEAIIHVLHSHKHPA
EFGADAQAAMKKALELFRNDIAAKYKELGFHG

>d1eco_ a.1.1.2 (-) Erythrocrutorin {Midge (Chironomus thummi thummi), fraction III}
LSADQISTVQASFDKVKGDPVGILYAVFKADPSIMAKFTQFAGKDLESIKGTAPFETHANRI
VGFFSKIIGELPNIEADVNTFVASHKPRGVTHDQLNNFRAGFVS YMKAH TDFAGAEAAWG
ATLD TFFGMIFSKM

>d1d8ua_ a.1.1.2 (A:) Non-symbiotic plant hemoglobin {Rice (*Oryza sativa*)}
 ALVEDNNAVAVSFSEEQEALVLKSWAILKKDSANIALRFFLKIFEVAPSASQMFSLRNSDV
 PLEKNPKLKTHAMSVFVMTCEAAQRLKAGKVTVRDRTLRLGATHLKYGVGDAHFV
 VKFALLDTIKEEVPADMWSPAMKSAWSEAYDHLVAAIKQEMKPAE

>d1cg5a_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Cartilaginous fish akai (*Dasyatis akajei*)}
 VLSSQNKKAIIEELGNLIKANAEGAWGADALARLFELHPQTKTYFSKFSGFEACNEQVKKHG
 KRVMNALADATHHLDNLHLHLEDLARKHGENLLVDPHNFHLFADCIVVTLAVNLQAFTP
 VTHCAVDKFLLELVAYELSSCYR

>d1spga_ a.1.1.2 (A:) Hemoglobin, alpha-chain {Teleost fish (*Leiostomus xanthurus*)}
 SLSATDKARVKALWDKIEGKSAELGAELGRMLVSFPQTKIYFSEWGQDLGPQTPQVRNH
 GAVIMAAVGKAVKSIDNLVGGLSQLSELHAFKL RVD PANFKILAHNIILVISMYPGDFTP
 VHLSVDKFLACLALALSEKYR

>d1cg5b_ a.1.1.2 (B:) Hemoglobin, beta-chain {Cartilaginous fish akai (*Dasyatis akajei*)}
 VKLSEDQEHYIKGVWKDV D HKQITAKALERVVVYPWTTRLFSKLQGLFSANDIGVQQH
 ADKVQRALGEAIDDLKKVEINFQNL SGKHQEIGVDTQNFKLLGQTFMVELALHYKKTR
 PKEHAAAYKFFRLVAEALSSNYH

>d1spgb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Teleost fish (*Leiostomus xanthurus*)}
 VDWTDAERAAIKALWGKIDVGEIGPQALSRL LIVYPWTQRHFKGFGNISTNAAILGNAKV
 AEHGKTVMGGLDRAVQNM DNIK NVYKQLSIKHSEKIHVDPDNFRLG EITMCVGAKFG
 PSAFTPEIHEAWQKFLAVVVSALGRQYH

>d1gcvb_ a.1.1.2 (B:) Hemoglobin, beta-chain {Houndshark (*Mustelus griseus*)}
 VHWTQEERDEISKTFQGTDMKTVVTQALDRMFKVYPWTNRYFQKRTDFRSSIHAGIVVG
 ALQDAVKHMD DVKTLFKDLSKKHADDLHVDPGSFHLLTDCIIVELAYLRKDCFTPHIQGI
 WDKFFEVIDAISKQYH

>d2lhb_ a.1.1.2 (-) Lamprey globin {Sea lamprey (*Petromyzon marinus*)}
 PIVDTGSVAPLSAAEKT KIRSAWAPVYSTYETSGVDILVKFFTSTPAAQEFPKFKGLTTADE
 LKKSADVRWHAERIINAVDDAVASMD DTEKMSMKLRNLSGKHAKSFQVDPEYFKVLAA
 VIADTVAAGDAGFEKLMSMICILLRSAY

>d1ash_ a.1.1.2 (-) Ascaris hemoglobin, domain 1 {Pig roundworm (*Ascaris suum*)}
 ANKTRELCMKSL E HAKVDTSNEARQD GIDLYKHM FENYPP LRKYFKSREEYTAEDVQND
 PFFAKQGQKILLACHVLCATYDDRET FNAYTRELLDRHARDHVHMPPEVWTD FWKLFEE
 YLGKKTTLDEPTKQAWHEIGREFAKEINK

>d1litha_ a.1.1.2 (A:) Hemoglobin {Innkeeper worm (*Urechis caupo*)}
 GLTAAQIKAIQDHWFLNIKGCLQAAADSIFFKYLTAYPGDLAFFHKFSSVPLYGLRSNPAYK
 AQTLTVINYLDKVV DALGGNAGALMKAKVPSHDAMGITPKHFGQLLKLVGGVFQEEFSA
 DPTTVAAGWDAAGVLVAAMK

>d1hlm_ a.1.1.2 (-) Hemoglobin, different isoforms {Sea cucumber (*Caudina* (*Molpadia*)
arenicola)}
 GATQSFQSVGDLTPAEKDLIRSTWDQLMTHRTGFVADV FIRIFHNDPTAQRKFPQMAGLSP
 AELRTSRQMHAHAIRVSALMTTYIDEMDTEVLPELLATLTRTHDKNHV GKKNYDLFGKV
 LMEAIKAELGVGFTKQVHDAWAKTFAIVQGV LITKHAS

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

AVYAYAENIEDPNSLMAVLKNIANKHASLGVKPEQYPIVGEHLLAAIKEVLGNAATDDIIS
AWAQAYGNLADVLMGMESELYERSAEQPGG

>d1ew6a_ a.1.1.2 (A:) Dehaloperoxidase {Marine worm (*Amphitrite ornata*)}
GFKQDIATIRGDLRTYAQDIFLAFLNKYPDERRYFKNYVGKSDQELKSMAKFGDHTEKVF
NLMMEVADRATDCVPLASDANTLVQMKQHSSLTGTFEKLFFVALVEYMRASGQSFDSQS
WDRFGKNLVSALSSAGMK

>d1f99a_ a.1.1.3 (A:) Phycocyanin {Red alga (*Polysiphonia urceolata*)}
MKTPLTEAIAAADSQGRFLSNTELQVVNGRYNRATSSLEAAKALTANADRLISGAANAVY
SKFPYTTQMPGPNYSSTAIGKAKCARDIGYYLRMVITYCLVVGGTGPMDDYLVAGLEEINR
TFELSPSWYIEALKYIKNNHGLSGDVANEANTYIDYAINTLS

>d1alla_ a.1.1.3 (A:) Allophycocyanin {Spirulina platensis}
SIVTKSIVNADAEARYLSPGELDRIKSFVTSGERRVRIAETMTGARERIIKQAGDQLFGKRP
DVVSPGGNAYGADMTATCLRDLDYYLRLITYGIVAGDVTPIEEIGVVGVREMYKSLGTPIE
AIAEGVRAMKSVATSLLSGADAAEAGSYFDYLIGAMS

>d1b33b_ a.1.1.3 (B:) Allophycocyanin {Cyanobacterium (*Mastigocladus laminosus*)}
MQDAITAVINSSDVQGKYLDAALEKLKSYFSTGELRVRAATTIAANAAAIKVEAVAKSLL
YSDITRPGGNMYTTTRYAACIRDLDYLLRYATYAMLADGPSILDERVLNGLKETYNLSLV
PISATVQAIQAMKEVTASLVGPDAGKEMGVYFDYICSGLS

>d1liaa_ a.1.1.3 (A:) Phycoerythrin {Red alga (*Polysiphonia urceolata*)}
MKSIVTTTISAADAAGRYPSTSDLQSVQGNIQRAAARLEAAEKLGSNHEAVVKEAGDACF
SKYGYNKNPGEAGENQEKINKCYRDIDHYMRLINYTLVVGGTGPLDEWGIAGAREVYRT
LNLPSAAYIAAFVFTDRDLCIPRDMSAQAGVEFCTALDYLINSLS

>d1liab_ a.1.1.3 (B:) Phycoerythrin {Red alga (*Polysiphonia urceolata*)}
MLDAFSRVVNSDSKAAAYVSGSDLQALKTFINDGNKRLDAVNYIVSNSSCIVSDAISGMIC
ENPGLITPGGNCYTNRRMAACLRDGEIILRYVSYALLAGDASVLEDRCNLGLKETYIALG
VPTNSTVRAVSIMKAAAVCFISNTASQRKVEVIEGDCSALASEVASYCDRVVAAS

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

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

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

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

>d1fafa_ a.2.3.1 (A:) Large T antigen, the N-terminal J domain {Murine polyomavirus}
MDRVLSRADKERLLELLKLPRQLWGDFGRMQQAYKQQSLLLHPDKGGSHALMQELNSL

WGTFKTEVYNLRMNLGGTGfQ

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

SHMREESLQLMDLLGLERSAWGNIPLMRKAYLKCKEFHPDKGGDEEKMKKMNTLYKK
MEDGVKYAHQPDFGGFWDATEIPTYGtDEWEQWWNAFNEENLFCSEEMPSSDDEAT

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

AALAEIVAQLNIYQSQVELIQQQMEAVRATISELEILEKTLSDIQGKDGSETLVPVGAGSFIK
AELKDTSEVIMSVGAGVAIKKNFEDAMESIKSQKNELESTLQKMGENLRAITDIMMKLSP
QAEELLAAVA

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

QNVQHQLAQFQQLQQQAQAIsvQKQTVEMQINETQKALEELSRADDAEVYKSSGNILI
RVAKDELTEELQEKLTLQLREKTIERQEERVMKKLQEMQVNIQEAMK

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

QDLDEARAMEAKRKAAEEHSSSHGDVDYAQASAELAKAIAQLRVIELTKK

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

DMLDLGAAKANLEKAQSELLGAADeATRAEIQUIRIEANEALVKAL

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

VHKLEPKDHLKPQNLEGISNEQIEPHFEAHYKGYVAKYNEIQEKLADQNFADRSKANQNY
SEYRELKVEETFNYMGVVLHELyFGMLTP

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

VIQLKRYEFPQLPYKVDALePYISKDIIDVHYNGHHKGYVNGANSLLDRLEKLIKGDLPQ
GQYDLQGILRGLTFNINGHKLHAIYWNMA

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

PYPFKLPDLGYPYEALePHIDAKTMEIHhQKHGAYVTNLNAALEKYPYLHGVEVEVLL
RHLAALPQDIQTAVRNNGGHLNHSLFWRLTTP

>d1qnnal a.2.11.1 (A:1-84) Cambialistic superoxide dismutase {Porphyromonas
gingivalis}

MTHELISLPYAVDALAPVISKETVEFHhGKHLKTYVDNLNKLIGTEFENADLNTIVQKSE
GGIFNNAQQTLNHNLYFTQFRPG

>d1h9ea_ a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}

PEFLEDPSVLTKDKLSELVANNVTLPAGEQRKDVYVQLYLQHLTARNRPPLPAGT

>d1h9fa_ a.140.1.1 (A:) Thymopoietin, LAP2 {Human (Homo sapiens)}

RQEDKDDLdVTELTNEDLLDQLVKYGVNPGPIVGTTTRKLYEKLLKLREQGTESRSS

>d1c75a_ a.3.1.1 (A:) Cytochrome c6 (synonym: cytochrome c553) {Bacillus
pasteurii}

VDAEAVVQKcISCCHGGDLTGASAPAIKAGANYSEEEILDILNGQGGMPGGIAKGAEAE
AVAAWLAEEKK

>d1ctj_ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Monoraphidium
braunii}

EADLALGKAVFDGNCAACHAGGGNNVIPDHTLQKAAIEQFLDGGFNIEAIVYQIENGKGA

MPAWDGRLEDEDEIAGVAAYVYDQAAGNKW

>d1c53__ a.3.1.1 (-) Cytochrome c6 (synonym: cytochrome c553) {Desulfovibrio vulgaris, different strains}

ADGAALYKSCVVGCHGADGSKQAMGVGHAVKGQKADELFKKLKGYADGSYGGEKKAV
MTNLVKRYSDEEMKAMADYMSKL

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

QADGAKIYAQCAGCHQQNGQGIPGAFPLAGHVAEILAKEGGREYLILVLLYGLQGQIEV
KGMKYNGVMSSFAQLKDEEIAAVLNHIATAWGDAAKKVKGFKPFTAEVKKLRRAKLTLPQ
QVLAERKKLGLK

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

>d1yc__ a.3.1.1 (-) Mitochondrial cytochrome c {Baker's yeast (Saccharomyces cerevisiae)}

AKESTGFKPGSAKKGATLFKTRCQQCHTIEEGPNKVGPNLHGIFGRHSGQVKGYSYTD
IINKNVKWEDESMSEYLTNPKKYIPGTKMAFAGLKKEKDRNDLITYMTKAAK

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

EDAKAGEAVFKQCMTCHRADKNMVG PALAGVVGRKAGTAAGFTYSPLNHNSGEAGLV
WTADNIVPYLADPN AFLKKFLTEK GKADQAVGVTKMTFKLANEQQRKDVVAYLATLK

>d155c__ a.3.1.1 (-) Cytochrome c2 {Paracoccus denitrificans}

NEGDAAKEGEKEFNKCKACHMIQAPDGTDIKGGKTGPNLYGVVGRKIASSEEGFKYGE
GILEVAEKNPDLTWTEANLIEYVTDPKPLVKKMTDDKGAKTKMTFKMGKNQADVVAFLAQD
DPDAXXXXXXXXXXXXXX

>d1cc5__ a.3.1.1 (-) Cytochrome c5 {Azotobacter vinelandii}

GGGARSGDDVVAKYCNACHGTGLLNAPKVGDSAAWKTRADAKGGLDGLLAQSLSGLN
AMPPKGTCAADCSDDELKAAIGKMSGL

>d1cch__ a.3.1.1 (-) Cytochrome c551 {Pseudomonas stutzeri}

QDGEALFKSKPCAACHSVDTKMVG PALKEVAAKNAGVEGAADTLALHIKNGSQGVWGP
IPMPNPVTEEEAKILAEWVLSLK

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

APQFFNIIDGSPLNFDDAMEEGRDTEAVKHFLFLETGENVYNEDPEILPEAEELYAGMCSGCH
GHYAEKGIGPGLNDAYWTYPGNETDVGLFSTLYGGATGQMGP MWGSLTLDEMLRTMAW
VRHLYTGDPKDASWLTDEQKAGFTPFQP

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

DGESIYINGTAPTCCSCHDRGVAGAPELNAPEDWADRPSSVDELVESTLAGKGAMPAYDG
RADREDLVKAIEYMLSTL

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

YDAAAGKATYDASCAMCHKTGMMGAPKVGDKAAWAPHIAKGMNVMVANSIKGYKGT
KGMMPAKGGNPKLTDAQVGNAYMVGQSK

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

GDTSPAQLIAGYEAAAGAPADAERGRALFLSTQTGGKPDTPSCTTCHGADVTRAGQTRTG
KEIAPLAPSATPDRFTDSARVEKWLGRNCNSVIGRDCTPGEKADLLAWLAAQ

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

DVTNAEKLVIKYTNIAHSANPMYEAPSITDGKIFFNRKFKTPSGKEAACASCHTNNPANV
GKNIVTGKEIPPLAPRVNTRKFTDIDKVEDEFTKHCNDILGADCSPSEKANFIAYLLTETKP
TK

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

SQWGSQGNLYDKVCGHCHKPEVGVGPVLEGRGLPEAYIKDIVRNGFRAMPAFPASYVDD
ESLTQVAEYLSLPA

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

AGDAEAGQGKVAVCGACHGVDGNSPAPNFPKLAGQGGERYLLKQLQDIKAGSTPGAPEGV
GRKVLEMTGMLDPLSDQDLEDIAAYFSSQKGSV

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

GYADPALAKQGEKLFRRGGKLDQGMPTGCHAPNGVGNDLGFPKLGQHAAYTAKQL
TDFREGNRTNDGDTMIMRGVAAKLSNKDIEALSSYIQGLH

>d1fcd1 a.3.1.4 (C:1-80) Flavocytochrome c sulfide dehydrogenase, FCSD, cytochrome subunit
{*Purple phototrophic bacterium (Chromatium vinosum)*}

EPTAEMLTNNCAGCHGTHGNSVGPASPSIAQMDPMVFVEVMEGFKSGEIASTIMGRIAKG
YSTADFEKMAGYFKQQTYP

>d1fcd2 a.3.1.4 (C:81-174) Flavocytochrome c sulfide dehydrogenase, FCSD, cytochrome subunit
{*Purple phototrophic bacterium (Chromatium vinosum)*}

AKQSFDALADTGAKLHDKYCEKCHVEGGKPLADEEDYHILAGQWTPYLQYAMSDFRE
ERRPMEKKMASKLRELLKAEGDAGLDALFAFYASQQ

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

DALHDQASALFKPIPEQVTELRGQPISQQRELGKKLFFDPRLSRSHVLSCHNTCHNVGTGG
ADNVPTSVGHGWQKGPRNSPTVFNAVFNAQFWDGRAKDLGEQAKGPIQNSVEMHSTP
QLVEQTLGSIPEYVDAFRKAFPKAGKPVSFNMLAIEAYEATLV

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

TPDSPFDLYLKGDDKALDAQKKGLKAFMDSGCSACHNGINLGGQAYFPFGLVKKPDAS
VLPBGDKGRFAVTKTQSDEYVFRAAPLRNVALTAPYFHSGQVWELKDAVAIMGNAQLGK
QLAPDDVENIVAFHLSLGGKQPRVEYPLLPASTETTPRAE

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

VTGEEVLQNACAACHVQHEDGRWERIDAARKTPEGWDMTVTRMMRNHGVLEPEERA
AIVRHLSDTGRGLSLAETEERRYILEREP

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

VAWDEGPDTSMTQTGCRCHSYARVALQRRTPEDWKHLVNFHLGQFPTLEYQALARDRD
WWGIAQAEIIPFLARTYPLGEA

>d1jmx1 a.3.1.7 (A:2-85) Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
{*Pseudomonas putida*}

EQGPSLLQNKCMGCHIPEGNDTYSRISHQRKTPEGWLMSIARMQVMHGLQISDDDRRTL
VKYLADKQGLAPSETDGVRYAMERR

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

cerevisiae))

TKPYRGHRFTKENVRILESWFAKNENPYLDTKGLENLMKNTSLSRIQIKNWVSNRRRKE
KTITIAPELADLLSGEPL

>d2lfb__ a.4.1.1 (-) Transcription factor LFB1 {Rat (Rattus rattus)}

MARIDPTKKGRRNRFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPS
QAQGLGSNLVTEVRVYNWFANRRKEEAFRHKLAMDTYKLN

>d1ocp__ a.4.1.1 (-) Oct-3 POU Homeodomain {Mouse (Mus musculus)}

METLVQARKRKRTSIENRVRWSLETMFLKCPKPSLQQITHIANQLGLEKDVVVRVWFCNRR
QKGKRSS

>d1b72a__ a.4.1.1 (A:) Homeobox protein hox-b1 {Human (Homo sapiens)}

ARTFDWMKVKNRPPKTAKVSEPLGSPGLRTNFTTRQLTELEKEFHFNKYLSRARRVEIA
ATLELNETQVKIWFQNRRMKQKKRERE

>d1b72b__ a.4.1.1 (B:) pbx1 {Human (Homo sapiens)}

RKRRNFNKQATEILNEYFYSHLSNPYPSEEAKEELAKKCGITVSQVSNWFGNKRIRYKKN
GKFQEEANIYAA

>d1bw5__ a.4.1.1 (-) Insulin gene enhancer protein isl-1 {Rat (Rattus norvegicus)}

MKTTRVRTVLNEKQLHTLRTCYAANPRPDALMKEQLVEMTGLSPRVIRVWFQNKRCCKD
KRSIMMK

>d1vnd__ a.4.1.1 (-) VND/NK-2 protein {Fruit fly (Drosophila melanogaster)}

ASDGLPNKKRKRRLVFTKAQTYELERRFRQQRYLSAPEREHSLIRLTPTQVKIWFQNH
RYKTKRAQNEKGYEGHP

>d1fjla__ a.4.1.1 (A:) Paired protein {Fruit fly (Drosophila melanogaster)}

KQRRSRTTFSASQLDELERAFERTQYPDIYTREELAQRNTLTEARIQVWFQNRRLRKQH
TSVS

>d1hcra__ a.4.1.2 (A:) HIN recombinase (DNA-binding domain) {Synthetic}

GRPRAINKEQEQISRLLEKGHPRQQLAIFGIGVSTLYRYFPASSIKKRMN

>d1gdtal 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}

PRGSALSDTERAQLDVMKLLNVSLHEMSRKISRSRHCIQVYLKDPVSYGTS

>d2ezl__ a.4.1.2 (-) Ibeta subdomain of the mu end DNA-binding domain of phage mu transposase
{Bacteriophage mu}

MIARPTLEAHDYDREALWSKWDNASDSQRRLAEKWLPVQAADEMLNQGISTKTAFATV
AGHYQVSASTLRDKYYQVQKFAKPDWAAALVDGRGASRRN

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

MNVHKSEFDEDAWQFLIADYLRPEKPAFRKCYERLELAAREHGWSIPSRATAFRRIQQLD
EAMVVACREGEHALM

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

EVKKSSWTEEDRIIFEAHKVLGNRWAEIAKLLPGRTDNAVKNHWNSTIKRKVDT

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

NPELNKGPWTKEEDQRVIEHVQKYGPKRWSIAKHLKGRIGKQCRERWHNHLNPEVK

>d1fexa__ a.4.1.3 (A:) Rap1 {Human (Homo sapiens)}

GRIAFDADDVAILTYVKENARSPSSVTGNALWKAMEKSSLTQHSWQSLKDRYLKHLRG

>d1ligna1 a.4.1.6 (A:360-445) DNA-binding domain of rap1 {Baker's yeast (Saccharomyces

cerevisiae))

KASFTDEEDEFILDVVRKNPTRRTTHTLYDEISHYVPNHTGNSIRHRFRVYLSKRLEYVYE
VDKFGKLVRDDDGNIKTkVLPSSI

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

KRKFSADEDYTLAIAVKKQFYRDLFQIDPDTGRSLITDEDTPTAIARRNMTMDPNHVPGSE
PNFAAYRTQSRRGPIAREFFKHFAEEHAAHTENAWRDRFRKFLLAYGIDDYISYYEAEKAQ
NREPEPMKNLTNRPKRPGVPTPGNYNS

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

MGPKRRLTFREKSRIIQEVEENPDLRKGEIARRFNIPPSTLSTILKNKRAILASERKYGVAS
TCR

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

KTNKLSPYDKLEGLLIAWFQQIRAAGLPVKGIILKEKALRIAEEELGMDDFTASNGWLDRFR
RRRS

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

DAITIHSILDWIEDNLESPLSLEKVSERSGYSKWHLQRMFKKETGHSLGQYIRS

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

RKMTEIAQKLKESNEPILYLAERYGFESQQTLTRTFKNYFDVPPHKYRMTNMQGESRFLH
PL

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

RRLSKSAVALRLTARPILDIALQYRFDSQQTFTRAFFKKQFAQTPALYRRSPEWSAFGIRPPLR
LG

>d1a6i_1 a.4.1.9 (2-67) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}

SRLDKSKVINSALELLNEVGIEGLTTRKLAQKLGVEQPTLYWHVKNKRALLDALAVEILA
RHHDYS

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

NLKDKILGVAKELFIKNGYNATTTGEIVKLSESSKGNLYYHFKTENLFLEILNIEESKWQE
QWKKEQIKA

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

MRSSAQEELVKAFKALLKEEFSSQGEIVAALQEQGFDNINQSKVSRMLTKFGAVRTRN
AKMEMVYCLPAELGVPTT

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

KGQRHIKIREIITSNEIETQDELVDMLKQDGYKVTQATVSRDIKELHLVKVPTNNGSYKYS
LPADQRFNPLSKLKR

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

DVTGRIAQTLLNLAKQPDAMTHPDGMQIKITRQEIGQIVGCSRETVGRILKMLEDQNLISA
HGKTIVVYGT

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

rubrum}
 DIKQRIAGFFIDHANTTGRQTQGGVIVSVDFTVEEIANLIGSSRQTTSTALNSLIKEGYISRQ
 GRGHYTIPNLVRLKAAA
 >d1jgsa_ a.4.5.28 (A:) Multiple antibiotic resistance repressor, MarR {Escherichia coli}
 LFNEIPLGRLIHMVNQKKDRLLNEYLSPLDITAAQFKVLCsircaacITPVELKKVLSVDL
 GALTRMLDRLVCKGWVERLPNPNDKRGVLVKLTTGGAAICEQCHQLVGQDLHQELTKNL
 TADEVATLEYLLKKVLP
 >d1hsja1 a.4.5.28 (A:373-487) staphylococcal accessory regulator A homolog, SarR
 {Staphylococcus aureus}
 MSKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKEIAKCSEFKPY
 YLTkALQKLKDLKLLSKKRSIQDERTVIVYVTDtQKANIQKLISELEEYIKN
 >d1fzpb_ a.4.5.28 (B:) Pleiotropic regulator of virulence genes, SarA {Staphylococcus aureus}
 AITKINDCFELLSMVTYADKLKSLIKKEFSISFEFAVLTYISENKEKEYYLKDIINHLNYKQ
 PQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVnKRIT
 >d1repc1 a.4.5.10 (C:15-143) RepE54 {Escherichia coli, mini-F plasmid}
 SPRIVQSNDLTEAAYSLSRDQKRMLYLFVDQIRKSDGTLQEHDGICEIHVAKYAEIFGLTSA
 EASKDIRQALKSFAGKEVVFYRPEEDAGDEKGYESFPWFIKPAHSPSRGLYSVHINPYLIPF
 FIGLQ
 >d1repc2 a.4.5.10 (C:144-246) RepE54 {Escherichia coli, mini-F plasmid}
 NRFTQFRLSETKEITNPYAMRLYESLCQYRKPDGSGIVSLKIDWIIERYQLPQSYQRMPDFR
 RRFLQVCVNEINSRTPMRLSYIEKKKGRQTTHIVFSFRDIT
 >d1hqca1 a.4.5.11 (A:243-318) Holliday junction helicase RuvB {Thermus
 thermophilus}
 LGLEKRDREILEVLILRFGGGPVGLATLATALSEDPGTLEEVHEPYLIRQGLLKRTPRGRVP
 TELAYRHLGYPPPv
 >d1fnna1 a.4.5.11 (A:277-388) CDC6, C-terminal domain {Archaeon Pyrobaculum aerophilum}
 ISEEVLIGLPLHEKLFLLAIVRSLSKISHTPYITFGDAEESYKIVCEEYGERPRVHSQLWSYLN
 DLREKGIVETRQNKRGEGVRGRTTLISIGTEPLDTLEAVITKLIKEELR
 >d1foka3 a.4.5.12 (A:287-386) Restriction endonuclease FokI, N-terminal (recognition)
 domain {Flavobacterium okeanokoites}
 VPKRVYWEMLATNLTDKEYVRTRRALILEILIKAGSLKIEQIQDNLKKLGFDEVIETIENDI
 KGLINTGIFIEIKGRFYQLKDHILQFVIPNRGVTKQLV
 >d2foka1 a.4.5.12 (A:5-143) Restriction endonuclease FokI, N-terminal (recognition) domain
 {Flavobacterium okeanokoites}
 IRTFGWVQNPGKFENLKRvVQVFDRNSKVHNEVKNIKPTLVKESKIQKELVAIMNQHDLI
 YTYKELVGTGTSIRSEAPCDaiIQATIADQGNKKGYIDNWSSDGFLRWAHALGFIEYINKSD
 SFVITDVGLAYSKSAD
 >d2foka2 a.4.5.12 (A:144-286) Restriction endonuclease FokI, N-terminal (recognition)
 domain {Flavobacterium okeanokoites}
 GSAIEKEILIEAISSYPPAIRILTLEDGQHLLTKFDLGKNLGFSGESGFTSLPEGILLDTLANA
 MPKDKGEIRNNWEGSSDKYARMIGGWLDKLGVLKQKGKEFIPTLGKPDNKEFISHAFKI
 TGEGLKVLRRAKGSTKFTR
 >d1fp1d1 a.4.5.29 (D:19-128) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}
 QTEDSACLsAMVLTTNLVYPavLNAAIDLNLFEIIAKATPPGAFMSPSEIASKLPASTQHSDL

PNRLDRMLRLLASYSVLTSTTRTIEDGGAERVYGLSMVGKYLVPDES
>d1fp2a1 a.4.5.29 (A:8-108) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}
RKPSEIFKAQALLYKHIYAFIDSMCLKWAVEMNIPNIIQNHGKPISLSNLVSILQVPSSKIGNV
RRLMRYLAHNGFFEIITKEEESYALTVASELLVRGSD
>d1e17a_ a.4.5.14 (A:) Afx (Foxo4) {Human (Homo sapiens)}
SRRNAWGNQSYAELISQAIESAPEKRLTLAQIYEWVVRTVPYFKDKGDSNSSAGWKNSIR
HNLSLHSHKFIKVHNEATGKSSWWMLNPEGG
>d2hdca_ a.4.5.14 (A:) Genesis {Rat (Rattus norvegicus)}
VKPPYSYIALITMAILQSPQKKLTLSGICEFISNRFYYREKFPWQNSIRHNLSLND CFVKI
PREPGNPGKGNYWTLDPQSEDMFDNGSFLRRRKR
>d1cf7a_ a.4.5.17 (A:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}
SRHEKSLGLLTTFVSLLEAKDGVLDLKLAAADTLAVRQKRRIYDITNVLEGIGLIEKKSK
NSIQWK
>d1cf7b_ a.4.5.17 (B:) Cell cycle transcription factor e2f-dp {Human (Homo sapiens)}
GKGLRHFSMKVCEKVQRKGTTSYNEVADELVSEFTNSNNHLAADSAYDQKNIRRRVYDA
LNVLMAMNIIISKEKKEIKWIGLP
>d1qgpa_ a.4.5.19 (A:) Z-alpha domain of dsRNA-specific adenosine deaminase, ADAR1 {Human (Homo sapiens)}
LSSHFAQELSIYQDQEQRILKFLEELGEGKATTAHDLSGKLGTPKKEINRVLYSLAKKGKLG
KEAGTPPLWKIAVSD
>d1j75a_ a.4.5.19 (A:) Dlm-1 {Mouse (Mus musculus)}
NLEQKILQVLSDDGGPVKIGQLVKKCQVPKKTNLNQVLYRLKKEDRVSSPEPATWSIG
>d1xgsa1 a.4.5.25 (A:195-271) Methionine aminopeptidase, insert domain {Archaeon Pyrococcus furiosus}
GQVIEVPPTLIYMYVRDVPVRVAQARFLLAKIKREYGTLPFAYRWLQNDMPEGQLKLALK
TLEKAGAIYGYVPLKEI
>d1b6a_1 a.4.5.25 (375-448) Methionine aminopeptidase, insert domain {Human (Homo sapiens)}
HDDMECSHYMKNFVDVGHVPIRLPRTKHLNVINENFGTLAFCRRWLDRLGESKYLMAK
NLCDLGIVDPYPPLC
>d1opc_ a.4.6.1 (-) OmpR {Escherichia coli}
VIAFGKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNLARGREYSA
MERSIDVQISRLRRMVEEDPAHPRIYQTVWGLGYVFVPD
>d1kgsa1 a.4.6.1 (A:124-225) PhoB {Thermotoga maritima}
SKSTKLVCGLDLDATKKAYRGSKEIDLTKEYQILEYLMNKNRVVTKEELQEHLWSFD
DEVFSDVLRSHIKNLRKKVDKGFKKKIHTVRGIGYVARDE
>d1qgia_ a.4.6.1 (A:) PhoB {Escherichia coli}
MAVEEVIEMQGLSLDPTSHRVMAGEEPLMGPTFKLLHFFMTHPERVYSREQLLNHVW
GTNVYVEDRTVDVHIRRLRKALEPGGHDRMVQTVRGTGYRFSTRF
>d1fsea_ a.4.6.2 (A:) Germination protein GerE {Bacillus subtilis}
SKPLLTKREREFELLVQDKTTKEIASSELFISEKTVRNHISNAMQKLGVKGRSQAVVELLR
MGELEL
>d1a04a1 a.4.6.2 (A:150-216) Nitrate/nitrite response regulator (NarL) {Escherichia coli}
ERDVNQLTPTPRERDILKLIAQGLPNKMIARRLDITESTVKVHVKHMLKKMKLKS RVEAAV
WVHQERIF

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

MRVPFSWLKAYVPELESPEVLEERLAGLGFETDRIERVXEEVVDLEVTPNRPDALGGLGL
ARDLHALGYALVEPEAA

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

PPEAIPFRPEYANRLLGTSYPEAEQIAILKRLGCRVEGEGPTYRVTPPSHRLDLRLEEDLVEE
VARIQGYETIPL

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

ESYYSIGEVSCLANVSIKALRYDYDKIDLFKPAYVDPDTSYRYYTDSQLIHLDLIKSLKYIGT
PLEEMKKAQDLEMEELFAFYTEQERQIREKLDFLSALEQTISLVKKRMKRQMEYPA

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

KYQVKQVAEISGVSIRTLHHYDNIELNPSALTADAGYRLYSDADLERLQQILFFKEIGFRLD
EIKEMLDHPNFDKRAALQSQKEILMKKKQRMDEMIQTIDRTLLS

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

QNLDLQLYMRDCELAESWMSAREAFNADDDANAGGNVEALIKKHEDFDKAINGHEQK
IAALQTVADQLIAQNHYASNLVDEKRKQVLERWRHLKEGLIEKRSRLGD

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

MVHQFFRDMDDEESWIKKLLVSSSEDYGRDLTGVDNLRRKKHKLRLAELAAHEPAIQSV
LDTGKKLSDDNTIGKEEIQQLAQFVDHWKELKQLAAARGQRLEESLEYQ

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

QFVANVEEEEAWINEKMTLVASEDYGDTLAAIQGLKKHEAFETDFTVHKDRVNDVCAN
GEDLIKNNHHVENITAKMKGLKGKVSLEKAAAQRKAKLDENSA

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

SSAVNQENERLMEEYERLASELLEWIRRTIPWLENRTPEKTMQAMQKKLEDFRDYRRKH
KPPKVQEKQCLEINFNTLQTKLRISNRPAFMPSEGKMSVSDIAGAWQRLEQAEGYEEWLL
NEIRRL

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

HANERLRRQFAAQANAIGPWIQNKMEEIARSSIQITGALEDQMNQLKQYEHNIINYKNNID
KLEGDHQLIQEALVFDNKHTNYTMEHIRVGWELLLTTIARTINEVETQILTRD

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

GSSNEIRRLERLEHLAEKFRQKASTHETWAYGKEQILLQKDYESASLTEVRALLRKHEAFE
SDLAAHQDRVEQIAAIAQELNELDYHDAVNVDRCQKICDQWDRLGTLTQKRREALERM
EKLL

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

ETIDQLHLEFAKRAAPFNNWMEGAMEDLQDMFIVHSIEEIQSLITAHEQFKATLPEADGER
QSIMAIQNEVEKVIQSYNIRISSNPYSTVTMDELRTKWDKVKQLVPIRDQSLQEELARQH
AN

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

DESRVENPDERVVIQHNWHELRLFMWDYVGIVRTTKRLERLRITMLQQEIDEYYAHFR
VSNLLELRNLVQVAELIVRCAMMRKESRGLHFTLDYPELLTHSGPSILSP

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

DGGENWAKIRDEMGLAMEEGCGIYRTPELMQKTIDKLAELQERFKRVITDTSSVFNTDL
LYTIELGHGLNVAECMAHSAMARKESRGAHQRLDEGCTERDDVNFLKHTLAFRDADGTT

RLEYSDEVKITLPP

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

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

TADDVNPEYILPWQGLVRLQKIMDEYAAGIATYKTNEKMLQRALELLAFLKEDLEKLAA
RDLHELMRAWELVHRVWTAEAHVRHMLFRKETRWPGYYYRTDYPELNDEEWKCFVCS
KYDAEKDEWTFEKVPYVQVIEWSF

>d2erl__ a.10.1.1 (-) ER-1 {Euplotes raikovi}
DACEQAAIQCVESACESLCTEGEDRTGCMYIYSNCPYV

>d1ery__ a.10.1.1 (-) ER-11 {Euplotes raikovi}
DECANAAAQCSITLCNLYCGPLIEICELTVMQNCEPPFS

>d1aca__ a.11.1.1 (-) Acyl-CoA binding protein {Cow (Bos taurus)}
SQAEDKAAEEVKHLKTKPADEEMLFYSHYKQATVGDINTERPGMLDFKKGAKWDAW
NELKGTSKEDAMKAYIDKVEELKKKYGI

>d1hbka_ a.11.1.1 (A:) Acyl-CoA binding protein {Plasmodium falciparum}
HMAQQVFEEECVSFINGLPRTINNLPNELKLDLYKYKQSTIGNCNIKEPSAHKYIDRKKY
EEAWKSVENLNREDAQKKRYVDIVSEIFPYWQD

>d1efla1 a.11.2.1 (A:88-198) Moesin {Human (Homo sapiens)}
DVSEELIQDITQRLFFLQVKEGILNDDIYCPPETAVLLASYAVQSKYGDFNKEVHKSGYLA
GDKLLPQRVLEQHKLNDQWEERIQVWHEEHRGMLREDAVLEYLKIAQDL

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

>d2lisa_ a.19.1.1 (A:) Lysin {Red abalone (Haliotis rufescens)}
HYVEPKFLNKAFEVALKVQIIAGFDRGLVKWLRVHGRTLSTVQKKALYFVNRRYMQTHW
ANYMLWINKKIDALGRTPVVGDYTRLGAEIGRRIDMAYFYDFLKDKNMIPKYLPMEEIN
RMRPADVPVKYM

>d1gaka_ a.19.1.1 (A:) SP18 {Abalone (Haliotis fulgens)}
FDDVVVSRQEQSYVQRGMVNFLDEEMHKLVKFRFRDMRWNLGPGFVFLKKVNRERMM
RYCMDYARYSKKILQLKHLVPNKKTLTKMGRFVGYRNYGVIRELYADVFRDVQGFRGPK
MTAAMRKYSSKDPGTFPCKNE

>d1aab__ a.21.1.1 (-) HMG1, domains A and B {Rat (Rattus norvegicus)}
GKGDPKKPRGKMSSYAFFVQTSREEHKKKHPDASVNFSEFSKKCSERWKTMSAKEKGKF
EDMAKADKARYEREMKTYIPPKGE

>d1qrva_ a.21.1.1 (A:) HMG-D {Drosophila melanogaster}
SDKPKRPLSAYMLWLNSARESIKRENPBGKIVTEVAKRGGELWRAMKDKSEWEAKAAKA
KDDYDRAVKEFEANG

>d1cg7a_ a.21.1.1 (A:) NHP6a {Baker's yeast (Saccharomyces cerevisiae)}
MVTPREPKKRTTRKKKDPNAPKRALSAYMFFANENRDIVRSENPDITFGQVGKKLGEKW
KALTPEEKQPYEAKAQADKKRYESEKELYNATLA

>d1j46a_ a.21.1.1 (A:) SRY {Human (Homo sapiens)}
MQDRVKRPMNAFIVWSRDQRRKMALENPRMRNSEISKQLGYQWKMLTEAEKWPFQFE
AQKLQAMHREKYPNYKYRPRRKAKMLPK

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

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

>d1eqza_ a.22.1.1 (A:) Histone H2A {Chicken (Gallus gallus), erythrocytes}
SGRGKQGGKARAKAKSRSSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAADVLEYLT
AEILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLKGVTIAQGGVLPNIQAVLLPKKT
DSHKA

>d1eqzb_ a.22.1.1 (B:) Histone H2B {Chicken (Gallus gallus), erythrocytes}
VTKTQKKGDKKRKKSRSKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFVNDIFERIA
SRLAHYNKRSTITSREIQTAVRLLLPGLAKHAVSEGTKAVTKYTSSK

>d1eqzg_ a.22.1.1 (G:) Histone H3 {Chicken (Gallus gallus), erythrocytes}
PRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTELLIRKLPFQRLVREIAQ
DFKTDLRFQSSAVMALQEASEAYLVGLFEDTNLCAIHAKRVTIMPKDIQLARRIRGERA

>d1eqzh_ a.22.1.1 (H:) Histone H4 {Chicken (Gallus gallus), erythrocytes}
KGLGKGGAKRHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLNVIRD
AVTYTEHAKRKTVTAMDVVYALKRQGRITLYGFGG

>d1a7w_ a.22.1.2 (-) Archaeal histone {Archaeon Methanothermobacter fermentans, histone B}
MELPIAPIGRIIKDAGAERVSDDARITLAKILEEMGRDIASEAIKLARHAGRKTIKAEDIELA
VRRFK

>d1flea_ a.22.1.2 (A:) Archaeal histone {Archaeon Methanopyrus kandleri}
ELPKAAIERIFRQGIGERRLSQDAKDTIYDFVPTMAEYVANAAKSVLDASGKKTLMEEHL
KALADVLMVEGVEDYDGELFGRATVRRILKRAGIERASSDAVDLYNKLICRATEELGEKA
AEYADEDEDGRKTVQGEDVEKAITYSMPKGDEL

>d1tafa_ a.22.1.3 (A:) TAF(II)42 {Fruit fly (Drosophila melanogaster)}
PKDAQVIMSILKELNVQEYEPVVNQLELTFRYVTSILDDAKVYANHARKKTIDLDDVR
LATEVTLD

>d1tafb_ a.22.1.3 (B:) TAF(II)62 {Fruit fly (Drosophila melanogaster)}
MLYSSISAESMKVIAESIGVGSLSDDAAKELAEDVSIKLRIVQDAKFMNHAKRQKLS
VRDIDMSLV

>d1bh9a_ a.22.1.3 (A:) TAF(II)18 {Human (Homo sapiens)}
LFSKELRCMMYGFQDDQNPYTESVDILEDLVIEFITEMTHKAMSI

>d1bh9b_ a.22.1.3 (B:) TAF(II)28 {Human (Homo sapiens)}
FSEEQNLNRYEMYRRSAFPKAAIKRLIQSITGTSVSNVVIAMSGISKVFVGEVVEEALDVC
EKWGEMPPPLQPKHMRVAVRRLKSKGQIP

>d1jfia_ a.22.1.3 (A:) Negative cofactor 2, NC2, alpha chain {Human (Homo sapiens)}
ARFPPARIKKIMQTDEEIGKVAAAVPVIISRALELFLESLLKKACQVTQSRNAKTMTTSHLK
QCIE

>d1jfib_ a.22.1.3 (B:) Negative cofactor 2, NC2, beta chain {Human (Homo sapiens)}

DDLTIPRAAINKMIKETLPNVRVANDARELVVNCCTEFIHLISSEANEICNKSEKKTISPEHVI
QALESLGFGSYISEVKEVLQECKTVALKRRKASSRLENLGIPEEEELLRQQQELFAKARQQQ
AELAQQEWLQ

>d2ccya_ a.24.3.2 (A:) Cytochrome c' {Rhodospirillum molischianum}

QSKPEDLLKLRQGLMQTLKSQWVPIAGFAAGKADLPADAAQRAENMAMVAKLAPIGWA
KGTEALPNGETKPEAFGSKSAEFLEGWKALATESTKLAAAAGKAGPDALKAQAAATGKVC
KACHEEFKQD

>d1bbha_ a.24.3.2 (A:) Cytochrome c' {Chromatium vinosum}

AGLSPEEQIETRQAGYEFMGWNMGKIKANLEGEYNAAQVEAAANVIAAIANS GMGALY
GPGTDKNVGDVKTRVKPEFFQN MEDVGKIAREFVGAANTLAEVAATGEAEAVKTAFGDV
GAACKSCHEKYRAK

>d1jafa_ a.24.3.2 (A:) Cytochrome c' {Rhodocyclus gelatinosus}

QFQKPGDAIEYRQSAFTLIANHFRVAAMAQKGKAPFDAKVAAENIALVSTLSKLPLTAFGP
GTDKGHGTEAKPAVWSDAAGFKAAADKFAAAVDKLDAAAGKTGDFAQIKAAVGETGGAC
KGCHDKFKE

>d1cpq_ a.24.3.2 (-) Cytochrome c' {Rhodobacter capsulatus}

ADTKEVLEAREAYFKSLGGSMKAMTGVAKAFDAEAAKVEAAKLEKILATDVAPLFPAGT
SSTDLPQGTEAKAAIWANMDDFGAKGKAMHEAGGAVIAAANAGDGAAFGAALQKLGG
TCKACHDDYREED

>d1a7va_ a.24.3.2 (A:) Cytochrome c' {Rhodopseudomonas palustris}

QTDVIAQRKAILKQMGEATKPIAAMLKGEAKFDQAVVQKSLAAIADDSKKLPALFPADSK
TGGDTAALPKIWEDKAKFDDLFAKLAAAATAAQGTIKDEASLKANIGGV LGNCKSCHDD
FRAKKS

>d1ei7a_ a.24.5.1 (A:) Tobacco mosaic virus coat protein {Tobacco mosaic virus, vulgare strain}

SYSITTPSQFVFLSSAWADPIELINLCTNALGNQFQTQQARTVVQRQFSEVWKPSQVTVR
FPDSDFKVYRYNAVLDPLVTALLGAFDTRNRIIEVENQANPTTAETLDATTRVDDATVAIRS
AINNLIVELIRGTGSYNRSSFESSSGLVWTSGPAT

>d1cgme_ a.24.5.1 (E:) Cucumber green mottle mosaic virus {Cucumber green mottle mosaic virus,
strain watermelon}

AYNPITPSKLIAFSASYVPVRTLLNFLVASQGTAFQTQAGRDSFRESLSALPSSVVDINSRFP
DAGFYAFLNGPVLRLPIFVSLLSSTDTRNRVIEVVDPSNPTTAESLNAV KRTDDASTAARAEI
DNLIESISKGFDVYDRASFEEAFSVVWSEATT SKA

>d1dowa_ a.24.9.1 (A:) alpha-catenin {Mouse (Mus musculus)}

KAHVLAASVEQATENFLEKGDKIAKESQFLKEELVVAVEDVRKQGDLMKSAAGEFADDP
CSSVKRGNMVRARALLSAVTRLLILADMADVYKLLVQLKVVEDGILKLRNAGNEQDL
GIQYKALKPEVDKLNIMAAKRQQELKDVGNRDQMAAARGILQKNVPILYTASQACLQHP
DVAAYKANRDLIYKQLQQA VTTGISNAAQA

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

DLRRQLRKAVMDHVSDSFLETNVPLLVLIEAAKNGNEKEVKEYAQVFREHANKLIEVANL
ACISISNNEEGVKLVRMSASQLEALCPQVINAALALAAKPQSKLAQENMDLFKEQWEKQV
RVLTDVDDITS

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

IDDFLAVSENHILEDVNKC VIALQEKDVDGLDRTAGAIRGRAARVIHVVTSEMDNYEPGV
YTEKVL EATKLLSNTVM PRFTEQVEAAVEALSSDPAQPM DENEFIDASRLVYDGIRDIRKA

VLM

>d1qkra_ a.24.9.1 (A:) Vinculin {Chicken (Gallus gallus)}

KDEEFPEQKAGEAINQPMMAARQLHDEARKWSSKGNDIIAAAKRMALLMAEMSRLVR
GGSGNKRALIQCAKDIAKASDEVTRLAKEVAKQCTDKRIRTNLLQVCERIPTISTQLKILST
VKATMLGRTNISDEESEQATEMLVHNAQNLMQSVKETVREAEAASIKIRTDAGFTLRWVR
K

>d1hela_ a.24.11.1 (A:) ExoS toxin {Pseudomonas aeruginosa}

ASSAVVFKQMVLLQALPMTLKGLDKASELATLTPEGLAREHSRLASGDGALRSLSTALAG
IRAGSQVEESRIQAGRLLERSIGGIALQQWGTTGGAASQLVLDASPELRREITDQLHQVMS
EVALLRQAVESEVS

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

SKQPLLDIALKGLKRTLPLEQMDGNSLRENFQEMASGNGPLRSLMTNLQNLNKIPEAKQ
LNDYVTTLTNIQVGVARFSQWGTGCGEVERWVDKASTHELTQAVKKIHVIAKELKNVTA
ELEKIEAGAPM

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

TSFSDSIKQLAAETLPKYMQQNLSDAEMLKQNHQDFATGSGPLRGSITQCQGLMQFCGG
ELQAEASAILNTPVCGIPFSQWGTIGGAASAYVASGVDLTQAANEIKGLAQMQKLLSLM

>d1jpnal a.24.13.1 (A:1-88) Signal sequence recognition protein Ffh {Thermus aquaticus}

MFQQLSARLQEAIGRLRGRGRITEEDLKATLREIRRALMDADVNLVARDFVERVREEAL
GKQVLESLTPAEVILATVYEALKEALGG

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

LLDNLRDVTVRKFLTGSSSYDKAVEDFIKELQKSLISADVNVKLVFSLTNKIKERLKNEKPPT
YIERREWFIVYDELSNLFGG

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

RSLLKTKENLGSGFISLFRGKKIDDDLFEELLEEQLLIADVGVETTRKIITNLTEGASRKQLR
DAEALYGLLKEEMGEILAKVDE

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

GAMEKFKTLLYDPIECMEVSEEIISYAKLQLGKKLNDSIYVSLTDHINFAIQRNQKGLDIKN
ALLWETKRLYKDEFAIGKEALVMVKNKTGVSLPEDEAGFIALHIVNAELNEE

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

MPNIINITKVMEEILSIVKYHFKIEFNESLHYRFTDLKFFAQRLFNGLTHMESEDDFLLD
TVKEYHRALECTKKIQTIEREYEHKLTSDELLYLTIDIERVVK

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

MKSLKGSRTENILTAFAGESQARNRYNYFGGQAKKDGFVQISDIFAETADQEREHAKRLF
KFLEGGDLEIVAAPAGIADTHANLIASAAGEHHEYTEMYPFARIAAREEGYEEIARVFI
AVAEFHEKRFLDFARNIKEGRV

>d1jgca_ a.25.1.1 (A:) Bacterioferritin (cytochrome b1) {Rhodobacter capsulatus}

MKGDAKVIEFLNAALRSELTAISQYWVHFRLQEDWGLAKMAKKSREESIEEMGHADKIIA
RILFLEGHPNLQKLDPLRIGEGPRETLECDLAGEHDALKLYREARDYCAEVGDIVSKNIFE
SLITDEEGHVDLETQISLYDRLGPQG FALLNAAPMDAA

>d1krqa_ a.25.1.1 (A:) Non-hem ferritin {Campylobacter jejuni}

MLSKEVVKLLNEQINKEMYAANLYLSMSSWCYENSLDGAGAFLEHASEESDHAKKLIT
YLNETHSHVELQEVKQPEQNFKSLLDVFEKTYEHEQFITKSINTLVEHMLTHKDYSTFNFL

QWYVSEQHEEEALFRGIVDKIKLIGEHGNGLYLADQYIKNIALSR

>d1dpsa_ a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Escherichia coli}

SKATNLLYTRNDVSDSEKKATVELLNQRQVIQFIDLSLITKQAHWNMRGANFIAVHEMLDG
FRTALIDHLDTMAERAVQLGGVALGTTQVINSKTPLKSYPLDIHNVQDHLKELADRYAIVA
NDVRKAIGEAKDDDDTADILTAASRDLDKFLWFIECNIE

>d1qgha_ a.25.1.1 (A:) Dodecameric ferritin homolog DPS {Listeria innocua}

VDTKEFLNHQVANLNVFTVKIHHQIHWYMRGHNFFTLHEKMDDLYSEFGEQMDEVAERLL
AIGGSPFSTLKEFLENASVEEAPYTKPKTMDQLMEDLVGTLELLRDEYKQGIELTDKEGD
DVTNDMLIAFKASIDKHIWMFKAFLGKAPLE

>d1h96a_ a.25.1.1 (A:) (Apo)ferritin {Mouse (Mus musculus)}

TSQIRQNYSTEVEAAVNRLVNLHLRASYTYLSLGGFFDRDDVALEGVGHFFRELAEEKRE
GAERLLEFQNDRGGRALFQDVQKPSQDEWGKTQEAMEAALAMEKNLNQALLDLHALG
SARADPHLCDFLESHYLDKEVKLIKMGHNLNRRVAGPQPAQTGAPQGSLGEYLFERL
TLK

>d1mtyb_ a.25.1.2 (B:) Methane monooxygenase hydrolase, beta and alpha subunits
{Methylococcus capsulatus}

ERRRGLTDPEMAAVILKALPEAPLDGNNKMGYFVTPRWKRLTEYEALTVYAQPNADWIA
GGLDWGDWTQKFHGGPSWGNETTELRTVDWFKHRDPLRRWHAPYVKDKAEWRYT
DRFLQGYSDGQIRAMNPTWRDEFINRYWGAFLFNEYGLFNAHSQGAREALSDVTRVSL
AFWGFDKIDIAQMIQLERGFLAKIVPGFDESTAVPKAEWTNGEVYKSARLAVEGLWQEVF
DWNESAFSVHAVYDALFGQFVRREFFQRLAPRFGDNLTFFINQAQTYFQIAKQGVQDLY
YNCLGDDPEFSDYNRTVMRNWTGKWLEPTIAALRDFMGLFAKLPA GTTDKEEITASLYRV
VDDWIEDYASRIDFKADRDQIVKAVLAGLK

>d1mtyd_ a.25.1.2 (D:) Methane monooxygenase hydrolase, beta and alpha subunits
{Methylococcus capsulatus}

AANRAPTSVNAQEVHRWLQSFNWDKNNRTKYATKYKMANETKEQFKLIAKEYARMEA
VKDERQFGSLQVALTRLNAGVRVHPKWNETMKVVSNFLEVGEYNAIAATGMLWDSAQA
AEQKNGYLAQVLDEIRHHTHCAYVNYYFAKNGQDPAGHNDARRTRTIGPLWKGMKRVF
SDGFISGDAVECSNLQLVGEACFTNPLIVAVTEWAAANGDEITPTVFLSIETDEL RHMANG
YQTVVSIANDPASAKYLNTDLNNAFWTQQKYFTPVLGMLFEYGSKFKVEPWVKTWDRW
VYEDWGGIWIGRLGKYGVESPRSLKDAKQDAYWAHHDLYLLAYALWPTGFFRLALPDQE
EMEWFEANYPGWYDHYGKIYEEWRARGCEDPSSGFIPLMWFIENNHPIYIDRVSQVPFCP
SLAKGASTLRVHEYNGEMHTFSDQWGERMWLAEPERYECQNIFEQYEGRELSEVIAELH
GLRSDGKTLIAQPHVRGDKLWTLDDIKRLNCVFKNPVKAF

>d1jqca_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Escherichia coli}

AYTTFSQTKNDQLKEPMFFGQPVNVARYDQQKYDIFEKLIKQLSFFWRPEEVDVSRDRI
DYQALPEHEKHIFISNLKYQTLLDSIQGRSPNVALLPLISPELETWVETWAFSETIHSRSYT
HIIRNIVNDPSVVFDDIVTNEQIQKRAEGISSYYDELIEMTSYWHLLGEGTHTVNGKTVTV
SLRELKKKLYLCLMSVNALEAIRFYVSFACSFAPAERELMEGNAKIIRLIARDEALHLTGTQ
HMLNLLRSGADDPMAEIAEECKQECYDLFVQAAQQEKDWADYLF RDGSMIGLNKDILC
QYVEYITNIRMQAVGLDLPFQTRSNIPIWINTWLV

>d1kgna_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Corynebacterium ammoniagenes}

SNEYDEYIANHTDPVKAINWNVIPDEKDLEVWDRLTGNFWLPEKIPVSNDIQSWNKMT
PQEQLATMRVFTGLTLLDTIQGTVGAISSLPAETMH EEA VYTNIAFMESVHAKSYSNIFMT

LASTPQINEAFRWSEENENLQRKAKIIMSYNGDDPLKKKVASTLLESFLFYSGFYLPMYL
SSRAKLTNTADIIRLIIRDESVHGYYIGYKYQQGVKKLSEAEQEEYKAYTFDLMYDLYENE
IEYTEDIYDDLGWTEDEVKRFLRYNANKALNNLGYEGLFPTDETKVSPAILSSLS

>d1jk0a_ a.25.1.2 (A:) Ribonucleotide reductase R2 {Baker's yeast (Saccharomyces cerevisiae)}
LNKELETLREENRVKSDMLKEKLSKDAENHKAYLKSHQVHRHKLKEMEKEEPLLNEDE
RTVLFPIKYHEIWQAYKRAEASFWTAEIDLSKDIHDWNNRMNENERFFISRVLAFFAASD
GIVNENLVENFSTEVQIPEAKSFYGFQIMINISETYSLLIDTYIKDPKESEFLNAIHTIPEI
GEKAEWALRWIQDADALFGERLVAFASIEGVFFSGSFASIFWLKCRGMMMPGLTFSNELICR
DEGLHTDFACLLFAHLKNKPDPAIVEKIVTEAVEIEQRYFLDALPVALLGMNADLMNQYV
EFVADRLLVAFGNKKYKVENPFDPMEN

>d1afra_ a.25.1.2 (A:) delta 9-stearoyl-acyl carrier protein desaturase {Castor bean (Ricinus communis)}

MPPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKWCWQPQDFLPDPASDGFDE
QVRELREAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRA
WTAEENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERAT
FISHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVLAFADMMR
KKISMPAHLMYDGRDDNLFDFHSAVAQRLGVYTAKDYADILEFLVGRWKVDKLTGLSAE
GQKAQDYVCRLPPRIRLEERAQGRAKEAPTMPFSWIFDRQVKL

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

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

>d1lrb_ a.26.1.1 (B:) Interleukin-6 {Human herpesvirus 8, Kaposi's sarcoma herpes-virus}
EFEKDLIQRNLNWLWVIDECFRDLCYRTGICKGILEPAAIFHLKLPAINDTDHCGLIGFNE
TSCLKKLADGFFEFVLFKFLTTEFGKSVINVDVMELLTKTLGWDIQEELNKLTKTHYSPP
KFDRGLLGRLQGLKYWVRHFASFYVLSAMEKFAGQAVRVLDSIP

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

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

>d1f6fa_ a.26.1.1 (A:) Placental lactogen {Sheep (Ovis aries)}
AQHPPYCRNQPGKCQIPLQSLFDRATTVANYSKLAGEMVNRFDQYGGQINSSESKVINC
HTSSITTPNSKAEAINTEDEKILFKLVISLLHSWDEPLHHAVTELANSKGTSPALLTKAQEIKE
KAKVLVDGVEVIQKRIHPGEKNEPYPVWSEQSSLTSDQDENVRRVAFYRLFHCLHRDSSKIY
TYLRILKCRLTSC

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

PHRRDLCSRSIWLARKIRSDLTALTESYVKHQGLNKNINLDSADGMPVASTDQWSELTEAE
 RLQENLQAYRTFHVLLARLLEDQQVHFTPTGDFHQAIHTLLLQVAAFAYQIEELMILLEY
 KIPRNEADGMPINVGDGGLFEKKLWGLKVLQELSQWTVRSIHDLRFISSHQTGIP

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

IQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAVYQQIL
 TSMPSRNVIQISNDLENLRDLLHVLAFSKSKCHLPEASGLETLDLGGVLEASGYSTEVAL
 SRLQGSQDMLWQLDLSPGC

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

GSCSKEYRVLLGQLQKQTDLMQDTSRLDPYIRIQGLDVPKLREHCRERPGAFPSEETLRG
 LGRRGFLQTLNATLGCVLHRLADLEQRLPKAQDLERSGLNIEDLEKLQMARPNILGLRNN
 IYCMAQLLDNSDTAEPTKAGRGASQPPTPTPASDAFQRKLEGCRFLHGYHRFMHSVGRVF
 SKW

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

QNLLRAVSNMLQKARQTLEFYPTCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRET
 SFITNGSCLASRKTSFMMALCLSSIEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAV
 IDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS

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

APPRLICDSRVLERYLLEAKEAEKITTGCAEHCSLNEKITVPDTKVNIFYAWKRMEVGQQA
 VEVWQGLALLSEAVLRGQALLVKSSQPWEPLQLHVDKAVSGLRSLTLLRALGAQKEAIS
 NSDAASAAPLRTITADTFRKLFRVYSNFLRGKLKLYTGEACRTGDR

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

RSPSPSTQPWEHVNAIQEARRLLNLSRDTAEMNETVEVISEMFDLQEPTCLQTRLELYKQ
 GLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFDCWEP

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

HKCDITLQAIKTLNSLTEQKTLCTELTVTDIFAASKNTTEKETFCRAATVLRQFYSHHEKD
 TRCLGATAQQFHRHKQLIRFLKRLDRNLWGLAGLNSCPVKEANQSTLENFLERLKTIMRE
 KYSKCSS

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

IPTSALVKETLALLSTHRTLLIANETLRIPVPVHKNHQLCTEEIFQGIGTLESQTVQGGTVER
 LFKNLSLIKKYIDGQKKKCGEERRRVNQFLDYLQEFLGVMNTEWI

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

SEYCSHMIGSGHLQSLQRLIDSQMETSCQITFEFVDQEQLKDPVCYLKKAFLLVQDIMEDT
 MRFRDNTPNIAIAIVQLQELSLRLKSCFTKDYEEDHKACVRTFYETPLQLLEKVKNVFNET
 KNLLDKDWNIFSKNCNNSFAECSSQGH

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

TQDCSFQHSPISDFAVKIRELSDYLLQDYPVTVASNLQDDELCGGLWRLVLAQRWMERL
 KTVAGSKMQGLLERVNTEIHFTVKCAFQPPPSCLRFVQTNISRLQETSEQLVALKPWITRQ
 NFSRCLELQCQP

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

NVKDVTKLVANLPKDYMITLKYVPGMDVLPSCWISSEMVVQLSDSLTDLLDKFSNISEGL
 SNYSIIDKLVNIVDDLVECVKENSSKDLKKSFKSPEPRLFTPEEFFRIFNRSIDAFKDFVBASE
 TSDCVVS

>d3inkc_ a.26.1.2 (C:) Interleukin-2 (IL-2) {Human (Homo sapiens)}
STKKTQLQLEHLLDLQMLNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCLEEEELKP
LEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEFLNRWITFAQSII
STLT

>d1jli_ a.26.1.2 (-) Interleukin-3 (IL-3) {Human (Homo sapiens)}
ANCSIMIDEIIHHLKRPPNPLLDPNNLNSEDMDILMERNLRTPNLLAFVRAVKHLENASAIE
SILKNLLPCLPLATAAPTRHPIHIKDGDWNEFRKLTFFYLKTLENAQAQQ

>d1ga3a_ a.26.1.2 (A:) Interleukin-13 (IL-13) {Human (Homo sapiens)}
GGPVPSTALRELIEELVNITQNQKAPLCNGSMVWSINLTAGMYCAALESINVSGCSAIEK
TQRMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKKLFREGRFN

>d2ilk_ a.26.1.3 (-) Interleukin-10 (cytokine synthesis inhibitory factor, CSIF) {Human (Homo sapiens)}
TQSENSCTHFPGNLPNMLRDLRDAFSRVKTFFQMKDQLDNLLKESLLEDFKGYLGCA
LSEMIQFYLEEVMQAENQDPDIKAHVNSLGENLKTLLRLRLRRCHRFLPCENKSKAVEQV
KNAFNKLQEKGIYKAMSEFDIFINYIEAYMTMKIRN

>d1aula_ a.26.1.3 (A:) Interferon-beta {Human (Homo sapiens)}
MSYNLLGFLQRSSNFQCQKLLWQLNGRLEYCLKDRMNFDIPEEIKQLQQFQKEDAALTIY
EMLQNIFAIFRQDSSSTGWNETIVENLLANVYHQINHLKTVLEEKLEKEDFTRGKLMSSLH
LKRYYYGRILHYLKAKEYSHCAWTIVRVEILRNIFYFINRLTGYLNRN

>d1b5l_ a.26.1.3 (-) Interferon-tau {Sheep (Ovis aries)}
CYLSRKMLLDARENKLLDRMNRLSPHSCLQDRKDFGLPQEMVEGDQLQKDQAFPVLY
EMLQQSFNLFYTEHSSAAWDTTLLEQLCTGLQQQLDHLDTCRGQVMGEEDSELGNMDPI
VTVKKYFQGIYDYLQKEGYSDCAWIVRVEMMRALT VSTTLQKRLTK

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

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

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

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

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

EVQNFINVLSNFYLDYGKDILYIEQRDSHIRRSMQTVLYQILVDMTKLLAPILVHTAEEV
WSHTPHVKEESVHLADMPKVVEVDQALLDKWRTFMNLRDDVNRALETARNEKVIGKSL
EAKVTIASNDKFNASEFLTSFDALHQLFIVSQVKVVDKLLDDQATAYEHGDIVIEHADGEKC
ERCWNYSEDLGAVDELTHLCPRCQQVVKSLV

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

ANKLYNAARFVLLSREGFQAKEDTPTLADRFMRSLSRGVEEITALYEALDLAQAAAREVY
ELVWSEFCDWYLEAAKPALKAGNAHTLRTLEEVLAVLLKLLHPMMPFLTSELYQALTGKE
ELALEAWPEPGGRDEEAERAFAEALKQAVTAVRALKAEAGLPPAQEVVRVYLEGETAPVEEN
LEVFRFLSRADLLPERPAKALVKAMPRVTARMPLEGLLDVEEWRRRQEKRLKELLALAER
SQRKLASPGFREKAPKEVVEAEEARLKENLEQAERIREALSQIG

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

DTGPYLQYAH SRLSVERNASGITQEKWINADFSLLKEPAAKLLIRLLGQYPDVLRNAIKT
HEPTTVVTYLFKLTHQVSSCYDVLWVAGQTEELATARLALYGAARQVLYNGMRLLGLTP
VERM

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

GDTGPYVQYAHARAHSILRKAGEWGAPDLSQATPYERALALDLLDFEEAVLEAAEERTPH
VLAQYLLDLAASWNAYYNARENGQPATPVLTAPEGLRELRLSLVQSLQRTLATGLDLLGIP
APEVM

>d1acp__ a.28.1.1 (-) Acyl carrier protein {Escherichia coli}

STIEERVKKIIGEQLGVKQEEVTNNASFVEDLGADSLDTVELVMALEEEFDTEIPDEEAEKI
TTVQAAIDYINGHQA

>d1af8__ a.28.1.1 (-) Actinorhodin polyketide synthase acyl carrier protein, ACT ACP
{Streptomyces coelicolor, A3(2)}

MATLLTTDDLRRALVECAGETDGTDLSGDFDLRFEDIGYDSLALMETAARLESRYGVSIP
DDVAGRVDTPRELLDLINGALAEAA

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

PKAQNIRQGAKEPYPEFVDRLLSQIKSEGHPQEISKFLTDTLTIQNANEECRNAMRHLRPED
TLEEKMYACRDIG

>d1qrjbl a.28.3.1 (B:131-214) HTLV-I capsid protein {Human T-cell leukemia virus type 1}

PSWASILQGLEEPYHAFVERLNIALDNGLPEGTPKDPILRSLAYSNANKECQKLLQARGHT
NSPLGDMLRACQWTWPKDKTKVL

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

GPWADITQGPSESFVDFANRLIKAVEGSDLPPSARAPVIIDCFRQKSQPDIIQLIRAAPSTLT
TPGEIIKYVLDRQKIAP

>d1b91a_ a.29.2.1 (A:) P300/CAF histone acetyltransferase bromodomain {Human (Homo
sapiens)}

GSHMSKEPRDPDQLYSTLKSILQQVKSHQSAWPFMEPVKRTEAPGYEYEVIRSPMDLKTMS
ERLKNRYVYVSKKLFMADLQRVFTNCKEYNAPESYYKCANILEKFFFSKIKEAGLIDK

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

GTTVHCDYLNRPKHSIHRRRTDPMVTLSSILESIIINDMRDLPNTYPFHTPVNAKVVKDY
KIITRPMDLQTLRENVKRRLYPSREEFHLELIVKNSATYNGPKHSLTQISQSMLDLCDEK

LKEKEDKLARLEKAINP

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

VRLTPTMMLYSGRSQDGSLLKSGRYLQQELPVRIAHRIKGFRSLPFIIGCNPTILHVHELYI
RAFQKLTDFFPIKDQADEAQYCQLVRQLLDDHKDVVTLLAEGLRESRKHIEDEKLVRYFL
DKTLTSRLGIRMLATHHLALHEDKP

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

ASLAGAPKYIEHFSKFSPLSMKQFLDFGSSNACEKTSFTFLRQELPVRLANIMKEINLLP
DRVLSTPSVQLVQSWYVQSLLDIMEFLDKDPEDHRTLSQFTDALVTIRNRHNDVVPTMAQ
GVLEYKDTYGDDPVSNQNIQYFLDRFYLSRISIRMLINQHTLIFD

>d1legda1 a.29.3.1 (A:242-396) Medium chain acyl-CoA dehydrogenase {Human (*Homo sapiens*)}

GAGFKVAMGAFDKERPVVAAGAVGLAQRALDEATKYALERKTFGKLLVEHQAISFMLAE
MAMKVELARMSYQRAAWEVDSGRNNTYYASIAKAFAGDIANQLATDAVQILGGNGFNT
EYPVEKLMRDAKIYQIYGGTSQIQLIVAREHIDKYKN

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

KGVYVLMISGLDLERLVLAGGPLGLMQAVLDHTIPYLHVREAFGQKIGHFQLMQGKMAD
MYTRLMACRQYVYNVAKACDEGHCTAKDCAGVILYSAECATQVALDGIQCFGGNGYIN
DFPMGRFLRDAKLYEIGAGTSEVRRLVIGRAFNAD

>d1joya_ a.30.2.1 (A:) EnvZ histidine kinase {*Escherichia coli*}

MAAGVKQLADDRTLLMAGVSHDLRTPLTRIRLATEMMSEQDGYLAESINKDIEECNAIIE
QFIDYLR

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

SQTVRVDieKLDNLMDLMGELVIARSRIETLKKYNIKELDESLSHLSRITLQNVVMKIR

>d1llib_ a.35.1.2 (B:) lambda C1 repressor, DNA-binding domain {Bacteriophage lambda (*Escherichia coli*)}

STKKKPLTQEQLDARRLKAIYEKKKNELGLSQESLADKLGMGQSGIGALFNGINALNAY
NAALLAKILKVSVEEFSPSIAREIYEMYEAVS

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

MQTLSERLKKRRIALKMTQTELATKAGVKQQSIQLIEAGVTKRPRFLFEIAMALNCDPVW
LQYGT

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

MNTQLMGERIRARRKKLKIRQAALGKMVGVSNAISQWERSETEPNGENLLALSALQC
SPDYLLKGDLSQTNVAY

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

MEQRITLKDYAMRFGQTKTAKDLGVYQSAINKAIHAGRKIFLTINADGSVYAEVVKPFPSN
KTTA

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

CSNEKARDWHRADVIAGLKKRKLSSALSRSQFGYAPTTLANALERHWPKEQIIANALET
KPEVIWPSRYQAGE

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

GFDLNDLFLEQLRQMKNMGGMASLMGKLPGMGQIPDNVKSQMDDKVLVRMEAIINSMT
MKERAKPEIIKGSRRRIAAGSGMQVQDVNRLKQFDDMQRMMKMK

>d1qb2a_ a.36.1.1 (A:) SRP54M {Human (*Homo sapiens*)}

QFTLRDMYEQFQNMKMGPFSQLGMIPGFGTDFMSKGNEQESMARLKKLMTIMDSMND
QELDSTDGAKVFSKQPGRIQRVARGSGVSTRDVQELLTQYTKFAQMVK
>d1an2a_ a.38.1.1 (A:) Max protein {Mouse (Mus musculus)}
ADKRAHHNALERKRRDHKDSFHSLRDSVPSLQGEKASRAQILDKATEYIQYMRRKNHT
HQQDIDDLKRQNALLEQQVRALEKARS
>d1mdya_ a.38.1.1 (A:) Myod B/HLH domain {Mouse (Mus musculus)}
MELKRKTTNADRRKAATMRERRRLSKVNEAFETLKRSTSSNPQNQLPKVEILRNAIRYIEG
LQALLRD
>d1an4a_ a.38.1.1 (A:) Usf B/HLH domain {Human (Homo sapiens)}
MDEKRRAQHNEVERRRRDKINNWIVQLSKIIPDSSMESTKSGQSKGGILSKASDYIQELRQ
SNHR
>d1a0aa_ a.38.1.1 (A:) Pho4 B/HLH domain {Baker's yeast (Saccharomyces cerevisiae)}
MKRESHKHAEQARRNRLAVALHELASLIPAEWKQQNVSAAPSKATTVEAACRYIRHLQQ
NGST
>d1am9a_ a.38.1.1 (A:) SREBP-1a {Human (Homo sapiens)}
QSRGEKRTAHNAIEKRYRSSINDKIIEKDLVVGTEAKLNKSAVLRKAIDYIRFLQHSNQKL
KQENLSLRTAVHKSLSLK
>d1k2ha_ a.39.1.2 (A:) Calcyclin (S100) {Rat (Rattus norvegicus), s100a1}
GSELETAMETLINVFHAHSGKEGDKYKLSKKELKDLLQTELSSFLDVQKDADAVDKIMKE
LDENG DGEVDFQEFVVLVAALT VACNNFFWENS
>d1psra_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), psoriasin s100a7}
SNTQAERSIIGMIDMFHKYTRRDDKIDKPSLLTMMKENFPNFLSACDKKGTNYLADVFEK
KDKNEDKKIDFSEFLSLLGDIATDYHKQSHGAAPCSGGSQ
>d1qlsa_ a.39.1.2 (A:) Calcyclin (S100) {Pig (Sus scrofa), calgizzarin s100c (s100a11)}
PTETERCIESLIAIFQKHAGRDGNNTKISKTEFLIFMNTLAAFTQNQKDPGVLD RMMKKL
DLDS DGQLDFQEFLNLIGGLAIACHDSFIKSTQK
>d1irja_ a.39.1.2 (A:) Calcyclin (S100) {Human (Homo sapiens), s100a9 (mrp14)}
TCKMSQLERNIETIINTFHQYSVKLGHPDTLNQGEFKELVRKDLQNFLKKENKNEKVIEHI
MEDLDTNADKQLSFEEFIMLMARL
>d1ncx_ a.39.1.5 (-) Troponin C {Chicken (Gallus gallus)}
ASMTDQQA EARAFLSEEMIAEFKAAAFDMFDADGGGDISTKELGTVMRMLGQNPTKEEL
DAIIIEVDEDDGSGTIDFEEFLVMMVRQMKE DAKGKSEEELANCFRIFDKNADGFIDIEELG
EILRATGEHVTEEDIEDLMKDS DKNNDGRIDFDEFLKMMEGVQ
>d2scpa_ a.39.1.5 (A:) Sarcoplasmic calcium-binding protein {Sandworm (Nereis diversicolor)}
SDLWVQKMKTYFNRIDFDKDGAITRMD FESMAERFAKESEMKA EHAKVLMDSLTGVWD
NFLTAVAGGKGIDETTFINS MKEMVKNPEAKSVVEGPLPLFFRAVD TNEDNNISRDEY GIFF
GMLGLDKTMAPASFDAIDTNNDGLLSLEEFVIAGSDFFMNDGDSTNKVFWGPLV
>d2sas_ a.39.1.5 (-) Sarcoplasmic calcium-binding protein {Amphioxus (Branchiostoma lanceolatum)}
GLNDFQKQKIKFTFDFFLDMNHDGSIQDND FEDMMTRYKEVNKGSLSDADYKSMQASL
EDEWRDLKGRADINKDDVVSWE EYLAMWEKTIATCKSVADLPWCQNRIPFLFKGMDV
SGDGIVDLEEFQNYCKNFQLQCADVPAVYNVITDGGKVTFDLNRYKELYRLLTSPAADA
GNTLMGQKP
>d1c7va_ a.39.1.5 (A:) Calcium vector protein {Amphioxus (Branchiostoma

lanceolatum)}

EEEILRAFKVFDANGDGVIDFDEFKFKIMQKVGEEPLTDAEVEEAMKEADEDGNGVIDIPEF
MDLIKKS

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

AAPKARALGPEEKDECMKIFDIFDRNAENIAPVSDTMDMLTKLGQTYTKRETEAIMKEAR
GPKGDKKKNIGPEEWLTLCSKWVRQDD

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

SSKYAVKLKTDFDNPRWIKRHKHMFDFLDINGNGKITLDEIVSKASDDICAKLEATPEQTK
RHQVCVEAFFRGCMEYGKEIAFPQFLDGWKQLATSELKKWARNEPTLIREWGDVDFDIF
DKDGSGTITLDEWKAYGKISGISPSQEDCEATFRHCDLNSGDLVDDEMTRQHLGFWYTL
DPEADGLYGNVP

>d1jffa_ a.39.1.5 (A:) EHCABP {Entamoeba (Entamoeba histolytica)}

MAEALFKEIDVNGDGAVSYEEVKAFVSKKRAIKNEQLQLIFKSIDADNGEIDQNEFAKF
YGSIQGQDLSDDKIGLKVLYKLMDVDGDGKLTKEEVTSFFKKHGIEKVAEQVMKADANG
DGYITLEEFLEFSL

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

STDDSPYKQAFSLFDRHGTGRIPKTSIGDLLRACGQNPTLAEITEIESTLPAEVDMEQFLQV
LNRPNFGDMPGDPPEEFVKGFQVFDKDATGMIGVGELRYVLTSLGEKLSNEEMDELLKGV
PVKDGMVNYHDFVQMILAN

>d1wdcb_ a.39.1.5 (B:) Myosin Essential Chain {Bay scallop (Aequipecten irradians)}

LPQKQIQEMKEAFSMIDVDRDGFVSKEDIKAISEQLGRAPDDKELTAMLKEAPGPLNFTM
FLSIFSDKLSGTDSEETIRNAFAMFDEQETKKLNIEYIKDLLENMGDNFNKDEMRTFKEA
PVEGGKFDYVKFTAMIKSGE

>d2mysb_ a.39.1.5 (B:) Myosin Essential Chain {Chicken (Gallus gallus)}

FDETEIEDFKEAFTVIDQNADGIIDKDDLRETFAAMGRLNVKNEELDAMIKEASGPINFV
FLTMFGEKLKGADPEDVIMGAFKVLDPDGKSGSIKKSFLEELLTTGGGRFTPEEIKNMWAA
FPPDVAGNVVDYKNICYVITHGEDA

>d1wdcc_ a.39.1.5 (C:) Myosin Regulatory Chain {Bay scallop (Aequipecten irradians)}

LSQDEIDDLKDVFELDFDWDGRDGAVDFAKLGDVCRCLGINPRNEDVFAVGGTHKMGEK
SLPFEEFLPAYEGLMDCEQGTADYMEAFKTFDREGQGFISGAELRHVLTALGERLSDEDV
DEIIKLTDLQEDLEGNVKEYEDFVKKVMAGPYP

>d1auib_ a.39.1.5 (B:) Calcineurin regulatory subunit (B-chain) {Human (Homo sapiens)}

SYPLEMCSHFDADKRLGKRFFKLDLNSGSLSVVEEFMSLPQLQNPLVQRVIDIFDITDG
NGEVDFKEFIEGVSQFSVKGDKEQKLRFRIYDMDKDGYISNGELFQVLKMMVGNLKL
DTQLQQIVDKTIINADKDGGRISFEFCVAVGGLDIHKKMVVDV

>d1rec_ a.39.1.5 (-) Recoverin {Cow (Bos taurus)}

LSKEILEELQLNTKFTTEELSSWYQSFLKECPSGRITRQEFQTIYSKFFPEADPKAYAQHVF
SFDANS DGTLD FKEYVIALHMTSAGKTNQKLEWAFSLYDVGNGTISKNEVLEIVTAIFK
MISPEDTKHLPEDENTPEKRAEKIWGFFGKKDDDKLTEKEFIEGTLANKEILRLIQFEPQKV
KECLK

>d1fpwa_ a.39.1.5 (A:) Frequenin (neuronal calcium sensor 1) {Baker's yeast (Saccharomyces cerevisiae)}

MGAKTSKLSKDDLTCLKQSTYFDRREIQQWHKGFRLDCPSGQLAREDFVKIYKQFFPFGS
PEDFANHLFTVFDKDNNGFIHFEEFITVLSTTSRGTLEEKLSWAFELYDLNHDGYITFDEML
TIVASVYKMMGSMVTLNEDEATPEMRVKKIFKLMDKNEDGYITLDEFREGSKVDPSIIGA
LNLYDGLI

>d1jbaa_ a.39.1.5 (A:) Guanylate cyclase activating protein 2, GCAP-2 {Cow (Bos taurus)}

GQQFSWEEAEENGAVGAADAAQLQEYKKFLEECPSGTLFMHEFKRFFKVPDNEEATQY
VEAMFRAFDTNGDNTIDFLEYVAALNLVLRGTLEHKLKWTFKIYDKDRNGCIDRQELLDI
VESIYKLLKACSVVEAEQQGKLLTPEEVVDRIFLVDENGDGQLSLNEFVEGARRDKWV
MKMLQMDLNP

>d1dgua_ a.39.1.5 (A:) Calcium- and integrin-binding protein, CIB {Human (Homo sapiens)}

SKELLAEYQDLTFLTKQEILLAHRRFCELLPQEQRSVESLRAQVPFEQILSLPELKANPFKE
RICRVFSTSPAKDSLSFEDFLDLLSVFSdTATPDIKSHYAFRIFDFFDDGTLNREDLSRLVNC
LTGEGEDTRLSASEMKQLIDNILEESDIDRDGTINLSEFQHVISRSPDFASSFKIVL

>d1qjta_ a.39.1.6 (A:) Eps15 {Mouse (Mus musculus)}

LSLTQLSSGNPVYKYYRQVEAGNTGRVLALDAAFLKKSGLPDLILGKIWDLADTDGK
GVLSKQEFFVALRLVACAQNGLEVSLSSLSLAVPPPRFHD

>d1c07a_ a.39.1.6 (A:) Eps15 {Human (Homo sapiens)}

TWVVSPAEEKAKYDEIFLKTDKMDGFGVSGLEVREIFLKTGLPSTLLAHIWSLCDTKDCGK
LSKDQFALAFHLISQKLIKIDPPHVLTPEMIPPS

>d1iq3a_ a.39.1.6 (A:) Pob1 {Human (Homo sapiens)}

GSLQDNSSYPDEPWRITEEQREYYVNQFRSLQPDPSFISGSVAKNFFTKSKLSIPELSYIWE
LSDADCDGALTPEFCAAFHLIVARKNGYPLPEGLPPTLQPEFIVTD

>d1hqva_ a.39.1.8 (A:) Apoptosis-linked protein alg-2 {Mouse (Mus musculus)}

PGPGGGPGPAAGAALPDQSFLWNVFQRVDKDRSGVISDNELQQALSNGTWTFPNPVTVR
SIISMFDRENKAGVNFSEFTGVWKYITDWQNVFRTYDRDNSGMIDKNELKQALSGFGYR
LSDQFHDILIRKFDRQGRGQIAFDDFIQGCIVLQRLTDIFRRYDTDQDGWIQVSYEQYLSM
VF

>d1juoa_ a.39.1.8 (A:) Sorcin {Human (Homo sapiens)}

FPGQTQDPLYGYFAAVAGQDGQIDADELQRCLTQSGIAGGYKPFNLETCLRMVSMMLDRD
MSGTMGFNEFKELWAVLNGWRQHFI SFDTDRSGTVDPQELQKALTTMGFRLSPQAVNSIA
KRYSTNGKITFDDYIACCVKLRLALTD SFRRRDTAQQGVVNFPYDDFIQCVMSV

>d1djb1 a.39.1.7 (B:158-298) Phosphoinositide-specific phospholipase C,
isozyme D1 (PLC-D!) {Rat (Rattus norvegicus)}

NKMNFKELKDFLKNLQVDDGYARKIFRECDHSQTDSLEDEEIEIFYKMLTQRAEIDRAF
EEAAGSAETLSVERLVTFHQHQQREEEAGPALALSLIERYPSETAKAQRQMTKDGFLMY
LLSADGNAFSLAHRRVYQDM

>d1kfull a.39.1.7 (L:515-700) Calpain large subunit, C-terminal domain (domain IV) {Human
(Homo sapiens)}

EIEANLEEFDISEDDIDDGVRRLFAQLAGEDAEISAFELQTLRRVLAKRQDIKSDGFSIETC
KIMVDMMLSDSGSKLGLKEFYILWTKIQKYQKIYREIDVDRSGTMNSYEMRKALEEAGF
KMPCQLHQVIVARFADDQLIIDFDNFVRCLVRLETFLKIFKQLDPENTGTIELDLISWLCFS
VL

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

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

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

>d1h8ba_ a.39.1.7 (A:) alpha-Actinin {Human (Homo sapiens)}
 MADTDTAEQVIASFRILASDKPYILAEELRRELPPDQAQYCIKRMPAYSGPGSVPGALDYA
 AFSSALYGESDL

>d1c3za_ a.39.2.1 (A:) Thp12-carrier protein {Yellow mealworm (Tenebrio molitor)}
 ETPREKLKQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAFCILKRAGFIDASGEFQ
 LDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPQHSSADFFKCVHDNRS

>d1dqa_ a.39.2.1 (A:) Pheromone binding protein {Silkworm (Bombyx mori)}
 SQEVMKNLSLNF GKALDECKKEMTLTDAINEDFYNFWKEGYEIKNRETGCAIMCLSTKL
 NMLDPEGNLHHGNAMEFAKKHGADETM AQLIDIVHGCEKSTPANDDKCIWTLGVATCF
 KAEIHKLNWAPSMDDVAVGE

>d1cpo_1 a.39.3.1 (0-119) Cloroperoxidase {Fungus (Caldariomyces fumago)}
 EEPGSGIGYPYDNNTLPYVAPGPTDSRAPCPALNALANHGYPHDGRAISRETLQNAFLNH
 MGIANSVIELALTNAFVVCEYVTGSDCGDSLNLTLAEPHAFEHDSFSRKDYKQGVA

>d1cpo_2 a.39.3.1 (120-298) Cloroperoxidase {Fungus (Caldariomyces fumago)}
 NSNDFIDNRNFD AETFQTS LDVVAGKTHFDYADMNEIRLQRESLSNELDFPGWFTESKPIQ
 NVESGFIFALVSDFNLPDNDENPLVRIDWWKYWFTNESFPYHLGWHPSPAREIEFVTSAS
 SAVLAASVTSTPSSLPSGAIGPGA EAVPLSFASTMTFP LLATNAPYYAQDPTLGPND

>d1h67a_ a.40.1.1 (A:) Calponin {Chicken (Gallus gallus)}
 MPQTERQLRVWIEGATGRRIGDNFMDGLKDG VILCELINKLQPGSVQKVNDPVQNWHL
 ENIGNFLRAIKHYGVKPHDIFEANDLFENTNHTQVQSTLIALASQAKTK

>d1aoa_1 a.40.1.1 (121-251) N-terminal actin-crosslinking domain from fimbrin {Human (Homo sapiens)}
 YSEEEKYAFVNWINKALENDPCRHVIPMNPNTDDL FKA VGDGIVLCKMINLSVPDTIDE
 RAINKKKLTPII QENLN LALSASAIGCHVVNIGAEDLRAGKPHLV LGLLWQIIKIGLFADI
 ELSRNEAL

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

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

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

VKNVMKNIMAGLQQTNSEKILLSWVRQSTRNYPQVNVINFTTSWSDGLALNALIHSRHP
DLFDWNSVVSQQSATQRLEHAFNIARYQLGIEKLLDPEDVDTTYPDKKSILMYITSLFQVL
PQQVSIE

>d1b28a_ a.43.1.1 (A:) Arc repressor {Salmonella bacteriophage P22}

MKGMSKMPQFNLRWPREVLDLVRKVAEENGMSVNSYIYQLVMESFKKEGRIGA

>d1mnta_ a.43.1.1 (A:) Mnt repressor {Salmonella bacteriophage P22}

ARDDPHFNFRMPMEVREKLKFRAEANGRSMNSELLQIVQDALSKPSPVTGYRND AERLA
DEQSELV

>d2cpga_ a.43.1.2 (A:) Transcriptional repressor CopG {Streptococcus agalactiae}

MKKRLTITLSESVLENLEKMAREMGLSKSAMISVALENYKKGQ

>d1cmba_ a.43.1.2 (A:) Met repressor, MetR {Escherichia coli}

AEWSGEYISPYAEHGKKSEQVKKITVSIPLKVLKILTDERTRRQVNNLRHATNSELLCEAFL
HAFTGQPLPDDADLRKERSDEIPEAAKEIMREMGINPETWEY

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

GGDLGKDLTQAWAVAMALGVEDKVTVPVFEGVQKTQTIRSASDIRDVFINAGIKGEEYDA
AWNS

>d1bed_1 a.44.1.1 (63-126) Disulphide-bond formation facilitator (DSBA), insertion domain
{Vibrio cholerae}

GNMGQAMSKAYATMIALEVEDKMVPVMFNRIHTLRKPPKDEQELRQIFLDEGIDAAKFD
AAYNG

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

GLYGKDQQEAAALVDMVNDGVEDLRCKYISLIYTNYEAGKDDYVKALPGQLKPFETLLSQ
NQGGKTFIVGDQISFADYNLLDLLLIHEVLAPGCLDAFPLLSAYVGRLSARPKLKAFLASP
EYVNLPIGNGKQ

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

RKHNMCGETEEEEKIRVDIIENQVMDFRTQLIRLCYSSDHEKLPQYLEELPGQLKQFSMFL
GKFSWFAGEKLTFVDFTYDILDQNRIFDPKCLDEFPNLKAFMCRFEALEKIAAYLQSDQF
CKMPINNKKMAQWGNKPVC

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

DLYGKDMKERALIDMYSEGILDLTEMIMQLVICPPDQKEAKTALAKDRTKNRYLP AFEKV
LKSHGQDYLVGNKLTRVDIHLLELLLYVEEFDASLLTSFPLLKAFKSRISLPLNVKKFLQPG
SQRKLPMDAKQIEEARKIYKF

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

TPDHWYPSDLQARARVHEYLGWHAD CIRGTFGIPLWVQVLGPLIGVQVP EEEKVERNRTA
MDQALQWLEDKFLGDRPFLAGQQVTLADLMALEELMQPVALGYELFEGRPRLAAWRGR
VEAFLGAELCQEAHSIILSILEQA AKKTLTPSPEAYQAMLLRIARIP

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

DLAGKTELEQCQVDAVVDTLDDFMSLFPWAEENQDLKERTFNDLLTRQAPHLLKDLD TY
LGDKEWFIGNYVTWADFYWDICSTLLVLKPDLLGIYPRLVSLRNKVQAIP AISAWILKRP
QTKL

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

LDGKTSLEKYRVDEITETLQDIFNDVVKIKFAPEAAKEAVQQNYEKSCKRLAPFLEGLLV
NGGGDGGFFVGNMTLADLHCYVALEVPLKHTPELLKDCPKIVALRKRVAECPKIAAYLKK
RPVRDF

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

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

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

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

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

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

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

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

>d1k0ma1 a.45.1.1 (A:92-240) Chloride intracellular channel 1 (cltc1) {Human (Homo sapiens)}
RYPKLAALNPESNTAGLDIFAKFSAYIKNSNPALNDNLEKGLLKALKVLDNYLTSPLEGV
DETSAEDEGVSRKFLDGNELTLADCNLLPKLHIVQVVKKYRGFTIPEAFRGVHRYLSN
AYAREEFASCTPDDEEIELAYEQVAKAL

>d1dn1b_ a.47.2.1 (B:) Syntaxin 1A N-terminal domain {Rat (Rattus norvegicus)}
DRFMDEFFEQVEEIRGFIDKIAENVVEVVKRKHSAISPNDPEKTKEELEELMSDIKKTANK
VRSKLKSIEQSIEQEEGLNRSSADLRIRKTHSTLSRKFVEVMSEYNATQSDYRERCKGRI

QRQLEITGRTTTTSEELEDMLESGNPAIFASGIIMDSSISKQALSEIETRHSEIIKLENSIRELHD
 MFMDMAMLVESQGEMIDRIEYNVEHAVDYVERAV
 >d1fioa_ a.47.2.1 (A:) Sso1 {Baker's yeast (Saccharomyces cerevisiae)}
 MHDFVGFNMKISQINRDLDDKYDHTINQVDSLHKRLLTEVNEEQASHLRHSLDNFVAQATD
 LQFKLKNEIKSAQRDGIHDTNKQAQAENSRQRFLKLIQDYRIVDSNYKEENKEQAKRQY
 MIIQPEATEDEVEAAISDVGQIFSQALLNANRRGEAKTALAIEVQARHQELLKLEKSMA
 ELTQLFNDMEELVIEQQ
 >d1hs7a_ a.47.2.1 (A:) Vam3p N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
 TNQKTKELSNLIETFAEQSRVLEKECTKIGSKRDSKELRYKIETELIPNCTSVRDKIESNILIH
 QNGKLSADFKNLKTKYQSLQQSYNQKSLFPLK
 >d1cfaa_ a.50.1.1 (A:) C5a anaphylotoxin {Human (Homo sapiens)}
 MLQKKIEEIAAKYKHSVVKKCCYDGASVNDETCEQRAARISLGPRCIKAFTECCVVASQ
 LRANISHKDMC
 >d0c3a_ a.50.1.1 (-) C3a anaphylotoxin {Human (Homo sapiens)}
 SVQLTEKRMNKVGKYPKELRKCCEDGMRQNPMRFSCQRRTRFISLGEACKKVFLDCCNY
 ITELRRQHARASHLGLAR
 >d1hyp_ a.52.1.1 (-) Soybean hydrophobic protein {Soybean (Glycine max)}
 PSCPDLSICLNILGGSLGTVDCCALIGGLGDIEAIVCLCIQLRALGILNLRNLQLILNSCG
 RSYPSNATCPRT
 >d1fk5a_ a.52.1.1 (A:) Plant non-specific lipid-transfer protein (ns-LTP) {Maize (Zea mays)}
 AISCGQVASAIAPCISYARGQSGPSAGCCSGVRSLNNAARTTADRRAACNCLKNAAAGV
 SGLNAGNAASIPSKCGVSIPYTISTSTDCSRVN
 >d1hssa_ a.52.1.2 (A:) 0.19 alpha-amylase inhibitor {Wheat (Triticum aestivum)}
 MCYPGQAFQVPALPACRPLLRLQCNGSQVPEAVLRDCCQQLAHISEWCRCGALYSMLDS
 MYKEHGAQEGQAGTGAFPCRREVVKLTAASITAVCRLPIVVDDASGDGAYVCKDVAAYP
 DA
 >d1tmqb_ a.52.1.2 (B:) Trypsin/alpha-amylase inhibitor RBI {Ragi (Elucine coracana gaertneri), seeds}
 SVGTSCIPGMAIPHNPLDSCRWYVSTRTCGVGPRLATQEMKARCCRQLEAIPAYCRCEAVR
 ILMGVTSSSGQHEGRLLQDLPGCPQVQRAFAPKLVTEVECNLATIHGGPFCLSL
 >d1ihfa_ a.55.1.1 (A:) Integration host factor (IHF) {Escherichia coli}
 ALTKAEMSEYLFDKLGLSKRDAKELVELFFEEIRRALENGEQVKLSGFGNFDLRDKNQRP
 GRNPKTGEDIPITARRVVTFRPGQKLKSRVENASPK
 >d1ihfb_ a.55.1.1 (B:) Integration host factor (IHF) {Escherichia coli}
 MTKSELIERLATQQSHIPAKTVEDAVKEMLEHMASTLAQGERIEIRGFGSFSLSHYRAPRTG
 RNPKTGDKVELEGKYVPHFKPGKELRDRANIYG
 >d1hns_ a.55.1.1 (-) DNA-binding domain of H1 protein, (H-NS) {Escherichia coli}
 AQRPAKYSYVDENGETKTWTGQGRTPAVIKKAMDEQGKSLDDFLIKQ
 >d1b8za_ a.55.1.1 (A:) HU protein {Thermotoga maritima}
 MNKKELIDRVAKKAGAKKDVKLILDTILETITEALAKGEKVQIVGFGSFEVRKAAARKG
 VNPQTRKPITIPERKVPKFKPGKALKEKVK
 >d1lexa_ a.55.1.1 (A:) Transcription factor 1, TF1 {Bacteriophage SPO1 (Bacillus subtilis)}
 MNKTELIKAIAQDTGLTQVSVSKMLASFEEKIITETVAKGDKVQLTGFLNIKPVARQARKGF

NPQTQEAL E I A P S V G V S V K P G E S L K K A A E G L K Y E D F A K

>d1h1ra1 a.56.1.1 (A:81-193) Aldehyde oxidoreductase, domain 2 {Desulfovibrio gigas}
Q P E N L H P L Q K A W V L H G G A Q C G F C S P G F I V S A K G L L D T N A D P S R E D V R D W F Q K H R N A C R
C T G Y K P L V D A V M D A A A V I N G K K P E T D L E F K M P A D G R I W G S K Y P R P T A V A K V T G T L

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

N K G V L H A V Q E G F Y K E H G L Q C G F C T P G M L M R A Y R F L Q E N P N P T E A E I R M G M T G N L C R C T
G Y Q N I V K A V Q Y A A R K L Q E

>d1b4fa_ a.60.1.2 (A:) EphB2 receptor {Human (Homo sapiens)}

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

>d1coka_ a.60.1.2 (A:) C-terminal domain of p73 {Human (Homo sapiens)}

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

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

N K Q E R T L F K E L I K T N G V G P K L A L A I L S G M S A Q Q F V N A V E R E E V G A L V K L P G I G K K T A E R L I
V E M K D R F K G L H G D L F T P

>d1bvsa2 a.60.2.1 (A:64-134) DNA helicase RuvA subunit, middle domain {Mycobacterium leprae}

D A E N R D L F L A L L S V S G V G P R L A M A T L A V H D A A A L R Q A L A D S D V A S L T R V P G I G R R G A E R I
V L E L A D K V G P V

>d1coo__ a.60.3.1 (-) C-terminal domain of RNA polymerase alpha subunit {Escherichia coli}

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

>d1doqa_ a.60.3.1 (A:) C-terminal domain of RNA polymerase alpha subunit {Thermus
thermophilus}

E Q E E E L D L P L E E L G L S T R V L H S L K E E G I E S V R A L L A L N L K D L K N I P G I G E R S L E E I K E A L E K K
G F T L K E

>d1dk2a_ a.60.6.1 (A:) DNA polymerase beta, N-terminal (8 kD)-domain {Rat (Rattus norvegicus)}

S K R K A P Q E T L N G G I T D M L V E L A N F E K N V S Q A I H K Y N A Y R K A A S V I A K Y P H K I K S G A E A K K
L P G V G T K I A E K I D E F L A T G K L R K L E K

>d1jmsa1 a.60.6.1 (A:148-242) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}

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

>d1tfr_1 a.60.7.1 (183-305) T4 RNase H {Bacteriophage T4}

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

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

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

>d1xola1 a.60.7.1 (A:186-290) T5 5'-exonuclease {Bacteriophage T5}

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

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

LTREKLIELAILVGTDYNPGGIKGIGLKKALEIVRHSKDPLAKFQKQSDVDLYAIKEFFLNPP
 VTDNYNLVWRDPDEEGILKFLCDEHDFSEERVKNGLERLKKAIKSGKQSTLESWFKR
 >d1f44a1 a.60.9.1 (A:20-129) Cre recombinase {Bacteriophage P1}
 SDEVKRNLMDFRDRQAFSEHTWKMLLSVCRSWAAWCKLNNRKWFPAEPEDVRDYLL
 YLQARGLAVKTIQQHLGQLNMLHRRSGLPRPSDSNAVSLVMRRIRKENVDAGE
 >d1a0p_1 a.60.9.1 (3-100) Recombinase XerD {Escherichia coli}
 QDLARIEQFLDALWLEKNLAENTLNAYRRDLSSMMVEWLHHRGLTLATAQSDDLQALLAE
 RLEGGYKATSSARLLSAVRRLFQYLYREKFRREDDPSAHL
 >d1f1oa1 a.60.9.1 (A:2-129) F1p recombinase {Baker's yeast (Saccharomyces
 cerevisiae)}
 PQFDILCKTPPKVLVRQFVERFERPSGEKIALCAAELTYLCWMITHNGTAIKRATFMSYNTI
 ISNSLSFDIVNKSLLQFKYKTQKATILEASLKKLIPAWFEFTIIPYYGQKHQSDITDIVSSLQLQF
 ES
 >d1aep__ a.63.1.1 (-) Apolipoprotein III {African locust (Locusta migratoria)}
 NIAEAVQQLNHTIVNAAHELHETLGLPTPDEALNLLTEQANAFKTKIAEVTTSKQEAKEKH
 QGSVAEQLNAFARNLNNSIHDAATSLNLQDQLNSLQSALTNVGHQWQDIATKTQASAE
 AWAPVQSALQEAEEKTKAANLQNSIQSAVQK
 >d1eq1a_ a.63.1.1 (A:) Apolipoprotein III {Manduca sexta}
 DAPAGGNAFEEMEKHAKFQKTFSEQFNSLVNSKNTQDFNKALKDGSQSVLQQLSAFSSS
 LQGAISDANGKAKEALEQARQNVKTAEEELRKAHPDVEKEANAFKDKLQAAVQTTVQE
 SQKLAKAVASNMEETNKKLAPKIKQAYDDFVKHAEVQKKLHEAATKQ
 >d1hm6a_ a.65.1.1 (A:) Annexin I {Pig (Sus scrofa)}
 AMVSEFLKQAWFIDNEEQEYIKTVKSGSGGPGSAVSPYPTFNPSSDVEALHKAITVKGVD
 EATIIELTKRTNAQRQKIAAYLQEKGKPLDEALKKALTGHLEVALALLKTPAQFDADEL
 RAAMKGLGTDEDTLNEILASRTNREIREINRVYKEELKRDIAKDITSQDYSQKALLSLA
 KGDRSEDLAINDDLADTDARALYEAGERRKGTDLNVFITILTTRSYPHLRVRFQKYSKYSK
 HDMNKVLDLELKGDIENCLTVVVKCATSKPMFFAEKLHQAMKGIGTRHKTILIRIMVSRSE
 IDMNIDIKACYQKLYGISLCQAILDETGDYKILVALCG
 >d1dk5a_ a.65.1.1 (A:) Annexin 2 (ca32) {Bell pepper (Capsicum annuum)}
 HHHHMASLTPAHVPSAAEDCEQLRSAFKGWTNEKLIISILAHRTAAQRKLIRQTYAETF
 GEDLLKELDLRELTHDFEKLVLVWTLDPSEDAHLAKEATKRWTNSFVLVELACTRSPKE
 LVLAREAYHARYKKSLEEDVAYHTTGDRKLLVPLVSSYRYGGEEVDLRLAKAESKILHE
 KISDKAYSDDDEVIRILATRSKAQLNATLNHYKDEHGEDIKQLEDGDEFVALLRATIKGLV
 YPEHYFVEVLRDAINRRGTEEDHLTRVIATRAEVDLKIIDEYQKRDSIPLGRAIAKDTRGD
 YESMILLALLGQE
 >d1azsc1 a.66.1.1 (C:86-201) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}
 GEKATKVQDIKNNLKEAIIETIVAAMSNLVPPVELANPENQFRVDYILSVMNVPDFDFPPEF
 YEHAALWEDEGVRCYERSNEYQLIDCAQYFLDKIDVIKQDDYVPSDQDLLRCR
 >d1tada1 a.66.1.1 (A:57-177) Transducin (alpha subunit), insertion domain {Cow (Bos taurus)}
 YSLEECLEFIIYGNLTLSILAIVRAMTTLNIIQYGD SARQDDARKLMHMADTIEEGTMPK
 EMSDIIQLRWKDSGIQACFDRASEYQLNDSAGYYLSDLERLVTPGYVPTEQDVLSRVKT
 >d1e79a1 a.69.1.1 (A:380-510) C-terminal domain of alpha and beta subunits of F1 ATP synthase
 {Cow (Bos taurus)}
 TRAMKQVAGTMKLELAQYREVAFAQFGSDLDAAATQQLSRGVRLTELLKQGQYSPMAI

EEQVAVIYAGVRGYLDKLEPSKITKFENAFLSHVISQHQALLGKIRTDGKISEESDAKLKEI
VTNFLAGFEA

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

MDPNIVGSEHYDVARGVQKILQDYKSLQDIILGMDELSEEDKLTVSRARKIQRFLSQPF
QVAEVFTGHLGKLVPLKETIKGFQQILAGEYDHLPEQAFYMVGPIDEEAVAKADKLAE

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

NSIIQRISKFDNILKDKTIINQQDLRQISWNGIPKIHRPVVWKLIGYLPVNTKRQEGFLQRK
RKEYRDSLKHTFSDQHSRDIPTWHQIEIDIPRTNPHIPLYQFKSVQNSLQRILYLWAIHPAS
GYVQGINDLVTPFFETFLTEYLPSPQIDDEIKDPSTYMVDEQITDLEADTFWCLTKLLEQI
TDNYIH

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

GQPGILRQVKNSQLVKRIDADLYNHVFQNEHVEFIQFAFRWMNCLLMREFQMGTVIRMW
DTYLSETSQEVTSSYSMSSNDIKPPVTPTEPRVASFVTPTKDFQSPTTALSNTMPNNAVEDS
GKMRQSSLNEFHVFVCAAFLIKWSDQLMEMDFQETITFLQNPPTKDWTTETDIEMLLSEAF
IWQSLYK

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

PIVQNLQGGQMVHQAISPRTLNAWVKVVEEKAFSPEVIPMFSALESEGATPQDLNMTMLNTVG
GHQAAMQMLKETINEEAAEWDRLHPVHAGPIAPGQMREPRGSDIAGTTSTLQEQIGWMT
HNPPIPVGEIYKRWIILGLNKIVRMY

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

PRGYTTWVNTIQTNGLLNEASQNLFGILSVDCTSEEMNAFLDVVPGQAGQKQILLDAIDK
IADDWDNRHPLPNAPLVAPPQGPIPMTARFIRGLGVPRERQMEPAFDQFRQTYRQWIIEM
SEGIKVMIGK

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

PVMHPHGAPPNHRPWQMKDLQAIKQEVSAAPGSPQFMQTIRLAVQQFDPTAKDLQDLL
QYLCSSLVASLHHQQLDSLISEAETRITSYNPLAGPLRVQANNPQQQGLRREYQQWLWA
AFAALPGSAKDPSWA

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

PVVIKTEGPAWTPLEPKLITRLADTVRTKGLRSPITMAEVEALMSSPLLPHDVTNLMRVILG
PAPYALWMDAWGVQLQTVIAAATRDPRHPANGQGRGERTNLNRLKGLADGMVGNPQGG
AALLRPGELVAITASALQAFREVARLA

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

DIHTYLREMEVKCKPKVGYMKKQPDITNSMRAILVDWLVEVGEEYKLQNETLHLAVNYI
DRFLSSMSVLRGKLQLVGTAAMLLASKFEEIYPPEVAEFVYITDDTYTKKQVLRMEHLVL
KVLAFDLAA

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

PTINQFLTQYFLHQQPANCKVESLAMFLGELSLIDADPYLKYLPSVIAAAAFHLALYTVTG
QSWPESLVQKTGYTLETLPCLLDLHQTYLRAPQHAQQSIREKYKNSKYHGVSLNPPET
LNL

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

WTFSSSEQLARLRADANRKFRCKAVANGKVLPNPVPFLEPHEEMTLCKYYEKRLLEFCS
VFKPAMPRSVVGTACMYFKRFYLNNSVMEYHPRIIMLTCAFLACKVDEFNVSSPQFVGNL
RESPLGQEKALEQILEYELLLIQQLNFHLIVH

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

NPYRPFEGFLIDLKTRYPILNPEILRKTADDFLNRIALTDAYLLYTPSQIALTAILSSASRAGI
TMESYLSSESLMLKENRTCLSQLLDIMKSMRNLVKKYEPPRSEEVAVLKQKLDLRCHSAELA
L

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

RVLNNLKLRELLLPKFTSLWEIQTEVTVDNRTILLTWMHLLCESFELDKSVFPLSVSILDY
LCKKQGTKKTLQKIGAACVLIGSKIRTVKPMTVSKLTYLSCDCFTNLELINQEKDILEALK
WDE

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

AVLATDFLIPLCNALKIPEDLWPQLYEAASTTICKALIQPNIALLSPLGICAGGLTTIETDNT
NCRPWTCTYLEDLSSILNFSNTNVRTVKDQVSEAFSLYD

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

FQGFLDSSLLNEEDCRQMIYRSEREHDARMVGVNVDQHFTSQYRKVLTTWMFCVCKDL
RQDNNVFPLAVALDELFLSTRIDRENYQSTAVALHIAGKVRAYMPIKATQLAYLCGGAT
TADKLLTLEVKS LDTLSWVADR

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

CLSTDLCYILHIMHAPREDYLNINLCRPKIFCALCDGRSAMKRPVLITLACMHLTMNQK
YDYYENRIDGVCKSLYITKEELHQCCDLVDIAIVSFDENYFKINA

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

LCEDRIFYNILEIEPRFLTSDSVFGTFQQSLTSHMRKLLGTWMFVCQEYNLEPNVVALAL
NLLDRLLLIKQVSKEHFQKTGSACLLVASKLRS LTPISTSSLCYAAADSFSRQELIDQEKELL
EKLAWRTE

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

AVLATDVTSFLLLKLVGGSQHLDWFHHEVNTLITKALVDPLTGSLPASIIAAGCALLVPAN
VIPQDTHSGGVVPQLASILGCDVSVLQA AVEQILTSVSDFDLRI

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

AMMNAFKEITTMADRINLPRNKVDRTNNLFRQAYEQSLKGRANDAIASACLYIACRQE
GVPRTFKEICAVSRISKKEIGRCFKLILKALETSD

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

LITTGDFMSRFCNLCLPKQVQMAATHIARKAVELDLVPGRSPISVAAAAIYMASQASAEK
RTQKEIGDIAGVADV TIRQSYRLIYPRAPDLFPTDFKFDTPVDKLPQL

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

NLAFALSELDRITAQLKLPRHVEEEAARLYREAVRKGLIRGRSIESVMAACVYAACRLLKV
PRTLDEIADIARVDKKEIGRSYRFIARNLNLTPKKLF

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

VKPTDYVNKFADELGLSEKVRRRRAIEILDEAYKRGLTSGKSPAGLVAAALYIASLLEGEKRT
QREVAEVARVTEVTVRNRYKELVEKLKIKVPIA

>d1guxa_ a.74.1.3 (A:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}
NTIQQLMMILNSASDQPSLENLISYFNNCTVNPKEISILKRVKDIGYIFKEKFAKAVGGQGCVEI
GSQRYKLGVRLLYYRVMESMLKSEERLSIQNFSKLLNDNIFHMSLLACALEVVMATYSRS
TSQNLDSTGTDLSFPWILNVLNLKAFDFYKVIESFIKAEGNLTREMIKHLERCEHRIMESLA
WLSDSPLFDLIKQSK

>d1guxb_ a.74.1.3 (B:) Retinoblastoma tumor suppressor domains {Human (Homo sapiens)}
TSLSLFYKKVYRLAYLRLNTLCERLLSEHPELEHIIWTLFQHTLQNEYELMRDRHLDQIM
MCSMYGICKVKNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEEYDSIIVFYNSVFMQRLKT
NILQYASTRPPTLSPIPHI

>d1rss_ a.75.1.1 (-) Ribosomal protein S7 {Thermus thermophilus}
LQPDLVYGDVLVTAFINKIMRDGKKNLAARIFYDACKIIQEKTGQEPLKVFKQAVENVKPR
MEVRSRRVGGANYQVPMEVSPRRQQSLALRWLVQAANQRPERRAAVRIAHELMDAAEG
KGGAVKKKEDVERMAEANRAYAHYRW

>d1iqva_ a.75.1.1 (A:) Ribosomal protein S7 {Archaeon Pyrococcus horikoshii}
IKVMGRWSTEDVEVKDPSLKPYINLEPRLPHTHGRHAKKHFGKANVHIVERLINKVMRS
GGSHYKVAGHFMRREHRSLSNKKVRAYEVVKEAFKIIKRTGKNPIQVLVWAIENAAPRE
DTTSVMFGGIRYHVAVDISPLRRLDVALRNIALGASAKCYRTKMSFAEALAEIILAANKD
PKSYAYSKKLEIERIAESSR

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

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

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

>d1iqpa1 a.80.1.1 (A:233-327) Replication factor C {Archaeon Pyrococcus furiosus}
RAPEDIREMMLLALKGNFLKAREKLREILLKQGLSGEDVLVQMHKEVFNLPIEEPKKVL
LADKIGEYNFRLVEGANEI IQLEALLAQFTLIGKK

>d1ngr_ a.77.1.1 (-) p75 low affinity neurotrophin receptor {Rat (Rattus norvegicus)}
GNLYSSLPLTKREEVEKLLNGDTWRHLAGELGYQPEHIDSFTHEACPVRALLASWGAQDS
ATLDALLAALRRIRADIVESLCSE

>d1ddf_ a.77.1.1 (-) Fas {Human (Homo sapiens)}
METVAINLSDVDLSKYITTIAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKVQ
LLRNWHQLHGKKEAYDTLIKDLKKANLCTLAEKIQTIILKDITSDSENSNFRNEIQSLVLEH
HHHHH

>d1a1w_ a.77.1.1 (-) FADD (Mort1) {Human (Homo sapiens)}
MDPFLVLLHSVSSSLSSSELTELKYLCLGRVGKRKLERVQSGLDLFSMLLEQNDLEPGHTE
LLRELLASLRRHDLRLRRVDDFE

>d1e41a_ a.77.1.1 (A:) FADD (Mort1) {Human (Homo sapiens)}

GSHMGEEDLCAAFNVICDNVGKDWRRRLARQLKVS DTKIDSIEDRYPRNLTERVRESLRIW
 KNTOKENATVAHLVGALRSCQMNLVADLVQEVQQARDLQNRSGA

>d3crd__ a.77.1.1 (-) Raidd CARD domain {Human (Homo sapiens)}
 MEARDKQVLRSLRLELGAEVLVEGLVLQYLYQEGILTENHIQEINAQTTGLRKTMLLLDIL
 PSRGPKAFDTFLDSLQEFPPWREKLKKAREEAMTDLPAG

>d1cy5a_ a.77.1.1 (A:) Apoptotic protease activating factor 1, APAF-1 {Human (Homo sapiens)}
 MDAKARNCLLQHREALEKDIKTSYIMDHMISDGFLTISEEEKVRNEPTQQQRAAMLIKMI
 LKKDNDYSYVSFYNNALLHEGYKDLAALLHDGIPV

>d3ygs_ a.77.1.1 (P:) Procaspase 9 prodomain {Human (Homo sapiens)}
 SMDEADRLLRRCLRLVEELQVDQLWDVLLSRELFRPHMIEDIQRAGSGSRRDQARQLII
 DLETRGSQALPLFISCLEDTGQDMLASFLRTNRQAG

>d1dgn_ a.77.1.1 (A:) Iceberg {Human (Homo sapiens)}
 ADQLLRKKRRIFIHVSAGTINALLDCLLEDEVISQEDMNKVRDENDTVMDKARVLIDL
 TGKGPCKSCCKFIKHLCEEDPQLASKMGLH

>d1d2za_ a.77.1.1 (A:) Pelle death domain {Drosophila melanogaster}
 LDNTMAIRLLPLPVRAQLCAHLDAALDVWQQLATAVKLYPDQVEQISSQKQRGRSASNEFL
 NIWGGQYNHTVQTLFALFKKLKLHNAMRLIKDYVSEDLHKYI

>d1d2zb_ a.77.1.1 (B:) Tube death domain {Drosophila melanogaster}
 LSSKYSRNTELRRVEDNDIYRLAKILDENSCWRKLMSIIPKGMVDVQACSGAGCLNFP AEIK
 KGFKYTAQDVFQIDEAANRLPPDQSKSQMMIDEWKTSGLNERPTVGVLQLLVQAELF
 SAADFVALDFLNESTPARPVDPGPGALISLE

>d1eyva_ a.79.1.1 (A:) Antitermination factor NusB {Mycobacterium tuberculosis}
 GRHQARKRAVALLFEAEVRGISAAEVVDTRAALAEAKPDIA RLHPYTA AVARGVSEHAAH
 IDDLITAHLRGWTLDR LPAVDRAILRVSVWELLHAADVPEPVVVDEAVQLAKELSTDDSP
 GFVNGVLGQVM

>d1eyla_ a.79.1.1 (A:) Antitermination factor NusB {Escherichia coli}
 MKPAARRRARECAVQALYSWQLSQNDIADVEYQFLAEQDVKDVDVLYFRELLAGVATNT
 AYLDGLMKPYLSRLLEELGQVEKAVLRALYELSKRSDVPYKVAINAEI ELAKSFGAEDSH
 K FVNGVLDKAAPVIRPNKK

>d1qk1a1 a.83.1.1 (A:1-102) Creatine kinase, N-terminal domain {Human (Homo sapiens),
 mitochondria}
 AASERRRLYPSPA EYPDLRKHNNCMASHLTPAVYARLCDKTTPTGWTL DQCIQTGV DNP G
 HPFIKTVGMVAGDEETYE VFADLFDPVIQERHNGYDPRTMKH

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

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

>d1hc2_1 a.85.1.1 (5-135) Hemocyanin, N-terminal domain {Spiny lobster (Panulirus
 interruptus)}
 TGNAQKQQDINHLLDKIYEPTKY PDLKDIAENFNPLGDTSIYNDHGA AVETLMKELNDHR
 LLEQRHWYSLFNTRQRKEALMLFAVLNQCKEWCYFRSNAAYFRERMNEGEFVYALYVSV
 IHSKLG DGIVLP

>d1lla_2 a.86.1.1 (110-379) Hemocyanin {Horseshoe crab (*Limulus polyphemus*)}
PVQEIPDKFIPSA AINEAFKKAHV RPEFDESPILVDVQDTGNILDPEYRLAYYREDVGINA
HHWHWHLVYPSTWNPKYFGKKKDRKGELFYMHQMCARYDCERLSNGMHRMLPFN
NFDEPLAGYAPHLTHVASGKYSPRPDGLKLRDLGDIEISEMVRMRERILDSIHLGYVISED
GSHKTLDELHGTDILGALVESSYESVNHEY YGNLHNWGHVTMARIHDPDGRFHEEPGVM
SDTSTSLRDPIFYNWHRFIDNIFHEYKNTLK

>d1hc2_2 a.86.1.1 (136-398) Hemocyanin {Spiny lobster (*Panulirus interruptus*)}
PLYQITPHMFTNSEVIDKAYSAMTQKPGTFNVSTGTCKNREQRVAYFGEDIGMNIHHVT
WHMDFPFWWEDSYGYHLDRKGELFFVHHQLTARFDFERLSNWLDPVDELHWDRIIRE
GFAPLTSYKYGGFEPVRPDNIHFEDVDGVAHVHDLEITESRIHEAIDHG YITDSDGHTIDIR
QPKGIELLDIIESSKYSSNVQYYGSLHNTAHVMLGRQGDPHGKFNLPPGVMEHFETATR
DPSFFRLHKYMDNIFKKHTDSF

>d1js8a1 a.86.1.1 (A:2503-2791) Functional unit from octopus hemocyanin {Giant octopus (*Octopus dofleini*)}
AIIRKNVNSLTPSDIKELRDAMAKVQADTSDNGYQKIASYHGIPLSCHYENG TAYACCQH
GMVTFPNWHRLTKQMEDALVAKGSHVGIPYWDWTTTFANLPVLVTEEKDNSFHHAHID
VANTDTTRSPRAQLFDDPDKGDKSFFYRQIALALEQTDFCDFEIQFEIGHNAIHSWVGSS
PYGMSTLHYTSYDPLFYLHHSNTDRIWSVWQALQKYRGLPYNTANCEINKLVKPLKPFNL
DTNPNAVTKAHSTGATSF DYHKLGYDYDNLNFHGMTIPELEEHLKEIQH

>d1dbha1 a.87.1.1 (A:198-404) Son of sevenless-1 (sos-1) {Human (*Homo sapiens*)}
EQTY YDLVKA FMAEIRQYIRELNLIKVREPFVSNSKLFSANDVENIFSRIVDIHEL SVKLL
GHIEDTVEMTDEGSPHPLVGSCFEDLAEELAFDPYESYARDILRPGFHDRFLSQLSKPGAA
LYLQSIGEGFKEAVQYVLPRLLLAPVYHCLHYFELLKQLEEKSEDQEDKECLKQAITALLN
VQSGMEKICKSLAKRRLSESA

>d1byla_ a.87.1.1 (A:) beta-pix {Human (*Homo sapiens*)}
MKGFDTTAINKSYYNVVLQNILETENEYSKELQTVLSTYLRPLQTSEKLSSANISYLMGNL
EEICSFQQMLVQSLEECTKLPEAQQRVGGCFLNLMPQMKTLYLT YCANHPSAVNVLTEHS
EELGEFMETKGASSPGILVLTGLSKPFMRLLDKYPTLLKELERHMEDYHTDRQDIQKSMA
AFKNLSAQCCQEVRRKKELELQILTEAIR

>d1f5xa_ a.87.1.1 (A:) RhoGEF Vav {Mouse (*Mus musculus*)}
MKGDEIYEDLMRLESVPTPPKMTEYDKRCCCLREIQQT EEEKYTDTLGSIQQHFMKPLQRF
LKPQDMETIFVNIEELFSVHTHFLKELKDALAGPGATTLYQVFIKYKERFLVYGRYCSQVE
SASKHLDQVATAREDVQMKLEEC SQRANNGRFTLRDLLMVP MQRVLKYHLLLQELVKH
TQDATEKENLRLALDAMRDLAQCVNEVKR

>d1foea1 a.87.1.1 (A:1034-1239) GEF of TIAM1 (T-Lymphoma invasion and metastasis inducing protein 1) {Mouse (*Mus musculus*)}
QLSDADKL RKVICELLETER TYVKDLNCLMERYLKPLQKETFLTQDELDVLFGNLTEMVE
FQVEFLKTLEDGVRLVPDLEKLEKVDQFKKVLFSLGG SFLYADRFKLYSAFCASHTKVP
KVLVKAKTDTAFKAFLDAQNPRQQHSSTLESYLIKPIQRVLKYPLLLREL FALTD AESEEH
YHLDVAIKTMNKVASHINEMQKIHE

>d1e6ya1 a.89.1.1 (A:1284-1569) Alpha chain {Archaeon *Methanosarcina barkeri*}
RRARGPNEPGGLSFGHLSDIVQTSRVS EDPAKIALEVVGAGCMLYDQIWLG SYMSGGVGF
TQYATAAYTDDILDNNTYYDV DYINDKYNGAATVGKDNKV KASLEVVKDIATESTLYGIE
TYEKFTALEDHF GGSQRATVLAAAAGVACSLATGNANAGLSGWYLSMYLHKEAWGRL

GFFGFDLQDQCGATNVLSYQGDEGLPDELRGPNYPNYAMNVGHQGGYAGIAQAAHSGR
GDAFTVNPLLKVCFADDLLPFNFAEPRREFGRGAIREFVPAGERSLVIPA
>d1hbn1 a.89.1.1 (B:189-443) Beta chain {Archaeon Methanobacterium thermoautotrophicum}
GYALRNIMVNHVVAATLKNTLQAAAALSTILEQTAMFEMGDAVGAFERMHLGLAYQGM
NADNLVFDLVKANGKEGTVGSVIADLVERALEDGVIVKEKELTDYKVYGTDDLAMWNA
YAAAGLMAATMVNQGAARAAQGVSSSTLLYYNDLIEFETGLPSVDFGKVEGTAVGFSFFSH
SIYGGGGPGIFNGNHIVTRHSKGFAIPCVAAAMALDAGTQMFSPEATSGLIKEVFSQVDEF
REPLKYVVEAAAEIKNEI
>d1agre_ a.91.1.1 (E:) Regulator of G-protein signalling 4, RGS4 {Rat (Rattus norvegicus)}
VSQEEVKKWAESLENLINHECGLAAFKAFLKSEYSEENIDFWISCEEYKKIKSPSKLSPKA
KKIYNEFISVQATKEVNLDSC TREETS RNMLEPTITCFDEAQKKIFNLMEKDSYRRFLKSRF
YLDLT
>d1fqia_ a.91.1.1 (A:) RGS9, RGS domain {Cow (Bos taurus)}
KLVDIPTKMRVERWAFNFSELIRDPKGRQSFQHFRLKEFSGENLGFWEACEDLKYGDQSK
VKEKAEIYKLFLAPGARRWINIDGKTMDITVKGLKHPHRYVLDAAQTHIYMLMKDSY
ARYLKSPIYKEMLAKEIEP
>d1dk8a_ a.91.1.1 (A:) Axin RGS-homologous domain {Human (Homo sapiens)}
GSASPTPPYLKWAESLHSLDDQDGLSLFRTFLKQEGCADLLDFWFACTGFRKLEPCDSNE
EKRLKLARAIYRKYILDNNGIVSRQTKPATKSFIKGCIMKQLIDPAMFDQAQTEIQATMEEN
TYP SFLKSDIYLEYTRTGSESPKV
>d1iapa_ a.91.1.1 (A:) p115RhoGEF {Human (Homo sapiens)}
SQFQSLEQVKRRPAHLMALLQHVALQFEPGPLLCCLHADMLGSLGPKEAKKAFLDFYHSF
LEKTAVLRVPVPPNVA FELDRTRADLISEDVQRRFVQEVVQSQQVAVGRQLED FR SKRLM
GMTPW EQELAQLEAWVGRDRASYEARERHVAERLLMHLEEMQHTISTDEEKSAAVVNAI
GLYMRHLGVRT
>d1htjf_ a.91.1.1 (F:) PdZ-RhoGEF RGS-like domain {Human (Homo sapiens)}
ESDIIFQDLEKLKSRPAHLGVFLRYIFSQADPSPLL FYLC AEVYQQASPKDSRSLGKDIWNIF
LEKNAPLRVKIPEMLQAEIDSRLRNSEDARGVLCEAQEAAMPEIQEQIH DYRTKRTLGLGS
LYGENDLLDLGDPLRERQVAEKQLAALGDILSAYAADRSAPMDFALNTYMSHAGIRL
>d1jdra_ a.93.1.1 (A:) Cytochrome c peroxidase, CCP {Baker's yeast (Saccharomyces cerevisiae)}
TTPLVHVASVEKGRSYEDFQKVYNAIALKLREDDEYDNYIGYGPVLVRLAWHTSGTWDK
HDNTGGSYGGTYRKFKEFN DPSNAGLQNGFKFLEPIHKEFPWISSGDLFSLGGVTAVQEM
QGPKIPWRCGRVDT PEDTTPDN GR LPPADK DADYVRTFFQRLNMNDREVVALMGAHTL
GKTHLKNSGYEGPWTANNVFDNSFYLNLLNEDWKLEKNDANNEQWDSKSGYMMMLPT
DYSLIQDPKYLSIVKEYANDQDKFFKDFSKAFEKLLENGITFPKDAPSPFIFKTLEEQGL
>d1mn2_ a.93.1.1 (-) Manganese peroxidase {Basidiomycetes fungus (Phanerochaete
chrysosporium)}
AVCPDGTRVSHAACCAFIPLAQDLQETIFQNECGQDAHEVIRLTFHDAIAISRSQGP KAGG
GADGSMLLFPTVEPNFSANNGIDDSVNNLIPFMQKHNTISAADLVQFAGAVALSNC PGAPR
LEFLAGRPNKTI AAVDGLIPEPQDSVTKILQRFEDAGGFTPFEVVSLLASHSVARANKVDQ
TIDAAPFDSTPFTFDTQVFLEVLLKGVGFPGSANNTGEVASPLPLGSGSDTGEMRLQSDFA
LAHDPRTACIWQGFVNEQAFMAASFRAAMSKLAVLGHNRLSLIDCSDVVPVPK PATGQPA
MFPASTGPQDLELSCP SERFPTLTTPGASQSLIAHCPDGSMSCPGVQFN GPA
>d1apxa_ a.93.1.1 (A:) Ascorbate peroxidase {Pea (Pisum sativum)}

GKSYPTVSPDYQKAIEKAKRKLRGFIAEKKCAPLILRLAWHSAGTFDSKTKTGGPFGTIKH
QAELAHGANGLDIAVRLLEPIKEQFPIVSYADFYQLAGVVAVEITGGPEVPFHPGREDKPE
PPPEGRLPDATKGSDDLRLDVFGKAMGLSDQDIVALSGGHTIGAAHKERSGFEGPWTSNPLI
FDNSYFTELLTGEKDGLLQLPSDKALLTDSVFRPLVEKYAADEDVFFADYAEHLKLSELG
FAEA

>d1bgp__ a.93.1.1 (-) Plant peroxidase {Barley (*Hordeum vulgare*), peroxidase 1}

AEPPVAPGLSFDFYWQTCPRAESIVREFVQEAVRKDIGLAAGLLRLHFHDCFVQGCDAV
LLDGSATGPGEQQAPPNLTLPKSAFKAVNDIRDLERECRGAVVSCSDILALAARDSVVVS
GGPDYRVPLGRRDSRFASTQDVLSDLPGPSSNVQSLALLGRLGLDADTLVTISGGHTIGL
AHCSSFEDRLFPRPDPTISPTFLSRLKRTCPAKGTDRRTVLDVRTPNVFDNKYYIDLNVREG
LFVSDQDLFTNAITRPIVERFAQSQQDFEQFGVSGKMGQMRVRTSDQGEVRRNCSVRNP
GPG

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

CPEQDKYRTITGMCNNRRSPTLGASNRAFVRWLPAEYEDGFSLPYGWTPGVKRNGFPVA
LARAVSNEIVRFPTDQLTPDQERSLMFMQWGQLLDHDLDFTEPAXVNCETSCVQQPPCF
PLKIPPNDPRIKNQADCIPFFRSCPACPGSNITIRNQINALTSFVDASMVYGSEELARNLRN
MSNQLGLLAVNQRFQDNGRALLPFDNLHDDPCLLTNRSARIPCFLAGDTRSSPELTSMT
HTLLLREHNRLATELKSINPRWDGERLYQEARKIVGAMVQIITYRDYLPVLGPTAMRKY
LPTYRSYNDSVDPRIANVFTNAFRYGHITLIQPFMFRLDNRYQPMENPRVPLSRVFFASWR
VVLEGGIDPILRGLMATPAKLNRQNQIAVDEIRERLFEQVMRIGLDLPALNMQRSRDHGLP
GYNAWRRFCGLPQPETVGQLGTVLRNLKLARKLMEQYGTNNIDIWMGGVSEPLKRKG
RVGPLLACIIGTQFRKLRLDGRFWWENEGVFSMQQRQALAQISLPRIICDNTGITTVSKNN
IFMSNSYPRDFVNCSTLPALNLASWREA

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

FLTRIKLLLKPTPNTVHYILTHFKGVWNIVNNIPFLRSLIMKYVLTSRSLIDSPPTYNVHYG
YKSWEAFSNLSYYTRALPPVADDCPTPMGVKGNKELPDSKEVLEKVLLRREFIPDPQGSN
MMFAFFAQHFTAQFFKTDHKRGPGFTRGLGHGVLDLNHIYGETLDRQHKLRLFKDGKLY
QVIGGEVYPPTVKDTQVEMIYPHIPENLQFAVGQEVFGLVPGLMMYATIWLREHQRVCDI
LKQEHPEWGDEQLFQTSKLILIGETIKIVIEDYVQHLSGYHFKLKFDPELLFNQQFQYQNRI
ASEFNTLYHWHPLPDFTNIEDQEYSFKQFLYNNISILLEHGLTQFVESFTRQIAGRVAGGRN
VPIAVQAVAKASIDQSREMKYQSLNEYRKRFSKPYTSFEELTGEKEMAAELKALYSIDIV
MELYPALLVEKPRPDAIFGETMVELGAPFSLKGLMGNPICSPQYWKPSTFGGEVGFKIINT
ASIQSLICNNVKGCPFTSFNVQ

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

MQASQFSAQVLDWYDKYGRKTLPWQIDKTPYKVLSEVMLQQTQVATVIPYFERFMAR
FPTVTDLANAPLDEVHLWTGLGYARARNLHKAQQVATLHGGKFPETFEEVAALPGV
GRSTAGAILSLSLGKHFPILNGNVKRVLARCYAVSGWPGKKEVENKLWSLSEQVTPAVGV
ERFNQAMMDLGAMICTRSKPKCSLCPLQNGCIAAANNSWALYPGKKPK

>d1keaa__ a.96.1.2 (A:) Thymine-DNA glycosylase {Archaeon *Methanobacterium thermoformicicum*}

DATNKKRKVFVSTILTFWNTDRRDFPWRHTRDPYVILITEILLRRTTAGHVKKIYDKFFVK
YKCFEDILKTPKSEIAKDIKEIGLSNQRAEQLKELARVVINDYGGRVPRNRKAILDLPGVG
KYTCAAVMCLAFGKKAAMVDANFVRVINRYFGGSYENLNYNHKAELWELAEITLVPGGKC
RDFNLGLMDFSAIICAPRKPKCEKCGMSKLCSSYYEKC

>d1mpgal a.96.1.3 (A:100-282) 3-Methyladenine DNA glycosylase II (gene alkA or aidA) {Escherichia coli}

AARPGRLRPGCVDAFEQGVRAILGQLVSVAMAAKLTARVAQLYGERLDDFPEYICFPTPQR
LAAADPQALKALGMPLKRAEALIHLANAALEGLPMTIPGDVEQAMKTLQTFPGIGRWT
ANYFALRGWQAKDVFLPDDYLIKQRFPGMTPAQIRRYAERWKPWRSYALLHIWYTEGW
QPDEA

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

DPIECFLSFICSSNNNIARITGMVERLCQAFGPRLIQLDDVTYHGFPSLQALAGPEVEAHLR
KLGLGYRARYVSASARAILEEQGGLAWLQQLRESSYEEAHKALCILPGVGTKVADCICLM
ALDKPQAVPVDVHMHIAQRDYSWHPTTSQAKGSPSQTNKELGNFFRSLWGPYAGWAQ
AVLFSADL

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

LPLPEPGEEAALAGLRAFLEAKLPRYAEERDRLDGEGGSRLSPYFALGVLSPLAAWEAER
RGEGEGARKWVAELLWRDFSyhLLYHFPWMAERPLDPRFQAFWQEDEALFQAWYEGKT
GVPLVDAAMRELHATGFLSNRARMNAAQFAVKHLLLPWKRCEEAFRHLLLDGDRAVNL
QGWQWAGGLGVDAAPYFRVFNPLVQGERHDPEGRWLKRWAPEYPSYAPKDPVVDLEEA
RRYRLRLARD

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

PVEPGETAAIARLQEFCDRAIADYDPQRNFPAEAGTSGLSALKFGAIGIRQAWQAASAAH
ALSRSDEARNSIRVWQQELAWREFYQHLYHFPSLADGPYRSLWQQFPWENREALFTAW
TQAQTGYPIVDAAMRQLTETGWMHNRCRMIVASFLTkdLIIDWRRGEQFFMQHLVDGDL
AANNGGWQWSASSGMDPKPLRIFNPASQAKKFDATATYIKRWLPelRHVHPKDLISGEIT
PIERRGYPAIVNHNLRQKQFKALYNQLKAAI

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

GAGHFVKMVHNGIEYGDMQLICEAYHLMKDVGLGLGHKEMAKAFEEWNKTELDSFLIEIT
ASILKFQDADGKHLLPKIRDSAGQKGTGKWTASALEYGVPVTLIGEAVFARCLSSLKDER
IQASKKLKGPQNIPFEGDKKSFLDIRKALYASKIISYAQGFMLLRQAATEFGWTLNYGGIA
LMWRGGCIIRSVFLGKIKDAFDRNPGLQNLLDDFFKSAVENCQDSWRAISTGVQAGIP
MPCFTTALSfydGYRHAMLPANLIQAQRDYFGAHTYELLAKPGQFIHTNWTGHGG

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

GAGSCVKMYHNSGEYAILQIWGEVFDILRAMGLNNDVAAVLEDWKSknFLKSYMLDIS
IAAARAKDKDGSYLTEHVMDRIGSKGTGLWSAQEALeIGVPAPSLNMAVVSrqFTMYKT
ERQANASNAPGITQSPGYTLKNKSPSGPEIKQLYDSVCIAIISCYAQMFQCLREMDKVHNF
GLNLPATIAFRAGCILQGYLLKPMTEAFekNPnISnlMCAFQTEIRAGLQNYRDMVALITS
KLEVSIPVLSASLNYVTAMFTPTLKYGQLVSLQRDVfGRHGYERVdKdGRESFQWPELQ

>d1gai__ a.102.1.1 (-) Glucoamylase {Aspergillus awamori, variant x100}

ATLDSWLSNEATVARTAILNnIGADGAWVSGADSGIVVASpSTDNPdYfYTWTRDSGLVIK
TLVDLFRNGDtdLLStIEHYISSQAIiQGVSnpSGDLSSGGLGEPKfNVdeTAYtGSWGRpQ
RDGPALRATAMIGFGQWLLDNGYtSAATEiVwPLVRNDLSYVAQYWNQtGYDLWEEVN
GSSFFtIAVQHRALVEGSaFATAVGSScSWCDsQAPQILCYLQsFWtGSYILANFDSSRSgK

DTNTLLGSIHTFDPEAGCDDSTFQPCSPRALANHKEVVDSFRSIYTLNDGLSDSEAVAVGR
YPEDSYYNNGNPWFLCTLAAAEQLYDALYQWDKQGSLEITDVSLDFFKALYSGAATGTYS
SSSTYSSIVSAVKTFADGFVSIVETHAASNGSLSEQFDKSDGDELSARDLTWSYAALLTANN
RRNSVPPSWGETSASSVPGTCAATSASGTYSSTVTTSWPSIVATG

>dlayx__ a.102.1.1 (-) Glucoamylase {Baker's yeast (*Saccharomyces fibuligera*)}

AYPSFEAYSNYKVDRTDLETFLDKQKEVSLYLLQNIAYPEGQFNNGVPGTVIASPSTSNP
DYQQWTRDSAITFLTVLSELEDNNFNNTLAKAVEYYINTSYNLQRTSNPSGSFDDENHK
GLGEPKFNTDGSAYTGAWGRPQNDGPALRAYAISRYLNDVNSLNEGKLVLTDSGDINFSST
EDIYKNIKPDLEYVIGYWDSTGFDLWEENQGRHFFTSLVQQKALAYAVDIAKSFDDGDFA
NTLSSTASTLESYLSGSDGGFVNTDVNHIVENPDLLQQNSRQGLDSATYIGPLLTHDIGESS
STPFDVDNEYVLQSYLLLEDNKDRYSVNSAYSAGAAIGRYPEDVYNGDGSSEGNPWFL
ATAYAAQVPYKLAYDAKSASNDITINKINYDFFNKYIVDLSTINSAYQSSDSVTIKSGSDEF
NTVADNLVTFGDSFLQVILDHINDDGSLEQLNRYTGYSTGAYSLTWSSGALLEAIRLRNK
VKALA

>d1cem__ a.102.1.2 (-) CelA cellulase {*Clostridium thermocellum*}

AGVPFNTKYPYGPTSIADNQSEVTAMLKAEWEDWKSKRITSNGAGGYKRVQRDASTNY
DTVSEGMMGYGLLLAVCFNEQALFDDLYRYVKSHFNGNGLMHHWHIDANNVNTSHDGGDG
AATDADEDIALALIFADKQWGSSGAINYGQEARTLINNLYNHCVEHGSYVLKPGDRWGGS
SVTNPSYFAPAWYKVYAQYTGDRWNQVADKCYQIVEEVKKYNNGTGLVPDWCTASGT
PASGQSYDYKYDATRYGWRTAVDYSWFGDQRAKANCDMLTKFFARDGAKGIVDGYTIQ
GSKISNNHNASFIGPVAAASMTGYDLNFAKELYRETAVKDEYYGYGNSLRLLTLLYIT
GNFPNPLSDL

>d1tf4a1 a.102.1.2 (A:1-460) Endo/exocellulase:cellobiose E-4, N-terminal domain
{*Thermomonospora fusca*}

EPAFNIAEALQKSMFFYEAQRSGKLPENNRVSWRGDSGLNDGADVGLDLTGWWYDAGD
HVKFGFPMAFTATMLAWGAIESPEGYIRSGQMPYLDKNLRWVNDYFIKAHPSPNVLYVQ
VGDGDADHKWWGPAEVMMPMERPSFKVDPSCPGSDVAAETAAMAASSIVFADDDPAYA
ATLVQHAKQLYTFADTYRGVYSDCVPAFAFYNSWSGYQDELVWGAYWLYKATGDDSYL
AKAEYEYDFLSTEQQTDLRSYRWTIWDDKSYGTYVLLAKETGKQKYIDDANRWLDYW
TVGVNGQRPYSPGGMVLDLTDWALRYAANTAFVALVYAKVIDDPVRKQRYHDFAVRQI
NYALGDNPRNSSYVVGFGNNPPRNPHRTAHGSWTDSPASPAENRHVLYGALVGGPGSPN
DAYTDDRQDYVANEVATDYNAGFSSALAMLVEEYGGTPLADFPPTTEPDG

>d1clc_1 a.102.1.2 (135-575) CelD cellulase {*Clostridium thermocellum*}

AMNVYEDAFKTAMLGMYLLRCGTSVSATYNGIHYSHGPCHTNDAYLDYINGQHTKKDS
TKGWHADAGDYNKYVVNAGITVGSMFLAWEHFKDQLEPVLEIPEKNNSIPDFLDELKYEI
DWILTMQYPDGSGRVAHKVSTRNFGGFIMPENEHDERFFVPWSSAATADFVAMTAMAARI
FRPYDPQYAEKCINAAKVSYEFLKNNPANVFANQSGFSTGEYATVSDADDRLWAAAEMW
ETLGDEEYLRDFENRAAQFSKKIEADFDWDNVANLGMFTYLLSERPGKNPALVQSIKDSL
LSTADSIVRTSQNHGYGRTLGTYYWGCNGTVVRQTMILQVANKISPNNDYVNAALDAIS
HVFGRNYNRSYVTGLGINPPMNPHDRRSGADGIWEPWPGYLVGGGWPGPKDWVDIQD
SYQTNEIAINWNAALIYALAGFVNYN

>d1faea__ a.102.1.2 (A:) Processive endocellulase CelF (Cel48F) {*Clostridium cellulolyticum*}

ASSPANKVYQDRFESMYSKIKDPANGYFSEQGIPYHSIETLMVEAPDYGHVTTSEAMSY

MWLEAMHGRFSGDFTGFDKSWSVTEQYLIPTEKDQPNTSMSRYDANKPATYAPEFQDPS
KYPSPLDTSQPVGRDPINSQLTSAYGTSMLYGMHWILDVDNWWYGFGARADGTSKPSYINT
FQRGEQESTWETIPQPCWDEHKFGGQYGFLLDFTKDTGTPAKQFKYTNPADADARAVQA
TYWADQWAKEQGKSVSTSVGKATKMGDYLRYSFFDKYFRKIGQPSQAGTGYDAAHYLL
SWYYAWGGGIDSTWSWIIGSSHNHFGYQNPFAAWVLSTDANFKPKSSNGASDWAKSLDR
QLEFYQWLQSAEGAIAGGATNSWNGRYEAVPSGTSTFYGMGYVENPVYADPGSNTWFG
MQVWSMQRVAELYYKTGDARAKLLDKWAKWINGEIKFNADGTFQIPSTIDWEGQPDT
WNPTQGYTGNANLHVKVNYGTDLGCASSLANTLTYYAAKSGDETSRQNAQKLLDAM
WNNYSDSKGISTVEQRGDYHRFLDQEVFVPAGWTGKMPNGDVIKSGVKFIDIRSKYKQD
PEWQTMVAALQAGQVPTQRLHRFWAQSEFAVANGVYAILFPD

>d1d12a_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Baker's yeast
(*Saccharomyces cerevisiae*)}

GAGEMRDRIESMFLESWRDYSKHGWGYDVYGPiEHTSHNMPRGNQPLGWIIVDSVDTL
MLMYSNSTLYKSEFEAEIQRSEHWINDVLDLFDIDAENVVFETTIRMLGGLLSAYHLSDVLE
VGNKTVYLNKAIDLGDRLALAFLLSTQTGIPYSSINLHSGQAVKNHADGGASSTAETTLQ
MEFKYLAYLTGNRTYWELVERVYEPLYKNNDLLNTYDGLVPIYTFPDTGKFGASTIRFGSR
GDSFYEYLLKQYLLTHETLYYDLYRKSMEGMKKHLLAQSKPSSLWYIGEREQGLHGQLSP
KMDHLVCFMGGLLASGSTEGLSIHEARRRPFFSKSDWDLAKGITDTCYQMYKQSSSGLAP
EIVVFNDGNIKQDGWWRSSVGDFVVKPLDRHNLQRPETVESIMFMYHLSHDHKEYREWG
AEIATSFENTCVCDCNDPKLRRFTSLDCITLPTKKSNNMESFWLAETLKYLYILFLDEFDL
TKVVFNTEAHPFVLDEEILKSQSLTTGWSL

>d1hcua_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {*Trichoderma reesei*}
KRGSPNPTRAAVKAQTSWNAYHHFAFPHDDLHPVNSFDDERNGWGSSAIDGLDTAI
LMGDADIVNTILQYVPQINFNTTAVANQGSSVFETNIRYLGLLSAYDLLRGPFSSLATNQT
LVNSLLRQAQTLANGLKVAFTTPSGVPDPTVFFNPTVRRSGASSNNVAEIGSLVLEWTRLS
DLTGNPQYLAQKGESYLLNPKGSPEAWPGLIGTFVSTSNQTFQDSSGSWSGLMDSFYE
YLIKMYLYDPVAFAHYKDRWVLGADSTIGHLGSHPSTRKDLTFLSSYNGQSTSPNSGHLA
SFGGGNFILGILLNEQKYIDFGIKLASSYFGTYTQTASGIGPEGFAWVDSVTGAGGSPSS
QSGFYSSAGFWVTAPYYILRPETLESYYAYRVTGDSKWQDLAWEALSAIEDACRAGSAY
SSINDVTQANGGGASDDMESFWFAEALKYAYLIFAEESDVQVQATGGNKVFVNTEAHPFSI
RS

>d1fo3a_ a.102.2.1 (A:) Class I alpha-1;2-mannosidase, catalytic domain {Human (*Homo sapiens*)}
QGPVHLNRYRQKGVLDVFLHAWKGYRKFAWGHDELKPVSRSEWFGGLTLIDALDTM
WILGLRKEFEARKWVSKKLHFEKDVDVNLFEISTIRILGGLLSAYHLSGDSLFLRKAEDFG
NRLMPAFRTPSKIPYSDVNIGTGVAHPPRWTSDSTVAEVTIQLEFRELSRLTGDKKFQEAV
EKVTQHIHGLSGKKDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQWIQGGKQE
TQLEDYVEAIEGVTRTHLLRHSEPSKLTfVgELAHGRFSAKMDHLVCFLPGTLALGVYHG
LPASHMELAQELMETCYQMNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNLRLPE
TVESLFYLYRVTGDRKYQDWGWEILQSFSRFRVPSGGYSSINNVQDPQKPEPRDKMESF
FLGETLKYLLFLFSDDPNLLSLDAYVFNTEAHPPIWT

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

GTAELIMKRVMLDLKKPLRNMDKVAEKNLNTLQPDGSWKDVYPYKDDAMTNWLPNNHL
LQLETIIQAYIEKDSHYYGDDKVFDQISKAFKYWYDSDPKSRNWWHNEIATPQALGEMLI

LMRYGKKPLDEALVHKLTERMKRGEPEKKTGANKTDIALHYFYRALLTSDEALLSFAVKE
LFYPVQFVHYEEGLQYDYSYLQHGPKLQISSYGAVFITGVLKLANYVRDTPYALSTEKLAI
FSKYRDSYLKAIRGSYMDFNVEGRGVSRPDILNKKAEKKRLLVAKMIDLKHTEEWADAI
ARTDSTVAAGYK

>d1flsa1 a.102.3.2 (A:249-619) Hyaluronate lyase {Streptococcus agalactiae}

EDNFTKLLDKWNDVTIGNYVYDTNDSNMQKLNQKLDETNAKNIEAIKLDNRNFLWKDL
DNLNNSAQLTATYRRLEDLAKQITNPHSTIYKNEKAIRTVKESLAWLHQNFYNVNDIEGS
ANWWDFEIGVPRSITGTLNLMNNTFTDAEIKTYTDPIEHFVPDAEYFRKTLVNPFKALGGN
LVDMMGRVKIIEGLLRKDNTHIEKTSLSKNLFTTATKAEGFYADGSYIDHTNVAYTGAYGN
VLIDGLTQLLPIIQTQDYKISNQELDMVYKWINQSFLPLIVKGELMDMSRGRSISREAASSH
AAAVEVLRGFLRLANMSNEERNLDLKSTIKTIITSNKFYNVFNLSYSDIANMKNLLNDS
TVATKP

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

APAYARTLDRAVEYLLSCQKDEGYWWGPLXISPVWDTGLAVLALRAAGLPADHDLVKA
GEWLLDRQITVPGDWAVKRPNLKPGGFAFQFDNVYYPDVCDTAVVVWALNTLRLPDERR
RRDAMTKGFRWIVGMQSSNGGWGAYDNDTSNLPNHIPFSDFGVTDPPSEDVTAHVLE
CFGSGFYDDAWKVIRRAVEYLRKREQKPDGSWFRWGVNYLYGTGAVVSALKAVGIDTRE
PYYIKALDWVEQHQNPDGGWGEDCRSYEDPAYAGKGASTPSQTAWALMALIAGGRAESE
AARRGVQYLVEVTPQPDGGWDEPYTGTGFPDGYLGYTMYRHVFPTLALGRYKQAIER

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

LSNVTMEAEYVLLCHILDRVDRDRMEKIRRYLLHEQREDGTWALYPGGPPDLDTTIEAYV
ALKYIGMSRDEEPMQKALRFIQSQGGIESSRVFTRMWLALVGEYPWEKVPMVPPEIMFLG
KRMPLNIYEFGSWARATVVALSIVMSRQPVFPLPERARVPELYETDVPPRRRGAKGGGGW
IFDALDRALHGYQKLSVHPFRRAAEIRALDWLLERQAGDGSWGGIQPPWFYALIALKILD
MTQHPAFIKGWEGLELYGVELDYGGWMFQAS

>d1d8db_ a.102.4.3 (B:) Protein farnesyltransferase, beta-subunit {Rat (Rattus norvegicus)}

PVWSEPLYSLRPEHARERLQDDSVETVTSIEQAKVEEKIQEVFSSYKFNHLVPRVLVQREK
HFHYLKRGLRQLTDAYECLDASRPWLCYWILHSLELLDEPIPQIVATDVCQFLELCQSPDG
GFGGGPGQYPHLAPTYAAVNALCIIGTEEAYNVINREKLLQYLYSLKQPDGSFLMHVGG
VDVRSAYCAASVASLTNIITPDLFEGTAEWIARCQNWEGGIGGVPGMEAHGGYTFCGLAA
LVILKKERSLNLKSLQWVTSRQMRFEFGFQGRCNKLVDGCYSFWQAGLLPLLHRALHA
QGDPAISMHSWMFHQQALQEYILMCCQCPAGLLDKPGKSRDFYHTCYCLSGLSIAQHF
GSGAMLHDVVMGVPENVLQPTHVPVYNIGPDKVIQATTHFLQKPVPGF

>d1dceb_ a.102.4.3 (B:) Rab geranylgeranyltransferase, beta subunit {Rat (Rattus norvegicus)}

TQQKDVTIKSDAPDTLLLEKHADYIASYGSKKDDYEYCMSEYLRMSGVYWGLTVMDLM
GQLHRMNKEEILVFIKSCQHECGVSASIGHDPHLLYTLASVQILTLYDSIHVINVDKVVAY
VQSLQKEDGSFAGDIWGEIDTRFSFCVATLALLGKLDAINVEKAIEFVLSCMNFDGGFGC
RPGSESHAGQIYCCTGFLAITSQLHQVNSDLLGWVLCERQLPSGGLNGRPEKLPDVCYS
WWVLASLKIIGRLHWIDREKLRSFILACQDEETGGFADRPMDVDPFHTLFGIAGLSLLGE
EQIKPVSPVFCMPPEVLQRVNVQPELVS

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

ASSTNLKDILADLIPKEQARIKTRQQHGNATVGGQITVDMMYGGMRGMKGLVYETSVLD

PDEGIRFRGYSIPECQKMLPKAKGGEEPLPEGLFWLLVTGQIPTEEQVSWLSKEWAKRAA
LPSHVVTMLDNFPTNLHPMSQLSAAITALNSESNFARAYAEIGHRTKYWELIYEDCMDLIA
KLPCVAAKIYRNLYREGSSIGAIDSKLDWSHNFTNMLGYTDAQFTELMRLYLIHSDHEGG
NVSHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLTQLQKEVGKDVSE
KLRDIWNTLNNGRVVPGYGHAVLRKTDPRYTCQREFALKHLPDPMFKLVAQLYKIVPN
VLLEQGGKAKNPWPNVDAHSGVLLQYYGMTEMNYYTVLFGVSRALGVLAQLIWSRALG
FPLERPKSMSTDGLIKLVDSK

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

LAKGLEDVYIDQTNICYIDGKEGKLYYRGYSVEELAELSTFEVVYLLWWGKLPSLSELE
NFKKELAKSRGLPKEVIEIMEALPKNTHPMGALRTIISYLGNIIDSGDIPVTPEEVYRIGISV
TAKIPTIVANWYRIKNGLEYVPPKEKLSHAANFLYMLHGEEPPKEWEKAMDVALILYAEH
EINASTLAVMTVGSTLSDYYSAILAGIGALKGPIHGGAVEEAIKQFMEIGSPEKVEEWFFKA
LQQRKIMGAGHRVYKTYDPRARIFKKYASKLGDKKLFEIAERLERLVEEYLSKKGISINV
DYWSGLVIFYGMKPIELYTTIFAMGRIAGWTAHLAEYVSHNRIIRPRLQYVGEIGKKYLP
LRR

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

EPTIHKLAGVTADVTAISKVNSDTNSLLYRGYPVQELAAKCSFEQVAYLLWNSLNDSE
LKAFVNFERSHRKLDENVKGAIDLLSTACHPMDVARTAVSVLGANHARAQDSSPEANLEK
AMSLATFPSVVAYDQRRRRGEELIEPREDLDYSANFLWMTFGEEAAPEVVEAFNVSMIL
YAEHSFNASTFTARVITSTLADLHSAVTGAIGALKGPLHGGANEAVMHTFEEIGIRKDESLD
EAATRSKAWMVDALAQKKKVMGFGHRVYKNGDSRVPTMKSALDAMIHYDRPEMLGL
YNGLEAAMEEAKQIKPNLDYPAGPTYNLMGFDTEMFTPLFIAARITGWTAHIMEQVADN
ALIRPLSEYNGPEQRQVP

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

LAPLPPHVPEHLVDFDMYNPSNLSAGVQEAWAVLQESNVPDLVWTRCNGGHWIATRQ
LIREAYEDYRHSSECPFIPREAGEAYDFIPTSMDPPEQRQFRALANQVVGMPVVDKLENR
IQELACSLIESLRPQGQCNTEDYAEPFPIRIFMLLAGLPEEDIPHLKYLTQDMTRPDGSM
TFAEAEALYDYLIPIIEQRRQKPGTDAISIVANGQVNGRPITSDEAKRMCGLLVGGDLTVV
NFLSFSMEFLAKSPEHRQELIQRPERIPAAACEELLRRFSLVADGRILTSDYEFHGVQLKKGD
QILLPQMLSGLDERENACPMHVDFSRQKVSHTTFGHGSHLCLGQHARREIIVTLKEWLT
RIPDFSIAPGAQIQHKSGIVSGVQALPLVWDPATTKAV

>d1jpa_ a.104.1.1 (A:) Cytochrome P450 bm-3 {*Bacillus megaterium*}

TIKEMPQPKTFGELKNLPLLNTDKPVQALMKIADELGEIFKFEAPGRVTRYLSSQRLIKEAC
DESRFDKNLSQALKFVRDFAGDGLFTSWTHEKNWKKAHNILLPSFSQQAMKGYHAMMV
DIAVQLVQKWERLNADEHIEVPEDMTRLTDLTIGLCGFNYRFNSFYRDQPHPFITSMVRAL
DEAMNKLQRANPDDPAYDENKRQFQEDIKVMNDLVDKIIADRKASGEQSDDLTHMLNG
KDPETGEPLDDENIRYQITFLIAGHETTSGLLSFALYFLVKNPHVLQKAAEEAARVLVDPV
PSYKQVKQLKYVGMVLNEALRLWPTAPAFSLYAKEDTVLGGEYPLEKGDELMLVLPQLH
RDKTIWGDVVEEFRPERFENPSAIPQHAFKPFNGQRACIGQQFALHEATLVLGMMMLKHF
DFEDHTNYELDIKETLTLKPEGFVVKAKSKKIPLGGI

>d1jfa_ a.104.1.1 (A:) Cytochrome P450-NOR, nitric reductase {Fungus (*Fusarium oxysporum*)}

APSFPFSRASGPEPPAEFAKLRTNPVSQVKLFDGSLAWLVTKHKDVCFVATSEKLSKVRT
RQGFPELSASGKQAAKAKPTFVDMDPPEHMHQSRSMVEPTFTPEAVKNLQPYIQRVDDL
LEQMKQKGCANGPVDLVKEFALPVPSYIYTLLGVFPNDLEYLTQQNAIRTNGSSTAREAS

AANQELLDYLAILVEQRLVEPKDDIISKLCTEQVKPGNIDKSDAVQIAFLLLVAGNATMVN
MIALGVATLAQHPDQLAQLKANPSLAPQFVEELCRYHTASALAIKRTAKEDVMIGDKLVR
ANEGIIASNQSANRDEEVFENPDEFNMNRKWPPQDPLGFGFGDHRCIAEHLAKAELTTVF
STLYQKFPDLKVAVPLGKINYTPLNRDVGIVDLPVIF

>d1jipa_ a.104.1.1 (A:) Cytochrome P450-ERYF {Saccaropolyspora erythraea}

TTVPDLESDFSFHDWYRTYAELRETAPVTPVRFLGQDAWLVTGYDEAKAALSDDLRLSSDP
KKKYPGVEVEFPAYLGFPEVDVRNYFATNMGTSDDPPTHRLRKLVSQEFTVRRVEAMRPRV
EQITAELLDEVGDSGVVDIVDRFAHPLPIKVICELLGVDEKYRGEFGRWSSEILVMDPERAE
QRGQAAREVVNFILDLVERRRTEPGDDLSSALIRVQDDDDGRLSADELTSIALVLLLAGFE
SSVSLIGIGTYLLLTHPDQLALVRRDPSALPNAVEEILRYIAPPETTTTRFAAEEVEIGGVAIPQ
YSTVLVANGAANRDPKQFPDPHRFDVTRDTRGHLSFGQGIHFCMGRPLAKLEGEVALRAL
FGRFPALSLGIDADDVVWRRSLLLRGIDHLPVRLDG

>d1cpt_ a.104.1.1 (-) Cytochrome P450-TERP {Pseudomonas sp.}

MDARATIEPHIARTVILPQGYADDEVITYPAFKWLRDEQPLAMAHIEGYDPMWIATKHADV
MQIGKQPGLFSNAEGSEILYDQNNFAFMRSISGGCPHVIDSLTSMDPPTHTAYRGLTLNWF
QPASIRKLEENIRRIAQASVQRLDFDGECDFMTCALYYPLHVMTALGVPEDEDEPLML
KLTQDFFGVEAARRFHETIATFYDYFNGFTVDRRSCPKDDVMSLLANSKLDGNYIDDKYI
NAYYVAIATAGHDTTSSSSGAIIGLSRNEQLALAKSDPALIPRLVDEAVRWTAPVKSFM
TALADTEVRGQNIKRGRIMLSYPSANRDEEVFSNPDEFDITRFPNRHLGFGWGAHMCLG
QHLAKLEMKIFFEELLPKLKSVELSGPPRLVATNFVGGPKNVPIRFTKA

>d1e9xa_ a.104.1.1 (A:) Cytochrome p450 14 alpha-sterol demethylase (cyp51) {Mycobacterium tuberculosis}

MSAVALPRVSGGHDEHGHLEEFRTDPIGLMQRVRDECGDVGTFQLAGKQVVLLSGSHAN
EFFFRAGDDDLQAKAYPFMTPIFGEGVVFDA SPERRKEMLHNAALRGEQMKGHAATIE
DQVRRMIADWGEAGEIDLDFFAELTIYTSSACLIGKKFRDQLDGRFAKLYHELERGTDPL
AYVDPYLPISFRRRDEARNGLVALVADIMNGRIANPPTDKSDRDMLDVLI AVKAETGTPR
FSADEITGMFISMMFAGHHTSSGTASWTIELMRHRDAYAAVIDELDELYGDGRSVSFHAL
RQIPQLENVLKETLRLHPLIILMRVAKGEFEVQGHRHIEGDLVAASPAISNRIPEDFPDPHD
FVPARYEQPRQEDLLNRWTWIPFGAGRHRVCVGAFAIMQIKAIFSVLLREYEFEMAQPPES
YRNDHSKMVVQLAQ PACVRYRRRT

>d1io7a_ a.104.1.1 (A:) CYP119 {Archaeon Sulfolobus solfataricus}

MYDWFSEMRKKDPVYYDGNIWQVFSYRYTKEVLNNFSKFSSDLTGYHERLEDLRNGKIR
FDIPTRYTMLTSDPPLHDELRSMSADIFSPQKLQTLET FIRETTRSLLDSIDPREDDIVKKLA
VPLPIIVISKILGLPIEDKEKFKEWSDLVAFRLGKPGEIFELGKKYLELIGYVKDHLNSGTEV
VSRVNSNLSIDIEKLGYYILLIAGNETTTNLISNSVIDFTRFNLWQRIREENLYLKAIEEALR
YSPPVMRTVRKTKERVKLGDQTIEEGEYVRVWIASANRDEEVFHDGEKFIPDRNPNPHLS
FGSGIHLCLGAPLARLEARIAIEEFSKRFRHIEILDTEKVPNEVLNGYKRLVVRLKS

>d1dt6a_ a.104.1.1 (A:) Mammalian cytochrome p450 2c5 {Rabbit (Oryctolagus cuniculus)}

PPGPTPFPIIGNILQIDAKDISKSLTKFSECYGPVFTVYLG MKPTVVLHG YEAVKEALVDLG
EEFAGRGSVPILKVKGLGIAFSNAKTWKEMRRFSLMTRLNFGMGKRSIEDRIQEEARCL
VEELRKTNASPCDPTFILGCAPCNVICSVIFHNRFDYKDEEFLKLMESLHENVLLGTPWL
QVYNNFPALLDYFPGIHKTLKKNADYIKNFIMEKVKEHQKLLDVNNPRDFIDCFLIKMEQ
ENNLEFTLES L VIAVSDLFGAGTETTSTTLRYSLLLLLKHPEVAARVQEEIERVIGRHRSPCM

QDRSRMPYTD A VIHEIQR FIDLLPTNLPHAVTRDVRFRNYFIPKGTDIITSLTSVLHDEKA FP
NPKVFDPGHFLDESGNFKKSDYFMPFSAGKRM CVGEGLARMELFLFLTSILQNFKLQSLV
EPKDL DITAVVNGFVSVPPSYQLCFIPIHH

>d1etob_ a.105.1.1 (B:) FIS protein {Escherichia coli}

MFEQ RVNSDVLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLA EVE
QPLLD MVMQYTLGNQTRAALMMGINRGTLRKKLK KYGMN

>d1ntca_ a.105.1.1 (A:) DNA-binding domain of NTRC {Salmonella typhimurium}

MDLPGELFEASTPDSPSHLPPDSWATLLAQWADRALRSGHQ NLLSEAQPELERTLLTTALR
HTQGHKQEAARLLGWGAATLTAKLKELGME

>d1aora1 a.110.1.1 (A:211-605) Aldehyde ferredoxin oxidoreductase {Archaeon Pyrococcus
furiosus}

IADKQKFMLVVREKVNKL RNDPVAGGGLPKYGTAVLVNIINENGLYPVKNFQTGVYPYAY
EQSGEAMAAKYLV RNKPCYACPIGCGRVNRLPTVGETEGPEYESVWALGANLGINDLASII
EANHMCDELGLDTISTGGTLATAMELYEKGHIKDEELGDAPPFRWGNT EVLHYYIEKIAK
REGFGDKLAEGSYRLAESYGHPELSMTVKKLELPAYDPRGAEGHGLGYATNNRGGCHIK
NYMISPEILGYPYKMDPHDVSDDKIKMLILFQDLTALIDSAGLCLFTTFGLGADDYRDLLN
AALGWDFTTEDY LKIGERIWNAERL FNLKAGLDPARDDTLPKRFLEEPMP EGPKNKGHTV
RLKEMLP RYKLRGWTE DGKIPKEKLEELGIAEFY

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

DKEELKKLSQEAYNEILNSPGYPFWKRQGTMAAVEWCNTNYALPTRNFSDGYFEFARSID
GYTMEGMKVQQRGCPYCNMPCGNVVLD AEGQSELDYENVALLGSNLGIGK LNEVSVL
NRIADEMGMDTISLGVSIAHVME AVERGILKEGPTFGDFKGAKQLALDIAYRK GELGNLA
AEGVKAMAEKLGTHDFAMHVKGLEVSGYNCYIYPAMALAYGTSAIGAHHKEAWVIAWE
IGTAPIEGEKA EKVEYKISYDPIKAQKVVELQRLRGGLFEMLTACRLPWVEVGLSLDYYPK
LLKAITGVTYTWDDLYKAADRVYSLIRAYWVREFNGKWDRKMDYPPKRWFTEGLKSGP
HKGEHLDEKKYDELLSEYYRIRGWDERGIPKKETL KELDLD FVIPELEKVTNLE

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

TCSTSD DADDPTPPNERDDEAFASRVAAAKRELEGTGTVCQINNGETDLAAKFHKS LPHD
DLGQVDADAF AALED CILNGDLSICEDVPVGNSEGD PVGRLVNPTAAFAIDISGPAFSATTI
PPVPTLPSP ELAAQLAEVYWMALARDVPFMQYGTDDITVTAAANLAGMEGF PNLD AVSI
GSDGTVDPLSQLFRATFVG VETGPFISQLLVNSFTIDSITVEPKQETFA PDVNYMVDFDEWL
NIQNGGPPAGPELLDDELRFVRNARDLARVTFTDNINTEAYRGALILLGLDAFN RAGVNG
PFIDIDRQAGFVNFGISHYFRLIGAAELAQRSSWYQKWQVHRFARPEALGGTLHLTIK GEL
NADFDLSLLENAELLKRVAAINAAQNPNNEVTYLLPQAIQEGSP THPSYPSGHATQNGAFA
TVLKALIGLDRGGDCYPDPVYPDDDGLKLIDFRGSCLT FEGEINKLAVNVAFGRQMLGIHY
RFDGIQGLLLGETITVRTLHQELMTFAEESTFEFRLFTGEVIKLFQDGTFTIDGFKC PGLVYT
GVENCV

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

GIPADNLQSRKASFDTRVAAAELALARGAVPSFANGEELLYRNSETGDPSFIGSFTKGLPH
DDNGAIIDPDDFLAFVRAINSGDEKEIAALT LGPARDPETGLPIWRSDLANSLDLEVRGWE
NSSAGLTFDLEGPDAQSVAMPPAPVLT SPELIAEMAELYLMALGRDIEFSEF DSPKNAAFIR
SAIERLNGLEWFNTPAKLGDPPAEIRRRRGEVTVGNLFRGILPGSEVGPYLSQFIIVGSKQIG

SATVGNKTLVSPNAADEFDGEIAYGSITISQVRVIATPGRDFMTDLKVFLDVQDAADFRGF
ESYEPGARLIRTIRDLATWVHFDSLYEAYLNAACLILLANGVPFDPNLPFQQEDKLDNQDVF
VNFGSAHVLSLVTEVATRALKAVRYQKFNIHRRRLPEATGGLISVNKNAFLKSESVFPEVD
VLVEELSSILDDSASSNEKQNIADGDVSPGKSFLLPMAFAEGSPFHPSYSGSHAVVAGACV
TILKAFFDANFQIDQVFEVDTDKLVKSSFPGLTVAGELNKLADNVAIGRNMAGVHYFS
DQFESLLLGEQIAIGILEEQSLTYGENFFFNLPKFDGTTIQI

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

RGQDTLFSVLDETRTAPGRRLQLSWLRHPLLDGRPLEARLDRVEGFVREGALREGVRRLL
YRLADLERLATRLELGRASPKDLGALRRSLQILPELRALLGEEVGLPDLSPKKEELEAALV
EDPPLKVSEGLIREGYDPDLALRAAHREGVAYFLELEERERERTGIPTLKVGYNAVFGY
YLEVTRPYERYVPKEYRPVQTLKDRQRYTLPEMKEKEREVYRLEALIRRREEEVFLEVRE
RAKRQAEALREAARILAELDVYAALAEVAVRYG

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

DAATRRNLEITQNLAGGAENTLASVLDCTVTPMGSRMLKRWLHMPVRDTRVLLERQQT
GALQDFTAGLQPVLRQVGDLERILARLALRTARPRDLARMRHAFQQLPELRAQLETVDSA
PVQALREKMGFEALRDLLERAIIIDTPVLVRDGGVIASGYNEELDEWRALADGATDYLE
RLEVRERERTGLDTLKVGFNAVHGYIYQISRGQSHLAPINYMRRQTLKNAERYIPELKEY
EDKVLTSKGKALALEKQLYEELFDLLLPHLEALQQSASALAEELDLVNLAERAYTLN

>d1tx4a_ a.116.1.1 (A:) p50 RhoGAP domain {Human (Homo sapiens)}

PLPNQQFGVSLQHLQEKNPQEPIPIVLRETVAYLQAHALTTEGIFRRSANTQVVREVQQK
YNMGLPVDFDQYNALHLPVILKTFLRELPEPLTFDLYPHVVGFLNIDESQRVPATLQVLQ
TLPEENYQVLRFLTAFLVQISAHSDQNKMTNTNLAVVFGPNLLWAKDAAITLKAINPINTF
TKFLLDHQGELF

>d1pbwa_ a.116.1.1 (A:) p85 alpha subunit RhoGAP domain {Human (Homo sapiens)}

LPDLAEQFAPPDIAPPLIKLVEAIEKKGLECSTLYRTQSSSNLAELRQLLDCDTPSVDLEMI
DVHVLADAFKRYLLDLPNPVIPAAVYSEMISLAPEVQSSEEYIQLLKKLIRSPSIPHQYWLT
LQYLLKHFFKLSQTSSKNLLNARVLSEIFSPMLFRFSAASSDNTENLIKVIEILISTEW

>d1f7ca_ a.116.1.1 (A:) Graf {Chicken (Gallus gallus)}

AQLDSIGFSIIKKCIHAVETRGINEQGLYRIVGVNSRVQKLLSILMDPKTATETETEICAWEI
KTITSALKTYLRMLPGPLMMYQFQRSFIKAAKLENQESRVSEIHSVLVHRLPEKNRQMLHLL
MNHLAKVADNHKQNLMTVANLGVVFGPTLLRPQEETVAAIMDIKFQNVIEILIEIENHEKIF
NTVPE

>d1wer__ a.116.1.2 (-) p120GAP domain {Human (Homo sapiens)}

MPEEYSEFKELILQKELHVYALSHVCGQDRTLLASILLRIFLHEKLESLLLCTLNDREIS
MEDEATTLFRATTLASTLMEQYMKATATQFVHHALKDSILKIMESKQSCELSPSKLEKNED
VNTNLTHLLNILSELVEKIFMASEILPPTLRYIYGCLQKSVQHKWPTNTTMRTRVVSGFVFL
RLICPAILNPRMFNIISDSPSIAARTLILVAKSVQNLANLVEFGAKEPYMEGVNPFIKSNKH
RMIMFLDELGNVPELPDTTEHSRTDLSRDLAALHEICVAHSDELRTLSNERGAQQHVLLKK
LLAITELLQQKQNQYT

>d1nfla_ a.116.1.2 (A:) GAP related domain of neurofibromin {Human (Homo sapiens)}

ERLVELVTMMGDQGELPIAMALANVVPCSQWDELARVLVTLFDSRHLLYQLLWNMFSKE
VELADSMQTLFRGNSLASKIMTFCFKVYGATYLQKLLDLLRIVITSSDWQHVSFEVDPTR
LEPSESLEENQRNLLQMTEKFFHAISSSEFPQLRSVCHCLYQVVSQRFPQNSIGAVGSA
MFLRFINPAIVSPYEAGILDKKPPPIIERGLKLSKILQSIANHVLFTEEHRPFNDFVKS

FDAARRFFLDIASDCPTSDAVNHSLSFISDGNVLALHRLWNNQEKIGQYLSSNRDHKAVG
RRPFDKMATLLAYLGPPE

>d1h6oa_ a.146.1.1 (A:) TRF1 {Human (Homo sapiens)}

EDAGLVAEAEAVAAGWMLDFLCLSLCRAFRDGRSEDFRRTNRNSAEAIHGLSSLTACQLRT
IYICQFLTRIAAGKTLDAQFENDERITPLESALMIWGSIEKEHDKLHEEIQNLIQIAIAVCM
ENGNFKEAEVFERIFGDPNSHMPFKSKLLMIISQKDTFHSFFQHFSYNHMMEEKIKSYVNY
VLSEKSSTFLMKAAAKVVE

>d1h6pa_ a.146.1.1 (A:) TRF2 {Human (Homo sapiens)}

AGEARLEEAVNRWVLKFYFHEALRAFRGSRYGDFRQIRDIMQALLVRPLGKEHTVSRLLR
VMQCLSRIEENLDCSFDMEAELTPLESAINVLEMITEFTLTEAVVRESSRKLKVEAAVVIC
IKNKEFEKASKILKKHMSKDPTTQKLRNDLLNIIREKNLAHPVIQNFSEYTFQKMLRFLE
SHLDDAEPYLLTMAKKALK

>d1jdha_ a.118.1.1 (A:) beta-Catenin {Human (Homo sapiens)}

AVVNLINYQDDAELATRAIPELTKLLNDEDQVVVNKAAMVHQLSKKEASRHAIMRSPQ
MVSIVRTMQNTNDVETARCTAGTLHNLSHHREGLLAIFKSGGIPALVKMLGSPVDSVLF
YAITTLHNLLHQEGAKMAVRLAGGLQKMVALLNKTNVKFLAITTDCLQILAYGNQESKL
IILASGGPQALVNIMRTYTYEKLLWTTSRVLKVLSVCSSNKPAIVEAGGMQALGLHLDPS
QRLVQNCLWTLRNLSDAATKQEGMEGLLGLTLVQLLGSDDINVVTCAAGILSNLTCNNYK
NKMMVCQVGGIEALVRTVLRAKDREDITEPAICALRHLSRHQEAEMAQNAVRLHYGLP
VVVKLLHPPSHWPLIKATVGLIRNLALCPANHAPLREQGAIPRLVQLLVRAHQDTQRRTS
MGGTQQQFVEGVRMEEIVEGCTGALHILARDVHNIRIVIRGLNTIPLFVQLLYSPIENIQRVA
AGVLCELAQDKEAAEAIEAEGATAPLTELHLSRNEG VATYAAAVLFRMS

>d1iala_ a.118.1.1 (A:) Importin alpha {Mouse (Mus musculus)}

DEQMLKRRNVSSFPDDATSPLQENRNNQGTVNWSVEDIVKGINNNLESQEQATQAARK
LLSREKQPPIDNIIRAGLIPKFVSFLGKTDCSPIQFESAWALTNISGTSEQTKAVVDGGAIPA
FISLLASPHAHISEQAVWALGNIAGDGSFRDLVIKHGAIDPLLALLAVPDLSTLACGYLRN
LTWTLNLNCRKNPAPPLDAVEQILPTLVRLHHNDPEVLADSCWASISYLTGDPNERIEMV
VKKGVPQLVKLLGATELPIVTPALRAIGNIVTGTDEQTQKVIDAGALAVFPSLLTNPKTNI
QKEATWTMSNITAGRQDQIQVVNHGLVPFLVGVLSKADFKTQKEAAWAITNYTSGGTV
EQIVYLHCGIIEPLMNLLSAKDTKIIQVILDAISNIFQAAEKLGETEKL SIMIEECGGLDKIE
ALQRHENESVYKASLNLEKYF

>d1qgra_ a.118.1.1 (A:) Importin beta {Human (Homo sapiens)}

MELITILEKTVSPDRLELEAAQKFLERAAVENLPTFLVELSRVLANPGNSQVARVAAGLQIK
NSLTSKDPDIKAQYQQRWLAIANARREVKNYVLHTLGTETYPSSASQCVAGIACAEIP
VNQWPPELIPQLVANVTNPNSTEHMKESTLEAIGYICQDIDPEQLQDKSNEILTAAIQGMRKE
EPSNNVKLAATNALLNSLEFTKANFDKESERHFIMQVVCEATQCPDTRVRVAALQNLVKI
MSLYYQYMETYMGPALFAITIEAMKSDIDEVALQGIEFWSNVCDEEMDLAIEASEAAEQG
RPPEHTSKFYAKGALQYLVILTQTLTKQDENDDDDDDWNPCKAAGVCLMLLATCCEDDIV
PHVLPFIKEHIKNPDWRYRDAAVMAFGCILEGPEPSQLKPLVIQAMPTLIELMKDPSVVVR
DTAAWTVGRICELLPEAAINDVYLAPLLQCLIEGLSAEPRVASNVCWAFSSLAEEAYEAAD
VADDQEEPATYCLSSSFELIVQKLETTDRPDGHQNNLRSSAYESLMEIVKNSAKDCYPV
QKTTLVIMERLQQVLQMESHQSTSDRIQFNDLQSLLCATLQNVLRKVQHQDALQISDVV
MASLLRMFQSTAGSGGVQEDALMAVSTLVEVLGGEFVKYMEAFKPFGLGKLYAEYQV
CLAAVGLVGDLCRALQSNIIPFCDEVMQLLENLGNENVHRSVKPQILSVFGDIALAIGGE

FKKYLEVVLNTLQQASQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDQENVHP
DVMLVQPRVEFILSFIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVCLKLVEARPMIHEL
LTEGRRSKTNKAKTLARWATKELRKLKNQA

>d1qbk_b_ a.118.1.1 (B:) Karyopherin beta2 {Human (Homo sapiens)}

YEWKPDEQGLQQILQLLKESQSPDTTIQRTVQQKLEQLNQYPDFNNYLIFVLTKLSEDEP
TRSLSGILKNNVKAHFQNFNGVTDIFIKSECLNIGDSSPLIRATVGILITTIASKGELQNW
PDLLPKLCSLLDSEDYNTCEGAFGALQKICEDSAEILDSVDLDRPLNIMIPKFLQFFKHSSP
KIRSHAVACVNQFIISRTQALMLHIDSFTENLFALAGDEEPEVRKNVCRALVMLEVRMDR
LLPHMHNIVEYMLQRTQDQDENVALEACEFWLTAEQPICKDVLVRHLPKLIPVLVNGMK
YSDIDIILLKGDVEEDETIPDSEQDIRPRFHRSTVAQQHDEDGIEEEDDDDDDEIDDDDTISD
WNLKRCSSAAALDVLANVYRDELLPHILPLLKELLFHHEWVVKESGILVLGAIAEGCMQG
MIPYLPPELIPHLIQCLSDKKALVRSITCWTLSTRYAHWVVSQPPDTYLKPLMTELLKRILDSN
KRVQEAACSAFATLEEEACTELVPYLAYILDTLVFAFSKYQHKNLLILYDAIGTLADSVGH
HLNKPEYIQMLMPPLIQKWNMLKDEKDLFPLLECLSSVATALQSGFLPYCEPVYQRCVN
LVQKTLAQAMLNNAQPDQYEAPDKDFMIVALDLLSGLAEGLGGNIEQLVARSNILTLMYQ
CMQDKMPEVRQSSFALLGDLTKACFQHVKPCIADFMPIGTNLNPEFISVCNNATWAIGEI
SIQMGIEMQPYIPMVHLQVEIINRPNTPKTLLENTAITIGRLGYVCPQEVAPMLQQFIRPW
CTSLRNIRDNEEKDSAFRGICTMISVNPSGVIQDFFCFDAVASWINPKDDLDRDMFCKILHG
FKNQVGDENWRRFSDQFPLPLKERLAAFYGV

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

AAADGDDSLYPIAVLIDELRNEDVQLRLNSIKKLSTIALALGVERTRSELLPFLTDTIYDEDE
VLLALAEQLGTFTTLVGGPEYVHCLLPPLSLATVEETVVVRDKAVESLRAISHEHSPSDLE
AHFVPLVKRLAGGDWFTSRTSACGLFSVCYPRVSSAVKAELRQYFRNLCSDDTPMVRRA
AASKLGEFAKVLELDNVKSEIIPMFSNLASDEQDSVRLAVEACVNIAQLLPQEDLEALVM
PTLRQAAEDKSWRVRYMVADKFTTELQKAVGPEITKTDLVPAFQNLMKDCEAEVRAAASH
KVKEFCENLSADCRENVIMSQILPCIKELVSDANQHVKSSALASVIMGLSPILGKDNTIEHLL
PLFLAQLKDECPEVRLNIISNLDVNEVIGIRQLSQSLLPAIVELAEDAKWRVRLAIIYEMPL
LAGQLGVEFFDEKLNSLCMAWLVDHVYAIREAATSNLKKLVEKFGKEWAHATIIPKVLAM
SGDPNYLHRMTTLFCINVLSEVCGQDITTKHMLPTVLRMAGDPVANVRFNVAKSQKIGP
ILDNSTLQSEVKPILEKLTQDQDQDVVKYFAQEALTVLSLA

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

SDPENIKTQELFRKVRSLNKLTPQMFMNQLMKQVSGLTVDTEERLKGVIDLVFEKAIDEPSF
SVAYANMCRCCLVTLKVPMAKPGNTVNFRKLLLNRQKEFEKDKADDDVFEKKQKELE
AASAPEERTRLHDELEEAKDKARRRSIGNIKFIGELFKLKMTEAIMHDCVVKLLKNHDEE
SLECLCRLTTIGKDLDFEKAKPRMDQYFNQMEKIVKERKTSSRIRFMLQDVIDLRLCNW
VS

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

TEDHLESICKVGEKSACSLESNLEGLAGVLEADLPNYKSKILRLLCTVARLLPEKLTIIYTT
LVGLLNARNYNFGGEFVEAMIRQLKESLKANNYNEAVYLVRFLSDLVNCHVIAAPSMVA
MFENFVSVTQEEDVPQVRRDWYVYAFLSSLPWVGKELYEKKDAEMDRIFANTESYLRKR
QKTHVPMLQVWTADKPHPQEEYLDCLWAQIQKLKKDRWQERHILRPYLAFDSILCEALQ
HNLPPTPPHTEDSVYPMPRVIFR

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

MFDTYDDPEGPVMPGSHSVERFVIEENLHCHIKSHWKERTCAAQLVSYPGKNKIPLNYHI
VEVIFAEELFQLPAPPHIDVMTTLLIELCKLQPGSLPQVLAQATEMLYMRLDTMNTTCVDR
FINWFSHLSNFQFRWSWEDWSDCLSQDPESPCKPKFVREVLEKCMRLSYHQRILDIVPPTF
SALCPSN

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

PTCIYKYGDESSNSLPGHSVALCLAVAFKSKATNDEIFSILKDVPNPNQDDDDDEGFSFNPL
KIEVFVQTLHLAAKSFHSFSALAKFHEVFKTAESEDEGKLHVLRVMFEVWRNHPQMIA
VLVDKMIRTQIVDCAAVANWIFSSLSRDFTRLFVWEILHSTIRKMKNKHVLKIQKELEEAK
EKLARQHDGVLEEQUIERLQEKVESAQSEQKNLFLVIFQRFIMILTEHLVRCETDGTSVLTPW
YKNCIERLQQIFLQHHQIIQQYMVTLENLLFTAELDPHILAVFQQFCALQA

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

PLALLDSSLEGEFDLVQRIIYEVDPSLPNDEGITALHNAVCAGHTEIVKFLVQFGVNVNA
ADSDGWTPLHCAASCNNVQVCKFLVESGAAVFAMTYSDMQTAADKCEEMEEGYTQCSQ
FLYGVQEKMG

>d1awcb_ a.118.2.1 (B:) GA binding protein (GABP) beta 1 {Mouse (Mus musculus)}

DLGKKLLEAARAGQDDEVRLMANGAPFTTDWLGTSPHLAAQYGHFSTTEVLLRAGVS
RDARTKVDRTPLHMAASEGHANIVEVLLKHGADVNAKDMLKMTALHWATEHNNHQEVV
ELLIKYGADVHTQSKFCKTAFDISIDNGNEDLAEILQ

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

VCVGDRLSGAAARGDVQEVRRLLHRELVHPDALNRFGKTALQVMMFGSPAVALLELLKQ
GASPNVQDASGTSPVHDAARTGFLDTLKVLEHADVNAALDSTGSLPIHLAIREGHSSVV
SFLAPESDLHHRDASGLTPELARQRGAQNLMDILQGHMMIP

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

DGDSFLHLAIIHEEKALTMEVIRQVKGDLAFLNFQNNLQQTPLHLAVITNQPEIAEALLGA
GCDPELRDFRGNTPLHLACEQGCLASVGVLTQSCTTPHLHSILKATNYNGHTCLHLASIHG
YLGIVELLVSLGADVNAQEPNGRTALHLAVDLQNPDLVSLLLKCGADVNRVITYQGYSPY
QLTWGRPSTRIQQQLGQLTLENLQMLPESEDEESYDTES

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

EDGDTPLHIAVVQGNLPAVHRLVNLFFQQGGRELDIYNNLRQTPLHLAVITTLPSVVRLVT
AGASPMALDRHGQTAAHLACEHRSPTCLRALDSPAAGTLDLEARNYDGLTALHVAVNT
ECQETVQLLLERGADIDAVDIKSGRSPLIHAVENNSLSMVQLLLQHGANVNAQMYSGSSA
LHSASGRGLLPLVRTLVRSADSSLNCHNDTPLMVARSRVIDILRG

>d1myo_ a.118.2.1 (-) Myotrophin {Rat (Rattus norvegicus)}

MCDKEFMWALKNGDLDEVKDYVAKGEDVNRTLEGGRKPLHYAADCGQLEILEFLLLKG
ADINAPDKHHITPLLSAVYEGHVSCVKLLLSKGADKTVKGPDGLTALEATDNQAIKALLQ

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

GPIITFTHDLTSDLSSPLKIMKALPSPVNDNEQKMKLEAFLQRLLFPEIQEMPTSLNND
SNRNSEGGSSNQQQHVSFDSLLQEVNDAFPNTQLNLNIPVDEHGNTPLHWLTSIANLEL
VKHLVKHGSNRLYGDNMGESCLVKAVKSVNNYDSGTFEALLDYLYPCLILED SMNRILH
HIIITSGMTGCSAAAKYYLDILMGWIVKKQNRPIQSGTNEKESKPNDKNGERKDSILENLD
LKWIIANMLNAQDSNGDTCLNIAARLGNISIVDALLDYGADPFIANKSGLRPVDFGAG

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

ADTAAKLHSLCEAVKTRDIFGLLQAYADGVDLTEKIPLANGHEPDETALHLAVRSVDRTSL
HIVDFLVQNSGNLDKQTGKGSTALHYCCLTDNAECLKLLLRGKASIEIANESGETPLDIAK
RLKHEHCEELLTQALSGRFNHSHVHVEYEWRL

>d1d8da_ a.118.6.1 (A:) Protein farnesyltransferase alpha-subunit {Rat (Rattus norvegicus)}

FLSLDSPTYVLYRDRAEWADIDPVPQNDGSPVQIIYSEKFRDVYDYFRAVLQRDERSER
AFKLTRDAIELNAANYTVWHFRRVLLRSLQKDLQEEMNYIIAIIIEQPKNYQVWHHRRVL
VEWLKDPSQELEFIADILNQDAKNYHAWQHRQWVIQEFRLWDNELQYVDQLLKEDVRN
NSVWNQRHFVISNTTGYSRAVLEREVQYTLEMIKLVPHNESAWNYLKGILQDRGLSRYP
NLLNQLLDLQPSHSPYLIAFLVDIYEDMLENQCDNKEDILNKALELCEILAKEKDTIRKEY
WRYIGRSLQSKHSRES DIPASV

>d1dcea1 a.118.6.1 (A:1-240,A:351-443) Rab geranylgeranyltransferase alpha-subunit, N-terminal domain {Rat (Rattus norvegicus)}

MHGRCLKVKTSEEQAEAKRLEREQKLKLYQSATQAVFQKRQAGELDES VLELTSQILGANP
DFATLWNCRREVLQHLETEKSPEESAALVKAELGFLESCLRVNPKSYGTWHHRCWLLSRL
PEPNWARELELCARFLEADERNFHCWDYRRFVAAQAAPAEELAFDSDLITRNFNSYSS
WHYRSCLLPQLHPQPDSPQGRLPENVLLKELELVQNAFFTDPNQSAWIFYHRWLLGRA
EXLFRCELSVEKSTVLQSELESCKELQELEPENKWCLLTIILLMRALDPLLYEKETLQYFST
LKAVDPMRAAYLDDLRSKFLENSVLKMEYADV

>d1a17_ a.118.8.1 (-) Protein phosphatase 5 {Human (Homo sapiens)}

PPADGALKRAEELKTQANDYFKAKDYENAIKFYSQAIELNPSNAIYYGNRSLAYLRTECY
GYALGDATRAIELDKKYIKGYRRASNMALGKFRAALRDYETVVVKVPHDKDAKMK
YQECNKIVKQKAFERAIAGDEHKRSVVDSDIESMTIEDEYS

>d1elra_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}

GKQALKEKELGNDAYKKKDFDTALKHYDKAKELDPTNMTYITNQAAYFEKGDYNKCR
ELCEKAIEVGRENREDYRQIAKAYARIGNSYFKEEKYKDAIHFYNKSLAEHRTPDVLKKC
QQAELKEQ

>d1elwa_ a.118.8.1 (A:) Hop {Human (Homo sapiens)}

EQVNELKEKGNKALSVGNIDDALQCYSEAIKLDPHNHVLYSNRSAAYAKKGDYQKAYED
GCKTVDLKPDWKGKYSRKAAALEFLNRFEAKRTYEEGLKHEANNPQLKEGLQNMPEAR

>d1qgea_ a.118.8.1 (A:) Vesicular transport protein sec17 {Baker's yeast (Saccharomyces cerevisiae)}

ISDPVELLKRAEKKGVPSSGFMKLFSGSDSYKFEEAADLCVQAATYRLRKELNLAGDSFL
KAADYQKKAGNEDEAGNTYVEAYKCFKSGGNSVNAVDSLENAIQIFTHRGQFRRGANFK
FELGEILENDLHDYAKAIDCYELAGEWYAQDQSVALSNKCFIKCADLKALDGGYIEASDIY
SKLIKSSMGNRLSQWSLKDYFLKKGLCQLAATDAVAAARTLQEGQSEDPNFADSRESNFL
KSLIDAVNEGDSEQLSEHCKEFDNFMRLDKWKITILNKIKESIQQQEDD

>d1hh8a_ a.118.8.1 (A:) Neutrophil cytosolic factor 2 (NCF-2, p67-phox) {Human (Homo sapiens)}

SLVEAISLWNEGVLAAADKKDWKGALDAFSVQDPHSRICFNIGCMYTILKNMTEAEKAFT
RSINRDKHLAVAYFQRGMLYYQTEKYDLAIKDLKEALIQLRGNQLIDYKILGLQFKLFACE
VLYNIAFMYAKKEEWKKAEEQLALATSMKSEPRHSHKIDKAMECVWKQKLYEPVVIPVGR
LFRPNERQVAQL

>d1fcha_ a.118.8.1 (A:) Peroxin pex5 (peroxisomal targeting signal 1 (PTS1) receptor) {Human (Homo sapiens)}

SATYDKGYQFEEENPLRDHPQPFEEGLRRLQEGDLPNAVLLFEAAVQQDPKHMEAWQYL
GTTQAENEQELLAISALRRCLKPDNQTALMALAVSFTNESLQRQACEILRDWLRYTPAY
AHLVTPAEEGAGGAGLGP SKRILGSLSDSLFLEV KELFLAAVRLDPTSIDPDVQCGLGVLF
NLSGEYDKAVDCFTAALSVRPNDYLLWNKLGATLANGNQSEEAVAAYRRALELQPGYIRS
RYNLGISCINLGAHREAVEHFLEALNMQRKSRGPRGEGGAMSENIWSTLRLALSMLGQSD
AYGAADARDLSTLLTMFGLPQ

>d1ihga1 a.118.8.1 (A:197-365) Cyclophilin 40 {Cow (Bos taurus)}

GSGDSHPDFPEDADVDLKDVDKILLISED LKNIGNTFFKSQNWEMAIKKYTKVLRVVEGS
RAAAEDADGAKLQPVALSCVLNIGACKLKMSDWQGAVDSCLEALEIDPSNTKALYRRAQ
GWQGLKEYDQALADLKKAEIAPEDKAIQAELLKVQKIKAKQDKKEKAAAY

>d1dvpa1 a.118.9.2 (A:1-145) Hrs {Fruit fly (Drosophila melanogaster)}

MFRSSFCKNLNATSHLRLEPDWPSILLICDEINQKDVTPKNAFAAIKKKMNSPNPHSSCYS
LLVLESIVKNCGAPVHEEVFTKENCMEFSSFLESTPHENVRQKMLELVQTWAYAFRSSDK
YQAIKDTMTILKAKGHTFPELRE

>d1elka_ a.118.9.2 (A:) Tom1 protein {Human (Homo sapiens)}

SDFLLGNPFSSPVGQRIEKATDGSLQSEDWALNMEICDIINETEEGPKDALRAVKKRIVGNK
NFHEVMLALTVLET CVKNCGHRFHV LVASQDFVESVLVR TILPKNNPPTIVHDKVLNLIQS
WADAFRSSPDLTG VVTIYEDLRRKGLEFPM

>d1juqa_ a.118.9.2 (A:) Gga3 {Human (Homo sapiens)}

ESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG PQIAVRLLAHKIQSPQEWEALQALT
VLEACMKNCGRFRFHNEVGKFRFLNELIKVVSPKYL GDRVSEKVKTKVIELLYSWTMALP
EEAKIKDAYHMLKRQGIVQSDPPIPVDR TLI

>d2tct_2 a.121.1.1 (68-208) Tetracyclin repressor (Tet-repressor, TetR) {Escherichia coli}

LPAAGESWQSFLRNAMSFRALLRYRDGAKVHLGTRPDEKQYD TVETQLRFMTENGFS
LRDGLYAISAVSHFTLGAVLEQQEHTAALTDRPAAPDENLPPLLREALQIMDSDDGEQAF L
HGLES LIRGFEVQLTALLQIV

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

KTNREKFYLYNELSLTTEYYYPLQNAIIEFYTEYYKTNSINEKMNKLENKYIDAYHVIFKE
GNLNGEWSINDVNAVSKIAANAVNGIVTFTHEQNINERIKLMNKFSQIFLNGLS

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

VSWDSL PDELLLGIF SCLCLPELLKVSGVCKRWYRLASD

>d1fqvb1 a.122.1.1 (B:85-160) Skp1-Skp2 dimerisation domains {Human (Homo sapiens)}

IPVWDQEFLKVDQGT LFELILAANYLDIKGLLDVTCKTVANMIKGKTP EEIRKTFNIK NDF
TEEEEAQVRKENQWC

>d1g5ya_ a.123.1.1 (A:) Retinoid-X receptor (RXR-alpha) {Human (Homo sapiens)}

PVERILEAE LAVEPKTETYVEANMGLNPSSPNDPVTNICQAADKQLFTLVEWAKRIPHSE
LPLDDQVILLRAGWNELLIASFSHRSAVKDGILLATGLHVHRNSAHSAGVGAIFDRVLTEL
VSKMRDMQMDKTELGCLRAIVLFNPDSKGLSNPAEVEALREKVYASLEAYCKHKYPEQP
GRFAKLLLRLPALRSIGLKCLEHLFFFKLIGDTPIDTFLMEMLEAP

>d1fcya_ a.123.1.1 (A:) Retinoic acid receptor gamma (RAR-gamma) {Human (Homo sapiens)}

ASPQLEELITKVSKAHQETFP SLCQLGKYTTNSSADHRVQLDLGLWDKFSELATKCIKIVE
FAKRLPGFTGLSIADQITLLKAACLDILMLRICTRYTPEQDTMTFSDGLTLNRTQMHNAGF
GPLTDLVFAFAGQLLPLEMDDTETGLLSAICLICGDRMDLEEPEKVDKLQEPLLEALRLYA

RRRRPSQPYMFPRMLMKITDLRGISTKGAERAITLKMEIPGMPPLIREMLE

>d1a28a_ a.123.1.1 (A:) Progesterone receptor {Human (Homo sapiens)}

QLIPPLINLLMSIEPDVIYAGHDNTKPDTSSTSLNQLGERQLLSVVKWSKSLPGFRNLHI
DDQITLIQYSWMSLMVFGLGWSYKHVSGQMLYFAPDLILNEQRMKESFYSLCLTMWQ
IPQEFVKLQVSQEEFLCMKVLLLLNTIPLEGLRSQTQFEEMRSSYIRELIKAIGLRQKGVVS
SSQRFYQLTKLLDNLHDLVKQLHLYCLNTFIQSRALSVEFPPEMMSEVIAAQLPKILAGMVK
PLLFHK

>d3erda_ a.123.1.1 (A:) Estrogen receptor alpha {Human (Homo sapiens)}

SLALSITADQMVSAALLDAEPPILYSEYDPTRPFSEASMMGLLTNLADRELHMINWAKRVP
GFVDLTLDQVHLLCAWLEILMIGLVWRSMEHPGKLLFAPNLLDRNQGKCVEGMVEIF
DMLLATSSRFRMMNLQGEFVCLKSIILLNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLI
HLMAGAGLTQQQHQLAQLLLILSHIRHMSNKGMEHLYSMKCKNVVPLYDLLEMLD
AHLRH

>d2prga_ a.123.1.1 (A:) Peroxisome proliferator activated receptor gamma, PPAR-gamma {Human (Homo sapiens)}

ESADLRALAKHLYDSYIKSFPLTKAKARAILTGKTTDKSPFVIYDMNSLMMGEDKIKFKHI
TPLQEQSKEVAIRIFQGCQFRSVEAVQEITEYAKSIPGFVNLDLNDQVTLLKYGVHEIITYM
LASLMNKDGVLISEGQGFMTRFLKSLRKPFGDFMEPKFEFAVKFNALELDDSDLAIFI
ILSGDRPGLLNPKPIEDIQDNLLQALELQLKLNHPESQLFAKLLQKMTDLRQIVTEHVQL
LQVIKKTETDMSLHPLLQEIKDLY

>d1ilga_ a.123.1.1 (A:) Pregnane x receptor, PXR {Human (Homo sapiens)}

GLTEEQRMMIRELMDAQMKTFDTSFHFKNFRLPGVLSSGCELPESLQAPSREEAAKWSQ
VRKDLCSLKVSLQLRGEDGSVWNYKPPADSGGKEIFSLPHMADMSTYMFKGIIISFAKVI
SYFRDLPIEDQISLLKGAAFELCQLRFNTVFNAETGTWECGRLSYCLEDTAGGFQQLLEP
MLKFHYMLKKLQLHEEEYVLMQAISLFSPDRPGVLQHRVVDQLQEQFAITLKSIECNRP
QPAHRFLFLKIMAMTELRSINAQHTQRLRLRIQDIHPFATPLMQELFGI

>d1ie9a_ a.123.1.1 (A:) Vitamin D nuclear receptor {Human (Homo sapiens)}

DSLRLPKLSEEQQRIIAILLDAHHKTYDPTYSDFCQFRPPVRVNDGGGSVTLELSQLSMLPH
LADLVSYSIQKVIGFAKMIPGFRDLTSEDQIVLLKSSAIEVIMLRSNESFTMDDMSWTCGN
QDYKYRVSDVTKAGHSLELIEPLIKFQVGLKKLNLHEEEHVLLMAICIVSPDRPGVQDAA
LIEAIQDRLSNTLQTYIRCRHPPPGSHLLYAKMIQKLADLRSLNEEHSKQYRCLSFQPECSM
KLTPLVLEVFG

>d1bsxa_ a.123.1.1 (A:) Thyroid hormone receptor beta (TR-beta) {Human (Homo sapiens)}

KPEPTDEEWELIKTVTEAHVATNAQGSWKQKRKFLPEDIGQAPIVNAPEGGKVDLEAFS
HFTKIITPAITRVVDFAKKLPMFCELPCEDQIILLKGCCMEIMSLRAAVRYDPESETLTLNGE
MAVTRGQLKNGGLGVVSDAIFDLGMSLSSFNLDDETEVALLQAVLLMSSDRPGLACVERIE
KYQDSFLLAFEHYINYRKHHVTHFWPKLLMKVTDLRMIGACHASRFLHMKVECPTELP
PLFLEVFE

>d1hg4a_ a.123.1.1 (A:) Ultraspiracle protein, usp {Drosophila melanogaster}

FSIERIIEAEQRAETQCGDRALTFLRVGPYSTVQPDYKGAVSALCQVVNKQLFQMVEYAR
MMPHFAQVPLDDQVILLKAAWIELLIANVAWCSIVSLDDGGAGGGGGGLGHDGSFERRSP
GLQPQQLFLNQSFYHRNSAIKAGVSAIFDRILSELSVKMKRLNLDRELSCLKAILYNPD
IRGIKSRAEIEMCREKVYACLDEHCRLEHPGDDGRFAQLLLRLPALRSISLKCQDHLFLFRI
TSDRPLEELFLEQLEAPPPG

>d1ah7__ a.124.1.1 (-) Bacterial phospholipase C {Bacillus cereus}

WSAEDKHKEGVNSHLWIVNRAIDIMSRNTTLVKQDRVAQLNEWRTLENGIYAADYENP
YYDNSTFASHFYDPDNGKTYIPFAKQAKETGAKYFKLAGESYKNKDMKQAFFYLGLSLH
YLGDVNQPMHAANFTNLSYPQGFHISKYENFVDTIKDNKYKVTGNGYWNWKGTPPEEW
IHGAAVVAKQDYSIVNDNTKDWVFKAAVSQEYADKWRAEVTTPMTGKRLMDAQRVTA
GYIQLWFDTYGDR

>d1cal_1 a.124.1.1 (1-249) Alpha-toxin, N-terminal domain {Clostridium perfringens}

WDGKIDGTGTHAMIVTQGVSIENDLSKNEPESVRKNLEILKENMHQLGSTYPDYDKN
AYDLYQDHFWDPTDNNFSKDNSWYLAYSIPDTGESQIRKFSALARYEWQGRNYKQATF
YLGEAMHYFGDIDTPYHPANVTAVDSAGHVKFETFAEERKEQYKINTVGCKTNEDFYADI
LKNKDFNAWSKEYARGFAKTGKSIYYSHASMSHSWDDWDYAAKVTLANSSQKGTAGYIY
RFLHDVSEGNPD

>d1gnia1 a.126.1.1 (A:3-196) Serum albumin {Human (Homo sapiens)}

HKSEVAHRFKDLGEENFKALVLIAFAQYLQQCPFEDHVKLVNEVTEFAKTCVADESAENC
DKSLHTLFGDKLCTVATLRETYGEMADCCAKQEPERNECFLQHKDDNPNLRLVRPEVD
VMCTAFHDNEETFLKKYLYEIARRHPYFYAPELLFFAKRYKAAFTECCQAADKAACLLPK
LDELREDEGKASSAKQ

>d1gnia2 a.126.1.1 (A:197-388) Serum albumin {Human (Homo sapiens)}

RLKCASLQKFGERAFAKAWAVARLSQRFPKAEFAEVSKLVTDLTQVHTECCHGDLLECADD
RADLAKYICENQDSISSKLKECCEKPLLEKSHCIAEVENDEMPADLPSLAADFVESKDVCK
NYAEAKDVFLGMFLYEYARRHPDYSVVLRLAKTYETTLEKCCAAADPHECYAKVFDE
FKPLVEEPQNL

>d1gnia3 a.126.1.1 (A:389-584) Serum albumin {Human (Homo sapiens)}

KQNCSELFELGEYKFQNALLVRYTKKVPQVSTPTLVEVSRNLGKVGSKCKHPEAKRMP
CAEDYLSVVLNQLCVLHEKTPVSDRVTKCTESLVNRRPCFSALEVDETYVPKEFNAETF
TFHADICTLSEKERQIKQTALVELVKHKPKATKEQLKAVMDDFAAFVEKCKADDKETC
FAEEGKKLVAAASQAALG

>d1j78a1 a.126.1.1 (A:13-198) Vitamin D binding protein {Human (Homo sapiens)}

CKEFSLHGKEDFTSLSLVLYSRKFPSPGTFEQVSQLVKEVVSLEACCAEGADPDCYDTRTS
ALSAKSCESNSPFPVHPGTAECCTKEGLERKLCMAALKHQPFQTYVEPTNDEICEAFRK
DPKEYANQFMWEYSTNYGQAPLSLLVSYTKSYLSMVGSCCTSASPTVCFLKERLQLKHL
LLTT

>d1j78a2 a.126.1.1 (A:199-386) Vitamin D binding protein {Human (Homo sapiens)}

LSNRVCSQYAAYGEKKSRLSNLIKLAQKVPTADLEDVLPLAEDITNLSKCCESASEDCMA
KELPEHTVKLCDNLSTKNSKFEDCCQEKAMDFVCTYFMPAAQLPELPDVELPTNKDV
CDPGNTKVMKYTFELSRRLHLEPVFLSKVLEPTLKSLECCDVEDSTTCFNAKGPLLKK
ELSSFIDK

>d1j78a3 a.126.1.1 (A:387-457) Vitamin D binding protein {Human (Homo sapiens)}

GQELCADYSENTFTEYKKKLAERLKAKLPDAPTELAKLVNKRSDFASNCCSINSPLYCD
SEIDAELKNI

>d1jswa_ a.127.1.1 (A:) L-aspartate ammonia lyase {Escherichia coli}

MSNNIRIEEDLLGTREVPADAYYGVHTLRAIENFYISNNKISDIPEFVRGMVMVKKAAAM
ANKELQTIPKSVANAIACDEVLLNNGKCMDQFPVDVYQGGAGTSVNMNTNEVLANIGL

ELMGHQKGEYQYLNPNDHVNKCQSTNDAYPTGFRIAVYSSLIKLVDAINQLREGFERKAV
EFQDILKMGRITQLQDAVPMTLGQEFRAFSILLKEEVKNIQRTAELLLEVNLGATAIGTGLN
TPKEYSPLAVKKLA EVTGFPCVPAEDLIEATSDCGAYVMVHGALKRLAVKMSKICNDLRL
LSSGPRAGLNEINLPELQAGSSIMPAKVNPPVPEVVNQVCFKVIGNDTTVMMAAEAGQLQ
LNVMEPVIGQAMFESVHILTNACYNLLEKCCINGITANKEVCEGYVYNSIGIVTYLNPFIGH
HNGDIVGKICAETGKSVREVVLERGLLTEAELDDIFSV

>d1yfm_ a.127.1.1 (-) Fumarase {Baker's yeast (*Saccharomyces cerevisiae*)}
SFRTEIDAFGEIHVPADKYWGAQTQRSFQNFKIGGARERMPLPLVHAFGVLKKSAAIVNE
SLGGLDPKISKAIQQADEVASGKLDDHFPLVVFQTGSGTQSNMNANEVISNRAIEILGGK
IGSKQVHPNNHCNQSSSNDTFPTVMHIAASLQIQNELIPELTNLKNALEAKSKEFDHIVKI
GRTHLQDATPLTLGQEFSGYVQQVENGIQ RVAHSLKTL SFLAQGGTAVGTGLNTKPGFDV
KIAEQISKETGLKFQTAPNRFEALAAHDAIVECSGALNTLACSLFKIAQDIRYLGSGPRCGY
HEMLPENEPGSSIMPGKVNPTQNEALTQVCVQVMGNNAITFAGSQGFELNVFKPVM
ANLLNSIRLITDAAYSFRVHCVEGIKANEPRIHELLTKSLMLVTALNPKIGYDAASKVAKNA
HKKGITLKESALELGVLTEKEFDEWVPEHML

>d1i0aa_ a.127.1.1 (A:) Argininosuccinate lyase/delta-crystallin {Turkey (*Meleagris gallopavo*),
delta-crystallin}

GRFVGSVDPIEILSSSISTEQRLTEVDIQASMAYAKALEKASILTKTELEKILSGLEKISEES
SKGVLVMTQSDEDIQTAIERRLKELIGDIAGKLQTGRSRNEQVVTDLKLLLKSSISVISTHL
LQLIKTLVERAAIEIDIIMPGYTHLQKALPIRWSQFLLSHAVALTRDSERLGEVKKRITVLPL
GSGVLAGNPLEIDRELLRSELDMTSITLNSIDAISERDFVVELISVATLLMIHLSKLAEDLIIF
STTEFGFVTLSDAYSTGSSLLPQKKNPDSLELIRSKAGRVFGRLAAILMVLKGIPSTFSKDL
QEDKEAVLDVVDTLTAVLQVATGVISTLQINKENMEKALTPELLSTDALYLVKGMPIRQ
AQTAGSKAVHLAETKGITINLTLEDLKSISPLFASDVSQVFSVVNSVEQYTAVGGTAKSSV
TAQIEQLRELLKKQK

>d1c3ca_ a.127.1.1 (A:) Adenylosuccinate lyase {*Thermotoga maritima*}

VERYSLSMPKDLWTEEAKEYRRWLEVELAVTRAYEELGMIPKGVTERIRNNAKIDVELFKK
IEEKTNHDVVA FVEGIGSMIGEDSRFFHYGLTSSDVLDTANSLALVEAGKILLESKEFCDV
LWEVANRYKHTPTIGRTHGVHAEPTSFGLKVLGWYSEMKNRVQRLERAIEEVSYGKISGA
VGNVANVPPEVEEKALSYLGLKPEPVSTQVVPDRRHAFYLSLTAIVAAGIERIAVEIRHLQR
TEVLEVEEPFRKGQRGSSAMPHKKNPITCERLTGLSRMMRAYVDPSLENIALWHERDISHS
SVERYVFPDATQTLYYMIVTATNVVRNMKVNEERMKKNIDLTGGLVFSQRVLLKLIKGL
TRKEAYDIVQRNALKTWNSEKHFLEYLLEDEEVKKLVTKEELEELFDISYYLKHVDHIFER
FEK

>d1dofa_ a.127.1.1 (A:) Adenylosuccinate lyase {*Archaeon Pyrobaculum aerophilum*}

HVSPFDWRYGSEEIRRLFTNEAIINAYLEVERALVCALEELGVAERGCCEKVNKASVSADE
VYRLERETGHDILSLVLLLEQKSGCRYVHYGATSNDIIDTAWALLIRRALAAVKEKARAVG
DQLASMARKYKTLEMVGRTHGQWAEPITLGFKFANYYYELYIACRQLALAEFIRAKIGG
AVGTMASWGELGLEVRRRVAERLGLPHHVITTQVAPRESFAVLASALALMAAVFERLAVEI
RELSRPEIGEVEGGGGSSAMPHKANPTASERIVSLARYVRALTHVAFENVALWHERDLTN
SANERVWIPEALLALDEILTSALRVLKNVYIDEERITENLQKALPYILTEFHMNRMIKEGAS
RAEAYKKAKEVKALTFEYQKWPVERLIEDALSLKLC

>d1dila_ a.128.1.4 (A:) Aristolochene synthase {Fungus (*Penicillium roqueforti*)}

TPPPTQWSYLCHPRVKEVQDEVDGYFLENWKFPSPKAVRTFLDAKFSEVTCLYFPLALDD

RIHFACRLTLVFLIDDVLEHMSFADGEAYNNRLIPISRGDVLDPDRTPKEEFILYDLWESMR
AHDAELANEVLEPTFVFMRAQTDRLRSIHELGHYLEYREKDVGKALLSALMRFSMGLR
LSADELQDMKALEANCAKQLSVVNDIYSYDKEEEASRTGHKEGAFLCSAVKVLAEE SKL
GIPATKRVLWSMTREWETVHDEIVAEEKIASPDGCSEAAKAYMKGLE YQMSGNEQWSKTT
R

>d1ps1a_ a.128.1.4 (A:) Pentalenene synthase {*Streptomyces* sp., UC5319}

QDVDFHIPLPGRQSPDHARAEAEQLAWPRSLGLIRSDAAAERHLRGGYADLASRFYPHAT
GADLDLGVLDMSWFFLFDLFDGPRGENPEDTKQLTDQVAAALDGPLPDTAPPIAHGFAD
IWRRTCEGMTPAWCARSARHWRNYFDGYVDEAESRFWNAPCDSAAQYLAMRRHTIGVQ
PTVDLAERAGRFEVPHRVFDSAVMSAMLQIAVDVNLLNDIASLEKEEARGEQNNMVMIL
RREHGWSKSRSVSHMQNEVRARLEQYLLLESCLPKVGEIYQLDTAEREALERYRTDAVRT
VIRGSYDWHRSSG

>d1psj_ a.133.1.2 (-) Snake phospholipase A2 {Chinese water moccasin (*Agkistrodon halys pallas*), different isoforms}

SLIQFETLIMKVAKKSGMFWYSNYGCYCGWGGQGRPQDATDRCCFVHDCCYGKVTGCD
PKMDVYSFSEENGDIVCGGDDPCKKEICECDRAAAICFRDNLTYNDKKYWAFGAKNCP
QEESEPC

>d1hn4a_ a.133.1.2 (A:) Phospholipase A2 {Pig (*Sus scrofa*), pancreas}

GISSRALWQFRSMIKCAIPGSHPLMDFNNYGCYCGLGSGTPVDELDRCCETHDNCYRDA
KNLDSCKFLVDNPYTESYSYSCSNTEITCNSKNNACEAFICNCDRNAAICFSKAPYNKEHK
NLDTKKYC

>d1kbhb_ a.153.1.1 (B:) Nuclear receptor coactivator CBP/p300 ibid domain {Mouse (*Mus musculus*)}

PNRSISPSALQDLLRTLKSPSSPQQQQVNLILKSNPQLMAAFIKQRTAKYVANQPQGMQ

>d1kbha_ a.153.1.1 (A:) Nuclear receptor coactivator ACTR {Human (*Homo sapiens*)}

EGQSDERALDQLHTLLSNTDATGLEEIDRALGIPELVNQGALEPK

>d1gg2g_ a.137.3.1 (G:) Transducin (heterotrimeric G protein), gamma chain {Cow (*Bos taurus*)}

SIAQARKLVEQLKMEANIDRIKVSAAAADLMAYCEAHAKEDPLLTPVPASENPF

>d1tbge_ a.137.3.1 (E:) Transducin (heterotrimeric G protein), gamma chain {Cow (*Bos taurus*)}

APVINIEDLTEKDKLKMEVDQLKKEVTLERMLVSKCCEEFRDYVEERSGEDPLVKGIPED
KNPFKELK

>d1aqe_ a.138.1.1 (-) Cytochrome c3 {*Desulfovibrio desulfuricans*, different strains}

TFEIPESVTMSPKQFEGYTPKKGDVTFNHASHMDIACQQCHHTVPDITYTIESCMTEGCHD
NIKERTEISSVERTFHTTKDSEKSCVGCHRELKRQGSPDAPLACNSCHVQ

>d2cy3_ a.138.1.1 (-) Cytochrome c3 {*Desulfovibrio desulfuricans*, different strains}

ADAPGDDYVISAPEGMKAKPKGDKPGALQKTVPFPHTKHATVECVQCHHTLEADGGAV
KKCTTSKGCHDSLEFRDKANAKDIKLVENAFHTQCIDCHKALKKKDKKPTGPTACGKCHTT
N

>d1wad_ a.138.1.1 (-) Cytochrome c3 {*Desulfovibrio gigas*}

VDVPADGAKIDFIAGGEKNLTVVFNHSTHKDVKCDDCHHDPGDKQYAGCTTDGCHNILD
KADKSVNSWYKVVDHAKGGAKPTCISCHKDKAGDDKELKKKLTGCKGSACHP

>d3caoa_ a.138.1.1 (A:) Cytochrome c3 {*Desulfovibrio africanus*}

EDMTHVPTDAFGKLERPAAVFNHDEHNEKAGIESCNACHHVWVNGVLAEEDEDSVGTPCS
DCHALEQDGDTPGLQDAYHQQCWGCHEKQAKGPVMCGECHVKN

>d1hh5a_ a.138.1.1 (A:) Cytochrome c7 (cytochrome c551.5) {Desulfuromonas acetoxidans}

ADVVTYENKKGNVTFDHKAHAIEKLGCDACHEGTPAKIAIDKKS AHKDACKTCHKSNG
PTKCGGCHIK

>d19hca_ a.138.1.1 (A:) Nine-haem cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

AALEPTDSGAPSAIVMFPVGEKPNPKGAAMKPVVFNHLEKKIADCETCHHTGDPVSCS
TCHTVEGKAEGDYITLDRAMHATDIAARAKGNTPTSCV SCHQSETKERRECAGCHAITTP
KDDEAWCATCHDITPSMTPSEM QKGIAGTLLPGDNEALAAETVLAEATVAPVSPMLAPYK
VVIDALADKYEPSDFTHRRHLTSLMESIKDDKLAQAFHDKPEILCATCHHRSPLSLTPPKC
GSCHTKEIDAADPGRPNLMAAYHLECMGCHKGMAVARPRD TDCTTCHKAAA

>d1fgja_ a.138.1.3 (A:) Hydroxylamine oxidoreductase, HAO {Nitrosomonas europaea}

DISTVPDETYDALKLDRGKATPKETYEALVKRYK DPAHGAGKGTMGDYWEPIAISIYMDP
NTFYKPPVSPKEVAERKDCVECHSDETPVWVRAWKRSTHANLDKIRNLKSDDPLYYYKKG
KLEEVENNL RSMGKLGEKETLKEVG CIDCHVDVNKKDKADHTKDIRMPTADTCGTCHL
REFAERESERDTMVWPNGQWPAGRPSHALDYTANIETT VWATMPQREVAEGCTMCHTN
QNKCDNCHTRHEFSAAESRKPEACATCHSGVDHNNWEAYTMSKHGKLAEMNRDKWN
WEVRLKDAFSKGGQNAPTCAACHMEYEGEYTHNITRKTRWANYPFVPGIAENITSDWSE
ARLDSWVL TCTQCHSERFARSYLDLMDKGTLEGLAKYQEANAIVHKMYEDGTLTGQKT
NRPNPPEPEKPGFGIFTQLFWSKGNNPASLELKVLEMGENNLAKMHVGLAHVNP GGWTY
TEGWGPMNRAYVEIQDEYTKMQELSALQARVN

>d1ft5a_ a.138.1.3 (A:) Cytochrome c554 {Nitrosomonas europaea}

ADAPFEGRKKCSSCHKAQAQSWKDTAHAKAMESL KPNVKKEAKQKAKLDPKDYTQD
KDCVGCHVDGFGQKGGYTIESPKPMLTG VGCE SCHGPGRNFRGDHRKSGQAF EKSGKKT
PRKDLAKKGQDFHFEERCSACHLNYEGSPWKGAKAPYTPFTPEVDAKYTFKFDEMVKE
VKAMHEHYKLEGVFEGEPKFKFHDEFQASAKPAKKGK

>d1ddca_ a.138.1.3 (A:) Dimeric di-heme split-soret cytochrome c {Desulfovibrio desulfuricans, ATCC 27774}

RFDQVGGAFGWKPHKLDPK ECAQVAYDGYWYKGF GCGFGAFYSIVGLMGEKYGAPYN
QFPFAMLEANKGGISDWGTIYGALYGAAATFSLFWGRKEVHPMVNELFRWYEVTKLPIFN
PGDAAQGVKGDLPMSASDSVLCHISVSKWCYENKIEATSKQRSERAGRLTADAAFKAAEI
INTKIDQGKDFKSTFPMQASVSSCGECHMTKGNDANWAKGIMDCTPCHSGTAATQNK FV
NH

>d1qdba_ a.138.1.3 (A:) Cytochrome c nitrite reductase {Sulfurospirillum deleyianum}

GIAGKEKSEEWAKYYPRQFDSWKKTK EYDSFTDMLAKDPALVIAWSGYAFSKDYNSPRG
HYALQDNVNSLRTGAPVDAKTGPLPTACWTCKSPDVPR LIEEDGELEYFTGKWAKYGS
QIVNVIGCANCHDDKTAELKVRVPHLNRGLQAAGLKT FEESTHQDKRTLVC AQCHVEYY
FKKTEWKDAKGADKTAMVVTLPWANGVGKDGNAGVEGMIKYYDEINFSDWTHNISKTP
MLKAQHPGFEFWKSGIHGQKGVSCADCHMPYTQEGSVKYS DHQVKENPLDSMDQSCM
NCHRESESKLRGIVHQKYERKEFLNKVAFDNIGKAHLETGKAIEAGASDEELKEVRKLIRH
GQFKADMAIAAHGNYFHAEETLRLLAAGSDDAQKARLLL VKILAKHGVMDYIAPDFDT
KDKAQKLAKVDIAALAAEKMFKQTLEQEWKKEAKAKGRANPELYKD VDTINDGKSS

WNKK

>d1e39a1 a.138.1.3 (A:1-102) Flavocytochrome c3 (respiratory fumarate reductase), N-terminal domain {Shewanella frigidimarina}

ADNLAEFHVQNQECDSCHTPDGELSNDSTLYENTQCVSCHGTLAEVAETTKHEHYNAHA
SHFPGEVACTSCHSAHEKSMVYCDSCSFDFNMPYAKKWLRDE

>d1neu__ b.1.1.1 (-) Myelin membrane adhesion molecule P0 {Rat (Rattus norvegicus)}

IVVYTDREVGAVGSQVTLHCSFWSSEWVSDDISFTWRYQPEGGRDAISIFHYAKGQPYID
EVGTFKERIQWVGDPSPWKDGSIVIHNLDSYDNGTFTCDVKNPPDIVGKTSQVTLYVFE

>d1eaja_ b.1.1.1 (A:) Coxsackie virus and adenovirus receptor (Car), domain 1 {Human (Homo sapiens)}

FARSLSITTPEEMIEKAKGETAYLPCKFTLSPEDQGPLDIEWLISPADNQKVDQVILYSGDK
IYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKKAPGVANKKIHLVVL
V

>d1qfoa_ b.1.1.1 (A:) N-terminal domain of sialoadhesin {Mouse (Mus musculus)}

TWGVSSPKNVQGLSGSCLLIPCIFYPADVPVSNGITAIWYYDYSGKRQVVIHSGDPKLVD
KRFRGRAELMGNMDHKVCNLLLKDLKPEDSGTYNFRFEISDSNRWLDVKGTTVTVTT

>d1bqhg_ b.1.1.1 (G:) CD8 {Mouse (Mus musculus)}

KPQAPELRIFPKKMDAELGQKVDLVCEVLGSVSQGCSWLFQNSSSKLPQPTFVVYMASSH
NKITWDEKLNSSKLFSAMRDTNNKYVLTNLKFSKENEGYYFCSVISNSVMYFSSVVPVLQ
KV

>d1cdy_1 b.1.1.1 (1-97) N-terminal domain of CD4 {Human (Homo sapiens)}

KKVVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTSPSKLNDRADSRRS
LWDQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLV

>d1wioa2 b.1.1.1 (A:179-291) N-terminal domain of CD4 {Human (Homo sapiens)}

FQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAERASSSKSWITFDLKNKEVSV
KRVTQDPKLQMGKKLPLHLTPQALPQYAGSGNLTALAEAKTGKLHQEVNLVV

>d1hnf_1 b.1.1.1 (4-104) CD2, first domain {Human (Homo sapiens)}

TNALETWGALGQDINLDIPSFQMSDDIDDIKWEKTSDDKKIAQFRKEKETFKEDTYKLF
KNGTLKIKHLKTDDQDIYKVSIDYDTKGKNVLEKIFDLKIQE

>d1qa9b_ b.1.1.1 (B:) CD2-binding domain of CD58, N-terminal domain {Human (Homo sapiens)}

SSQQIYGVKYGNVTFHVP SNQPLKEVLWKKQKDKVAELENSEFRAFSSFKNRVYLDTKSG
SLTIYNLTSSDEDEYEMESPNITDSMKFFLYVGES

>d1dr9a1 b.1.1.1 (A:1-105) CD80, N-terminal domain {Human (Homo sapiens)}

VIHVTKEVKEVATLSCGHNVSV EELAQTIRYWQKEKKMVLTMMSGDMNIWPEYKNRTIF
DITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVK

>d1i85a_ b.1.1.1 (A:) CD86 (b7-2), N-terminal domain {Human (Homo sapiens)}

MLKIQAYFNETADLPCQFANSQNQSLSELVVFWDQENLVLNEVYLGKEKFDSVHSKYM
GRTSFSDSDSWTLRLHNLQIKDKGLYQCIIHHKKPTGMIRIHQMNSELSVLA

>d1f97a1 b.1.1.1 (A:27-128) Junction adhesion molecule, JAM, N-terminal domain {Mouse (Mus musculus)}

KGSVYTAQSDVQVPENESIKLTCTYSGFSSPRVEWKFFVQGSTTALVCYNSQITAPYADRV
T FSSSGITFSSVTRKDNGEYTCMVSEEGQNYGEVSIHLTVL

>d1jmaa_ b.1.1.1 (A:) HSV glycoprotein D {Herpes simplex virus type 1}

KYALADASLKMADPNRFRGKDLPLVDQLTDPGVRVYHIQAGLPDPFPQPPSLPITVYYAV

LERACRSVLLNAPSEAPQIVRGASEDVRKQPYNLTIWFRMGGNCAIPITVMEYTECSYN
KSLGACPIRTQPRWNYYSFSAVSEDNLGFLMHAPAFETAGTYLRLVKINDWTEITQFILE
HRAKGSCKYALPLRIPPSACLSPQAYQQGVTVDSIGMLPRFIPENQRTVAVYSLKIAGWHG
PKAPYTSTLLPPELSE

>d1hzhhl b.1.1.1 (H:1-113) Immunoglobulin (variable domains of L and H chains) {Intact IgG B12 antibody (human), kappa L chain}

QVQLVQSGAEVKKPGASVKVSCQASGYRFSNFIHWVRQAPGQRFQFEWMGWINPYNGNK
EFSAKFQDRVTFADTSANTAYMELRSLRSADTAVYYCARVGPYSWDDSPQDNYYMDV
WGKGTTVIVSS

>d1a3rll b.1.1.1 (L:1-114) Immunoglobulin (variable domains of L and H chains) {Fab 8F5 (mouse), kappa L chain}

DIVMTQSPSSLTVTTGEKVTMTCKSSQSLLNSRTQKNYLTWYQQKPGQSPKLLIYWASTR
ESGVPDRFTGSGSGTDFTLISGVQAEDLAVYYCQNNYNYPLTFGAGTKLELKRADAAPT

>d1fn4b1 b.1.1.1 (B:1-106) Immunoglobulin (variable domains of L and H chains) {Fab 198 against acetylcholine receptor, (rat)}

QVQLLESGLVRPSETLSLTCTVSGFSLTSFSVSWVRHPSGKGPEWMGRMWDGYTAY
NSALKSRLSISRDTSKNQVFLKMNSLQTDGTYYCTRDLYGGYPLGFWYDFWGP

>d1jtpa_ b.1.1.1 (A:) Immunoglobulin (variable domains of L and H chains) {Camel (Camelus dromedarius), anti-lysozyme antibody}

DVQLQASGGGSVQAGGSLRLSCAASGYTIGPYCMGWFRQAPGKEREGVAAINMGGGITY
YADSVKGRFTISQDNAKNTVYLLMNSLEPEDTAIYYCAADSTIYASYIECGHGLSTGGYG
YDSWGQGTQVTVSSRR

>d1mcwwl b.1.1.1 (W:1-111) Immunoglobulin (variable domains of L and H chains) {Heterologous L chain dimer MCG-WEIR hybrid (human)}

ESALTQPASVSGSPGQSITVSCAGHTSDVADSNSISWFQQHPDKAPKLLIYAVTFRPSGIPLR
FSGSKSGNTASLTISGLLPDDEADYFCMSYLSASFSVFGSGTKVTVLR

>d1b88a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

MQQVRQSPQSLTVWEGTAILNCSYENSAFDYFPWYQQFPGEGPALLISILSVSNKKEDGR
FTIFFNKREKKLSLHIADSQPGDSATYFCAASASFGDNSKLIWGLGTSLVVNP

>d1fo0a_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

KVTQTQTSISVMEKTTVTMDCVYETQDSSYFLFWYKQTASGEIVFLIRQDSYKKENATVG
HYSLNFQPKSSIGLIITATQIEDSAVYFCAMRGDYGGSGNKLIFGTGTLTSVKP

>d1i9ea_ b.1.1.1 (A:) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

QSVTQPDARVTVSEGASLQLRCKYSYSATPYLFWYVQYPRQGLQLLLKYYSGDPVVQGV
NGFEAEFSKSNSSFHLRKASVHWSDSAVYFCAVSGFASALTFGSGTKVIVLPYIQN

>d1bec_1 b.1.1.1 (3-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

AVTQSPRNKVAVTGGKVTLSQQTNHNNMYWYRQDTGHGLRLIHYSYGAGSTEKGDIP
DGYKASRPSQEQLILELATPSQTSVYFCASGGGRGSYAEQFFGPGTRLTVLE

>d1kb5b_ b.1.1.1 (B:) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

VTLLEQNPRWRLVPRGQAVNLRCLKNSQYPWMSWYQQDLQKQLQWLFTLRSPGDKEV
KSLPGADYLATRVTDTELRLQVANMSQGRTLYCTCSAAPDWGASAETLYFGSGTRLTVL

>d1nfdb1 b.1.1.1 (B:1-117) T-cell antigen receptor {Mouse (Mus musculus), beta-chain}

DSGVVQSPRHIIKEKGRSVLTCIPISGHSNVVWYQQTLGKELKFLIQHYEKVERDKGFLP

SRFSVQQFDDYHSEMNSALELEDSAMYFCASSLRWGDEQYFGPGTRTLVLE
>d1hxma1 b.1.1.1 (A:1-120) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}
AIELVPEHQTVPVSIGVPATLRCSMKGEAIGNYYINWYRKQTQGNMTFTIYREKDIYGPFGK
DNFQGDIDIAKNLAVLKILAPSERDEGSYYCACDTLGMGGEYTDKLIFGKGTRVTVEPR
>d1hxmb1 b.1.1.1 (B:1-123) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
AGHLEQPQISSTKTLSTARLECVVSGITISATSVYWYRERPGEVIQFLVSISYDGTVRKESG
IPSGKFEVDRIPETSTSTLTIHNVEKQDIATYYCALWEAQQELGKKIKVFGPGTKLIITD
>d1tvda_ b.1.1.1 (A:) T-cell antigen receptor {Human (Homo sapiens), delta-chain}
DKVTQSSPDQTVASGSEVLLCTYDTVYSNPDLFWYRIRPDYSFQFVFGDDSRSEGADF
TQGRFSVKHILTQKAFHLVISPVRTEDSATYYCAFTLPPPTDKLIFGKGTRVTVEP
>d1ahl__ b.1.1.1 (-) Immunoreceptor CTLA-4 (CD152), N-terminal fragment {Human
(Homo sapiens)}
AMHVAQPAVVLASSRGIA SFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMMGNEL
TFLDDSICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYLIGINGTQIYVIDPEPC
PDSDQEPK
>d3frua1 b.1.1.2 (A:179-269) Fc (IgG) receptor, alpha-3 domain and beta subunit {Rat (Rattus
norvegicus)}
KEPPSMRLKARPGNSGSSVLTCAAFSFYPPPELKFRFLRNGLASGSGNCSTGPNGDGSFHA
WSLLEVKRGDEHHYQCQVEHEGLAQPLTVDL
>d1i4fb1 b.1.1.2 (B:) Class I MHC, beta2-microglobulin and alpha-3 domain {Human (Homo
sapiens), HLA-A2.1}
MIQRTPKIQVYSRHPAENGKSNFLNCYVSGFHPSDIEVDLLKNGERIEKVEHSDLSFSKDW
SFYLLYYTEFTPTKEDEYACRVNHVTLSPKIVKWDRDM
>d1zaga1 b.1.1.2 (A:184-277) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}
QDPPSVVVTS HQAPGEKKKLKCLAYDFYPGKIDVHWTRAGEVQEPEL RGDV LHN GNGT
YQSWVVAVPPQDTAPYSCHVQHSSLAQPLVVPWEA
>d1hyrc1 b.1.1.2 (C:181-274) MHC I homolog {Human (Homo sapiens), Mic-a}
TVPPMVNVTRSEASEGNITVTCRASGFYPWNITLSWRQDGVSLSHDTQQWGDVLPDGNG
TYQTWVATRICQGEEQRFTCYMEHSGNHSTHPVPS
>d1c16a1 b.1.1.2 (A:181-276) MHC I homolog {Mouse (Mus musculus), t22}
RSDPPKAHVTRHPRPEGDVTLRCWALGFYPADITLTWQLNGEELTQDMELVETRPAGDGT
FQKWAAVVVPLGKEQSYTCHVYHEGLPEPLILRWGG
>d1igtb3 b.1.1.2 (B:236-361) Immunoglobulin (constant domains of L and H chains) {Intact IgG2a
antibody Mab231 (mouse), kappa L chain}
PCPPCKCPAPNLLGGPSVFIFPPKIKDVLMSLSPIVTCVVVDVSEDDPDVQISWVNNNEV
HTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKG
>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}
GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRG
GKYAATSQVLLPSKDVMAGTDEHV VCKVQH PNGNKEKNVPLPV
>d2ig2h2 b.1.1.2 (H:120-231) Immunoglobulin (constant domains of L and H chains) {Fab KOL
(human), lambda L chain}
STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPQPVTVSWNSGALTSGVHTFPAVLQSSGL
YSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCP

>d2fbjh2 b.1.1.2 (H:119-220) Immunoglobulin (constant domains of L and H chains) {Fab J539 (mouse), kappa L chain}

ESARNPTIYPLTLPPALSSDPVIIGCLIHDFYPSGTMNVTWKGSGKDITTVNFPPALASGGRY
TMSNQLTLPAVECPGESVKCSVQHDSNPVQELDVNCSG

>d1aqkl2 b.1.1.2 (L:112-216) Immunoglobulin (constant domains of L and H chains) {Fab B7-15A2 (human), lambda L chain}

QPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVNAGVETTKPSKQS
NNKYAASSYLSLTPEQWKSHKSYSCQVTHEGSTVEKTVAPAEC

>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}

RADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVAWAIDGSAAANGVLNSWTDQDS
KDSTYSMSSTLTLTADYEYAANSYTCAATHKTSTSPIVKSFNANEC

>d1fp5a1 b.1.1.2 (A:336-438) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgE}

VSAYLSRPSFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGT
LTVTSTLPVGTRDWIEGETYQCRVTHPLPRALMRSTTKTSG

>d1fp5a2 b.1.1.2 (A:439-543) Immunoglobulin (constant domains of L and H chains) {Fc (human) IgE}

PRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKT
KSGSFFVFSRLEVTRAWEQKDEFICRAVHEAASPSQTVQRAVSV

>d1pfc__ b.1.1.2 (-) Immunoglobulin (constant domains of L and H chains) {Fc (guinea pig)}

RTISKAKGPPRIPEVYLLPPPRNELSKKKVSLTCMITGFYPADINVEWDSSEPSDYKNTPPVF
DTDGSFFLYSRLKVDTDANNNGESFTCSVMHEALPNHVIQKSISRSPG

>d1g84a_ b.1.1.2 (A:) Immunoglobulin (constant domains of L and H chains) {C epsilon2 domain from IgE (human)}

SRDFTPTVKILQSSSDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQ
EGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKS

>d1tcr2 b.1.1.2 (A:118-213) T-cell antigen receptor {Mouse (Mus musculus), alpha-chain}

IQNPEPAVYALKDPRSQDSTLCLFTDFDSQINVPKTMESGTFITDATVLDKAMDSKSNGA
IAWSNQTSFTCQDIFKETNATYPSSDVP

>d1bd2e2 b.1.1.2 (E:119-247) T-cell antigen receptor {Human (Homo sapiens), beta-chain}

DLKNVFPPEVAVFEPSEAEISHTQKATLVCLATGFYPDHVELSWWVNGKEVHSGVSTDPQ
PLKEQPALNDSRYALSSRLRVSATFWQDPRNHFRCQVQFYGLSENDEWTQDRAKPVTVQIV
SAEAWGRAD

>d1hxma2 b.1.1.2 (A:121-206) T-cell antigen receptor {Human (Homo sapiens), gamma-chain}

SQPHTKPSVFMKNGTNVACLKVFYPKDIRINLVSSKKITEFDPAIVISPSGKYNAVKLGK
YEDSNSVTCSVQHDNKT VHSTDFE

>d1hxmb2 b.1.1.2 (B:124-230) T-cell antigen receptor {Human (Homo sapiens), delta-chain}

KQLDADVSPKPTIFLPSIAETKLQKAGTYLCLLEKFFPDVIKIHWEKKSNITLGSQEGNTM
KTNDTYMKFSWLTVPKSLDKEHRCIVRHENNKNGVDQEIIFFPI

>d1cd1a1 b.1.1.2 (A:186-279) CD1, beta2-microglobulin and alpha-3 domain {Mouse (Mus musculus)}

QEKPAWLSSVPSSAHGHRQLVCHVSGFYPKPVWVMWMRGDQEQQGTHRGDFLPNAD
ETWYLQATLDVEAGEEAGLACRVKHSSSLGGQDIILYW

>d1hdma1 b.1.1.2 (A:94-196) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}

SRGFPIAEVFTLKPFEFGKPNLVCFVSNLFPPMLTVNWHDHSPVEGFGPTFVSAVDGLS
FQAFSYLNFTPEPSDIFSCIVTHEPDRYTAIAYWVPRNALPS

>d1hdmb1 b.1.1.2 (B:88-185) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DM}

TRPPSVQVAKTTPFNTREPVMACVWGFYPAEVTITWRKNGKLMHSSAHKTAQPNGD
WTYQTLSHLALTPSYGDTYTCVVEHIGAPEPILRDWTPG

>d1aqdb1 b.1.1.2 (B:93-190) Class II MHC, C-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DR1}

RRVEPKVTVYPSKTQPLQHNNLLVCSVSGFYPGSIEVRWFRNGQEEKAGVVSTGLIQNGD
WTFQTLVMLETVPRSGEVYTCQVEHPSVTSPLTVEWRA

>d2iada1 b.1.1.2 (A:83-186) Class II MHC, C-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-AD}

TNEAPQATVFPKSPVLLGQPNTLICFVDNIFPPVINITWLRNSKSVTDGVYETSFLVNRDHS
FHKLSYLTFFIPSDDDIYDCKVEHWGLEEPVLKHWEPEISSADLVPR

>d1vcaa1 b.1.1.3 (A:91-199) Second domain of vascular cell adhesion molecule-1 (VCAM-1) {Human (Homo sapiens)}

FPKDPEIHLSPLEAGKPITVKCSVADVYPFDRLEIDLLKGDHLMKSQEFLEDADRKSLET
KSLEVTFTPVIEDIGKVLVCRAKLHIDEMDSVPTVRQAVKELQVYISP

>d1ic1a1 b.1.1.3 (A:83-190) Second domain of intercellular cell adhesion molecule-1 (ICAM-1) {Human (Homo sapiens)}

YWTPERVELAPLPSWQPVGKNLTLRCQVEGGAPRANLTVVLLRGEKELKREPAVGEPAEV
TTTVLVRRDHHGANFSCRTDLRPQGLELFENTSAPYQLQTFVLPAT

>d1zxq_1 b.1.1.3 (87-192) Second domain of intercellular cell adhesion molecule-2 (ICAM-2) {Human (Homo sapiens)}

PPRQVILTQLPTLVAVGKSFTIECRVPTVEPLDSLTLFLFRGNETLHYETFGKAAPAPQEATA
TFNSTADREDGHRNFSCLAFLDLMSRGGNIFHKHSAPKMLEIY

>d1cdy_2 b.1.1.3 (98-178) CD4 {Human (Homo sapiens)}

FGLTANS DTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTL SVSQLELQDSGTWTC
TVLQNQKKVEFKIDIVVLA

>d1wioa4 b.1.1.3 (A:292-363) CD4 {Human (Homo sapiens)}

MRATQLQKNLTCEVWGPTSPKLMLSLKLENKEAKVSKREKAVWVLNPEAGMWQCLLSD
SGQVLLESNIKVLP

>d1hnf_2 b.1.1.3 (105-182) CD2, second domain {Human (Homo sapiens)}

RVSKPKISWTCINTTLTCEVMNGTDPELNLYQDGKHLKLSQRVITHKWTTSLSAKFKCTA
GNKVSKESSVEPVSCPEK

>d1dr9a2 b.1.1.3 (A:106-200) CD80, second domain {Human (Homo sapiens)}

ADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKL
DFNMTTNHSMCLIKYGHRLRVNQTFNWN TA

>d1vcaa2 b.1.1.4 (A:1-90) N-terminal domain of vascular cell adhesion molecule-1 (VCAM-1) {Human (Homo sapiens)}

FKIETTPESRYLAQIGDSVSLTCSTTGCESPFFSWRTQIDSPNGKVTNEGTTSTLTMNPVSF
GNEHSYLC TATCESRKLEKGIQVEIYS

>d1iam_2 b.1.1.4 (1-82) N-terminal domain of intracellular adhesion molecule-1, ICAM-1 {Human (Homo sapiens)}

QTSVSPSKVILPRGGSVLVTCSTSCDQPKLLGIETPLPKKELLPGNNRKVYELSNVQEDSQ
PMCYSNCPDGQSTAKTFLTV

>d1zxq_2 b.1.1.4 (1-86) N-terminal domain of intracellular adhesion molecule-2, ICAM-2 {Human (Homo sapiens)}

KVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVGGLETSLNKILLDEQAQWKHYLVSNIS
HDTVLCQCHFTCSGKQESMNSNVSVYQ

>d1epfa1 b.1.1.4 (A:1-97) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}

LQVDIVPSQGEISVGESKFFLCQVAGDAKDKDISWFSPNGEKLSPNQQRISVWVNDSSST
LTIYNANIDDAIGYKCVVTAEDGTQSEATVNVKIFQ

>d1epfa2 b.1.1.4 (A:98-189) Neural cell adhesion molecule (NCAM) {Rat (Rattus norvegicus)}

KLMFKNAPTQEFKEGEDAVIVCDVSSLPPTIIWKHKGRDVILKKDVRFIVLSNNYLQIR
GIKKTDEGTYRCEGRILARGEINFKDIQVIV

>d1ie5a_ b.1.1.4 (A:) Neural cell adhesion molecule (NCAM) {Chicken (Gallus gallus)}

GKDIQVIVNVPPSVRARQSTMNATANLSQSVTLACDADGFPEPTMTWTKDGEPIEQEDNE
EKYSFNYDGSSELIKKVKDSDEAEYICIAENKAGEQDATIHLKVFAK

>d1gsma1 b.1.1.4 (A:1-90) Mucosal addressin cell adhesion molecule-1 (MADCAM-1) {Human (Homo sapiens)}

VKPLQVEPPEPVVAVALGASRQLTCRLACADRGASVQWRGLDTSLGAVQSDTGRSVLTVR
NASLSAAGTRVCVCGSCGGRTFQHTVQLLVY

>d1gsma2 b.1.1.4 (A:91-206) Mucosal addressin cell adhesion molecule-1 (MADCAM-1) {Human (Homo sapiens)}

AFPNQLTVSPAALVPGDPEVACTAHKVTPVDPNALSFSLLVGGQELEGAQALGPEVQEEEE
EPQGDEDVLFVRTERWRLPPLGTPVPPALYCQATMRLPGLELSHRQAIPVLIEGR

>d1fhga_ b.1.1.4 (A:) Telokin {Turkey (Meleagris gallopavo)}

AEEKPHVKPYFTKTILDMEVVEGSAARFDCKVEGYPDPEVMWFKDDNPVKESRHFQIDY
DEEGNCSLTISEVCGDDDAKYTCKAVNSLGEATCTAELLVETM

>d1glca_ b.1.1.4 (A:) Titin {Human (Homo sapiens), different modules}

SMEAPKIFERIQSQTVGQGSDAHFRVRVVGKPDPECEWYKNGVKIERSDRIYWYWPEDN
VCELVIRDVTGEDSASIMVKAINIAGETSSHAFLVQAK

>d1nct_ b.1.1.4 (-) Titin {Human (Homo sapiens), different modules}

SKTTLAARILTKPRSMTVYEGESARFSCDTDGEPVPTVTWLRKGQVLSTSARHQVTTTKY
KSTFEISSVQASDEGNYSVVVENSEGKQEAFTLTIQK

>d1koa_1 b.1.1.4 (6265-6361) Twitchin {Nematode (Caenorhabditis elegans)}

QPRFIVKPYGTEVGEGQSANFYCRVIASSPPVVTWHKDDRELKQSVKYMKRYNGNDYGL
TINRVKGDDKGEYTVRAKNSYGTKEEIVFLNVTRHSEP

>d1wiu_ b.1.1.4 (-) Twitchin {Nematode (Caenorhabditis elegans)}

LKPKILTASRKIKIKAGFTHNLEVDFIGAPDPTATWTVGDSGAALAPELLVDAKSSTTSIFFP
SAKRADSGNYKLKVKNELGEDEAIFEVIVQ

>d1tiu_ b.1.1.4 (-) Twitchin {Human (Homo sapiens), Ig repeat 27}

LIEVEKPLYGVEVFVGETAHFEIELSEPDVHGQWKLKGQPLTASPDCEIIEDGKKHILILHN
CQLGMTGEVSFQAANAKSAANLKVKEK

>d1iray1 b.1.1.4 (Y:1-101) Type-1 interleukin-1 receptor {Human (Homo sapiens)}

DKCKEREEKIILVSSANEIDVRPCPLNPNEHKGTITWYKDDSKTPVSTEQASRIHQHKEKL
WFVPAKVEDSGHYVCVVRNSSYCLRIKISAKFVENEPNLC

>d1iray2 b.1.1.4 (Y:102-204) Type-1 interleukin-1 receptor {Human (Homo sapiens)}
YNAQAIFKQKLPVAGDGLVCPYMEFFKNENNELPKLQWYKDCKPLLLDNIHFSGVKDR
LIVMNVAEKHRGNYTCHASYTYLGKQYPITRVIEFITLEENKPT

>d1iray3 b.1.1.4 (Y:205-311) Type-1 interleukin-1 receptor {Human (Homo sapiens)}
RPVIVSPANETMEVDLGSQIQLICNVTGQLSDIAYWKWNGSVIDEDDPVLGEDYYSVENP
ANKRRSTLITVLNISEIESRFYKHPFTCFANKTHGIDAAYIQLIYPV

>d1evsc1 b.1.1.4 (C:149-250) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens),
FGFR1}
MPVAPYWTSPEKMEKKLHAVPAAKTVKFKCPSSGTPQPTLRWLKNGKEFKPDHRIGGYK
VRYATWSIIMDSVVP SDKGNYTCIVENEYGSINHTYQLDVVER

>d1ev2e2 b.1.1.4 (E:251-360) Fibroblast growth factor receptor, FGFR {Human (Homo sapiens),
FGFR2}
RSPHRPILQAGLPANASTVVGGDVEFVCKVYSDAQPHIQWIKHVEKNGSKYGPDGLPYLK
VLKAAGVNTTDKEIEVLYIRNVTFEDAGEYTCLAGNSIGISFHSAWLTVL

>d1biha1 b.1.1.4 (A:5-98) Hemolin {Moth (Hyalophora cecropia)}
KYPVLKDQPAEVLFRENNPTVLECIIEGNDQGVKYSWKKGKSYNWQEHNAALRKDEG
SLVFLRPQASDEGHYQCFAETPAGVASSRVISFRKT

>d1biha2 b.1.1.4 (A:99-209) Hemolin {Moth (Hyalophora cecropia)}
YLIASPAKTHEKTPIEGRPFQLDCVLPNAYPKPLITWKKRLSGADPNADVTDFDRRITAGP
DGNLYFTIVTKEDVSDIYKYVCTAKNAAVDEEVVLVEYEIKGVTKDNSGY

>d1biha3 b.1.1.4 (A:210-306) Hemolin {Moth (Hyalophora cecropia)}
KGEPVPQYVSKDMMAKAGDVTMIYCMYGSNPMGYPNYFKNGKDVNGNPEDRITRHNH
TSGKRLFLKTTLPEDEGVYTCEVDNGVGKPKQHSLKLTVV

>d1biha4 b.1.1.4 (A:307-395) Hemolin {Moth (Hyalophora cecropia)}
SAPKYEQKPEKVIVVKQGQDVTIPCKVTGLPAPNVVWSHNAKPLSGGRATVTD SGLVIKG
VKNGDKGYYGCRATNEHGDKYFETLVQVN

>d1cs6a1 b.1.1.4 (A:7-103) Axonin-1 {Chicken (Gallus gallus)}
RSYGPVFEEQPAHTLFPEGSAAEEKVTLTCRARANPPATYRWKMNGTELKMGPDSRYRLVA
GDLVISNPVKAKDAGSYQCVATNARGTVVSREASLRF

>d1cs6a2 b.1.1.4 (A:104-208) Axonin-1 {Chicken (Gallus gallus)}
GFLQEFSAEERDPVKITEGWGMFTCSPPHYPALSYRWLLNEFPNFIPADGRRFVSQTTG
NLYIAKTEASDLGNYSCFATSHIDFITKSVFSKFSQLSLAAEDA

>d1cs6a3 b.1.1.4 (A:209-299) Axonin-1 {Chicken (Gallus gallus)}
RQYAPSIKAKFPADTYALTGQMVTLECFAGNPVPQIKWRKLDGSQTSKWLSSEPLLHIQN
VDFEDEGTYECEAENIKGRDTYQGRIIHA

>d1cs6a4 b.1.1.4 (A:300-388) Axonin-1 {Chicken (Gallus gallus)}
QPDWLDVITDTEADIGSDLRWSCVASGKPRPAVRWLRDQGQPLASQNRIEVSGGELRFSKL
VLED SGMYQCVAENKHGTVYASAELTVQA

>d1gl4b_ b.1.1.4 (B:) Perlecan Ig3 domain {Mouse (Mus musculus)}
PIMVTVEEQRSQSVRPGADVTFICTAKSKSPAYTLVWTRLHNGKLPSRAMDFNGILTIRNV
QPSDAGTYVCTGSNMFAMDQGTATLHVQ

>d1f97a2 b.1.1.4 (A:129-238) Junction adhesion molecule, JAM, C-terminal domain

{Mouse (*Mus musculus*)}

VPPSKPTISVPSSVTIGNRAVLTCSEHDGSPPEYSWFKDGISMLTADAKKTRAFMNSSFTID
PKSGDLIFDPVTAFDSTGEYYCQAQNGYGTAMRSEAAHMDAVELNVGG

>d1fltx_b.1.1.4 (X:) Second domain of the Flt-1 receptor {Human (*Homo sapiens*)}

GRPFVEMYSEIPEIIHMTEGRELVIPCRVTSPNITVTLKKFPLDTLIPDGKRIIWDSRKGFIIISN
ATYKEIGLLTCEATVNGHLYKTNYLTHRQT

>d1he7a_b.1.1.4 (A:) NGF binding domain of trkA receptor {Human (*Homo sapiens*)}

SHMPASVQLHTAVEMHHWCIPFSVDGQPAPSLRWLFNGSVLNETSFIFTEFLEPAANETVR
HGCLRLNQPTHVNNGNYTLLAANPFGQASASIMAAFMNDNPFEFNPE

>d1fcga1_b.1.1.4 (A:4-88) Fc gamma receptor ectodomain (CD32) {Human (*Homo sapiens*), IIa}

APPKAVLKLEPPWINVLQEDSVTLTCQGARSPESDSIQWFHNGNLIPTHTQPSYRFKANN
DSGEYTCQTGQTSLSDPVHLTVLF

>d1fnla2_b.1.1.4 (A:87-175) Fc gamma receptor ectodomain (CD32) {Human (*Homo sapiens*), III}

HIGWLLLQAPRWVFKEEDPIHLRCHSWKNTALHKVTYLQNGKDRKYFHHNSDFHIPKAT
LKDSGSYFCRGLVGSKNVSSSETVNITITQA

>d1nkr_1_b.1.1.4 (6-101) Killer cell inhibitory receptor {Human (*Homo sapiens*), p58-cl42 kir}

RKPSLLAHPGPLVKSEETVILQCWSDVMFEHFLLHREGMFNDTLRLIGEHHHDGVSKANFSI
SRMTQDLAGTYRCYGSVTHSPYQVSAPSDPLDIVI

>d1g0xa1_b.1.1.4 (A:2-97) Ligand binding domain of lir-1 (ilt2) {Human (*Homo sapiens*)}

HLPKPTLWAEPGSVITQGSPVTLRCQGGQETQEYRLYREKKTAPWITRIPQELVKKGQFPIIP
SITWEHAGRYRCYYGSDTAGRSESSDPLELVVTG

>d1g0xa2_b.1.1.4 (A:98-198) Ligand binding domain of lir-1 (ilt2) {Human (*Homo sapiens*)}

AYIKPTLSAQSPVVNSGGNVTLCDSQVAFDGFILCKEGEDEHPQCLNSQPHARGSSRAI
FSVGPVSPSRRWWYRCYAYDSNSPYEWSLPSDLLELLVLG

>d1f42a1_b.1.1.4 (A:1-87) The p40 domain of interleukin-12 (IL-12 beta chain), N-terminal domain {Human (*Homo sapiens*)}

IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF
GDAGQYTCHKGGEVLSHLLLLHKED

>d1jba1_b.1.1.4 (A:101-186) CD3 gamma chain ectodomain fragment {Mouse (*Mus musculus*)}

KKDGSQTNKAKNLVQVDGSRGDGSVLLTCGLTDKTIKWLKDGSIISPLNATKNTWNLGN
NAKDPRGTYQCQGAKETSNPLQVYYRM

>d1jba2_b.1.1.4 (A:1-100) CD3 epsilon chain ectodomain fragment {Mouse (*Mus musculus*)}

DDAENIEYKVSISGTSVELTCPLSDENLKWEKNGQELPQKHDKHLVLQDFSEVEDSGYY
VCYTPASNKNTYLYLKARVGSADDAKKDAAKKDDAKKDDA

>d1k3ia1_b.1.1.5 (A:538-639) Galactose oxidase, C-terminal domain {Fungi (*Fusarium spp*)}

GNLATRPKITRTSTQSVKVGGRITISTDSSISKASLIRYGTATHTVNTDQRRIPLTLTNNGGNS
YSFQVPSDSGVALPGYWMLFVMNSAGVPSVASTIRVTQ

>d1qba_1_b.1.1.5 (781-885) Bacterial chitinase, c-terminal domain {*Serratia marcescens*}

GETHFVDTQALEKDWLRFANILGQRELAKLDKGGVAYRLPVPGARVAGGKLEANIALPGL
GIEYSTDGGKQWQRYDAKAKPAVSGEVQVRSVSPDGKRYRAEKV

>d1svb_1_b.1.1.5 (303-395) Envelope glycoprotein, domain III (C-terminal) {Tick-borne encephalitis virus}

TYTMCDKTKFTWKRAPTDSGHDTVVMEVTFSGTKPCRIPVRAVAHGSPDVNVAMLITPN

PTIENNGGGFIEMQLPPGDNIYVVGELSHQWFQK

>d1kclal b.1.1.5 (A:496-581) Cyclodextrin glycosyltransferase, domain E {Bacillus circulans, different strains}

TATPTIGHVGPMMAKPGVTITIDGRGFGSSKGTVYFGTTAVSGADITSWEDTQIKVKIPAVA
GGNYNIKVANAAGTASNVDNFEV

>d1smaal b.1.1.5 (A:1-123) Maltogenic amylase, N-terminal domain {Thermus sp.}

MRKEAIHHRSTDNFAYAYDSETHLRLQTKKNDVDHVELLFGDPYEWHDGAWQFQTMP
MRKTGSDGLFDYWLAEVKPPYRRLRYGFVLRAGGEKLVYTEKGFYHEAPSDDTAYYFCF
PFLHRV

>d1bvza1 b.1.1.5 (A:1-120) Maltogenic amylase, N-terminal domain {Thermoactinomyces vulgaris, TVaII}

MLLEAIFHEAKGSYAYPISETQLRVRLRAKKGDVVRCEVLYADRYASPEEELAHALAGKA
GSDERFDYFEALLECSTKRKYVFLLTGPQGEAVYFGETGFSAERSKAGVFQYAYIHRSE

>d1eh9a1 b.1.1.5 (A:1-90) Glycosyltrehalose trehalohydrolase, N-terminal domain {Archaeon Sulfolobus solfataricus, km1}

TFAYKIDGNEVIFTLWAPYQKSVKLKVLEKGLYEMERDEKGYFTITLNNVKVRDRYKYVL
DDASEIPDPASRYQPEGVHGSPSQIIQESKE

>d1bf2_1 b.1.1.5 (1-162) Isoamylase, N-terminal domain {Pseudomonas amyloclavata}

AINSMGLGASYDAQANITFRVYSSQATRIVLYLYSAGYGVQESATYTLSPAGSGVWAVTV
PVSSIKAAGITGAVYYGYRAWGPNWPYASNWGGKSGAGFVSDVDANGDRFNPKNLLLD
PYAQEVSQDPLNPSNQNGNVFASGASYRTTDSGIYAPKGVVLV

>d1lla_3 b.1.1.5 (380-628) Hemocyanin, C-terminal domain {Horseshoe crab (Limulus polyphemus)}

PYDHDVLFNPDQVQDVTLHARVDNVVHTFMREQEELKHGINPGNARSIAKARYYHLDH
EPFSYAVNVQNNASDKHATVRIFLAPKYDELGNEIKADELRRTAIELDKFKTDLHPGKNT
VVRHSLDSSVTLSHQPTFEDLLHGVGLNEHKSEYCSGWPShLLVPKGNIGMEYHLFV
MLTDWDKDKVDGSESVACVDASVYCGARDHKYPDKKPMGFPDRPIHTEHISDFLTNNM
FIKDIKIKFHE

>d1hc2_3 b.1.1.5 (399-653) Hemocyanin, C-terminal domain {Spiny lobster (Panulirus interruptus)}

PPYTHDNLEFSGMVVNGVAIDGELITFFDEFQYSLINAVDSGENIEDVEINARVHRLNHNEF
TYKITMSNNNDGERLATFRIFLCPIEDNNGITLTLEARWFCIELDKFFQKVPSGPETIERSS
KDSSVTVPDMPFSQSLKEQADNAVNGGHDLDLSAYERSGIPDRMLLPKSKPEGMEFNLY
VAVTDGDKDTEGHNGGHDYGGTHAQCGVHGEAYPDNRPLGYPLERRIPDERVIDGVSNI
KHVVVKIVHHL

>d1js8a2 b.1.1.5 (A:2792-2892) C-terminal domain of octopus hemocyanin {Giant octopus (Octopus dofleini)}

EDRVFAGFLLRTIGQSADVNFVCTKDGECTFGGTFCILGGEHEMFVAFDRLFKYDITTS
LKHRLDAHDDFDIKVTIKGIDGHVLSNKYLSPTVFLAPA

>d1clc_2 b.1.1.5 (35-134) CelD cellulase, N-terminal domain {Clostridium thermocellum}

IETKVSAAKITENYQFDSRIRLNSIGFIPNHSKKATIAANCSTFYVVKEDGTIVYTGTATSMF
DNDTKETVYIADFSSVNEEGTYYLAVPGVGKSVNFKI

>d1flsa2 b.1.1.5 (A:171-248) Hyaluronate lyase precatalytic domain {Streptococcus agalactiae}

SEHPQPVTQTIEKSVNTALNKNYVFNKADYQYTLTNPSLGKIVGGILYPNATGSTTVKISD

KSGKIIKEVPLSVTAST

>d1edqa1 b.1.1.5 (A:24-132) Chitinase A, N-terminal domain {*Serratia marcescens*}

AAPGKPTIAWGNTKFAIVEVDQAATAYNNLVKVKNAADVSVSWNLWNGDTGTAKVLL
NGKEAWSGPSTGSSGTANFKVNKGGRYQMQUALCNADGCTASDATEIVVAD

>d1fl3a1 b.1.1.5 (A:5-190) Transglutaminase N-terminal domain {Human (*Homo sapiens*)}

RTAFGGRRAVPPNNSNAEDDLPTVELQGVVPRGVNLQEFLNVTSVHLFKERWDTNKVD
HHTDKYENNNKLIVRRGQSIFYVQIDFSRPYDPRRDLFRVEYVIGRYPQENKGTYPVPIVSEL
QSGKWGAKIVMREDRSVRLSIQSSPKCIVGKFRMYVAVWTPYGVLRTSRNPETDTYILFN
PWCED

>d1g0da1 b.1.1.5 (A:6-140) Transglutaminase N-terminal domain {Red sea bream (*Chrysophrys major*)}

GLIVDVNGRSHENNLAHRTREIDRERLIVRRGQPFSTLQCSDSLPPKHHLELVHLGKRDE
VVIKVQKEHGARDKWWFNQQGAQDEILLTLHSPANAVIGHYRLAVLVMSPDGHIVERAD
KISFHMLFNPWCRD

>d1eut_1 b.1.1.5 (403-505) Sialidase, "linker" domain {*Micromonospora viridifaciens*}

GICAPFTIPDVALEPGQQTVPVAVTNQSGIAVPKPSLQLDASPDWQVQGSVEPLMPGRQA
KGQVTITVPAGTTPGRYRVGATLRTSAGNASTTFTVTVGLLD

>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}

KPAPSAEHSYAEGLVKVFDNAPAEFTIFAVDTKGVARTDGGDPFEVAINGPDGLVVDAK
VTDNNDGTYGVVYDAPVEGNYNVNVTLRGNPIKNMPIDVKCIE

>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}

GANGEDSSFGSFTFTVAAKNKKGEVKTYGGDKFEVSITGPAAEITLDAIDNQDGTYYTAAYS
LVGNGRFSTGVKLNGKHIEGSPFKQVLGNPGKKNPVKSFTTTRTAN

>d1doab_ b.1.1.5 (B:) Rho GDP-dissociation inhibitor 1, RhoGDI {Cow (*Bos taurus*)}

EPTAEQLAQIAAENEDEHSVNYKPPAQKSIQEIQLDKDDESLRKYKEALLGRVAVSADP
NVPNVVVTRLTLVCSTAPGPLELDTGDLESFKKQSFVLKEGVEYRIKISFRVNREIVSGMK
YIQHTYRKGVKIDKTDYMGVSYGPRAEEYEFLTPMEEAPKGMLARGSYNIKSRTDDDR
TDHLSWEWNLTIKKEWKD

>d1cfla1 b.1.1.5 (A:10-182) Arrestin {Cow (*Bos taurus*), visual arrestin}

HVIFKKISRDKSVTIYLGKRDYIDHVERVEPVDGVVLVDPELVKGKRVYVSLTCAFRYQQE
DIDVMGLSFRRDLYFSQVQVFPPVGASGATTRLQESLIKKLGANTYPFLTFPDYLPSCVM
LQPAPQDVGKSCGVDFEIKAFATHSTDVEEDKIPKKSSVRLLRKVQHAPR

>d1g4ma2 b.1.1.5 (A:176-393) Arrestin {Cow (*Bos taurus*), beta-arrestin 1}

ERPGPQPTAETTRQFLMSDKPLHLEASLDKEIYYHGEPISVNVHVTNNTNKTVMKKIKISVR
QYADICLFNTAQYKCPVAMEEADDTVAPSSTFCKVYTLTPFLANNREKRGALDGLKHE
DTNLASSTLLREGANREILGIIVSYKVKVCLVSRGGLLDLASSDVAVELPFTLMHPKPK
EPPHREVPEHETPVDNLIELDTNDDDIVFEDFAR

>d1a02n1 b.1.1.5 (N:577-678) Transcription factor NFATC, C-terminal domain {Human (*Homo sapiens*)}

LPMVERQDTSCLVYGGQQMILTGQNFTSESKVVFTEKTTDGQQIWEMEATVDKDKSQP
NMLFVEIPEYRNKHIRTVPKVNIFYVINGKRKRSQPQHFTYHPV

>d1imhc1 b.1.1.5 (C:368-468) Transcription factor TONEBP, C-terminal domain {Human (*Homo sapiens*)}

sapiens)}}
VPEILKKSLHSCSVKGEEEVFLIGKNFLKGTKVIFQENVSDENSWKSEAEIDMELFHQNHL
IVKVPPYHDQHITLPVSVGIYVVTNAGRSHDVQPFTYTPD
>d1nfia1 b.1.1.5 (A:190-314) p65 subunit of NF-kappa B (NFKB), C-terminal domain {Human (Homo sapiens)}
NTAELKICRVNRNSGSLGGDEIFLLCDKVQKEDIEVYFTGPGWEARGSFQADVHRQVAI
VFRTPPYADPSLQAPVRVSMQLRRPSDRELSEPMEFQYLPDTDDRHRIEEKRKRTYETFKSI
MK
>d1ahm_ b.1.1.5 (-) Major mite allergen {House-dust mite (Dermatophagoides farinae), Der f 2}
DQVDVKDCANNEIKKVMVDGCHGSDPCIIHRGKPFLEALFDANQNTKTAKIEIKASLDG
LEIDVPGIDTNACHFVKCPLVKGQQYDIKYTWNVPKIAPKSENVVTVKLIGDNGVLACA
IATHGKIRD
>d1soxa1 b.1.1.5 (A:344-466) Sulfite oxidase, C-terminal domain {Chicken (Gallus gallus)}
ELPVQSAVTQPRGAAVPPGELTVKGYAWSGGGREVVVRVDVSLDGGRTWKVARLMGDK
APPGRAWAWALWELTVPEAGTELEIVCKAVDSSYNVQPDSVAPIWNLRGVLSTAWHRVR
VSVQD
>d1lcra1 b.1.1.5 (A:351-432) Gingipain R (RgpB), C-terminal domain {Porphyromonas gingivalis}
PTEMQVTAPANISASAQTFEVACDYNGAIATLSDDGDMVGTAIVKDGKAIKLNESIADET
NLTLTVVGYNKVTVIKDVKVE
>d1h6ta1 b.1.1.6 (A:241-321) Internalin B {Listeria monocytogenes}
ECLNKPINHQS NLVVPNTVKNTDGLSVTPEIISDDGDYEKPNVKWHLPEFTNEVSFIFYQP
VTIGKAKARFHGRVTQPLKE
>d1ehxa_ b.1.1.6 (A:) Cellulosomal scaffoldin protein CipC, module x2.1 {Clostridium cellulosyticum}
MQDPTINPTSISAKAGSFADTKITLTPNGNTFNGISELQSSQYTKGTNEVTLLASYLNTLPE
NTTKTLTFDFGVGTKNPKLITVLPKDIPGLE
>d1im3d_ b.1.1.6 (D:) Cytomegalovirus protein US2 {Human cytomegalovirus}
PWFQIEDNRCYIDNGKLFARGSIVGNMSRFVDPKADYGGVGENLYVHADDVEFVPGESL
KWNVRNLDVMPFIFETLALRLVLQGDVIWLRCVPEL
>d1jjua3 b.1.1.6 (A:274-351) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}
AAPQVLAVAPARLKIGEETQLRVAGTGLGSDLTLPEGVAGSVESAGNGVTVLKLTATGTPG
PVSLELGGQKVDLVAYD
>d1jjua4 b.1.1.6 (A:352-489) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Paracoccus denitrificans}
RPDRISIVPDLTIARIGNGGPIPKVPAQFEAMGWLNGPDGQPGTGDDIALGAFPASWATD
NFDEEA EKMQDAKYAGSIDD TGLFTPAEAGPNPERPMQTNNAGNLKVIATVDAEGEPLSA
EAHLYATVQRFVDAPIR
>d1jmx3 b.1.1.6 (A:282-363) Quinohemoprotein amine dehydrogenase A chain, domains 4 and 5 {Pseudomonas putida}
GKARLLAVQPAFIKAGGESEITLVGSLAGKPD LGAGVEVTEVLEQTPTLVRLKARAAAD
AKPGQREVAVGTLKGVNLAVYD
>d2hft_1 b.1.2.1 (1-106) Extracellular region of human tissue factor {Human (Homo sapiens)}

SGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLT
DEIVKDVVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLET

>d2hft_2 b.1.2.1 (107-211) Extracellular region of human tissue factor {Human (Homo sapiens)}
NLGQPTIQSFEQVGTKVNVTVEDERTLVRRNNTFLSLRDVFGKDLYTLYYWKSSSQEKG
EFRSGKKTAKTNTNEFLIDVDKGENYCFSVQAVIPSRTVNRKSTDSPVECMG

>d1fnf_1 b.1.2.1 (1142-1235) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
PLSPPTNLHLEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVVHADQSSCT
FDNLSPGLEYNVSVYTVKDDKESVPISDTIIPA

>d1fnf_2 b.1.2.1 (1236-1326) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
VPPPTDLRFTNIGPDTMRVTWAPPPSIDLTNFLVRYSPVKNEEDVAELSPSDNAVVLTNLL
PGTEYVVS SVSSVYEQHESTPLRGRQKTG

>d1fnha1 b.1.2.1 (A:3-92) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
PAPTDLKFTQVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSSSVVVSGL
MVATKYEVSVYALKDTLTSRPAQGVVTTLE

>d1fnha2 b.1.2.1 (A:93-182) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
NVSPRRARVTDATETTITISWRTKETITGFQVDAPANGQTPIQRTIKPDVRSYITITGLQP
GTDYKIYLYTLNDNARSSPVVIDASTA

>d1j8ka_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
NIDRPKGLAFTDVDVDSIKIAWESPQGQVSRYRVYSSPEDGIHELFPAPDGEEDTAELQGL
RPGSEYTVSVVALHDDMESQPLIGTQSTAIPA

>d2fnba_ b.1.2.1 (A:) Fibronectin, different Fn3 modules {Human (Homo sapiens)}
MRGSEVPQLTDLSFVDITDSSIGLRWTPLNSSTIIGYRITVVAAGEGIPIFEDFVDSSVGYTY
VTGLEPGIDYDISVITLINGGESAPTTLTQQT

>d2mfn_1 b.1.2.1 (1-92) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}
GLDSPTGFDSSDITANSFTVHWVAPRAPITGYIIRHHAESVGRPRQDRVPPSRNSITLTNLN
PGTEYVVSIIAVNGREESPLIGQQATVS

>d2mfn_2 b.1.2.1 (93-184) Fibronectin, different Fn3 modules {Mouse (Mus musculus)}
DIPRDLEVIASPTSLISWEPPAVSVRYRITYGETGGNSPVQEFTVPGSKSTATINNIKPGA
DYTITLYAVTGRGDSPASSKPVSYNYKT

>d1qr4a1 b.1.2.1 (A:1-87) Tenascin {Chicken (Gallus gallus)}
DNPKDLEVSDPTETTLRLWRPVAKFDRYRLTYVSPSGKKNEMEIPVDSTSFILRGLDAG
TEYTISLVAEKGRHKS KPTTIKGSTV

>d1qr4a2 b.1.2.1 (A:88-175) Tenascin {Chicken (Gallus gallus)}
VGSPKGISFSDITENSATVSWTPPRS RVDSYRVSYVPITGGTPNVVTVDGSKTRTKLVKLVP
GVDYNNVNIISVKGFESEPISGILKT

>d1ten_ b.1.2.1 (-) Tenascin {Human (Homo sapiens)}
RLDAPSQIEVKDVTDTTALITWFKPLAEIDGIELTYGIKDVPGDRTTIDLTEDENQYSIGNLK
PDTEYEVSLISRRGDMSSNPAKETFTT

>d1cfb_1 b.1.2.1 (610-709) Neuroglian, two amino proximal Fn3 repeats {Drosophila melanogaster}
IVQDVPNAPKLTGITCQADKAEIHWEQQGDNRSPILHYTIQFNTSFTPASWDAAYEKVPNT
DSSFVVMSPWANYTFRVIAFNKIGASPPSAHSDSCTTQ

>d1cfb_2 b.1.2.1 (710-814) Neuroglian, two amino proximal Fn3 repeats {Drosophila melanogaster}
PDVPFKNPNDNVVGQGTEPNNLVISWTPMPEIEHNAPNFHYVSWKRDIPAAAWENNIFD
WRQNNIADIADQPTFVKYLIKVVAINDRGESNVAAEEVVGYSGEDR

>d1qg3a1 b.1.2.1 (A:1126-1217) Integrin beta-4 subunit {Human (Homo sapiens)}
DLGAPQNPNAKAAGSRKIHFNWLPSPGKPMGYRVKYWIQGDSESEAHLLDSKVPSVELT
NLYPYCDYEMKVCAYGAQGEGPYSSLVSCRTHQ

>d1qg3a2 b.1.2.1 (A:1218-1320) Integrin beta-4 subunit {Human (Homo sapiens)}
EVPSEPGRLAFNVVSSTVTQLSWAEPATNGETAYEVCYGLVNDDNRPIGPMKKVLVDN
PKNRMILLIENLRESQPYRYTVKARNAGAGWGPEREAIINLATQP

>d1axib1 b.1.2.1 (B:32-130) Growth hormone receptor {Human (Homo sapiens)}
EPKFTKCRSPERETFSCHWTDEVHHGTKNEGPIQLFYTRRNTQEWTEWKECPDYVSAG
ENSCYFNSSFTSIAIPYCIKLTSNGGTVDKCFVSVDEIVQ

>d1axib2 b.1.2.1 (B:131-236) Growth hormone receptor {Human (Homo sapiens)}
PDPPIALNWTLLNVSLTGIHADIQVRWEAPRNADIQKGMVLEYELQYKEVNETKWK
MDPILTTSPVYSLKVDKEYEVRVRSKQRNSGNYGEFSEVLYVTLPQM

>d1eerb1 b.1.2.1 (B:8-116) Erythropoietin (EPO) receptor {Human (Homo sapiens)}
DPKFESKAALLAARGPEELLCFTEERLEDLVCFWEEAASAGVGPQYSFSYQLEDEPWKLC
RLHQAPTARGAVRFWCSLPTADTSSFPVLELRVTAASGAPRYHRVIHIN

>d1eerb2 b.1.2.1 (B:117-220) Erythropoietin (EPO) receptor {Human (Homo sapiens)}
EVVLLDAPVGLVARLADESGHVLRWLPPPETPMTSHIRYEVDVSAGQGAGSVQRVEILE
GRTECVLSNLRGRTRYTFAVRARMAEPSFGGFVSEWSEPVSLLT

>d1bp3b1 b.1.2.1 (B:202-300) Prolactin receptor {Human (Homo sapiens)}
LPPGKPEIFKCRSPNKETFTCWWRPGTDGGLPTNYSILTYHREGETLMHECPDYITGGPNSC
HFGKQYTSMWRTYIMMVNATNQMGSSFSDELYVDVTYI

>d1bp3b2 b.1.2.1 (B:301-404) Prolactin receptor {Human (Homo sapiens)}
VQDPPELEAVEVKQPEDRKPYLWIKWSPPTLIDLKTGWFTLLYEIRLKPEKAAEWIHF
GQQTEFKILSLHPGQKYLVRCKPDHGYWSAWSPATFIQIPS

>d1iarb1 b.1.2.1 (B:1-96) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}
FKVLQEPTCVSDYMSISTCEWKMNPTNCSTELRLLYQLVFLLEAHTCIPENNGGAGCV
CHLLMDDVVSADNYTDLWAGQQLLWKGSKFPSEHV

>d1iarb2 b.1.2.1 (B:97-197) Interleukin-4 receptor alpha chain {Human (Homo sapiens)}
KPRAPGNLTVHTNVSDTLLLTWSNPYPDPNYLYNHLTYAVNIWSENDPADFRIYNVTYLEP
SLRIAASLTKSGISYRARVRAWAQAYNTTWSEWSPSTKWH

>d1egja_ b.1.2.1 (A:) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}
IQMAPPSLNVTKDGSYSLRWETMKMRYEHIDHTFEIQYRKDTATWKDSKTETLQNAHS
MALPALEPSTRYWARVRVRSRTGYNGIWSEWSEARSWDTES

>d1gh7a1 b.1.2.1 (A:1-103) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}
EETIPLQTLRCYNDYTSHITCRWADTQDAQRLVNVTLIRRVNEDLLEPVSCDLSDDMPWS
ACPHPRCVPRRCVIPCQSFVVTDDVDFSFQPDRLGTRLTVTL

>d1gh7a2 b.1.2.1 (A:104-217) Common beta-chain in the GM-CSF, IL-3 and IL-5 receptors {Human (Homo sapiens)}
TQHVQPPEPRDLQISTDQDHFLTWSVALGSPQSHWLSPGDLEFEVVYKRLQDSWEDAAI
LLSNTSQATLGPEHLMPSSTYVARVRTRLAPGSRLSGRPSKWSPEVCWDSQPGD

>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 AVLSCSWEV RKEVASSVSFGLFYKPSPDAGSAVLLREEECSPVLREG
LGLSLHTRHHCQIPVPDPATHGQYIVSVQPRRAEKHIKS

>d1cd9b1 b.1.2.1 (B:1-107) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse
(Mus musculus)}

AGYPPASPSNLSCLMHLTTNSLVCQWEPGPETHLPTSFILKSFRSRADCQYQGDTPDCVAK
KRQNNCSIPRKNLLLYQYMAIWVQAENMLGSSSESPKLCLDPMDVV

>d1cd9b2 b.1.2.1 (B:108-213) Granulocyte colony-stimulating factor (GC-SF) receptor {Mouse
(Mus musculus)}

KLEPPMLQALDIGPDVVSHQPGCLWLSWKPWKPSEYMEQECELRYQPQLKGANWTLVF
HLPSSKDQFELCGLHQAPVYTLQMRCIRSSSLPGFWSPWSPGLQLRPTM

>d1fyhb1 b.1.2.1 (B:12-109) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}
VPTPTNVTIESYNMNPVYWEYQIMPQVPVFTVEVKNYGVKNSEWIDACINISHHYCNISD
HVGDPNSLSLWVRVKARVGQKESAYAKSEEFACVCRDGK

>d1fyhb2 b.1.2.1 (B:110-223) Interferon-gamma receptor alpha chain {Human (Homo sapiens)}
IGPPKLDIRKEEKQIMIDIFHPSVFNVDGEQVDYDPETTCYIRVYNVYVRMNGSEIQYKIL
TQKEDDCDEIQCLAIQVSSLNSQYCVSAEGLVHVGVTTEKSKEVCITIFN

>d1bqua1 b.1.2.1 (A:5-99) Cytokine receptor gp130 cytokine-binding domains {Human (Homo
sapiens)}

GLPPEKPKNLSCIVNEGKKMRCEWDGGRETHLETNFTLKSEWATHKFADCKAKRDTPTS
CTVDYSTVYFVNIEVWVEAENALGKVTSDHINFDPV

>d1bqua2 b.1.2.1 (A:100-214) Cytokine receptor gp130 cytokine-binding domains {Human
(Homo sapiens)}

YKVKPNPPHNLVINSEELSSILKLTWTNPSIKSVIILKYNIQYRTKDASTWSQIPPEDTASTR
SSFTVQDLKPFTEYVFRIRCMKEDGKGYWSDWSEEASGITYEDRPSKEPSF

>d1liral b.1.2.1 (A:2-101) Cytokine receptor gp130 cytokine-binding domains {Human (Homo
sapiens)}

LLDPCGYISPSPVQLHSNFTAVCVLKEKCMDYFHVNANYIVWKTNHFTIPKEQYTIINR
TASSVTFTDIASLNILTCNLTFGQLEQNVYGITISG

>d1j7vr1 b.1.2.1 (R:2-100) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}
GTELPSPSPVWFEEFFHHILHWTPIPQQSESTCYEVALLRYGIESWNSISQCSQTLSDYDLTA
VTLDLYHSNGYRARVRAVDGSRHSQWTVTNTRFSVD

>d1j7vr2 b.1.2.1 (R:101-206) Interleukin-10 receptor 1, IL-10R1 {Human (Homo sapiens)}
EVTLTVGSVNLEIHNGFILGKIQLPRPKMAPAQDTYESIFSHFREYEIAIRKVPQGQFTFTHKK
VKHEQFSLTSGEVGEFCVQVKPSVASRSNKGMSKEECISLT

>d1bpv__ b.1.2.1 (-) Type I titin module {Human (Homo sapiens)}
SPIDPPGKPVPLNITRHTVTLKWAKPEYTGFGKITSYIVEKRDLPNGRWLKANFSNILENEF
TVSGLTEDAAAYEFRIAKNAAGASPPSEPSDAITCRDDVEA

>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)}

GIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTC
GAATLSAERVGRDNKEYEYSVEQCEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRD
II

>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)}

KPDPPKNLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTD
KTSATVICRKNASISVRAQDRYYSSSWSEWASVPCS

>d1jz8a1 b.1.4.1 (A:220-333) beta-Galactosidase, domains 2 and 4 {Escherichia coli}
TQISDFHVATRFNDDFSRAVLEAEVQMCGELRDYLRVTVSLWQGETQVASGTAPFGGEIID
ERGGYADRVTLRLNVENPKLWSAEIPNLYRAVVELHTADGTLIEAEACDVGFR

>d1jz8a2 b.1.4.1 (A:626-730) beta-Galactosidase, domains 2 and 4 {Escherichia coli}
FFQFRLSGQTIEVTSEYLFRHSDNELLHWMVALDGGKPLASGEVPLDVAPQGGKQLIELPELP
QPESAGQLWLTVRVVPNATAWSEAGHISAWQQWRLAENLSVTL

>d1bhga1 b.1.4.1 (A:226-328) beta-Glucuronidase {Human (Homo sapiens)}
TYIDDITVTTVEQDSGLVNYQISVKGSNLFKLEVRLDAENKVANGTGTQGGQLKVPGV
SLWWPYLMHERPAYLSLEVQLTAQTSGLPVSDFYTLPGVIRT

>d1fl3a2 b.1.5.1 (A:516-627) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}
SNVDMDFEVENAVLGKDFKLSITFRNNSHNRYTITAYLSANITFYTGVPKAEFKKETFDVT
LEPLSFKKEAVLIQAGEYMGQLEQASLHFFVTARINETRDVLAKQKSTVL

>d1fl3a3 b.1.5.1 (A:628-728) Transglutaminase, two C-terminal domains {Human (Homo sapiens)}
TIPEIIKVRGTQVVGSMDMTVTVEFTNPLKETLRNVVHLDGPGVTRPMKKMFREIRPNST
VQWEEVCRPWVSGHRKLIASMSSDSLHVYGELDVQIQRR

>d1g0da2 b.1.5.1 (A:472-583) Transglutaminase, two C-terminal domains {Red sea bream
(Chrysophrys major)}
RLQLSIKHAQPVFGTDFDVIVEVKNEGGRDAHAQLTMLAMAVTYNSLRRGECQRKTISVT
VPAHKAHKEVMRLHYDDYVRCVSEHHLIRVKALLDAPGENGPIMTVANIPLS

>d1g0da3 b.1.5.1 (A:584-684) Transglutaminase, two C-terminal domains {Red sea bream
(Chrysophrys major)}
TPELLVQVPGKAVVWEPLTAYVSFTNPLPVPLKGGVFTLEGAGLLSATQIHVNGAVAPSGK
VSVKLSFSPMRTGVRKLLVDFDSDRLKDVKGVTTVVVHKK

>d1ncia_ b.1.6.1 (A:) N-cadherin (neural) {Mouse (Mus musculus)}
GSDWVIPPINLPENSRGPFQELVRIRSGRDKNLSLRYSVTGPGADQPPTGIFIINPISGQLSV
TKPLDRELIARFHLRAHAVDINGNQVENPIDIVINVID

>d1ncja2 b.1.6.1 (A:102-215) N-cadherin (neural) {Mouse (Mus musculus)}
NDNRPEFLHQVWNGSVPEGSKPGTYVMTVTAIDADDPNALNGMLRYRIVSQAPSTPSPN
MFTINNETGDIITVAAGLDREKVQQYTLIIQATDMEGNPTYGLSNTATAVITVTD

>d1noa__ b.1.7.1 (-) Neocarzinostatin {Streptomyces carzinostaticus}
AAPTATVTPSSGLSDGTVVKVAGAGLQAGTAYDVGQCAWVDTGVLACNPADFSSVTADA
NGSASTSLTVRRSFEGFLFDGTRWGTVDCTTAACQVGLSDAAGNGPEGVAISFN

>d1akp__ b.1.7.1 (-) Kedarcidin (apo form) {Actinomycete, strain L585-6}
ASAAVSVPATGLADGATVTVSASGFATSTSATALQCAILADGRGACNVAEFHDFSLSGGE
GTTSVVVRRSFTGYVMPDGPEVGAVDCDTPAGGCEIVVGGNTGEYGNAAISFG

>d1srda_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Spinach (Spinacia
oleracea)}
ATKKAVAVLKGTSNVEGVVTLTQEDDGPTTVNVRISGLAPGKHGFLHEFGDTTNGCMST
GPHFNPDKKTHGAPEDEV RHAGDLGNIVANTDGVAEATIVDNQIPLTGPNSSVGRALVVH
ELEDDLKGGGHELSPTTGNAGGRLACGVVGLTPV

>d1eqwa_ b.1.8.1 (A:) Cu,Zn superoxide dismutase, SOD {Salmonella typhimurium}
NTLTVKMNDALSSGTGENIGEITVSETPYGLLFTPHLNLTPGIHGFHVHTNPSCMPGMKD

GKEVPALMAGGHLDPKGTGKHLGPYNDKGHLGDLPLGLVNNADGTATYPLLAPRLKSLSE
LKGHSLMIHKGGDNYSKDPAPLGGGGARFACGVIE

>d1jk9b1 b.1.8.1 (B:74-245) Copper chaperone for superoxide dismutase, C-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}

GKPNSSAVAIETFQKYTIDQKKDTAVRGLARIVQVGENKTLFDITVNGVPEAGNYHASIH
EKGDVSKGVESTGKVWHKFDEPIECFNESDLGKNLYSGKTFLSAPLPTWQLIGRSFVSKS
LNHPENEPSSVKDYSFLGVIARSAGVWENNKQVCACTGKTVWEERKDALA

>d1qtsa1 b.1.10.1 (A:692-824) Alpa-adaptin AP2, N-terminal subdomain {Mouse (*Mus musculus*)}
GSPGIRLGSSDNFARFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFLNF
TPTLICADDLQTNLNLQTKPVDPTVDGGAQVQVQVNNIECISDFTEAPVLNIQFRYGGTFQN
VSVKLPITLNK

>d1e42a1 b.1.10.1 (A:705-824) Beta2-adaptin AP2, N-terminal subdomain {Human (*Homo sapiens*)}

GGYVAPKAVWLPAVKAKGLEISGTFTHRQGHIYMEMNFTNKALQHMTDFAIQFNKNSFG
VIPSTPLAIHTPLMPNQSIDVSLPLNTLGPVMKMEPLNNLQVAVKNNIDVFYFSCLIPLNV

>d1jv2a1 b.1.15.1 (A:439-598) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (*Homo sapiens*)}

PVITVNAGLEVYPSILNQDNKTCSLPGTALKVSCFNVRFLKADGKGVLPRLNLFQVELL
LDKLGKQGAIRRALFLYSRSPSHSKNMTISRGGMLQCEELIAYLRDESEFRDKLTPITIFME
YRLDYRTAADTTGLQPILNQFTPANISRQAHIILLDCGE

>d1jv2a2 b.1.15.1 (A:599-737) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (*Homo sapiens*)}

DNVCKPKLEVSVDSDQKKIYIGDDNPLTLIVKAQNNQGEAYEAELIVSIPLQADFIGVVRN
NEALARLSCAFKTENQTRQVVCDDLGNPMKAGTQLLAGLRFSVHQQSEMDTSVKFDLIQI
SSNLFDKVSPPVSHKVDLA

>d1jv2a3 b.1.15.1 (A:738-956) Thigh, calf-1 and calf-2 domains of integrin alpha {Human (*Homo sapiens*)}

VLAAVEIRGVSSPDHVFPIPNWEHKENPETEEDVGPVVQHIYELRNNGPSSFSKAMLHLQ
WPYKYNNNTLLYILHYDIDGPMNCTSDMEINPLRIKISSLQTTEKNDTVAGQGERDHLITK
RDLALSEGDIHTLGCQVAQCLKIVCQVGRDLRGKSAILYVKSLLWTETFMNKENQNHSYS
LKSSASFNVIEFPYKNLPIEDITNSTLVTTNVTWGIQ

>d1jv2b1 b.1.15.1 (B:55-106,B:355-434) Hybrid domain of integrin beta {Human (*Homo sapiens*)}
EFPVSEARVLEDRPLSDKSGDSSQVTQVSPQRIALRLRPDDSKNFSIQVRQXVELEVRL
PEELSLSFNATCLNNEVIPGLKSCMGLKIGDTVFSFIEAKVRGCPQEKEKSFTIKPVGFKDS
LIVQVTFDCD

>d1qpxa1 b.1.11.1 (A:1-124) Pilus chaperone PapD, N-domain {Escherichia coli}
AVSLDRTRAVFDGSEKSMTLDISNDNKQLPYLAQAWIENENQEKIITGPVIATPPVQRLDPG
AKSMVRLSTTPDISKLQDRESLFYFNLRIPRSEKANVVQIALCTKIKLFYRPAAIKTRP

>d1quna1 b.1.11.1 (A:1-121) Periplasmic chaperone FimC {Escherichia coli}

GVALGATRVIYPAGQKQVQLAVTNNDENSTYLIQSWVENADGVKDGRFIVTPPLFAMKGG
KENTLRILDATNNQLPQDRESLFWMNVAIPSMDSKLTENTLQLAIISRIKLYRPAKLA

>d1dqia_ b.1.13.1 (A:) Superoxide reductase (SOR) {Archaeon *Pyrococcus furiosus*}
MISSETIRSGDWKGEKHVPVIEYEREGELVKVKVQVGKEIPHPNTTEHHIRYIELYFLPEGEN
FVYQVGRVEFTAHGESVNGPNTSDVYTEPIAYFVLKTKKKGKLYALSYCNIHGLWENEVT

LE

>d1dfx_1 b.1.13.1 (37-125) Desulfoferrodoxin C-terminal domain {Desulfovibrio desulfuricans}

VEGSTDGAMEKHVPVIEKVDGGYLIKVGSVPHPMEEKHWIEWIELLADGRSYTKFLKPG
DAPEAFFAIDASKVTAREYCNLHGHWKAEN

>d1f00i1 b.1.14.1 (I:658-752) Intimin {Escherichia coli}

ASITEIKADKTTAVANGQDAITYTVKVMKGDKPVSNQEVTFTTTLGKLSNSTEKTDTNGY
AKVTLTSTTPGKSLVSARVSDVAVDVKAPEVEFFT

>d1f00i2 b.1.14.1 (I:753-841) Intimin {Escherichia coli}

TLTIDDGNIEIVGTGVKGKLPTVWLQYGQVNLKASGGNGKYTWRSANPAIASVDASSGQ
VTLKEKGTTTISVISSDNQTATYTIATPNS

>d1cwva2 b.1.14.1 (A:597-692) Invasin {Yersinia pseudotuberculosis}

TIAADKSTLAAVPTSIIADGLMASTITLELKDTYGDPQAGANVAFDRTLGNMGVITDHNDG
TYSAPLTSTTLGVATVTVKVDGAAFSVPSVTVNFT

>d1cwva3 b.1.14.1 (A:693-795) Invasin {Yersinia pseudotuberculosis}

ADPIPDAGRSSFTVSTPDILADGTMSSTLSFVPVDKNGHFISGMQGLSFTQNGVPVSISPITE
QPDSYTATVVGNSVGDVTITPQVDTLILSTLQKKISLFPV

>d1cwva4 b.1.14.1 (A:796-886) Invasin {Yersinia pseudotuberculosis}

PTLTGILVNGQNFAATDKGFPKTIFKNATFQLQMDNDVANNTQYEWSSSFTPNVSVNDQGG
VTITYQTYSEVAVTAKSKKFPSYSVSYRFYP

>d1exh__ b.2.2.1 (-) Exo-1,4-beta-D-glycanase (cellulase, xylanase), cellulose-binding domain, CBD {Cellulomonas fimi}

ASSGPAGCQVLWGVNQWNTGFTANVTVKNTSSAPVDGWTLTFSFSPSGQQVTQAWSSTVT
QSGSAVTVRNAPWNGSIPAGGTAQFGFNGSHTGTNAAPTAFLNGTPCTVG

>d1hejc_ b.2.2.1 (C:) Endo-1,4-beta xylanase D, xylan binding domain, XBD {Cellulomonas fimi}

TGSCSVSAVRGEEWADRFNVTYSVSGSSSWVVTGLNGGQSVQSSWNAALTGSSGTVTA
RPNNGSGNSFGVTFYKNGSSATPGATCATG

>d1g43a_ b.2.2.2 (A:) Cellulosomal scaffolding protein A, scaffoldin {Clostridium cellulolyticum}

AGTGVVSVQFNNGSSPASSNSIYARFKVTNTSGSPINLADLKLRYYYTQDADKPLTFWCD
HAGYMSGSNYIDATSKVTGSFKAVSPAVTNADHYLEVALNSDAGSLPAGGSIEIQTRFARN
DWSNFDQSNDSYTAAGSYMDWQKISAFVGGTLAGSTP

>d1tf4a2 b.2.2.2 (A:461-605) Endo/exocellulase:cellobiose E-4, C-terminal domain {Thermomonospora fusca}

PEIFVEAQINTPGTTTFTEIKAMIRNQSGWPARMLDKGTFRYWFTLDEGVDPADITVSSAYN
QCATPEDVHHVSGDLYYVEIDCTGEKIFPGGQSEHRREVQFRIAGGPGWDPSNDWSFQGI
GNELAPAPYIVLYDDGVPVWGTA

>d1aoha_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

AVRIKVDTVNAKPGDTRIPVRFSGPSKGIANCDFVYSYDPNVLEIIEIEPGELIVDPNPTK
SFDTAVYPDRKMIVFLFAEDSGTGAYAITEGDFVATIVAKVKSGAPNGLSVIKFVEVGGFAN
NDLVEQKTQFFDGGVNVG

>d1g1ka_ b.2.2.2 (A:) Cohesin domain {Clostridium thermocellum, cellulosome, various modules}

ASLKVTVTGTANGKPGDTRVPTVFADVAKMKNVGTCNFYLGYDASLLEVVSVDAGPIVK
NAAVNFSSASNGTISFLDNTITDELITADGVFANIKFKLKSVTAKTTTTPTVTFKDGGAFG
DGTMSKIASVTKTNGSVTIDPG

>d1qunb1 b.2.3.2 (B:1-158) Mannose-specific adhesin FimH {Escherichia coli}
 FACKTANGTAIPIGGGSANVYVNLAPVVNVGQNLVVDLSTQIFCHNDYPETITDYVTLQR
 GSAYGGVLSNFSGTVKYSGSSYPFPTTSETPRVVYNSRTDKPWPVALYLTPVSSAGGVAIK
 AGSLIAVLILRQTNNYNSDDFQFVWNIYANNDVVVPT

>d1qunb2 b.2.3.2 (B:159-279) Mannose-specific adhesin FimH {Escherichia coli}
 GGCDVSARDVTVTLPDYPGSGVPIPLTVYCAKSQNLGYLSGTTADAGNSIFTNTASFSPAQ
 GVGVLQTRNGTIIPANNTVSLGAVGTSASVSLGLTANYARTGGQVTAGNVQSIIGVTFVYQ

>d1pdkb_ b.2.3.2 (B:) PapK pilus subunit {Escherichia coli}
 LLDRPCHVSGDSLKNHVVFKTRASRDFWYPPGRSPTESFVIRLENCHATAVGKIVTLTFKG
 TEEAALPGHLKVTGVNAGRLGIALLDTDGSSLLKPGTSHNKGGQGEKVTGNSLELPFGAYV
 VATPEALRTKSVVPGDYEATATFELTYR

>d1ycsa_ b.2.5.1 (A:) p53 tumor suppressor, DNA-binding domain {Human (Homo sapiens)}
 VPSQKTYQGSYGFRGLHSGTAKSVTCTYSPALNKMFCQLAKTCPVQLWVDSTPPPGTR
 VRAMAIYKQSQHMTEVVRRCPHHERCSDSDGLAPPQHLIRVEGNLRVEYLDDRNTFRHS
 VVVPYEPPEVGSDCTTIHYNMCMSSCMGGMNRRPILTIITLEDSSGNLLGRNSFEVRVCA
 CPGRDRRTEEE

>d1imhc2 b.2.5.1 (C:188-367) Transcription factor TONEBP, DNA-binding domain {Human (Homo sapiens)}
 KKSPMLCGQYPVKSEGKELKIVVQPETQHRARYLTEGSRGSVKDRTQQGFPTVKLEGHN
 EPVVLQVFVGNDSGRVKPHGFYQACRVTGRNTTPCKEVDIEGTTVIEVGLDPSNNMTLAV
 DCVGILKLRLNADVEARIGIAGSKKKSTRARLVFRVNIMRKDGSTLTQLTPSSPILCTQPAG

>d1nfka2 b.2.5.1 (A:39-250) p50 subunit of NF-kappa B (NFKB), N-terminal domain {Mouse (Mus musculus)}
 GPYLQILEQPKQRGFRFRYVCEGSPSHGGLPGASSEKNKKSYPQVKICNYVGPAAKVVIVQLVT
 NGKNIHLHAHSLVKGHCEDGVCTVTAGPKDMVVGAFANLILHVTKKKVFETLEARMTEA
 CIRGYNPGLLVHSDLAYLQAEGGGDRQLTDREKEIIRQAAVQQTKEMDLSVVRLMFTAFL
 PDSTGSFTRRLEPVVSDAIYDSKAPNASNLKI

>d1bvoa_ b.2.5.1 (A:) Dorsal homologue Gambifl {African malaria mosquito (Anopheles gambiae)}
 PYVEITEQPHPKALRFRYECEGRSAGSIPGVNTTAEQKTFPSIQVHGYRGRAVVVVSCVTK
 EGPEHKPHPHNLVGKEGCKKGVCVEINSTTMSYTFNNLGIQCVKKKDVEEALRLRQEIR
 VDPFRITGFHGAKEPGSIDLNAVRLCFQVFLEGQQRGRFTEPLTPVVSIIYDKK

>d1xbra_ b.2.5.1 (A:) T domain from Brachyury transcription factor {African clawed frog (Xenopus laevis)}
 ELKVSLEERDLWTRFKELTNEMIVTKNGRRMFPVLKVSMGLDPNAMYTVLLDFVAADN
 HRWKYVNGEWWPGGKPEPQAPSCVYIHPDSPNFGAHWMKDPVSFSKVKLTKNMNGGG
 QIMLSNLHKYEPRIHIVRVGGTQRMITSFSFPETQFIAVTAYQNEEITALKIKHNPFKAFLD
 AKERN

>d1bgl2 b.2.5.1 (A:322-575) STAT3b {Mouse (Mus musculus)}
 VVERQPCMPMHPDRPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGS
 RKFNILGTNTKVMNMEESNNGSLSAEFKHLTLREQRCGNGGRANCDAASLIVTEELHLITFE
 TEVYHQGLKIDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWD
 QVAEVLWSQFSSTTKRGLSIEQLTTLAEKLLGPGVNYSGCQITWAKFCKENMAGKGFSEFW
 VWLDNIIDLKVKY

>d1h9da_ b.2.5.1 (A:) Acute myeloid leukemia 1 protein (AML1), RUNT domain {Human (Homo sapiens)}

VLADHPGELVRTDSPNFLCSVLPTHWRCNKTLPIAFKVVALGDVPDGLTVTMAGNDEN
YSAELRNATAAMKNQVARFNDLRFVGRSGRGKSFTLTITVFTNPPQVATYHRAIKITVDGP
REPRR

>d1qhoa2 b.3.1.1 (A:577-686) Cyclodextrin glycosyltransferase, C-terminal domain {Bacillus stearothermophilus, maltogenic alpha-amylase}

LSGTQTSVVFTVKSAPPTNLGDKIYLTGNIPELGNWSTDTSGAVNNAQGPLLAPNYPDW
YVFSVPAGKTIQFKFFIKRADGTIQWENGSNHVATTPTGATGNITVTWQN

>d1acz_ b.3.1.1 (-) Glucoamylase, granular starch-binding domain {Aspergillus niger}

CTTPTAVAVTFDLTATTTYGENIYLVGSISQLGDWETSDGIALSADKYTSSDPLWYVTVTL
PAGESFEYKFIRIESDDSVESDPNREYTVPQACGTSTATVTDWTR

>d1cqya_ b.3.1.1 (A:) beta-amylase {Bacillus cereus}

TPVMQTIIVVKNVPTTIGDTVYITGNRAELGSWDTKQYPIQLYYDSHSNDWRGNVVLPAER
NIEFKAFIKSKDGTVKSWQTIQQSWNPVPLKTTSTSSW

>d1dmha_ b.3.6.1 (A:) Catechol 1,2-dioxygenase {Acinetobacter calcoaceticus}

VKIFNTQDVQDFLRVASGLEQEGGNPRVKQIIHRVLSPLYKAIEDLNITSDEYWAGVAYLN
QLGANQEAGLLSPGLGFDHYLDMRMDAEDAALGIENATPRTIEGPLYVAGAPESVGYAR
MDDGSDPNGHTLILHGTIFDADGKPLPNAKVEIWHANTKGFYSHFDPTGEQQAFNMRRSI
ITDENGQYRVRTILPAGYGCPPEGPTQQLNLGRHGNRPAHIIHYFVSADGHRKLTQINV
AGDPYTYDDFAATREGLVVDVEHTDPEAIKANDVEGPFAEMVFDLKLRLVDGVDNQ
VVDRPRLAV

>d1eo9a_ b.3.6.1 (A:) Protocatechuate-3,4-dioxygenase, alpha chain {Acinetobacter calcoaceticus, adp1}

ELKETPSQTGGPYVHIGLLPKQANIEVFEHNLDNNLVQDNTQGQRIRLEGQVFDGLSLPLR
DVLIEIWQADTNGVYPSQADTQGKQVDPNFLGWGRTGADFGTGFWSFNTIKPGAVPGRK
GSTQAPHISLIIFARGINIGLHTRVYFDDEAEANAKDPVLNSIEWATRRQTLVAKREERDGE
VVYRFDIRIQGENETVFFDI

>d1eo9b_ b.3.6.1 (B:) Protocatechuate-3,4-dioxygenase, beta chain {Acinetobacter calcoaceticus, adp1}

IIWGAYAQRNTEDHPPAYAPGYKTSVLRSPKNALISIAETLSEVTAPHFSADKFGPKDNDLI
LNYAKDGLPIGERVIVHGYVRDQFGRPVKNALVEVWQANASGRYRHPNDQYIGAMDPNF
GGCGRMLTDDNGYYVFRTIKPGYPWRNRINEWRPAHIIHFSLIADGWAQRLISQFYFEGD
TLIDSCPILKTIPSEQRRALIALEDKSNFIEADSRCYRFDITLRGRRATYFENDLT

>d1c3ga1 b.4.1.1 (A:180-259) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}

ETVQVNLPVSLEDLFVGKKKSFKIGRKGPHGASEKTQIDIQLKPGWKAGTKITYKNQGDY
NPQTGRRKTLQFVIEKSHP

>d1c3ga2 b.4.1.1 (A:260-349) Heat shock protein 40 Sis1 {Baker's yeast (Saccharomyces cerevisiae)}

NFKRDGDDLIYTLPLSFKESLLGFSKTIQTIDGRTLPLSRVQPVQPSQTSTYPGQGMPTPKN
PSQRGNLIVKYKVDYPISLNDQAQKRAID

>d1id2a_ b.6.1.1 (A:) Amicyanin {Paracoccus versutus (Thiobacillus versutus)}

QDKITVTSEKPVAAADVPAADVVGIEKMKYLTPEVTIKAGETVYWVNGEVMPHNVAFK

KGIVGEDAFRGEMMTKDQAYAITFNEAGSYDYFCTPHPFMRGKVIVE
>d1kdj__ b.6.1.1 (-) Plastocyanin {Fern (*Adiantum capillus-veneris*)}
AKVEVGDEVGNFKFYPPDSITVSAGEAVEFTLVGETGHNIVFDIPAGAPGTVASSELKAASMD
ENDLLSEDEPSFKAKVSTPGTYTFYCTPHKSANMKGTLTVK
>d1nin__ b.6.1.1 (-) Plastocyanin {*Anabaena variabilis*}
ETYTVKLGSDKGLLVFEPAKLTIKPGDTVEFLNNKVPPHNVVFDAAALNPAKSADLAKSLS
HKQLLMSPGQSTSTTFPADAPAGEYTFYCEPHRGAGMVGKITVAG
>d1bqk__ b.6.1.1 (-) Pseudoazurin {*Achromobacter cycloclastes*}
ADFEVHMLNKGKDGAMVFEPASLKVAPGDTVTFIPTDKGHNIVETIKGMIPDGAEAFKSKI
NENYKVTFAPGVYGVKCTPHYGMGMVGVVQVGDAPANLEAVKGAKNPKKAQERLDA
ALAALGN
>d2cbp__ b.6.1.1 (-) Plantacyanin {Cucumber (*Cucumis sativus*)}
AVYVVGSGSGWTFNTESWPKGKRFRAGDILLFNYNPSMHNVVVVNQGGFSTCNTPAGA
KVYTSGRDQIKLPKGQSYFICNFPGHCQSGMKIAVNAL
>d1cc3a__ b.6.1.1 (A:) Azurin {*Pseudomonas aeruginosa*}
AECSVDIQGNDQMVFNTNAITVDKSKQFTVNLSHPGNLPKNVMGHNWVLSTAADMQG
VVTGDMASGLDKDYLPDDSRVIAHTKLIGSGEKDSVTFDVSCLKKEGEQYMFFCSELCGI
NHALMKGTLTLK
>d1qhqa__ b.6.1.1 (A:) Auracyanin {*Chloroflexus aurantiacus*}
ANAPGGSNNVNETPAQTVEVRAAPDALAFAQTSLSLPANTVVRLDFVNQNNLGVQHNW
VLVNGGDDVAAAVNTAAQNNADALFVPPDTPNALAWTAMLNAGESGSVTFRTAPPGTY
LYICTFPGHYLAGMKGTLTVTP
>d1e30a__ b.6.1.1 (A:) Rusticyanin {*Thiobacillus ferrooxidans*}
LDTTWKEATLPQVKAMLEKDTGKVS GDTVYSGKTVHVVA AAVLPGFPPSFVHDKKN
PTLEIPAGATVDVTFINTNKGFGHSFDITKKGPPYAVMPVIDPIVAGTGFSPVPKDGKFGYT
NFTWHPTAGTYYYVCQIPGHAATGQFGKIVVK
>d1jer__ b.6.1.1 (-) Stellacyanin {Cucumber (*Cucumis sativus*)}
MQSTVHIVGDNTGWSVPSSPNFYSSQWAAGKTRVGDLSLQFNFPANAHNHHEMETKQSFD
ACNFVNSDNDVERTSPVIERLDELGMHYFVCTVGTHCSNGQKLSINVVAAN
>d1libya__ b.6.1.4 (A:) Red copper protein nitrosocyanin {*Nitrosomonas europaea*}
EHNFNVINAYDTTIPELNVGVTVKNI RAFNV LNEPETLVVKKGD AVKVVENKSPISEG
FSIDAFGVQEVIKAGETKTISFTADKAGAFIWCQLHPKNIHLPGTLNVVE
>d1fwxa1 b.6.1.4 (A:452-581) Nitrous oxide reductase, C-terminal domain {*Paracoccus denitrificans*}
SVWDRNDPMWAETRAQAEADGVDIDNWTEEVIRDGNKVRVYMSSVAPSFSIESFTVKEG
DEVTIVITNLDEIDDLTHGFTMGNYGVAMEIGPQMTSSVTFVAANPGVYWYYCQWFCHA
LHMEMRGRMLVEPK
>d1ffb1 b.6.1.2 (B:118-283) Quinol oxidase (CyoA) {*Escherichia coli*}
KPLAHDEKPITIEVVSMDWKWFFIYPEQGIATVNEIAFPANTPVYFKVTSNSVMNSFFIPRL
GSQIYAMAGMQTRLHLIANEPGTYDGISASYS GPGFSGMKFKAIATPDRAAFDQWVAKAK
QSPNTMSDMAAFEKLAAPSEYNQVEYFSNVKPDLFADVINKFMA
>d1ar1b1 b.6.1.2 (B:108-252) Cytochrome c oxidase {*Paracoccus denitrificans*}
NDPDLVIKAIHQWYWSY EYPNDGVAFDALMLEKEALADAGYSEDEYLLATDNPVVVP
VGKKVLVQVTATDVIHAWTIPAFAVKQDAVPGRIAQLWFSVDQEGVYFGQCSELCGINHA

YMPIVVKAVSQEKYEAWLAGAKEEFAA

>d2cuab_ b.6.1.2 (B:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AYTLATHTAGVIPAGKLERVDPTTVRQEGPWADPAQAVVQTGPNQYTVYVLAFAGFYQPN
PIEVPQGAIEVFKITSPDVIHGFHVVEGTNINVEVLPGEVSTVRYTFKRPGEYRIICNQYCGLG
HQNMFGTIVVKE

>d1j9qa1 b.6.1.3 (A:4-166) Nitrite reductase, NIR {Alcaligenes faecalis, strain s-6}

ATAAEIAALPRQKVELVDPPFVHAHSQVAEGGPKVVEFTMVIEKKIVIDDAGTEVHAMA
FNGTVPGLMVVHQDDYLELTLPETNTLMHNNFHAATGALGGGGLTEINPGEKTILRF
KATKPGVFVYHCAPPGMVPWHVVS GMNGAIMVLPREGLHDGK

>d1gs7a2 b.6.1.3 (A:160-336) Nitrite reductase, NIR {Alcaligenes xylosoxidans}

QGKPLHYDRAYTIGFEFDLYIPKGPDKYKDYATLAESYGDTVQVMRTLTPSHIVFNGKVG
ALTGANALTAKVGETVLLIHSQANRDTRPHLIGGFGDWVWETGKFANPPQRDLETWFIRG
GSAGAALYTFKQPGVYAYLNHNLIIEAFELGAAGHIKVEGKWNDLMLKQIKAPAPIPR

>d1kbva1 b.6.1.3 (A:13-163) Nitrite reductase, NIR {Neisseria gonorrhoeae, AniA}

ELPVIDAVTTHAPEVPPAIDRDYPAKVRVKMETVEKTMKMDDGVEYRYWTFDGDVPGR
MIRVREGDTVEVEFSNNPSSTVPHNVDFHAATGQGGGAAATFTAPGRTSTFSFKALQPGLY
IYHCAVAPVGMHIANGMYGLILVEPKEGLPKV

>d1kbva2 b.6.1.3 (A:164-314) Nitrite reductase, NIR {Neisseria gonorrhoeae, AniA}

DKEFYIVQGDFYTKGKKGAQGLQPFDMDKAVAEQPEYVVFNGHVGALTGDNALKAKAG
ETVRMYVGNNGPNLVSSFHVIGEIFDKVYVEGGKLINENVQSTIVPAGGSAIVEFKVDIPG
NYTLVDHSIFRAFNKGALGQLKVEGAENPEIM

>d1kv7a1 b.6.1.3 (A:31-170) multi-copper oxidase CueO {Escherichia coli}

RPTLPIPDLLTTDARNRIQLTIGAGQSTFGGKTATTWGYNGNLLGPAVKLQRGKAVTVDIY
NQLTEETTLHWHGLEVPGEVDGGPQGIIPPGGKRSVTLNVDQPAATCWFHPHQHGKTGR
QVAMGLAGLVVIEDDEILKL

>d1kv7a2 b.6.1.3 (A:171-335) multi-copper oxidase CueO {Escherichia coli}

MLPKQWGIDDPVIVQDKKFSADGQIDYQLDVMATAAVGWFGDTLLTNGAIYPQHAAPRG
WLRLRLNLCNARSLNFATSDNRPLYVIASDGGLLPEPVKVSELPLVMGERFEVLVEVND
NKPFDLVTLPLVSQMGMAIAPFDKPHPMRIQPIAISASGALPDTLS

>d1kv7a3 b.6.1.3 (A:336-516) multi-copper oxidase CueO {Escherichia coli}

SLPALPSLEGLTVRKLQLSMDPMLDMMGMQMLMEKYGDQAMAGMDHSQMMGHMGMH
GNMNMNMNHGGKFDFFHHANKINGQAFDMNKPMFAAAKGQYERWVISGVGDMMLHPFHI
HGTQFRILSENGKPPAAHRAGWKDVTVKVEGNVSEVLVKNHHDAPKEHAYMAHCHLLEH
EDTGMMMLGFTV

>d1aoza1 b.6.1.3 (A:1-129) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}

SQIRHYKWEVEYMFWAPNCNENIVMGINGQFPGPTIRANAGDSVVVELTNKLHTEGVVIH
WHGILQRGTPWADGTASISQCAINPGETFFYNFTVDNPGTFFYHGHLGMQRSAGLYGSLIV
DPPQGKKE

>d1aoza2 b.6.1.3 (A:130-338) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}

PFHYDGEINLLLSDWWHQSIHKQEVGLSSKPIRWIGEPQTILLNGRGQFDCSIAAKYDSNL
EPCKLKGSSECAPYIFHVSPKKTYRIRIASTTALAALNFAIGNHQLLVVEADGNYVQPFYTS
DIDIYSGESYSVLITTDQNPSENYWVSVGTRARHPNTPPGLTLLNYLPNSVSKLPTSPPPQT
PAWDDFDRSKNFTYRITAAMGSPK

>d1aoza3 b.6.1.3 (A:339-552) Ascorbate oxidase {Zucchini (Cucurbita pepo medullosa)}

PPVKFNRRIFLLNTQNVINGYVKWAINDVSLALPPTPYLGAMKYNLLHAFDQNPPPEVFPE
DYDIDTPPTNEKTRIGNGVYQFKIGEVDVILQANMMKENLSETHPWHLHGHDFWVLG
YGDGKFSAAEESSLNLKNPPLRNTTVVIFPYGWTAIRFVADNPGVWAFHCHIEPHLMGMG
VFAEGVEKVGRIPTKALACGGTAKSLINNPKNP

>d1hfua1 b.6.1.3 (A:1-131) Laccase {Inky cap fungus (Coprinus cinereus)}
AIVNSVDTMTLTNANVSPDGFTRAGILVNGVHGPLIRGGKNDNFELNVNDLDNPTMLRP
TSIHHWGLFQRGTNWADGADGVNQCISPFGHAFLYKFTPAGHAGTFWYHSHFGTQYCDG
LRGPMVIYDDND

>d1hfua2 b.6.1.3 (A:132-303) Laccase {Inky cap fungus (Coprinus cinereus)}
PHAALYDEDDENTIITLADWYHIPAPSIQGAAQPDATLINGKGRYVGGPAAELSIVNVEQG
KKYRMRLISLSCDPNWQFSIDGHELTIIIEVDGELTEPHTVDRLQIFTGQRYSFVLNANQPVD
NYWIRAQPNKGRNGLAGTFANGVNSAILRYAGAANADPTTSANPNPAQL

>d1hfua3 b.6.1.3 (A:304-503) Laccase {Inky cap fungus (Coprinus cinereus)}
NEADLHALIDPAAPGIPTGAADVNLRFQLGFSGGRFTINGTAYESPSVPTLLQIMSGAQSA
NDLLPAGSVYELPRNQVVELVVPAGVLGGPHPFHLHGHAHSVRSAGSSTYNFVNPVKR
DVVSLGVTGDEVITIRFVTDNPGPWFFHCHIEFHLMNGLAIVFAEDMANTVDANNPPVEW
AQLCEIYDDLPEATSIQTV

>d1kew_1 b.6.1.3 (1-192) Ceruloplasmin {Human (Homo sapiens)}
KEKHYIIGIIEETTWDYASDHGEKKLISVDTEHSNIYLQNGPDRIGRLYKKALYLQYTDETF
RTTIEKPVWLGLFLGPIIKAETGDKVYVHLKNLASRPYTFHSHGITYYKEHEGAIPDNTTD
FQRADDKVYPGEQYTYMLLATEEQSPGEGDGNCVTRIHSHIDAPKDIASGLIGPLICKK
DSLDEKEKEK

>d1kew_3 b.6.1.3 (347-553) Ceruloplasmin {Human (Homo sapiens)}
IRGKHVRHYIIAAEEIHWNYAPSGIDIFTKENLTAPGSDSAVFFEQGTTRIGGSYKKLVYREY
TDASFTNRKERGPREEHLGILGPVIWAEVGDITRVTFHNKGAYPLSIEPIGVRFNKNNEGTY
YSPNYNPQSRSPPSASHVAPTETFTYEWTVPKEVGPTNADPVCLAKMYYSAVDPTKDIF
TGLIGPMKICKKGS LHANGRQK

>d1kew_4 b.6.1.3 (554-705) Ceruloplasmin {Human (Homo sapiens)}
DVDKEFYLFPTVFDENESLLEDNIRMFTTAPDQVDKEDEDFQESNKMHSMNFGMYGNQ
PGLTMCKGDSVVWYLFSAAGNEADVHGIYFSGNTYLWRGERRDANLFPQTSLTLMWPD
TEGTFNVECLTTDHYTGGMKQKYTVNQCRQSED

>d1qsa2 b.7.1.1 (A:626-756) PI-specific phospholipase C isozyme D1 (PLC-D1), C-terminal domain {Rat (Rattus norvegicus)}
WRPERLRVRIISGQQLPKVNKNKNSIVDPKVIVEIHGVGRDTGSRQTAVITNNGFNPRWDM
EFEFEVTVPDALVRFMVEDYDSSSKNDFIGQSTIPWNSLKQGYRHVHLLSKNGDQHPSA
TLFVKISIQD

>d1rlw__ b.7.1.1 (-) Domain from cytosolic phospholipase A2 {Human (Homo sapiens)}
SSHKFTVVVLRATKVTKGAFGDMLDTPDPYVELFISTTPDSRKTRHFNNNDINPVWNETF
EFILDPNQENVLEITLMDANYVMDETLGTATFTVSSMKVGEKKEVPFIFNQVTEMVLEMS
LEVASS

>d1d5ra1 b.7.1.1 (A:188-351) Pten tumor suppressor (Phosphoinositide phosphatase), C-terminal domain {Human (Homo sapiens)}
YRPVALLFHKMMFETIPMFSGGTCNPQFVVCQLKVKIYSSNSGPTRREDKFMFYFEPQPLP
VCGDIKVEFFHKQNKMLKKDKMFHFWVNTFFIPGPVEVDNDKEYLVLTLTKNDLKANK

DKANRYFSPNFKVKLYFTKTV

>d1e8xa2 b.7.1.1 (A:357-522) Phosphoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}

CDRKFRVKIRGIDIPVLPRTADLTVFVEANIYQGQQVLCQRRTPSPKPFTEEVLWNVWLEFSI
KIKDLPGKALLNLQIYCGKAPALSGKTS AEMPSPEKSGKAQLLYVNLLIDHRFLLRHGE
YVLHMWQLSGKGEDQGSFNADKLTSATNPDKENSMSISILLDN

>d1bdya_ b.7.1.1 (A:) Domain from protein kinase C delta {Rat (Rattus norvegicus)}

MAPFLRISFNSYELGSLQAEDDASQPFCAVKMKEALTDRGKTLVQKKPTMYPEWKSTFD
AHIEGRVIQIVLMRAAEDPMSEVTVGVSVLAERCKKNNGKA EFWLDLQPQAKVLMCV
QYFLE

>d1gmia_ b.7.1.1 (A:) Domain from protein kinase C epsilon {Rat (Rattus rattus)}

MVVFNGLLKIKICEAVSLKPTAWSLRDAVGPRPQTFLDPYIALNVDDSRIGQTATKQKTN
SPAWHDEFVTDVCNGRKIELAVFHDAPIGYDDFVANCTIQFEELLQNGSRHFEDWIDLEPE
GKVYVIIDLSGSSG

>d1k5wa_ b.7.1.2 (A:) Synaptogamin I {Rat (Rattus norvegicus)}

KLGDICFSLRYVPTAGKLTVVILEAKNLKKMDVGGSDPYVKIHLMQNGKRLKKKKTTIK
KNTLNPYYNESFSFEVPFEIQKVQVVTVLDYDKIGKND AIGKVFGYNSTGAELRHW
SDMLANPRRPIAQWHTLQVEEEVDAMLAV

>d1rsy__ b.7.1.2 (-) Synaptogamin I {Rat (Rattus norvegicus)}

GGGILDSMVEKEEPKEEEKLGKLQYSLDYDFQNNQLLVGIIQAAELPALDMGGTSDPYVK
VFLLPDKKKKFETKVHRKTLNPFVNEQFTFKVPYSELGGKTLVMAVYDFDRFSKHDIIGEF
KVPMNTVDFGHVTEEWRLQSA

>d1dsya_ b.7.1.2 (A:) C2 domain from protein kinase c (alpha) {Rat (Rattus norvegicus)}

TEKRGRILIYKAEVTDEKLHVTVRDAKNLIPMDPNGLSDPYVKLKLIPDPKNESKQKTKTI
RSTLNPQWNESTFTKLKPSDKDRRLSVEIWDWDRTRNDFMGSLSGVSELMKMPASGW
YKLLNQEEGEYYNVPIPE

>d1qpxa2 b.7.2.1 (A:125-215) PapD {Escherichia coli}

NEVWQDQLILNKVSGGYRIENPTYVYTVIGLGGSEKQAE EGEFETVMLSPRSEQTVKSA
NYNTPYLSYINDYGGRPVLSFICNGSRCVK

>d1quna2 b.7.2.1 (A:122-205) FimC {Escherichia coli}

LPPDQAAEKLRFRRSANSLTLINPTPYLTVTTELNAGTRVLENALVPPMGESAVKLPSDAG
SNITYRTINDYGALTPKMTGVME

>d1kvp__ b.10.1.1 (-) Bacteriophage capsid proteins {Bacteriophage phi-X174}

SNIQTGAERMPHDLSHLGFLAGQIGRLITISTTPVIAGDSFEMDAVGALRLSPLRRGLAIDS
TVDIFTFYVPHRHVYGEQWIKFMKDGVNATPLPTVNTTGYIDHAAFLGTINPDTNKIPKHL
FQGYLNIYNNYFKAPWMPDRTEANPNELNQDDARYGFRCCHLKNIWTAPLPPELTSRQ
MTTSTGMAPVTTKFRDVPNLSGTPLIFRDNKGRTIKTGQLGIGPVDAGFLVAQNTAQAAAN
GERAIPSNLWADLSNATSIDIMGLQAAYANLHTDQERDYFMQRYRDVISSFGGKTSYDAD
NRPLLVMRSNLWASGYDVGTDQTSLGQFSGRVQQTYKHSVPRFFVPEHGTMTLALVR
FPPTATKEIQYLNAGALTYTDIAGDPVLYGNLPPREISMKDVFRSGDSSKKFKIAEGQWY
RYAPSYVSPAYHLLLEGFPFIQEPPSGDLQERVLIRHHDYDQCFQSVQLLQWNSQVKFNVTV
YRNLPTTRDSIMTS

>d1gff2_ b.10.1.1 (2:) Bacteriophage capsid proteins {Bacteriophage G4}

MFQKFISKHNAPINSTQLAATKTPAVAAPVLSVPNLSRSTILINATTTAVTTHSGLCHVVRID
ETNPTNHHALSIAGSLSNVPADMIAFAIRFEVADGVVPTAVPALYDVYPIETFNNGKAISFK

DAVTIDSHPRTVGNDVYAGIMLWSNAWTASTISGVLSVNQVNREATVLQPLK

>d1stma_ b.10.1.2 (A:) SPMV coat protein {Satellite panicum mosaic virus}

AAATSLVYDTCYVTLTERATTSFQRQSFPTLKGMDRAFQVVAFTIQGVSAAPLMYNARL
YNPGDTSVHATGVQLMGTVPRTVRLTPRVGQNNWFFGNTEEAETILADGLVSTKGANA
PSNTVIVTGCFLAPSELQSS

>d1a34a_ b.10.1.2 (A:) STMV coat protein {Satellite tobacco mosaic virus}

TGDNNSNVVTMIRAGSYPKVNPTPTWVRAIPFEVSVQSGIAFKVPVGSLSANFRDTSFTSV
TVMSVRAWTQLTPPVNEYSFVRLKPLFKTGDSTEEFEGRASNINTRASVGYRIPTNLRQNT
VAADNVCEVRSNCRQVALVISCCFN

>d2stv_ b.10.1.2 (-) STNV coat protein {Satellite tobacco necrosis virus}

TMRAVKRMINTHLEHKRFALINSGNTNATAGTVQNLSNGIIQGDDINQRSGDQVRIVSHKL
HVRGTAITVSQTFRFIWFRDNMNRGTTPTVLEVLNTANFMSQYNPITLQQKRFTILKDVTL
NCSLTGESIKDRIINLPGQLVNYNGATAVAASNGPGAIFMLQIGDSLVLWDSSYEAVYTDA

>d1smvc_ b.10.1.2 (C:) SMV coat protein {Sesbania mosaic virus}

QAGISMAPSAQGAMVRIRNPAVSSSRGAITVLHCELTAIEGVTDSIVVSSELVMPYTVGTW
LRGVADNWSKYSWLSVRYTYIPSCPSSTAGSIHMGFYDMADTVPVSVNKLNLRGYVS
GQVWSGSAGLCFINNSRCSDTSTAISTTLDVSELGKKWYPYKTSADYATAVGVDVNIATDL
VPARLVIALLDGSSSTAVAAGRIYDITYTIQMIPTASALNL

>d1f2nc_ b.10.1.2 (C:) RYMV capsid protein {Rice yellow mottle virus}

AEPQLQRAPVAQASRISGTVPGPLSSNTWPLHSVEFLADFKRSSTSADATTYDCVPFNLPR
VWSLARCYSMWKPTRWDVVYLPEVSATVAGSIEMCFLYDYADTIPRYTGKMSRTAGFVT
SSVWYGAEGCHLLSGGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVVNTILPARLAVR
SSIKPTVSDTPGKLYVIASMLRDPVDPTLNT

>d1bmvl_ b.10.1.2 (1:) BPMV coat protein {Bean pod mottle virus}

SISQQTVWNQMATVRTPLNFDSSKQSFCQFSVDLLGGGISVDKTGDWITLVQNSPISNLLR
VAAWKKGCLMVKVVMMSGNAAVKRSDWASLVQVFLTNSNSTEHFDACRWTKSEPHSWEL
IFPIEVCGPNNGFEMWSSEWANQTSWHLNFLVDNPKQSTTFDVLLGISQNFIEIAGNTLMPA
FSVPQ

>d1bmvl2_ b.10.1.2 (2:) BPMV coat protein {Bean pod mottle virus}

METNLFKLSLDDVETPKGSMLDLKISQSKIALPKNTVGGTILRSDLLANFLTEGNFRASVD
LQRTTHRIKGMIMVATVGIPENTGIALACAMNSSIRGRASSDIYTICSQDCELWNPACTKA
MTMSFNPNPCSDAWSLEFLKRTGFHCDIICVTGWTATPMQDVQVTIDWFISSQECVPRTYC
VLNPQNPFVLNRWMGKLTFPQGTSRSVKRMPLSIGGGAGAKSAILMNPNAVLSMWRYF
VGDLVFEVSKMTSPYIKCTVSFFIAFGNLADDTINFEAFPHKLVQFGEIQEKVVLKFSQEEF
LTAWSTQVRPATLLADGCPYLYAMVHDSSVSTIPGDFVIGVKLTIENMCAYGLNPGISGS
RLLGTIPQ

>d1a6ca1 b.10.1.2 (A:1-176) TRSV capsid protein {Tobacco ringspot virus}

AVTVVPDPTCCGTLSEFKVPKDAKKGKHLGTFDIRQAIMDYGGLHSQEWCAKGIVNPTFT
VRMHAPRNAFAGLSIACTFDDYKRIDLALGNECPPSEMFEPTKVFMKLDADVHEWQF
NYGELTGHGLCNWANVATQPTLYFFVASTNQVTMAADWQCIVTMHVDMGPVIDRFELN

>d1a6ca2 b.10.1.2 (A:177-348) TRSV capsid protein {Tobacco ringspot virus}

PTMTWPIQLGDTFAIDRYYEAKEIKLDGSTSMLSISYNFGGPVKHKKHAISYSRAVMSRN
LGWSGTISGSVKSVSLLFCTASFVIFPWECEAPPTLRQVLWGPHQIMHGDGQFEIAIKTRLH
SAATTEEGFGRLGILPLSGPIAPDAHVGSYEFIVHINTWRPDSQVHPPM

>d1a6ca3_b.10.1.2 (A:349-513) TRSV capsid protein {Tobacco ringspot virus}

FSSSELYNWFTLTNLKPDANTGVVNFIDIPGYIHDFASKDATVTLASNPLSWLVAATGWHY
GEVDLCISWSRSKQAQAQEGSVSITTNYRDWGAYWQQQARIYDLRRTEAEIPIFLGSYAG
ATPSGALGKQNYVRISIVNAKDIVALRVCLRPKSIKFWGRSATLF

>d2tbvc_b.10.1.2 (C:) TBSV coat protein {Tomato bushy stunt virus}

IITHVGGVGGSIMAPVAVSRLVGSKPKFTGRTSGGVTVTSHREYLTQVNNSSGFVVNGGI
VGNSLQLNPSNGTLFSWLPALASNFDQYSFNSVVLDDYVPLCGTTEVGRVALYFDKDSQDP
EPADRVELANFGVLKETAPWAEAMLRIPTDKVKRYCND SATVDQKLIDLGQLGIATYGGA
GADAVGELFLARSVTLYFPQPTNTLLSSKRLDLTGSLADATGPGYLVLTPTVLTHTFRAT
GTFNLSSGGLRCLTSLTLGATGAVVINDIL AIDNVGTASDYFLNCTVSSLPATVTFTVSGVAA
GILLVGRARANVVNLL

>d1cwpa_b.10.1.2 (A:) Cowpea chlorotic mottle virus {Host: cowpea (Vigna unguiculata), (L.)}

KAIAWTGYSVSKWTASCAA AEAKVTSAITISLPNELSSERNKQLKVGRVLLWLGLLPSV
SGTVKSCVTETQTAAASFQVALAVADNSKDVVAAMYPEAFKGITLEQLAADLTIYLYSSA
ALTEGDVIVHLEVEHVRPTFDDSFTPVY

>d1c8nc_b.10.1.2 (C:) TNV coat protein {Tobacco necrosis virus}

GVSRAAGFVTAPVIGAMVTRPTVPRFGMRGNSTVVSNSSELILNLTPIALAYTVQSLPLIATQ
PAWLGTIADNYSKWRWVSLRIIYSPKCPTTSTGTVAMCLSYDRNDVAPGSRVQLSQTYSKAI
NFPPYAGYDGAAILNTDVTPTSAIYVDVDVTRFDKAWYSTIGTAAFAALTAFDQNFQFCPT
VHIGSDGGPAVAVPPGDIFFKYVIELIEPINPTMN

>d1auyb_b.10.1.2 (B:) TYMV coat protein {Turnip yellow mosaic virus}

MEIDKELAPQDRVTVTATVLPVAVPGPSPLTIKQPFQSEVLFAGTKDAEASLTIANIDSVSTLT
TFYRHASLESLSWVTIHPTLQAPTFTTVGVCWVPAQSPVTPAQITKTYGGQIFCIGGAIQTL
SPLIVKCPLEMMQPRVKDSIQYLDSPKLLISITAQPTAPPASTCIITVSGTLSMHSPILTDTST

>d1e57b_b.10.1.2 (B:) PHMV coat protein {Physalis mottle virus}

VVKVKQASIPAPGSILSQPNTEQSPAIVLPFQFEATTFGTAEATAAQVSLQTADPITKLTAPYR
HAQIVECKAILTPTDLAVSNPLTVYLAWVPANSPATPTQILRVYGGQS FVLGGAISA AKTIE
VPLNLD SVNRM LKDSVTYTDTPKLLAYS RAPTNPSKIPTASIQISGRIRLSKPM LIAN

>d1f15b_b.10.1.2 (B:) CMV coat protein {Cucumber mosaic virus, strain fny}

DANFRVLSQQLSRLNKT LAAGRPTINHPTFVG SERCRPGYTFTSITLKPPKIDRGSYYGKRL
LLPDSVTEYDKKLVSRLQIRVNPLPKFDSTVWVTVRKVPASSDLSVA AISAMFADGAS PVL
VYQYAASGVQANNKLLYDLSAMRADIGDMRKYAVLVYSKDDALETDELVLHVDIEHQRI
PTSGVL PV

>d1nove_b.10.1.3 (C:) Nodavirus capsid protein {Nodamura virus}

RRRAAPRQQQRQQSNRASNQPRRRRARTRRQQRMAATNNMLKMSAPGLDFLKCAFAS
PDFSTDPGKGIPDKFQGLVLPKKHCLTQSITFTPGKQTMLLVAPIPGIACLKAEANVGASF
GVPLASVEFPFGDQLFGTSATDTAANVTAFRYASMAAGVYPTSNLMQFAGSIQVYKIPLK
QVLNSYSQTVATVPPTNLAQNTIAIDGLEALDLPNNNYSGSFIEGCYSQSVCNEPEFEFHP
IMEGYASVPPANVTNAQASMFTNLTFSGARYTGLGMDAIAILVTPTGAVNTAVLKVWA
CVEYRPNPNSTLYEFARESPANDEYALAA YRKIARDIPIAVACKDN

>g1f8v.1_b.10.1.3 (A:,D:) Nodavirus capsid protein {Pariacoto virus}

NRNKRKARKVVSRTALVPMAPASQRTGPAPRKPRKRNQALVRNPRLTDAGLAFLKCAFAA
PDFSVDPGKGIPDNFHGRTLAIKDCNTTSVVFTPN TDTYIVVAPVPGFAYFRAEVAVGAQPT
TFVGVPPYPTYATNFGAGSQNGLPAVNNYSKFRYASMACGLYPTSNMMQFSGSVQVWRVD

LNLS EAVNPAVTAITPAPGVFANFVDKRINGLRGIRPLAPRDNYSGNFIDGAYTFAFDKSTD
FEWCDFVRSLEFSESNVLGAATAMKLLAPGGGTDTTLTGLGNVNTLVYKISTPTGAVNTAI
LRTWNCIELQPYTDSALFQFSGVSPFPDPLALECYHNLKMRFPVAVSSRENXSKFWEGVLR
VLNQISGTLVIPGPVGTISAGVHQLTGMYM

>d1dnv__ b.10.1.3 (-) *Galleria mellonella* densovirus capsid protein {Wax moth (*Galleria mellonella*), densovirus}

VYIIPRPF SNFGKKLSTYTKSHKFMIFGLANNVIGPTGTGTTAVNRLTTCLAEIPWQKLPL
YMNQSEFDLLPPGSRVVECNVKVIFRTNRIAFETSSTVTKQATLNQISNVQTAIGLNKLGW
GINRAFTAFQSDQPMIPTATTAPKYEPVTGDTGYRGMIA DYYGADSTNDTAFGNAGNYPH
HQVSSFTFLQNYCYMYQQTNQGTGGWPCLAEHLQQFDSKTVNNQCLIDVTYKPKMGLI
KSPLNYKIIGQPTVKGTISVGDNLVNMRGAVVTNPPEATQNVAESTHNLTRNFPADLFNIYS
DIEKSQVLHKGPWGHENPQIQPSVHIGIQAVPALTTGALLINSSPLNSWTD SMGYIDVMSS
CTVMEAQPTHFPFSTEANTNPGNTIYRINLT PNSLTSAFNGLYGNGATLGN

>d1b35a_ b.10.1.3 (A:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (*Teleogryllus commodus*)}

VMGEDQQIPRNEAQHG VHPISIDTHRISNNWSPQAMCIGEKVVSIRQLIKRFGIFGDANTL
QADGSSFFVAPFTVTSPTKTLTSTRNYTQFDY YYYLYAFWRGSMRIKMVAETQDGTGTPR
KKTNFTW FVRMFNSLQDSFNSLISTSSSAVTTTVLPSGTINMGPSTQVIDPTVEGLIEVEVP
YYNISHITPAVTIDDGTPSMEDY LKGHSPPCLLTFSPRDSISATNHIITASFMRALGDDFSFM
YLLGVPPLVNVARA

>d1b35b_ b.10.1.3 (B:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (*Teleogryllus commodus*)}

ENSHIENEDKRLTSEQKEIVHFVSEG VTPSTTALPDIVNLSTNYLDKNTREDRIHSIKDFLSR
PIIIATNLWSVSDPVEKQLYTANFPEVLISNAMYQDKLKG FVGLRATLVVKVQVNSQP FQQ
GRLMLQYIPYAQYMPNRVTLINETLQGRSGCPRTDLELSVGTEVEMRIPYVSPHLYYNLIT
GQGSFGSIYVVVYSQLHDQVSGTGSIEYTVWAHLEDVDVQYPTGANIFTGNEAYIKGTSR
YDAAQKAHAA

>d1b35c_ b.10.1.3 (C:) Cricket paralysis virus (CRPV) {Host: australian black field cricket (*Teleogryllus commodus*)}

SKPTVQGGKIGECKLRGQGRMANFDGMDMSHKMAL SSTNEIETNEGLAGTSLDVM DLSR
VLSIPNYWDRFTWKTSDVINTVLWDNYVSPFKVKPYSATITDRFRCTHMGKVANAFTYW
RGSMVYTFKFVKTQYHSGRLRISFIPY YYYNTTISTGTPDVSRTQKIVVDLRTSTAVSFTVPYI
GSRPWLYCIRPESSWLSKDNTDGALMYNCVSGIVRVEVLNQLVAAQNVFSEIDVICEVNG
GPDLEFAGPTCPRYVPYAGDFTLADTRKIEAERTQEYSNNED

>d1sida_ b.10.1.4 (A:) Murine polyomavirus coat protein vp1 {Murine polyoma virus, strain small-plaque 16}

KACPRPAPVPKLLIKGGMEVLDLVTGPDSVTEIEAFLNPRMGQPPTPESLTEGGQYYGWSR
GINLATSDTEDSPGNNTLPTWSMAKLQLPMLNEDLTCDTLQMWEAVSVKTEVVGSGSLL
DVHGFNKPTDTVNTKGISTPVEGSQYHVF AVGGEPLDLQGLVTDARTKYKEEGVVTIKTIT
KKDMVNKDQVLNPISKAKLDKDGMY PVEIWHPDPAKNENTRYFGNYTGGTTTPPVLQFT
NTLT TVLLDENG VGPLCKGEGLYLSCVDIMGWRVTRNYDVHHWRGLPRYFKITLRKRWV
KNPYPMASLISSLFNNMLPQVQGQPMEGENTQVEEV RVYDGT EPPGDPDMTRYVDRFG
KTKTVFPG

>d1fmd2_ b.10.1.4 (2:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs,

1860)}

DKKTEETTLLLEDRLTTRNGHTTSTTQSSVGVTFGYATAEDSTSGPNTSALETRVHQAERFF
KMALFDWVPSQNFQGHMHKVVLPHPEKGVYGGVLVKSAYMRNGWDVEVTAVGNQFNG
GCLLVALVPEMGDISDREKYQLTLYPHQFINPRTNMTAHITVPYVGVNRYDQYKQHRPWT
LVVMVVAPLTTNTAGAAQIKVYANIAPTNVHVAGELPSKE

>d1qqp1_ b.10.1.4 (1:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

TTSAGESADPVTTTVENYGGGETQIQRRQHTDVSFIMDRFVKVTPQNQINILDLMQVPSHTL
VGALLRASTYYFSDLEIAVKHEGDLTWVPNGAPEKALDNTTNPTAYHKAPLTRALPYTA
PHRVLATVYNGECRYSRNAVPNLRGDLQVLAQKVARTLPTSFNYGAIKATRVTELLYRMK
RAETYCPRPLLAHPTEARHKQKIVAPVK

>d1qqp3_ b.10.1.4 (3:) Foot-and-mouth disease virus {Foot-and-mouth disease virus, (strain bfs, 1860)}

GIFPVACSDGYGGLVTTDPKTADPVYGVFNPPRNQLPGRFTNLLDVAEACPTFLRFEGGV
PYVTTKTDSDRVLAQFDMSLAAKHMSNTFLAGLAQYYTQYSGTINLHFMFTGPTDAKAR
YMVAYAPPGMEPPKTPEAAAHCIAEWDGTLNSKFTFSIPYLSAADYTYTASDVAETTNV
QGWVCLFQITHGKADGDALVVLASAGKDFELRLPVDARAE

>d1mvma_ b.10.1.4 (A:) MVM coat protein {Murine minute virus, strain i}

GVGVSSTGSYDNQTHYRFLGDGWVEITALATRLVHLNMPKSENYCRIRVHNTTDTSVKGN
MAKDDAHEQIWTPWSLVDANAWGVWLQPSDWQYICNTMSQLNLVSLDQEIFNVVLKTV
TEQDSGGQAIIYNNDLTACMMVAVDSNNILPYTPAANSMETLGFYPWKPTIASPYRYFYF
VDRDLSVTYENQEGTIEHNVMGTPKGMNSQFFTIENTQQITLLRTGDEFATGTYYFDNPNV
KLHTTWQTNRQLGQPPLLSTFPEADTDAGTLTAQGSRHGATQMEVNWVSEAIRTPAQV
GFCQPHNDFEASRAGPFAAPKVPADVTDQGMREANGSVRYSYGKQHGENWAAHGAPE
RYTWDETNGFSGRDTRDGFISAPLVVPPPLNGILTNNANPIGTKNDIHFNSVFNSTYGPLTTF
SHPSPVYPQGQIWDKELDLEHKPRLHITAPFVCKNNAPGQMLVRLGPNLTDQYDPNGATL
SRIVTYGTFFWKGLTMRACLKLRANTTWNPNVYQVSVEDNGNSYMSVTKWLPTATGNMQS
VPLITRPVARNTY

>d1hxs1_ b.10.1.4 (1:) Poliovirus {Poliovirus type 1, strain Mahoney}

GSSSTDNTVRETVGAATSRDALPNTEASGPTHSEIPALTAVETGATNPLVPSDTVQTRHVV
QHRSRSESSIESFFARGACVTIMTVDNPASTTNKDKLFAVWKITYKDTVQLRRKLEFFTY
RFDMEFTFVV TANFTETNNGHALNQVYQIMYVPPGAPVPEKWDDYTWTSSNPSIFYTY
GTAPARISVPYVGISNAYSHFYDGFYSKVPKLDQSAALGDSLYGAASLNDGILAVRVNDH
NPTKVTSKIRVYLKPKHIRVWCPRPPRAVAYYGPVVDYKDGTLLPLSTKDLTTY

>d1pov0_ b.10.1.4 (0:) Poliovirus {Poliovirus type 1, strain Mahoney}

GAQVSSQKVGAHENSNRAYGGSTINYTTINYRDSASNAASKQDFSQDPSKFTEPIKDVLI
KTAPMLNSPNIACGYSDRVLQLTLGNSTITTQEAANSVVAYGRWPEYLRDSEANPVDQP
TEPDVAACRFYTLDTVSWTKESRGWWKLPDALRDMGLFGQNMYYHYLGRSGYTVHV
QCNASKFHQ GALGVFAVPEMCLAGDSNTTMMHTSYQNANPGEKGGTFTGTFTPDNNQTS
PARRFCPV DYLLGNGTLLGNAFVFPHQIINLRTNNCATLVLPYVNSLSIDSMVKHNNWGIA
ILPLAPLNFASSEPEIPTLTIAPMCCEFNGLRNITLPLRLQ

>d1eah3_ b.10.1.4 (3:) Poliovirus {Poliovirus type 2, strain Lansing}

GLPVLNTPGSNQYLTADNYQSPCAIPEFDVTPPIDIPGEVRNMMELAEIDTMIPLNLTNQRK
NTMDMYRVELNDAAHS DTPILCLSLSPASDPRLAHTMLGEILNYTHWAGSLKFTFLFCG

SMMATGKLLVSYAPPGAEAPKSRKEAMLGTHVIWDIGLQSSCTMVVPWISNTTYRQTIND
SFTEGGYISMFYQTRVVVPLSTPRKMDILGFVSACNDFSRLRRDTHISQEA

>d1aym1_ b.10.1.4 (1:) Rhinovirus coat protein {Human rhinovirus 16}

NPVERYVDEVLNEVLVVPNINQSHPTTSNAAPVLDAAEAGHTNKKIQPEDTIETRYVQSSQT
LDEMSVESFLGRSGCIHESVLDIVDNYNDQSFTKWNINLQEMAIKKFEMFTYARFDSEI
TMVPSVAAKDGHHIGHVMQYMYVPPGAPIPTTRDDYAWQSGTNASVFWQHGGQPFPRFSL
PFLSIASAYYMFYDGYDGDYKSRYGTVVTNDMGTLCSRIVTSEQLHKVKVVTIRIYHKA
KHTKAWCPRPPRAVQYSHHTTNYKLSSEVHNDVAIRPRTNLTTV

>d1bev1_ b.10.1.4 (1:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

QAAGALVAGTSTSTHSVATDSTPALQAAETGATSTARDESMIETRTIVPTHGHIHETSVESSFG
RSSLVGMPLLATGTSITHWRIDFREFVQLRAKMSWFTYMRFDVEFTIATSSSTGQNVTTTEQ
HTTYQVMYVPPGAPVPSNQDSFQWQSGCNPSVFADTDGPPAQFSVPMSSANAYSTVYD
GYARFMDTDPDRYGILPSNFLGFMYFRTLEDAAHQVRFRIYAKIKHTSCWIPRAPRQAPYK
KRYNLVFGSDSDRICSNRASLTSY

>d1bev3_ b.10.1.4 (3:) Bovine enterovirus coat protein {Bovine enterovirus, VG-5-27}

GLPTKPGPGSYQFMTTDEDCSPCILPDFQPTPEIFIPGKVNNLLEIAQVESILEANNREGVEG
VERYVIPVSVQDALDAQIYALRLELGGSGPLSSSLGLTAKHYTQWSGSVEITCMFTGTFTM
TTGKVLLEYTPPGGDMPRNREEAMLGTHVIWDFGLQSSITLVIPWISASHFRGVSNDDEL
NYQYYAAGHVTIWYQTNMVIPPGFPNTAGIIMMIAAQPNFSFRIQKDREDMTQTALQ

>d1tme3_ b.10.1.4 (3:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

SPIAVTVREHKGCFYSTNPDTTVPIYGKTISTPNDYMCGEFSDLLELCKLPTFLGNPNSSNK
RYPYFSATNSVPTTSLVDYQVALSCSCMCNSMLAAVARNFNQYRGSLNFLVFTGAAMVK
GKFLIAYTPPGAGKPTTRDQAMQATYAIWDLGLNSSFVFTAPFISPHTYRQTSYTSATIASV
DGWVTWVQLTPLTPSGTPVNSDILTLVSAGDDFTLRMPISPTKWVPQ

>d1tmf1_ b.10.1.4 (1:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

GVDNAEKGVSNDDASVDFVAEPVKLPENQTRVAFFYDRAVPIGMLRPGQNMETTFNYQ
ENDYRLNCLLLTPLPSFCPDSSSGPQKTKAPVQWRWVRSRGVNGANFPLMTKQDYAFLC
FSPFTFYKCDLEVTVSALGTDTVASVLRWAPTGAPADVTDQLIGYTPSLGETRNPHMWLV
GAGNSQVSFVVPYNSPLSVLPAAWFNGWSDFGNTKDFGVAPNADFGRLWIQGNSTASVRI
RYKKMKVFCPRPTLFFPWPTPTTTKINADNPVPILELE

>d1tmf2_ b.10.1.4 (2:) Theiler's murine encephalomyelitis virus {Theiler's murine encephalomyelitis virus, strain da}

DQNTTEEMENLSDRVASDKAGNSATNTQSTVGRLCGYGKSHHGEHPASCADTATDKVLAA
ERYYTIDLASWTTSQEAFFSHIRIPLPHVLAGEDGGVFGATLRRHYLCKTGWRVQVQCNAS
QFHAGSLLVFMAPEFYTGKGTGTMEPSDPFTMDTEWRSPQGAPTGYRYDSRTGFFATN
HQNQWQWTVYPHQILNLRNTTVDLEVPYVNVAPSSSWTQHANTWTLVVAVLSPLQYATG
SSPDVQITASLPVNPVFNGLRHETVIAQ

>d1dzla_ b.10.1.4 (A:) L1 protein {Human papillomavirus type 16}

KVVSTDEYVARTNIYYHAGTSRLLAVGHPYFPIKKPNNNKILVPKVSGLQYRVFRIHLDPD
NKFGFPDTSFYNPDTQRLVWACVGVGVGRGQPLGVGISGHPLLKLDDETENASAYAANA

GVDNRECISMDYKQTQLCLIGCKPPIGEHWGKGSPTQVAVQPGDCPPLELINTVIQDGD
MVDTGFGAMDFTTLQANKSEVPLDICTSICKYPDYIKMVSEPYGDSLFFYLRRQMFVRH
LFNRAGTVGENVPDDLYIKGSGSTANLASSNYFPTPSGSMVTSDAQIFNKPYWLQRAQGH
NNGICWGNQLFVTVVDTRSTNMSLCAAISTSETTYKNTNFKEYLRHGEEYDLQFIFQLC
KITLTADVMTYIHSMNSTILEDWNFGLQPPPGGTLEDTYRFVTSQAIACQKHTPPAPKEDP
LKKYTFWEVNLKEKFSADLDQFPLGRKFLLQLGL

>d1ihma_b.10.1.4 (A:) Calcivirus capsid protein {Norwalk virus}

DPLAMDPVAGSSTAVATAGQVNPIDPWIINNFBVQAPQGEFTISPNNTPGDVLFDSLGPLN
PFLHLSQMYNGWVGNMVRIMLAGNAFTAGKIIVSCIPPFGSHNLTAQATLFPHVIAD
VRTLDPIEVPLEDVRNVLFHNNDNRNQQTMLVCMLYTPLRTGGGTGDSFVVAGRVMTCF
SPDFNFLFLVPPTVEQKTRPFTLPNPLSSLSNSRAPLPISSMGISPDNVQSVQFQNGRCTL
GRLVGTTTPVSLSHVAKIRGTSNGTVINLTDLGTFPHFEGPAPIGFPDLGGCDWHINMTQF
GHSSQTQYDVTTPDTFVPHLGSIQANGIGSGNYVGVLSWISPPSHPSGSQVDLWKIPNYG
SSITEATHLAPSVYPPGFGFVLVFFMSKMPGPGAYNLPCLLPQEYISHLASEQAFTVGEAAL
LHYVDPDTGRNLGEFKAYPDGFLTCVPNGASSGPQQLPINGVFVFSWVSRFYQLKPVGT
AS

>d1amm_1 b.11.1.1 (1-85) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GKITFYEDRGFQGHCEYECSSDCPNLQPYFSRCNSIRVDSGCWMLYERPQYQGHQYFLRRG
DYPDYQQWMGFNDSSIRSCRLIPQHT

>d1amm_2 b.11.1.1 (86-174) gamma-Crystallin {Cow (Bos taurus), isoform II (B)}

GTFMRRIYERDDFRGQMSEITDDCPSLQDRFHLTEVHSLNVLEGSWVLYEMPYSYRGRQYL
LRPGEYRRYLDWGAMNAKVGSLRRVMDFY

>d1bd7a_b.11.1.1 (A:) beta-Crystallin {Rat (Rattus norvegicus), isoform E}

EHKIILYENPNFTGKKMEIVDDDVPSFHAHGYQEKVSSVRVQSGTWVGYQYPGYRGLQY
LLEKGDYKDNSDFGAPHPQVQSVRRIRDMQGNPKIIFEQENFQGHSELSGPCPNLKETG
MEKAGSVLVQAGPWVGYEQANCKGEQVFVEKGEYPRWDSWTSSRRTDSLSSLRPIK

>d1npsa_b.11.1.1 (A:) Protein S {Myxococcus xanthus}

ANITVFYNEDFQKGQVDLPPGNYTRAQLAALGIENNTISSVKVPPGVKAILYQNDGFAGD
QIEVVANAEELGPLNNNVSSIRVISVPV

>d1hdfa_b.11.1.1 (A:) Spherulin 3a (S3a) {Slime mold (Physarum polycephalum)}

SVCKGVSGNPAKGEVFLYKHVNFQGDSWKVTGNVYDFRSVSGLNDVSSVKVGPNTKA
FIFKDDRFNGNFIRLEESSQVTDLTTRNLNDAISSMIVATFE

>d1ik3a2 b.12.1.1 (A:9-167) Plant lipoxigenase {Soybean (Glycine max), isozyme L3}

GHKIKGTVVLMRKNVLDVNSVTSVGGIIGQLDLVGSTLDTLTAFLGRSVSLQLISATKAD
ANGKGLKGFATFLEGIITSLPTLGAGQSAFKINFEWDDGSGIPGAFYIKNFMQTEFFLVSLT
LEDIPNHGSIHFVCNSWIYNAKLFKSDRIFFANQTY

>d1lox_2 b.12.1.1 (2-112) 15-Lipoxygenase {Rabbit (Oryctolagus cuniculus)}

GVYRVCVSTGASIYAGSKNKVELWLVGQHGEVELGSLRPNRKEEEFKVNVSKYLGSL
FVRLRKKHFLKEDAWFCNWISVQALGAAEDKYWFPCYRWVVG DGVSQSLPVG

>d1pgs_1 b.13.1.1 (4-140) Peptide:N-glycosidase F, PNGase F {Flavobacterium meningosepticum}

DNTVNIKTFDKVKNAFGDGLSQAEGTFTFPADVTTVKTIKMFIKNECPNKTCDWEDRYA
NVYVKNKTTGEWYEIGRFITPYWVGTEKLPRGLEIDVTDFKSLLSGNTELKIYTETWLAK
GREYSVDFDIVYGTDPY

>d1pgs_2 b.13.1.1 (141-314) Peptide:N-glycosidase F, PNGase F {Flavobacterium meningosepticum}

KYSAVVPVIQYNKSSIDGVYPYGKAHTLGLKKNQLPTNTEKAYLRTTISGWGHAKPYDAG
SRGCAEWCFRTHITIAINNANTFQHQLGALGCSANPINNQSPGNWTPDRAGWCPGMAVPT
RIDVLNNSLTGSTFSYEEKFQSWTNNGTNGDAFYAISSFVIAKSNTPIAPVVTN

>d1phm_1 b.13.1.2 (45-198) Peptidylglycine alpha-hydroxylating monooxygenase, PHM
{Rat (Rattus norvegicus)}

NECLGTIGPVTPLDASDFALDIRMPGVTPKESDITYFCMSMRLPVDEEAFVIDFKPRASMDT
VHHMLLFGCNMPSSSTGSYWFCDEGTCTDKANILYAWARNAPPTRLPGKVGFRVGGGETGS
KYFVLQVHYGDISAFRDNHKDCSGSVSVHLTRVPQ

>d1phm_2 b.13.1.2 (199-354) Peptidylglycine alpha-hydroxylating monooxygenase, PHM
{Rat (Rattus norvegicus)}

PLIAGMYLMMSVDTVIPPGEKVVNADISCQYKMYPMHVFAYRVHTHHLGKVVSgyrvr
NGQWTLIGRQNPQLPQAFYPVEHPVDVTFGDILAARCVFTGEGRTEATHIGGTSSDEMCN
LYIMYYMEAKYALSfMTCTKNVAPDMFRTIPAEANIPI

>d1hx6a1 b.13.2.1 (A:15-244) Coat protein p3 {Bacteriophage prd1}

LRNQQAAMAANLQARQIVLQQSYPIQQVETQTFDPANRSVFDVTPANVGIVKGFLVKVTA
AITNNHATEAVALTDFGPANLVQRVIYYDPDNQRHTETSGWHLHFVNTAKQGAPFLSSMV
TDSPIKYGDVMNVIDAPATIAAGATGELTMYWVPLAYSETDLTGAVLANVPQSKQRLKL
EFANNNTAFAAVGANPLEAIYQGAGAADCEFEIEISYTVYQSYLDQLPVGQ

>d1hx6a2 b.13.2.1 (A:245-384) Coat protein p3 {Bacteriophage prd1}

NGYILPLIDLSTLYNLENSAQAGLTPNVDFVQYANLYRYLSTIAVFDNGGSFNAGTDINYL
SQRTANFSDTRKLDPKTWAAQTRRRIATDFPKGVIYCDNRDKPIYTLQYGNVGFVVPKPT
VNQNARLLMGYEYFTSRT

>d1ruxa1 b.13.2.2 (A:5-636) Adenovirus hexon {Human adenovirus type 5}

MMPQWSYMHISGQDASEYLSPLGVQFARATETYFSLNNKFRNPTVAPTHDVTDRSQRLT
LRFIPVDREDTAYSYKARFTLAVGDNRLDMASTYFDIRGVLDRGPTFKPYSGTAYNALAP
KGAPNPCEWDEAATALEINLEEEDDDNEDEVDEQAEQQKTHVFGQAPYSGINITKEGIQIG
VEGQTPKYADKTFQPEPQIGESQWYETEINHAAGRVLKKTPMKPCYGSYAKPTNENG
QGILVKQQNGKLESQVEMQFFSTTEATAGNGDNLTPKVVLVSEDVDIETPDTHISYMP
TIK EGNSRELMGQQSMPNRPNYIAFRDNFIGLMYYNSTGNMGVLAGQASQLNAVVDLQDRN
TELSYQLLLDSIGDRTRYFSMWNQAVDSYDPDVRIIENHGTEDELPNYCFPLGGVINTETLT
KVKPKTGQENGWEKDATEFSKDNEIRVGNNFAMEINLNANLWRNFLYSNIALYLPDKLKY
SPSNVKISDNPNPTYDYMNKRVVAPGLVDCYINLGARWSLDYMDNVNPNFHHNRNAGLRY
RSMLLGNGRYVPFHIQVPQKFFAIKNLLLLPGSYTYEWNFRKDVNMVLQSSLGNDLRVD
GASIKFDSICLYATFFPMAHNTASTLEAMLRND

>d1ruxa2 b.13.2.2 (A:637-946) Adenovirus hexon {Human adenovirus type 5}

TNDQSFNDYLSAANMLYPIPANATNPISIPSRNWAAFRGWAFTRLKTKETPSLGSGYDPY
YTYSGSIPYLDGTFYLNHTFKKVAITFDSSVSWPGNDRLLTPNEFEIKRSVDGEGYNVAQC
NMTKDWFVLVQMLANYNIGYQGFYIPESYKDRMYSFFRNFPMSRQVVD DTKYKDYQQV
GILHQHNSGFVGYLAPT MREGQAYPANFPYPLIGKTAVDSITQKKFLCDRTLWRIPFSSNF
MSMGALTDLGQNLLYANSAHALDMTFEVDPMDEPTLLYVLFEVFDVVRVHRPHRGVIET
VYL RTPFSA

>d1shsa_ b.15.1.1 (A:) Small heat shock protein {Archaeon Methanococcus

jannaschii}

TGIQISGKGFMPIIIEGDQHIKVIAWLPGVNKEDIILNAVGDLEIRAKRSPLMITESERIIYS
EIPEEEEIYRTIKLPATVKEENASAKFENGVLVLPKAESSIKKGINIE

>d1gmea_ b.15.1.1 (A:) Small heat shock protein {Wheat (*Triticum aestivum*)}

SIVRRSNVFDPFADLWADPFDTRFSIVPAISGGGSETAAAFANARMDWKETPEAHVFKADLP
GVKKEEVKVEVEDGNVLVVSIGERTKEKEDKNDKWHRVERSSGKFVRRFRLLLEDKVEE
VKAGLENGVLTVTVPKAEVKKPEVKAIQISG

>d1a44_ b.17.1.1 (-) Phosphatidylethanolamine binding protein, PEBP {Cow (*Bos taurus*)}

PVDLSKWSGPLSLQEVDERPQHPLQVKYGGAEVDELGKVLTPQVKNRPTSITWDGLDP
GKLYTLVLTPDAPSRKDPKYREWVHFLVNMKGNNISSGTVLSDYVGSPPKGTGLHR
YVWLVEYEQEPLKCDPILSNRSGDHRGKFKVASFRKKYELGAPVAGTCYQAEWDDYVP
KLYEQLSG

>d1qoua_ b.17.1.1 (A:) Centroradialis protein Cen {Garden snapdragon (*Antirrhinum majus*)}

GRVIGDVVDHFTSTVKMSVIYNSNNSIKHVYNGHELFPASVTSTPRVEVHGGDMRSFFTLI
MTDPDVPGPSDPYLRHLHWIVTDIPGTTDSSFGKEVVSYEMPRPNIGIHRFVLLFKQKK
RGQAMLSPPVVCRDGFNTRKFTQENELGLPVA AVFFNCQRET

>d1k3ia2 b.18.1.1 (A:-12-150) Galactose oxidase, N-terminal domain {Fungi (*Fusarium* spp)}

IPEGSLQFLSLRASAPIGSAISRNNWAVTCDSAQSGNECNKAIDGNKDTFWHTFYGANGDP
KPPHTYTIDMKTTQNVNGLSMLPRQDGNQNGWIGRHEVYLSSDGTNWGSPVASGSWEA
DSTTKYSNFETRPARYVRLVAITEANGQPWTSIAEINVFQASS

>d1eut_2 b.18.1.1 (506-647) Sialidase, C-terminal domain {*Micromonospora viridifaciens*}

QARMSIADVDSEETAREDGRASNVIDGNPSTFWHTEWSRADAPGYPHRISLDLGGTHTIS
GLQYTRRQNSANEQVADYEIYTSNLGTTWDGPVASGRFTTSLAPQRAVFPARDARYIRLVA
LSEQTGHKYAAVAELEVEGQR

>d1ji6a1 b.18.1.3 (A:503-652) delta-Endotoxin, C-terminal domain {*Bacillus thuringiensis*, CRY3bb1}

FFNTIDAELITQLPVVKAYALSSGASIIIEGPGFTGGNLLFLKESSNSIAKFKVTLNSAALLQR
YRVRIRYASTTNLRLRFVQNSNNDLFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKN
ELIIGAESFVSNEKIYIDKIEFIPVQL

>d1ciy_1 b.18.1.3 (462-609) delta-Endotoxin, C-terminal domain {*Bacillus thuringiensis*, CRYIA (A)}

NNIIPSSQITQIPLTKSTNLGSGTSSVVKGPFGFTGGDILRRTSPGQISTLRVNITAPLSQRYRVRI
RYASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTPFNFSNGSSVFTLSAH
VFNSGNEVYIDRIEFVPAEVT

>d1i5pa1 b.18.1.3 (A:473-633) delta-Endotoxin, C-terminal domain {*Bacillus thuringiensis* subsp. *kurstaki*, CRY2AA}

NIYAAANENGTMIHLAPEDYTGTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNTTARY
TLRGNGNSYNLYLRVSSIGNSTIRVTINGRVYTVSNVNTTTNNDGVNDNGARFSDINIGNIV
ASDNTNVTLTDLNINSGTDFDLNIMFVPTNLPLPY

>d1jz8a3 b.18.1.5 (A:13-219) beta-Galactosidase {*Escherichia coli*}

RRDWENPGVTQLNRLAAHPPFASWRNSEEARTDRPSQQLRSLNGEWRFAWFAPEAVPES
WLECDLPEADTVVPSNWQM HGYDAPITYNTVYPITVNPFFVPTENPTGCYSLTFNVEDS
WLQEGQTRIIFDGVNSAFHLWCNGRWVGYGQDSRLPSEFDLSAFLRAGENRLAVMVLRW

SDGSYLEDDQDMWRMSGIFRDVSLHKPT

>d1bhga2 b.18.1.5 (A:22-225) beta-Glucuronidase {Human (Homo sapiens)}

GLQGGMLYPQESPSRECKELDGLWSFRADFSNRRRGFEEQWYRRPLWESGPTVDMVPV
SSFNDISQDWRLRHFVGVWYEREVILPERWTQDLRTRVVLRIKSAHSYAIVWVNGVDT
LEHEGGYLPFEADISNLVQVGPLPSRLRITIAINNTLTPTTLPPGTIQYLTDTSKYPKGYFVQ
NTYFDFFNAGLQRSVLLYTTPT

>d1cx1a_ b.18.1.6 (A:) Cellulose-binding domain {Cellulomonas fimi}

ASLDSEVELLPHTSFAESLGPWSLYGTSEPVFADGRMCVDLPGGQGNPWDAGLVYNGVP
VGEGESYVLSFTASATPDMPVRLVGEAGGAYRTAFEQGSAPLTGEPATREYAFTSNLTFPP
DGDAPGQVAFHLGKAGAYEFCISQVSLTTSAT

>d1lulo_ b.18.1.6 (-) Cellulose-binding domain {Cellulomonas fimi}

ASPIGEGTFDDGPEGWVAYGTDGPLDTSTGALCVAVPAGSAQYGVGVVLNGVAIEEGTTY
TLRYTATASTDVTVRALVGQNGAPYGTVLDTSPALTSEPRQVTETFTASATYPATPAADDPE
GQIAFQLGGFSADAWTLCLDDVALDSEVEL

>d1bvp12 b.19.1.1 (1:121-254) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain
{Bluetongue virus}

PARQPYGFFLETEETFQGRWFMRAAQAVTAVVCGPDMIQVSLNAGARGDVQQIFQGRN
DPMMIYLVWRIENFAMAQGNSQQTQAGVTVSVGGVDMRAGRIIAWDGQAALHVHNPT
QQNAMVQIQVVFYISMD

>d1ahsa_ b.19.1.1 (A:) Virus capsid protein vp7 (BTV-10 vp7), central (top) domain {African
horse sickness virus}

TGPYAGAVEVQQSGRYYPQGRTRGGYINSNIAEVCMDAGAAGQVNALLAPRRGDAVMI
YFVWRPLRIFCDPQGASLESAPGTFVTVDGVNVAAGDVVAWNTIAPNVGNPAGARRSILQ
FEVLWYT

>d1qhda2 b.19.1.1 (A:149-332) vp6, the major capsid protein of group A rotavirus {Bovine
rotavirus}

GFTFHKPNIFYSASFTLNRSQPAHDNLMGTMWLNAGSEIQVAGFDYSCAINAPANTQQFE
HIVQLRRVLTTATITLLPDAERFSFPRVITSADGATTWYFNPVILRPNNVEIEFLNGQIINTY
QARFGTIIARNFDTIRLSFQLMRPPNMTPAVAALFPNAQPFEHHATVGLTLRIESAVCE

>d1jsma_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}

DQICIGYHANNSTEQVDTIMEKNVTVTHAQDILEKTHNGKLCDLNGVKPLILRDCSVAGW
LLGNPMCDEFLNVPEWSYIVEKDNPNVNGLCYPENFNDYEELKHLSSSTNHFEEKIRIIPRSS
WSNHDASSGVSSACPYNGRSSFFRNVWLIKKNAYPTIKRSYNNNTNQEDLLILWGIHHP
NDAAEQTKLYQNPTTYVSVGTSTLNQRSVPEIATRPKVNGQSGRMEFFWTILKPNDAINFE
SNGNFIAPYAYKIVKKGGS AIMKSGLEYGNCNTKCQTPMGAINSSMPFHNIHPLTIGEC
KYVKSGLVLATGLRNVP

>d2viua_ b.19.1.2 (A:) Hemagglutinin {Influenza A virus, different strains}

STATLCLGHHAVPNGTLVKTITDDQIEVTNATELVQSSTGKICNNPHRILDGIDCTLIDALL
GDPHCDVFQNETWDLFVERSKAFSNCYPYDVPDYASLRSLVASSGTLEFITEGFTWTGVIQ
NGGSNACKRGP GSGFFSRLNWLTKSGSTYPVLNVTMPNNDNFDKLYIWGIHHPSTNQEQ
TSLYVQASGRVTVSTRSQQTII PNIGSRPWVRGLSSRISYWTIVKPGDVLVINSNGNLIAPR
GYFKMRTGKSSIMRSDAPIDTCISECITPNGSIPNDKPFQNVNKITYGACPKYVKQNTLKL
ATGMRNVPEKQT

>d1qhva_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus}

type 2}

AITIGNKNDDKLTWTTDPSPNCRIHSDNDCKFTLVLTCKGSQVLATVAALAVSGDLSSM
TGTVASVSIFLRFQNGVLMENSSLKKHYWNFRNGNSTNANPYTNAVGFMPNLLAYPKT
QSQTAKNNIVSQVYLHGDKTKPMILTITLNGTSESTETSEVSTYSMSFTWSWESGKYTTET
FATNSYTFSYIAQE

>d1h7za_ b.21.1.1 (A:) Adenovirus fiber protein head domain (knob domain) {Human adenovirus type 3}

KNNTLWTGPKPEANCIIEYGKQNPDSKLTLLVKNGGIVNGYVTLMGASDYVNTLTKNKN
VSINVELYFDATGHILPDSSSLKTDLELKYQTADFSARGFMPSTTAYPFVLPNAGTHNEN
YIFGQCYYKASDGALFPLEVTVMNLNKRPLDSRTSYVMTFLWSLNAGLAPETTQATLITSPF
TFSYIREDD

>d1aly_ b.22.1.1 (-) Extracellular domain of CD40 ligand {Human (Homo sapiens)}

GDQNPQIAAHVISEASSKTTSVLQWAEKGYTMSNNLVTLENGKQLTVKRQGLYYIYAQV
TFCSNREASSQAPFIASLCLKSPGRFERILLRAANTHSSAKPCGQQSIHLGGVFELQPGASV
FVNVTDPSPQVSHGTGFTSFGLLKL

>d1c28a_ b.22.1.1 (A:) 30 kd adipocyte complement-related protein {Mouse (Mus musculus)}

MYRSAFSVGLETRVTPNVPIRFTKIFYNQNNHYDGSTGKFYCNIPGLYYFSYHITVYMKD
VKVSLFKKDKAVLFTYDQYQEKNVDAQSGSVLLHLEVGDQVWLQVYGDGDHNGLYAD
NVNDSTFTGFLLYHDT

>d1tnra_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}

KPAAHLIGDPSKQNSLLWRANTDRAFLQDGFSLSNSLLVPTSGIYFVYSQVVFSGKAYSP
KATSSPLYLAHEVQLFSSQYPFHVPLSSQKMVYPGLQEPWLHSMYHGAAAFQLTQGDQLS
THTDGIPHLVLSPSTVFFGAFAL

>d4tsva_ b.22.1.1 (A:) Tumor necrosis factor (TNF) {Human (Homo sapiens)}

DKPVAHVVANPQAEGQLQWSNRRANALLANGVELRDNQLVVPIEGLFLIYSQVLFKGQG
CPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLEKGD
RLSAEINRPDYLDFAESGQVYFGIIL

>d1dg6a_ b.22.1.1 (A:) Apoptosis-2 ligand, apo2l/TRAIL {Human (Homo sapiens)}

QRVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIHEKG
FYYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYPAPILLMKSARNSCWSKDAEYGLY
SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG

>d1jtzx_ b.22.1.1 (X:) TRANCE/RANKL cytokine {Mouse (Mus musculus)}

QPFAHLTINAASIPSGSHKVTLSWYHDRGWAKISNMTLSNGKLRVNQDGFYLYANICFR
HHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLMMKGGSTKNWSGNSEFHFYSINVGGFKL
RAGEEISIQVSNPSLLDPDQDATYFGAFKVQDID

>d1jh5a_ b.22.1.1 (A:) Soluble part of TALL-1, sTALL-1 {Human (Homo sapiens)}

VTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALKEENKILVKETGYFFIYGQVLYTD
KTYAMGHILQRKKVHVFGDELSLVTLFRICIQNPETLPNNSCYSAGIAKLEEGDELQLAIP
RENAQISLDGDVTFFGALKLL

>d1sfp_ b.23.1.1 (-) Acidic seminal fluid protein (ASFP) {Cow (Bos taurus)}

LPRNTNCGGILKEESGVATYYGPKTNCVWTIQMPPEYHVRVSIQYLQLNCNKESLEIIDGL
PGSPVLGKICEGSLMDYRSSGSIMTVKYIREPEHPASFYEVLYFQDPQA

>d1sppb_ b.23.1.1 (B:) Major seminal plasma glycoprotein PSP-II {Pig (Sus scrofa)}

ARINGPDECGRVIKDTSGSISNTDRQKNLCTWTILMKPDQKVRMAIPYLNACGKEYVEV

FDGLLSGPSYGKLCAGAAIVFLSTANTMTIKYNRISGNSSSPFLIIFYGSSP
>d1cb8a2 b.24.1.1 (A:600-700) Chondroitinase AC {Pedobacter heparinus (Flavobacterium heparinum)}
PKVLANTNQLQAVYHQQLDMVQAIFYTAGKLSVAGIEIETDKPCAVLIKHINKQVIWAA
DPLQKEKTAVLSIRDLKTGKTNRVKIDFPQQEFAGATVELK
>d1legua2 b.24.1.1 (A:815-893) Hyaluronate lyase {Streptococcus pneumoniae}
SSLIENNETLQSVYDAKQGVWGIVKYDDSVSTISNQFQVLKRGVYTIRKEGDEYKIAYYN
PETQESAPDQEVFKKLEQH
>d1flsa3 b.24.1.1 (A:920-984) Hyaluronate lyase {Streptococcus agalactiae}
SKQQVIYDKNSQTWAVIKHDNQESLINNQFKMNKAGLYLVQKVGNDYQNVYYQPQTMT
KTDQLAI
>d1ddl1a_ b.26.1.1 (A:) Smad4 tumor suppressor C-terminal domain {Human (Homo sapiens)}
NGHLQHHPMPHPGHYWPVHNELAFQPPISNHPAPEYWCSIAFYFEMDVQVGETFKVPSS
CPIVTVDGYVDPSPGGDRFCLGQLSNVHRTEAIERARLHIGKGVQLECKGEGDVWVRCLS
DHAVFVQSYLDREAGRPGDAVHKIYPSAYIKVFDLRQCHRQMQQQAATAQAAAAAQ
AAAVAGNIPGPSVGGIAPISLSAAAGIGVDDLRLRLCILRMSFVKGWGPDYPRQSIKETPC
WIEIHLHRALQLLDEVLTMP
>d1khxa_ b.26.1.1 (A:) Smad2 MH2 domain {Human (Homo sapiens)}
PVTYSEPAFWCSIAYYELNQRVGETFHASQPSLTVDGFTDPSNSERFCLGLLSNVNRNATV
EMTRRHIGRGVRLYYIGGEVFAECLSDSAIFVQSPNCNQRYGWHPATVCKIPPGCNLKIFN
NQEFAALLAQSVNQGFQAVYQLTRMCTIRMSFVKGWGAEYRRQTVTSTPCWIELHLNGP
LQWLDKVLTMGSPSVRCSSMS
>d1k3ja_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}
ATQRFLIEKFSQEQIGENIVCRVICTTGQIPIRDLSDISQVLKEKRSIKKVWTFGRNPACDY
HLGNISRLSNKHFQILLGEDGNLLNDISTNGTWLNGQKVEKNSNQLLSQGDEITVGVG
ESDILSLVIFINDKFKQCLEQNKVDRIR
>d1qu5a_ b.26.1.2 (A:) Phosphotyrosine binding domain of Rad53 {Baker's yeast (Saccharomyces cerevisiae)}
EAETREQKLLHSNNTENVKSSKKKGNGRFLTLKPLPDSIIQESLEIQQGVNPFFIGRSEDCN
CKIEDNRLSRVHCFIFKKRHAVGKSMYESPAQGLDDIWYCHTGTNVSYLNNRMIIQGTKF
LLQDGDDEIKIWDKNNKFVIGFKVEINDTTGLFNEGLGMLQEQRVVLKQTAEKDLVKKL
>d1lns_ b.29.1.1 (-) Concanavalin A {Jack bean (Canavalia ensiformis)}
ADTIVAVELDTYPNTDIGDPSYPHIGIDIKSVRSKKTAKWNMQNGKVGTAHIIYNSVDKRL
SAVVSYPNADSATVSYDVLNVLPEWVRVGLSASTGLYKETNTILSWSFTSKLKSNSH
ETNALHFMFNQFSKDQKDLILQGDATTGTDGNLELTRVSSNGSPQGSSVGRALFYAPVHI
WESSAVVASFEATFTFLIKSPDSHPADGIAFFISNIDSSIPSGSTGRLLGLFPDAN
>d1hqla_ b.29.1.1 (A:) Legume lectin {Griffonia simplicifolia, lectin I-b4}
SVSFTFPNFWSDVEDSIIFQGDANTTAGTLQLCKTNQYGTPLQWSAGRALYSDPVQLWDN
KTESVASFYTEFTFFLKITGNGPADGLAFLAPPDSDVKDAGEYLGLFNKSTATQPSKNQV
VAVEFDTWTNPNFPEPSYRHIGINVNSIVSVATKRWEDSDIFSGKIATARISYDGSAEILTVV
LSYPDGSDYILSHSVDMRQNLPESVRVGISASTGNNQFLTIVYILSWRFSSNL
>d2pela_ b.29.1.1 (A:) Legume lectin {Peanut (Arachis hypogaea)}
AETVSFNFNSFSEGNPAINFQGDVTVLNNGNIQLTNLKNVNSVGRVLYAMPVRIWSSATGN

VASFLTSTFSFEMKDIKDYDPADGIIFFIAPEDTQIPAGSIGGGTLGVSDTKGAGHFVGVFEFDT
YSNSEYNDPPTDHSVGDVNSVDSVKTPWNSVSGAVVKVTVIYDSSTKTLSSVAVTNDNGD
ITTIAQVVLDLAKLPERVKFGFSASGSLGGRQIHLIRWSFTSTLITT

>d1g7ya_ b.29.1.1 (A:) Legume lectin {Horse gram (*Dolichos biflorus*), different isoforms}

ADIQSFSFKNFNSSSFIQGDATVSSSKLRLTKVKGNGLPTLSSLGRAFYSSPIQIYDKSTGA
VASWATSFTANIFAPNKSSSADGIAFALVPVGSEPKSNSGFLGVFDSVDYDNSAQTVAVEFD
TFSNTDWDPTSRHIGIDVNSIKSIRTASWGLANGQNAEILITYNAATSLLVASLVHPSRRTSY
IVSERVDITNELPEYVSIGFSATTGLSEGYTETHDVLSWSFASKLPDDSTTEPLDIASYLVRN
VL

>d1dhkb_ b.29.1.1 (B:) Phytohemagglutinin-L, PHA-L, also arcelin {Kidney bean (*Phaseolus vulgaris*)}

ATETSFIIIDAFNKTNLILQGDATVSSNGNLQLSYNSYDSMSRAFYSAPIQIRDSTTGNVASFD
TNFTMNIRTHRQANSAGLDVFLVPVQPESKGDVTVEFDTFLSRISIDVNNNDIKSVPWD
VHDYDGQNAEVRITYNSSTKVFSVLSNPSTGKSNNVSTTVELEKEVYDWWVSGFSATSG
AYQWSYETHDVLSWSFSSKF

>d1gbg_ b.29.1.2 (-) *Bacillus* 1-3,1-4-beta-glucanase {*Bacillus licheniformis*}

QTGGSFYEPFNNTGLWQKADGYSNGNMFNCTWRANNVSMTSLGEMRLSLTSPSYNK
FDCGENRSVQTYGYGLYEVNMKPAKNVGIVSSFFTYTGPTDGTWPWEIDIEFLGKDTTKV
QFNYYTNGVGNHEKIVNLGFDAANSYHTYAFDWQPNSEIKWYVDGQLKHTATTQIPQTPG
KIMMNLWNGAGVDEWLGSYNGVTPLYAHYNWVRYTKR

>d1dypa_ b.29.1.2 (A:) kappa-Carrageenase, catalytic
{*Pseudoalteromonas carrageenovora*}

SMQPPIAKPGETWILQAKRSDEFNVKDATKWNFQNTENYGVWSWKNENATVSKGKLKLT
TKRESHQRTFWDGCNQQQVANYPLYTSGVAKSRATGNYGYEARIKGASTFPGVSPAF
WMYSTIDRSLTKEGDVQYSEIDVVELTQKSAVRESHDHLHNIVVKNGKPTWMRPGSFPQT
NHNGYHLPFDPRNDFHTYGVNVTDKKITWYVDGEIVGEKDNLYWHRQMNLTLSQGLRA
PHTQWKCNQFYPSANKSAEGFPTSMEVDYVRTWVKV

>d1bkza_ b.29.1.3 (A:) S-lectin, different isoforms {Human (*Homo sapiens*)}

SNVPHKSSLPEGIRPGTVLRIRGLVPPNASRFHVNLLCGEEQGSDAALHFNPRLDTSEVVF
NSKEQGSWGREERGPVFPFQRGQPFVLIASDDGFKAVVGDAQYHHFRHRLPLARVRLV
EVGGDVQLDSVRIF

>d1hlca_ b.29.1.3 (A:) S-lectin, different isoforms {Human (*Homo sapiens*)}

ELEVKNMDMKPGSTLKITGSIADGTDGFINLGGQTDKLNLFNPRFSESTIVCNSLDGSN
WGQEQREDHLCFSPGSEVKFTVTFESDKFKVKLPDGHELTFPNRLGHSHLSYLSVRGGFN
MSSFKLKE

>d1a78a_ b.29.1.3 (A:) S-lectin, different isoforms {Toad (*Bufo arenarum*)}

ASAGVAVTNLNLKPGHCVEIKGSIPPDCGFAVNLGEDASNLLHFNARFDLHGDVKNKIVC
NSKEADAWGSEQREEVFPFQQGAEVMVCFEYQTQKIIKFSSGDQFSFPVRKVLPSIPFLSL
EGLAFKSITTE

>d1hdka_ b.29.1.3 (A:) Charcot-Leyden crystal (CLC) protein {Human (*Homo sapiens*)}

SLLPVPYTEAASLSTGSTVTIKGRPLVCFLNEPYLQVDFHTEMKEESDIVFHFQVCFGRRV
VMNSREYGAWKQQVESKNMPFQDGQEFELSSVLPDKYQVMVNGQSSYTFDHRIKPEAV
KMVQVWRDISLTKFNVSYL

>d1a3k_ b.29.1.3 (-) Galectin-3 CRD {Human (*Homo sapiens*)}

LIVPYNLPLPGGVVPRMLITILGTVKPNANRIALDFQRGNDVAFHFNPRFNENNRRVIVCN
TKLDNNWGREERQSVFPFESGKPKFIQVLVEPDHFKVAVNDAHLLQYNHRVKKLNEISKL
GISGDIDLTSASYTMI

>d1c1la_b.29.1.3 (A:) Congerin I {Conger eel (Conger myriaster)}

GGLQVKNFDFTVGKFLTVGGFINNSPQRFSVNVGESMNSLSLHLDHRFNYGADQNTIVM
NSTLKGDNGWETEQRSTNFTLSAGQYFEITLSYDINKFYIDILDGPNLEFPNRYSKFLPFL
SLAGDARLTLVKLE

>d1d2sa_b.29.1.4 (A:) Sex hormone-binding globulin {Human (Homo sapiens)}

PPAVHLSNGPGQEPIAVMTFDLTKITKTSSSEFVRTWDPEGVIFYGDTNPKDDWFMLGLRD
GRPEIQLHNHWAQLTVGAGPRLDDGRWHQVEVKMEGDSVLLEVDGEEVLRLRQVSGHPI
MRIALGGLLFPASNLRLPLVPALDGCLRRDSWLDKQAEISASAPTSRSC

>d1dyka1 b.29.1.4 (A:2744-2932) Laminin alpha2 chain {Mouse (Mus musculus)}

HGPCVAESEPALLTGSKQFGLSRNSHIAIAFDDTKVKNRLTIELEVRTEAESGLLFYMARIN
HADFATVQLRNGFPYFSYDLGSGDTSTMIPTKINDGQWHKIKIVRVKQEGILYVDDASSQT
ISPKKADILDVVGILYVGGLPINYTTRRIGPVTYSLDGCVRNLHMEQAPVDLDQPTSSFHV
GTCFA

>d1dyka2 b.29.1.4 (A:2933-3117) Laminin alpha2 chain {Mouse (Mus musculus)}

NAESGTYFDGTGFAKAVGGFKVGLDLLVEFEFRTRPTGVLLGVSSQKMDGMGIEMIDEK
LMFHVDNGAGRFTAIYDAEIPGHMCNGQWHKVTAKKIKNRLELVVDGNQVDAQSPNSA
STSADTNDPVFVGGFPGGLNQFGLTTNIRFRGCIRSLKLTGKTGKPLEVNFKALELRGVQ
PVSCPT

>d1c4ra_b.29.1.4 (A:) Ligand-binding domain of neuexin 1beta {Rat (Rattus norvegicus)}

HAGTTYIFSKGGGQITYKWPPNDRPSTRADRLAIGFSTVQKEAVLVRVDSSSGLGDYLELH
IHQGKIGVKFNVGTDDIAIEESNAIINDGKYHVVRFRTRSGGNATLQVDSWPVIERYPAGRQ
LTIFNSQATHIIGGKEQGQPFQGGQLSGLYNGLKVLNMAAENDANIAIVGNVRLVGEV

>d1a8d_1 b.29.1.6 (1-247) Tetanus neurotoxin {Clostridium tetani}

MKNLDCWVDNEEDIDVILKKSTILNLDINNDIISDISGFNSSVITYPDACLVPINGKAIHLV
NNESEVIVHKAMDIEYNDMFNNFTVSFWLRVPKVSASHLEQYGTNEYSISSMKKHLSI
GSGWSVSLKGNNLIWTLKDSAGEVRQITFRDLPDKFNAYLANKWVFITITNDRSSANLYI
NGVLMGSAEITGLGAIREDDNNITLKLDRCNNNNQYVSIDKFRIFCKALNPKEIEKLYTSYLS
>d1epwa1 b.29.1.6 (A:862-1079) Botulinum neurotoxin {Clostridium botulinum, serotype B}
NIILNLRYKDNNLIDLSGYGAKVEVYDGVELNDKNQFKLTSSANSKIRVTQNQNIIFNSVFL
DFSVSFWIRIPKYKNDGIQNYIHNEYTIINCMKNNSGWKISIRGNRIIWTLIDINGKTKSVFF
EYNIREDISEYINRWFFVTITNNLNNAKIYINGKLESNTDIKDIREVIANGEIIFKLDGDIDRT
QFIWMKYFSIFNTELSQSNIERYKIQSY

>d1kit_1 b.29.1.8 (25-216) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}

ALFDYNATGDTEFDSPAKQGWMDNTNNGSGVLTNADGMPAWLVQGIGGRAQWTYSLS
TNQHAQASSFGWRMTTEMKVLSSGGMITNYANGTQRVLPISLDSSGNLVVEFEGQTGRT
VLATGTAATEYHKFELVFLPGSNPSASFYFDGKLIRDNIQPTASKQNMIVWNGSSNTDGV
AAYRDIKFEIQGD

>d1kit_2 b.29.1.8 (347-543) Vibrio cholerae sialidase, N-terminal and insertion domains {Vibrio cholerae}

DVTDQVKERSFQIAGWGGSELYRRNTSLNSQQDWQSNAKIRIVDGAANQIQVADGSRKY

VVTLSIDESGGLVANLNGVSAPIILQSEHAKVHSFHDYELQYSALNHTTTTLFVDGQQITTW
AGEVSQENNIQFGNADAQIDGRLHVQKIVLTQQGHNLFEDAFYLAQQTPEVEKDLEKLG
WTKIKTGNTMSLYGNAS

>d6cel__ b.29.1.10 (-) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma
reesei, Cel7A}

ESACTLQSETHPPLTWQKCSSGGTCTQQTGSSVIDANWRWTHATNSSTNCYDGNTWSST
LCPDNETCAKNCCLDGAAYASTYGVTTSGNSLSIDFVTQSAQKNVGARLYLMASDTTYQ
EFTLLGNEFSFDVDVSQLPCGLNGALYFVSMADGGVSKYPTNTAGAKYGTGYCDSQCP
RDLKFINGQANVEGWEPSSNNANTGIGGHGSCCSQMDIWEANSISEALTPHPCTTVGQEIC
EGDGCGGTYSDNRYGGTCDPDGCDWNPYRLGNTSFYGPSSFTLDTTKKLTVVVTQFETS
GAINRYYVQNGVTFQQPNAELGSYSGNELNDDYCTAEEAEFGSSFSKGGTLQFKKATS
GGMVLVMSLWDDYYANMLWLDSTYPTNETSSTPGAVRGSCSTSSGVPQVESQSPNAKV
TFSNIKFGPIGSTGNPSG

>d1eg1a_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Trichoderma
reesei, Endoglucanase I}

EQPGTSTPEVHPKLTTYKCTKSGGCVAQDTSVVLDWNYRWMHDANYNSCTVNGGVNTT
LCPDEATCGKNCFIEGVDAASGVTTSGSSLTMNQYMPSSSGGYSSVSPRLLYLLSDGEYV
MLKLNGQELSFDVDLSALPCGENGSLYLSQMDENGGANQYNTAGANYGSGYCDACQPV
QTRWNGTLNTSHQGFCNEMDILEGNSRANALTPHSCTATACDSAGCGFNPYGSYKSY
YGPAGDTVDTSKFTIITQFNTDNGSPSGNLVSITRKYQQNGVDIPSAQPGGDTISSCPSASA
YGG LATMGKALSSGMVLVFSIWNDNSQYMNWLDSGNAGPCSSTEGNPSNILANNPNTHV
VFSNIRWGDIGSTT

>d3ovwa_ b.29.1.10 (A:) Cellobiohydrolase I (cellulase, Endoglucanase I, CBH1) {Fusarium
oxysporum}

ETPDKAKEQHPKLETYRCTKASGCKKQTNIVADAGIHGIRQKNGAGCGDWGQKPNATA
CPDEASCAKNCILSGMDSNAYKNAGITTSGNKLRLQLINNQLVSPRVYLLEENKKKYEM
LHLTGTEFSFDVEMEKLPCGMNGALYLSEMPQDGGKSTSRNSKAGAYYGAGYCDACQY
VTPFINGVGNIKGQGVCCNELDIWEANSRATHIAPHPCSKPGLYGCTGDECGSSGICDKAG
CGWNHNRINVTDFYGRGKQYKVDSTRKFTVTSQFVANKQGDLELHRHYIQDNKVIESA
VVNISGPPKINFINDKYCAATGANEYMRLLGGTKQMGMDSRGMVLAMSVWWSEGDFM
AWLDQGVAGPCDATEGDPKNIVKVQPNPEVTFNIRIGEIGSTSSV

>d1qh7a_ b.29.1.11 (A:) Xylanase II {Bacillus agaradhaerens}

EIVTDNSIGNHGDYDYEFWKDSGGSGTMILNHGGTFSAQWNNVNNILFRKGKKFNETQT
HQQVGNMSINYGANFQPNNGNAYLCVYGTVDPLVEYYIVDSWGNWRPPGATPKGTITV
DGGTYDIYETLRVNQPSIKGIATFKQYWSVRRSKRTSGTISVSNHFRAWENLGMNMGKM
YEALTVEGYQSSGSANVYSNTRRINGNPLS

>d1bk1__ b.29.1.11 (-) Xylanase II {Aspergillus kawachii}

AGINYVQNYNGNLGDFTYDESAGTFSMYWEDGVSSDFVVLGLWTTGSSNAITYSAEYSA
SGSSSYLAVYGWVNYPQAEYYIVEDYGDYNPCSSATSLGTVYSDGSTYQVCTDTRTNEPS
ITGTSTFTQYFSVRESTRSGTVTVANHFNFWAQHGFNSDFNYQVMAVEAWSGAGSASV
TIS

>d2nlra_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain
{Streptomyces lividans, CelB2}

DTTICEPFGTTTIQGRYVVQNNRWGSTAPQCVTATDTGFRVTQADGSAPTNGAPKSYPSVF

NGCHYTNCSPGTDLPVRLDTVSAAPSSISYGFVDGAVYNASYDIWLDPTARTDGVNQTEI
MIWFNRVGPIQPIGSPVGTASVGGRTWEVWSSGGNGSNDVLSFVAPSAISGWSFDVMDFVR
ATVARGLAENDWYLTSVQAGFEPWQNGAGLAVNSFSSTVET

>d1h8va_ b.29.1.11 (A:) Endo-1,4-beta-glucanase (cellulase) catalytic domain
{*Trichoderma reesei*, Cel12A}

ETSCDQWATFTGNGYTVSNNLWGASAGSGFGCVTAVSLSGGASWHADWQWSGGQNNV
KSYQNSQIAIPQKRTVNSISSMPTTASWSYSGSNIRANVAYDLFTAANPNHVTYSGDYELM
IWLKGYGDIGPIGSSQGTNVNKGQSWTLYYGYNGAMQVYSFVAQTNTTNYSGDVKNFFN
YLRDNKGYNAAGQYVLSYQFGTEPFTGSGTLNVASWTASIN

>d1oac1 b.30.2.1 (A:301-724) Copper amine oxidase, domain 3 (catalytic)
{*Escherichia coli*}

PAVKPMQIIEPEGKNYTITGDMIHWRNWDHLSMNSRVGPMISTVTYNDNGTKRKVMYE
GSLGGMIVPYGDPDYGWYFKAYLDSGDYGMGTLTSPARGKDAPSNVLLNETIADYTG
PMEIPRAIAVFERIYAGPEYKHQEMGQPNVSTERRELVRWISTVGNADYIFDWIFHENG
TIDAGATGIEAVKGVKAKTMHDETAKDDTRYGTLIDHNIVGTTHQHIYNFRLDLDVDGEN
NSLVAMDPVVKPNTAGGPRTSTMQVNQYNIGNEQDAAQKFDPGTIRLLSNPNKENRMGN
PVSYQIIPYAGGTHPVAKGAQFAPDEWIYHRLSFMDKQLWVTRYHPGERFPEGKYPNRST
HDTGLGQYSKDNESLDNTDAVVWMTTGTTHVARAEWPIMPTEWVHTLLKPWNFFDET
PTLGALK

>d1ksia1 b.30.2.1 (A:207-647) Copper amine oxidase, domain 3 (catalytic) {*Pea*
seedling (Pisum sativum)}

VSKQSPFPGPKQHSLTSHQPQGPFGQINGHSVSWANWKFHIGFDVRAGIVISLASIYDLEK
HKSRRLVLYKGYISELFVPYQDPTEEFYFKTFDFSGEFGFGLSTVSLIPNRDCPPHAQFIDTY
VHSANGTPILLKNAICVFEQYGNIMWRHTENGIPNESIEESRTEVNLIVRTIVTVGNADNVI
DWEFKASGSIKPSIALSGILEIKGTNIKHKDEIKEDLHGKLVANSIGIYHDHFYIYYLDFDI
DGTHNSFEKTSKTVRIKDGSSKRKSYWTTETQTAKTESDAKITIGLAPAEVNVNPNIKT
AVGNEVGYRLIPAIPAHPLLTEDDYPQIRGAFTNYNVWVTAYNRTEKWAGGLYVDHSRGD
DTLAVWTKQNREIVNKDIVMWHVVGIIHVPAQEDFPIMPLLSTSFELRPTNFFERNPVLKT
LSPRDVAWPGC

>d1av4_1 b.30.2.1 (212-628) Copper amine oxidase, domain 3 (catalytic) {*Arthrobacter*
globiformis}

PLRTTQKPISITQPEGPSFTVTGGNHIEWEKWSLDVGFVREGVVLHNIAFRDGDRLRPIIN
RASIAEMVVPYGDPSPIRSWQNYFDTGEYLVGQYANSLELGCDCLGDITYLSPVISDAFGN
PREIRNGICMHEEDWGILAKHSDLWSGINYTRNRMRMVISFFTTIGNADYGFYWYLYLDG
TIEFEAKATGVVFTSAFPEGGSNDISQLAPGLGAPFHQHIFSARLDMAIDGFTNRVEEEDVV
RQTMGPGNERGNAFSRKRTVLTRESEAVREADARTGRTWIISNPESKNRLNEPVGKYLHA
HNQPTLLADPGSSIARRAAFATKDLWVTRYADDERYPTGDFVNQHSGGAGLPSYIAQDRD
IDGQDIVVWHTFGLTHFPRVEDWPIMPVDTVGFKLRPEGFFDRSPVLDVPAN

>d1a2va1 b.30.2.1 (A:237-672) Copper amine oxidase, domain 3 (catalytic) {*Yeast*
(*Hansenula polymorpha*)}

PEAPPINVTQPEGVSFKMTGNVMEWSNFKFHIGFNYREGIVLSDVSYNDHGNVRPIFHRIS
LSEMIVPYGSPEFPHQRKHALDIGEYGAGYMTNPLSLGCDCKGVIHYLDAHFSDRAGDPI
TVKNAVCIHEDDGLLFKHSDFRDNFATSLVTRATKLVVSQIFTAANAHEYCLYWVFMQDG
AIRLDIRLTGILNTYILGDDEEAGPWGTRVYPNVNAHNHQLFSLRIDPRIDGDGNSAAAC

DAKSSPYPLGSPENMYGNAFYSEKTTFTKTVKDSLTYNESATGRSWDIFNPKNVNPYSGKP
PSYKLVSTQCPPLAKEGSLVAKRAPWASHSVNVVPYKDNRLYPSGDHVPQWSGDGVRG
MREWIGDGSENIDNTDILFFHTFGITHFPAPEDFPLMPAEPITLMLRPRHFFTENPGLDIQPS
YAMTTSEAKRAV

>d1cb8a3 b.30.3.1 (A:336-599) Chondroitinase AC {*Pedobacter heparinus* (*Flavobacterium heparinum*)}

IEPYHHQFWNGDYVQHLPAYSFNVRMVSKRTRRSESGNKENLLGRYLSDGATNIQLRGP
EYYNIMPVWEWDKIPGITSRDYLTDRPLTKLWGEQGSNDFAGGVSDGVYGASAYALDYD
SLQAKKAWFFFDKEIVCLGAGINSNAPENITTTLNQSWLNGPVISTAGKTGRGKITTFKAQ
GQFWLLHDAIGYYFPEGANLSLSTQSQKGNWFHINNSHSHKDEVSGDVFKLWINHGARPE
NAQYAYIVLPGINKPEEIKKYNGTA

>d1flsa4 b.30.3.1 (A:620-919) Hyaluronate lyase {*Streptococcus agalactiae*}

LKSNLSTFNSMDRLAYYNAKKDFGFALSLHSKRTLNYEGMNDENTRGWYTGDMFYIY
NSDQSHYSNHFWPTVNPYKMAGTTTEKDAKREDTTKEFMSKHSKDAKEKTGQVTGTSDF
VGSVKLNDHFALAAMDFTNWDRTLTAQKGWVILNDKIVFLGSNIKNTNGIGNVSTTIDQR
KDDSKTPYTTYVNGKTIDLKQASSQQFTDTKS VFLESKEPGRNIGYIFFKNSTIDIERKEQT
GTWNSINRTSKNTSIVSNPFITISQKHDNKGDSYGYMMVPNIDRTSFDKLANKEVELLEN
S

>d1ezve1 b.33.1.1 (E:87-215) ISP subunit of the mitochondrial cytochrome bc₁-complex, watersoluble domain {*Baker's yeast* (*Saccharomyces cerevisiae*)}

DVLAMAKVEVNLAAPLGNVVKWQKPVFIRHRTPEIQEANSVDMSALKDPQTDA
DRVKDPQWLIMLGICHTLGCVPIGEAGDFGGWFCPCHGSHYDISGRIRKGPAPLNLEIPAY
EFDGDKVIVG

>d1rfs_ b.33.1.1 (-) ISP subunit from chloroplast cytochrome bf complex {*Spinach* (*Spinacia oleracea*)}

TIAKDALGNDVIAAEWLKTHAPGDRTLQGLKGDPTYLVVESDKTLATFGINAVCTHLGC
VVPFNAAENKFICPCHGSQYNNQGRVVRGPAPLSLALAHCDVDDGKVVFVPWTETDFRT
GEAPWWSA

>d1g8kb_ b.33.1.1 (B:) Arsenite oxidase Rieske subunit {*Alcaligenes faecalis*}

RTTLAYPATAVSVAKNLAANEPVSFTYPDTSSPCVAVKLGAPVPGGVGPDDDIVAYSVLCT
HMGCPSTYDSSSKTFSCPCHFTFDEAEKAGQMICEATADLPRVLLRYDAASDALTAGV
DGLIYGRQANVI

>d1fqta_ b.33.1.1 (A:) Rieske-type ferredoxin associated with biphenyl dioxygenase {*Burkholderia cepacia*}

MKFTRVCDRRDVPEGEALKVESGGTSVAIFNVGELFATQDRCTHGDWSLSGGYLEGD
VVECSLHMGKFCVRTGKVKSPPPCEALKIFPIRIEDNDVLVD FEAGYLAP

>d1byma_ b.34.1.2 (A:) Diphtheria toxin repressor (DtxR) {*Corynebacterium diphtheriae*}

NPPIGLDELGVGNSDAAAPGTRVIDAATSMPRKVRIVQINEIFQVETDQFTQLLDADIRVGS
EVEIVDRDGHITLSHNGKDVELLDDLAHTIRIEEL

>d1fx7a3 b.34.1.2 (A:145-230) Iron-dependent regulator IdeR {*Mycobacterium tuberculosis*}

GADDANLVRLTELPAGSPVAVVVRQLTEHVQGDIDLITRLKDAGVVPNARVTVETTPGGG
VTIVIPGHENVTLPEMAHAVKVEKV

>d1neb__ b.34.2.1 (-) SH3 domain from nebulin {Human (Homo sapiens)}
TAGKIFRAMYDYMAADADEVSKFDGDAIINVQAIDEGWMYGTVQRTGRTGMLPANYVE
AI

>d2abl_1 b.34.2.1 (75-139) Abl tyrosine kinase, SH3 domain {Human (Homo sapiens)}
MGPSNDPNLFVALYDFVASGDNTLSITKGEKLRVLGYNHNGEWCEAQTKNGQGWWVPSN
YITPVN

>d1pht__ b.34.2.1 (-) Phosphatidylinositol 3-kinase (p85-alpha subunit, pi3k), SH3
domain {Human (Homo sapiens)}
AEGYQYRALYDYKKEREEDIDLHLGDILTVNKGSLVALGFSDGQEARPEEIGWLNNGYNET
TGERGDFPGTYVEYIGRKKISPP

>d1g2ba_ b.34.2.1 (A:) alpha-Spectrin, SH3 domain {Chicken (Gallus gallus)}
MDRQGFVPAAYVKKLDSGTGKELVLALYDYQEKSPREVTMKKGDILLNSTNKDWWK
VEVN

>d1awj__ b.34.2.1 (-) IL-2 inducible T-cell (Itc) kinase {Mouse (Mus musculus)}
KKPLPPTPEDNRRSFQEPEETLVIALYDYQTNDPQELALRCDEEYLLDSSEIHWWRVQDK
NGHEGYAPSSYLVEKS

>d1fmk_1 b.34.2.1 (82-145) c-src tyrosine kinase {Human (Homo sapiens)}
MVTTFVALYDYESRTETDLSFKKGERLQIVNNTEGDWWLAHSLSTGQTGYIPSNYVAPSD
SIQA

>d1gl5a_ b.34.2.1 (A:) tyrosine kinase tec {Mouse (Mus musculus)}
GSEIVVAMYDFQATEAHDRLRLERGQEYIILEKNDLHWWWRARDKYGSEGYIPSNYVTGKK
SNNLDQYD

>d1gria2 b.34.2.1 (A:157-217) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal
domains {Human (Homo sapiens)}
QPTYVQALFDFDPQEDGELGFRRGDFIHVMDNSDPNWWKGACHGQTGMFPRNYVTPVN
RNV

>d1gbra_ b.34.2.1 (A:) Growth factor receptor-bound protein 2 (GRB2), N- and C-terminal domains
{Mouse (Mus musculus)}
GSRRASVGSMEIAIKYDFKATADDELSFKRGDILKVLNEECDQNWYKAELNGKDGFIK
NYIEMKPHPEFIVTD

>d2hsp__ b.34.2.1 (-) Phospholipase C, SH3 domain {Human (Homo sapiens)}
GSPTFKCAVKALFDYKAQREDELTFIKSAIQNVEKQEGGWWRGDYGGKKQLWFPSNYV
EEMVNPEGIHRD

>d1ycsb2 b.34.2.1 (B:457-519) 53BP2 {Human (Homo sapiens)}
IMNKGVIYALWDYEPQNDDLEPMKEGDCMTIIHREDEDEIEWWWARLNDKEGYVPRNLL
GLYP

>d1bb9__ b.34.2.1 (-) Amphiphysin 2 {Rat (Rattus norvegicus)}
TTGRLDLPPGFMFKVQAQHDYTATDDELQLKAGDVVLVIPFQNPEEQDEGWLMGVKES
DWNQHKELEKCRGVFPENFTEVQ

>d1i07a_ b.34.2.1 (A:) EPS8 SH3 domain {Mouse (Mus musculus)}
KKYAKSKYDFVARNSELVSMKDDVLEILDDRQWWKVRNASGDSGFVPNNILDIMRTP

>d1k1za_ b.34.2.1 (A:) Vav N-terminal SH3 domain {Mouse (Mus musculus)}
RAQDKKRNELGLPKMEVFQEYYGIPPPGAFGGFLRLNPGDIVELTKAEAEHNWWEGRN
TATNEVGWFPNCRVHPYVH

>d1i1ja_ b.34.2.1 (A:) Melanoma inhibitory activity protein {Human (Homo sapiens)}
 GPMPKLADRKLCADQECSHPI SMAVALQDYMAPDCRFLTIHRGQVVYVFSKLGKGRGLF
 WGGSVQGDYYGDLAARLGYPSSIVREDQTLKPGKVDVKTDKWDFYC

>d1k1ja_ b.34.2.1 (A:430-525) Psd-95 {Rat (Rattus norvegicus)}
 GFYIRALFDYDKTKDCGFLSQALSFRFGDVLHVIDAGDEEWWQARRVHSDSETDDIGFIP
 SKRRVERREWSRLKAKDWGSSSGSQGREDSVLSYET

>d2mysa1 b.34.3.1 (A:34-79) Myosin S1 fragment, N-terminal domain {Chicken (Gallus gallus),
 pectoral muscle}
 AKSSVFVHHPKQSFVKGTIQSKEGGKVTVKTEGGETLTVKEDQVFS

>d1b7ta1 b.34.3.1 (A:29-76) Myosin S1 fragment, N-terminal domain {Bay scallop (Aequipecten
 irradians)}
 DGKKNCWVPDEKEGFASAEIQSSKGDEITVKIVADSSTRTVKKDDIQS

>d1lvk_1 b.34.3.1 (34-79) Myosin S1 fragment, N-terminal domain {Slime mold (Dictyostelium
 discoideum)}
 YIWYNPDPKERDSYECGEIVSETSDSFTFKTSDGQDRQVKKDDANQ

>d1jj2s_ b.34.5.1 (S:) Ribosomal proteins L24 (L24p) {Archaeon Haloarcula
 marismortui}
 SKQPDKQRKSQRRAPLHERHKQVRATLSADLREEYGQRNVRVNAGDTVEVLRGDFAGEE
 GEVINVDLDKAVIHVEDVTLEKTDGEEVPRPLDTSNVRVTDLDLEDEKREARLESEDDSA

>d1jj2p_ b.34.5.1 (P:) Ribosomal proteins L21e {Archaeon Haloarcula marismortui}
 PSSNGPLEGTRGKLKNKPRDRGTSPQRAVEEFDDGEKVHLKIDPSVPNGRFHPRFDGQT
 GTVEGKQGDAYKVDIVDGGKEKTIIVTAAHLRRQE

>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}
 KNSKFKNFRVYYREGDQLWKGP GELLWK GEGAVLLKVGTDIKVVP RRKAKI IKD

>d1jh2a_ b.35.1.1 (A:) Chaperonin-10 (GroES) {Mycobacterium tuberculosis}
 AKVNIKPLEDKILVQANEAE TTTASGLVIPDTAKEKPQEGTVVAVGPGRWDEDEGEKRIPLD
 VAEGDTVIYSKYGGTEIKYNGE EYLILSARDVLAVVSK

>d1g31a_ b.35.1.1 (A:) GP31 co-chaperonin {Bacteriophage T4}
 QQLPIRAVGEYVILVSEPAQAGDEEVTESGLIIGKRVQGEVPEL CVVHSVGPDPVPEGFCEVG
 DLTSLPVGQIRNVPHPFVALGLKQPKEIKQKFVTCHYKAIPCLYK

>d1e3ia1 b.35.1.2 (A:1-174,A:325-376) Alcohol dehydrogenase {Mouse (Mus musculus), class II}
 GTQGKVIKCKAAIAWK TGSPLCIEIEVSPPKACEVRIQVIATCVCPTDINATDPKKKALFP
 VVLGHECAGIVESVGPVTFNFKPGDKVIPFFAPQCKRCKLCL SPLTNLCGKL RNFKYPTID
 QELMEDRTSRFTCKGRSIYHFMGVSSFSQYTVVSEANLARVDDEANLERVCXKSVDSVPN
 LVSDYKNKKFDL DLLVTHALPFESINDAIDLMKEGKSIRTILTF

>d1ykfa1 b.35.1.2 (A:1-150,A:315-352) Bacterial secondary alcohol dehydrogenase
 {Thermoanaerobacter brockii}
 MKGFAMLSIGKVGWIEKEKPAPGPFDAIVRPLAVAPCTSDIHTVFEGAIGERHNMILGHEA
 VGEVVEVGSEVKDFKPGDRVVPAITPDWRTSEVQRGYHQHSGGMLAGWKFSNVKDG
 V FGEFFHVNDADMNLAHL PKEIPLEAAVMIPDXDPSKLVTHVFRGFDNIEKAFMLMKDKPK

DLIKPVVILA

>d1e3ja1 b.35.1.2 (A:4-150,A:314-351) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly (*Bemisia argentifolii*)}

DNLSAVLYKQNDLRLEQRPIPEPKEDVLLQMAYVGICGSDVHYEHGRIADFIVKDPMVI
GHEASGTVVKVGKNVHLLKKGDRVAVEPGVPCRRCQFCKEGKYNLCPDLTFCATPPDDG
NLARYYVHAADFCHKLPD NVSLEEGALXNVKQLVTHSFKLEQTVDAFEAAARKKADNTIK
VMISCRQ

>d1qora1 b.35.1.2 (A:2-135,A:266-327) Quinone oxidoreductase {*Escherichia coli*}

ATRIEFHKHGGPEVLQAVEFTPADPAENEIQVENKAIGINFIDTYIRSGLYPPPSLPSGLGTEA
AGIVSKVSGSVKHIKAGDRVVYAQSALGAYSSVHNIIADKAAILPAAISFEQAAASFLKGL
TVYYLLRKTXLQGYITTREELTEASNELFSLIASGVIKVDVAEQQKYPLKDAQRAHEILES
RATQGSSLLIP

>d1kwaa_ b.36.1.1 (A:) Cask/Lin-2 {Human (*Homo sapiens*)}

RSRLVQFQKNTDEPMGITLKMNELNHCIVARIMHGGMIHRQGT LHV GDEIREINGISVANQ
TVEQLQKMLREMRSITFKIVPSYREF

>d1be9a_ b.36.1.1 (A:) Synaptic protein PSD-95 {Rat (*Rattus norvegicus*)}

FLGEEDIPREPRRIVHRGSTGLGFNIIGGEDGEGIFISFILAGGPADLSGELRKGDQILSVNG
VDLRNASHEQAAIALKNAGQTVTIIAQYKPEEYSRFEANSRVNSSGRIVTN

>d1qava_ b.36.1.1 (A:) Syntrophin {Mouse (*Mus musculus*)}

GSLQRRRVTVRKADAGGLGISIKGGRENKMPILISKIFKGLAADQTEALFVGDAILSVNGE
DLSSATHDEAVQALKKTGKEVVLEV KYMK

>d1b8qa_ b.36.1.1 (A:) Neuronal nitric oxide synthase, NNOS {Rat (*Rattus norvegicus*)}

GSHMIEPNVISVRLFKRKVGGLGLV KERVSKPPVIISDLIRGGAAEQSGLIQAGDIILAVND
RPLVDLSYDSALEVLRGIASETHVVLILRGPEGFTTHLETTFTGDGTPKTIRVTQPLGPPTK
AV

>d3pdza_ b.36.1.1 (A:) Phosphatase hPTP1e {Human (*Homo sapiens*)}

PKPGDIFEVELAKNDNSLGISVTGGVNTSVRHGGIYVKAVIPQGA AESDGRIHKGDRV LAV
NGVSLEGATHKQAVETLRNTGQVVHLLLEKGQSPT

>d1g9oa_ b.36.1.1 (A:) Na⁺/H⁺ exchanger regulatory factor, NHERF {Human (*Homo sapiens*)}

RMLPRLCCLEKGPNGYGFHLHGEKGKLGQYIRLVEPGSPA EKAGLLAGDRLVEVNGENV
EKETHQQVVSIRAAALNAVRLLVDPETDEQL

>d1ihja_ b.36.1.1 (A:) Inad {Fruit fly (*Drosophila melanogaster*)}

GELIHMVTLDKTGKKSFGICIVRGEVKDSPNTKTTGIFIKGIVPDSPAHL CGRLKVGDRILS
LNGKDVRNSTEQAVIDLIKEADFKIELEIQTF

>d1fc6a3 b.36.1.3 (A:157-248) Photosystem II D1 C-terminal processing protease {Algae (*Scenedesmus obliquus*)}

AGSVTGVGLEITYDGGSGKD VVVLT PAPGGPAEKAGARAGDVIVTV DGTAVKGMSLYDV
SDLLQGEADSQVEVVLHAPGAPSNTRTLQLTRQ

>d1k32a1 b.36.1.3 (A:763-853) Tricorn protease {Archaeon *Thermoplasma acidophilum*}

GRIACDFKLDGDHYVVA KAYAGDYSNEGEKSPIFEY GIDPTGYLIEDIDGETVGAGSNIYR
VLSEKAGTSARIRLSGKGGDKRDLMIDIL

>d1g3p_2 b.37.1.1 (91-217) N-terminal domains of the minor coat protein g3p {Bacteriophage M13}

EYGDTPIPGYTYINPLDGTYP PGTEQN PANPNPSLEESQPLNTFMFQNNRFRNRQGALT VY
TGTVTQGTDPVKTY YQYTPVSSKAMYDAYWNGKFRDCAFHSGFNEDIFVCEYQGQSSDL

PQPPVNA

>d1fgp_ b.37.1.1 (-) N-terminal domains of the minor coat protein g3p {Bacteriophage fd}
ETVESCLAKPHTENSFTNVWKDDKTLDYRANYEGCLWNATGVVVCTGDETQCYGTWVP
IGLAIPENAAAH

>d1b34a_ b.38.1.1 (A:) D1 core SNRNP protein {Human (Homo sapiens)}
KLVRFLMKLSHETVTIELKNGTQVHGTITGLVDVSMNTHLKAVKMTLKNREPQVLETLSIR
GNNIRYFILPDSLPLDTLLV

>d1b34b_ b.38.1.1 (B:) D2 core SNRNP protein {Human (Homo sapiens)}
TGPLSVLTQSVKNNTQVLINCRNNKLLGRVKAFFDRHCNMVLENVKEMWTEVPKSGKG
KKKSKPVNKDRYISKMFLRGDSVIVVLRNPLIAGK

>d1d3ba_ b.38.1.1 (A:) D3 core SNRNP protein {Human (Homo sapiens)}
GVPIKVLHEAEGHIVTCETNTGEVYRGKLEAEDNMNCQMSNITVTYRDGRVAQLEQVYI
RGCKIRFLILPD

>d1d3bl_ b.38.1.1 (L:) B core SNRNP protein {Human (Homo sapiens)}
TVGKSSKMLQHIDYRMRCILQDGRIFIGTFKAFFDKHMLNLILCDCDEFKIKPKNSKQAERE
EKRVLGLVLLRGENLVSMTEGPPPKDTG

>d1i81a_ b.38.1.1 (A:) Archaeal homoheptameric Sm protein {Archaeon Methanobacterium
thermoautotrophicum}
RVNVQRPLDALGNSLNSPVIKLGKDREFRGVLKSFDLHMNLVLNDAEELEDGEVTRRLG
TVLIRGDNIVYISP

>d1ltrd_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IB}
APQSITELCSEYHNTQIYTINDKILSYTESMAGKREMVITFKSGATFQVEVPGSQHIDSQK
KAIERMKDTRLITYLTETKIDKLCVWNNKTPNSIAAISMEKLYAGA

>d1tiid_ b.40.2.1 (D:) Heat-labile toxin {Escherichia coli, type IIB}
GASQFFKDNCRNTASLVEGVELTKYISDINNNTDGMVVSSTGGVWRISRAKDYPDNV
MTAEMRKIAMAAVLSGMRVNMCASSPNVIWAELEA

>d1c4qa_ b.40.2.1 (A:) Verotoxin-1/shiga-toxin, B-pentamer {Escherichia coli}
TPDCVTGKVEYTKYNDDDTFTVKVGDKELATNRANLQSLLSAQITGMTVTIKTNACHN
GGGFSEVIFR

>d1prtb1_ b.40.2.1 (B:90-199) Pertussis toxin S2/S3 subunits, C-terminal domain
{Bordetella pertussis}

TTRNTGQPATDHYYSNVTATRLLSSTNSRLCAVFVRSGQPVIGACTSPYDGKYWSMYSRL
RKMLYLIYVAGISVRVHVSKEEQYYDYEDATFETYALTGISICNPGSSLC

>d1prtd_ b.40.2.1 (D:) Pertussis toxin S4 subunit {Bordetella pertussis}
DVPYVLVKTNMVVTSVAMKPYEVTPTRMVLCGIAAKLGAAASSPDAHVPFCFGKDLKRP
GSSPMEVMLRAVFMQQRPLRMFLGPKQLTFEGKPALELIRMVECSGKQDCP

>d1prtf_ b.40.2.1 (F:) Pertussis toxin S5 subunit {Bordetella pertussis}
LPHTLYKNFTVQELALKLKGNQEFCLTAFMSGRSLVRACLS DAGHEHDTWFDTMLGFAI
SAYALKSRIALTVEDSPYPGTPGDLELQICPLNGYCE

>d1esfa1_ b.40.2.2 (A:1-120) Staphylococcal enterotoxin A, SEA {Staphylococcus
aureus}

SEKSEEINEKDLRKKSELQGTALGNLKQIYYYNEKAKTENKESHDQFLQHTILFKGFFTDH
SWYNDLLVDFDSKDIVDKYKGKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLHDNNR
LT

>d3tss_1 b.40.2.2 (5-93) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}
 NIKDLLDWYSSGSDTFTNSEVLDNSLGSMRIKNTDGSISLIIFSPSPYYSPAFTKGKVDLNT
 KRIKKSQHTSEGTWIHFQISGVTNTEK

>d3seb_1 b.40.2.2 (1-121) Staphylococcal enterotoxin B, SEB {Staphylococcus aureus}
 ESQDPKPKDELHKSSKFTGLMENMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKLGNY
 DNVRVEFKNKDLADKYKDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCMYGGV
 TEH

>d1enf1 b.40.2.2 (A:2-101) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}
 DLHDKSELTDLALANAYGQYNHPFIKENIKSDEISGEKDLIFRNQGDSGNDLRVKFATADL
 AQKFKNKVNDIYGASFYYKCEKISENISECLYGGTTLNS

>d1an8_1 b.40.2.2 (3-95) Streptococcal superantigen Spe-C {Streptococcus pyogenes}
 KKDISNVKSDLLYAYTITPYDYKDCRVNFSTHTLNIDTQKYRGKDYIISSEMSYEASQKF
 KRDDHVDVFGFLFYILNSHTGEYIYGGITPAQN

>d1et9a1 b.40.2.2 (A:1-95) Streptococcal superantigen Spe-H {Streptococcus pyogenes}
 NSYNTTNRHNLESYKHDSNLIEADSIKNSPDIVTSHMLKYSVKDKNLSVFFEKDWISQEF
 KDKEVDIYALSAQEVCECPGKRYEAFGGITLNS

>d1eu3a1 b.40.2.2 (A:2A-96) Streptococcal superantigen Smez-2 {Streptococcus pyogenes}
 GLEVDNNSLLRNIYSTIVYEYSDIVIDFKTSHNLVTKKLDVRDARDDFFINSEMDEYAANDF
 KTGDKIAVFSVPFDWNYLSKGKVTAYTYGGITPYQK

>d1eoa1 b.40.4.1 (A:71-204) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}
 AKDNYGKLP LIQSRSDRTGQKRVKFVDLDEAKSDSKEVLFRRVHNTRQQGATLAFLT
 LRQQASLIQGLVKANKEGTISKNMVKWAGSLNLESIVLVRGIVKKVDEPIKSATVQNLEIHI
 TKIYTISETPEAL

>d1b8aa1 b.40.4.1 (A:1-103) Aspartyl-tRNA synthetase (AspRS) {Archaeon Pyrococcus kodakaraensis}
 MYRTHYSSEITEELNGQKVKVAGVWWEVKDLGGIKFLWIRDRDGIVQITAPKKKVDPPELF
 KLIPKLRSDEVVAVEGVVNFTPKAKLGFEILPEKIVVLNRAET

>d1c0aa1 b.40.4.1 (A:1-106) Aspartyl-tRNA synthetase (AspRS) {Escherichia coli}
 MRTEYCGQLRLSHVGQQVTLCGWVNRRRDLGSLIFIDMRDREGIVQVFFDPDRADALKL
 ASELRNEFCIQVTGTVRARDEKNINRDMATGEIEVLASSLTINRAD

>d1bbua1 b.40.4.1 (A:11-154) Lysyl-tRNA synthetase (LysRS) {Escherichia coli, gene lysS}
 VVDLNNELKTRREKLANLREQGIAFPNDFRRDHTSDQLHAEFDGKENELEALNIEVAVA
 GRMMTRRIMGKASFVTLQDVGGRIQLYVARDDLPEGVYNEQFKKWDLGDILGAKGKLF
 KTKTGELSIHCTELRLLTKALRPLPD

>d1cuk_3 b.40.4.2 (1-64) DNA helicase RuvA subunit, N-terminal domain {Escherichia coli}
 MIGRLRGIIIEKQPPLVLIIEVGGVGYEVHMPMTCFYELPEAGQEAI VTFHFVVREDAQLLY
 GFN

>d1bvsa3 b.40.4.2 (A:1-63) DNA helicase RuvA subunit, N-terminal domain {Mycobacterium

leprae}

MIFSVRGEVLEVALDHAVIEAAGIGYRVNATPSALATLNQGSQARLV TAMVVREDSMTLY
GFS

>d3ulla_ b.40.4.3 (A:) ssDNA-binding protein {Human (Homo sapiens), mitochondria}

LERSLNRVHLLGRVGQDPVLRQVEGKNPVTIFSLATNEMWRS GDSEVYQLGDVSQKTTW
HRISVFRPGLRDVAYQYVKKGSRIYLEGKIDYGEYMDKNNVRRQATTIIADNIIFL

>d1qvca_ b.40.4.3 (A:) ssDNA-binding protein {Escherichia coli}

ASRGVNKVLVGNLGDPEVRYMPNGGAVANITLATESWRDKATGEMKEQTEWHRVV L
FGKLAEVASEYLRKGSQVYIEGQLRTRKWT DQSGQDRYTTEVVVNVGGTMQMLGGRQG
GGAPAGGNIGGGQPQGGWGQPQQPQGGN

>d1ewia_ b.40.4.3 (A:) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

MVGQLSEGAIAAIMQKGD TNIKPILQVINIRPIT TGNSPPRYRLLMSDGLNTLSSFMLATQL
NPLVEEEQLSSNCVCQIHRFIVNTLKDGR RVVILMELEV LKSAEAVGVKIGN

>d1fgua1 b.40.4.3 (A:181-298) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

MSKVVPISLTPYQSKWTICARVTNKSQIRTWSNSRGE GKLFSLELVDES GEIRATAFNEQV
DKFFPLIEVNKVYYFSKGT LKIANKQFTAVKNDYEMTFNNETSVMPCEDDHHLPTV

>d1fgua2 b.40.4.3 (A:299-426) Replication protein A 70 KDa subunit (RPA70) fragment {Human (Homo sapiens)}

QFDFTGIDDLNENKSKDSLVDIIGICKSYEDATKITVRSNNREVA KRNIYLMDSGKVV TATL
WGEDADKFDGSRQPVLAIKGARVSDFGGRSLSVLSSSTIIANPD IPEAYKLRGWFDAEGQA
LDGVS

>d1quqa_ b.40.4.3 (A:) Replication protein A 32 KDa subunit (RPA32) fragment {Human (Homo sapiens)}

HIVPCTISQLLSATLVDEVFRIGNVEISQVTIVGIIRHAEKAPT NIVYKIDDMTAAPMDVRQ
WVDTDTSSENTVPPET YVKVAGHLRSFQNK KSLVAFKIMPLEDMNEFTTHILEVINAH
MVLSK

>d1quqb_ b.40.4.3 (B:) Replication protein A 14 KDa (RPA14) subunit {Human (Homo sapiens)}

DMMDLPRSRINAGMLAQFIDKPVCFVGRLEKIHP TGMFILSDGEGKNGTIELMEPLDEEI
SGIVEVVGRTAKATILCTSYVQFKEDSHPFDLGLYNEAVKIIHDFPQFYPLG

>d1jb7a1 b.40.4.3 (A:36-204) Telomere end binding protein alpha subunit {Oxytricha nova}

YEYVELAKASLTSAQPQH FYAVVIDATFPYKTNQERYICSLKIVDPTLYLKQQKGAGDASD
YATLVLYAKRFEDLP IIHRAGDIIRVHRATLR LYNQ RQFNANVFYSSSWALFSTDKRSVTQ
EINNQDAVSDTTPFSFSSKHATIEKNEISILQNL RKWANQYFSSYS

>d1jb7a2 b.40.4.3 (A:205-328) Telomere end binding protein alpha subunit {Oxytricha nova}

VISSDMYTALNKAQAQKGDFDVVAKILQVHELDEYTNELKLKDASGQVFYTL SLKLKFP
HVRTGEVVRIRSATYDETSTQKKVLILSHYSNIITFIQSSKLAKELRAKI QDDHSVEVASLK
KNV

>d1jb7a3 b.40.4.3 (A:329-495) Telomere end binding protein alpha subunit {Oxytricha nova}

SLNAVVLTEVDKKHAALPSTSLQDLFHHADSDKELQAQDTFRTQFYVT KIEPSDVKEWVK
GYDRKTKKSSSLKGASGKGDNIFVQVQLVKDASTQLNNNTYRVLLY TQDGLGANFFNVK
ADNLHKNADARKKLED SAELLTKFNSYVD AVERRNGFYLIKDTKLIY

>d1jb7b_ b.40.4.3 (B:) Core domain of telomere end binding protein beta subunit {Oxytricha nova}

QQQSAFKQLYTELFNNEGDFSKVSSNLKKPLKCYVKESYPHFLVTDGYFFVAPYFTKEAV
 NEFHAKFPNVNIVDLTDKVIVINNWSLELRRVNSAEVFTSYANLEARLIVHSFKPNLQERL
 NPTRYPVNLFRDDEFKTTIQHFRHTALQAAINKTVKGDNLVDISKVADAAGKKKGKVDAGI
 VKASASKGDEFSDFSFKEGNTATLKIADIFVQKEG
 >d1jjcb3 b.40.4.4 (B:39-151) Domain B2 of PheRS-beta, PheT {Thermus thermophilus (Thermus aquaticus)}
 FPIPRGVVFARVLEAHPIPGTRLKRLVLDAGRTVEVVSGAENARKGIGVALALPGTELPGL
 GQKVGGERVIQGVRSFGMALSPRELGVGEYGGGLLEFPEDALPPGTPLSEAWP
 >d1fl0a_ b.40.4.4 (A:) EMAP II {Human (Homo sapiens)}
 IDVSRLDLRIGCIITARKHPDADSLYVEEVDVGEIAPRTVVSGLVNHVPLEQMQRNMVILL
 CNLKPAKMRGVLSQAMVMCASSPEKIEILAPPNGSVPGDRITFDAFPGEPPDKELNPKKKI
 WEQIQPDLHTNDECVATYKGVPPFEVKGKGVCRQAQTMSNSGIKL
 >d1gd7a_ b.40.4.4 (A:) CsaA {Thermus thermophilus}
 MTPLEAFQILDLRVGRVLRAEPHEKARKPSYKLWVDLGLPLGVKQSSAQITELYRPEDLVG
 RLVVCAVNLGAKRVAGFLSEVLVLGVLPDEAGRVVLLAPDREVPLGGKVF
 >d1h95a_ b.40.4.5 (A:) Y-box protein 1 cold shock domain (YB1-CSD) {Human (Homo sapiens)}
 MKKVIATKVLGTVKWFNVRNGYGFNRNDTKEDVFVHQTAIKNNPRKYLRVSGDGET
 VEFDVVEGEKGAEAAANVTGPG
 >d1sro_ b.40.4.5 (-) S1 RNA-binding domain of polyribonucleotide phosphorylase, PNPase {Escherichia coli}
 AEIEVGRVYTGKVTRIVDFGAFVAIGGGKEGLVHISQIADKRVEKVTDYLMGQEVVPKV
 LEVDROGRIRLSIKEA
 >d1hh2p1 b.40.4.5 (P:127-198) S1 domain of NusA {Thermotoga maritima}
 FEKYSELKGTVTTAEVIRVMGEWADIRIGKLETRLPPKKEWIPGEEIKAGDLVKVYIIDVVK
 TTKGPKILVSR
 >d1k0ra1 b.40.4.5 (A:108-183) S1 domain of NusA {Mycobacterium tuberculosis}
 STREGEIVAGVIQRDSRANARGLVVVRIGTETKASEGVIPAAEQVPGESYEHGNRLRCYVV
 GVTRGAREPLITLSR
 >d1go3e_ b.40.4.5 (E:) RNA polymerase II subunit RBP4 (RpoE) {Archaeon Methanococcus jannaschii}
 MYKILEIADVVKVPPEEFGKDLKETVKKILMEKYEGRLDKDVGFVLSIVDVKDIGEGKVV
 HGDGSAYHPVVFETLVYIPEMYELIEGEVVDVVEFGSFVRLGPLDGLIHVSQIMDDYVSY
 DPKREAIIGKETGKVLEIGDYVRARIVAISLKAERKRGSKIALTMRPYLGKLEWIEEKA
 KKQ
 >d1hr0w_ b.40.4.5 (W:) Translational initiation factor 1, IF1 {Escherichia coli}
 AKEKDTIRTEGVVTEALPNATFRVKLDGPEILAYISGKMRMHYIRILPGDRVVVEITPYDP
 TRGRIVYRK
 >d1jt8a_ b.40.4.5 (A:) Archaeal initiation factor-1a, aIF1a {Archaeon Methanococcus jannaschii}
 MAEQQQEQQIRVRIPRKEENEILGIIQMLGASRVVRCLDGKTRLGRIPGRLKNRIWVRE
 GDVVIVKPWEVQGDQKCDIIWRYTKTQVEWLKRKGYLDELL
 >d1d7qa_ b.40.4.5 (A:) Translation initiation factor-1a, eIF1a {Human (Homo sapiens)}
 PKNKGKGGKNRRRGKNENESEKRELVFKEDGQEYAQVIKMLGNRLEAMCFDGVKRLC
 HIRGKLRKKVWINTSDIILVGLRDYQDNKADVILKYNADEARSLKAYGELPEHAKINETD
 TFGPGDDDEIQFDDIGDDDEDIDDI

>d1a62_2 b.40.4.5 (48-125) Rho termination factor, RNA-binding domain {Escherichia coli}
DIFGDGVLEILQDGFGLRSADSSYLAGPDDIYVSPSQIRRFNLRTGDTISGKIRPPKEGERY
FALLKVNEVNFDPKE

>d1bkb_2 b.40.4.5 (75-139) C-terminal domain of eukaryotic initiation translation factor 5a
{Archaeon Pyrobaculum aerophilum}
IIEKFTAQILSVSGDVIQLMDMRDYKTIEVPMKYVEEEAKGRLAPGAEEVWQILDRIKII
RVKG

>d1jj2a2 b.40.4.5 (A:1-90) N-terminal domain of ribosomal protein L2 {Archaeon Haloarcula
marismortui}
GRRIQGQRRGRGTSTFRAPSHRYKADLEHRKVEDGDVIAGTVVDIEHDPARSAPVAAVEF
EDGDRRLILAPEGVGVGDELQVGVD AEIAP

>d1fjgl_ b.40.4.5 (L:) Ribosomal protein S12 {Thermus thermophilus}
PTINQLVRKGREKVRKSKVPALKGAPFRRGVCTVVRTVTPKKPNSALRKVAKVRLTSGY
EVTAYIPGEGHNLQEHSVVLIRGGRVKDLPGVRYHIVRGVYDAAGVKDRKKSRSKYGTK
KPKEAA

>d1fjgq_ b.40.4.5 (Q:) Ribosomal protein S17 {Thermus thermophilus}
PKKVLTVGVVSDKMQKTVTVLVERQFPHPYLGKVIKRSKKYLAHDPEEKYKLGDVVEIIE
SRPISKRRKRFRVLRVLESGRMDLVEKYLIRRQNYQSLSKRGGKA

>d1ckma1 b.40.4.6 (A:239-327) RNA guanylyltransferase (mRNA capping enzyme) {Chlorella
virus, PBCV-1}
THHTIDFIIMSEDGTIGIFDPNLRKNVPVGKLDGYYNKGSIVECGFADGTWKYIQGRSDKN
QANDRLTYEKTLLNIEENITIDELDLF

>d1a0i_1 b.40.4.6 (241-349) ATP-dependent DNA ligase {Bacteriophage T7}
PENEADGIIQGLVWGKGLANEGKVIGFEVLLESGRLVNATNISRALMDEFTETVKEATLS
QWGGFFSPYGIGDNDACTINPYDGWACQISYMEETPDGSLRHPSFVMFR

>d1fvial b.40.4.6 (A:190-293) ATP-dependent DNA ligase {Chlorella virus, PBCV-1}
FKDAEATIISMALFKNTNTKTKDNFGYSKRSTHKS GKVEEDVMGSIEVDYDGVVFSIGT
GFDADQRRDFWQNKESYIGKMKFKYFEMGSKDCPRFPVFIGIR

>d1dgsa2 b.40.4.6 (A:315-400) NAD⁺-dependent DNA ligase {Thermus filiformis}
AEEKETRLLDVVFQVGRTGRVTPVGVLPEVFI EGSEVSRVTLHNESYIEELDIRIGDWVLV
HKAGGVIPEVLRVLKERRTGKERPI

>d1gvp__ b.40.4.7 (-) Gene V protein {Filamentous bacteriophage (f1, M13)}
MIKVEIKPSQAQFTTRSGVSRQGKPYSLNEQLCYVDLGNEYPVLVKITLDEGQPAYAPGLY
TVHLSSFVKGQFGSLMIDRLRLVPAK

>d1pfsa_ b.40.4.7 (A:) Gene V protein {Pseudomonas bacteriophage pf3}
MNIQITFTDSVRQGTSAKGNPYTFQEGFLHLEDKPHPLQCQFFVESVIPAGSYQVPYRINV
NNGRPELAFDFKAMKRA

>d1gpc__ b.40.4.7 (-) Gene 32 protein (gp32) core {Bacteriophage T4}
GFSSSEDKGEWKLKLDNAGNGQAVIRFLPSKNDEQAPFAILVNHGFKKNGKWIETCSSTH
GDYDSCPVCQYISKNDLYNTDNKEYSLVKRKTSYWANILVVKDPAAPENEGKVFKYRFG
KKIWDKINAMIAVDVEMGETPVDVTCPWEGANFVLVKVKQVSGFSNYDESKFLNQSAIPNI
DDES FQKELFEQMVDLSEMTSKDKFKSFEELNTKFGQVM

>d1je5a_ b.40.4.7 (A:) gp2.5 {Bacteriophage T7}
MAKKIFTSALGTAEPYAYIAKPDY GNEERGFGNPRGVYKVDLTIPNKDPRCQRMVDEIVK

CHEEAYAAAVEEYEANPPAVARGKKPLKPYEGDMPFFDNGDGTTFKFKCYASFQDKKTK
ETKHINLVVDSKGGKMEDVPIIGGGSKLKVKYSLVPYKWNTAVGASVKLQLESVMLVE
LATFGGGEDDWADEVEEN

>d1e9ga_b.40.5.1 (A:) Inorganic pyrophosphatase {Baker's yeast (Saccharomyces cerevisiae)}
TYTTRQIGAKNTLEYKVYIEKDGPVSAFHDIPLYADKENNIFNMVVEIPRWTNAKLEITK
EETLNPIIQDTKKGKLRFVRNCFPHHGYIHNYGAFPQTWEDPNVSHPETKAVGDNDPIDVL
EIGETIAYTGQVKQVKALGIMALLDEGETDWKVIAIDINDPLAPKLNDIEDVEKYFPGLLR
ATNEWFRIYKIPDGKPENQFAFSGEAKNKKYALDIKETDHSWKQLIAGKSSDSKGIDLTN
VTLPDTPTYSKAASDAIPASLKADAPIDKSIDKWFFISG

>d1i40a_b.40.5.1 (A:) Inorganic pyrophosphatase {Escherichia coli}
SLLNVPAGKDLPEDIYVVIEIPANADPIKYEIDKESGALFVDRFMSTAMFYPCNYGYINHTL
SLDGPVDVLVPTPYPLQPGSVTRCRPVGVLKMTDEAGEDAKLVAVPHSKLSKEYDHIKD
VNDLPELLKAQIAHFFEHYKDLEKGKWKVEGWENAEAAKAEIVASFERAANK

>d1h9ma1_b.40.6.2 (A:1-73) Cytoplasmic molybdate-binding protein ModG {Azotobacter vinelandii}

MKISARNVFKGTVSALKEGAVNAEVDILLGGGDKLAAVVTLESARSLQLAAGKEVVAVV
KAPWVLLMTDSSGY

>d1h9ra1_b.40.6.2 (A:123-199) C-terminal domain of molybdate-
dependent transcriptional regulator ModE {Escherichia coli}
MQTSARNQWFGTITARDHDDVQQHVVDVLLADGKTRLKVAITAQSGARLGLDEGKEVLIL
LKAPWVGITQDEAVAQNA

>d1h9ra2_b.40.6.2 (A:200-261) C-terminal domain of molybdate-
dependent transcriptional regulator ModE {Escherichia coli}
DNQLPGIISHIERGAEQCEVLMALPDGQTLCAVTPVNEATSLQQGQNVNTAYFNADSVIIATL

>d1g2913_b.40.6.3 (1:241-301) Maltose transport protein MalK, C-terminal domain
{Archaeon Thermococcus litoralis}

GSPPMNFLDAIVTEDGFVDFGEFRLKLLPDQFEVLGELGYVGREVIFGIRPEDLYDAMFAQ

>d1g2914_b.40.6.3 (1:302-372) Maltose transport protein MalK, C-terminal domain
{Archaeon Thermococcus litoralis}

VRVPGENLVRVVEIVENLGSERIVRLRVGGVTFVGSFRSESRVREGVEVDVVFDMMKKIHI
FDKTTGKAIF

>d1b3qa2_b.40.7.1 (A:540-671) Histidine kinase CheA, C-terminal domain {Thermotoga maritima}
TLAIICALLVKVNNLVYAIPIANIDTILSISKEDIQRVQDRDVIVIRGEVIPVYRLWEVLQIEH
KEELEEMEAVIVRVGNRKYGIVVDDLQDDIVIKSLGKVFSEVKEFSGAAILGDGSIALII
NVSGIV

>d1k0sa_b.40.7.1 (A:) Chemotaxis protein CheW {Thermotoga maritima}

MKTLADALKEFEVLSFEIDEQALAFDVDNIEMVIEKSDITPVPKSRHFVEGVINLRGRIIPV
VNLAKILGISFDEQKMKSIIVARTKDVEVGFLVDRVLGVLRITENQLDLTNVSDKFGKKSK
GLVKT DGRLLIYLDIDKIIIEITVKEGV

>d1bla__b.42.1.1 (-) Basic FGF (FGF2) {Human (Homo sapiens)}

MAEGEITTLPALPEDGGSGAFPPGHFKDPKRLYCKNGGFFLRHPDGRVDGVREKSDPHIK
LQLQAEERGVSIVKGVSANRYLAMKEDGRLLASKSVTDECFFFERLESNNYNTYRSRKYT
SWYVALKRTGQYKLGSKTGPQKAILFLPMSAKS

>d1ihka_b.42.1.1 (A:) Fibroblast growth factor 9, FGF9 {Human (Homo sapiens)}

TDLDHLKGILRRRQLYCRTGFHLEIFPNGTIQGTRKDHSRFGILEFISIAVGLVSIRGVDSGLY
LGMNEKGELYGSEKLTQECVFREQFEENWYNTYSSNLYKHVDTGRRYYVALNKDGT
PRE
GTRTKRHQKFTHFLPRPVDPAKVPPELYKDILSQS

>d1i1b__ b.42.1.2 (-) Interleukin-1beta {Human (Homo sapiens)}

VRSLNCTLRDSQQKSLVMSGPYELKALHLQGQDMEQQVVFMSFVQGEESNDKIPVALG
LKEKNLYLSCVLKDDKPTLQLESVDPKNYPKKKMEKRFVFNKIEINNKLFEFSAQFPNWY
ISTSQAENMPVFLGGTKGGQDITDFTMQFVSS

>d1lr1_ b.42.1.2 (1:) Interleukin-1 receptor antagonist protein {Human (Homo sapiens)}

SKMQAFRIWDVNQKTFYLRNNQLVAGYLQGPVNLEEKIDVVPPIEPHALFLGIHGGKMC
LSCVKSGDETRLQLEAVNITDSENKQDKRFAFIRSDSGPTTSFESAACPGWFLCTAMEA
DQPVSLTNMPDEGVMVTKFYFQEDE

>d2ila__ b.42.1.2 (-) Interleukin-1alpha {Human (Homo sapiens)}

NVKYNFMRIIKYEFILNDALNQSIIRANAQYLTAALHNLDEAVKFDMGAYKSSKDDAKIT
VILRISKTLQYVTAQDEDQPVLLKEMPEIPKTITGSETNLLFFWETHGKKNYFTSVAHPNLF
ATKQDYWVCLAGGPPSITDFQILE

>d1abr1 b.42.2.1 (B:1-140) Plant cytotoxin B-chain (lectin) {Abrus precatorius}

IVEKSKICSSRYEPTVRIGGRDGMCDVDYDNGYHNGNRHIMWKCKDRLEENQLWTLKSD
KTIRSNKGCLTTYGYAPGSYVMIYDCTSAVAEATYWEIWDNGTIINPKSALVLSAESSMG
GTLTVQTNEYLMRQGWRTGN

>d1ce7b2 b.42.2.1 (B:134-255) Plant cytotoxin B-chain (lectin) {European mistletoe
(Viscum album)}

TAPREVTIYGFNDLCMESGGGSVTVETCSSGKADKWALYGDGSIRPEQNQAQCLTSGGDS
VAGVNIVSCSGAASGQRWVFTNEGAILNLKNGLAMDVANPGGGRIIYPATGKPNQMWLP
VF

>d1hwmb2 b.42.2.1 (B:136-266) Plant cytotoxin B-chain (lectin) {Sambucus ebulus,
ebulin}

DVQPIATLIVGYNEMCLQANGENNNVWMEDCDVTSVQQQWALFDDRTIRVNNSRGLCV
TSNGYVSKDLIVIRKCQGLATQRWFFNSDGSVVNLKSTRVMDVKESDVSLEQEVIIIPATGN
PNQQWRTQVPQI

>d1xyfa1 b.42.2.1 (A:313-436) Endo-1,4-beta-xylanase C-terminal domain {Streptomyces
olivaceoviridis}

GQIKGVGSGRCLDVPNASTTDGTQVQLYDCHSATNQQWQTYTDAGELRVYGDKCLDAAG
TGNGTKVQIYSCWGGDNQKWRLNSDGSIVGVQSGLCCLDAVGGGTANGTLIQLYSCSNGS
NQRWTRT

>d1j1xa1 b.42.3.1 (A:1-153) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}

AGLPVIMCLKSNNHQKYLRYQSDNIQQYGLLQFSADKILDPLAQFEVEPSKTYDGLVHIKS
RYTNKYLVWRSPNHYWITASANEPDENKSNWACTLTKPLYVEEGNMKKVRLHLHVQLGH
YTQNYTVGGSFVSYLFAESSQIDTGSKDVFHVID

>d1j1xa2 b.42.3.1 (A:154-299) Agglutinin {Love-lies-bleeding (Amaranthus caudatus)}

WKSIFQFPKGYVTFKGNNGKYLGVITINQLPCLQFGYDNLNDPKVAHQMFVTSNGTICIKS
NYMNKFWRLSTDDWILVDGNDPRETNEAAALFRSDVHDFNVISLLNMQKTWFIKRFTSG
KPGFINCMNAATQNVDATALEIHEL

>d1wba__ b.42.4.1 (-) Winged bean albumin 1 {Goa bean (Psophocarpus tetragonolobus)}

DDPVYDAEGNKLVRGKYTIVSFSDGAGIDVVATGNENPEDPLSIVKSTRNIMYATSISSED

KTPPQPRNILENMRLKINFATDPHKGDVWSVVDVFQPDGQQLKLAGRYPNQVKGAFTIQK
GSNTPRTYKLLFCPVGSPCKNIGISTDPEGKKRLVVSYSQSDPLVVKFHRH
>d1eyla_ b.42.4.1 (A:) chymotrypsin inhibitor WCI {Winged bean (Psophocarpus tetragonolobus)}

EFDDDLVDAEAGNLVENGGTYYLLPHIWAHGGGIETAKTGNEPCPLTVVRSPNEVSKGEPIR
ISSQFLSLFIPRGSVALGFANPPSCAASPWWTVVDSPQGPAVKLSQQKLPEKDILVFKFEK
VSHSNIHVYKLLYCQHDEEDVKCDQYIGIHRDRNGNRRLVVTEENPLELVLLKAKS
>d1avac_ b.42.4.1 (C:) Amylase/subtilisin inhibitor {Barley (Hordeum vulgare), seed}

ADPPPVHDTDGHEL RADANYVLSANRAHGGGLTMAPGHGRHCPLFVSQDPNGQHDGF
PVRITPYGVAPSDKIIRLSTDVRI SFRAYTTCLQSTEW HIDESELAAGRRHVITGPVKDPSPSG
RENAFRIEKYSGAEVHEYKLMSCGDWCQDLGVFRDLKGGAWFLGATEPYHVVVFKKAP
PA

>d1a8d_2 b.42.4.2 (248-452) Tetanus neurotoxin {Clostridium tetani}

ITFLRDFWGNPLRYDTEYYLIPVASSSKDVQLKNITDYM YLTNAPS YTN GKLN IYYRRLYN
GLKFIIKRYTPNNEIDSFVKSGDFIKLYVS YNNNEHIVGYPKDGNAFN NLDRI LRVGYNAP
GIPLYKKMEAVKLRLD KTYSVQLKLYDDKNASLGLVGTHNGQIGNDPNRDILIASNWYFN
HLKDKILGCDWYFVPTDEGWTND

>d3btaa2 b.42.4.2 (A:1079-1295) Botulinum neurotoxin {Clostridium botulinum, serotype A}

NEKEIKDLYDNQSN SGILKDFWGDY LQYDKPYMLNLYDPNKYVDVNNVGIRGYMYLK
GPRGSVM TTN IYLNSSLYRGTKFIIKKYASGNKDNIVRNNDRVYINVVVNKEYRLATNAS
QAGVEKILSALEIPDVGNLSQVVVMKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNI
AKLVASNWYNRQIERSSRTLGC SWEFIPVDDGWGERPL

>d1lepwa2 b.42.4.2 (A:1080-1290) Botulinum neurotoxin {Clostridium botulinum, serotype B}

SEY LKDFWGNPLMYNKEYYMFNAGNKNSYIKLKKDSPVGEILTRSKYNQNSKYINYRDL
YIG EKFIIRKSNSQSINDDIVRKEDYIYLDFFNLNQEW RVYTYKYFKKEEEKLFLAPISDS
DEFYNTIQIKEYDEQPTYSCQLLFKKDEESTDEIGLIGIHRFYESGIVFEEYKDYFCISKWYL
KEVKRKPYNLKLGCNWQFIPKDEGWTE

>d1dfca1 b.42.5.1 (A:1008-1140) Fascin {Human (Homo sapiens)}

EAVQIQFGLINCGNKYLTA EAFGFKVNASASSLKKKQIWTLEQPPDEAGSAAVCLRSHLGR
YLAADKDG NVTCEREVPGPDCRFLIVAHDDGRWSLQSEAHRRYFGGTEDRLSCFAQTVSP
AEKWSVHIAMHP

>d1dfca2 b.42.5.1 (A:1141-1259) Fascin {Human (Homo sapiens)}

QVNIYSVTRKRYAHL SARP ADEIAVDRDVPWGVDSLITLAFQDQRYSVQTADHRFLRHDG
RLVARPEPATGYTLEFRSGKVAFRDCEGRYLAPSGPSGTLKAGKATKVGKDELFALEQS

>d1dfca3 b.42.5.1 (A:1260-1382) Fascin {Human (Homo sapiens)}

CAQVVLQAANERNVSTRQGMDLSANQDEETDQETFQLEIDRDTKKCAFRTHTGKYWTL
TATGGVQSTASSKNASCYFDIEWRDRRITLRASNGKFVTSKKNQQLAASVETAGDSELFL
MKLIN

>d1dfca4 b.42.5.1 (A:1383-1493) Fascin {Human (Homo sapiens)}

RPIIVFRGEHGFICRKVTGTL DANRSSYDVFQLEFNDGAYNIKDSTGKYWTVGSDSAVTS
SGDTPVDFFFEFC DYNKVAIKVGGRYLKGDHAGVLKASAETVDPASLWEY

>d1i8da1 b.43.4.3 (A:1-93) Riboflavin synthase {Escherichia coli}

MFTGIVQGTAKLVSIDEKPNFRTHVVELPDHMLDGL ETGASVAHNGCCLTVTEINGNHVS
FDLMKETLRITNLGDLKVG DWVNVERAAKFSDE

>d1i8da2 b.43.4.3 (A:94-206) Riboflavin synthase {Escherichia coli}
 IGGHLMMSGHIMTTAEVAKILTSENNRQIWFKVQDSQLMKYILYKGFIDGISLTVGEVTPT
 RFCVHLIPETLERTTLGKKKLGARVNIIDPQTQAVVDTERVLAARENAM

>d1jb9a1 b.43.4.2 (A:6-162) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Maize (Zea mays), root isoform}
 SRSKVSVAPLHLESAKEPPLNTYKPKEPFTATIVSVESLVGPKAPGETCHIVIDHGGNVPYW
 EGQSYGVIPPGENPKKPGAPQNVRLYSIASTRYGDNFDGRTGSLCVRRAVYYDPETGKED
 PSKNGVCSNFLCNSKPGDKIQLTGPSGKIMLLPEE

>d1fdr_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Escherichia coli}
 ADWVTGKVTKVQNWTDALFSLTVHAPVLPFTAGQFTKLGLEIDGERVQRAYSYVNSPDN
 PDLEFYLVTPDGKLSPLAALKPGDEVQVVSEAAGFFVL

>d1a8p_1 b.43.4.2 (2-100) Ferredoxin reductase (flavodoxin reductase) N-terminal domain {Azotobacter vinelandii}
 SNLNVERVLSVHHWNTLFSFKTTRNPSLRFENGQFVMIGLEVDGRPLMRAYSIASPNYE
 EHLEFFSIKVQNGPLTSRLQHLKEGDELMVSRKPTGTLV

>d1qfja1 b.43.4.2 (A:1-97) NAD(P)H:flavin oxidoreductase {Escherichia coli}
 TTLSCKVTSVEAITDTVYRVRIVPDAAFSFRAGQYLMVVMDERDKRPFSMASTPDEKGF
 ELHIGASEINLYAKAVMDRILKDHQIVVDIPHGEAWL

>d1i7pa1 b.43.4.2 (A:29-153) cytochrome b5 reductase {Rat (Rattus norvegicus)}
 HHHMITLENPDIKYPLRLIDKEILSHDTRRFRFALPSPQHILGLPIGQHIYLSTRIDGNLVIRP
 YTPVSSDDDKGFVDLVVKVYFKETHPKFPAGGKMSQYLENMNIGDTIEFRGPNGLLVYQ
 GK

>d2pia_1 b.43.4.2 (1-103) Phthalate dioxygenase reductase {Pseudomonas cepacia, db01}
 TTPQEDGFLRLKIASKEKIARDIWSFELTDPQGAPLPPFEAGANLTVAVPNGSRRTYSLCND
 SQERNRYVIAVKRDSNGRGGISFIDDTSEGDAVEVSLPRN

>d1lep3b1 b.43.4.2 (B:2-102) Dihydroorotate dehydrogenase B, PyrK subunit {Lactococcus lactis, isozyme B}
 SQLQEMMTVVSQREVAYNIFEMVLKGTLDVEMDLPQGFLHLAVPNGAMLLRRPISISSWD
 KRAKTCTILYRIGDETTGTYKLSKLESGAKVDVMGPLNGF

>d1cqxa2 b.43.4.2 (A:151-261) Flavohemoglobin, central domain {Alcaligenes eutrophus}
 WKGWRTFVIREKRPESDVITSFILEPADGGPVVNFEPGQYTSVAIDVPALGLQQIRQYSLSD
 MPNGRTYRISVKREGGGPQPPGYVSNNLHDHVNVDQVKLAAPYGSFHI

>d1ja1a1 b.43.4.1 (A:240-518) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}
 SSIRQYELVVHEDMDVAKVYTGENMRLKSYENQKPPFDAKNPFLAAVTANRKLNQGTER
 HLMHLELDISDSKIRYESGDHVAVYPANDSALVNQIGEILGADLDVIMSLNNLDEESNKKH
 PFPCPTTYRTALTYLDITNPPRTNVLYELAQYASEPSEQEHLHKMASSSGEGKELYLSWV
 VEARRHILAILQDYPSLRPPIDHLCELLPRLQARYYAIASSSKVHPNSVHICAVAVEYEAKS
 GRVNGVATSWLRAKEPAGENGGRALVPMFVRKSQF

>d1ddga1 b.43.4.1 (A:226-446) Sulfite reductase flavoprotein {Escherichia coli}
 IHTSPYSKDAPLVASLSVNQKITGRNSEKDVRHIEIDLGDGLRYQPGDALGVWYQNDPAL
 VKELVELLWLKGDEPVTVEGKTLPLNEALQWHFELTVNTANIVENYATLTRSETLLPLVGD

KAKLQHYAATTPIVDMVRFSPAQLDAEALINLLRPLTPRLYSIASSQAEVENEHVTVGVV
 RYDVEGRARAGGASSFLADRVEEEGEVRFIEHNDNFR

>d1f20a1 b.43.4.1 (A:963-1232) Neuronal nitric-oxide synthase FAD/NADP+ domain
 {Rat (*Rattus norvegicus*)}

SWKRNFRLTYVAEAPDLTQGLSNVHKRVSAARLLSRQNLQSPKSSRSTIFVRLHTNGN
 QELQYQPGDHLGVFPGNHEDLVNALIERLEDAPPANHVVKVEMLEERNTALGVISNWKD
 ESRLPPCTIFQAFKYYLDITTPPTPLQLQQFASLATNEKEKQRLVLVSKGLQEYEEWKWGK
 NPTMVEVLEEFPISQMPATLLLTQLSLLQPRYYSISSSPDMYPDEVHLTVAIVSYHTRDGEG
 PVHHGVCSSWLNRIQADDVVPCFVRGAP

>d1exma1 b.43.3.1 (A:213-312) Elongation factor Tu (EF-Tu), domain 2 {*Thermus thermophilus*}

PVRDVKPFLMPVEDVFTITGRGT VATGRIERGKVKVGDEVEIVGLAPETRKT VVTGVEM
 HRKTLQEG IAGDNVGVLLRGVSREEVERGQVLAKPGSITP

>d1jnya1 b.43.3.1 (A:228-322) Elongation factor eEF-1alpha, domain 2 {*Archaeon Sulfolobus solfataricus*}

PVDKPLRIPIQDVYSISGVGTVPVGRVESGVLKVGDKIVFMPAGKVGEVRSIETHHTKMDK
 AEPGDNIGFNVRGVEKKDIKRGDVVGHPPNPPTV

>d1dar_1 b.43.3.1 (283-400) Elongation factor G (EF-G), domain II {*Thermus thermophilus*}

PLDIPPIKGTTPGEVVEIHPDPNGPLAALAFKIMADPYVGRLT FIRVYSGTLTSGSYVYNTT
 KGRKERVARLLRMHANHREEVEELKAGDLGAVVGLKETITGDTLVGEDAPRVILE

>d1g7sa1 b.43.3.1 (A:228-328) Initiation factor IF2/eIF5b, domains 2 and 4 {*Archaeon Methanobacterium thermoautotrophicum*}

EDSPARGTILEVKEETGLGMTIDAVIYDGILRKDDTIAMMTSKDVISTRIRSLKPRPLEEM
 RESRKKFQKVDEVVAAAGIKIVAPGIDDMAGSPLRVVT

>d1g7sa2 b.43.3.1 (A:460-587) Initiation factor IF2/eIF5b, domains 2 and 4 {*Archaeon Methanobacterium thermoautotrophicum*}

IIKPASIRLIPKLVFRQSKPAIGGVEVL TG VIRQGYPLMNDDGETVGTVESMQDKGENLKSA
 SRGQKVAMAIKDAVYGKTIHEGDTLYVDIPENHYHILKEQLSGDLTDEELDLMDKIAEIKR
 KKNPD

>d1d1na_ b.43.3.1 (A:) Initiation factor IF2/eIF5b, domains 2 and 4 {*Bacillus stearothermophilus*}

YEEKVIGQAEVRQTFKVS KVG TIAGCYVTDGKITRDSKVRLIRQGIVVYEGEIDSLKRYKD
 DVREVAQGYECGLTIKNFNDIKEGDVIEAYVMQEVARA

>d1d2ea2 b.44.1.1 (A:349-451) Elongation factor Tu (EF-Tu) {*Cow (Bos taurus)*, mitochondrial}

HQKVEAQVYILTKEEGRHKPFVSHFMPVMFSLTWDMACRIILPPGKELAMPGEDLKLTL
 ILRQPMILEKGQRFTLRDGNRTIGTGLVTDTPAMTEEDKNIKW

>d1f60a2 b.44.1.1 (A:335-441) Elongation factor eEF-1alpha, C-terminal domain
 {*Baker's yeast (Saccharomyces cerevisiae)*}

CASFNATVIVLNHPGQISAGYSPVLDCHTAHIACRFDELLEKNDRRSGKKLEDHPKFLKSG
 DAALVKFVPSKPMCVEAFSEYPPLGRFAVRDMRQTVAVGVIKSVDK

>d1flma_ b.45.1.1 (A:) FMN-binding protein {*Desulfovibrio vulgaris*, strain Miyazaki F}

MLPGTFFEVLKNEG VVAIATQGEDGPHLVNTWNSYLKVL DGNRIVVPVGGMMHKTEANVA
 RDERVLMTLGSRKVAGRNGPGTGFLIRGSAAFR TDGPEFEAIARFKWARAALVITVVS AEQ
 TL

>d1ci0a_ b.45.1.1 (A:) Pyridoxine 5'-phosphate oxidase (PNP oxidase) {*Baker's yeast (Saccharomyces cerevisiae)*}

FTLNEKQLTDDPIDLFTKWFNEAKEDPRETLPEAITFSSAELPSGRVSSRILLFKELDHARGFT
IYSNWGTSRKAHDIATNPNAIIVFFWKDLQRQVRVEGITEHVNRETSERYFKTRPRGSKIG
AWASRQSDVIKNREELDELTKNTERFKDAEDIPCPDYWGGLRIVPLEIEFWQGRPSRLHD
RFVYRRKTENDPWKVVR LAP

>d1eja_ b.45.1.2 (A:) FMN-binding protein MTH152 {Archaeon Methanobacterium
thermoautotrophicum}

GSQAAHMMMSDMFEDFPVESAHRI LTPRPTVMVTTVDEEGNINAAPFSFTMPV SIDPPV VAF
ASAPDHHTARNIESTHEFVINITPADIIERMWVTARDIPAGENELEAAGLAWTSSRRVKPPRI
VEAPGHLECELLRMFEVGDHNLITGSVVSASVRSGAVKEGLLDVESVKPVLHVGGNK FV
VGDHVRHVE

>d1i0ra_ b.45.1.2 (A:) Ferric reductase {Archaeon Archaeoglobus fulgidus}

MDVEAFYKISYGLYIVTSESNGRKGQIANTVFQLTSKPVQIAVCLNKENDTHNAV KESGA
FGVSVLELETPMEFIGRFGFRKSSEFEKFDGVEYKTGKTGVPLVTQHAVAVIEAKVVKECD
VGHTTLFVGEAVDAEVLKDAEVLTYADYHLMKKGKTPRT

>d1k28d1 b.106.1.1 (D:4-200) Baseplate structural protein gp27 {Bacteriophage T4}
LQRPGYPNLSVKLFDSYDAWSNNRFVELAATITTLTMRDSLYGRNEGMLQFYDSKNIHTK
MDGNEIIQISVANANDINN VKTRIYGCKHFSVSVDSKGDNI IAIELGTIHSIENLKFGRPFFP
DAGESIKEMLGVIYQDR TLLTPAINAINAYVPDIPWTSTFENYLSYVREVALAVGSDKFVFV
WQDIMGVNMMDY

>d1k28d2 b.106.1.1 (D:201-376) Baseplate structural protein gp27 {Bacteriophage T4}
DMMINQEPYPMIVGEPSLIGQFIQELKYPLAYDFVWLTKSNPHKRDP MKNATIYAH SFLDS
SIPMITTGKGENSIVVSRSGAYSEMTYRNGYEEAIRLQTMAQYDGYAKCSTIGNFNLT PGV
KIIFNDSKNQFKTEFYVDEVIHEL SNNSVTHLYMFTNATKLETIDPVKV KNEF

>d1arb_ b.47.1.1 (-) Achromobacter protease {Achromobacter lyticus, strain m497-1}
GVSGSCNIDVVCPEGDGRDII RAVGAYSKSGTLACTGSLVNNTANDRKMYFLTAHHC GM
GTASTAASIVVYWNYQNSTCRAPNTPASGANGDGSMSQTQSGSTVKATYATSDFTLLELN
NAANPAFNLFWAGWDRRDQNYPGAIAIHHPNVAEKRISNSTSPTS FVAWGGGAGTTHLNV
QWQPSGGVTEPGSSGSPISPEKRVLGQLHGGPSSCSATGTNRSDQYGRVFTSWTGGGAA
ASRLSDWLDPASTGAQFIDGLDS

>d1qq4a_ b.47.1.1 (A:) alpha-Lytic protease {Lysobacter enzymogenes, 495}
ANIVGGIEYSINNASLCSVGFSVTRGATKGFVTAGHCGTVNATARIGGAVVGTF AARVFPG
NDRAWVSLTSAQTLLPRVANGSSFVTVRGSTEAAVGA AVCHSGRTTGYQCGTITAKNVT A
NYAEGAVRGLTQSNACMGRGDSGGSWITSAGQAQGVMSGGNVQSNNGNCGIPASQRSSL
FERLQPILSQYGLSLVTG

>d2sfa_ b.47.1.1 (-) Serine proteinase {Streptomyces fradiae}
IAGGEAIYAAGGGRCSLGFNVRSSSGATYALTAGHCTEIASTWYTNSGQTSLLGTRAGTSF
PGNDYGLIRHSNASAADGRVYLYNGSYRDITGAGNAYVGQTVQRSGSTTGLHSGRVTGL
NATVNYGGGDIVSGLIQTNVCAEPGDSGGALFAGSTALGLTSGGSGNCRTGGTTFFQP VTE
ALSAYGV SIL

>d1qtfa_ b.47.1.1 (A:) Exfoliative toxin B {Staphylococcus aureus}
KEYSAEEIRKLKQKFVPPTDKELYTHITDNARSPYNSVGT V FVKGSTLATGV LIGKNTIVT
NYHVAREAAKNPSNIIFTPAQNRDAEKNEFPTPYGKFEAE EIKESPYGQGLDLAIKLPNE
KGESAGDLIQPANIPDHIDIAKGDKYSLLGYPNYSAYSLSYQSQIEMFNDSQYFGYTEVGN
SGSGIFNLKGELIGHSGKGGQHNLPIGVFFNRKISSLYSVDNTFGDTLGN DLKKRAKLDK

>d1gdna_ b.47.1.2 (A:) Trypsin(ogen) {Mold (*Fusarium oxysporum*)}

IVGGTSASAGDFPFIVSISRNGGPWCGGSLNANTVLTAAHCVSGYAQSGFQIRAGSLSRTS
GGITSSLSVVRVHPSYSGNNNDLAILKLSTSPSGGNIGYARLAASGSDPVAGSSATVAGWG
ATSEGGSSSTPVNLLKVTVPVSRATCRAQYGTSAITNQMFCAVSSGGKDSCQGDSGGPIV
DSSNTLIGAVSWGNGCARPNYSGVYASVGALRSFIDTYA

>d1eq9a_ b.47.1.2 (A:) (alpha,gamma)-chymotrypsin(ogen) {Red fire ant (*Solenopsis invicta*)}

IVGGKDAPVGKYPYQVSLRLSGSHRCGASILDNNNVLTAAHCVDGLSNLNLKLVHVG
TN YLSESGDVYDVEDAVVNKNYDDFLLRNDVALVHLTNPIKFNDLVQPIKLSTNDEDLES
NP CTLTGWGSTRLGNTPNALQEIELIVHPQKQCERDQWRVIDSHICTLTKRGEACHGDSG
GPLVANGAQIGIVSFGSPCALGEPDVYTRVSSFSVSWINANLKK

>d1azza_ b.47.1.2 (A:) Crab collagenase {Atlantic sand fiddler crab (*Uca pugilator*)}

IVGGVEAVPNSWPHQAALFIDDMYFCGGSLISPEWILTAAHCMGAGFVDVVLGAHNIRE
DEATQVTIQSTDFTVHENYNSFVISNDIAVIRLPVPVTLTAAIATVGLPSTDVGVGTVVTP
TG WGLPSDSALGISDVLQVDVPIMSNADCAVYGIVTDGNICIDSTGGKGTCTNGDSGGPLN
YNGLTYGITSFGAAAGCEAGYPDAFTRVTYFLDWIQTQTGITP

>d2hlca_ b.47.1.2 (A:) HL collagenase {Common cattle grub (*Hypoderma lineatum*)}

IINGYEAYTGLFPYQAGLDITLQDQRRVWCGGSLIDNKWILTAAHCVHDAVSVVVYL
GSA VQYEGEAVVNSEIRIISHSMFNPDTYLNDVALIKIPHVEYTDNIQPIRLPSGEELN
NKFENIW ATVSGWGQSNTDTVILQYTYNLVIDNDRCAQEYPPGIIVESTICGDTSDGK
SPCFGDSGGPFLVSDKNLLIGVVSFVSGAGCESGKPVGFSRVTSYMDWIIQNTGIKF

>g1jou.1 b.47.1.2 (A:,B:) Thrombin {Human (*Homo sapiens*)}

SEYQTFNPRTFGSGEADCGLRPLFEKKSLEDKTERELLESYIDGXIVEGSDAEIGMSPWQ
VMLFRKSPQELLCGASLISDRWVLTAAHCLLYPPWDKNFTENDLLVRIGKHSRTRYERNIE
KISMLEKIYIHPRYNWRENLDRIALMKLKKPVAFSDYIHPVCLPDRETAASLLQAGYKGR
VTGWGNLKETWTANVGKGQPSVLQVVNLPIVERPVCKDSTRIRITDNMFCAGYKPDEGK
RGDACEGDAGGPFVMMKSPFNRRWYQMGIVSWGEGCDRDGKYGFYTHVFRLLKKWIKV
IDQFGE

>d1pytc_ b.47.1.2 (C:) Procarboxypeptidase A-S6 subunit III (zymogen E) {Cow (*Bos taurus*)}

SRPSSRVVNGEDAVPYSSWSWQVSLQYEKDGAFHHTCGGSLIAPDWVVTAGHCISTSR
TYQ VVLGEYDRSVLQGSEQVIPINAGDLFVHPLWNSNCVACGNDIALVKLSRSAQLGDKV
QLA NLPPAGDILPNEAPCYISGWGRLYTGGLPKLQEALLPVVDYEHCSQYDWWGITV
KKT MVCAGGDTRSGCDGDSGGPLNCPAADGSWQVHGVTSFVSAFGCNTIKKPTVFTRV
SAFI DWINETIASN

>d1a7s_ b.47.1.2 (-) Heparin binding protein, HBP {Human (*Homo sapiens*)}

IVGGRKARPRQFPFLASIQNQGRHFCGGALIHARFVMTAASCFPGVSTVVLGAYDLRR
RE RQSRQTFSISSMSENGYDPQQNLNDLMLQLDREANLTSSVTILPLPLQNATVEAGTRCQV
AGWGSQRSGGRLSRFPRFVNVTVPEDQCRPNNVCTGVLTTRGGICNGDGGTPLVCEGL
AHGVASFSLGPCGRGPDDFTRVALFRDWIDGVLNNPGPGPA

>d1a0la_ b.47.1.2 (A:) beta-Tryptase {Human (*Homo sapiens*)}

IVGGQEAPRSKWPWQVSLRVHGPYWMHFCGGSLIHPQWVLTAAHCVGPDVKDLAALRV
QLREQHLYYQDQLLPVSRIIVHPQFYTAQIGADIALLEELPVKVSSHVHTVTLPPASETF
PMPGCWVTGWGDVDNDERLPPPFPLKQVKVPIMENHICDAKYHLGAYTGDDVRIVRDDM
LCAGNTRRDSCQGDSGGPLVCKVNGTWLQAGVVSWGEGCAQPNRPGIYTRVTYYLDWI
HHYVPPKK

>d1danh_ b.47.1.2 (H:) Coagulation factor VIIa {Human (Homo sapiens)}

IVGGKVC PKGEC PWQV LLLVNGAQLCGGTLINTIWVVSAAHCFDKIKNWRNLI AVLGEH
DLSEHDGDEQSRRVAQVIIPSTYVPGTTNHDIALRLHQPVVLT DHVPLCLPERTFSERTL
AFVRFSLVSGWGQLLDRGATALELMVLNVPRMTQDCLQQSRKVGDS PNITEYMFCAGY
SDGSKDSCKGDSGGPHATHYRG TWYLTGIVSWGQGCATVGHFGVYTRVSQYIEWLQKL
MRSEPRPGVLLRAPFP

>d1lea_ b.47.1.2 (A:) Factor B {Human (Homo sapiens)}

ADPDESQSLSLCGMVWEHRKGT DYHKQPWQAKISVIRPSKGHESCMGAVVSEYFVLTA
HCFTVDDKEHSIKVSVGG EKRDLEIEVVL FHPNYNINGKKEAGIPEFYDYDVALIKLKNKL
KYGQTIRPICLPCTEGTTRALRLPPTTTCQQQKEELLPAQDIKALFVSEEEKLTRKEVYIK
NGDKKGSCERDAQYAPGYDKVKDISEVVT PRFLCTGGVSPYADPNTCRGDSGGPLIVHKR
SRFIQVGVISWGVVDVCKNQKRQKQVPAHARDFHINLFQVLPWLKEKLQDEDLGFL

>d1bio_ b.47.1.2 (-) Factor D {Human (Homo sapiens)}

ILGGREAEAHARPYMASVQLNGAHL CGGV LVAEQWVLSAAHCLEDAADGKVQVLLGA
HSLSQPEPSKRLYDVLRAVPHPD SQPDTIDHDL LLLQLSEKATLGPAVRPLPWQRVDRDVA
PGTLCDVAGWGIVNHAGRRPDSLQH VLLPVLD RATCNRRTHHDGAITERLMCAESNRD
SCKGDSGGPLVCGGVLEGVVTSGSRVCGNRKKPGIYTRVASYAAWIDSVLA

>d1a5ia_ b.47.1.2 (A:) Single chain tissue plasminogen activator {Vampire bat (Desmodus rotundus)}

TCGLRKYKEPQLHSTGGLFTDITSH PWQAAIFAQNRSSGERFLCGGILISSCWVLTA AHCF
QESYLPDQLKVVLGR TYRVKPGEEEQTFKVKKYIVHKEFDDDTYNNDIAL LQLKSDSPQC
AQESDSVRAICLPEANLQLPDWTECELSGYGKHKSSSPFYSEQLKEGHVRLYPSSRCAPKF
LFNKTVTNMMLCAGDTRSGEIYPNVHDACQGD SGGPLVCMNDNHMTLLGIISWGVGCG
EKDVPGVYTKVTNYLGWIRDNMHL

>d1bqya_ b.47.1.2 (A:) Plasminogen activator from snake venom, TSV-PA {Chinese green tree viper (Trimeresurus stejnegeri)}

VFGGDECNINEHRSLVVLFN SNGFLCGGTLINQDWVVTAAHCDSNNFQLLFGVH SKKILN
EDEQTRDPKEKFFCPNRKKDDEV DKDIMLIKLDSSVSNSEHIAPLSLPSSPPSVG SVCRIMG
WGKTIPTKEIYPDVPHCANINILDH AVCRTAYSWRQVANTTLCAGILQGGRDTCHFD SGGP
LICNGIFQGIVSWG GHPCGQPGEPGVYTKVFDYLDWIKSIIAGNKDATCPP

>d1ao5a_ b.47.1.2 (A:) Kallikrein-13 {Mouse (Mus musculus)}

VVGGFNCEKNSQPWQVAVYYQKEHICGGVLLDRNWVLTAAHCYVDQYEVWL GKNKLF
QEEPSAQHRLVSKSFPHPGFNMSLLMLQTIPPGADFSDDLMLRLSKPADITDVVKPIALPT
KEPKPGSKCLASGWGSITPTRWQKPDDLQCVFITLLPNENCAKVYLQKVTDVMLCAGEM
GGGKDTCRDDSGGPLICD GILQGTTSYGPVPCGKPGVPAIYTNLIKFN SWIKDTMMKNA

>d1elva1 b.47.1.2 (A:410-668) Complement C1s protease, catalytic domain {Human (Homo sapiens)}

CGVPREPFE EKQRIIGGSDADIKNFPWQVFFDNPWAGGALINEYWVLTAAHVVEGNREPT
MYVGSTSVQTSRLAKSKMLTPEHVF IHPGWKLLAVPEGR TNFDNDIALVRLKDPVKMGPT
VSPICLPGTSSDYNLMDGDLGLISGWGRTEKRDRAVRLKAARLPVAPLRKCKEVKVEKPT
ADAEAYVFTPNMICAGGEKGMDSCKGDSGGAF AVQDPNDKTKFYAAGLVSWGPQCGTY
GLYTRVKNYVDWIMKTMQENS

>d1fi8a_ b.47.1.2 (A:) Granzyme B {Rat (Rattus norvegicus)}

IIGGHEAKPHSRPYMAYLQIMDEYSGSKKCGGFLIREDFVLTAAHCSGSKIQVTLGAHNIK

EQEKMQQIIPVVKIIPHPAYNSKTISNDIMLLKLKSKAKRSSAVKPLNLP RRNVKVKPGDVC
YVAGWGKLGPMGKYSDTLQEVELTVQEDQKCESYLKNYFDKANEICAGDPKIKRASFRG
DSGGPLVCKKVAAGIVSYGQNDGSTPRAFTKVSTFLSWIKKTMKK

>g1fiz.1 b.47.1.2 (L:,A:) Beta-acrosin {Pig (*Sus scrofa*)}

ATCDGPCGLRFRQXVVGGMSEAEPGAWPVMVSLQIFMYHNNRRYHTCGGILLNSHWVLT
AAHCFKNKKKVTDWRLIFGANEVVWGSNKPVKPPLQERFVEEIIHEKYVSGLEINDIALI
KITPPVPCGPFIFPGCLPQFKAGPPRAPQTCWVTGWGYLKEKGPRTSPTLQEARVALIDLE
LCNSTRWYNGRIRSTNVCAGYPRGKIDTCQGDSGGPLMCRDRAENTFVVVGITSWGVC
ARAKRPGVYTSTWPYLNWIASKIGSNALQMVQLGTPPR

>d1eaa_ b.47.1.2 (A:) Matriptase MTSP1 {Human (*Homo sapiens*)}

VVGGTDADEGEWPWQVSLHALGQGHCASLISPNWLVSAAHCYIDDRGFRYSDPTQWT
AFLGLHDQSQRSAPGVQERRLKRIISHPPFNDFTFDYDIALLELEKPAEYSSMVRPICLPDA
SHVFPAGKAIWVTGWGHTQYGGTGALILQKGEIRVINQTTCEMLPQQITPRMMC VGFLS
GGVDSCQGDSGGPLSSVEADGRIFQAGVVSWDGCAQRNKPVGVT RLPLFRDWIKENTG
V

>d1svpa_ b.47.1.3 (A:) Viral capsid protein {Sindbis virus}

ALKLEADRLFDVKNEDGDVIGHALAMEGKVMKPLHVKG TIDHPVLSKLKFTKSSAYDM
EFAQLPVNMRSEAFYTYTSEHPEGFYNNWHGAVQYSGGRFTIPRGVGGRGDAGRPIMDNS
GRVVAIVLGGADEGTRTALS VVTWNSKGKTIKTTPEGTEEWSA

>d1cula1 b.47.1.3 (A:705-720,A:3-186) NS3 protease {Human hepatitis C virus (HCV), different isolates}

GSVVIVGRIILSGSGSXITAYSQQTRGLLGCITSLTGRDKNQVEGEVQVVSTATQSFLATCV
NGVCWTVYHGAGSKTLAGPKGPITQMYTNVDQDLVGWQAPPGARSLTPCTCGSSDLYLV
TRHADVIPVRRRGDSRGSLLSPRPVSYLKSSGGPLLCPSGHAVGIFRAAVCTRGVAKAVD
FVPVESMETTMRSPVFTD

>d1bfa_ b.47.1.3 (A:) NS3 protease {Dengue virus serotype 2}

WDVPSPPPVGKAELEDGAYRIKQKGILGYSQIGAGVYKEGTFHTMWHVTRGAVLMHKG
KRIEPSWADVKKDLVSCGGGWKLEGEWKEGEEVQVLALEPGKNPRAVQTKPGLFKTNA
GTIGAVSLDFSPGTSGSPIIDKKGKVVG IYGNVVT RSGAYVSAIAQTEKSIEDNPEIEDD

>d1cqqa_ b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human rhinovirus type 2}

GPEEEFGMSLIKHNSCVITTENGKFTGLGVYDRFVVVPTHADPGKEIQVDGITT KVIDSYD
LYNKNGIKLEITVLKLD RNEKFRDIRRYIPN NEDDYPNCNLALLANQPEPTIINVGDVVS Y
GNILLSGNQ TARM LKYSYPTKSGYCGGVLYKIGQVLGIHVGGNGR DGFSAMLLRSYFT

>d1hava_ b.47.1.4 (A:) 3C cysteine protease (picornain 3C) {Human hepatitis A virus}

STLEIAGLVRKNLVQFGVGEKNGSVRWVMNALGVKDDWLLVPSHAYKFEKDYEMMEFY
FNRGGTYYSISAGNVVIQSLDVGFQDVVLMKVPTIPKFRDITQHFIKKGDVPRALNRLATL
VTTVNGTPMLISEGPLKMEEKATYVHKKNDGTTVDLTVDQAWRGKGEGLPGMCGGALV
SSNQSIQNAILGIHVAGGNSILVAKLVTQEMFQIDKKI

>d2hrva_ b.47.1.4 (A:) 2A cysteine proteinase {Human rhinovirus 2}

GPSDMYVHVGNLIYRN LHLFNSEMHESILVSYSSDLIIYRTNTV GDDYIPSCDCTQATYYC
KHKNRYFPITVTSHDWYEQESEYYPKH IYQYNLLIGEGPCEPGDCGGKLLCKHGVIGIVTA
GGDNHVAFIDLRHFHCA

>d1maba2 b.49.1.1 (A:10-94) N-terminal domain of alpha and beta subunits of F1 ATP synthase {Rat (*Rattus norvegicus*)}

SSILEERILGADTSVDLEETGRVLSIGDGIARVHGLRNVQAEEMVEFSSGLKGMSLNLEPD
NVGVVVVFGNDKLIKEGDIVKRTGAI

>d1skye2 b.49.1.1 (E:1-82) N-terminal domain of alpha and beta subunits of F1 ATP synthase
{Bacillus sp., strain ps3}

MTRGRVIQVMGPVVDVKFENGHLPAIYNALKIQHKARNENEVDIDLTLEVALHLGDDTVR
TIAMASTDGLIRGMEVIDTGAP

>d1bd0a1 b.49.2.1 (A:2-11,A:245-382) Alanine racemase {Bacillus stearothermophilus}
NDFHRDTWAEXFSLHSRLVHVKKLQPGKEKVSYGATYTAQTEEWIGTIPIGYADGWLRRLQ
HFHVLVDGQKAPIVGRICMDQCMIRLPGLPVGTKVTLIGRQGDEVISIDVARHLETINY
EVPCTISYRVPRIFRHKRIMEVRNAIG

>d1d7ka1 b.49.2.1 (A:7-43,A:284-427) Eukaryotic ornithine decarboxylase
{Human (Homo sapiens)}

EEFDCHFLDEGFTAKDILDQKINEVSSSDDKDAFYVAXFTLAVNIIAKKIVLKEQTGSDDDED
ESSEQTFMYVYVNDGVYGSFNCILYDHAHVKPLLQKRPKPDERYYSSSIWGPTCDGLDRIV
ERCDLPEMHVGDWMLFENMGAYTVAAASTFNGFQRPTIYYVMSGPAWQLMQQFQNPDP
PP

>d1hvc__ b.50.1.1 (-) Human immunodeficiency virus type 1 protease {Human immunodeficiency
virus type 1}

PQITLWQRPLVTIRIGGQLKEALLDTGADDTVLEEMNLPGKWPKMIGGIGGFIKVRQYD
QILIEICGHKAIGTVLVGPTPVNIIGRNLLTQIGCTLNFGGSSGPQITLWQRPLVTIKIGGQLK
EALLDTGADDTVLEEMSLPGRWKPKMIGGIGGFIKVRQYDQILIEICGHKAIGTVLVGPTP
VNIIGRNLLTQIGCTLNF

>d4fiv__ b.50.1.1 (-) Feline immunodeficiency virus (FIV) protease {Feline immunodeficiency
virus}

VGTTTTLEKRPEILIFVNGYPIKFLLDTGADITILNRRDFQVKNSIENGRQNMIGVGGGKRG
TNYINVHLEIRDENYKTQCIFGNVCVLEDNSLIQPLLGRDNMIKFNIRLVM

>d1baia_ b.50.1.1 (A:) Rous sarcoma virus protease {Rous sarcoma virus, strain pr-C}

LAMTMEHKDRPLVRVILTNTGSHPVKQRSVYITALLDTGADDTVISEEDWPTDWPVMEA
ANPQIHGIGGGIPVRKSRDMIELGVINRDGSLERPLLLFPLVAMTPVNILGRDCLQGLGLRL
TNL

>d1fmb__ b.50.1.1 (-) EIAV protease {Equine infectious anemia virus}

VTYNLEKRPTTIVLINDTPLNVLLDTGADTSVLTTAHYNRLKYRGRKYQGTGIGGVGGNV
ETFSTPVTIKKKGRHIKTRMLVADIPVTILGRDILQDLGAKLVL

>d2er7e_ b.50.1.2 (E:) Endothiapepsin {Chestnut blight fungus (Endothia parasitica)}

STGSATTPIDSLDDAYITPVQIGTPAQTNLDFDTGSSDLWVFSSETTASEVDGQTIYTPSK
STTAKLLSGATWSISYGDGSSSGDVYTDTVSVGGTLVTGQAVESAKKVSSSFTEGSTIDG
LLGLAFSTLNTVSPQQKTFFDNAKASLDSPVFTADLGYPHAPGTYNFGFIDTTAYTGSITYT
AVSTKQGFWEWTSTGYAVGSGTFKSTSIDGIADTGTTLLYLPATVVSAYWAQVSGAKSSSS
VGGYVFPCSATLPSFTFGVGSARIVPGDYIDFGPISTGSSSCFGGIQSSAGIGINIFGDVALK
AAFVVFNAGATTPTLGFASK

>d2apr__ b.50.1.2 (-) Acid protease {Bread mold (Rhizopus chinensis)}

AGVGTVPMTDYGNDIEYYGQVTIGTPGKKFNLDFTGSSDLWIASTLCTNCGSGQTKYDP
NQSSTYQADGRTWSISYGDGSSASGILAKDNVNLGGLLIKGTIELAKREAASFASGPNDG
LLGLGFDTTITVRGVKTPMDNLISQGLISRPFGVYLKAKNNGGGGEYIFGGYDSTKFKGS

LTTVPIDNSRGWWGITVDRATVGTSTVASSFDGILDTGTTLLILPNNIAASVARAYGASDNG
DGYTITISCDTSAFKPLVFSINGASFQVSPDSLVEEFQGGQCIAGFGYGNWGFALIGDTFLKN
NYVVFNQGVPEVQIAPVAE

>d1eaga_ b.50.1.2 (A:) Acid protease {Yeast (Candida albicans)}

QAVPVTLHNEQVTYAADITVGSNNQKLNIVVDTGSSDLWVPDVNVDCQVTYSDQTADFC
KQKGTYPDPSGSSASQDLNTPFKIGYGDGSSSQGTLYKDTVGFGGVSIKNQVLADVSTSI
DQGILGVGYKTNEAGGSYDNVPVTLKKQGVIKNAISLYLNSPDAATGQIIFGGVDNAK
YSGSLIALPVTSDRELRLISLGSVEVSGKTINTDNVDVLLDSGTTITYLQQDLADQIIKAFNG
KLTQDSNGNSFYEVDCNLSGDVVFNFNFSKNAKISVPASEFAASLQGDDGQPYDKCQLLFDV
NDANILGDNFLRSAYIVYDLDDNEISLAQVKYTSASSISALT

>g1htr.1 b.50.1.2 (P:,B:) Pepsin(ogen) {Human (Homo sapiens), progastricsin
(pepsinogen C)}

AVVKVPLKKFKSIRETMKEKGLLGEFLRTHKYDPAWKYRFGDLXSVTYEPMAYMDAAAYF
GEISIGTPPQNFLVLFDTGSSNLWVPSVYCQSQACTSHSRFNPSESSTYSTNGQTFSLQYGS
GSLTGFFGYDTLTVQSIQVPNQEFGLSENEPGTNFVYAQFDGIMGLAYPALSVDEATTAMQ
GMVQEGALTSPVFSVYLSNQQGSSGAVVFGVDSSLYTGQIYWAPVTQELYWQIGIEEF
LIGGQASGWCSEGCQAIVDTGTSLTVPQQYMSALLQATGAQEDEYGGFLVNCNSIQNLPL
SLTFIINGVEFPLPPSSYILSNNGYCTVGVEPTYLSSQNGQPLWILGDVFLRSYYSVYDLGN
NRVGFATAA

>d1mpp_ b.50.1.2 (-) Pepsin {Mucor pusillus}

GSDVTPGLYDFDLEEYAI PVSIGTPGQDFYLLFDTGSSDTWVPHKGCDNSEGCVGKRFFDP
SSSSTFKETDYNLNITYGTGGANGIYFRDSITVGGATVKQQTLAYVDNVSGPTAEQSPDSE
LFLDGIFGAAYPDNTAMEAEYGDYNTVHVNLKQGLISSPVFSVYMTNDGGGQVVFG
GVNNTLLGGDIQYTDVLKSRGGYFFWDAPVTGVKIDGSDAVSFDGAQAFTIDTGTNFFIA
PSSFAEKVVKAALPDATESQQGYTVPCSKYQDSKTTFSLVLQKSGSSSDTIDVSVPIKMLL
PVDKSGETCMFIVLPDGGNQFIVGNLFLRFFVNVYDFGKNRIGFAPLASGYEND

>d1hrna_ b.50.1.2 (A:) Chymosin (synonym: renin) {Human (Homo sapiens)}

GNTTSSVILTNYMDTQYYGEIGITPPQTFKVVFDTGSSNVWVPSSKCSRLYTACVYHKLF
DASDSSSYKHNGTELTRYSTGTVSGFLSQDIITVGGITVTQMFGEVTEMPALPFMLAEFD
GVVGMGFIEQAIGRVTPFDNIISQGVVKEDVFSFYNNRDSSENSQSLGGQIVLGGSDPQHYE
GNFHYNLIK TG VWQIQMKGVS VGSSTLLCEDGCLALVD TGASYISGSTSSIEKLMEALGA
KKRLFDYVVKCNEGPTLPDISFHLGGKEYTLTSADYVFQESYSSKKLCTLAIHAMDIPPPT
GPTWALGATFIRKFYTEFDRRNNRIGFALAR

>d1fkna_ b.50.1.2 (A:) beta-secretase (memapsin) {Human (Homo sapiens)}

RRGSFVEMVDNLRGKSGQGYVEMTVGSPPQTLNVLVDTGSSNFAVGAAPHPFLHRYQ
RQLSSTYRDLRKGVYVPYTQGWEGELGTDLV SIPHPNVTVRANIAAITESDKFFINGSN
WEGILGLAYAEIARPDDSLEPFDFS LKQTHV PNLFS LQLCGAGFPLNQSEVLASVGGSMII
GGIDHS LYTGSLWYTPIRREWY YEVIIVRVEINGQDLKMDCKEYNYDKSIVDSGTTNLRPL
KKVFEEAAVKSIIKAASSTEKFPDGFWLGEQLVCWQAGTTPWNIFPVISLYLMGEVTNQSFRI
TILPQQYLRPVEDVATSQDDCYKFAISQSSTGTVMGAVIMEGFYVVFDRARKRIGFAVSAC
HVHDEFRTAAVEGPFVTLDMEDCGYN

>d1pfza_ b.50.1.2 (A:) Plasmepsin ii (a hemoglobin-degrading enzyme) {Plasmodium falciparum}

HLTIGFKVENAHDRILKTIKTHKLKNYIKESVNFLNSGLTKTNYLGSSNDNIELVDFQNMIF
YGDAEVGDNQQPFTFILTGSANLWVPSVKCTTAGCLTKHLYDSSKSRTYEKDGTKVEM

NYVSGTVSGFFSKDLVTVGNLSLPYKFIEVIDTNGFEPTYTASTFDGILGLGWKDLSIGSVDP
PIVVELKNQNKIENALFTFYLPVHDKHTGFLTIGGIEERFYEGPLTYEKLNDLYWQITLDA
HVG NIMLEKANCIVDSGTSAITVPTDFLNKMLQNLDVIKVPFLPFYVTLCNN SKLPTEFT
SENGKYTLEPEYYLQHIEDVGPGLCMLNIIGLDFVPTFILGDPFMRKYFTVFDYDNH SVG
IALAKKNL

>d1ile_2 b.51.1.1 (198-386) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}
KEIQDPSVYVRFPLKEPKKLGLEKASLLIWTTTPWTLPGNVAAAVHPEYTYAAFQVGDEA
LILEEGLGRKLLGEGTQVLKTFPGKALEGLPYTPPYPALEKGYFVVLADYVSQEDGTGI
VHQAPAFGAEDLETARVYGLPLLKTVDDEGKLLVEPFKGLYFREANRAILRDLRGRGLLF
KEESYLHSY

>d1ffya2 b.51.1.1 (A:201-394) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}
HDKRSASIYVAFNVKDDKGVVDADAKFIIWTTTPWTIPSNVAITVHPELKYGQYNVNGEK
YIIAEALSDAVAEALDWDKASIKLEKEYTGKELEWVVAQHPFLDRESLVINGDHVTTDAG
TGCVHTAPGHGEDDYIVGQQYELPVISPIDDKGVFTEEGGQFEGMFYDKANKAVTDLLTE
KGALLKLD FITHSY

>d1gaxa2 b.51.1.1 (A:190-342) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}
TEPTPGKLYTLRYEVEGGGFIEIATVRPETVFADQAI AVHPEDERYRHLLGKRARIPLTEVWI
PILADPAVEKDFGTGALKVTPAHDPLDYEIGERHGLKPVSVINLEGRMEGERVPEALRGLD
RFEARRKAVELFREAGHLVKEEDYTIALA

>d1gmua1 b.107.1.1 (A:1-70) Urease metallochaperone UreE, N-terminal domain {Klebsiella aerogenes}
MLYLTQRLEIPAAATASVTLPIDVRVKSRVKVTLNDGRDAGLLLPRGLLLRGGDVLSNEEG
TEFVQVIAA

>d1eara1 b.107.1.1 (A:1-74) Urease metallochaperone UreE, N-terminal domain {Bacillus pasteurii}
MVITKIVGHIDDL SHQIKKVDWLEVEWEDLNKRILRKETENGTDIAIKLENSGTLRYGDVL
YESDDTLIAIRTK

>d1aa6_1 b.52.2.2 (565-715) Formate dehydrogenase H {Escherichia coli}
PIDKLTDEYPMVLSTVREVGHYSCRSMTGNCAALAA LADEPGYAQINTEDAKRLGIEDEA
LVWVHSRKGGKIITRAQVSDRPNGAIYMTYQWWIGACNELVTENLSPITKTPEYKYCAVR
VEPIADQRAAEQYVIDEYNKLKTRLREAAALA

>d1tmo_1 b.52.2.2 (632-798) Trimethylamine N-oxide reductase {Shewanella massilia}
ERSHGGPGSDKHPIWLQSCHPDKRLHSQMCE SREYRETYAVNGREPVIISP VDAKARGIK
DGDIVRVFNDRGQLLAGAVVSDNFPKGIVRIHEGAWYGPVGKDGSTEGGA EVGALCSYG
DPNTLTLDIGTSKLAQACSAYTCLVEFEKYQGKVPKVSSFDGPIEVEI

>d1g8ka1 b.52.2.2 (A:683-825) Arsenite oxidase large subunit {Alcaligenes faecalis}
LPATVQQQKDKYRFWLNNGRNNEVWQTAYHDQYNSLMQERYPMAYIEMNPDDCKQLD
VTGGDIVEVYNDFGSTFAMVYPVAEIKRGQTFMLFGYVNGIQGDVTTDWTDRDIIPYYKG
TWGDIRKVGSMSEFKRTVSFKSRRFG

>d2napa1 b.52.2.2 (A:601-723) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}
AAEEPDAEYPLYLTSMRVIDHWHTATMTGKVP ELQKANPIAFVEINEEDAARTGIKHGDS
VIVETRRDAMEL PARVSDVCRPGLI AVPPFDPKKLVNKLFLDATDPVSREPEYKICAA RVR
KA

>d1qcsa1 b.52.2.3 (A:0-85) N-terminal domain of NSF-N, NSF-Nn {Hamster (Cricetulus griseus)}

NMAGRSMQAARCPTDELSLNCVAVSEKDYQSGQHVIVRTSPNHKYIFTLRTHPSVVPGS
 VAFSLPQRKWAGLSIGQEIEVALYSF

>d1cr5a1 b.52.2.3 (A:26-107) N-terminal domain of NSF-N, NSF-Nn {Baker's yeast
 (*Saccharomyces cerevisiae*), sec18p}
 TRHLKVSNCNNNSYALANVAAVSPNDFPNNIYIIIDNLFVFTTRHSNDIPPGTIGFNGNQRT
 WGGWSLNQDVQAKAFDLFKY

>d1cz4a1 b.52.2.3 (A:1-91) N-terminal domain of VAT-N, VAT-Nn {Archaeon
Thermoplasma acidophilum}
 MESNNGIILRVAEANSTDPGMSRVRLDESSRRLD AEIGDVVEIEKVRKTVGRVYRARPED
 ENKGIVRIDSVMRNNCGASIGDKVKVRKVR

>d1e32a1 b.52.2.3 (A:21-106) Membrane fusion atpase p97 N-terminal domain , P97-Nn {Mouse
 (*Mus musculus*)}
 NRPNRLIVDEAINEDNSVVSLSQPKMDELQLFRGDTVLLKGKKRREAVCIVLSDDTCSDE
 KIRMNRVVRNNLRVRLGDVISIQPCP

>d1dfup_ b.53.1.1 (P:) Ribosomal protein L25 {*Escherichia coli*}
 MFTINAEVRKEQGKGASRRRLRAANKFPPIYGGKEAPLAIELDHDKVMNMQAKAEFYSE
 VLTIVVDGKEIKVKAQDVQRHPYKPKLQHIDFVRA

>d1feua_ b.53.1.1 (A:) Ribosomal protein TL5 (general stress protein CTC) {*Thermus
 thermophilus*}
 MEYRLKAYYREGEKPSALRRAGKLPGLMYNRHLNRKVYVDLVEFDKVFRQASIIHHVIVL
 ELPDGQSLPTLVRQVNLDRRRRPEHVDFFVLSDEPVEMYVPLRFVGTAGVRAGGVQLQE
 IHRDILVKVSPRNIPEFIEVDVSGLEIGDSLHASDLKLPPGVELAVSPEETIAAVPPEDVEKL
 AE

>d1mai_ b.55.1.1 (-) Phospholipase C delta-1 {Rat (*Rattus norvegicus*)}
 GLQDDPDLQALLKGSQLLKVKSSSWRRERFYKLQEDCKTIWQESRKVMRSPESQLFSIED
 IQEVRMGHRTEGLEKFARDIPEDRCFSIVFKDQRNTLDLIAPSPADAQHWVQGLRKIIH

>d1dro_ b.55.1.1 (-) beta-spectrin {Fruit fly (*Drosophila melanogaster*)}
 GSGTGAGEGHEGYVTRKHEWDSTTKKASNRSWDKVYMAAKAGRISFYKDQKGYSNP
 ELTFRGEPSYDLQNA AIEIASDYTKKKHVLRVKLANGALFLLQAHDDTEMSQWVTS LKA
 QSDSTA

>d1dyna_ b.55.1.1 (A:) Dynamin {Human (*Homo sapiens*)}
 ILVIRKGWLTINNIGIMKGSKEYWFLTAENLSWYKDDEEKEKKYMLSVDNLKLRDVE
 KGMSSKHIFALFNTEQRNVYKDYRQLELACETQEEVDSWKASFLRAGVYPERV

>d1btka_ b.55.1.1 (A:) Bruton's tyrosine kinase {Human (*Homo sapiens*)}
 AAVILESIFLKRSQQKKKTSPNFKKCLFLLTVHKLSYYEYDFERGRRGSKKGSIDVEKITC
 VETVVPEKNPPPERQIPRRGEESSEMEQISIIERFPYPFQVVYDEGPLYVFSPTEELRKRWIH
 QLKNVIRYNSDLVQKYHPCFWIDGQYLCCSQ TAKNAMGCQILEN

>d1pls_ b.55.1.1 (-) Pleckstrin, N-terminal domain {Human (*Homo sapiens*)}
 MEPKRIREGYLVKKGSVFNTWKPMWVVLLEDGIEFYKKKSDNSPKGMIPLKGSTLTSPCQ
 DFGKRMFVFKITTTKQQDHFFQAAFL EERDAWVRDINKAIKCIEGLEHHHHHHH

>d1dbha2 b.55.1.1 (A:418-550) Son of sevenless-1 (sos-1) {Human (*Homo sapiens*)}
 AIKKMNEIQKNIDGWEGKDIGQCCNEFIMEGTLTRVGAKHERHIFLFDGLMICCKSNHGQ
 PRLPGASNAEYRLKEKFFMRKVQINDKDDTNEYKHAF EILKDENS VIFS AKSAEEKNNW
 MAALISLQYRSTL

>d1foea2 b.55.1.1 (A:1240-1401) GEF of TIAM1 (T-Lymphoma invasion and metastasis inducing protein 1) {Mouse (Mus musculus)}

EFGAVFDQLIAEQTGEKKEVADLSMGDLLLLHTSVIWLNPASLGKWKKEPELAAAFVFKTA
VVLVYKDGSKQKKKLVGSHRLSIYEEWDPFRFRHMIPTEALQVRALPSADAEANAVCEIV
HVKSESEGRPERVFHLCCSSPESRKDFLKS SVHSILRDKHRRQ

>d1bak__ b.55.1.1 (-) G-protein coupled receptor kinase 2 (beta-adrenergic receptor kinase 1) {Human (Homo sapiens)}

GSHMGKDCIMHGYMSKMGNPFLTQWQRRYFYLFNRLWRGEGEAPQSLLTMEEIQSVE
ETQIKERKCLLLKIRGGKQFILQCDSDPELVQWKELRDYREAQQLVQRPVKMKNKPRS

>d1faoa_ b.55.1.1 (A:) Dual adaptor of phosphotyrosine and 3-phosphoinositides DAPP1/PHISH {Human (Homo sapiens)}

PSLGTKEGYLTKQGGLVKTWKTRWFTLHRNELKYFKDQMSPEPIRILDLTECSAVQFDYS
QERVNCFCLVFPRTFYLC AKTGVEADEWIKILRWKLSQI

>d1fgya_ b.55.1.1 (A:) Grp1 {Mouse (Mus musculus)}

TFFNPREGWLLKLGGRVKTWKRRWFILTDNCLYYFEYTTDKEPRGIIPLENLSIREVLDP
RKPNCFELYNP SHKGQVIKACKTEADGRVVEGNHVYRISAPSPEEKKEEWMKSIKASISRD
PFYDM

>d1fhoa_ b.55.1.1 (A:) UNC-89 {Nematode (Caenorhabditis elegans)}

MGDTGKLGRIRHDAFQVWEGDEPPKLRVYVFLFRNKIMFTEQDASTSPPSYTHYSSIRLDK
YNIRQHTTDEDITIVLQPQEPGLPSFRIKPKDFETSEYVRKAWLRDIAEEQEKYAAERD

>d1aqca_ b.55.1.2 (A:) X11 {Human (Homo sapiens)}

MEDLIDGIIFAANYLGSTQLLSDKTPSKNVRMMQAQEAVSRIKMAQKLAKSRKKAPEGES
QPMTEVDLFILTQRIKVLNADTQETMMDHPLRTISYIADIGNIVVLMARRRIPRSNSQENVE
ASHPSQDGKRQYKMICHVFESEDAQLIAQSIGQAFSVAYQEFLR

>d1qqga1 b.55.1.2 (A:12-114) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

DVRKVGYL RKP KSMHKRFFVLRAASEAGGP ARLEY YENEKKWRHKSSAPKRSIPLESCF
NINKRADSKNKH LVALYTRDEHFAIAADSEAEQDSWYQALLQLH

>d1qqga2 b.55.1.2 (A:159-262) Insulin receptor substrate 1, IRS-1 {Human (Homo sapiens)}

AFKEVWQVILKPKGLGQTKNLIGIYRLCLTSKTISFVKLNSEAAVVLQLMNIRRCGHSN
FFFIEVGRSAVTGPGEFWMQVDDSVVAQNMHETILEAMRAMSD

>d1shca_ b.55.1.2 (A:) Shc adaptor protein {Human (Homo sapiens)}

GSHMGQLGGEEWTRHGSFVNKPTRGWLHPNDKVMGPGVSYLVRYMGCVEVLQSMRAL
DFNTRTQVTREAI SLVCEAVPGAKGATRRRKPCSRPLSSILGRSNLKFAGMPITLTVSTSSLN
LMAADCKQIIANHHMQSISFASGGDPDTAEYVAYVAKDPVNQRACHILECPEGLAQDVIST
IGQAFELRFKQYLR

>d1ddma_ b.55.1.2 (A:) Numb {Fruit fly (Drosophila melanogaster)}

HQWQADEEAVRSATCSFSVKYLGCEVEVFESRGMQVCEEALKVLRQSRRRPV RGLLHVSG
DGLRVVDDET KGLIVDQTIEKVSFCAPDRNHERGFSYICRDGTTRRWMCHGFLACKDSGE
RLSHAVGCAFAVCLER

>d1legxa_ b.55.1.4 (A:) Vasodilator-stimulated phosphoprotein (VASP) {Human (Homo sapiens)}

MSETVICSSRATVMLYDDGNKRWLPA GTGPQAFSRVQIYHNPTANSFRVVG RKM QPDQQ
VVINCAIVRGVKYNQATPNFHQWRDARQVWGLNFGSKEDAAQFAAGMASALEALEG

>d1ddwa_ b.55.1.4 (A:) Homer {Rat (Rattus norvegicus)}

MGEQPIFSTRAHV FQIDPNTKKNWVPTSKHAVTVSYFYDSTRNVYRIISLDGSKAIINSTITP

NMTFTKTSQKFGQWADSRANTVYGLGFSSEHHLKFAEKFQEFKEAAR
>d1e5wa2 b.55.1.5 (A:199-346) Moesin {Human (Homo sapiens)}
EMYGVNYFSIKNKKGSELWLGVDALGLNIYEQNDRLTPKIGFPWSEIRNISFNDKKFVIKPI
DKKAPDFVIFYAPRLRINKRILALCMGNHELYMRRRKPDITIEVQQMKAQAREEKHKQKME
RAMLENEKKKREMAEKEKEKIEREKEE
>d1gg3a2 b.55.1.5 (A:188-279) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
GVDLHKAKDLEGVDIILGVCSSGLLVYKDKLRINRFPWPKVLKISYKRSSFFIKIRPGEQEQ
YESTIGFKLPSYRAAKKLWKCVEHHTFFR
>d1ytfcl b.56.1.1 (C:) Transcription factor IIA (TFIIA), N-terminal domain {Baker's yeast
(Saccharomyces cerevisiae)}
ENLMLCLYDKVTRTKARWKCSLKDGVVTINRNDYTFQKAQVEAEWV
>d1ytfcl2 b.56.1.1 (D:55-119) Transcription factor IIA (TFIIA), N-terminal domain
{Baker's yeast (Saccharomyces cerevisiae)}
NTQSKLTVKGNLDYGFCDVWTFIVKNCQVTVEDSHRDASQNGSGDSQSVISVDKLRI
VACNSK
>d1iega_ b.57.1.1 (A:) Human cytomegalovirus protease {Human cytomegalovirus}
QAVAPVYVGGFLARYDQSPDEAELLPRDVVEHWLHAQGGQPSLSVALPLNINHDDTA
VVGHVAAAMQSVRDGLFCLGCVTSRPFLEIVRRASEKSELVSRGPVSPLQPKVVEFLSGSY
AGLSLASRRCDDEQATSLSGSETTPFKAVALCSVGRRRGTLAVYGRDPEWVTQRFPDLT
AADRDGLRAQWQRCGSTAVDASGDPFRSDSYGLLGNSVDALYIRERLPKLRYDKQLVGV
TERESYVKA
>d1at3a_ b.57.1.1 (A:) HSV-2 protease {Herpes simplex virus type 2}
RAVPIYVAGFLALYDSGDPGELALDPDTVRAALPPENPLPINVDHRARCEVGRVLAVVNDP
RGPFFVGLIACVQLERVLETAASAAIFERRGPALSREERLLYLITNYLPSVSLSTKRRGDEVP
PDRTLFAHVALCAIGRRLGTIVTYDTSLDAAIAPFRHLDPATREGVRREAAEAELALAGRT
WAPGVEALTHTLSTAVNNMMLRDRWSLVAERRRQAGIAGHTYLQA
>d1fl1a_ b.57.1.1 (A:) KSHV protease {Kaposi's sarcoma-associated herpes virus}
AQGLYVGGFVDVVSCKLEQELYLDPDQVTDYLPVTEPLPITIEHLPETEVGWTGLGLFQVS
HGIFCTGAITSPAFLELASRLADTSHVARAPVKNLPKEPLLEILHTWLPGLSLSSIHPRELSQ
TPSGPVFQHVSLCALGRRRGTVAVYGHDAEWVVSFRFSSVSKSERAHILQHVSSCRLEDLS
TPNFVSPLETLMAKAIDAGFIRDRLDLLKTDRGVASILSPVYLKA
>d1a49a1 b.58.1.1 (A:116-217) Pyruvate kinase (PK) {Rabbit (Oryctolagus cuniculus)}
PEIRTLGIKSGTAEVELKKGATLKITLDNAYMEKCDENILWLDYKNICKVVDVGSKVYV
DDGLISLQVKQKGPDFLVTEVENGGFLGSKKGVNLPGAAYDL
>d1e0ta1 b.58.1.1 (A:70-167) Pyruvate kinase (PK) {Escherichia coli}
PEIRTMKLEGGNDVSLKAGQTFFTTDKSVIGNSEMVAVTYEGFTTDLSVGNTVLVDDGLI
GMEVTAIEGNKVICKVLNNGDLGENKGVNLPGVSIAL
>d1i2da1 b.58.1.2 (A:2-170) ATP sulfurylase N-terminal domain {Fungus (Penicillium
chrysogenum)}
ANAPHGGVLKDLLARDAPRQAELAAEAESLPAVTLTERQLCDLELIMNGGFSPLEGFMNQ
ADYDRVCDENRLADGNVFSMPITLDASQEVIDEKKLQAGSRITLRDFRDDRNLAILTIDDI
YRPDKTKEAKLVFGGDPEHPAIVYLNNTVKEFYIGGKIEAVNKLNHYD
>d1jhda1 b.58.1.2 (A:1-173) ATP sulfurylase N-terminal domain {unnamed symbiont
of Riftia pachyptila}

MIKPVGSDELKPLFVYDPEEHHKLSHEAESLPSVVISSQAAGNAVMMGAGYFSPLQGFMN
VADAMGAAEKMTLSDGSSFPVVLCLLENTDAIGDAKRIALRDPNVEGNPVLAVMDIEAI
EEVSDEQMAVMTDKVYRTTDMDHIGVKTFNSQGRVAVSGPIQVLNFSYFQADF

>d1hbq_ b.60.1.1 (-) Retinol binding protein {Cow (Bos taurus)}

ERDCRVSSFRVKENFDKARFAGTWYAMAKKDPEGLFLQDNIVAEFSVDENGQMSATAKG
RVRLNNWDVCADMVGTFDTEDPAKFKMKYWGWASFLQKGNDHWHIITDYETFAVQ
YSCRLNLDGTCADSYSFVFARDPSGFSPEVQKIVRQRQEELCLARQYRLIPHNGYCNGK

>d1hn2a_ b.60.1.1 (A:) Odorant-binding protein {Cow (Bos taurus)}

AQEEAEQNLSELSGPWRTVYIGSTNPEKIQENGPFRTYFRELVDDEKGTVDYFYSVKRD
GKWKNVHVKATKQDDGTYVADYEGQNVFKIVSLSRTHLVAHNINVDKHGQTTELTFLV
KLNVEDEDLEKFWKLTEDKGIDKKNVNFLENENHPHPE

>d1bj7_ b.60.1.1 (-) Lipocalin allergen {Cow (Bos taurus), bos d 2}

IDPSKIPGEWRIIYAAADNKDKIVEGGPLRNYRRIECINDCESLSITFYLDQGTCLLLTEV
AKRQEGYVYVLEFYGTNTLEVIHVSENMLVTYVENYDGERITKMTEGLAKGTSFTPEELE
KYQQLNSERGVPNENIENLIKTDNCPP

>d1ew3a_ b.60.1.1 (A:) Lipocalin allergen {Horse (Equus caballus), equ c 1}

VAIRNFDISKISGEWYSIFLASDVKEKIEENGSMRVFVDVIRALDNSSLYAEYQTKVNGECT
EFPMVFDKTEEDGVYSLNYDGYNVFRISEFENDEHIILYLVNFDKDRPFQLFEFYAREPDVS
PEIKEEFVKIVQKRGIVKENIIDLTIDRCFQLRG

>d1e5pa_ b.60.1.1 (A:) Aphrodisin, a sex pheromone {Golden hamster (Mesocricetus auratus)}

FAELQGKWYTIVIAADNLEKIEEGPLRFYFRHIDCYKNCSEMEITFYVITNNQCSKTTVIG
YLGKNGTYETQFEGNNIFQPLYITSDKIFFTNKNMDRAGQETNMIVVAGKGNALTPEENEI
LVQFAHEKKIPVENILNLTATDTCPE

>d1exsa_ b.60.1.1 (A:) beta-Lactoglobulin {Pig (Sus scrofa)}

VEVTPIMTELDTQKVAGTWHTVAMAVSDVSLDAKSSPLKAYVEGLKPTPEGDLEILLQK
RENDKCAQEVLLAKKTDIPAVFKINALDENQLFLDTDYDSHLLLCMENSASPEHSLVCQS
LARTLEVDDQIREKFEDALKTSLVPMRILPAQLEEQCRV

>d1epba_ b.60.1.1 (A:) Retinoic acid-binding protein {Rat (Rattus norvegicus), albino}

VKDFDISKFLGFWYEIFASKMGTPGLAHKEEKMGAMVVELKENLLALTTTYSEDHCV
LEKVTATEGDGPAPKFQVTRLSGKKEVVVEATDYLTIAIIDITSLVAGAVHRTMKLYSRSLD
DNGEALYNFRKITSDHGFSETDLYILKHDLCVKVLQSAA

>d1qqsa_ b.60.1.1 (A:) Neutrophil gelatinase-associated lipocalin (NGAL) {Human (Homo sapiens)}

TSDLIPAPPLSKVPLQQNFQDNQFQGGKWWVGLAGNAILREDKDPQKMYATIYEEKEDAS
YNVTSVLFRKKKCDYAIRTFVPGCQPGFTLGNIKSYPGLTSYLVRVVSTNYNQHAMVFF
KKVSQNREYFKITLYGRTELSELKNNFIRFSKSLGLPENHIVFPVPIDQCID

>d1bbpa_ b.60.1.1 (A:) Bilin-binding protein {Cabbage butterfly (Pieris brassicae)}

NVYHDGACPEVKPVDNFDWSNYHGKWWWEVAKYPNSVEKYGKCGWAEYTPEGKSVKVS
NYHVIHGKEYFIEGTAYPVGDSKIGKIYHKLTYYGGVTKENVFNVLSTDNKNYIIGYYCKY
DEKKKGHQDFVWVLSRSKVLGTGEAKTAVENYLIGSPVVDSQLVYSDFSEAACKVN

>d1i4ua_ b.60.1.1 (A:) Alpha-crustacyanin {European lobster (Homarus gammarus)}

DKIPDFVVPGKCASVDRNKLWAEQTPNRNSYAGVWYQFALTNNPYQLIEKCVRNEYSFD
GKQFVIESTGIAYDGNLLKRNGKLYPNPFGEPHLSIDYENSFAAPLVILETDYSNYACLYSCI
DYNFGYHSDFSFISRSANLADQYVKKCEAAFKNINVDTTFRVKTQVQSSCPYDTQKTL

>d1qfta__b.60.1.1 (A:) Histamine binding protein {Brown ear tick (Rhipicephalus appendiculatus)}
NQPDWADEAANGAHQDAWKSLKADVENVYYMVKATYKNDPVGNDFTCVGVMAND
VNEDEKSIQAEFLFMNNADTNMQFATEKVTAVKMYGYNRENAFRYETEDGQVFTDVIAY
SDDNCDVIYVPGTDGNEEGYELWTTDYDNIPANCLNKFNEYAVGRETRDVFTSACLEIAA
A

>d1npl1a__b.60.1.1 (A:) Nitrophorin 1 {Rhodnius prolixus}
KCTKNALAQTGFNKDKYFNGDVWYVTDYLDLEPDDVPKRYCAALAAGTASGKLKEALY
HYDPKTQDTFYDVSELQEESPGKYTANFKKVEKNGNVKVDVTSGNYTFTVMYADDSS
ALIHTCLHKGNKDLGLYAVLNRNKDTNAGDKVKGAVTAASLKFSDFISTKDNKCEYDN
VSLKSLTK

>d1lfc__b.60.1.2 (-) Intestinal fatty acid binding protein {Rat (Rattus norvegicus)}
AFDGTWKVDRNENYEKFMEKMGINVVKRKLGAHDNLKLTITQEGNKFTVKESSNFRNID
VVFELGVDFAYSLADGTELTGTWTMEGNKLVGKFKRVDNGKELIAVREISGNELIQTYTY
EGVEAKRIFKKE

>d1b56__b.60.1.2 (-) Epidermal fatty acid binding protein {Human (Homo sapiens)}
TVQQLEGRWRLVDSKGFDEYMKELGVGIALRKMGAMAKPDCIITCDGKNLTIKTESTLKT
TQFSC TLGEKFEETTADGRKTQTVCNFTDGALVQHQEWDGKESTITRKLKDGKLVVECV
MNNVTCTRIYEKVE

>d1mdc__b.60.1.2 (-) Fatty acid-binding protein {Tobacco hornworm (Manduca sexta)}
SYLGKVYSLVKQENFDGFLKSAGLSDDKIQALVSDKPTQKMEANGDSYSNTSTGGGGAK
TVSFKSGVEFDDVIGAGDSVKSMYTVDGNVVTHVVKGDAGVATFKKEYNGDDLVTITS
SNWDGVARRYKA

>d1ftpa__b.60.1.2 (A:) Fatty acid-binding protein {Desert locust (Schistocerca gregaria)}
VKEFAGIKYKLDSQTNFEEYMKAIGVGAIERKAGLALSPVIELEILDGDKFKLTSKTAIKNT
EFTFKLGEEFDEETLDGRKVKSTITQDGPKNLVHEQKGDHPTIIREFSKEQCVITIKLGLDV
ATRIYKAQ

>d1cbs__b.60.1.2 (-) Cellular retinoic-acid-binding protein (CRABP) {Human (Homo sapiens),
CRABP-II}
PNFSGNWKIIRSENFEELLKVLGVNVMLRKIAVAAASKPAVEIKQEGDTFYIKTSTTVRTTE
INFKVGEEFEEQTVDGRPCKSLVKWESENKMOVCEQKLLKGEGPKTSWTRELTNDGELILT
MTADDVVCTRVYVRE

>d1ggla__b.60.1.2 (A:) Cellular retinol-binding protein III {Human (Homo sapiens)}
PPNLTGYRFSVQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTVRTLSTFRNY
TVQFDVGVEFEEDLRSVDGRKCQTIVTWEEHLVCVQKGEVPNRGWRHWLEGEMLYLE
LTARDAVCEQVFRKVH

>d1lfo__b.60.1.2 (-) Liver fatty acid binding protein {Rat (Rattus norvegicus)}
MNFSGKYQVQSQENFEPFMKAMGLPEDLIQKGKDIKGVSEIVHEGKKVKLTITYGSKVIH
NEFTLGEECELETMTGEKVKAVVKMEGDNKMVTTFKGIKSVTEFNGDTITNTMTLGDIV
YKRVSRI

>d1leal__b.60.1.2 (-) Ileal lipid binding protein {Pig (Sus scrofa)}
AFTGKYEIESEKNYDEFMKRLALPSDAIDKARNLKIIEVKQDQGNFTWSQQYPGGHSITN
TFTIGKECDIETIGGKKFKATVQMEGGKVVVNSPNYHHTAEIVDGKLVEVSTVGGVSYER
VSKKLA

>d1swga__b.61.1.1 (A:) Streptavidin {Streptomyces avidinii}

SRYVLTGRYDSAPATDGSGTALGWTVAWKNNYRNAHSATTWSGQYVGGAEARINTQWL
LTSGTTEANAWKSTLVGHDTFTKVKPSAASGGGSAEAGITGTWYNQLGSTFIVTAGADGA
LTGTYESA

>d1ij8a_ b.61.1.1 (A:) Avidin {Chicken (Gallus gallus)}

KCSLTGKWTNDLGSNMTIGAVNSRGEFTGTYTTAVTATSNEIKESPLHGTENTINKRTQPTF
GFTVNWKFESESTTVFTGQCIFDRNGKEVLKTMWLLRSSVNDIGDDWKATRVGINIFTRL

>d1smpi_ b.61.2.1 (I:) Metalloprotease inhibitor {Erwinia chrysanthemi}

SSLRLPSAAELSGQWVLSGAEQHCDIRLNTDVLDTGTTWKLADGTACLQKLLPEAPVGWR
PTPDGLTLTQADGSAVAFFSRNRDRYEHKLVDSVRTLKKK

>d1jiwi_ b.61.2.1 (I:) Metalloprotease inhibitor {Pseudomonas aeruginosa, aprin}

SSLILLSASDLAQWTLQQDEAPAICHLELRDSEVAEASGYDLGGDTACLTRWLPSEPRAW
RPTPAGIALLERGGLTMLLGRQGEGDYRVQKGDGGQLVLRAT

>d1ei5a1 b.61.3.1 (A:336-417) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum
anthropi}

EVSrVEADSAWFGSWLDDDETGLVLSLEDAGHGRMKARFGTSPeMMDVVSANEARSaVT
TIRRDGETIELVRASENLRLSMKR

>d1ei5a2 b.61.3.1 (A:418-520) D-aminopeptidase, middle and C-terminal domains {Ochrobactrum
anthropi}

VKGEAKHDIIGRYHSDELADLLLVSEGGAIYGAFEGFLGKSDMYPLYSVGSDVWLLPVQ
RSMdAPSPGEWKLVRFRDDKGEITGLSVGCWLARGVEYRRVQP

>d1jjua5 b.61.4.1 (A:166-273) Quinohemoprotein amine dehydrogenase A chain, domain 3
{Paracoccus denitrificans}

PDAYADDASGAYVLAGRQPGRGdyTGRLVLKKAGEDYEVTMTLDFADGSRsFSGTGRIL
GAGEWRATLSdGTVTIRQIFALQDGRFSGRWHDADSDVIGGRLAAVKAD

>d1jmxa5 b.61.4.1 (A:163-281) Quinohemoprotein amine dehydrogenase A chain, domain 3
{Pseudomonas putida}

ESAaWAeWQKARPKADALPGQWAFSGHMLAKGDVRGVMSVTPDQGDtFKVEVKGAYA
DGTPFNGSGSAILYNGYEWrgNVKVGdANLRQVFAALDGEMKGRMFEAeHDERGLDFT
AVKE

>d1ihga2 b.62.1.1 (A:2-196) Cyclophilin 40 isomerase domain {Cow (Bos taurus)}

SHpSPQAKPSNPSNPRVFFdVDIGGERVGRIVLELFADIVPKTAENFRALCTGEKGIGPTTG
KPLHfKGCPFHRIKKFMIQGGDFSNQNGTGGESIYGEKFEDENfHYKHdKEGLLSMANA
GSNTNGSQQFITTVPtPHLDGKHVVFgQVIKGMGVAKILENVEVKGEKPAKLCVIAECGE
LKEGDDWGIFPKD

>d1clh_ b.62.1.1 (-) Bacterial cyclophilin {Escherichia coli}

AKGDpHVLLTTSAGNIELELDKQKAPVSVQNFVDYVNSGFYNNTTFHRVIPGFMIQGGGF
TEQMqQKKPNPPIKNEADNGLRNTRGTIAMARTADKDSATSQFFINVADNAFLDHGQRDF
GYAVFGKVVKGMdVADKISQVPTHdVGPYQNVPSKPVVILSAKVLP

>d1c39a_ b.64.1.1 (A:) Cation-dependent mannose 6-phosphate receptor, extracytoplasmic domain
{Cow (Bos taurus)}

EKTCDLVGEKGKESEKELALLKRLTPLfQKSfESTVGQSPDMYSYVFRVCREAGQHSSGA
GLVQIQKSNGKETVVGRFNETQIFQGSNWIMLIYKGGDEYDNHCGREQRRAVVMISCNR
HTLADNFNPVSEERGKVQDCfYLFEMDSSLACS

>d1e6fa_ b.64.1.1 (A:) Cation-independent mannose-6-phosphate receptor (MIR-receptor)

{Human (Homo sapiens)}

DDCQVTNPSTGHLFDLSSLSGRAGFTAAYSEKGLVYMSICGENENCPPGVGACFGQTRISV
GKANKRLRYVDQVLQLVYKDGSPCPSKSGLSYKSVISFVCRPEAGPTNRPMLISLDKQTC
TLFFSWHTPLACE

>d1f3ua_ b.65.1.1 (A:) TFIIF beta subunit, Rap30 {Human (Homo sapiens)}

AERGELDLTGAKQNTGVWLKVPKYLSQQWAKASGRGEVGLRIAKTQGRTEVSFTLNE
DLANIHDIGGKPASVSAPREHPFVLQSVGGQTLTVFTESSDKLSLEGIVVQRAECRPA

>d1f3ud_ b.65.1.1 (D:) TFIIF alpha subunit, Rap74 {Human (Homo sapiens)}

SSQNVTEYVVRVPKNTTKKYNIMAFNAADKVN FATWNQARLERDLSNKKIYQEEEMPES
GAGSEFNRLREEARRKKYGIVLKEFRPEDQPWLLRVNGKSGRKFKGIKKGGVTENTSY
YIFTQCPDGAFAFPVHNWYNFTPLARHRTLTAEEAEEEWERRN

>d1hxn_ b.66.1.1 (-) Hemopexin {Rabbit (Oryctolagus cuniculus)}

ESTRCDPDLVLSAMVSDNHGATYVFSGSHYWRLDTNRDGWHSWPIAHQWPQGPSTVDA
AFSWEDKLYLIQDTKVYVFLTKGGYTLVNGYPKRLEKELGSPVISLEAVDAAFVCPGSSR
LHIMAGRRLWWLDLKSQAQATWTELPWPHEKVDGALCMEKPLGPNSCSTSGPNLYLIHG
PNLYCYRHVDKLNAAKNLPQQRVSRLGCTH

>d1qhual b.66.1.1 (A:24-215) Hemopexin {Rabbit (Oryctolagus cuniculus)}

IEQCSDGWSFDATTLDDNGTMLFFKDEFVWKSHRGIRELISERWKNFIGPVDAAFRHGHT
SVYLIKGDKVWVYTSEKNEKVYPKSLQDEFPGIPFLDAAVECHRGECQDEGILFFQGNR
KWFWDLTTGTTKERSWPAVGNCTSALRWLG RYYCFQGNQFLRFNPVSGEVPPGYPLDVR
DYFLSCPGRGHRS

>d1gen_ b.66.1.1 (-) Gelatinase A (MMP-2), C-terminal domain {Human (Homo sapiens)}

LGPVTPEICKQDIVFDGIAQIRGEIFFFKDRFIWRTVTPRDKPMGPLL VATFWPELPEKIDAV
YEAPQEEKAVFFAGNEYWIYSASTLERGYPKPLTSLGLPPDVQRVDAAFNWSKNKKTYIF
AGDKFWRYNEVKKKMDPGFPKLIADAWNAIPDNLD AVVDLQGGGHSYFFKGAYYKLE
NQSLKSVKFGSIKSDWLGC

>d1fbl_1 b.66.1.1 (272-466) Collagenase, C-terminal domain {Pig (Sus scrofa)}

PQTPQVCD SKLTFDAITTLRGELMFFKDRFYMRTNSFYPEVELNFISVFWPQVPNGLQAAY
EIADRDEV RFFKG NKYWAVRGQDVLYGYPKDIHRSFGFPSTVKNIDA AVFEEDTGKTYFF
VAHECWRYDEYKQSM DTGYPKMIAEEFPGIGNKVD AVFQKDGLYFFHGTRQYQFDFKT
KRILTLQKANSWFNC

>d3sil_ b.68.1.1 (-) Salmonella sialidase {Salmonella typhimurium, strain lt2}

EKSVVFKAEGEHFTDQKGNTIVGSGSGGTTKYFRIPAMCTTSKGTIVVFADARHNTASDQ
SFIDTAAARSTDGGKTWNKKIAIYNDRVNSKLSRVM DPTCIVANIQGRE TILVMVGKWN
NDKTWGAYRDKAPD TDWDLVLYKSTDDGVTF SKVETNIHDIVTKNGTISAMLGGVGSGL
QLNDGKLVFPVQMVRTKNITTVLNTSFIYSTDGITWSLPSGYCEGFGSENNIIEFNASLVNN
IRNSGLRRSFETKDFGKTWTEFPPMDKKVDNRNHGVQGSTITIPSGNKLVA AHSSAQKN
NDYTRSDISLYAHNLYSGEVKLIDDFYPKVG NASGAGYSCLSYRKNVDKETLYV VYEANG
SIEFQDL SRHLPVIKSYN

>d1f8ea_ b.68.1.1 (A:) Influenza neuraminidase {Influenza A virus, different strains}

RDFNNLT KGLCTINSWHIYGKDN AVRIGEDSDVLVTREPYVSCDPDECRFYALSQGT TIRG
KHSNGTIHDRSQYRALISWPLSSPPTVYNSRVECIGWSSTSCHDGKTRMSICISGPNNN NASA
VIWYNRRPVTEINTWARNILRTQESECVCHNGVCPVVFTDGSATGPAETRIYYFKEGKILK
WEPLAGTAKHIEECSCYGERAEITCTCRDNWQGSNRPVIRIDPVAMTHTSQYICSPVLTDN

PRPNDPTVGKCNDPYPGNNNGVKGFSYLDGVNTWLGRITISIASRSGYEMLKVPNALTD
DKSKPTQGQTIVLNTDWSGYSGSFM DYWAE GECYRACFYVELIRGRP KEDKVWWTSNSI
VSMCSSTEFLGQWDWPDGAKIEYFL

>d1inv__ b.68.1.1 (-) Influenza neuraminidase {Influenza B virus, different strains}

EPEWTPRLSCQGSTFQKALLISPHRFGEIKGNSAPLIIREPFVACGPKECRHFALTHYAAQP
GGYYNGTRKDRNKLRLHLSVKLGKIPTVENSIFHMAAWSGSACHDGREWTYIGVDGPDN
DALVKIKYGEAYTDTYHSYAHNLRITQESACNCIGGDCYLMITDGSASGISKCRFLKIREG
RIIKEILPTGRVEHTEECTCGFASNKTIEACRDNSYAKRPFVKLNVEDTAEIRLMCTKT
YLDTPRPDDGSIAGPCESNGDKWLGGIKGGFVHQRMASKIGRWYSRTMSKTNRMGME
LYVRYDGPWTDSDALTLSGVMVSIEEPGWYSFGFEIKDKKCDVPCIGIEMVHDGGKDTW
HSAATAIYCLMGSGQLLWDTVTGVDMAL

>d1e8ua_ b.68.1.1 (A:) Paramyxovirus hemagglutinin-neuraminidase head domain {Newcastle disease virus}

GAPIHDPDFIGGIGKELIVDNASDVTSFYPSAFQEHLNFIPAPTTGSGCTRIPSFDM SATHYC
YTHNVILSGCRDHSHSHQYLALGVLRTTATGRIFFSTLRSISLDDTQNRKSCSVSATPLGCD
MLCSKVTEETEEEDYNSAVPTLMAHGRLGFDGQYHEKDLDVTTLFEDWVANYPGVGGGS
FIDGRVWFVSVYGGKLPNSPSTVQEGKYVIYKRYNDTCPDEQDYQIRMAKSSYKPGRFG
GKRIQQAILSIVSTSLGEDPVLTVPPNTVTLMGAEGRILTVGTSHFLYQRGSSYFSPALLYP
MTVSNKTATLHSPYTFNAFTRPGSIPCQASARCPNSCVTGVYTDPLYFYRNHTLRGVFG
TMLDSEQARLNPA SAVEDSTSRSRITRVSSSSTKAAYTTSTCFKVVKTNKTYCLSIAEISNTL
FGEFRIVPLLVEILKND

>d1eur__ b.68.1.1 (-) Micromonospora sialidase, N-terminal domain {Micromonospora viridifaciens}

GEPLYTEQDLAVNGREGFPNYRIPALTVPDGDLLASYDGRPTGIDAPGPNSILQRRSTDGG
RTWGEQQVVSAGQTTAPIKGFSDPSYLVRETGTIFNFHVYSQRQGFAGSRPGTDPADPNV
LHANVATSTDGGLTWSHRTITADITPDPGWRSRFAASGEGQLRYGPHAGRLIQYTIINAA
GAFQAVSVYSDDHGR TWAGEAVGVGM DENKTVELSDGRVLLNSRDSARSGYRKVAVS
TDGGHSYGPVTIDRDL PDPTNNASIIRAFPDAPAGSARAKVLLFSNAASQTSRSQGTIRMS
CDDGQTWPVSKVFQPGSMSYSTLTALPDGTYGLLYEPGTGIRYANFNLA WLGGICAP

>d2sli_2 b.68.1.1 (277-759) Leech intramolecular trans-sialidase, C-terminal domain {North american leech (Macrobdella decora)}

GENIFYAGDVTESNYFRIPSLTLSTGTVISAADARYGGTHDSKSKINIAFAKSTDGGNTWS
EPTLPLKFDDYIAKNIDWPRDSVGKNVQIQGSASYIDPVLLEDKLT KRIFLFADLM PAGIGS
SNASVSGSGFKEVNGKKYLKLRWHK DAGRAYDYTIREKGVYNDATNQPTFEFRVDGEYNL
YQHDTNLTCKQYDYNFSGNNLIESKTDVDVNMNIFYKNSVFKAFTNYLAMRYSDDEGA
SWSDLDIVSSFKEVSKFLVVGPGIGKQISTGENAGRLLVPLYSKSSAELGFMYSDDHGDN
WTYVEADNLTGGATAEAQIVEMPDGSLKTYLRTGSNCIAEVTSIDGGETWSDRVPLQGIST
TSYGTQLSVINYSQPIDGKPAIILSPNATNGRKNGKIWIGLVNDTGNTGIDKYSVEWKYSY
AVDTPQMGSYSYCLAELPDGQVGLLYEKYDSWSRNELHLKDILKFEKYSISELTGQA

>d1kit_3 b.68.1.1 (217-346,544-781) Vibrio cholerae sialidase {Vibrio cholerae}

VIFRGPDRIPSIVASSVTPGVVTAFAEKRVGGDPGALSNTNDIITRTSRDGGITWDTELNLT
EQINVSDEFDFSDPRPIYDPSSNTVLVSYARWPTDAAQNGDRIKPWMPNGIFYSVYDVASG
NWQAPIXVNP GPGHGITLTRQQNISGSQNGRLIYPAIVLDRFFLNVMSIYSDDGGSNWQTG
STLPIFRWKSSSILETLEPSEADMVELQNGDLLLTARLDFNQIVNGVNYSPRQQFLSKDGG

ITWSLLEANNANVFSNISTGTVDASITRFEQSDGSHFLFTNPQGNPAGTNGRQNLGLWFS
FDEGVTWKGPQLVNGASAYSIDIYQLDSENAIVIVETDNSNMRILRMPITLLKQKLTLSQN
>d1jjub_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Paracoccus denitrificans}
RDYILAPARPDKLVIDTEKMAVDKVTIADAGPTPMVPMVAPGGRIAYATVNKSESLVKI
DLVTGETLGRIDLSTPEERVKSLFGAALSPDGKTLAIYESPVRLLETHFEVQPTRVALYDAE
TLSRRKAFAEAPRQITMLAWARDGSKLYGLGRDLHVMDPEAGTLVEDKPIQSWEAETYAQ
PDVLAVWNQHESGVMATPFYTARKDIDPADPTAYRTGLLTMDLETGEMAMREVRIMDV
FYFSTAVNPAKTRAFGAYNVLESFDLEKNASIKRVPLPHSYYSVNVSTDGSTVWLGGALG
DLAAYDAETLEKKGQVDLPGNASMSLASVRLFTRDE

>d1jmb_ b.69.2.2 (B:) Quinohemoprotein amine dehydrogenase B chain {Pseudomonas putida}
GPALKAGHEYMIVTNYPNNLHVVDVASDTVYKSCVMPDKFGPGTAMMAPDNRTAYVLN
NHYGDIYGIDLTCKNTFHANLSSVPGEVGRSMYSFAISPDGKEVYATVNPTQRLNDHYV
VKPPRLEVSTADGLEAKPVRTFPMPRQVYLMRAADDGSLYVAGPDIYKMDVKTGKYTV
ALPLRNWNRKGYAPDVLYFWPHQSPRHEFSMLYTIARFKDDKQDPATADLLYGYLSVDL
KTGKTHTQEFADLTELYFTGLRSPKDPNQIYGVLNRLAKYDLKQRKLIKAANLDHTYYCV
AFDKKGDKLYLGTFNDLAVFNPDLTLEKVKNIKLPGGDMSTTTPQVFIR

>d1tbga_ b.69.4.1 (A:) beta1-subunit of the signal-transducing G protein heterotrimer {Cow (Bos taurus)}
MSELDQLRQEAELKNQIRDARKACADATLSQITNNIDPVGRIQMRTRRTLGRHLAKIYA
MHWGTD SRLLV SASQDGKLIWDSYTTNKVHAIPLRSSWVMTCAYAPSGNYVACGGLDN
ICSIYNLKTREGNVRVSREL AGHTGYLSCCRFLDDNQIVTSSGDTTCALWDIETGQQTTF
TGHTGDVMSLSLAPDTRLFVSGACDASAKLWDVREGMCRQTFTGHESDINAICFFPNGN
AFATGSDDATCRLFDLRADQELMTYSHDNIICGITSVSFSKSGRLLLAGYDDFNCNVWDA
LKADRAGVL AGHDNRV SCLGVTDDGMAVATGSWDSFLKIWN

>d1erja_ b.69.4.1 (A:) Tup1, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
HYLVYPYNQRANHSKPIPPFLDLDSQSVPDALKKQTNDDYYILYNPALPREIDVELHKS LDH
TSVVCCKVFSNDGEY LATGCNKTTQVYRVSDGSLVARLSDDSAANKDPENLNTSSSPSSD
LYIRSVCFSPDGKFLATGAEDRLIRIWDIENRKIVMILQGHEQDIYSLDYFSPGDKLVSGSG
DRTVRIWDLRTGQC SLTSLIEDGVTTVAVSPGDGKYIAAGSLDRAVRVWDSETGFLVERLD
SENEGTGHKDSVYSVVFTRDGQSVVSGSLDRSVKLWNLQ NANNKSDSKTPNSGTCEVT
YIGHKDFVLSVATTQND EYILSGSKDRGVLFWDKKSGNPLLMLQGHRNSVISVAVANGSS
LGPEYNVFATGSGDCKARIWKYKKI

>d1k8kc_ b.69.4.1 (C:) Arp2/3 complex 41 kDa subunit ARPC1 {Cow (Bos taurus)}
AYHSFLVEPISCHAWNKDRTQIAICPNNHEVHIYEKSGNKWVQVHELKEHNGQVTGVDW
APDSNRIVTCGTDRNAYVWTLKGRTWKPTLVILRINRAARCVRWAPNEKKFAVGSGSRVI
SICYFEQENDWWVCKHIKKPIRSTVLSLDWHPNSVLLAAGSCDFKCRIFSAYIKEVEERPA
PTPWGSKMPFGELMFESSSSCGWVHGVCF SANGSRVAWVSHDSTVCLADADKKMAVATL
ASETLP LLAVTFITESSLVAAGHDCFPVLFTYDSAAGKLSFGGRLDVPKQSSQRGLTARERF
QNLDKKASSEGSAAGAGLDSLHKNSVSQISVLSGGKAKCSQFCTTGMDGGM SIWDVRS
LESALKDLKIV

>d1h4ia_ b.70.1.1 (A:) Methanol dehydrogenase, heavy chain {Methylobacterium extorquens}
NDKLVELSKSDDNWVMPGKNYDSNNFSDLKQINKGNVKQLRPAWTFSTGLLNGHEGAP

LVVDGKMYIHTSFPNNTFALGLDDPGTILWQDKPKQNPAARAVACCDLVNRGLAYWPGD
GKTPALILKTQLDGNVAALNAETGETVWKVENS DIKVGSTLT IAPYVVKDKVIIGSSGAEL
GVRGYLTAYDVKTGEQVWRAYATGPKDLLLASDFNIKNPHYGQKGLGTGTWEGDAWK
IGGGTNWGWYAYDPGTNLIYFGTGNPAPWNETMRPGDNKWTMTIFGRDADTGEAKFGY
QKTPHDEWDYAGVNVMMMLSEQDKDKGKARKLLTHPDRNGIVYTLDRTDGALVSANKLD
DTVNVFKSVDLKTGQPVRDPEYGTRMDHLAKDICPSAMGYHNQGHDSYDPKRELFFMG
INHICMDWEPFMLPYRAGQFFVGATLNMYPGPKGDRQNYEGLGQIKAYNAITGDYKWE
KMERFAVWGGTMATAGDLVFGTLDGYLKARDSDTGDLWKFKIPSGAIGYPMTYTHK
GTQYVAIYYGVGGWPGVGLVFDLADPTAGLGAVGAFKKLANYTQMGGGVVVFSLDGK
GPYDDPNVGEWK

>d1flga_b.70.1.1 (A:) Ethanol dehydrogenase {Pseudomonas aeruginosa}

KDVTWEDIANDDKTTGDVLQYGMGTHAQRWSPLKQVNADNVFKLTPAWSYSFGDEKQ
RGQESQAIVSDGVIYVTASYSRLFALDAKTGKRLWTYNHRLPDDIRPCCDVVNRGAAYG
DKVFFGTLDASVVALNKNTGKVVWKKKFADHGAGYTMTGAPTIVKDGTGKVLLIHGS
SGDEFGVVGRLFARDPDTGEEIWMRPFVEGHMGRLNGKDSVTGDVKAPSWPDDRNSPT
GKVESWSHGGGAPWQSASFDAETNTIIVGAGNPGPWNTWARTAKGGNPHDYDSLYTSG
QVGVDPSSEVKWFYQHTPNDAWDFSGNNELVLFDYKAKDGKIVKATAHADRNNGFFYV
VDRSNGKLQNAFPVDNITWASHIDLKTGRPVEREGQRPPLPEPGQKHGKAVEVSPPFLG
GKNWNPMAYSQDTGLFYVPANHWKEDYWTEEVSYTKGSAYLGMGFRIKRMYYDDHVGS
LRAMDPVSGKVVWEHKEHLPLWAGVLATAGNLVFTGTGDGYFKAFDAKSGKELWKFQT
GSGIVSPITWEQDGEQYLGVTVGYGGAVPLWGGDMADLTRPVAQGGSFVFKLPSW

>d1kb0a2_b.70.1.1 (A:1-573) Quinoprotein alcohol dehydrogenase, N-terminal domain
{Comamonas testosteroni}

TGPAAQAAAQVRVDGDFIRANAARTPDWPTIGVDYAETRYSRDLQINAANVKDLGLAW
SYNLESTRGVEATPVVVDGIMYVSASWSVVAIDTRTGNRIWYDTPQIDRSTGFKGCCDV
VNRGVALWKGVYVGAWDGRLLALDAATGKEVWHQNTFEGQKGLTITGAPRVFKGKV
IIGNGGAIEYGVRYITAYDAETGERKWRWFSPVGDPSKPFEDESMKRAARTWDPSGKW
WEAGGGGTMWDSMTFDAELNTMYVGTGNGSPWSHKVRSKGGDNLYLASIVALDPDT
GKYKWHYQETPGDNWDYTSTQPMILADIKIAGKPRKVILHAPKNGFFFVLDRTNKGFISA
KNFVPVNWASGYDKHGKPIGIAAARDGSKPQDAVPGPYGAHNWHPMSFNPQTGLVYLPA
QNVVNLMDKKWEFNQAGPGKPQSGTGWNTAKFFNAEPPKSKPFRLLAWDPVAQKA
AWSVEHVSPWNGGTLTTAGNVVFQGTADGRLVAYHAATGEKLWEAPTGTGVVAAPSTY
MVDGRQYVSVAVGWGGVYGLAARATERQGPVTYTFVVGGKARMPE

>d1e43a1_b.71.1.1 (A:394-483) Bacterial alpha-Amylase {Bacillus licheniformis}

YAYGAQHDFDHHDIVGWTREGDSSVANSGLAALITDGPGGAKRMYVGRQNAGETWH
DITGNRSEPVVINSEGWGEFHVNGGSVSIYVQR

>d1g94a1_b.71.1.1 (A:355-448) Bacterial alpha-Amylase
{Pseudoalteromonas haloplantis (Alteromonas haloplantis)}

NWAVTNWWDNTNNQISFGRGSSGHMAINKESTLTATVQTDMA SGQYCNVLKGELSAD
AKSCSGEVITVNSDGTINLNIGAWDAMAIHKNALN

>d1bag_1_b.71.1.1 (348-425) Bacterial alpha-Amylase {Bacillus subtilis}

QPEELSNPNGNNQIFMNQRGSHGVVLANAGSSSVSINTATKLDPGRYDNKAGAGSFQVN
DGKLTGTINARSAVLYPD

>d1gja1_b.71.1.1 (A:573-636) Maltosyltransferase {Thermotoga maritima}

GKFENLTTKDLVMYSYEKNGQKIVIAANVGKEPKEITGGRVWNGKWSDEEKVVLKPLEF
ALVVQ

>d1pama3 b.71.1.1 (A:407-496) Cyclodextrin glycosyltransferase {Bacillus sp., strain 1011}
GSTHERWINNDVIIYERKFGNNVAVVAINRNMNTPASITGLVTS�PRGSYNDVLGGILNGN
TLTVGAGGAASNFTLAPGGTAVWQYTTDA

>d1smd_1 b.71.1.1 (404-496) Animal alpha-amylase {Human (Homo sapiens)}
QPFTNWDYDNGSNQVAFGRGNRGFIVFNDDWTFSLTLQTGLPAGTYCDVISGDKINGNCT
GIKIYVSDDGKAHFSISNSAEDPFIAIHAESKL

>d2taaa1 b.71.1.1 (A:382-478) Fungal alpha-amylase {Aspergillus oryzae, Taka-amylase}
YKNPYIKDDTTIAMRKGTGDSQIVTILSNKGASGDSYTLSSGASYTAGQQLTEVIGCTTV
TVGSDGNVPVPMAGGLPRVLPTEKLAGSKICSDSS

>d1smaa2 b.71.1.1 (A:506-588) Maltogenic amylase {Thermus sp.}
GDVAFLTADDEVNHLVYAKTDGNETVMIIINRSNEAAEIPMPIDARGKWLVNLLTGERFAA
EAETLCVSLPPYGFVLYAVESW

>d1bvza2 b.71.1.1 (A:503-585) Maltogenic amylase {Thermoactinomyces vulgaris, TVaII}
GNVRSWHADKQANLYAFVRTVQDQHVGVVLNNRGEKQTVLLQVPESGGKTWLDCLTG
EEVHGKQGGQLKLTLPYQGMILWNGR

>d1eh9a2 b.71.1.1 (A:491-557) Glycosyltrehalose trehalohydrolase {Archaeon Sulfolobus
solfataricus, km1}
CDRRVNVVNGENWLIKGREYFSLYVFSKSSIEVKYSGTLLLSSNNSFPQHIEEGKYEFDKG
FALYK

>d1bf2_2 b.71.1.1 (638-750) Isoamylase {Pseudomonas amyloclavata}
YSGSQLTWYQPSGAVADSNYWNNTSNYAIAYAINGPSLGDNSNIYVAYNGWSSSVTFTLPA
PPSGTQWYRVTDTCWWDGASTFVAPGSETLIGGAGTTYGQCGQSLLLISK

>d1gcya1 b.71.1.1 (A:358-418) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase)
{Pseudomonas stutzeri}
RADSAISFHSYSGLVATVSGSQQLVVALNSDLGNPGQVASGSFSEAVNASNGQVRVWR
S

>d1avaa1 b.71.1.1 (A:347-403) Plant alpha-amylase {Barley (Hordeum vulgare), seeds, AMY2
isozyme}
HNESKLQIIEADADLYLAEIDGKVIVKLGPYDVGNLIPGGFKVAAHGNDYAVWEKI

>d1uok_1 b.71.1.1 (480-558) Oligo-1,6-glucosidase {Bacillus cereus}
GSYDLILENNPSIFAYVRTYGVKLLVIANFTAEECIFELPEDISYSEVELLIHNYDVENGPIE
NITLRPYEAMVFKLK

>d1g5aa1 b.71.1.1 (A:555-628) Amylosucrase {Neisseria polysaccharea}
RLVTFNTNNKHIIGYIRNNALLAFGNFSEYPQTVTAHTLQAMPFKAHDLIGGKTVSLNQDL
TLQPYQVMWLEIA

>d1leg3a3 b.72.1.1 (A:47-84) Dystrophin {Human (Homo sapiens)}
PASQHFLSTSVQGPWERAISPKNVPYYINHETQTTTCWD

>d1i5hw_ b.72.1.1 (W:) Ubiquitin ligase NEDD4 WWIII domain {Rat (Rattus norvegicus)}
GSPVDSNDLGPLPPGWEERTHTDGRVFFINHNKKTQWEDPRMQNVAITG

>d1jmqa_ b.72.1.1 (A:) Yap65 ww domain {Human (Homo sapiens)}
FEIPDDVPLPAGWEMAKTSSGQRYFKNHIDQTTTWQDPRKAMLSQM

>d1aiw__ b.72.2.1 (-) Cellulose-binding domain of endoglucanase Z {Erwinia chrysanthemi}

MGDCANANVYPNWVSKDWAGGQPTHNEAGQSIVYKGNLYTANWYTASVPGSDSSWTQ
VGSCN

>d1ed7a_ b.72.2.1 (A:) Chitin-binding domain of chitinase A1 {Bacillus circulans}

AWQVNTAYTAGQLVTYNGKTYKCLQPHTSLAGWEPSNPALWQLQ

>d1flja_ b.74.1.1 (A:) Carbonic anhydrase {Rat (Rattus norvegicus), isozyme III}

AKEWGYASHNGPEHWHELYPIAKGDNQSPIELHTKDIRHDPSLQPWSVSYDPGSAKTILN
NGKTCRVVFD DTFDRSMLRGGPLSGPYRLRQFHLHWGSSDDHGSEHTVDGVKYAAELH
LVHWNPKYNTFGEALKQPDGIAVVGIFLKIGREKGEFQILLDALDKIKTGKEAPFNHFDP
SCLFPACRDYWTYHGSFTTPPCEECIVWLLLKEPMTVSSDQMAKLRS LFASAENEPPVPLV
GNWRPPQPIKGRVVRAF SK

>d1znca_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme IV}

WCYEVQAESSNYPCLVPVKWGGNCQKDRQSPINIVTTAKAKVDKKLGRFFFSGYDKKQT
WTVQNNGHSVMMLLENKASISGGGLPAPYQAKQLHLHWSDLPYKGSEHSLDGEHFAME
MHIVHEKEKGT SRNVKEAQDPED EIAVL AFLVEAGTQVNEG FQPLVEALSNIPKPEMSTT
MAESSLLDLLPKEEKL RHYFRYLGSLTTP TCDEKVVWTVFREPIQLHREQILAFSQKLYYD
KEQTVSMKDNVRPLQQLGQRTVIKS

>d1jd0a_ b.74.1.1 (A:) Carbonic anhydrase {Human (Homo sapiens), isozyme XII}

KWTYFGPDGENSWSKKYPSCGGLLQSPIDLHSDILQYDASLTPLEFQGYNLSANKQFLLT
NNGHSVKLNLPSDMHIQGLQSRYSATQLHLHWGNPNDPHGSEHTVSGQHFAAELHIVHY
NSDLYPDASTASNKSEGLAVLAVLIEMGSFNPSYDKIFSHLQHVKYKGQEA FVPGFNIEEL
LPERTA EYYRYRGLTTPPCNPTVLWTVFRNPVQISQEQLLALETALYCTHMDDPSPREMI
NNFRQVQKFDERLVYTSFS

>d1koqa_ b.74.1.1 (A:) Carbonic anhydrase {Neisseria gonorrhoeae}

THWGYTGHDSPESWGNLSEEFRLCSTGKNQSPVNITETVSGKLPAIKVNYKPSMVDVENN
GHTIQVNYPEGGNTLT VNGRTYTLKQFHFLT VNGRTYTLKQFH FHVPSENQIKGRTFPME
AHFVHLDENKQPLVLAVLYEAGKTNGRLSLAVLYEAGKTNGRLSSIWNVMPMTAGKVKL
NQPFDASTLLPKRLKYRFA GSLTTPPCTEGVSWLV LKTYDHIDQAQAEKFTRAVGSENN
RPVQPLNARVVIE

>d1ji6a2 b.77.2.1 (A:291-502) delta-Endotoxin (insectocide), middle domain {Bacillus
thuringiensis, CRY3bb1}

LYSKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLQGIEFHTRLQPGYFG
KDSFNYWSGNYVETRPSIGSSKTITSPFYGDKSTEPVQKLSFDGQKVYRTIANTDVAAPWN
GKVYLGVTKVDFSQYDDQKNETSTQTYDSKRNNGHVSAQDSIDQLPPETTDEPLEKAYS
HQLNYAECFLMQDRRG TIPFFT WTHRSVD

>d1ciy_2 b.77.2.1 (256-461) delta-Endotoxin (insectocide), middle domain {Bacillus thuringiensis,
CRYIA (A)}

PIRTVSQLTREIYTNPVLENFDGSFRGMAQRIEQNIRQPHLMDILNSITIYTDVHRGFNYWS
GHQITASPVGFSGPEFAFPLFGNAGNAAPPVLVSLTGLGIFRTLSSPLYRRIILGSGPNNQELF
VLDGTEFSFASLT TNLPSTIYRQRTVDSL DVIPPQDNSVPPRAGFSHRLSHVTMLSQAAG
AVYTLRAPTF SWQHRS AEF

>d1i5pa2 b.77.2.1 (A:264-472) delta-Endotoxin (insectocide), middle domain {Bacillus
thuringiensis subsp. kurstaki, CRY2AA}

YQSLMVSSGANLYASGSGPQQTQSFTAQNWPFYLSLFQVNSNYILSGISGTRLSITFPNIGG
LPGSTTTHSLNSARVNYSGGVSSGLIGATNLNHNFNFCSTVLPPLSTPFVRSWLDSGTD RAG

VATSTNWQTESFQTTLRLRCGAFSARGNSNYFPDYFIRNISGVPLVIRNEDLTRPLHYNQIR
NIESPSGTPGGARAYLVSVHNRKN

>g1jot.2 b.77.3.1 (B:,A:) Lectin MPA {Osage orange (*Maclura pomifera*)}

RNGKSQSIIIVGPWGDRXGVTFDDGAYTGIREINFEYNSETAIGGLRVTYDLNGMPFVAEDH
KSFITGFKPVKISLEFPSEYIVEVSGYVGKVEGYTVIRSLTFKTNKQTYGPYGVNTGTPFSL
PIENGLIVGFKGSIGYWLDYFSIYLSL

>d1c3ma_ b.77.3.1 (A:) Heltuba lectin {Jerusalem artishoke (*Helianthus tuberosus*)}

ASDIAVQAGPWGGNGGKRWLQTAHGGKITSIIKGGTCIFSIFVYKDKDNIEYHSGKFGV
LGDKAETITFAEDEDITAISGTFGAYYHMTVVTSLTFQTNKKVYGPFGTVASSFSPLTKG
KFAGFFGNSGDVLDSSIGGVVVP

>d1jpc__ b.78.1.1 (-) Lectin (agglutinin) {Snowdrop (*Galanthus nivalis*)}

DNILYSGETLSTGEFLNYGSFVFIMQEDCNLVLYDVKPIWATNTGGLSRSCFLSMQTDGN
LVVYNPSNKPWASNTGGQNGNYVCILQKDRNVVIYGTDRWATGTHT

>d1dlpa2 b.78.1.1 (A:116-235) Fetuin-binding protein Scafet precursor {Bluebell (*Scilla campanulata*)}

GSVVVANNGNSILYSTQGNDNHPQTLHATQSLQLSPYRLSMETDCNLVLFDRDDRNVSTN
TAGKGTGCRAVLQPNGRMDVLTNQNIWVTSGNSRSAGRYVFLQPDRLAIYGGALWT
T

>d1lair__ b.80.1.1 (-) Pectate lyase {*Erwinia chrysanthemi*, type C}

ATDTGGYAATAGGNVTGAVSKTATSMQDIVNIIDAARLDANGKKVKGGAYPLVITYTGNE
DSLINAAAANICGQWSKDPGRGVEIKEFTKGITIGANGSSANFGIWKSSDVVVQNMRI
YLPGGAKDGMIRVDDSPNVWVDHNEFAANHECDGTPDNDTTFESAVDIKGASNTVTV
SYNYIHGVKKVGLDGSSSSDTGRNITYHHNYNDVNARLPLQRGGLVHAYNNLYTNITGS
GLNVRQNGQALIENNWFKAIPVTSRYDGKNFGTWVLKGNITKPADFSTYSITWTADT
KPYVNADSWTSTGTFTVAYNYSVSAQCCKDKLPGYAGVGKNLATLTSTAC

>d1pcl__ b.80.1.1 (-) Pectate lyase {*Erwinia chrysanthemi*, type E}

AVETDAATTGWATQNGGTTGGAKAAKAVEVKNISDFKKALNGTDSSAKIIVTGPIDISGG
KAYTSFDDQKARSQISPSNTTIIGVGSNGKFTNGSLVIKGVKNVILRNLYIETPVDVAPHYE
SGDGWNAEWDAVIDNSTNVWVDHVTISDGSFTDDKYTTKDGEKYVQHDGALDIKKGS
DYVTISYSRFEHDKTILIGHSDSNGSQDSGKLRVTFHNNVFDREVTERAPRVRFSGSIHAYN
NVYLGDVKHSVYPYLYSFGSGTSGSILSESNSFTLSNLKSIDGKNPECSIVKQFNSKVFSK
GSLVNGSTTTKLDTCGLTAYKPTLPYKYSAQMTMTSSLATSINNAGYGKL

>d1bn8a_ b.80.1.1 (A:) Pectate lyase {*Bacillus subtilis*}

ADLGHQTLGSNDGWGAYSTGTTGGSKASSNVYTVSNRNQLVSALGKETNTTPKIIYIKG
TIDMNVDDNLKPLGLNDYKDPEYDLKYLKAYDPSTWGKKEPSGTQEEARARSQKNQK
ARVMVDIPANTTIVGSGTNAKVVGNGFQIKSDNVIIRNIEFQDAYDYFPQWDPTDGSSGN
WNSQYDNITINGGTHIWDHCTFNDGSRPDSTSPKYGRKYQHHDGQTDASNGANYITM
SYNYHHDHDKSSIFGSSDSTSDGKLGITLHHNRYKNIVQRAPRVRFQVHVNNYYE
GSTSSSSYPFSYAWGIGKSSKIYAQNNVIDVPGLSAAKTISVFSGGTALYDSGTLLNGTQIN
ASAANGLSSSVGWTPSLHGSIDASANVKSNNVINQAGAGKLN

>d1ee6a_ b.80.1.1 (A:) Pectate lyase {*Bacillus* sp., strain ksmp15}

APTVVHETIRVPAGQTFDGKGQTYVANPNTLGDGSAENQKPIFRLEAGASLKNVVIGAP
AADGVHCYGDCTITNVIWEDVGEDALTKSSGTVNISGGAAYKAYDKVFQINAAGTINIR
NFRADDIGKLVQRNGGTTYKVVMNVENCNISRVKDAILRTDSSTSTGRIVNTRYSNVPTLF

KGFKSGNTTASGNTQY

>d1rmg__ b.80.1.3 (-) Rhamnogalacturonase A {*Aspergillus aculeatus*}

QLSGSVGPLTSASTKGATKTCNILSYGAVADNSTDVGPAITSAWAACKSGGLVYIPSGNYA
LNTWVTLTGGSATAIQLDGHIYRTGTASGNMIAVTDTTDFELFSSTSKGAVQGFGYVYHAE
GTYGARILRLTDVTHFSVHDIILVDAPAFHFTMDTCSDGEVYNMAIRGGNEGGLDGIDVW
GSNIWVHDVEVTNKDECVTVKSPANNILVESIYCNWSGGCAMSGLGADTDVTDIVYRNV
YTWSSNQMYMIKSNNGSGTVSNVLLENFIGHGNAYSLDIDGYWSSMTAVAGDGVQLNNI
TVKNWKGTEANGATRPPIRVVCSDTAPCTDLTLEDIAIWTESGSSELYLCRSAYGSGYCLK
DSSSHTSYTTTSTVTAAPSGYSATTMAADLATAFGLTASIPIPTIPTSFPGLTPYSALAG

>d1bhe__ b.80.1.3 (-) Polygalacturonase {*Erwinia carotovora*, subsp. *carotovora*}

SDSRTVSEPKTPSSCTTLKADSSTATSTIQKALNNCDQGKAVRLSAGSTSVFLSGPLSLPSG
VSLLDKGVTLRAVNNAKSFENAPSSCGVVVDKNGKGCDAFITAVSTTNSGIYGP GTIDGQG
GVKLQDKKVSWWELAADAKVKKLKQNTPRLIQINKSKNFTLYNVSLNSPNFHVVFSDG
DGFTAWKTTIKTPSTARNTDGIDPMSSKNITIAYSNIATGDDNVAIKAYKGRAETRNISILHN
DFGTGHGMSIGSETMGVYNVTVDLKMNGTTNGLRIKSDKSAAGVVNGVRYSNVVMK
NVAKPIVIDTVYEKKEGSNVPDWS DITFKDVTSETKGVVVLNGENAKKPIEVTMKNVKLT
SDSTWQIKNVNVKK

>d1hg8a_ b.80.1.3 (A:) Polygalacturonase {*Fusarium moniliforme*}

DPCSVTEYSGLATAVSSCKNIVLNGFQVPTGKQLDLSSLQNDSTVTFKGTTTTFATTADNDF
NPVVISGSNITITGASGHVIDGNGQAYWDGKGSSNSNSNQKPDHFIVVQKTTGNSKITNLNIQ
NWPVHCFDITGSSQLTISGLILDNRAGDKPNAKSGSLPAAHNTDGFDISSSDHVTLDNNHV
YNQDDCVAVTSGTNIVVSNMYCSGGHGLSIGSVGGKSDNVVDGVQFLSSQVVNSQNGCR
IKSNSGATGTINNVTYQNIALTNIISTYGVVDVQQDYLNNGGPTGKPTNGVKISNIKFIKVTGTV
ASSAQDWFILCGDGCSCGFTFSGNAITGGGKTSSCNYPTNTCPS

>d1xat__ b.81.1.3 (-) Xenobiotic acetyltransferase {*Pseudomonas aeruginosa*}

NYFESPFGRKLLSEQVSNPNIRVGRYSYYSGYHGHFSFDDCARYLMPDRDDVDKLVIGSF
CSIGSGAAAFIMAGNQGHRAEWASTFPFHFMEEPAFAGAVNGYQPAGDTLIGHEVWIGTE
AMFMPGVRVGHGAIIGSRALVTGDVEPYAIVGGNPARTIRKRFSDGDIQNLLMAWWDW
PLADIEAAMPLCTGDIPALYQHWKQRQA

>d1kk6a_ b.81.1.3 (A:) Xenobiotic acetyltransferase {*Enterococcus faecium*, VAT(D)}

MGPNPMKMYPIEGNKSVQFIKPILEKLENVEVGEYSYYSKNGETFDKQILYHYPILNDKL
KIGKFCSIGPGVTIIMNGANHRMDGSTYPFNLFNGWEKHMPKLDQLPIKGDTHGNDVWI
GKDVVIMPVGKIGDGAIVAANSVVVKDIAPYMLAGGNPANEIKQRFDQDTINQLLDIKW
WNWPIDIINENIDKILDNSIIREVIW

>d1fxja1 b.81.1.4 (A:252-329) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
C-terminal domain {*Escherichia coli*}

VMLRDPARFDLRLTHGRDVEIDTNVHIEGNVTLGHRVKIGTGCVIKNSVIGDDCEISPYT
VVEDANLAACTIGPF

>d1hm9a1 b.81.1.4 (A:252-459) N-acetylglucosamine 1-phosphate uridyltransferase GlmU,
C-terminal domain {*Streptococcus pneumoniae*}

VSVFNPEATYIDIDVEIAPEVQIEANVILKGQTKIGAETVLTNGTYVVDSTIGAGAVITNSMI
EESSVADGVTVPYAHIRPNSSLGAQVHIGNFVEVKGSSIGENTKAGHLTYIGNCEVGSNV
NFGAGTITVNYDGKNKYKTVIGDNNFVGSNSTIIPVELGDNSLVGAGSTITKDVPADAIAI
GRGRQINKDEYATRLPHHPKNQ

>d1fi2a_ b.82.1.2 (A:) Germin {Barley (*Hordeum vulgare*)}

TDPDPLQDFCVADLDGKAVSVNGHTCKPMSEAGDDFLFSSKLTAKAGNTSTPNGSAVTELD
VAEWPGTNTLGVSMMNRVDFAPGGTNPPHIHPRATEIGMVMKCELLVILGSLDSGNKLYS
RVVRAGETFVIPRGLMHFQFNVGKTEAYMVVSFNSQNPQIVFVPLTLFGSDPPIPTPVLTKA
LRVEAGVVELLKSKFAGGS

>d2phla1 b.82.1.2 (A:11-210) Seed storage 7S protein {French bean (*Phaseolus vulgaris*),
phaseolin}

DNPFYFNSDNSWNTLFKNQYGHIRVLQRFDDQSKRLQNLEDYRLVEFRSKPETLLLPQQA
DAELLVVRSGSAILVLVKPDDRREYFFLTSDNPIFSDHQIPAGTIFYLVNPDPKEDLRIIQL
AMPVNNPQIHEFFLSSTEAAQQSYLQEFKSHILEASFNSKFEEINRVLFEEEGQQEGVIVNIDS
EQIKELSKHAKSS

>d2phla2 b.82.1.2 (A:220-381) Seed storage 7S protein {French bean (*Phaseolus vulgaris*),
phaseolin}

NTIGNEFGNLTERTDNSLNLISSIEMEELGALFVPHYYSKAIVILVVNEGEAHVELVGPKGN
KETLEYESYRAELSKDDVFVIPAAYPVAIKATSNVNFTGFGINANNNNRNLLAGKTDNVIS
SIGRALDGKDVLTGTFSGSGDEVMLINKQSGSYFVDAH

>g1dgr.3 b.82.1.2 (M:,N:) Seed storage 7S protein {Jack bean (*Canavalia ensiformis*),
canavalin/vinculin}

QLRRYAATLSEGDIIVIPSSFPVALKAASDLNMVGIGVNAENNERNFLAGHKENVIRQIPRQ
VSDLTFPGSGEEVEELLENQKESYFVDGQPXDKPFNLRSRDPIYSNNYGLYEITPEKNSQ
LRDLIDLLNCLQMNEGALFVPHYNSRATVILVANEGRAEVELVGL

>d1fxa1 b.82.1.2 (A:10-248) Seed storage 7S protein {Soybean (*Glycine max*),
proglycinin}

NECQIQKLNALKPDNRIESEGLIETWNPNNKPFQCAGVALSRCTLRNALRRPSYTNQP
QEIIYIQQKGIFGMIYPGCPSTFEPPQQPQQRGQSSRPQDRHQKIYNFREGDLIAVPTGVAV
WMYNNEDTPVAVSIIDTNSLENQLDQMPRRFYLAGNQEQEFLKYQQEQGGHQSQKKG
HQQEENEGGSILSGFTLEFLEHAFSVDKQIAKNLQGENEGEDKGAIIVTVKGGLSVIKP

>d1fxa2 b.82.1.2 (A:297-470) Seed storage 7S protein {Soybean (*Glycine max*),
proglycinin}

ICTMLRHNIGQTSSPDIYNPQAGSVTTATSLDFPALSRLRLSAEFGSLRKNAMFVPHYNL
NANSIYALNGRALIQVVNCNGERVFDGELQEGRVLIVPQNFVVAARSQSDNFEYVSFKTN
DTPMIGTLAGANSLNALPEEVIQHTFNLKSQQARQIKNNNPFKFLVPPQES

>d1qjea_ b.82.2.1 (A:) Isopenicillin N synthase {Emericella nidulans}

SKANVPKIDVSPLFGDDQAAKMRVAQQIDAASRDTGFFYAVNHGINVQRLSQKTKEFHMS
ITPEEKWDLAIRAYNKEHQDQVRAGYYLSIPGKKAVESFCYLNPNFTPDHPRIQAKTPTHE
VNVWPDETKHPGFQDFAEQYYWDVFLSSALLKGYALALGKEENFFARHFKPDDTLASV
VLIRYPYLDPYPEAAIKTAADGTKLSFEWHEDVSLITVLYQSNVQNLQVETAAGYQDIEAD
DTGYLINCOSYMAHLTNYYKAPIHRVKWVNAERQSLPFFVNLGYDSVIDPFDPREPNGK
SDREPLSYGDYLNGLVSLINKNGQT

>d1dcs_ b.82.2.1 (-) Deacetoxycephalosporin C synthase {*Streptomyces clavuligerus*}

MDTTVPTFSLAELQQGLHQDEFRRCLRDKGLFYLTDCGLTDTLKSADLVIDFFEHGSE
AEKRAVTSVPVPTMRRGFTGLESESTAQITNTGSYSDYSMCMGTADNLFPSGDFERIWTQ
YFDRQYTASRAVAREVLRATGTEPDGGVEAFLDCEPLLRFYFPQVPEHRSAAEQPLRMA
PHYDLSMVTLIQQTTPCANGFVSLQAEVGGAFDTLPYRPDAVLVFCGAIALTVTGGQVKAP
RHHVAAPRRDQIAGSSRTSSVFFLRPNADFTFSVPLARECGFDVSLDGETATFQDWIGGNY

VNIRRTSKA

>d1gp6a_ b.82.2.1 (A:) Anthocyanidin synthase {Mouse-ear cress (Arabidopsis thaliana)}

VAVERVESLAKSGIISIPKEYIRPKEELESINDVFLEEKKEDGPQVPTIDLKNIESDDEKIREN
CIEELKKASLDWGMHLINHGIPADLMERVKKAGEEFFSLSVEEKEYANDQATGKIQGY
GSKLANNASGQLEWEDYFFHLAYPEEKRDLSIWPKTPSDYIEATSEYAKCLRLLATKVFKA
LSVGLGLEPDRLEKEVGGLEELLQMKINYYPKCPQPELALGVEAHTDVSALTFILHNMV
PGLQLFYEGKWVTAKCVPDSIVMHIGDTLEILSNGKYKSILHRGLVNKEKVRISWAVFCEP
PKDKIVLKPLPEMVSVESPAKFPPTFAQHIEHKLFGKEQEEL

>d1hw5a2 b.82.3.2 (A:1-137) Catabolite gene activator protein, N-terminal domain {Escherichia coli}

VLGKPQTDPTLEWFLSHCHIHKYPKSTLIHQGEKAETLYYIVKGSVAVLIKDEEGKEMILS
YLNQGDFIGELGLFEEGQERSAWVRAKTACEVAEISYKKFRQLIQVNPDILMRLSAQMAR
RLQVLAEKVGNLAFL

>d1cx4a1 b.82.3.2 (A:130-265) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}

RIIHPKTDDQRNRLQEACKDILLFKNLDPEQMSQVLDAMFEKLVKEGEHVIDQGDDGDNF
YVIDRGTFDIYVKCDGVGRCVGNYNDRGSFGELALMYNTPRAATITATSPGALWGLDRVT
FRIIVKNNAKKRKMY

>d1cx4a2 b.82.3.2 (A:266-412) Regulatory subunit of Protein kinase A {Rat (Rattus norvegicus)}

ESFIESLPFLKSLEVSRCLKVVDVIGTKVYNDGEQIIAQGDSADSFFIVESGEVRITMKRKG
KSDIEENGAVEIARCLRGQYFGELALVTNKPRAASAHAIGTVKCLAMDVQAFERLLGPCM
EIMKRNIATYEEQLVALFGTNMDIV

>d1ig3a1 b.82.6.1 (A:179-263) Thiamin pyrophosphokinase, substrate-binding domain {Mouse (Mus musculus)}

DSLIIYLLQPGKHRLHVDTGMEGSWCGLIPVGQPCNQVTTTGLKWNLNDVLGFGTLVST
SNTYDGSGLTVETDHPDLLWTMAIKS

>d1ig0a1 b.82.6.1 (A:224-319) Thiamin pyrophosphokinase, substrate-binding domain {Baker's yeast (Saccharomyces cerevisiae)}

TDLIFLIKNGTLIEYDPQFRNTCIGNCGLLPIGEATLVKETRGLKWDVKNWPTSVVTGRV
SSSNRFVGDNCCFIDTKDDIILNVEIFVDKLIDFL

>d1bdo_ b.84.1.1 (-) Biotinyl domain of acetyl-CoA carboxylase {Escherichia coli}

EISGHIVRSPMVGTfYRTPSPDAKAFIEVGQKVNVDGTLTCIVEAMKMMNQIEADKSGTVK
AILVESGQPVEFDEPLVIE

>d1dd2a_ b.84.1.1 (A:) Biotin carboxyl carrier domain of transcarboxylase (TC 1.3S) {Propionibacterium freudenreichii, subsp. shermanii}

AGAGKAGEGEIPAPLAGTVSKILVKEGDTVKAGQTVLVLEAMKMETEINAPTDGKVEKV
LVKERDAVQGGGGLIKIG

>d1htp_ b.84.1.1 (-) Protein H of glycine cleavage system {Pea (Pisum sativum)}

SNVLDGLKYAPSEWVKHEGSVATIGITDHAQDHLGEVVFVELPEPGVSVTKGKGFGAVE
SVKATSDVNSPISGEVIEVNTGLTGKPLINSSPYEDGWMIKIKPTSPDELESLLGAKEYTK
FCEEEDAAH

>d1gixa_ b.84.1.1 (A:) Ipoyl domain of dihydrolipoamide acetyltransferase {Neisseria meningitidis}

ALVELKVPDIGGHENVDIHAVEVNVGDTIAVDDTLITLETDKATMDVPAEVAGVVKEVKV

KVGDKISEGGLIVVVEAEGTA

>d1fyc__ b.84.1.1 (-) Ipoyl domain of dihydrolipoamide acetyltransferase {Human (Homo sapiens)}

GSNMSYPPHMQVLLPALSPMTMGTVQRWEKKVGEKLSEGDLLAEIETDKATIGFEVQEE
GYLAKILVPEGTRDVPLGTPLCIIVEKEADISAFADYRPTEVTDLK

>d1pmr__ b.84.1.1 (-) Lipoyl domain of the 2-oxoglutarate dehydrogenase complex {Escherichia coli}

SSVDILVPDLPESVADATVATWHKKPGDAVVRDEVLEIETDKVVLEVPASADGILDAVLE
DEGTTVTSRQILGRLREGN

>d1k8ma_ b.84.1.1 (A:) Lipoyl domain of the mitochondrial branched-chain alpha-ketoacid dehydrogenase {Human (Homo sapiens)}

MGQVVQFKLSDIGEGIREVTVKEWYVKEGDTVVSQFDSICEVQSDKASVTITSRDGVVKK
LYYNLDDIAYVGKPLVDIETEALKDLE

>d1dv1a1 b.84.2.1 (A:331-446) Biotin carboxylase subunit of acetyl-CoA carboxylase, C-terminal domain {Escherichia coli}

RGHAVECRINAEDPNTFLPSPGKITRFHAPGGFGVRWESHYAGYTVPPYYDSMIGKLICY
GENRDVAIARMKNALQELIIDGIKTNDLQIRIMNDENFQHGGTNIHYLEKKLGL

>d1gsoa1 b.84.2.1 (A:328-426) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia coli}

ERASLGVMMAAGGYPGDYRTGDVIHGLPLEEVAGGKVFHAGTKLADDEQVVTNGGRVL
CVTALGHTVAEAQKRAYALMTDIHWDDCFCKRDIGWRAIER

>d1b6ra1 b.84.2.1 (A:277-355) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

NNPSVMINLIGSDVNYDWLKLPLVHLHWYDKEVRPGRKVGHLNLTDSDTSRLTATLEALI
PLLPEYASGVIWAQSKFG

>d1eyza1 b.84.2.1 (A:319-392) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

GPAASAVILPQLTSQNVTFDNVQNAVGLDLQIRLFGKPEIDGSRRLGVALATAESVVDAIER
AKHAAGQVKVQG

>d2gpr__ b.84.3.1 (-) Glucose permease IIa domain, IIa-glc {Mycoplasma capricolum}

MWFFNKNLKVLPACDGTIITLDEVEDEVFKERMLGDGFAINPKSNDFHAPVSGKLVTAFP
TKHAFGIQTKSGVEILLHIGLDTVSLDGNGFESFVTQDQEVNAGDKLVTVDLKSVAKKVP
SIKSPIIFTNNGGKTLEIVKMGEVKQGDVVAILK

>d1glaf_ b.84.3.1 (F:) Glucose-specific factor III (glsIII) {Escherichia coli}

GLFDKLSLVSDDKKDTGTIEIIAPLSGEIVNIEDVPDVVFAEKIVGDGIAIKPTGNKMVAPV
DGTIGKIFETNHAFSIESDSGVELFVHFGIDTVELKGEGFKRIAEQGQVRVKGDTVIEFDLPL
LEEKAKSTLTPVVISNMDEIKELIKLSGSVTVGETPVIRIKK

>d1euwa_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Escherichia coli}

MMKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDARELAPGDTTLVPTGLAIHIAD
PSLAAMMLPRSGLGKHGIVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMI
FVPVVQAEFNLVEDF

>d1f7ra_ b.85.4.1 (A:) Deoxyuridine 5'-triphosphate nucleotidohydrolase (dUTPase) {Feline immunodeficiency virus}

MIIEGDGILDKRSEDAGYDLLAAKEIHLLPGEVKVIPTGVKLMPLPKGYWGLIIGKSSIGSKG
LDVLGGVIDEGYRGEIGVIMINVSRSITLMERQKIAQLIILPCKHEVLEQGKVVMDSERG
DNGYGSTGVF

>d1dfaa1 b.86.1.2 (A:1-180,A:416-454) PI-Scei intein {Baker's yeast (*Saccharomyces cerevisiae*)}
CFAKGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPRGRETMYSVVQKSQHRAH
KSDSSREVPELLKFTCNATHELVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVE
LVKEVSKSYPISEGPERANELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAXC
RGFYFELQELKEDDYGITLSDDSDHQFLLANQVNVHN

>d1dq3a1 b.86.1.2 (A:1-128,A:415-454) PI-Pfui intein {Archaeon *Pyrococcus furiosus*}
CIDGKAKIIFENEGEEHLTTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPEK
RVVKGKVNVIWKYELGKDVTKYEIITNKGTKILTSPWHPFFVLTPDFKIVEKRADELKEGD
ILIGGMXGLEVVRRHITTTNEPRTFYDLTVENYQNYLAGENGMIHVHN

>d1am2__ b.86.1.2 (-) GyrA intein {*Mycobacterium xenopi*}
ASITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNPVLADRLFHSGEHPVYA
VRTVEGLRVTGTANHPLLCLVDVAGVPTLLWKLIDEIKPGDYAVIQSAFSVDCAGFARGK
PEFAPTTYTVGVPGLVRFLEAHRDPDAKAIADELTDGRFYAKVASVTDAGVQPVSRLR
VDTADHAFITNGFVSHN

>d1umua_ b.87.1.1 (A:) UmuD' {*Escherichia coli*}
DYVEQRIDLNQLLIQHPSATYFVKASGDSMIDGGISDGDLLIVDSAITASHGDIVIAAVDGE
FTVKKLQLRPTVQLIPMNSAYSPTISSEDTLDVFGVVIHVVK

>d1jhfa2 b.87.1.1 (A:73-198) LexA C-terminal domain {*Escherichia coli*}
EEGLPLVGRVAADEPLLAQQHIEGHYQVDPSLFKPNADFLLRVSGMSMKDIGIMDGDLLA
VHKTQDVRNGQVVVARIDDEVTVKRLKKQGNKVPELLPENSEFKPIVVDLRQQSFTIEGLA
VGVIRN

>d1f39a_ b.87.1.1 (A:) lambda repressor C-terminal domain {Bacteriophage lambda virus}

ASASAFWLEVEGNSMTAPTGSKPSFPDGMILILVDPEQAVEPGDFCIARLGGDEFTFKKLIR
DSGQVFLQPLNPQYPMIPCNESCSVVGKVIASQWPEETFG

>d1aqt_2 b.93.1.1 (2-86) Epsilon subunit of F1F0-ATP synthase N-terminal domain {*Escherichia coli*}

STYHLDVVSAEQQMFSGLVEKIQVTGSEGELGIYPGHAPLLTAIKPGMIRIVKQHGHEEFIY
LSGGILEVQPGNVTVLADTAIRG

>d1e79h2 b.93.1.1 (H:15-100) Epsilon subunit of F1F0-ATP synthase N-terminal domain {Cow (*Bos taurus*)}

QMSFTFASPTQVFFNSANVRQVDVPTQTGAFGILAAHVPTLQVLRPGLVVVHAEDGTTSK
YFVSSGSVTVNADSSVQLLAEAEAVTL

>d1trea_ c.1.1.1 (A:) Triosephosphate isomerase {*Escherichia coli*}

MRHPLVMGNWKLNGSRHVMHELVSNLRLKELAGVAGCAVAIAPPEMYIDMAKREAEGSHI
MLGAQNVNLNLGAFTGETSAAMLKDIGAQYIIIGHSESRRTYHKESDELIAKKFAVLKEQG
LTPVLCIGETEAEAEAGKTEEVCAEQIDAVLKTQGAFAFEGAVIAYEPVWAIGTGKSATPA
QAQAVHKFIRDHIAKVDANIAEQVIIQYGGSVNASNAELFAQPDIDGALVGGASLKADA
FAVIVKAAEAAKQA

>d1hg3a_ c.1.1.1 (A:) Triosephosphate isomerase {Archaeon *Pyrococcus woesei*}

AKLKEPIIAINFKTYIEATGKRALEIAKAAEKVYKETGVTIVVAPQLVDLRMIAESVEIPVFA

QHIDPIKPGSHTGHVLP EAVKEAGAVGTLLNHSENRMILADLEAAIRRAEEVGLMTMVCS
NNPAVSAAVAALNP DYVAVEPPELIGTGIPVSKAKPEVITNTVELVKKVNPEVKVLCGAGIS
TGEDVKKAIELGT VGVLLASGVTKAKDPEKAIWDLVSGI

>d1qo2a_ c.1.2.1 (A:) Phosphoribosylformimino-5-aminoimidazole carboxamide ribotide
isomerase HisA {Thermotoga maritima}

MLVVP AIDLFRGKVARMIKGRKENTIFYEKDPVELVEKLIIEGFTLIHVVDLSNAIENSGEN
LPVLEKLSEFAEHIQIGGGIRSLDYAEKLRKLG YRRQIVSSKVLEDPSFLKSLREIDVEPVFS
LDTRGGRVAFK GWLAEEEEIDPV SLLKRLKEYGLEEIVHTEIEKDGT LQEHD FSLTKKIAIEA
EVK VLAAGGISSENSLKTAQKVHTETNGLLKG VIVGRAFLLEGILTVEVMKRYAR

>d1thfd_ c.1.2.1 (D:) Cyclase subunit (or domain) of
imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}

MLAKRIIACLDVKDGRVVKGSNFENLRDSGDPVELGKFYSEIGIDELVFLDITASVEKRKT
MLELVEKVAEQIDIPFTVGGGIHDFETASELILRGADKVSINTAAVENPSLITQIAQTFGSQA
VVVAIDAKRVDGEFMVFTYSGKKNTGILLRDWVVEVEKRGAGEILLTSIDRDGTSKGYDT
EMIRFVRPLTTLPIIASGGAGKMEHFLEAFLAGADAALAASVFHFREIDVRELKEYLKKHG
VNRLEGL

>d1jvna1 c.1.2.1 (A:230-552) Cyclase subunit (or domain) of
imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces
cerevisiae), His7}

DYSNYGLTRRIIACLDVRTNDQGD LVVTKGDQYDVREKSDGKGVRNLGKPVQLAQKYY
QQGADEVTF LNITSFRDCPLKDT PMLEVLKQAAKT V FVPLTVGGGIKDIVDVGTKIPALE
VASLYFRSGADKVSIGTDAVYAAEKYYELGNRGDGT SPIETISKAYGAQAVVISVDPKRVY
VNSQADTKNKVFETEYPPGNGEKYCWYQCTIKGGRESRDLGVWELTRACEALGAGEILL
NCIDKDG SNSGYDLELIEHVKDAVKIPVIASSGAGVPEHFEEAFLKTRADACLGAGMFHR
GEFTVNDVKEYLLEHGLKVRMDEE

>d1dbta_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Bacillus
subtilis}

MKNNLP IIALDFASAEETLAFLAPFQQEPLFVKVGMELFYQEGPSIVKQLKERNCEFLDL
KLHDIPTTVNKAMKRLASLGVDLVNVHAAGGKKMMQAALEGLEEGTPAGKKRPSLIAVT
QLTSTSEQIMKDELLIEKSLIDTVVHYSKQAEESGLDGVVCSVHEAKAIYQAVSPSFLT VTP
GIRMSEDAANDQVRVATPAIAREKGSSAIVVGRSITKAEDPVKAYKAVRLEWEGI

>d1dvja_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Archaeon
Methanobacterium thermoautotrophicum}

MDVMNRLILAMDLMNRDDALRV TGEVREYIDTVKIGYPLVLSEGMDIIAEFRKRFGCRIIA
DFKVADIPETNEKICRATFKAGADAIIVHGFPGADSVRACLNVAEEMGREVFLITEMSHPG
AEMFIQGA ADEIARMGVDLGVKNYVGPSTRPERLSRLREIIGQDSFLISPGVGAQGGDPGE
TLRFADAIIVGRSIYLADNPAAAAAGIIESIKDLLIPEDPAANKARKEAELAAATA

>d1dqwa_ c.1.2.3 (A:) Orotidine 5'-monophosphate decarboxylase (OMP decarboxylase) {Baker's
yeast (Saccharomyces cerevisiae)}

MHKATYKERAATHPSPVA AKLFNIMHEKQTNLCASLDVRTTKELLELVEALGPKICLLKT
HVDILTDFSMEGT VKPLKALSAKYNFLLFEDRK FADIGNTVKLQYSAGVYRIAEWADITN
AHGVVGP GIVSGLKQAAEEVTKEPRGLLMLAELSCKGSLSTGEYTKGTVDIAKSDKDFVI
GFIAQRDMGGRDEGYDWLIMTPGVGLDDKGDALGQQYRTVDDVVSTGSDIIIVGRGLFA
KGRDAKVEGERYRKAGWEAYLRRCGQQD

>d1pii_2 c.1.2.4 (255-452) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Escherichia coli}
GENKVCGLTRGQDAKAAAYDAGAIYGGILFVATSPRCVNVEQAQEVMAAAPLQYVGVFR
NHDIADVVDKAKVLSLAAVQLHGNEEQLYIDTLREALPAHVAIWKALSVGETLPAREFQH
VDKYVLDNGQGGSGQRFDWSLLNGQSLGNVLLAGGLGADNCVEAAQTGCAGLDFNSA
VESQPGIKDARLLASVFQTLRAY

>d1nsj__ c.1.2.4 (-) N-(5'phosphoribosyl)antranilate isomerase, PRAI {Thermotoga maritima}
MVRVKICGITNLEDALFSVESGADAVGFVFYPPKSKRYISPEDARRISVELPPFVFRVGVFVN
EEPEKILDVASYVQLNAVQLHGEEPIELCRKIAERILVIKAVGVSNERDMERALNYREFPILL
DTKTPEYGGSGKTFDWSLILPYRDRFRYLVLSSGGLNPENVRSAIDVVRPFAVDVSSGVEAF
PGKKDHDSIKMFIKNAKGL

>d1pii_1 c.1.2.4 (1-254) Indole-3-glycerophosphate synthase, IPGS {Escherichia coli}
MQTVLAKIVADKAIWVEARKQQQLASFQNEVQPSTRHFYDALQGARTAFIECKKASPS
KGVIRDDFDPARIAAIYKHYASISVLTDEKYFQGSFNFLPIVSQIAPQPILCKDFIIDPYQIY
LARYYQADACLLMLSVLDDDQYRQLAAVAHSLEMGVLTEVSNEEEQERAIALGAKVVGI
NNRDLRLDSIDLNRRELAPKLGHNVTVISESGINTYAQVRELSHFANGFLIGSALMAHDD
LHAARRRVLL

>d1a53__ c.1.2.4 (-) Indole-3-glycerophosphate synthase, IPGS {Archaeon Sulfolobus solfataricus}

PRYLKGWLKDVVQLSLRRPSFRASRQRPIISLNERILEFNKRNITAHAEYKRKSPSGLDVER
DPIEYSKFMERYAVGLSILTEEKYFNNGSYETLRKIASSVSIPILMKDFIVKESQIDDAYNLGA
DTVLLIVKILTERELESLEYARSYGMEPLIEINDENDLDIALRIGARFIGINSRDLETLEINK
ENQRKLISMIPSNVVKVAESGISERNEIEELRKLGVNAFLIGSSLMRNPEKIKEFIL

>d1qopa_ c.1.2.4 (A:) Trp synthase alpha-subunit {Salmonella typhimurium}
MERYENLFAQLNDRREGAFVPFVTLGDPGIEQSLKIIDTLIDAGADALELGVPFSDPLADG
PTIQNANLRAFAAGVTPAQCFEMLAIIREKHPTIPIGLLMYANLVFNNGIDAFYARCEQVGV
DSVLVADVPVEESAPFRQAALRHNIAPIFICPPNADDDLLRQVASYGRGYTYLLSRSGVTG
AENRGALPLHHLIEKLKEYHAAPALQGFGISSPEQVSAAVRAGAAGAISGSAIVKIIKENLA
SPKQMLAELRSFVSAMKAASR

>d1geqa_ c.1.2.4 (A:) Trp synthase alpha-subunit {Archaeon Pyrococcus furiosus}
MFKDGLSIPYLTAGDPDKQSTLNFLALDEYAGAIELGIPFSDPIADGKTIQESHYRALKNG
FKLREAFWIVKEFRHSSTPIVLMITYYNPIYRAGVRNFLAEAKASGVDGILVVDLPVFHA
KEFTEIAREEGIKTVFLAAPNTPDERLKVIDDMTTGfVYLVSLYGTGAREEIPKTAYDLLR
RAKRICRNKVAVGFGVSKREHVVSLLKEGANGVVVGSAVLVKIIGEKGREATEFLKKKVEE
LLGI

>d2dora_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme A}
MLNTTFANAKFANPFMNASGVHCMTIEDLEELKASQAGAYITKSSTLEKREGNPLPRYVD
LELGSINSMGLPNLGFDDYLDYVLKNQKENAQEGPIFFSIAGMSAAENIAMLKIKIESDFS
GITELNLSCPNVPGKPQLAYDFEATEKLLKEVFTFTKPLGVKLPPYFDLVHFDIMAEILNQ
FPLTYVNSVNSIGNGLFIDPEAESVVIKPKDGFGGIGGAYIKPTALANVRAFYTRLKPEIQII
GTGGIETGQDAFEHLLCGATMLQIGTALHKEGPAIFDRIIKELEEIMNQKGYQSIADFHGKL
KSL

>d1ep3a_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Lactococcus lactis, isozyme B}
MTENNRLSVKLPGLDLKNPIIPASGCFGFGEEYAKYYDLNKLGSIMVKATTLHPRFGNPTP
RVAETASGMLNAIGLQNPGLLEVIMTEKLPWLNNFPELPIIANVAGSEEADYVAVCAKIGD

AANVKAIELNISCNVKHGGQAFGTDPEVAAALVKACKAVSKVPLYVKLSPNVTDIVPIAK
AVEAAGADGLTMINLMGVRFDLKTRQPILANITGGLSGPAIKPVALKLIHQVAQDVDIPII
GMGGVANAQDVLEM YMAGASAVAVGTANFADPFVCPKIIDKLPELMDQYRIESLES LIQE
VKEGKK

>d1d3ga_ c.1.4.1 (A:) Dihydroorotate dehydrogenase {Human (Homo sapiens)}

MATGDERFYAEHLMPTLQGLLDPESAHRLAVRFTSLGLLPRARFQDSDMLEVRVLGHKFR
NPVGIAAGFDKHGEAVDGLYKMGFGFVEIGSVTPKPQEGNPRPRVFRLLPEDQAVINRYGF
NSHGLSVVEHRLRARQQKQAKLTEDGLPLGVNLGKNKTSVDAAEDYAEGVRVLGPLAD
YLVVNVSSPNTAGLRSLQGKAELRRLTKVLQERDGLRRVHRPAVLVKIAPDLTSQDKEDI
ASVVKELGIDGLIVTNTTVSRPAGLQGALRSETGGLSGKPLRDLSTQTIREMYALTQGRVPI
IGVGGVSSGQDALEKIRAGASLVQLYTALTFWGPPVVGKVKRELEALLKEQGFGGVTDI
GADHRR

>d1oyb_ c.1.4.1 (-) Old yellow enzyme (OYE) {Brewer's yeast (Saccharomyces
carlsbergensis)}

SFVKDFKPQALGDTNLFKPIKIGNNELLHRAVIPPLTRMRALHPGNIPNRDWAVEYYTQRA
QRPGMTIITEGAFIS PQAGGYDNAPGVWSEEQMVWTKIFNAIHEKKS FVWVQLWVLGW
AAFPDNLARDGLRYDSASDNVFMDAEQEAKAKKANNPQHSLTKDEIKQYIKEYVQAAK
NSIAAGADGVEIHSANGYLLNQFLDPHSNTRTDEYGGSIENRARFTLEVVDALVEAIGHEK
VGLRLSPYGVFNSMSGGAETGIVAQYAYVAGELEKRAKAGKRLAFVHLVEPRVTNPFLTE
GEGEYEGGSNDFVYSIWKGPIRAGNFALHPEVVREEVKDKRTLIGYGRFFISNPDLVDRL
EKGLPLNKYDRDTFYQMSAHGYIDYPTYEEALKLGWDDK

>d1huva_ c.1.4.1 (A:) Membrane-associated (S)-mandelate dehydrogenase
{Pseudomonas putida}

NLFNVEDYRKLAKRLPKMVYDYLEGGAEDEYGVKHNRDVFQQWRFKPKRLVDVSRR
SLQAEVLGKRQSMPLLIGPTGLNGALWPKGDLALARAATKAGIPFVLSTASNMSIEDLAR
QCDGDLWFQLYVIHREIAQGMVLKALHTGYTTVLTTDVAVNGYRERDLHNRFKIPPFLT
LKNFEGIDLGKMDKANLEMQAALMSRQMDASFNWEALRWLRDLWPHKLLVKGLLSAE
DADRCIAEGADGVILSNHGGRLDCAISPMEVLAQSVAKTGKPVLDISGFRRGSDIVKAL
ALGAEAVLLGRATLYGLAARGETGVDEVLTLLKADIDRTLAQIGCPDITSLSPDYLQNE

>d1h61a_ c.1.4.1 (A:) Pentaerythritol tetranitrate reductase {Enterobacter cloacae}

SAEKLFTPLKVGAVTAPNRVFMAPLTRLSIEPGDIPTPLMGEYYRQRASAGLIIEATQISA
QAKGYAGAPGLHSPEQIAAWKKITAGVHAEDGRIAVQLWHTGRISHSSIQPGGQAPVSAS
ALNANTRTSLRDENGNAIRVDTTTTPRALELDEIPGIVNDFRQAVANAREAGFDLVELHSAH
GYLLHQFLSPSSNQRTDQYGGSVENRARLVLEVVDVAVCNWSADRIGIRVSPIGTFQNVD
NGPNEEADALYLIEELAKRGIAYLHMSETDLAGGKPYSEAFRQKVRERFHGVIIGAGAYTA
EKAEDLIGKGLIDAVAFGRDYIANPDLVARLQKKAELNPQRPE SFYGGGAEGYTDYPSL

>d1djna1 c.1.4.1 (A:1-340) Trimethylamine dehydrogenase, N-terminal domain {Methylophilus
methylotrophus, w3a1}

ARDPKHDLFEPIQIGPKTLNRNFYQVPHCIGAGSDKPGFQSAHRSVKAEGGWAALNTEY
CSINPESDDTHRLSARIWDEGDVRNLKAMTDEVHKGALAGVELWYGGAHAPNMESRA
TPRGPSQYASEFETLSYCKEMDLS DIAQVQQFYVDAAKRSRDAGFDIVYVYGAHSYLP LQ
FLNPYYNKRTDKYGGSLNRRARFWLETLEKVKHAVGSDCAIATRFGVDTVYGPQGIEAE
VDGQKFVEMADSLVDMWDITIGDIAEWGEDAGPSRFYQQGHTIPWVKLVKQVSKKPV L
GVGRYTDPEKMIEIVTKGYADIIGCARPSIADPFLPQKVEQGRYD

>d1ltda1 c.1.4.1 (A:98-511) Flavocytochrome b2, C-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}

APGETKEDIARKEQLKSLLPPLDNIINLYDFEYLASQTLTKQAWAYYSSGANDEVTHRENH
NAYHRIFFKPKILVDVRKVDISTDMLGSHVDVPFYVSATALCKLGNPLEGEKDVARGCGQ
GVTKVPQMISTLASCSPEEIIAAPSDKQIQWYQLYVNSDRKITDDLKVNVEKLGVKALFV
TVDAPSLGQREKDMKLKFSNTKAGPKAMKKTNVEESQGASRALSKFIDPSLTWKDIEELK
KKTCLKPIVIKGVQRTEDVIKAAEIGVSGVLSNHGGRQLDFSRAPIEVLAETMPILEQRNL
KDKLEVFVDGGVRRGTDVLKALCLGAKGVGLGRPFLYANSCYGRNGVEKAIEILRDEIE
MSMRLLGVTSIAELKPDLLDLSTLKARTVGVNDVLYNEVYEGPTLTFEFDA

>d1h7wa2 c.1.4.1 (A:533-844) Dihydropyrimidine dehydrogenase, domain 4 {Pig (*Sus scrofa*)}

ISVEMAGLKFIPFGLASAAPTSSSMIRRAFEAGWGFALTCTFSLDKDIVTNVSPRIVRGT
TSGPMYGPQGSSFLNIELISEKTAAYWCQSVTELKADFPDNIVIASIMCSYNKNDWMELSR
KAEASGADALELNLSCPHGMGERGMGLACGQDPELVNRNICRWVRQAVQIPFFAKLTPNV
TDIVSIARAAGEGADGVTATNTVSGLMGLKADGTPWPAVGAGKRTTYGGVSGTAIRPIA
LRAVTTIARALPGFPILATGGIDSAESGLQLHSGASVLQVCSAVQNQDFTVIQDYCTGLKA
LLYLKSIE

>d1ea0a2 c.1.4.1 (A:423-1193) Alpha subunit of glutamate synthase, central and FMN domains {*Azospirillum brasilense*}

TTHLDELVKTASLKGEPSDMDKAELRRRQQAFLTMEDMELILHPMVEDGKEAIGSMGD
DSPIAVLSDKYRGLHHFFRQNFQVTNPPIDSLRERRVMSLKTRLGNLGNILDEDETQTRL
LQLESPVLTTAEFRAMRDYMGDTAAEIDATFPVDGGPEALRDALRRIRQETEDAVRGGAT
HVILTDEAMGPAAAAIPAILATGAVHHLIRSNLRTFTSLNVRTAEGLDTHYFAVLIGVGATT
VNAYLAQEAIAERHRRGLFGSMPLKGMANYKKAIDDGLLKIMSKMGISVISSYRGGGNF
EAIGLSRALVAEHFPAMVSRISGIGLNGIQKKVLEQHATAYNEEVVALPVGGFYRFRKSGD
RHGWEGGVIHTLQQAVTNDSTYTFKKYSEQVNKRPPMQLRDLELRSTKAPVPVDEVESI
TAIRKRFITPGMSMGALSPEAHGTLNVAMNRIGAKSDSGEGGEDPARFRPDKNGDNWNS
AIKQVASGRFGVTAEYLNQCRELEIKVAQGAKPGEGGQLPGFKVTEMIARLRHSTPGVML
ISPPPHHDIYSIEDLAQLIYDLKQINPDAAKVTVKLVSRSGIGTIAAGVAKANADIILISGNSGG
TGASPQTSIKFAGLPWEMGLSEVHQVLTNLRLRHRVRLRTDGGLKTGRDIVIAAMLGAEE
FGIGTASLIAMGCIMVRQCHSNTCPVGVCVQDDKLRQKFVGTPEKVVNLFTFLAEEVREI
LAGLGFRSLNEVIGRTDLLHQVSRGAEHLDDLNLNRLAQVDPG

>d1eepa_ c.1.5.1 (A:) Inosine monophosphate dehydrogenase (IMPDH) {Lyme disease spirochete (*Borrelia burgdorferi*)}

NKITKEALTFDDVSLIPRKSSVLPSEVSLKTQLTKNISLNIPFLSSAMDTVTESQMAIAIAKE
GGIGIIHKNMISIEAQRKEIEKVKTYKFQKTINTNGDTNEQKPEIFTAKQHLEKSDAYKNAE
HKEDFPNACKDLNNKLRVGAASIDIDTIERVEELVKAHVDILVIDSAHGHSTRIELIKKIK
TKYPNLDLIAGNIVTKEAALDLISVGADCLKVGIGPGSICTTRIVAGVGVQPITAICDVYEA
CNNTNICIIADGGIRFSGDVVKAIAAGADSVMIGNLFAGTKESPSEIIYNGKKFKSYVGM
GSISAMKRGSKSRYFQLENNEPKKLVPPEGIEGMVPYSGKLKDILTQLKGGLMSGMGYLGA
ATISDLKINSKFVKISHS

>d1ak5_1 c.1.5.1 (2-101,222-483) Inosine monophosphate dehydrogenase (IMPDH) {*Tritrichomonas foetus*}

AKYYNEPCHTFNEYLLIPGLSTVDCIPSNVNLSTPLVKFQKGQQSEINLKIPLVSAIMQSVS
GEKMAIALAREGGISFIFGSQSIESTAAMVHAVKNFKAXHNELVDSQKRYLVGAGINTRDF

RERVPALVEAGADVLCIDSSDGFSEWQKITIGWIREKYGDKVKVGAGNIVDGEGFRYLAD
AGADFIKIGIGGGSICITREQKGIGRGQATAVIDVVAERNKYFEETGIYIPVCSDGGIVYDYH
MTLALAMGADFIMLGRYFARFEESPTRKVTINGSVMKEYWGEGSSRARNWQRYDLGGK
QKLSFEEGVDSYVPYAGKLKDNVEASLNKVKSTMCNCGALTIPQLQSKAKITLVSSVSI

>d1jr1a1 c.1.5.1 (A:17-112,A:233-514) Inosine monophosphate dehydrogenase
(IMPDH) {Chinese hamster (*Cricetulus griseus*)}

GLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSAITKKITLKTPLVSSPMDTVTEAG
MAIAMALTGGIGFIHNCCTPEFQANEVRKVKKYEQXYPLASKDAKKQLLCGAAIGTHED
DKYRLDLLALAGVDVVLDSSQGNSIFQINMIKYMKEKYPNLQVIGGNVVTAAQAKNLI
DAGVDALRVGMGCGSICITQEV LACGRPQATAVYKVSEYARRFGVPVIADGGIQNVGHIA
KALALGASTVMMGSLAATTEAPGEYFFSDGIRLKKYRGMGSLDAMDKHLSSQNRYFSE
ADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVRAMMYSGELKFEKR
TSSAQVEGGVHSLHSYEKRLF

>d1bd0a2 c.1.6.1 (A:12-244) Alanine racemase {*Bacillus*
stearothermophilus}

VDLDAIYDNVENLRLLPDDTHIMAVVKANAYGHGDVQVARTALEAGASRLAVAFLDEA
LALREKGIEAPILVLGASRPADAALAAQQRIALTVFRSDWLEEASALYSGPFIHFLKMDT
GMGR LGVKDEEETKRIVALIERHPHFVLEGLYTHFATADEVNTDYFSYQYTRFLHMLEWL
PSRPPLVHCANSAASLRFPDRTFNMVRFGIAMYGLAPSPGIKPLLPYPLKEA

>d1d7ka2 c.1.6.1 (A:44-283) Eukaryotic ornithine decarboxylase {Human (*Homo sapiens*)}

DLGDILKKHLRWLKA LPRVTPFYAVKCND SKAIVKTLAATGTGFD CASKTEIQLVQSLGVP
PERIIYANPCKQVSQIKYAANNGVQMMTFDSEVELMKVARAHPKAKLVLR IATDDSKAVC
RLSVKFGATLRTSRLLLERAKELNIDVVGVSFHV GSGCTDPETFVQAISDARCVFDMGAE
VGFSMYLLDIGGGFPGSE DVKLK FEEITGVINPALDKYFPSDSGVRIIAEPGRYYYVASA

>d1exba_ c.1.7.1 (A:) Voltage-dependent K⁺ channel beta subunit {Rat (*Rattus norvegicus*)}

LQFYRN LGKSGLRV SCLGLGTWVTFGGQITDEMAEHLMTLAYDNGINLFD TAEVYAAGK
AEVVLGNIKKKGWRRSSLVITTKIFWGGKAETERGLSRKHIEGLKASLERLQLEYVDVV
FANRPDPNTPMEETVRAMTHVINQGMAMYWGTSRWSSMEIMEAYSVARQFNLI PPICEQ
AEYHMFQREKVEVQLPEL FHKIGVGAMTWSPLACGIVSGKYDSGIPPYSRASLKG YQWL
KDKILSEEGR RQQA KLKELQAIAERLGCTLPQLAIAWCLRN EGVSSVLLGASNAEQLMEN
IGAIQVLPKLSSSIVHEIDSILGNKPYS

>d2alr_ c.1.7.1 (-) Aldose reductase (aldehyde reductase) {Human (*Homo sapiens*)}

AASCVLLHTGQKMPLIGLGTWKSEPGQVKA AVKYALSVGYRHIDCAA IYGNEPEIGEALK
EDVGPGKAVPREELFVTSKLWNTKHHPEDVEPALRKT LADLQLEYLDLYLMHWPYA FER
GDNPFKPNADGTICYDSTHYKETWKALEALVAKGLVQALGLSNFNSRQID DILSVASVRPA
VLQVECHPYLAQNELIAHCQARGLEV TAYSPLGSSDRAW RDPDEPVLLEEPVVLALAEKY
GRSPAQILLRWQVQRKVICIPKSITPSRILQNIKVFDF TFSPEEMKQLNALNKNWRYIVPML
TVDGKRVPRDAGHPLYPFNDPY

>d1afsa_ c.1.7.1 (A:) 3-alpha-hydroxysteroid dehydrogenase {Rat (*Rattus norvegicus*)}

MDSISLRVALNDGNFIPVLGFGTTVP EKVAKDEVIKATKIAIDNGFRHFD SAYLYEVEEEVG
QAIRSKIEDGTVKREDIFYTSKLWSTFHRPELVRTC LEKTLKSTQLDYVDLYIIHFPMALQP
GDIFFPRDEHGKLLFETVDICDTWEAMEKCKDAGLAKSIGVSNFNCRQLERILNKPGLKY
KPV CNQVECHLYLNQSKMLDYCKSKDIILVSYCTLGSSRDKTWVDQKSPVLLDDPVLC AI
AKKYKQTPALVALRYQLQRGVVPLIRSFNAKRIKELTQVFEFQLASEDMKALDGLNRNFR

YNNAKYFDDHPNHPF

>d1hw6a_ c.1.7.1 (A:) 2,5-diketo-D-gluconic acid reductase A {Corynebacterium sp.}
TVPSIVLNDGNSIPQLGYGVFKVPPADTQRAVEEAEVGYRHIDTAAIYGNEEGVGAAIAA
SGIARDDLFTTKLWNRHDGDEPAAIAEESLAKLALDQVDLYLVHWPTPAADNYVHAW
EKMIELRAAGLTRSIGVSNHLVPHLERIVAATGVVPAVNQIELHPAYQQREITDWAAAHDV
KIESWGPLGQGKYDLFGAEPVTAAAAAHGKTPAQAVLRWHLQKGFVVPKSVRRERLEE
NLDVFDLFDLTDTEIAAIDAMDP

>d1e43a2 c.1.8.1 (A:1-393) Bacterial alpha-amylase {Bacillus
amyloliquefaciens/Bacillus licheniformis chimera}
VNGTLMQYFEWYTPNDGQHWKRLQNDAEHLSDIGITAVWIPPAYKGLSQSDNGYGPYDL
YDLGEFQQKGTVRTKYGTKSELQDAIGSLHSRNVQVYGDVVLNHHKAGADATEDVTAVE
VNPANRNQETSEEYQIKAWTDFRFPGRGNTYSDFKWHWYHFDGADWDESRKISRIFKFR
GEGKAWDWEVSSSENGNYDYLMYADVDYDHPDVVAETKKWGIWYANELSLDGFRIIDAA
KHIFSFRLRDWVQAVRQATGKEMFTVAEYWQNNAGKLENYLNKTSFNQSVFDVPLHFNL
QAASSQGGGYDMRKLLNGTVVSKHPLKSVTFVDNHDTPQGSLESTVQTFWKPLAYAFI
LTRESGYPQVFGDMYGTGKGSQREIPALKHKIEPILKARKQ

>d1g94a2 c.1.8.1 (A:1-354) Bacterial alpha-amylase {Pseudoalteromonas
haloplanctis (Alteromonas haloplanctis)}
TPTTFVHLFEWNWQDVAQECEQYLGPKGYAAVQVSPNEHITGSQWWTRYQPVSYLEQS
RGGNRAQFIDMVNRCSAAGVDIYVDTLINHMAAGSGTGTAGNSFGNKSFPYISPDHFES
CTINNSDYGNDRYRVQNCGLVGLADLTASNYVQNTIAAYINDLQAIGVKGFRFDASKHV
AASDIQSLMAKVNGSPVVFQEVIDQGGGEAVGASEYLSLSTGLVTEFKYSTELGNTFRNGSLA
WLSNFGEGWGFMPSSSAVVFDNHDNQRGHGGAGNVITFEDGRLYDLANVFMLAYPYG
YPKVMSSYDFHGD TDAGGPNVPVHNNGNLECFASNWKCEHRWSYIAGGVDFRNNTAD

>d1bag_2 c.1.8.1 (1-347) Bacterial alpha-amylase {Bacillus subtilis}
LTAPSIKSGTILHAWNWSFNTLKHNMKDIHDAGYTAIQTSPINQVKEGNQGDKSMSNWWY
WLYQPTSYQIGNRYLGTEQEFKEMCAAEEYGIKVIVDAVINHTTFDYAAISNEVKSIPNW
THGNTQIKNWSRWDVTQNSLLGLYDWNTQNTQVQSYLKRFLERALNDGADGFRFDAA
KHIELPDDGSYGSQFWPNITNTSAEFQYQGILQDSASRDAAYANYMDVTASNYGHSIRSA
LKNRNLGVSNISHYASDVSAADKLVTWVESHDITYANDDEESTWMSDDDIRLGWAVIASRS
GSTPLFFSRPEGGNGVRFPKGSQIGDRGSALFEDQAITAVNRFHNV MAG

>d1gja2 c.1.8.1 (A:1-572) Maltosyltransferase {Thermotoga maritima}
MLLREINRYCKEKATGKRIYAVPKLWIPGFFKKFDEKSGRCFVDPYELGAEITDWILNQSR
EWDYSQPLSFLKGEKTPDWIKRSVVYGS LPRTTAAYNHKSGSGYEEENDVLGFREAGTFFK
MMLLLPFVKSLGADAIYLLPVSRMSDLFKKGDAPSPYSVKNPMELDERYHDPLLEPFKVD
EEFKAFVEACHILGIRVILDFIPRTAARDSDLIREHPDWFYWIKVEELADYTPPRAEELPFK
VPDEDELEIYNKENVKRHLKKFTLPPNLIDPQKWEKIKREEGNILELIVKEFGIITPPGFSD
LINDPQPTWDDVTFLRLYLDHPEASKRFLDPNQPPYVLYDVIKASKFPKGEPNRELWEYL
AGVIPHYQKKYGIDGARLDMGHALPKELLDLIKNVKEYDPAFVMIAEELDMEKDKASK
EAGYDVILGSSWYFAGRVEEIGKLPDIAEELVLPFLASVETPDTPRIATRYASKMKKLAPF
VTYFLPNSIPYVNTGQEIGEKQPMNLGLDTPNLRKVLSP TDEFFGKLAFDHYVLHWDS
PDRGVLNFIKKLIKVRHEFLDFVLN

>d1qhoa4 c.1.8.1 (A:1-407) Cyclodextrin glycosyltransferase {Bacillus
stearothermophilus, maltogenic alpha-amylase}

SSSASVKGDVIYQIIIDRFYDGDTTNNNPAKSYGLYDPTKSKWKMYWGGDLEGVRQKLP
YLKQLGVTTIWLSPVLDNLDTLAGTDNTGYHGYWTRDFKQIEEHFGNWTTFDTLVNDAH
QNGIKVIVDFVPNHSTPFKANDSTFAEGGALYNNGTYMGNYFDDATKGYFHHNGDISNW
DDRYEAQWKNFTDPAGFSLADLSQENGITIAQYLTDAAVQLVAHGADGLRIDAVKHFNSGF
SKSLADKLYQKKDIFLVGEWYGDDPGTANHLEKVRVANNSGVNVLDLNTVIRNVFGT
FTQTMVLDLNNMVNQGTGNEYKYKENLITFIDNHDMRSRFLSVNSNKANLHQALAFILTSRG
TPSIYYGTEQYMAGGNDPYNRGMMPAFDTTTTAFKEVSTLAGLRRNNAAIQY

>d1hx0a2 c.1.8.1 (A:1-403) Animal alpha-amylase {Pig (Sus scrofa)}

EYAPQTQSGRTSIVHLFEWRWVDIALECERYLGPKGFGGVQVSPNENIVVTNPSRPWWE
RYQPVSYKLCSTRSGNENEFDMVTRCANNVGVRIYVDAVINHMCGSGAAAGTGTTCCGSYC
NPGNREFPAVPYSAWDFNDGKCKTASGGIESYNDPYQVRDCQLVGLLDLALEKDYVRSMI
ADYLNKLIDIGVAGFRIDASKHMWPGDIKAVLDKLNLTNTNWFAGSRPFIFQEVIDLGGE
AIKSSEYFGNGRVTEFKYGAKLGTVVVRKWSGEKMSYLNWGEWGFMPSPDRALVFVDN
HDNQRGHGAGGSSILTFWDARLYKIAVGFMLAHPYGFTRVMSSYRWARNFVNGEDVND
WIGPPNNNGVIKEVTINADTTCGNDWVCEHRWREIRNMVWFRNVVDG

>d2aaa_2 c.1.8.1 (1-381) Fungal alpha-amylases {Aspergillus niger, acid amylase}

LSAASWRTQSIYFLLTDRFGRDNTTATCNTGNEIYCGGSWQGIIDHLDYIEGMGFTAIWI
SPITEQLPQDTADGEAYHGYWQQKIYDVNSNFGTADNLKSLSDALHARGMYLMVDVVP
DHMGYAGNGNDVDYSVFDPPDSSSYFHPYCLITDWDNLTMVEDCWEGDTIVSLPDLDTT
ETAVRTIWDWVADLVSNYSVDGLRIDSLEVPDFPFGYNKASGVYCVGEIDNGNPASD
CPYQKVLDGVLNYPYWQLLYAFESSSGSISNLNMIKSVASDCSDPTLLGNFIENHDNPRF
AKYTSDYSAKNVLSYIFLSDGIPIVYAGEEQHYAGGKVPYNREATWLSGYDTSAEELYTW
IATTNAIRKLAIAADSAYIT

>d1smaa3 c.1.8.1 (A:124-505) Maltogenic amylase, central domain {Thermus sp.}

DLFQAPDWVKDTVWYQIFPERFANGNPAISPKGARPWGSEDPTPTSFFGGDLQGIIDHLDY
LADLGITGIYLTPIFRAPSNHKYDTADYFEIDPHFGDKETLKTTLVKRCHEKGIRVMLDAVFN
HCGYEFAPFQDVLKNGAASRYKDWFHIREFPLQTEPRPNYDTFAFVPHMPKLNTHPEVK
RYLLDVATYWIREFDIDGWRLDVANEIDHQFWREFRQAVKALKPDVYILGEIWHDAMPW
LRGDQFDAMNYPLADAALRFFAKEDMSASEFADRLMHVLHSPYKQVNEAAFNLLGSH
DTPRLLTVCGGDVRKVKLLFLFQLTFTGSPCIYYGDEIGMTGGNDPECRKCMVWDPEKQ
NKELYEHVKQLIALRKQYRALRR

>d1eh9a3 c.1.8.1 (A:91-490) Glycosyltrehalose trehalohydrolase, central domain
{Archaeon Sulfolobus solfataricus, km1}

FNNETFLKKEDLIYEIHVGTFTEGTFEGVIRKLDYLDLGITAIEIMPIAQFPGKRDWGYD
GVYLYAVQNSYGGPEGFRKLVDEAHKKGLGVILDVVYNHVGPEGNYMVKLGPYFSQKY
KTPWGLTFNFDDAESDEVKFILENVEYWIKEYNVDFRDLAVHAIIDTSPKHILEEIIADV
VHKYNRIVIAESDLNDPRVVNPKEKCGYNIDAQWVDDFHHSIHAYLTGERQGYTDFGN
LDDIVKSYKDVVYDGKYSNFRKTHGEPVGELDGCFVVIQNHQVGNRGKGERIHK
LVDRESYKIAAALYLLSPYIPMIFMGEEYGEENPFYFFSDFSLSKLIQGVREGRKKENGQD
TDPQDESTFNASKLSWKIDEEIFSFKILIKMRKELSIA

>d1bf2_3 c.1.8.1 (163-637) Isoamylase, central domain {Pseudomonas amyloclavata}

PSTQSTGTPKTRAQKDDVIYEVHVRGFTEQDTSIPAQYRGTYYGAGLKASYLASLGVTAV
EFLPVQETQNDANDVVPNSDANQNYWGYMTENYFSPDRRYAYNKAAGGPTAEFQAMV
QAFHNAGIKVYMDVVYNHTAEGGTWTSSDPTTATIYSWRGLDNATYYELTSGNQYFYDN

TGIGANFNTYNTVAQNLIIVDSLAYWANTMGVDGFRFDLASVLGNSCLNGAYTASAPNCP
NGGYNFDAADSNVAINRILREFTVRPAAGGSGLDLFAEPWAIGGNSYQLGGFPQGWSEWN
GLFRDSLRLQAQNELGSMTIYVTQDANDFSGSSNLFQSSGRSPWNSINFIDVHDGMTLKD
VYSCNGANNSQAWPYGPSDGGTSTNYSWDQGMASAGTGAARDQRRARTGMAFEMLSAG
TPLMQGGDEYLRTLQCNNNAYNLDSSANWLTYSWTTDQSNFYTFARLIAFRKAHPALR
PSSW

>d1gcy2 c.1.8.1 (A:1-357) G4-amylase (1,4-alpha-D-glucan maltotetrahydrolase)
{*Pseudomonas stutzeri*}

DQAGKSPNAVRYHGGDEILQGFHWNVREAPNDWYNILRQQAATIAADGFSAIWMPVP
WRDFSSWSGSKSGGEGYFWHDFNKNRGYGSQAQLRQAASALGGAGVKVLYDVVPN
HMNRGYPDKEINLPAGQGFWRNDCADPGNYPNDCDDGDRFIGGDADLNTGHPQVYGMF
RDEFTNLRISQYGAGGFRFDFVRGYAPERVNSWMTDSADNSFCVWELWKGPSSEYPNWDW
RNTASWQQIIKDWSDRAKCPVDFALKERMQNGSIADWKHGLNGNPDPRWREAVTFVD
NHDTGYSPGQNGGQHWWALQDGLIRQAYAYILTSPGTPVVYWDHMYDWGYGDFIRQLIQ
VRRAGV

>d1avaa2 c.1.8.1 (A:1-346) Plant alpha-amylase {Barley (*Hordeum vulgare*), seeds, AMY2
isozyme}

QVLFQGFNWESWKHNGGWYNFLMGKVDDIAAAGITHVWLPPASQSVAEQGYMPGRLY
DLDASKYGNKAQLKSLIGALHGKGVKAIADIVINHRTAEHKDGRGIYCIFEGGTPDARLD
WGPHMICRDDRYPADGTGNPDTGADFGAAPDIDHLNLRVQKELVEWLNWLKADIGFDG
WRFDFAKGYADVAKIYIDRSEPSFAVAEIWTSLAYGGDGKPNLNQDQHRQELVNWVDK
VGGKGPATTFDFTTKGILNVAVEGELWRLRGTDGKAPGMIGWWPAKAVTFVDNHDTGST
QHMWPFPSPDRVMQGYAYILTHPGTPCIFYDHFFDWGLKEEIDRLVSVRTRHGI

>d1uok_2 c.1.8.1 (1-479) Oligo-1,6, glucosidase {*Bacillus cereus*}

MEKQWWKESVVYQIYPRSFMDNNGDGIGDLRGIISKLDYKELGIDVIWLSPVYESPNDD
NGYDISDYCKIMNEFGTMEDWDELLHEMHERNMKLMMDLVNHTSDEHNWFIESRKS
DNKYRDYIWRPGKEGKEPNWGAAFSGSAWQYDEMTDEYYLHLFSKKQPDNLWDNE
KVRQDVYEMMKFWLEKGIDGFRMDVINFISKEEGLPTVETEEGYVSGHKHFMNGPNH
KYLHEMNEEVLSHYDITVGEPMGPVTTEEAKLYTGEERKELQMVVFQFEHMDLDSGEGG
KWDVKPCSLTLKENLTKWQKALEHTGWNSLYWNNHDQPRVVSFRGNDGMYRIESAK
MLATVLHMMKGTPYIYQGEEIGMTNVRFESIDEYRDIETLNMKYKEKVMERGEDIEKVMQ
SIYIKGRDNARTPMQWDDQNHAGFTTGEPWITVNPYKEINVKQAIQNKDSIFYYYKKLI
ELRKNNEIVVY

>d1g5aa2 c.1.8.1 (A:1-554) Amylosucrase {*Neisseria polysaccharea*}

SPNSQYLKTRILDIYTPEQRAGIEKSEDWRQFSRRMDTHFPKLMNELDSVYGNNEALLPM
LEMLLAQAWQSYSQRNSSLKDIDIARENPDWILSNKQVGGVCYVDLFAAGDLKGLKDKI
PYFQELGLTYLHMLPLFKCPEGKSDGGYAVSSYRDVNPALGTIGDLREVIAALHEAGISAV
VDFIFNHTSNEHEWAQRCAAGDPLDFNYIYFPDRRMPDQYDRTLREIFPDQHPGGFSQLE
DGRWVWTTFNSFQWDLNYSNPWVFRAMAGEMFLANLGVLDILRMDAVAFIWKQMGTS
CENLPQAHALIRAFNAVMMRIAAPAVFFKSEAIVHPDQVVQYIGQDECQIGYNPLQMAALLW
NTLATREVNLLHQALTYRHNLPHTAWVNYVRSHDDIGWTFADEDAAYLGISGYDHRQF
LNRFFVNRFDGSFARGVFPQYNPSTGDCRVSGTAAALVGLAQDDPHAVDRIKLLYSIALST
GGLPLIYLGDEVGTLNDDWSQDSNKSDDSRWAHRPRYNEALYAQRNDPSTAAGQIYQD
LRHMIAVRQSNPRFDGG

>d1eswa_ c.1.8.1 (A:) Amylomaltase MalQ {Thermus aquaticus}

MELPRAFGLLLHPTSLPGPYGVGVLGREARDFLRFLKEAGGRYWQVLPLGPTGYGDS
PYQSFSFAAGNPYLIDLRPLAERGYVRLEDPGFPQGRVDYGLLYAWKWPALKEAFRGFKE
KASPEEREAFAAFREREAWWLEDYALFMALKGAHGGLPWNRWPLPLRKREEKALREAK
SALAEVAFHAFTQWLFFRQWGALKAEAEALGIRIIGDMPIFVAEDSAEVWAHPEWFHLDE
EGRPTVVAGVPPDYFSETGQRWGNPLYRWDVLEREGFSFWIRRLEKALELFLVRIDHFRG
FEAYWEIPASCPTAVEGRWVKAPGEKLFQKIQEVFGEVPVLAEDLGVITPEVEALRDRFGL
PGMKVLQFAFDDGMENPFLPHNYPAHGRVVVYTGTHDNDTTLGWYRTATPHEKAFMAR
YLADWGITFREEEEVPWALMHLGMKSVARLAVYPVQDVLALGSEARMNYPGRPSGNWA
WRLLPGELSPEHGARLRAMAEATERL

>d1b1ya_ c.1.8.2 (A:) beta-Amylase {Barley (Hordeum vulgare)}

MKGNYVQVYVMLPLDAVSNNRFEKGDELRAQLRKLVEAGVDGVMVDVWWGLVEGK
GPKAYDWSAYKQLFELVQKAGLKLQAIMSFHQCGGNVGDAVNIPIQWVRDVGTRDPDI
FYTDGHGTRNIEYLTLGVDNQPLFHGRSAVQMYADYMTSFRENMKDFLDAGVIVDIEVG
LGPAGELRYPSYPQSHGWSFPGIGEFICYDKYLQADFKAAAAAVGHPEWEFPNDAGQYN
DTPERTQFFRDNGTYLSEKGRFFLAWYSNNLIKHGDRILDEANKVFLGYKVQLAIKIAGV
HWWYKVPASHAAELTAGYYNLHDRDGYRTIARMLKRHRASINFTCAEMRDSEQPPDAMS
APEELVQQVLSAGWREGLNVSCENALPRYDPTAYNTILRNARPHGINQSGPPEHKLFGFTY
LRLSNQLVEGQNYVNFKTFVDRMHANLPRDPYVDPMAPLPRSGPEISIEMILQAAQPKIQP
FPFQEHTDLPVGPTGGMGGQAEGPTCG

>d1b9za2 c.1.8.2 (A:1-417) Bacterial beta-amylase, catalytic domain {Bacillus cereus}

AVNGKGMNPDYKAYLMAPLKKIPEVTNWETFENDLRWAKQNGFYAITVDFWWGDMEK
NGDQQDFDSYAQRFAQSVKNAGMKMPIISTHQCGGNVGDDCNVPIPSWVWNQKSDDSL
YFKSETGTVNKETLNPLASDVIRKEYGELYTAFAAAMKPYKDVIAKIYLSGGPAGELRYPS
YTTSDGTGYPSRGKFQAYTEFAKSKFRLWVLNKYGSLNEVNKAWGTKLISELAILPPSDG
EQFLMNGYLSMYGKDYLEWYQGILENHTKLIGELAHNAFDTTFQVPIGAKIAGVHWQYN
NPTIPHGAEKPAYNDYSHLLDAFKSAKLDVTFTCLEMTDKGSYPEYSMPKTLVQNIATL
ANEKGIVLNGENALSIGNEEEYKRVAEMAFNYNFAGFTLLRYQDVMYNNSLMGKFKDLL
GV

>d1xyza_ c.1.8.3 (A:) Xylanase {Clostridium thermocellum, XynZ}

NALRDYAEARGIKIGTCVNYPFYNNSDPTYNSILQREFSMVVCENEMKFDALQPRQNVFD
FSKGDQLLAFAERNQMQRGHTLIWHNQNP SWLTNGNWNRDSLLAVMKNHITVMT
H YK GK IVEWDVANECMDDSGNGLRSSIWRNVIGQDYLDYAFRYAREADPDALLFYNDYNI
EDLGPKSNAVFNMKSMKERGVPIDGVGFQCHFIGMSPEYLASIDQNIKRYAEIGVIVSFT
EIDIRIPQSEN PATAFQVQANNYKELMKICLANPNCNTFVMWGFTDKYTWIPGTFPGYGNP
LIYDSNYNPKPAYNAIKEALM

>d1hiza_ c.1.8.3 (A:) Xylanase {Bacillus stearothermophilus, Xt6}

SYAKKPHISALNAPQLDQRYKNEFTIGAAVEPYQLQNEKDVQMLKRHFNSIVAENVMKPI
SIQPEEGKFNF EQADRIVKFAKANGMDIRFHTLVWHSQVPQWFFLDKEGKPMVNETDPV
KREQNKQLLLKRLETHIKTIVERYKDDIKYWDVVNEVVGGDDGKLNRNSPWYQIAGIDYIK
VAFQAARKYGGDNKLYMNDYNTEVEPKRTALYNLVKQLKEEGVPIDGIGHQSHIQIGWP
SEAEIEKTINMFAALGLDNQITELDVSMYGWPPRAYPTYDAIPKQKFLDQAARYDRLFKL
YEKLSDKISNVTFWGIADNHTWLDSRADVYYDANGNVVVDPNAPYAKVEKGKGKDA
PFVFGPDYKVKPAYWAIDHK

>d1bg4__ c.1.8.3 (-) Xylanase {*Penicillium simplicissimum*}

EASVSIDAKFKAHGGKYLGTIGDQYTLTKNTKNPAIHKADFGQLTPENSMKWDATEPNRG
QFTFSGSDYLVNFAQSNGLIRGHTLVWHSQLPGWVSSITDKNTLISVLKNHITVVMTRYK
GKIYAWDVLNEIFNEDGSLRNSVFYNVIGEDYVRIAFETARSVDPAKLYINDYNLDSAGY
SKVNGMVSHVKKWLAAGIPIDGIGSQTHLGAGAGSAVAGALNALASAGTKEIAITELDIA
GASSTDYVNVVNACLNQAKCVGITVWGVADPDSWRSSSSPLLFDGNYNPKAAAYNAIANA
L

>d1edg__ c.1.8.3 (-) Endoglucanase CelA {*Clostridium cellulolyticum*}

MYDASLIPNLQIPQKNIPNNDGMNFVKGLRLGWNLGNTFADFNGTNITNELDYETSWSGI
KTTKQMIDAIKQKGFNTVRIPVSWHPHVSQSDYKISDVWMNRVQEVVNYCIDNKMVIL
NTHHDVDKVKGYFPSSQYMASSKKYITSVWAQIAARFANYDEHLIFEGMNEPRLVGHAN
EWWPELTNSDVVDSINCINQLNQDFVNTVRATGGKNASRYLMCPGYVASPDGATNDYFR
MPNDISGNNNKIIVSVHAYCPWNFAGLAMADGGTNAWNINDSKDQSEVTWFMNDIYNK
YTSRGIPVIIGECGAVDKNNLKTREYMSYYVAQAKARGILCILWDNNNFSGTGELFGFFD
RRSCQKFPEIIDGMVKYAFGLIN

>d1ceo__ c.1.8.3 (-) Endoglucanase CelC {*Clostridium thermocellum*}

MVSFKAGINLGGWISQYQVFSKEHFDTFITEKDIETIAEAGFDHVRLPFDYPIIESDDNVGE
YKEDGLSYIDRCLEWCKKYNLGLVLDMMHAPGYRFQDFKTSTLFEDPNQKRFVDIWRFL
LAKRYINEREHIAFELLNQVVEPDSTRWNKLMLECIKAIREIDSTMWLYIGGNNYNPDEL
KNLADIDDDYIVYNFHFYNPFFFTHQKAHWSESAMAYNRTVKYPGQYEGIEEFVKNNPK
YSFMMELNNLKNKELLRKDLKPAIEFREKKKCKLYCGEFGVIAIADLESRIKWHEHYISL
LEEYDIGGAVWNYKKMDFEIYNEDRKPVSQELVNILAR

>d1cz1a__ c.1.8.3 (A:) Exo-beta-(1,3)-glucanase {*Yeast (Candida albicans)*}

AWDYDNNVIRGVNLGGWFVLEPYMTPSLFEPFQNGNDQSGVPVDEYHWTQTLGKEAAL
RILQKHWSTWITEQDFKQISNLGLNFVRIPIGYWAFQLLDNDPYVQGQVQYLEKALGWAR
KNNIRVWIDLHGAPGSQNGFDNSGLRDSYNFQNGDNTQVTLNVLNTIFKKYGGNEYS
VIGIELLNEPLGPVLNMDKLKQFFLDGYNSLRQTGSVTPVIIHDAFQVFGYWNNFLTVAEG
QWNVVVDHHHYQVFSGGELSRNINDHISVACNWGWDAKKESHWNVAGEWSAALTDCA
KWLNGVNRGARYEGAYDNAPYIGSCQPLLDISQWSDEHKTDTRRYIEAQLDAFEYTGGW
VFWSWKTENAPEWSFQTLTYNGLFPQPVTDRQFPNQCGFH

>d1ceca__ c.1.8.3 (A:) Endocellulase E1 {*Acidothermus cellulolyticus*}

AGGGYWHTSGREILDANNVPVRIAGINWFGFETCNVYVHGLWSRDYRSMLDQIKSLGYN
TIRLPYSDDILKPGTMPNSINFYQMNQDLQGLTSLQVMDKIVAYAGQIGLRILDRHRPDCS
GQSALWYTSSVSEATWISDLQALAQRYKGNPTVVGFDLHNEPHDPACWGCGDPSIDWRL
AAERAGNAVLNVNPNLLIFVEGVQSYNGDSYWWGGNLQGAGQYPVVLNVPNRLVYSAH
DYATSVYPQTWFSDFPNNMPGIWNKNWGYLFNQNIAPVWLGEFGTTLQSTTDQTWLK
TLVQYLRPTAQYGADSFQWTFWSWNPDSGDTGGILKDDWQTVDTVKDGYLAPIKSSIFD
PV

>d7a3ha__ c.1.8.3 (A:) Endoglucanase Cel5a {*Bacillus agaradhaerens*}

SVVEEHGQLSISNGELVNERGEQVQLKGMSSHGLQWYGQFVNYESMKWLRDDWGINVF
RAAMYTSSGGYIDDPVKEKVKEAVEAAIDLDIYVIIDWHILSDNDPNYKKEAKDFDEM
SELYGDYPNVIYEIANEPNGSDVTWGNQIKPYAEEVPIIRNNDPNNIIIVGTGTWSQDVHH
AADNQLADPNVMYAFHFYAGTHGQNLRDQVDYALDQGAAIFVSEWGTSATGDGGVFL
DEAQVWIDFMDERNLSWANWSLTHKDESSAALMPGANPTGGWTEAELSPSGTFVREKIR

ES

>d1g0ca_ c.1.8.3 (A:) Alkaline cellulase K catalytic domain {Bacillus sp.}

PAGMQAVKSPSEAGALQLVELNGQLTLAGEDGTPVQLRGMSTHGLQWFGEIVNENAFVA
LSNDWGSNMIRLAMYIGENGYATNPEVKDLVYEGIELAFEHDMYVIVDWHVHAPGDPRA
DVYSGAYDFFEEIADHYKDHPKNHYIHWELANESPNNNGGPGLTNDEKGWEAVKEYAEP
IVEMLREKGDNMILVGNPNWSQRPDLSDNPIDAENIMYSVHFYTGSHGASHIGYPEGTP
SSERSNVMANVRYALDNGVAVFATEWGTSQANGDGGPYFDEADVWLNFLNKHNISSWAN
WSLTNKNEISGAFTPFELGRTDATDLDPGANQVWAPEELSLSGEYVRARIKGIEYTPIDRTK

>d1bqca_ c.1.8.3 (A:) Beta-mannanase {Thermomonospora fusca}

ATGLHVKNRGLYEANGQEFIRGVSHPHNWYPQHTQAFADIKSHGANTVRVVLNSNGVRW
SKNGPSDVANVISLCKQNRLLICMLEVHDTTGYGEQSGASTLDQAVDYWIELKSVLQGEED
YVLINIGNEPYGND SATVAAWATDTSAAIQRRLRAAGFEHTLVVDAPNWGQDWTNTMRNN
ADQVYASDPTGNTVFSIHMYGVYSQASTITSYLEHFVNAGLPLIIGEFHGDHSDGNPDEDT
IMAEAERLKLGYIGWSWSGNGGGVEYLDMVYNFDGDNLSPWGERIFYGPNGIASTAKEA
VIFG

>d1qnra_ c.1.8.3 (A:) Beta-mannanase {Trichoderma reesei}

ASSFVTISGTQFNIDGKVG YFAGTNCYWCSFLT NHADVDSTFSHISSSGLKVVRVWGFND
VNTQPSPGQIWFQKLSATGSTINTGADGLQTLDYVVQSAEQHNLKLIIPFVNNWSDYGGI
NAYVNAFGGNATTWYTNTAAQTQYRK YVQAVVSRYANSTAIFAWELGNEPRCNGCSTDV
IVQWATSVS QYVKSLDSNHLVTLGDEGLGLSTGDGAYPYTYGEGTDFAKNVQIKSLDFGT
FHLYPDSWGTNYTWGNGWIQTHAAACLAAGKPCVFEEYGAQQNPCTNEAPWQTTSLTT
RGMGGDMFWQWGDTFANGAQSNSDPYTVWYNSSNWQCLVKNHVDAIN

>d1j9ya_ c.1.8.3 (A:) Mannanase 26A {Pseudomonas fluorescens, subsp. cellulosa}

PVTVKLVDSQATMETRSLFAFMQEQR RH SIMFGHQHETTQGLTITRTDGTQSDTFNAVGD
FAAVYGWDTLSIVAPKAEGDIVAQVKKAYARGGIITVSSHFDNPKTDTQKGVWPVGTSWD
QTPAVVDSLPGGAYNPVLNGYLDQVAEWANNLKDEQGRLIPVIFRLYHENTGSWFWWGD
KQSTPEQYKQLFRYSVEYLRDVKGV RNFLYAYSPNNFWDVTEANYLERYPGDEWVDVL
GFDTYGPVADNADWFRNVVANAALVARMAEARGKIPVISEIGIRAPDIEAGLYDNQWYRK
LISGLKADPDAREIAFLLVWRNAPQGVPGPNGTQVPHYWVPANRPENINNGTLED FQAFY
ADEFTAFNRDIEQVYQRPT

>d1ghsa_ c.1.8.3 (A:) Plant beta-glucanases {Barley (Hordeum vulgare), 1,3-beta-glucanase}

IGVCYGVIGNNLPSRSDVVQLYRSK GINGMRIYFADGQALSALRNSGIGLILDIGNDQLANI
AASTSNAASWVQNNVRPYYP AVNIKYIAAGNEVQGGATQSILPAMRNLNAALSAAGLGAI
KVSTSIRFDEVANSFPPSAGVFKNAYMTDVARLLASTGAPLLANVYPYFAYRDNPGSISLN
YATFQP GTTVRDQNNGLTYTSLFDAMVDAVYAALEKAGAPAVKV VVSES GWPSAGGFAA
SAGNARTYNQGLINHVG GGT PKKREALETYIFAMFNENQKTGDATERSFGLFNPDKSPAY
NIQF

>d1jz8a5 c.1.8.3 (A:334-625) beta-Galactosidase, domain 3 {Escherichia coli}

EVRIENGLLLLNGKPLLIRGVNRHEHHPLHGQVMDEQTMVQDILLMKQNNFNAVRC SHY
PNHPLWYTLCDRYGLYVVDEANIETHGMVPMNRLTDDPRWLPAMSERVTRMVQRDRNH
PSVIIWSLGNESGHGANHDALYRWIKSVDPSPRPVQYEGGGADTTATDIIICPMYARVDEDQP
FPAVPKWSIKKWLSLPGETRPLILCQYAHAMGNSLGGFAKYWQAFRQYPRLQGGFVWD
WVDQSLIKYDENGNPWSAYGGDFGDTPNDRQFCMNGLVFADRTPHPALTEAKHQQQ

>d1bhga3 c.1.8.3 (A:329-632) beta-Glucuronidase, domain 3 {Human (Homo sapiens)}

VAVTKSQFLINGKPFYFHGVNKHEDADIRGKGFDWPLLKDFNLLRWLGANAFRTSHYPY
AEEVMQMCDRYGIVVIDECPGVGLALPQFFNNVSLHHHMQVMEEVVRDKNHPAVVM
WSVANEPASHLESAGYYLKMVIAHTKSLDPSRPVTFVSNSNYAADKGAPYVDVICLSYY
SWYHDYGHLELIQLQLATQFENWYKKYQKPIIQSEYGAETIAGFHQDPPLMFTEEYQKSL
LEQYHLGLDQKRRKYVVGELIWNFADFMTEQSPTRVLGNKKGIFTRQRQPKSAAFLLRER
YWKIANE

>d1clxa_ c.1.8.3 (A:) Xylanase A, catalytic core {Pseudomonas fluorescens}
GLASLADFPIGVAVAASGGNADIFTSSARQNIVRAEFNQITAENIMKMSYMYSGSNFSFTNS
DRLVSWAAQNGQTVHGHALVWHPYQLPNWASDSNANFRQDFARHIDTVAAHFAGQVK
SWDVVNEALFDSADDPDGRGSANGYRQSVFYRQFGGPEYIDEAFRRARAADPTAELYYN
DFNTEENGAKTTALVNLVQRLLNNGVPIDGVGFQMHVMNDYPSIANIRQAMQKIVALSP
LKKITELDVRLNNPYDGNSSNDYTNRNDCAVSCAGLDRQKARYKEIVQAYLEVVPGR
GGITVWGIADPDSWLYTHQNLPDWPLLFNDNLQPKPAYQGVVEALS

>d1e4mm_ c.1.8.4 (M:) Plant beta-glucosidase (myrosinase) {White mustard (Sinapis alba)}
EITCQENLPFTCGNTDALNSSSFSSDFIFGVASSAYQIEGTIGRGLNIWDGFTHRYPNKSGPD
HGNGDTTCDSFSYWQKDIDVLDELNATGYRFSIAWSRIIPRGKRSRGVNEKGIDYYHGLIS
GLIKKGITPFVTLFHWDLPQTLQDEYEGFLDPQIIDDFKDYADLCFEFGDSVKYWLINQ
LYSVPTRGYGSALDAPGRCSPTVDPSCYAGNSSTEPYVAHHQLLAHAKVVDLYRKNYTH
QGGKIGPTMITRWFLPYNDTDRHSIAATERMKEFFLGWFMGPLTNGTYPQIMIDTVGERLP
SFSPEESNLVKGSYDFLGLNYYFTQYAQSPNPVNSTNHTAMMDAGAKLTYINASGHYIG
PLFEKDKADSTDNIYYYPKGIYSVMDYFKNKYNPLIYVTENGISTPGDENRNQSMIDYT
RIDYLCSHLCFLNKVIEKDVNVKGYLAWALGDNYEFNKGFTVRFGLSYIDWNNVTDRD
LKKSGQWYQSFISP

>d1pbga_ c.1.8.4 (A:) 6-phospho-beta-D-galactosidase, PGAL {Lactococcus lactis}
MTKTLPKDFIFGGATAAYQAEGATHTDGKGPVAWDKYLEDNYWYTAEPASDFYHKYPVD
LELAEEYGVNGIRISIAWSRIIPTGYGEVNEKGVEFYHKLFAECHKRHVEPFVTLHHFDT
EALHSNGDFLNRENIEHFIDYAAFCFEFPEVNYWTTFNEIGPIGDGQYLVGKFPPGIKYDL
AKVFQSHHNMVSHARAVKLYKDKGYKGEIGVVHALPTKYPDPENPADVRAAELEDII
HNKFILDATYLGHYSDKTMEGVNHILAENGELDLRDEDFQALDAAKDLNDFLGINYIM
SDWMQAFDGETEIIHNGKGEKSSKYQIKGVGRRVAPDYVPRTDWDWIIYPEGLYDQIMR
VKNDYPNYKKIYITENGLGYKDEFVDNTVYDDGRIDYVKQHLEVLSDAIADGANVKGYF
IWSLMDVFSWSNGYEKRYGLFYVDFDTQERYPKKSAHWYKKLAETQVIE

>d1qoxa_ c.1.8.4 (A:) Beta-glucosidase A {Bacillus circulans, subsp. alkalophilus}
SIHMFPSDFKWGVATAAYQIEGAYNEDGRGMSIWDTFHTPGKVKNGDNGNVACDSYHR
VEEDVQLKDLGVKVYRFSISWPRVLPQGTGEVNRAGLDYYHRLVDELLANGIEPFCTLY
HWDLPQALQDQGGWGSRTIDAFAYELMFELGGGIKQWITFNEPWCMAFLSNYLG
HAPGNKDLQLAIDVSHLLVAHGRAVTLFRELGISGEIGIAPNTSWAVPYRRTKEDMEACL
RVNGWSGDWYLDPIYFGEYPKFMDWYENLGYKPPIVDGDMELIHQPIDFIGINYTSSM
NRYNPGEAGGMLSSEAISMGAPKTDIGWEIYAEGLYDLLRYTADKYGNPTLYITENGACY
NDGLSLDGRIHDQRRIDYLAHMLIQASRAIEDGINLKGMEWSLMDNFEWAEGYGMRF
LVHVDYDTLVRTPKDSFYWYKGVISRGWLDL

>d1gowa_ c.1.8.4 (A:) beta-Glycosidase {Archaeon Sulfolobus solfataricus}
MYSFPNSFRFGWSQAGFQSEMGTGSEDNPNTDQYKQVHDPENMAAGLVSGDLPENGP
YWGNYKTFHDNAQKMGLKIARLNSEWSRQFPNPLPRPQNFDQVTEVEINENELKR

LDEYANKDALNHYREIFKDLKSRGLYFIQNMYHWPLPLWLHDPIRVRRGDFTPSGWLST
RTVYEFARFSAYTAWKFDDLVDYSTMNEPNVVGGLGYVGKSGFPPGYLSFELSRRAM
YNIIQAHARAYDGIKSVSKKPVGIIYANSSSQPLTDKDM EAVEMAENDNRWWFFDAIRGE
ITRGNEKIVRDDLKGRDLWIGVNYITRTVVKRTEKGYVSLGGYGHGCERNVSLAGLPT
SDFGWEFFPEGLYDVLTKYWNRYHLYMYVTENGIADDADYQRPYYLVSHVYQVHRAINS
GADVRYGLHWSLADNYEWASGFSMRFGLLKVDYNTKRLYWRPSALVYREIATNGAITDE
IEHLNSVPPVKPLRH

>d1nar__ c.1.8.5 (-) Seed storage protein {*Vicia narbonensis*, Narbonin}

PKPIFREYIGVKPNSTTLHDFPTEINTETLEFHYILGFAIESYYESGKGTGTFEESWDVELFG
PEKVKNLKRHPVVKVVISIGGRGVNTPFDPAEENVVWSNAKESLKLIIQKYSDDSGNLID
GIDIHYEHIRSDEPFATLMGQLITELKKDDDLNINVVSIAPSENNSSHYQKLYNAKKDYINW
VDYQFSNQKPVSTDDAFVEIFKSLEKDYHPHKVLPGFSTDPLDTKHNKITRDIFIGGCTR
LVQTFSLPGVFFWNANDSVIPKRDGDKPFIVELTLQQLAA

>d1cnv__ c.1.8.5 (-) Seed storage protein {Jack bean (*Canavalia ensiformis*), Concanavalin B}

DISSTEIAVYWGQREDGLLRDTCKTNKYKIVFISFLDKFGCEIRKPELELEGVCGPSVGNPC
SFLESQIKECQRMGVKVFLALGGPKGTYSACSADYAKDLAEYLHTYFLSERREGPLGKVA
LDGIHFDIQKPVDELNWDNLLEELYQIKDVYQSTFLLSAAPGCLSPDEYLDNAIQTRHFDY
IFVRFYNDRSCQYSTGNIQRIRNAWLSWTKSVYPRDKNLFLELPASQATAPGGGYIPPSALI
GQVLPYLPDLQTRYAGIALWNRQADKETGYSTNIIRYL

>d2ebn__ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {*Flavobacterium meningosepticum*, endoglycosidase F1}

TTKANIKLFSFTEVNDTNPLNNLNLFTLKNKGKPLVDMVVLFSANINYDAANDKV FVSNNP
NVQHLLTNRAKYLKPLQDKGIKVILSGNHDRSGIANLSTARAKAFAQELKNTCDLYNLD
GVFFDDEYSAYQTPPPSGFVTPSNNAARLAYETKQAMPNKLVTVYVYSRTSSFTAVDG
VNAGSYVDYAIHDYGGSYDLATNYPGLAKSGMVMSSQEFNQGRYATAQALRNIVTKGYG
GHMIFAMDPNRSNFTSGQLPALKLIKELYGDELVYSNTPYSKDW

>d1eoka__ c.1.8.5 (A:) Endo-beta-N-acetylglucosaminidase {*Flavobacterium meningosepticum*, endoglycosidase F3}

NGVCIAYYITDGRNPTFKLKDIPDKVDMVILFGLKYWSLQDTTKLPGGTGMMGSFKSYK
DLDTQIRSLQSRGIKVLQNIDDDVSWQSSKPGGFASAAAYGDAIKSIVIDKWKL DGISLDIE
HSGAKPNPIPTFGYAATGYNGWYSGSMAATPAFLNVISELTKYFGTTAPNNKQLQIASGI
DVYAWNKIMENFRNNFNYYIQLQSYGANVSRTQLMMNYATGTNKIPASKMVFGAYAEGGT
NQANDVEVAKWTPTQGAKGGMMIYTYNSNVSYANAVRDAVK

>d1edt__ c.1.8.5 (-) Endo-beta-N-acetylglucosaminidase {*Streptomyces plicatus*, endoglycosidase H}

KQGPTSVAYVEVNNNSMLNVGKYTLADGGGNAFDVAVIFAANINYDTGTKTAYLHFEN
VQRVLDNAV TQIRPLQQGQIKVLLSVLGNHQGAGFANFPSQQAASAFQKLSDAVAKYGL
DGVDFFDEYAEYGNNGTAQPNSSFFVHLVTALRANMPDKIISLYNIGPAASRLSYGGVDV
SDKFDYAWNPPYYGTWQVPGIALPKAQLSPA AVEIGRTSRSTVADLARRTVDEGYGVYLT
NLDGGDRTADVSAFTRELYGSEAVRT

>d1edqa2 c.1.8.5 (A:133-443,A:517-563) Chitinase A, catalytic domain {*Serratia marcescens*}

TDGSHLAPLKEPLLEKNKPYKQNSGKVVGSYFVEWGVYGRNFTVDKIPAQNLTHLLYGFI
PICGGNGINDSLKEIEGSFQALQRSCQGREDFKVSIHDPFAALQKAQKGVTA WDDPYKGN
FGQLMALKQAHPDLKILPSIGGWTLSDPFFFFMGDKVKRDRFVGSVKEFLQ TWKFFDGVDI

DWEFPGGKGANPNLGSPQDGETYVLLMKELRAMLDQLSVETGRKYELTS AISAGKDKID
KVAYNVAQNSMDHIFLMSYDFYGAFDLKNLGHQTALNAPAWKPD TAYTTVNGVNALLA
QGVKPGKIVVGTAMXDARSVQAKGKYVLDKQLGGLFSWEIDADNGDILNSMNASLGNS
AGVQ

>d1goia2 c.1.8.5 (A:3-291,A:380-446) Chitinase B, catalytic domain {*Serratia marcescens*}

TRKAVIGYYFIPTNQINNYTETDTSVVPFPVSNITPAKAKQLTHINFSFLDINSNLECAWDPA
TNDAKARDVVNRLTALKAHNPSLRIMFSIGGWYYSNDLGVSHANYVNAVKTPASRAKFA
QSCVRIMKDYGFDGVNIDWEYPQAAEVDGFIAALQEIRTLLNQQTITDGRQALPYQLTIA
GAGGAFFLSRYYSKLAQIVAPLDYINLMTYDLAGPWEKVTNHQAALFGDAAGPTFYNAL
REANLGWSWEELTRAFFSPFSLTVDAAVQQHLMMEGVPSAKIVMGVPFXDDAESFKYKA
KYIKQQQLGGVMFWHLGQDNRNGDLLAALDRYFNAADYDDSQLDMGTGLRYTGVGPG

>d1d2ka1 c.1.8.5 (A:36-292,A:355-427) Chitinase 1 {Fungus (*Coccidioides immitis*)}

GGFRSVVYFVNWAIYGRGHNPQDLKADQFTHILYAFANIRPSGEVYLSDTWADTDKHYPG
DKWDEPGNNVYGCIKQMYLLKKNRNLKTLLSIGGWYTSNFKTPASTEERKKFADTS
LKLMDLGFDFGIDIDWEYPEDEKQANDFVLLKACREALDAYS AKHPNGKKFLLTASPA
GPQNYNKLKLAEMDKYLD FWNLMAYDFSGSWDKVSGHMSNVFPSTTKPESTPFSSDKA
VKDYIKAGVPANKIVLGMPLXDTVKIAGKKA EYITKNMGGMGGMWWESSDKTG NESLV
GTVVNLGGTGKLEQRENELSYPE SVYDNLKNGMPS

>d1e9la1 c.1.8.5 (A:22-266,A:337-393) Chitinase-like lectin yml, saccharide binding domain {Mouse (*Mus musculus*)}

YQLMCYYTSWAKDRPIEGSFKPGNIDPCLCTHILYAFAGMQNNEITYTHEQDLRDYEALN
GLKDKNTELKTLLAIGGWKFGPAPFSAMVSTPQNRQIFIQSVIRFLRQYNFDGLNLDWQY
PGSRGSPPKDKHLFSVLVKEMRKA FEEESVEKDIPRLLLTSTGAGIIDVIKSGYKIPELSQSL
DYIQVMTYDLHDPKDG YTGENSPLYKSPYDIGKSADLNVD SIISYWKDHGAASEKLIVGF
PAXDNVRSFKLKAQWLKDNNLGGAVVWPLDMDDFSGSFCHQRHFPLTSTLKGDLNIHSA
S

>d1qba_3 c.1.8.6 (338-780) Bacterial chitinase (beta-N-acetylhexosaminidase) {*Serratia marcescens*}

FPYRGIFLDVARNFHKKDAVLRLLDQMAAYKLNKFHFLSDDEGWRIEIPGLPEL TEVGG
QRCHDLSETTCLLPQYGGPDVYGGFFSRQDYIDIIKYA QARQIEVIPEIDMPAHARA AVV
SMEARYKKLHAAGKEQEANEFR LVDPTDTSNTTSVQFFNRQSYLNPCLDSSQRFVDK VIG
EIAQMHKEAGQPIKTWHFGGDEAKNIRLGAGYTDKAKPEPGKGIIDQGNEDKPWAKSQV
CQTMKEGKVADMEHLPSYFGQEVSKLVKAHGIDRMQAWQDGLKDAESSKAFATSRVGV
NFWDTLYWGGFDSVNDWANKGYEVVVS NPDYVYMDFPYEVNPDERGYYWGTRFS DER
KVFSFAPDNMPQNAETSVDRDGNHFN AKSDKPWPGAYGLSAQLWSETQRTDPQMEY MIF
PRALSVAERSWHRAGWEQDYRAGREYKG

>d1jaka1 c.1.8.6 (A:151-506) beta-N-acetylhexosaminidase {*Streptomyces plicatus*}

YAWRSAMLDVSRHFFGVDEVKRYIDRVARYKY NKLHLHLSDDQGWR IADSWPRLATYG
GSTEVGGGPGGYTKAEYKEIVRYAASRHLEV VPEIDMPGHTNAALASYAELNCDGVAPP
LYTGTKVGFSSLCVDKDV TYDFVDDVIGELAALTPGRYLHIGGDEAHSTPKAD FVAFMKR
VQPIVAKYGKTVVGWHQLAGAEPVEGALVQY WGLDRTGDAEKA EAEVAEAA RGTGLILS
PADRTYLD MKYTKDTPLGLSWAGYVEVQ RSYDWD PAGYLP GAPADAVRGVEAPLWTET

LSDPDQLDYMAFPRLPGVAELGWSPASTHDWDITYKVRLAAQAPYWEAAGIDFYRSPQVP
WT

>d1i0da_ c.1.9.3 (A:) Phosphotriesterase {Pseudomonas diminuta}

DRINTVRGPITISEAGFTLTHEHICGSSAGFLRAWPEFFGSRKALAEKAVRGLRRARAAGV
RTIVDVSTFDIGRDVSLAEVSRAADVHIVAATGLWFDPLSMRLRSVEELTQFFLREIQYG
IEDTGIRAGIIKVATTGKATPFQELVLKAAARASLATGVPVTTHTAASQRDGEQQAAIFESE
GLSPSRVCIGHSDDDTDDLSYLTALAARGYLIGLDHIPHSAIGLEDNASASALLGIRSWQTRA
LLIKALIDQGYMKQILVSNDFLFGFSSYVTNIMDVMDRVNPDGMAFIPLRVIPFLREKGV
QETLAGITVTNPARFLSPTLRAS

>d1bf6a_ c.1.9.3 (A:) Phosphotriesterase homology protein {Escherichia coli}

SFDPTGYTLAHEHLHIDLSGFKNNVDCRLDQYAFICQEMNDLMTRGVRNVIEMTNRYMG
RNAQFMLDVMRETGINVVACTGYQQDAFFPEHVATRSVQELAQEMVDEIEQGIDGTELK
AGIIAEIGTSEGKITPLEEKVFIAAALAHNQTGRPISTHTSFSTMGLEQLALLQAHGVDLSR
VTVGHCCLKDNLDNILKMIDLGAYVQFDTIGKNSYYPDEKRIAMLHALRDRGLLNVRML
SMDITRRSHLKANGGYGYDYLLTTFIPQLRQSGFSQADVDVMLRENPSQFFQ

>d1jcla_ c.1.10.1 (A:) Deoxyribose-phosphate aldolase DeoC {Escherichia coli}

HMTDLKASSLRALKLMDLTTLNDDDTDEKVIALCHQAKTPVGNTAAICIYPRFIPIARKTL
KEQGTPEIRIATVTNPHGNDDIDIALAETRAAIYGADEVVFPYRALMAGNEQVGF
LVKACKEACAAANVLLKVIIETGELKDEALIRKASEISIKAGADFIKTSTGKVAVNATPESA
RIMMEVIRDMGVEKTVGFKPAGGVRTAEDAQKYLAIADELFGADWADARHYRFGASSLL
ASLLKALGHG

>d1nal1_ c.1.10.1 (1:) N-acetylneuraminate lyase {Escherichia coli}

NLRGVMAALLTPFDQQQALDKASLRRLVQFNIQQGIDGLYVGGSTGEAFVQSLSEREQVL
EIVAEKGKGIKLIHVGCVTTAESQQLAASAKRYGFDAVSAVTPFYYPFSFEHCDHYRA
IIDSADGLPMVVYNIPALSGVKLTLDQINTLVTLPGVGALKQTSGLDLYQMEQIRREHPDLV
LYNGYDEIFASGLLAGADGGIGSTYNIMGWRYQGIVKALKEGDIQTAQKLQTECNKVIDL
LIKTVFRGLKTVLHYMDVSVPLCRKPFPGPVDEKYQPELKALAQQLMQ

>d1f74a_ c.1.10.1 (A:) N-acetylneuraminate lyase {Haemophilus influenzae}

MRDLKGIFSALLVSFNEGTINEKGLRQIIRHNIDKMKVDGLYVGGSTGENFMLSTEEKKE
IFRIAKDEAKDQIALIAQVGSVNLKEAVELGKYATELG YDCLSAVTPFYKFSFPEIKHYD
TIIAETGSNMIVYSIPFLTGVNMGIEQFGELYKNPKVLGVKFTAGDFYLLERLKKAYPNHLI
WAGFDEMMLPAASLGV DGAIGSTFNVNGVRARQIFELTKAGKLKEALEIQHVTNDLIEGI
LANGLYLTIKELLKLEGVDAGYCREPMTSKATAEQVAKAKDLKAKFLS

>d1dhpa_ c.1.10.1 (A:) Dihydrodipicolinate synthase {Escherichia coli}

MFTGSIVAIVTPMDEKGNVCRASLKKLIDYHVASGTS AIVSVGTTGESATLNHDEHADVV
MMTLDLADGRIPVIAGTGANATAEAI SLTQRFND SGIVGCLTVTPYYNRPSQEGLYQHFK
AIAHTDLPQILYNVPSRTGCDLLPETVGRLAKVKNIIGIKEATGNLTRVNQIKELVSDDFVLL
SGDDASALDFMQLGGHGVISVTANVAARDMAQMCKLAAEGHFAEARVINQRLMPLHNK
LFVEPNPIPVKWACKELGLVATDTLRLPMTPTDSGRETVRAALKHAGLL

>d1adoa_ c.1.10.1 (A:) Fructose-1,6-bisphosphate aldolase {Rabbit (Oryctolagus cuniculus),
muscle isozyme}

PHSHPALTPEQKKELSDIAHRIVAPGKGILAADESTGSIKRLQSIGTENTEENRRFYRQLLL
TADDRVNPCIGGVILFHETLYQKADDGRPFQVIKSKGGVVGKVDKGVVPLAGTNGETT
TQGLDGLSERCAQYKKDGADFAKWRCVLKIGEHTPSALAIMENANVLARYASICQQNGI

VPIVEPEILPDGDHDLKRCQYVTEKVLAAVYKALSDHHIYLEGTLLKPNMVTTPGHACTQK
YSHEEIAMATVTALRRTPPAVTGVTFLSGGQSEEEASINLNAINKCPLLKPWALTFSYGRA
LQASALKAWGGKKENLKAAQEEYVKRALANSLACQGKYTSSGQAGAAASESLFISNHA
Y

>d1euaa_ c.1.10.1 (A:) KDPG aldolase {Escherichia coli}

MKNWKTSAESILTTGPVVPVIVVKKLEHAVPMAKALVAGGVRVLEVTLRTECAVDAIRAI
AKEVPEAIVGAGTVLNPQQLAEVTEAGAQAFAISPGLTEPLLKAATEGTIPLIPGISTVSELML
GMDYGLKEFKFFPAEANGGVKALQAIAGPFSQVRFCTGGISPANYRDYLA LKSVLCIGG
SWLVPADALEAGDYDRITKLAREAVEGAKL

>d1qfea_ c.1.10.1 (A:) Type I 3-dehydroquinate dehydratase {Salmonella typhi}

MKTVTVKNLIIGEGMPKIIIVSLMGRDINSVKAEALAYREATFDILEWRVDHFMDIASTQSV
LTAARVIRDAMPDIPLLFTRSAKEGGEQTITTQHLYTLNRAAIDSGLVDMIDLELFTGDAD
VKATVDYAHAHNVYVVM SNHDFHQTPSAEEMVSRLRKMQUALGADIPKIAVMPQSKHDV
LTLTATLEMQQHYADRPVITMSMAKEGVISRLAGEVFGSAATFGAVKQASAPGQIAVN DL
RSVLMILHNA

>d1f05a_ c.1.10.1 (A:) Transaldolase {Human (Homo sapiens)}

MESALDQLKQFTTVVADTGDFHAIDEYKPQDATTNPSLILAAAQMPAYQELVEEAIAYGR
KLGGSQEDQIKNAIDKLFVLFGAEILKKIPGRVSTEVDARLSFDKDAMVARARRLIELYKE
AGISKDRILIKLSSTWEGIQAGKELEEQHGIHCNMTLLFSFAQAVACAEAGVT LISPFVGRIL
DWHVANTDKKSYEPLEDPGVKS SVTKIYNYYKKFSYKTIVMGASFRNTGEIKALAGCDFLT
ISPKLLGELLQDNAKLVPVLSAKAAQASDLEKIHLD EKSFRWLHNEDQMAVEKLSDGIRK
FAADAVKLERMLTERMFN

>d1h7na_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Baker's yeast (Saccharomyces cerevisiae)}

MHTAEFLETEPTEISSVLAGGYNHPLLRQWQSERQLTKNMLIFPLFISDNPD DFEIDSLPNI
NRIGVNRLKDY LKPLVAKGLRSVILFGVPLIPGT KDPVGTAADDPAGPVIQGIKFIREYFPEL
YIICDVCLCEYTSHGHCGVLYDDGTINRERSVSRLAAVAVNYAKAGAHCVAPSD MIDGRIR
DIKRGLINANLAHKTFVLSYAAKFSGNLYGPFRDAACSAPSNGDRKCYQLPPAGRGLARR
ALERDMSEGADGIIVKPSTFYLDIMRDASEICKDLPICAYHVS GEYAMLHAAAEKGVVDL
KTIAFESHQGF L RAGARLIITYLAPEFLDWLDE

>d1b4ka_ c.1.10.3 (A:) 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase) {Pseudomonas aeruginosa}

YPYTRLRRNRDDFSRRLVRENVLTVDLILPVFVLDGVNQRESIPSM PGVERLSIDQLLIE
AEEWVALGIPALALFPVTPVEKKSLDAAEAYNPEGIAQRATRALRERFPELGIITDVALDPF
TTHGQDGILDDDGYVLNDV SIDVLVRQALSHAEAGAQQV VAPSDMMDGRIGAI REALES
GHTNVRIMAYS AKYASAYYGPFRDAVGSASNLGKG NKATYQMDPANSDEALHEVAADL
AEGADMVMVKPGMPYLDIVRRVKDEFRAPTFVYQVSGEYAMHMGAIQNGWLAESVILE
SLTAFKRAGADGILTYFAKQAAEQ LRR

>d1ggl1a_ c.1.10.4 (A:) 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase (DAHP synthase, AroG) {Escherichia coli}

DLRIKEIKELLPPVALLEKFPATENAANTVAHARKAIHKILKGND DRLLVIGPCSIHDPVAA
KEYATRLLALREELKDELEIVMRVYFEKPRTTVGWKGLINDPHMDNSFQINDGLRIARKLL
LDINDSGLPAAGEFLDMITPQYLADLMSWGAIGARTTESQVHRELASGLSCPVGFKNGTD
GTIKVAIDAINAAGAPHCFLSVTKWGHSAIVNTSGNGDCHIILRGGKEPNYS AKHVAEVKE

GLNKAGLPAQVMIDFSHANSSKQFKKQMDVCADVCCQIAGGEKAIIGVMVESHVLEGNQ
SLESGEPLAYGKSITDACIGWEDTDALLRQLANAVKARR

>d1d9ea_ c.1.10.4 (A:) 3-deoxy-D-manno-octulosonate 8-phosphate synthase (KDO8P synthase) {Escherichia coli}

MKQKVVSIGDINVANDLPFVLFGGMNVLERSDLAMRICEHYVTVTQKLGIPYVFKASFDK
ANRSSIHSYRGPGLLEGMKIFQELKQTFGVKIITDVHEPSQAQPVADVVDVIQLPAFLARQ
TDLVEAMAKTGAVINVKKPQFVSPGQMGNIVDKFKEGGNEKVILCDRGANFGYDNLVVD
MLGFSIMKKVSGNSPVIFDVTHALQCRDPFGAASGGRRRAQVAELARAGMAVGLAGLFIE
AHPDPEHAKCDGPSALPLAKLEPFLKQMKAIDDLKVGFEELDTSK

>d1ec7a1 c.1.11.2 (A:138-446) D-glucarate dehydratase {Escherichia coli}

DGQQRSEVEMLGYLFFVGNRKATPLPYQSQPDDSCDWYRLRHEEAMTPDAVVRLAEAA
YEKYGFNDFKLKGGVLAGEEEEAESIVALAQRFPPQARITLDPNGAWSLNEAIKIGKYLKGS
AYAEDPCGAEQGFSGREVMAEFRRATGLPTATNMIATDWRQMGHTLSLSQSVDIPLADPHF
WTMQGSVRVAQMCHIEFGLTWGSHSNNHFDISLAMFTHVAAAAPGKITAIDTHWIWQEGN
QRLTKEPFEIKGGLVQVPEKPGLGVEIDMDQVMKAHELYQKHGLGARD DAMGMQYLIPG
WTFDNKRPCMVR

>d1fhua1 c.1.11.2 (A:100-320) O-succinylbenzoate synthase {Escherichia coli}

QAANYRAAPLCNGDPDDLILKLADMPGEKVAKVKVGLYEAVRDGMVNNLLEAIPDLHL
RLDANRAWTPKGGQFAKYVNPDYRDRIAFLEEPCKTRDDSRFAFRETGIAIAWDESLRE
PDFAFVAEEGVRAVVIKPTLTGSLEKVVREQVQAAHALGLTAVISSSISSLGLTQLARIAAWL
TPDTIPGLDLDLMQAQQVRRWPGSTLPVVEVDALERLL

>d2mnr_1 c.1.11.2 (133-359) Mandelate racemase {Pseudomonas putida}

PVQAYDSHSLDGVKLATERAVTAAELGFRVKTIGYPALDQDLAVVRSIRQAVGDDFGI
MVDYNQSLDVPAAIKRSQALQQEGVTWIEEPTLQHDYEGHQRIQSKLNPVQMGENWL
GPEEMFKALSIGACRLAMPDAMKIGGVTGWIRASALAQQFGIPMSSHLFQEISAHLLAATP
TAHWLERLDLAGSVIEPTLTFEGGNAVIPDLPGVGIIWREKEIGKYL

>d2chr_1 c.1.11.2 (127-370) Chlormuconate cycloisomerase {Alcaligenes eutrophus}

PLRSAPIAWTLASGDTKRDLDSAVEMIERRRHNRFKVKLGFRSPQDDLIHMEALSNSLGS
KAYLRVDVNQAWDEQVASVYIPELEALGVELIEQPVGRENTQALRRLSNNRVAIMADES
LSTLASAFDLARDRSVDVFLKLCNMGGVSATQKIAAAEASGSIYGGTMLDSTIGTSVA
LQLYSTVPSLPGFCELGPFVLADTLSHEPLEIRDYELQVPTGVGHGMLTDEDKVRQYARV
S

>d1jpdx1 c.1.11.2 (X:114-321) L-Ala-D/L-Glu epimerase {Escherichia coli}

TLPETVITAQTVVIGTPDQMANSASTLWQAGAKLLKVKLDNHLISERMVAIRTAVPDATLI
VDANESWRAEGLAARCQLLADLGVAMLEQPLPAQDDAALENFIHPLPICADESCHTRSNL
KALKGRYEMVNIKLDKTGGLTEALALATEARAQGFSMLGCMMLCTSRASAAALPLVPQVS
FADLDGPTWLAVDVEPALQFTTGELHL

>d1jpmal c.1.11.2 (A:126-359) L-Ala-D/L-Glu epimerase {Bacillus subtilis}

YRDTLETDTVSVNSPEEMAADAENYLKQGFQTLKIKVGKDDIATDIARIQEIRKRVGSAV
KLRLDANQGWRPKEAVTAIRKMEDAGLIELVEQPVHKDDLGLKKVTDATDTPIMADE
SVFTPRQAFEVLQTRSADLINIKLMKAGGISGAEKINAMAEACGVECMVGSMIETKLGITA
AAHFAASKRNITRFDAPLMLKTDVFNGGITYSGSTISMPGKPGGLGIIGAAL

>d1kczal c.1.11.2 (A:161-413) beta-Methylaspartase {Clostridium tetanomorphum}

GAEINAVPVFAQSGDDRYDNVDKMIIEADVLPHALINNVEEKLGLKGEKLLEYVKWLR
DRIIKLRVREDYAPIFHIDVYGTIGAAFDVDIKAMADYIQTAEAAKPFHLRIEGPMDVEDR
QKQMEAMRDLRAELDGRGVDAELVADEWCNTVEDVKFFTDNKAGHVMVQIKTPDLGGV
NNIADAIMYCKANGMGAYCGGTCNETNRSAEVTTNIGMACGARQVLAKPGMGVDEGM
MIVKNEMNRVLALVGRRK

>d1dqua_ c.1.12.6 (A:) Isocitrate lyase {*Aspergillus nidulans*}

SYIEEDQRYWDEVA AVKNWWKDSRWRYTKRPFTAEQIVAKRGNLKIEYPSNVQAKKLW
GILERNFKNKEASFTYGCLDPTMVTQMAKYLDTVYVSGWQSSSTASSTDEPSPDLADYP
MNTVPNKVNHLWMAQLFHDRKQREERMTPKDQRHKVANVDYLRPIIADADTGHGGLT
AVMKLTCLFVERGAAGIHIEDQAPGTTKCGHMAGKVLVPISEHINRLVAIRAQADIMGTD
LLAIARTDSEATLITSTIDHRDHPFIIGSTNPDIQPLNDLMVMAEQAGKNGAELQAIEDEW
LAKAGLKLFNDAVVDAINNSPLPNKKAIEKYLTQSKGKSNLEARIAKEIAGTDIYFDW
EAPRTREGYYRYQGGTQCAINRAVAYAPFADLIWMESKLDPDYKQAKEFADGVHAVWPEQ
KLAYNLSPSFNWKKAMPREDEQETIYIKRLGALGYAWQFITLAGLHTTALISDTFAKAYAKQ
GMRAYGELVQEP EMANGVDVVTHQKWSGANYVDNMLKMITGG

>d1f8ma_ c.1.12.6 (A:) Isocitrate lyase {*Mycobacterium tuberculosis*}

ASVVGTPKSAEQIQEWD TNPRWKDVTRTYS AEDVVALQGSVVEEHTLARRGAEVLWE
QLHDLEWVNALGALTGNMAVQQVRAGLKAIYLSGWQVAGDANLSGHTYPDQSLYPANS
VPQVRRINNALQRADQIAKIEGDTSVENWLAPIVADGEAGFGGALNVYELQKALIAAGV
AGSHWEDQLASEKKCGHLGGKVLPTQQHIRTLSARLAADVADVPTVVIARTDAEAATLI
TSDVDERDQPFITGERTREGFYRTKNGIEPCIRAKAYAPFADLIWMETGTPDLEAARQFSE
AVKAEYPDQMLAYNCSPSFNWKKHLDDATIAKFQKELAAAMGFKFQFITLAGFHALNYSM
FDLAYGYAQNQMSAYVELQEREFAAEERGYTATKHQREV GAGYFDRIATTVDPNSSTTAL
TGSTEEGQF

>d1bura1 c.1.14.1 (A:148-475) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{*Spinach (Spinacia oleracea)*}

FQGPPHGIQVERDKLNKYGRPLLGCTIKPKLGLSAKNYGRAVYECLRGGLDFTKDDENV
NSQPFRMRWRDRFLFCAEALYKAQAETGEIKGHYLNATAGTCEDMMKRAVFARELGVPV
MHDYLTGGFTANTTSLHYCRDNGLLLHIHRAMHAVIDRQKNHGMHFRVLAKALRLSGG
DHIHSGTVVGKLEGERDITLGFVDLLRDDYTEKDRSRGIYFTQSWVSTPGVLPVASGGIHV
WHMPALTEIFGDDSVLQFGGTLGHPWGNAPGAVANRVALEACVQARNEGRDLAREGN
TIREATKWSPELAAACEVWKEIKFEFPAMDTV

>d5ruba1 c.1.14.1 (A:138-457) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{*Rhodospirillum rubrum*}

GPSVNISALWKVLGRPEVDGGLVVGTHKPKLGLRKPFAEACHAFWLGGDFIKNDEPQG
NQPFAPLRDTIALVADAMRRAQDETGEAKLFSANITADDPFEIARGEYVLETFGENASHV
ALLVDGYVAGAAAITARRRFPDNFLHYHRAGHGAVTSPQSKRGYTA FVHCKMARLQGA
SGIHTGTMGFGKMEGESSDRAIAYMLTQDEAQGPFYRQSWGGMKACTPIISGGMNALRM
PGFFENLGNANVILTAGGGAFGHIDGPVAGARSLRQAWQAWRDGVPVLDYAREHKELAR
AFESFPGDADQIYPGWRKALGV

>d1geha1 c.1.14.1 (A:137-443) Ribulose 1,5-bisphosphate carboxylase-
oxygenase {*Archaeon Thermococcus kodakaraensis*}

DGPAFGIEGVRKMLEIKDRPIYGVVPKPKVGYSPEEF EKLAYDLLSNGADYMKDDENLTS
PWYNRFEERA EIMAKIIDKVENETGEKKTWFANITADLLEMEQRLEV LADLGLKHAMVD

VVITGWGALRYIRDLAADYGLAIHGHRAMHAAFTRNPHYHGISMFVLAKLYRLIGIDQLHV
GTAGAGKLEGGKWDVIQNARILRESHYKPDENDVFHLEQKFYSIKAAPTSSGGLHPGNI
QPVIEALGTDIVLQLGGGTLGHPDGAAGARAVRQAIDAIMQGIPLDEYAKTHKELARAL
EKWGHVTP

>d4xiaa_ c.1.15.3 (A:) D-xylose isomerase {Arthrobacter, strain b3728}

VQPTPADHFTFGLWTVGWGTGADPFGVATRANLDPVEAVHKLAEFGAYGITFHDNDLIPFD
ATAAEREKILGDFNQALADTGLKVPMTTNLFSPVFKDGGFTSNDRSIRRFALAKVLHNI
DLAAEMGAETFVMWGGREGSEYDGSKDLAAALDRMREGVDTAAGYIKDKGYNLRIAL
EPKPNEPRGDIFLPTVGHGLAFIEQLEHGDIVGLNPETGHEQMAGLNFTHGIAQALWAEKL
FHIDLNGQRGIKYDQDLVFGHGDLSAFTVDLLENGFPNGGPKYTGPRHFDYKPSRTDG
YDGVWDSAKANMSMYLLLKERALAFRADPEVQEAMKTSGVFELGETTLNAGESAADL
MNDASAFAGFDAEAAAERNFAFIRLNQLAIEHLLGSR

>d1a0ea_ c.1.15.3 (A:) D-xylose isomerase {Thermotoga neapolitana}

AEFFPEIPKVQFEGKESTNPLAFKFYDPEEIIDGKPLKDHLKFSVAFWHTFVNEGRDPFGDP
TADRPWNRYTDPMDKAFARVDALFEFCEKLNIEYFCFHDRDIAPEGKTLRETNKILDKVV
ERIKERMKDSNVKLLWGTANLFSHPRYMHGAATTCSADVFAAAAQVKKALEITKELGG
EGYVFWGGREGYETLLNTDLGFELENLARFLRMAVDYAKRIGFTGQFLIEPKPKPEPTKHQ
YDFDVATAYAFKSHGLDEYFKFNIEANHATLAGHTFQHELRMARILGKLGSIDANQGDLL
LLGWDTDQFPTNVYDTTLAMYEVIKAGGFTKGGNFDKAVRRASYKVEDLFIGHIAGM
DTFALGFKVAYKLVKDGVLDFKIEEKYRSFREGIGRDIVEGKVDFEKL EYIIDKETIELPSG
KQEYLESLSYIVKTILELR

>d1luca_ c.1.16.1 (A:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}

MKFGNFLTQPPELSQT EVMKRLVNLGKASEGCGFDTVWLEHHFTEFGLLGNPYVAA
AHLLGATETLNVGTAAIVLPTAHPVRQAEDVNLLDQMSKGRFRFGICRGLYDKDFRVFGT
DMDNSRALMDCWYDLMKEGFNEG YIAADNEHIKFPKIQLNPSAYTQGGAPVYVVAESAS
TTEWAAERGLPMILSWIINTHEKKAQLDLYNEVATEHGYDVT KIDHCLSYITSVDHDSNRA
KDICRNFLGHWDYSYVNATKIFDDSDQTKGYDFNKGQWRDFVLKGHKDTNRRIDYSYEI
NPVGTPEECIAIIQQDIDATGIDNICCGFEANGSEEEIIASMKLFQSDVMPYLKEKQ

>d1lucb_ c.1.16.1 (B:) Bacterial luciferase (alkanal monooxygenase) {Vibrio harveyi}

MKFGFLFLNFMNSKRSSDQVIEEMLDTAHYVDQLKFDTLAVYENHFSNNGVVGAPLTV
GFLMGMTKNAKVASLNHVITTHHPVRVAEEACLLDQMSEGRFAFGFSDCEKSADMRRFFNR
PTDSQFQLFSECHKIINDAFTTGYCHPNNDFYSPKISVNP HAFTEGGPAQFVNATSKEVVE
WAAKGLPLVFRWDDSNAQRKEYAGLYHEVAQAHGVDVSQVRHKL TLLVNQNVDGEAA
RAEARVYLEEFVRESYSNTDFEQKMGE LLSENAIGTYEESTQAARVAIECCGAADLLMSFE
SMEDKAQQRAVIDVNNANIV

>d2ptd_ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Bacillus cereus}

ASSVNELENWSKWMQPIPD SIPLARISIPGTHDSGTFLQNPIKQVWGMTQEYDFRYQMD
HGARIFDIRGRLTDDNTIVLHHGPLYLYVTLHEFINEAKQFLKDN PSETIIMSLKKEYEDMK
GAEDSFSSTFEKKYFVDPIFLKTEGNIKLGDARGKIVLLKRYSGS NEPGGYNNFYWPDNET
FTTTVNQNANVTVQEKYKVS YDEKVKSIKDTMDETMNNS EDLNHLYINF TSLSSGGTAW
NSPYYYASYINPEIANYIKQKNPARVGWVIQDYINEKWSPLLYQEVIRANKSLI

>d2plc_ c.1.18.2 (-) Phosphatidylinositol-specific phospholipase C {Listeria monocytogenes}

VTTKQWMSALPDTTNLAALSIPGTHDTMSYNGDITWTLTKPLAQTQTMSLYQQLEAGIRY
IDIRAKDNLNIYHGPIFLNASLSGVLETITQFLKKNPKETIIMRLKDEQNSNDSFDYRIQPLI

NIYKDYFYTTPTDTSNKIPTLKDVGRKILLSENHTKKPLVINSRKFGMQFGAPNQVIQD
DYNGPSVKTKFKEIVQTAYQASKADNKLFLNHISATSLTFTPRQYAAALNNKVEQFVLNLT
SEKVRGLGILIMDFPEKQTIKNIKNKF

>d7reqa1 c.1.19.1 (A:4-560) Methylmalonyl-CoA mutase, alpha and beta subunits
{*Propionibacterium freudenreichii*, subsp. *shermanii*}

LPRFDSVDLGNAPVPADAARRFEELAAKAGTGEAWETAEQIPVGTLFNEVDYKDMDWLD
TYAGIPPFVHGPYATMYAFRPWTIRQYAGFSTAKESNAFYRRNLAAGQKGLSVAFDLPTHR
GYDSNPRVAGDVGMAGVAIDSIYDMRELFAGIPLDQMSVSMTMNGAVLPILALYVVTAE
EQGVKPEQLAGTIQNDILKEFMVRNTYIYPPQPSMRIISEIFAYTSANMPKWNSISISGYHM
QEAGATADIEMAYTLADGVDYIRAGESVGLNVDQFAPRLSFFWGIGMNFMEVAKLRAA
RMLWAKLVHQFGPKNPKSMLRTHSQTSGWSLTAQDVYNNVVRTCIEAMAATQGHTQSL
HTNSLDEAIALPTDFSARIARNTQLFLQQESGTTRVIDPWGSAYVEELTWDLARKAWGHI
QEVEKVGGMAKAIKGIKPMRIEAAARTQARIDSGRQPLIGVNKYRLEHEPPLDVLKVD
NSTVLAEQKAKLVKLRAERDPEKVKAALDKITWAAGNPDDKDPDRNLLKLCIDAGRAM
ATVGEMSDALEKVFGRYT

>d7reqb1 c.1.19.1 (B:16-475) Methylmalonyl-CoA mutase, alpha and beta subunits
{*Propionibacterium freudenreichii*, subsp. *shermanii*}

LTPTTSLAGDFPKATEEQWEREVEKVLRNRPPEKQLTFAECLKRLTVHTVDGIDIVPMY
RPKDAPKKLGYPGVAPFTRGTTVRNGDMDAWDVRALHEDPDEKFTRKAILEGLERGVTS
LLLVRDPDAIAPEHLDEVLSVDVLEMTKVEVFSRYDQGAAAEALVSVERSDKPAKDLAL
NLGLDPIGFAALQGTEPDLTVLGDWVRRLAKFSPDSRAVTIDANIYHNAGAGDVAELEWA
LATGAEYVRALVEQGFTATEAFDTINFRVTATHDQFLTIARLRALREAWARIGEVFGVDED
KRGARQNAITSWRELTREDPYVNILRGSIAFSAVSGGAESITLPTQALGLPEDDFPLRIA
RNTGIVLAAEEVNIGRVNDPAGGSYYVESLTRSLADAAWKEFQEVEKLGGMASKAVMTEHV
TKVLDACNAERAKRLANRKQPITAVSEFPMIGARSIE

>d1aj2_ c.1.21.1 (-) Dihydropteroate synthetase {*Escherichia coli*}

MKLFAQGTSLDLSHPHVMGILNVTGPSFSDGGTHNSLIDAVKHANLMINAGATHIDVGGES
TRPGAAEVSVEELQRPVVEAIAQRFEVWISVDTSKPEVIRESAKVGAHIINDIRSLSEPG
ALEAAAETGLPVCLMHMQGNPKTMQEAPKYDDVFAEVNRYFIEQIARCEQAGIAKEKLL
LDPGFGFGKNLSHNYSLARLAEFHFNPLLVGMSRKS MIGQLLNVGPSERLSGSLACA
VIAAMQGAHIIRVHDVKETVEAMRVVEATLSAKENKRYE

>d1ad1a_ c.1.21.1 (A:) Dihydropteroate synthetase {*Staphylococcus aureus*}

TKTKIMGILNVTGPSFSDGGKFNNVESAVTRVKAMMDEGADIIDVGGVSTRPGHEMITVE
EELNRVLPVVEAIVGFDVKISVDTFRSEVAEACLKLGVDIINDQWAGLYDHRMFQVVAKY
DAEIVLMHNGNGNRDEPVVEEMLTSLLAQAHQAKIAGIPSNKIWLDPGIGFAKTRNEEAE
VMARLDELVATEYPVLLATSRKRFTKEMMGYDTPVERDEVTAATTAYGIMKGVRAVRV
HNVELNAKLAKGIDFLKENENARHN

>d1uroa_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Human (*Homo sapiens*)}

GFPELKNDTFLRAAWGEETDYTPVWCMRQAGRYLPEFRETRAQQDFSTCRSPEACCELT
LQPLRRFPLDAAIIFSDILVVPQALGMEVTMVPKGPSFPEPLREEQDLERLRDPEVVASEL
GYVFQAITLTRQLAGRVPLIGFAGAPWTLMTYMVEGGGSSTMAQAKRWLYQRPQASHQ
LLRILTDALVPYLVGQVVAGAQAQLFESHAGHLGPQLFNKFALPYIRDVAKQVKARLRE
AGLAPVPMIIFAKDGHFALEELAQAQGYEVVGLDWTVPKKARECVGKTVTLQGNLDPCA
LYASEEEIGQLVKQMLDDFGPHRYIANLGHGLYPDMDPEHVGA FVDAVHKHSRLLRQ

>d1j93a_ c.1.22.1 (A:) Uroporphyrinogen decarboxylase, UROD {Tobacco (*Nicotiana tabacum*), UROD-III}

TQPLLLDAVRGKEVERPPVWLMRQAGRYMKSYQLLCEKYPLFRDRSENVDLVVEISLQP
WKVFRPDGVILFSDILTPLSGMNIPFDIIKKGKGPVIFDPLRTAADVEKVREFIPEKSVPYVGE
ALTILRKEVNNQAAVLGFVGAPFTLASVVEGGSSKNFTKIKRLAFAEPKVLHALLQKFAT
SMAKYIRYQADSGAQAVQIFDSWATELSPVDFEESLPYLKQIVDSVKLTHPNLPLILYASG
SGGLLERLPLTGVDVVSLDWTVDMA DGRRRLGPNVAIQGNVDPGVLFSGKEFITNRINDT
VKKAGKGKHILNLGHGIKVGTPREENFAHFFEIAKGLRY

>d1heta2 c.2.1.1 (A:175-324) Alcohol dehydrogenase {Horse (*Equus caballus*)}

GFSTGYGSAVKVAKVTQGSTCAVFLGGVGLSVIMGCKAAGAARIIGVDINKDKFAKAKE
VGATECVNPQDYKKPIQEVLTMSNGGVDFSFEVIGRLDTMTALSCCQEAYGVSIVGV
PPDSQNLSMNPMLLLSGRTWKGAIFGGFKS

>d1keva2 c.2.1.1 (A:151-314) Bacterial secondary alcohol dehydrogenase
{*Clostridium beijerinckii*}

MMTTGFHGAELADIQMGSSVVVIGIGAVGLMGIAGAKLRGAGRIIGVSRPICVEAAKFY
GATDILNYKNGHIVDQVMKLTNGKGVDRVIMAGGGSETLSQAVSMVKPGGIISNINYHGS
GDALLIPRVEWGCGMAHKTIKGGLCPGGRLRAEMLRDMVVYNRV

>d1e3ja2 c.2.1.1 (A:151-313) Ketose reductase (sorbitol dehydrogenase) {Silverleaf whitefly
(*Bemisia argentifolii*)}

LEPLSVGVHACRRAGVQLGTTVLVIGAGPIGLSVLAAKAYGAFVVCTARSPRRLEVAKN
CGADVTLVVDPAKEESSIIERIRSAIGDLPNVTIDCSGNEKCITIGINITRTGGTLMLVGMGS
QMVTVPVLNACAREIDIKSVFRYCNDYPIALEMVASGRC

>d1qora2 c.2.1.1 (A:136-265) Quinone oxidoreductase {*Escherichia coli*}

YEIKPDEQFLFHAAAGGVGLIACQWAKALGAKLIGTVGTAQKAQSALKAGAWQVINYRE
EDLVERLKEITGGKKVRVYDSVGRDTWERSLDCLQRRGLMVSFGNSSGAVTGVNLGIL
NQKGSlyVTRPS

>d1ek6a_ c.2.1.2 (A:) Uridine diphosphogalactose-4-epimerase (UDP-galactose 4-
epimerase) {Human (*Homo sapiens*)}

MAEKVLVTGGAGYIGSHTVLELLEAGYLPVVIDNFHNAFRGGGSLPESLRRVQELTGRSV
EFEEMDILDQGALQRLFKKYSFMAVIHFAGLKAVGESVQKPLDYRVNLTGTIQLLEIMKA
HGVKNLVFSSSATVYGNPQYLPLDEAHPTGGCTNPYGKSKFFIEEMIRDLQADKTWNAV
LLRYFNPTGAHASGCIGEDPQGIPNNLMPYVSQVAIGRREALNVFGNDYDTEGTGVRDY
IHVVDLAKGHIAALRKLKEQCGCRIYNLGTGTGYSVLQMVQAMEKASGKKIPYKVVAR
EGDVAACYANPSLAQEELGWTAALGLDRMCEDLWRWQKQNPSGFGT

>d1kewa_ c.2.1.2 (A:) dTDP-glucose 4,6-dehydratase (RmlB) {*Streptococcus suis*,
serotype 2}

MKILITGGAGFIGSAVVRHIIKNTQDTVVNIDKLTYAGNLESLSDISNRYNFEHADICDSA
EITRIFEQYQPDAMHLAAESHVDRSITGPAAFIETNIVGTYALLEVARKYWSALGEDKKN
NFRFHHISTDEVYGDLPHPDEVENSVTLPFTETTAYAPSSPYSASKASSDHLVRAWRRTY
GLPTIVTNCNNYGPYHFPEKLIPLVILNALEGKPLPIYGKGDQIRDWLYVEDHARALHNV
VTEGKAGETYNIGGHNEKKNLDVFTICDLLDEIVPKATSYREQITYVADRPGHDRRYAID
AGKISRELGWKPLETFESGIRKTVEWYLANQWVNNVKSGAYQSWIEQNYEGRQ

>d1e6ua_ c.2.1.2 (A:) GDP-4-keto-6-deoxy-d-mannose
epimerase/reductase (GDP-fucose synthetase) {*Escherichia coli*}

AKQRVFIAGHRGMVGSAIRRQLEQRGDVELVLRTRDELNLLDSRAVHDFFASERIDQVYL
AAAKVGGIVANNNTYPADFIYQNMIESNIIHAAHQNDVNKLLFLGSSCIYPKLAKQPMAE
SELLQGTLEPTNEPYAIAKIAGIKLCESYNRQYGRDYRSVMPTNLYGPHDNFHPNSNSHVIPA
LLRRFHEATAQKAPDVVVWGSCTPMREFLHVDDMAAASIHVMELAHEVWLENTQPMLS
HINVTGVDCTIRELAQTIKVVGYKGRVVFDAKPDGTPRKLLDVTRLHQLGWYHEISL
EAGLASTYQWFLENQ

>d1db3a_ c.2.1.2 (A:) GDP-mannose 4,6-dehydratase {Escherichia coli}

SKVALITGVTGQDGSYLAEFLLKGYEVHGIKRRASSFNTERVDHIYQDPHTCNPKFHLHY
GDLSDTSNLTRILREVQPDEVYNLGAMSHVAVSFESPEYTADVDMGTLRLLEAIRFLGLE
KKTRFYQASTSELYGLVQEIPQKETTPFYPRSPYAVAKLYAYWITVNYRESYGMACNGILF
NHESPRRGETFVTRKITRAIANIAQGLESCLYLGNMDSLRLDWGHAKDYVKMQWMMMLQQ
EQPEDFVIATGVQYSVRQFVEMAAQLGIKLRFEFTGVEEKGIVSVTGHDA PGVKPGD
VIIAVDPRYFRPAEVETLLGDPTKAHEKLGWKPEITLREMVSEMVANDLEAAKKHS

>d1eq2a_ c.2.1.2 (A:) ADP-L-glycero-D-mannoheptose 6-epimerase {Escherichia coli}

MIIVTGGAGFIGSNIVKALNDKGITDILVVDNLKDGTKFVNLDLNIADYMDKEDFLIQIM
AGEEFGDVEAIFHEGACSSSTTEWDGKYMMDNQYQSKELLHYCLEREIPFLYASSAATYG
GRTSDFIESREYEKPLNVYGYSKFLFDEYVRQILPEANSQIVGFRYFNVYGPREGHKGSMA
SVAFHLNTQLNNGESPKLFEGSENFKRDFVYVGDVADVNLFLENGVSGIFNLGTGRAES
FQAVADATLAYHKKKGQIEYIPFPDKLKGRYQAFQTADLTNLRAAGYDKPFKTVAEGVTEY
MAWLN

>d1qrra_ c.2.1.2 (A:) Sulfolipid biosynthesis protein SQD1 {Thale cress (Arabidopsis thaliana)}

KRVMVIGGDGYCGWATALHLSKKNYEVCIVDNLVRRFLDHQLGLESITPIASIHDRISRWK
ALTGKSIELYVGDICDFEFLAESFKSFEPDSVVHFGEQRSAPYSMIDRSRAVYTQHNNVIGT
LNVLFAlKEFGEECHLVKLGTMGEGTPNIDIEEGYITITHNGRTDTLPYPKQASSFYHLSK
VHDSHNIAFTCKAWGIRATDLNQG VVYGVKTDTEMHEELRNRLDYDAVFGTALNRFCV
QAAVGHPLTVYGGGQTRGYLDIRDTVQCVEIAIANPAKAGEFRVFNQFTEQFSVNELAS
LVTKAGSKLGLDVKKMTVPNPRVEAEHYNAKHTKLMELGLEPHYLSDSLSDSLLNFA
VQFKDRVDTKQIMPSVSWKKIGVKTKS

>d1k6xa_ c.2.1.2 (A:) Negative transcriptional regulator NmrA {Aspergillus nidulans}

QQKKTIAVVNATGRQAASLIRVAAVGHVRAQVHSLKGLIAEELQAIPNVTLFQGPLLN
NVPLMDTLFEGAHLAFINTTSQAGDEIAIGKDLADAAKRAGTIQHYIYSSMPDHSYGPW
PAVPMWAPKFTVENYVRQLGLPSTFVYAGIYNNNFTSLPYPLFQMEMLPDGTFEWHAPFD
PDIPLPWLD AEHDVGPALLQIFKDGPKWNGHRIALT FETLSPVQVCAAFSRALNRRVTY
VQVPKVEIKVNIPVGYREQLEAIEVVFGHEHKAPYFPLPEFSRPAAGSPKGLGPANGKGAGA
GMMQGPGGVISQRTDEARKLWSGWRDMEEYAREVFPIEEEANGLDWML

>d1cyda_ c.2.1.2 (A:) Carbonyl reductase {Mouse (Mus musculus)}

LNFSGLRALVTGAGKGIGRDTV KALHASGAKVVAVTRTNSDLVSLAKECPGIEPVCVDLG
DWDATEKALGGIGPVDLLVNNAALVIMQPFLEVTKEAFDRSFSVNLRSVFQVSQMVARD
MINRGVPGSIVNVSSMVAHVTFPNLITYSSTKGAMTMLTKAMAMELGPHKIRVNSVNPTV
VLTDMGKKVSADPEFARKLKERHPLRKFAEVEDV VNSILFLLSDRSASTSGGGILVDAGYL
AS

>d1oaa_ c.2.1.2 (-) Sepiapterin reductase {Mouse (Mus musculus)}

ADGLGCAVCVLTGASRGFGRALAPQLARLLSPGSVMLVSARSESMLRQLKEELGAQQPD
LKVVLAADLGTEAGVQRLLSAVRELPRPEGLQRLLLINNAATLGDVSKGFLNVNDLAEV

NNYWALNLTSMCLTSGTLNAFQDSPGLSKTVVNISSLCALQPYKGWGLYCAGKAARDM
LYQVLAEEPSVRVLSYAPGPLDNDMQQLARETSKDPELRSKLQKLKSDGALVDCGTSA
QKLLGLLQKDTFQSGAHVDFYD

>d1hdr_ c.2.1.2 (-) Dihydropteridin reductase (pteridine reductase) {Human (Homo sapiens)}
EARRVLVYGGRGALGSRCVQAFRARNWWVASVDVVENEEASASIIVKMTDSFTEQADQ
VTAEVGKLLGEEKVDAILCVAGGWAGGNAKSKSLFKNCDLMWKQSIWTSTISSHLATKH
LKEGGLLTLAGAKAALDGTGPMIGYGMAGAVHQLCQSLAGKNSGMPPGAAAIAVLPV
TLDTPMNRKSMPEADFSSWTPLEFLVETFDHWITGKNRPSSGSLIQVVTTEGRTELTPAYF

>d1e7wa_ c.2.1.2 (A:) Dihydropteridin reductase (pteridine reductase) {Leishmania major}
TVPVALVTGAAKRLGRSIAEGLHAEGYAVCLHYHRSAAEANALSATLNARRPNSAITVQA
DLSNVATAPVSGADGSAPVTLFTRCAELVAACYTHWGRCDVLVNNASSFYPTPLLRNDED
GHEPCVGDREAMETATADLFGSNAIAPYFLIKAFHRVAGTPAKHRGTNYSIINMVDAMT
NQPLLGYTIYTMAGALEGLTRSAALELAPLQIRVNGVGPGLSVLVDDMPPAVWEGHRSK
VPLYQRDSSAAEVSDVVIFLCSSKAKYITGTCVKVDGGYSLTRA

>d1fds_ c.2.1.2 (-) Human estrogenic 17beta-hydroxysteroid dehydrogenase {Human (Homo sapiens)}
ARTVVLTITGCSSGIGLHLAVRLASDPSQSFKVYATLRDLKTQGRLWEAARALACPPGSLET
LQLDVRDSKSVAAARERVTEGRVDVLCNAGLGLLGPLEALGEDAVASVLDVNVVGTVR
MLQAFLPDMKRRGSGRVLVTGSGGLMGLPFNDVYCASKFALEGLCESLAVLLLPGFVH
LSLIECGPVHTAFMEKVLGSPEEVLDRDTHFTFRFYQYLAHASKQVFREAAQNPEEVAEVF
LTALRAPKPTLRYFTTERFLPLLRMLDDPSGSNYVTAMHREVFQDV

>d1fmca_ c.2.1.2 (A:) 7-alpha-hydroxysteroid dehydrogenase {Escherichia coli}
MFNSDNLRLDGKCAITGAGAGIGKEIAITFATAGASVVVSDINADAANHVVDEIQQLGGQ
AFACRCDITSEQELSALADFAISKLGKVDILVNNAGGGGPKPFDMPMADFRRAYELNVFSF
FHLSQLVAPEMEKNNGGVILTITSMAAENKNINMTSYASSKAAASHLVRNMAFDLGEKNI
RVNGIAPGAILTDALKSVITPEIEQKMLQHTPIRRLGQPQDIANAALFLCSPAASWVSGQILT
VSGGGVQELN

>d1hdca_ c.2.1.2 (A:) 3-alpha,20-beta-hydroxysteroid dehydrogenase {Streptomyces hydrogenans}
NDLSGKTVIITGGARGLGAEARQAVAAGARVVLADVLDEEGAATARELGDAARYQHLD
VTIEEDWQRVVAYAREEFGSVDGLVNNAGISTGMFLETESVERFRKVVEINLTGVFIGMKT
VIPAMKDAGGGSIVNISSAAGLMGLALTSSYGASKWGVRLSKLAAVELGTDRIRVNSVH
PGMTYTPMTAETGIRQGEKNYPNTPMGRVGEPGEIAGAVVKLLSDTSSYVTGAELAVDGG
WTTGPTVKYVMGQ

>d1fjha_ c.2.1.2 (A:) 3-alpha-hydroxysteroid dehydrogenase {Comamonas testosteroni}
MSIIVISGCATGIGAATRKVLEAAGHQIVGIDIRDAEVIADLSTAEGRKQAIADVLAACSKG
MDGLVLCAGLGPQTKVLGNVSVNYFGATELMDAFLPALKKGHQPAAVVISSVASAHLA
FDKNPLALALEAGEEAKARAIVEHAGEQGGNLAYAGSKNALTVAVRKRAAAWGEAGVR
LNTIAPGATETPLLQAGLQDPRYGESIAKFVPPMGRRAEPSEMASVIAFLMSPAASYVHGA
QIVIDGGIDAVMRPTQF

>d1bdb_ c.2.1.2 (-) Cis-biphenyl-2,3-dihydrodiol-2,3-dehydrogenase {Pseudomonas sp., lb400}
MKLKGEAVLITGGASGLGRALVDRFVAEGAKVAVLDKSAERLAELETDHGDNVLGIVGD
VRSLEDQKQAASRCVARFGKIDTLIPNAGIWDYSTALVDLPEESLDAAFDEVFHINVKGYI
HAVKACLPALVASRGNVIFTISNAGFYPPNGGGPLYTAAKHAIVGLVRELAFELAPYVRVNG

VGSGGINSDLRGPSSLGMGSKAISTVPLADMLKSVLPIGRMPEVEEYTGAYVFFATRGD
APATGALLNYDGGLGVRGFFSGAGGNDLLEQLNIH

>d1b16a_ c.2.1.2 (A:) Drosophila alcohol dehydrogenase {Fruit fly (*Drosophila lebanonensis*)}
MDLTNKNVIFVAALGGIGLDTSRELVKRNLNKFNVILDRVENPTALAEKAINPKVNITFHT
YDVTVPVAESKLLKKIFDQLKTVDILINGAGILDDHQIERTIAINFTGLVNTTTAILDFWD
KRKGGPGGIIANICSVTGFNAIHQVPVYSASKAAVVSFTNSLAKLAPITGVTAYSINPGITRT
PLVHTFNSWLDVEPRVAELLLSHPTQTSEQCGQNFKVKAIEANKNGAIWKLDLGTLEAIEW
TKHWDSHI

>d1gcoa_ c.2.1.2 (A:) Glucose dehydrogenase {*Bacillus megaterium*}
MYKDLEGKVVVITGSSTGLGKSMAIRFATEKAKVVVNYSKEDEANSVLEEIKKVGGEAI
AVKGDVTVESDVINLVQSAIKEFGKLDVMINNAGLENPVSSHEMSLSDWNKVIDTNLTGA
FLGSREAIKYFVENDIKGTVINMSSVHEKIPWPLFVHYAASKGGMKLMTETLALEYAPKGI
RVNNIGPGAINTPINAEEKFADPEQRADVESMIPMGYIGEPEEIAAVAAWLASSEASYVTGIT
LFADGGMTQYPSFQAGRG

>d1gega_ c.2.1.2 (A:) meso-2,3-butanediol dehydrogenase {*Klebsiella pneumoniae*}
KKVALVTGAGQGIGKAIARLVKDGFAVAIADYNDATAKAVASEINQAGGHAVAVKVDVS
DRDQVFAAVEQARKTLGGFDVIVNNAGVAPSTPIESITPEIVDKVYNINVKGVWIGIAAV
EAFKKEGHGGKIINACSQAGHVGNPALAVYSSSKFAVRGLTQTAARDLAPLGITVNGYCP
GIVKTPMWAEIDRQVSEAAGKPLGYGTAEFAKRITLGRLEPEDVAACVSYLASPDSYDYM
TGQSLIDGGMVFN

>d1h5qa_ c.2.1.2 (A:) Mannitol dehydrogenase {Mushroom (*Agaricus bisporus*)}
PGFTISFVNKTIIVTGGNRGIGLAFTRAVAAAGANVAVIYRSAADAVEVTEKVGKEFGVKT
KAYQCDVSNITDIVTKTIQQIDADLGPIGLIANAGVSVPKATELTHEFAFVYDVNVFGV
FNTCRAVAKLWLQKQKGSIVVTSSMSSQIINQSSLNGSLTQVFYNSSKAACSNLVKGLAA
EWASAGIRVNALSPGYVNTDQTAHMDKKIRDHQASNIPLNRFAQPEEMTGQAILLSDHA
TYMTGGEYFIDGGQLIW

>d1i01a_ c.2.1.2 (A:) beta-keto acyl carrier protein reductase {*Escherichia coli*}
MNFEGKIALVTGASRGIGRAIAETLAARGAKVIGTATSENGAQASDYLGGANGKGLMLNV
TDPASIESVLEKIRAEFGVDILVNNAGITRDNLLMRMKDEEWNDIETNLSSVFRLSKAVM
RAMMKKRHGRITIGSVVGTMGNGGQANYAAAKAGLIGFSKSLAREVASRGITVNVVAP
GFIETDMTRALSDDQQRAGILAQVPAGRLGGAQEIANAVAFSLASDEAAAYITGETLHVNGGM

>d1eno_ c.2.1.2 (-) Enoyl-ACP reductase {Oil seed rape (*Brassica napus*)}
LPIDLRGKRAFIAGIADDNGYGWAVAKSLAAAGAEILVGTWVPALNIFETSLRRGKFDQSR
VLPDGSLMEIKKVYPLDAVFDNPEDVPEDVKANKRYAGSSNWTQEAECVRQDFGSIDI
LVHSLANGPEVSKPLLETSRKGYLAASASSYSFVSLLSHFLPIMNPGGASISLTYIASERIIP
GYGGGMSSAKAALES DTRVLAFEAGRKQNI RVNTISAGPLGSRAAKAIGFIDTMIEYSYN
NAPIQKTLTADEVGNAAAFVLSPLASAITGATIYVDNGLNSMGVALDSPVFK

>d1eny_ c.2.1.2 (-) Enoyl-ACP reductase {*Mycobacterium tuberculosis*, TB, gene *InhA*}
AGLLDGKRILVSGIITDSSIAFHARVAQEQAQLVLTGFDRRLRIQRITDRLPAKAPLLELD
VQNEEHLASLAGRVTEAIGAGNKLDGVVHSIGFMPQTGMGINPFFDAPYADVSKGIHISAY
SYASMAKALLPIMNPGGSIVGMDFDPSRAMPAYNWMTVAKSALESVNRFVAREAGKYGV
RSNLVAAGPIRTLAMSAIVGGALGEEAGAQIQLL EEGWDQRAPIGWNMKD ATPVAKTVC
ALLSDWLPATTGDIYADGGAHTQLL

>d1qg6a_ c.2.1.2 (A:) Enoyl-ACP reductase {*Escherichia coli*}

GFLSGKRILVTGVASKLSIAYGIAQAMHREGAELAFETYQNDKLKGRVEEFAAQLGSDIVLQ
CDVAEDASIDTMFAELGKVWPKFDGFVHSIGFAPGDQLDGDYVNAVTVREGFKIAHDISSY
SFVAMAKACRSMLNPGSALLTSLYGAERAIPNYNVMGLAKASLEANVRYMANAMGPE
GVRVNAISAGPIRTLAASGIKDFRKMLAHCEAVTPIRRTVTIEDVGNSAAFLCSDLSAGISG
EVVHVDGGFSIAAMNE

>d2ae2a_ c.2.1.2 (A:) Tropinone reductase {Jimsonweed (Datura stramonium), II}
AGRWNLEGCTALVTGGSRGIGYGIVEELASLGASVYTCSRNQKELNDCLTQWRSGFKV
EASVCDLSSRSERQELMNTVANHFHGHKLNLVNNAGIVYKEAKDYTVEDYSLIMSINFEA
AYHLSVLAHPFLKASERGNVVFISVSGALAVPYEAVYGATKGAMDQLTRCLAFEWAKD
NIRVNGVGPVGIATSLVEMTIQDPEQKENLNKLIDRCALRRMGEPKELAAMVAFLCFPAAS
YVTGQIIYVDGGLMANCGF

>d1g0oa_ c.2.1.2 (A:) 1,3,8-trihydroxynaphtalene reductase (THNR, naphtol reductase) {Rice blast
fungus (Magnaporthe grisea)}

KYDAIPGLPGQSASLEGKVALVTGAGRGIGREMAMELGRRGCKVIVNYANSTESAEEVV
AAIKKNGSDAACVKANVGVVEDIVRMFEEAVKIFGKLIVCSNSGVVSFGHVKDVTPEEF
DRVFTINTRGQFFVAREAYKHLEIGGRLILMGSI TGQAKAVPKHAVYSGSKGA IETFARCM
AIDMADKKITVNVVAPGGIKTDMYHAVCREYIPNGENLSNEEVDEYAAVQWSPLRRVGLP
IDIARVVCFLASNDGGWVTGKVIGIDGGACM

>d1hdoa_ c.2.1.2 (A:) Biliverdin IX beta reductase {Human (Homo sapiens)}
MAVKKIAIFGATGQTGLTTLAQAVQAGYEVTVLVRDSSRLPSEGPRPAHVVDVLQAAD
VDKTVAGQDAVIVLLGTRNDLSPTTVMSEGARNIVAAMKAHGVDKVVACTSAFLWDPT
KVPPRLQAVTDDHIRMHKVLRESGLKYVAVMPPHIGDQPLTGAYTVTL DGRGPSRVISKH
DLGHFMLRCLTTDEYDGHSTYPSHQY

>d1e6wa_ c.2.1.2 (A:) 3-hydroxyacyl-CoA dehydrogenase {Rat (Rattus norvegicus)}
SVKGLVAVITGGASGLGLSTAKRLVGQGATAVLLDVPNSEGETEAKKLGGNCIFAPANVTS
EKEVQAALTLAKEKFGRIDVAVNCAGIAVAIKTYHEKKNVHTLED FQRVINVN LIGTFNV
IRLVAGVMGQNEPDQGGQRGVIINTASVAAFEGQVGQAAYSASKGGIVGMTLPIARDLAPI
GIRVVTIAPGLFATPLLTLPDKVRNFLASQVPFPSRLGDP AEY AHLVQMVIENPFLNGEVIR
LDGAIRMQP

>d1hu4a_ c.2.1.2 (A:) Carbonyl reductase/20beta-hydroxysteroid dehydrogenase {Pig (Sus
scrofa)}

SSNTRVALVTGANKGIGFAIVRDLCRQFAGDVVLTARDVARGQAAVKQLQAEGLSPRFHQ
LDIIDLQSIRALCDFLRKEYGGDLVLVNNAIAFQLDNPTPFHQAELTMKTNFMGTRNVC
TELLPLIKPQGRVVNVSSTEGVRLNECSPELQQKFKSETITEELVGLMKNKFVEDTKNGV
HRKEGWSdstyGVTkIGVSVLSRIYARKLREQRAGDKILLNACCPGWVRTDMGGPKAPK
SPEVGAETPVYLALLPSDAEGPHGQFVTDKKVVEWGVPPESYPWVNA

>d1b7go1 c.2.1.3 (O:1-138,O:301-340) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Archaeon Sulfolobus solfataricus}

MVNVAVNGYGTIGKRVADAIKQPDMKLVGVAKTSPNYEAFIAHRRGIRIYVPQQSIKKFE
ESGIPVAGTVEDLIKTSDIVVDTTPNGVGAQYKPIYLQLQRNAIFQGGEKA EVADISFSALC
NYNEALGKKYIRVVSXESIVPENIDAIRASMKLMSAEDSMRITNESLGILKGYLI

>d1ggaa1 c.2.1.3 (A:1-164,A:334-358) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Trypanosoma brucei brucei, glycosome}

TIKVGINGFGRIGRMVFQALCDDGLLGNEIDVVAVVDMNTDARYFAYQMKYDSVHGKFK

HSVSTTKSKPSVAKDDTLVVNGHRILCVKAQRNPADLPWGKLGVEYVIESTGLFTVKSAA
EGHLRGGARKVVISAPASGGAKTFVMGVNHNHNNYNPREQHVVSNASXNEWGYSHRVVDL
VRHMAARDRAAKL

>d1gl3a1 c.2.1.3 (A:1-133,A:355-367) Aspartate beta-semialdehyde dehydrogenase {Escherichia coli}

MKNVGFIGWRGMVGSVLMQRMVEERDFDAIRPVFFSTSQLGQAAPSFGGTTGTLQDAFD
LEALKALDIIVTCQGGDYTNEIYPKLRESGWQGYWIDAASSLRMKDDAIILDPVNQDVIT
DGLNNGIRTFVGGXAAEPLRRMLRQLA

>d1ebfa1 c.2.1.3 (A:2-150,A:341-359) Homoserine dehydrogenase {Baker's yeast (Saccharomyces cerevisiae)}

STKVNVNAVIGAGVVGSAFLDQLLAMKSTITYNLVLLEAERSLISKDFSPNLVGSWDKA
ALAASTTKTLPLDDLIAHLKTSPKPVILVDNTSSAYIAGFYTKFVENGISIATPNKKAFFSSDL
ATWKALFSNKPTNGFVYHEATVGAGLXAAVTAAGVLGDVIKIAQRL

>d1e5qa1 c.2.1.3 (A:2-124,A:392-450) Saccharopine reductase {Rice blast fungus (Magnaporthe grisea)}

ATKSVLMLGSGFVTRPTLDVLTDSGIKVTVACRTLESAKKLSAGVQHSTPISLDVNDDAAL
DAEVAKHDLVISLIPYTFHATVIKSAIRQKKHVTTTSYVSPAMMELDQAAKDAGITVMNEI
GXYSAMAKLVGVPCAVAVKFVLDGTISDRGVLAPMNSKINDPLMKELKEYGIECKEKV
VA

>d1f06a1 c.2.1.3 (A:1-118,A:269-320) Diaminopimelic acid dehydrogenase (DAPDH) {Corynebacterium glutamicum}

MTNIRVAIVGYGNLGRSVEKLIQKQPDMDLVGIFSRRATLDTKTPVFDVADVVDKHADDVD
VLFLCMGSATDIPEQAPKFAQFACTVDITYDNHRDIPRHRQVMNEAATAAGNVALVSTGXR
NPDFTASSQIAFGRAAHMKQQGQSGAFTVLEVAPYLLSPENLDDLIARDV

>d1dih_1 c.2.1.3 (2-130,241-273) Dihydrodipicolinate reductase {Escherichia coli}

HDANIRVAIAGAGGRMGRQLIQAALALEGVQLGAALEREGSSLLGSDAGELAGAGKTGV
TVQSSLDVAVKDDFDVFIDFTRPEGTLNHLAFCRQHKGKGMVIGTTGFDEAGKQAIRDAAAD
IAIVFAANFSXMTFANGAVRSALWLSGKESGLFDMRDVLDLNNL

>d1k5ha2 c.2.1.3 (A:1-125,A:275-300) 1-deoxy-D-xylulose-5-phosphate reductoisomerase {Escherichia coli}

MKQLTILGSTGSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLEFSPPRYAVMDDEA
SAKLLKTMLQQQGSRTVLGSGQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGK
TILLANKXDMRTPIAHTMAWPNRVNSGVKPLDFC

>d1gcua1 c.2.1.3 (A:1-128,A:247-292) Biliverdin reductase {Rat (Rattus norvegicus)}

MDAEPKRKFGVVVVGVRAGSVRLRDLKDPRSA AFLNLIGFVSRRELGSLEVRQISLED
ALRSQEIDVAYICSESSSHEDYIRQLQAGKHVLEYPMTLSFAAAQELWELAAQKGRVLH
EEHVELLXKNIFLKDQDIFVQKLLDQVSAEDLAAEKKRIMHCLGLASDIQKLCH

>d1h6da1 c.2.1.3 (A:51-212,A:375-433) Glucose-fructose oxidoreductase, N-terminal domain {Zymomonas mobilis}

QAATLPAGASQVPTTPAGRPMPIAIRPMPEDRRFGYAIVGLGKYALNQILPGFAGCQHSRIE
ALVSGNAEKAKIVAAEYGVDPKRIYDYSNFDKIAKDPKIDAVYIILPNSLHAEFAIRAFKAG
KHVMCEKPMATSVADCQRMIDA AKAANKKLMIGYRCHYXNQFSAQLDHLAEAVINNKP
VRSPGEEGMQDVRLIQAIYEAARTGRP VNTDWGYVRQGGY

>d1dpga1 c.2.1.3 (A:1-181,A:413-426) Glucose 6-phosphate dehydrogenase, N-

terminal domain {Leuconostoc mesenteroides}

VSEIKTLVTFGGTGD LAKRKLYPSVFNLYKKGYLQKHFAIVGTARQALNDDEFKQLVRD
CIKDFTDDQAQAEAFIEHFSYRAHDVTD AASYAVLKEAIEEAADKFDIDGNRIFYMSVAPR
FFGTIAKYLKSEGLLADTGYNRLMIEKPFGT SYDTAAELQNDLEN AFDDNQLFRIDHYLG
XEPYERMIHDTMNGD

>d1qkia1 c.2.1.3 (A:12-199,A:435-449) Glucose 6-phosphate dehydrogenase, N-terminal domain {Human (Homo sapiens)}

VCGILREELFQGDAFHQSDTHIFIIMGASGDLAKKKIYPTIWWLFRDGLLPENTFIVGYARS
RLTVADIRKQSEPFKATPEEKLKLEDDFARN SYVAGQYDDAASYQRLNSHMNALHLGSQ
ANRLFYLALPPTVYEAVTKNIHESCMSQIGWNR IIVEKPFGRDLQSSDRLSNHISSLFREDQ
IYRIXDAYERLILDVFCGSQ

>d2naca1 c.2.1.4 (A:148-335) Formate dehydrogenase {Pseudomonas sp., strain 101}

ISVAEHVVMMLSLVRNYLPSHEWARKGGWNIADCVSHAYDLEAMHVGTVAAGRIGLAV
LRR LAPFDVHLHYTDRHRLPESVEKELNLTWHATREDMYPVCDVVTLCNPLHPETEHMI
NDETLKLFKRGAYIVNTARGKLCDRDAVARALESGRLAGYAGDVWFPQPAPKDHPWRTM
PYNGMTPHISG

>d1qp8a1 c.2.1.4 (A:83-263) Putative formate dehydrogenase {Archaeon Pyrobaculum aerophilum}

ADAVAEFALALLAPYKR IIQYGEKMKRGDYGRDVEIPLIQGEKVAVLGLGEIGTRVGKIL
AALGAQVRGFSRTPKEGPWRFTNSLEEALREARA AVCALPLNKHTRGLVKYQHLALMAE
DAVFVNVGRAEVLDRDGVLRILKER PQFIFASDVWWGRNDFAKDAEFFSLPNVVATPWV
AG

>d1dxy_1 c.2.1.4 (101-299) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}

SPAAIAEFALTDTLYLLRNMGKVQAQLQAGDY EKAGTFIGKELGQQTVGVMGTGHIGQV
AIKLFKGFGAKVIAYDPYPMKGDHPDFDYVSLEDL FKKQSDVIDLHVP GIEQNTHINEAAF
NLMKPGAIVINTARP NLDTQAMLSNLKSGKLAGVGIDTYEYETEDLLNLAKHGSFKDPL
WDELLGMPNVVLSPHIAYY

>d1gdha1 c.2.1.4 (A:101-291) D-glycerate dehydrogenase {Hyphomicrobium methylavorum}

VTVATAEIAMLLLLGSARRAGEGEGKMIRTRSWPGWEPELVLGKLDNKT LGIYGFGSIGQ
ALAKRAQGFDMDIDYFDTHRASSSDEASYQATFHDSLDSLLSVSQFFSLNAPSTPETRYFF
NKATIKSLPQGAIVVNTARGDLVDNELVVAALEAGRLAYAGFDVFAGEPNINEGYDLPNT
FLFPHIGSA

>d1psda1 c.2.1.4 (A:108-295) Phosphoglycerate dehydrogenase {Escherichia coli}

NTRSV AELVIGELLLLLRGVPEANAKAHRGVWNKLAAGSFEARGKKLGIIIGYGHIGTQLG
ILAESLGMVYFYFYDIENKLPLGNATQVQHLSDLLNMSDVVSLHVPENPSTKNMMGAKEIS
LMKPGSLLINASRGTVVDIPALCDALASKHLAGAAIDVFPTEPATNSDPFTSPLCEFDNVLL
TPHIGG

>d1pjca1 c.2.1.4 (A:136-303) L-alanine dehydrogenase {Phormidium lapideum}

AGRLSVQFGARFLERQQGGRGVLLGGVPGVKPGKV VILGGGVVGTEAAKMAVGLGAQV
QIFDINVERLSYLETFLGSRVELLYSNSAEIETAVAEADLLIGAVLVPGRRAPILVPASLVEQM
RTGSVIVDVAVDQGGCVETLHPTSHTQPTYEVFGVVHYGVPNMPGA

>d1f8ga1 c.2.1.4 (A:144-326) Nicotinamide nucleotide transhydrogenase dI component {Rhodospirillum rubrum}

AGYRAVIDGAYEFARAFPMMMTAAGTVPPARVLVFGVGVAGLQAIATAKRLGAVVMATD

VRAATKEQVESLGKFITVDDEAMKTAETAGGYAKEMGEEFRKKQAEAVLKELVKTDAI
TTALIPGKPAPVLITEEMVTKMKPGSVIIDLAVEAGGNCPLSEPGKIVVKHGVKIVGHTNVP
SR

>d1b3ra1 c.2.1.4 (A:190-352) S-adenosylhomocystein hydrolase {Rat (*Rattus norvegicus*)}
NLYGCRESLIDGIKRATDVMIAGKVAVVAGYGDVVGKCAQALRGFGARVIITEIDPINALQ
AAMEGYEVTMTDEACEKEGNIFVTTTGCVDIILGRHFEQMKDDAIVCNIGHFDVEIDVKWL
NENAVEKVNIPQVDRYLLKNGHRIILAEGRNVNLGCAMGH

>d1civa1 c.2.1.5 (A:12-193) Malate dehydrogenase {Flaveria bidentis, chloroplast}
LPAKQKPECFGVFCLTYDLKAEETKSWKKIINVAVSGAAGMISNHLFLKASGEVFGPDQ
PISLKLGSERSFAALEGVAMELEDSLYPLLRQVSIGIDPYEIFQDAEWALLIGAKPRGPGM
ERADLLDINGQIFAEQKALNAVASPNVKVMVVGNPCNTNALICLKNAPNIPPKNFHAL

>d2cmd_1 c.2.1.5 (1-145) Malate dehydrogenase {Escherichia coli}
MKVAVLGAAGGIGQALALLKTQLPSGSELSLYDIAPVTPGVAVDLSHIPTAVKIKGFSGED
ATPALEGADVVLISAGVRRKPGMDRSDLFNVNAGIVKNLVQQVAKTCPKACIGIITNPVNT
TVAIAAEVLKKAGVYDKNKLFG

>d2hpa1 c.2.1.5 (A:22-162) Malate dehydrogenase {Archaeon *Haloarcula marismortui*}
TKVSVVGAAGTVGAAAGYNIALRDIADDEVFVDIPDKEDDTVGQAADTNHGIAYDSNTR
VRQGGYEDTAGSDVVITAGIPRQPGQTRIDLAGDNAPIMEDIQSSLDEHNDDYISLTTSNP
VDLLNRHLYEAGDRSREQVIG

>d1hya1 c.2.1.5 (A:21-166) L-2-hydroxyisocaproate dehydrogenase, L-HICDH {Lactobacillus
confusus}
ARKIGIIGLGNVGA AVAHGLIAQGVADDYVFIDANEAKVKADQIDFQDAMANLEAHGNIV
INDWAALADADVISTLGNIKLQQDNPTGDRFAELKFTSSMVQSVGTNLKESGFHGVLVV
ISNPVDVITALFQHVTGFPAHKVIGT

>d5ldh_1 c.2.1.5 (1-162) Lactate dehydrogenase {Pig (*Sus scrofa*)}
ATLKEKLIAPVAQQETTIPDNKITVVGVGQVGMACAISILGKSLTDELALVDVLEDKLGGE
MMDLQHGSLFLQTPKIVANKDYSVTANSKIVVVITAGVRQQEGESRLNLVQRNVNVFKFII
PQIVKYSPNCIIIVSNPVDILTYVAWKLSGLPKHRVIG

>d1ceqa1 c.2.1.5 (A:19-163) Lactate dehydrogenase {Malaria parasite (*Plasmodium falciparum*)}
PKAKIVLVGSGMIGGVMATLIVQKNLGDVVLFDIVKNMPHGKALDTSHTNVMAYSNCKV
SGSNTYDDLADSDVVITAGFTKAPGKSDKEWNRDDLPLNNKIMIEIGGHIKKNCNPAFI
IVVTNPVDVMVQLLHQHSGVPPKNKIIGL

>d1ldna1 c.2.1.5 (A:15-162) Lactate dehydrogenase {Bacillus stearothermophilus}
MKNNGGARVVVIGAGFVGASYVFALMNQGIADIVLIDANESKAIGDAMDFNHGKVFAP
KPVDIWHGDYDDCRDADLVVICAGANQKPGETRLDLVDKNIAIFRSIVESVMASGFQGLF
LVATNPVDILTYATWKFSGLPHERVIGSG

>d1llda1 c.2.1.5 (A:7-149) Lactate dehydrogenase {Bifidobacterium longum, strain am101-2}
PTKLAVIGAGAVGSTLAFAAAQRGIAREIVLEDIAKERVEAEVLDMQHGSSFYPTVSDGS
DDPEICRDADMVVITAGPRQKPGQSRLELVGATVNILKAIMPNLVKVAPNAIYMLITNPVDI
ATHVAQKLTGLPENQIFGSG

>d1hyea1 c.2.1.5 (A:1-145) MJ0490, lactate/malate dehydrogenase {Archaeon
Methanococcus jannaschii}
MKVTIIGASGRVGSATALLAKEPFMKDLVLIGREHSINKLEGLREDIYDALAGTRSDANIY
VESDENLRIIDESDVVIITSGVPRKEGMSRMDLAKTNAKIVGKYAKKIAEICDTKIFVITNP

VDVMTYKALVDSKFERNQVFG

>d1qmg2 c.2.1.6 (A:82-307) Acetohydroxy acid isomeroeductase, ketoacid reductoisomerase (KARI) {Spinach (*Spinacia oleracea*)}

SATTFDFDSSVFKKEKVTLSGHDEYIVRGGRNLFPLLPDAFKGIKQIGVIGWGSQAPAQAQ
NLKDSLTEAKSDVVVKIGLRKGSNSFAEARAAGFSEENGTLGDMWETISGSDLVLLLISDS
AQADNYEKVFUSHMKPNSILGLSHGFLGLHLSLQSLGQDFPKNISVIAVCPKGMGPSVRRLYV
QGKEVNGAGINSSFAVHQDVDGRATDVALGWSIALGSPFTFATT

>d1pgja2 c.2.1.6 (A:1-178) 6-phosphogluconate dehydrogenase {Trypanosoma brucei}
SMDVGVVGLGVMGANLALNIAEKGFVAVFNRTYSKSEEFMKANASAPFAGNLKAFET
MEFAAASLKKPRKALILVQAGAATDSTIEQLKKVFEKGDILVDTGNAHFQDQGRRAQQLE
AAGLRFLGMGISGGEAGARKGPAFFPGGTLSVWEEIRPIVEAAAAKADDGRPCVTMNGS
G

>d1f0ya2 c.2.1.6 (A:12-203) Short chain L-3-hydroxyacyl CoA dehydrogenase {Human (*Homo sapiens*)}

KIIVKHVTVIGGGLMGAGIAQVAAATGHTVVVLVDQTEDILAKSKKGIEESLRKVAKKKFAE
NPKAGDEFVEKTLSTIATSTDAASVVHSTDLVVEAIVENLKVKNELFKRLDKFAAEHTIFA
SNTSSLQITSIANATTRQDRFAGLHFFNPVPMKLVEVIKTPMTSQKTFESLVDFSKALGKH
PVSCKDTP

>d1dlja2 c.2.1.6 (A:1-196) UDP-glucose dehydrogenase (UDPGDH) {Streptococcus pyogenes}

MKIAVAGSGYVGLSLGVLLSLQNEVTIVDILPSKVDKINNGLSPIQDEYIEYYLKSKQLSIK
ATLDSKAAYKEAELVIIATPTNYSRINYFDTQHVETVIKEVLSVNSHATLIKSTIPIGFITE
MRQKFQTDRIIFSPEFLRESKALYDNLPSRIIVSCEENDSPKVKADAEKFALLLKSAACKN
NVPVLIMG

>d1bg6_2 c.2.1.6 (4-187) N-(1-D-carboxylethyl)-L-norvaline dehydrogenase {Arthrobacter, strain 1c}

SKTYAVLGLGNGGHAFAYLALKGQSVLAWDIDAQRIKEIQDRGAIIAEGPGLAGTAHPD
LLTSDIGLAVKDADVLIVVPAIHHASIAANIASYISEGQLIILNPGATGGALEFRKILRENGA
PEVTIGETSSMLFTCRSERPGQVTVNAIKGAMDFACLPAAKAGWALEQIGSVLPQYVAVE

>d1levya2 c.2.1.6 (A:9-188) Glycerol-3- phosphate dehydrogenase {Trypanosome (*Leishmania mexicana*)}

KDELLYLNAKVFGSGAFGTALAMVLSKKCREVCVWHMNEEEVRLVNEKRENVLFLKG
VQLASNITFTSDVEKAYNGAEIILFVIPTQFLRGFFEKSGGNLIAYAKEKQVPVLVCTKGIER
STLKFP AEIIGEFLPSPLLSVLAGPSFAIEVATGVFTCVSIASADINVARRLQRMSTG

>d1ks9a2 c.2.1.6 (A:1-167) Ketopantoate reductase PanE {Escherichia coli}

MKITVLGCGALGQLWLTALCKQGHEVQGWLRVPQPYCSVNLVETDGSIFNESLTANDPDF
LATSDLLLVTLKAWQVSDAVKSLASTLPVTTPIILLHNGMGITIEELQNIQQPLLMTTTHA
ARRDGNVHHVANGITHIGPARQQDGDYSYLADILQTVLPDVAWHN

>d1jaya_ c.2.1.6 (A:) Coenzyme F420H2:NADP+ oxidoreductase (FNO) {Archaeon *Archaeoglobus fulgidus*}

MRVALLGGTGNLKGGLALRLATLGHEIVVGSRRREEKAEAKAAEYRRIAGDASITGMKNE
DAAEACDIAVLTPWEHAIDTARDLKNILREKIVVSPLVPVSRGAKGFTYSSERSAAEIVAE
VLESEKVVVSALHTIPAARFANLDEKFDWDVPVCGDDDESCKVVMSEIDGLRPLDAGP
LSNSRLVESLTPLILNIMRFNGMGELGIKFL

>d1bgva1 c.2.1.7 (A:195-449) Glutamate dehydrogenase {Clostridium symbiosum}
KARSFGGSLVRPEATGYGSVYYYVEAVMKHENDTLVGKTVALAGFGNVAWGAAKKLAEL
GAKAVTLSPDGYIYDPEGITTEEKINYMLEMNASGRNKVQDYADKFGVQFFPGEKPWD
QKVDIIMPCATQNDVDLEQAKKIVANNVYYIEVANMPTTNEALRFLMQQPNMVVAPSK
AVNAGGVLVSGFEMSQNSERLSWTAEVDSKLHQVMTDIHDGSAAAERYGLGYNLVA
GANIVGFQKIADAMMAQGIW

>d1gtma1 c.2.1.7 (A:181-419) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}
GGSLGRIEATARGASYTIREAAKVLGWDTLKGKTIAIQGYGNAGYYLAKIMSEDFGMKV
VAVSDSKGGIYNPDGLNADEVLKWKNEHGSVKDFPGATNITNEELLELEVVLAPAAIEE
VITKKNADNIKAKIVAEVANGPVTPEADEILFEKGILQIPDFLCNAGGVTVSFYFEWVQNITG
YYWTIEEVRERLDKKMTKAFYDVYNIAKEKNIHMRDAAYVVAVQRVYQAMLDRGWVK
H

>d1hwxal c.2.1.7 (A:209-501) Glutamate dehydrogenase {Cow (Bos taurus)}
HGRISATGRGVFHHGIENFIENASYMSILGMTPGFGDKTFAVQGFNGVGLHSMRYLHRFGA
KCVAVGESDGSIWNPDGIDPKELEDFKLQHGTLGFPKAKIYEGSILEVDCDILIPAASEKQL
TKSNAPRVKAKIIAEGANGPTTPQADKIFLERNIMVIPDLYLNAGGVTVSFYQILKNLNHV
SYGRLTFKYERDSNYHLLMSVQESLERKFGKHGGTIPIVPTAEFQDRISGASEKDIVHSL
AYTMERSARQIMRTAMKYNLGLDLRTAAYVNAIEKVFRVYNEAGVTFT

>d1lehal c.2.1.7 (A:135-364) Leucine dehydrogenase {Bacillus sphaericus}
GISPAFGSSGNPSPVTAYGVYRGMKAAAKEAFGSDSLEGLAVSVQGLGNVAKALCKKLNT
EGAKLVVTDVNKA AVSAVAEEGADAVAPNAIYGVTCDFAPCALGAVLNDFTIPQLKAK
VIAGSADNQLKDPRHGKYLHELGIYAPDYVINAGGVINVADELYGYNRTRAMKRVDGI
YDSIEKIFAISKRDGVPSYVAADRMAEERIAKVAKARSQFLQDQRNINLNGR

>d1cldal c.2.1.7 (A:149-349) Phenylalanine dehydrogenase {Rhodococcus sp.,
M4}
SAFTTAVGVFEAMKATVAHRGLGSLDGLTVLVQGLGAVGGSLASLAAEAGAQLLVADTD
TERVAHAVALGHTAVALDVLSTPCDVFAPCAMGGVITTEVARTLDCSVVAGAANNVIAD
EAASDILHARGILYAPDFVANAGGAIHLVGREVLGWSESVHERAVAIGDTLNQVFEISDN
DGVTPDEAARTLAGRRAREAS

>d1a4ial c.2.1.7 (A:127-296) Methylenetetrahydrofolate
dehydrogenase/cyclohydrolase {Human (Homo sapiens)}
LTSINAGRLARGDLNDCFIPCTPKGCELIKETGVPIAGRHAVVVGRSKIVGAPMHDLLLW
NNATVTTCHSKTAHLDEEVNKGDLVVATGQPEMVKG EWIKPGAIVIDCGINYVPDDKKP
NGRKVVGDVAYDEAKERASFITPVPGGVGPMTVAMLMQSTVESAKRFLE

>d1edzal c.2.1.7 (A:149-319) Methylenetetrahydrofolate
dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}
PCTPLAIVKILEFLKIYNNLLPEGNRLYGKKCIVINRSEIVGRPLAALLANDGATVYSVDVN
NIQKFTRGESLKLKHHVEDLGEYSEDLLKKCSLSDSVITGVPSSENYKFPTEYIKEGAVC
INFACKNFSDDVKEKASLYVPMTGKVVTIAMLLRNMLRLVRNVELSKE

>d1do8a1 c.2.1.7 (A:280-573) Mitochondrial NAD(P)-dependent malic enzyme {Human (Homo
sapiens)}
IQGTAVALAGLLAAQKVISKPISEHKILFLGAGEAALGIANLIVMSMVENGLSEQEAQKKI
WMFDKYGLLVKGRKAKIDSYQEPFTHSAPESIPDTFEDAVNILKPSTIIGVAGAGRLFTP
DVI RAMASINERPVIFALSNPTAQAECTAEAYTLTEGRCLFASGSPFGPVKLTDGRVFTPGQG

NNVYIFPGVALAVILCNTRHISDSVFLEAAKALTSQLTDEELAQGRLYPPLANIQEVSINIAI
KVTEYLYANKMAFRYPEPEDKAKYVKERTWRSEYDSLDPVYEW

>d1djna2 c.3.1.1 (A:490-645) Trimethylamine dehydrogenase, C-terminal domain
{Methylophilus methylotrophus, w3a1}

RWNTDGTNCLTHDPIPGADASLPDQLTPEQVMDGKKKIGKRVVILNADTYFMAPSLAEKL
ATAGHEVTIVSGVHLANYMHFTLEYPNMMRRLHELHVEELGDHFCRIEPGRMEIYNIWG
DGSKRITYRGPGVSPRDANTSHRWIEFDSLVLVTGRH

>d1cjca1 c.3.1.1 (A:107-331) Adrenodoxin reductase of mitochondrial p450 systems {Cow (Bos
taurus)}

HQALDIPGEELPGVFSARAFVGVWYNGLPENRELAPDLSCDTAVILGQGNVALDVARILLTP
PDHLEKTDITEAALGALRQSRVKTWVWVGRRGPLQVAFTIKELREMIQLPGTRPMLDPADF
LGLQDRIKEAARPRKRLMELLRLTATEKPGVEEAARRASASRAWGLRFFRSPQQVLPSPD
GRRAGIRLAVTRLEGIGEATRAVPTGDVEDLPCGLVLSSIGY

>d1h7wa3 c.3.1.1 (A:288-440) Dihydropyrimidine dehydrogenase, domain 3 {Pig (Sus scrofa)}
PKTDDIFQGLTQDQGFYTSKDFLPLVAKSSKAGMCACHSPLPSIRGAVIVLGAGDTAFDCA
TSALRCGARRVFLVFRKGFVNIRAVPEEVELAKEEKCEFLPFLSPRKVIVKGGRIVAVQFVR
TEQDETGWNEDEDQIVHLKADVVISAFGS

>d1coy_1 c.3.1.2 (4-318,451-506) Cholesterol oxidase {Brevibacterium sterolicum}
RTLADGDRVPALVIGSGYGGAVAALRLTQAGIPTQIVEMGRSWDTPGSDGKIFCGMLNPD
KRSMWLADKTDQPVSNFMGFGINKSIDRYVGVLDSERFSGIKVYQGRGVGGGSLVNGG
MAVTPKRNYPFEEILPSVDSNEMYNKYFPRANTGLGVNNIDQAWFESTEWYKFARTGRKT
AQRSGFTTAFVFNVDYFEYMKKEAAGQVTKSGLGGEVIYGNNAGKKSLDKTYLAQAAA
TGKLTITTLHRVTKVAPATGSGYSVTMEQIDEQGNVATKVVTADRVFFAAGSVGTSKLLV
SMKAQGHLPNLSSQVGEGWXGVLLNKATDNFGRLEPYPGLYVVDGSLVPGNVGVNPFV
TITALAERNMDKIISDI

>d1k0ia1 c.3.1.2 (A:1-173,A:276-394) p-Hydroxybenzoate hydroxylase, PHBH {Pseudomonas
aeruginosa}

MKTQVAIIAGPSGLLLGQLLHKAGIDNVILERQTPDYVLGRIRAGVLEQGMVDLLREAG
VDRRMARDGLVHEGVEIAFAGQRRRIDLKRLSGGKTVTVYQGTEVTRDLMEAREACGAT
TVYQAAEVRLLHDLQGERPYVTFERDGERLRLDCDYIAGCDGFHGISRQSIAPERXMQHGR
LFLAGDAAHIVPPTGAKGLNLAASDVSTLYRLLLKAYREGRGELLERYSAICLRIWKAER
FSWWMTSVLHRFPDADFQRIQQTELEYLSEAGLATIAENYVGLPYEEIE

>d1el8a1 c.3.1.2 (A:1-217,A:322-385) Sarcosine oxidase {Bacillus sp., strain b0618}
STHFDVIVVGAGSMGMAAGYQLAKQGVKTLLVDAFDPHTNGSHHGDTRIIRHAYGEGR
EYVPLALRSQELWYELEKETHHKIFTKTGVLVFGPKGESAFVAETMEAAKEHSLTVDLLE
GDEINKRWPGITVPENYNAIFEPNSGVLFSENCIRAYRELAARGAKVLTHTRVEDFDISPD
SVKIETANGSYTADKLIVSMGAWNSKLLSKLNLDPXDEHFIIDLHPEHSNVVIAAGFSGHG
FKFSSGVGEVLSQLALTGKTEHDISIFSINRPALKESLQ

>d1foha5 c.3.1.2 (A:1-240,A:342-461) Phenol hydroxylase {Soil-living yeast (Trichosporon
cutaneum)}

TKYSESYCDVLIVGAGPAGLMAARVLSEYVRQKPDCLKVRIIDKRSTKVYNGQADGLQCR
TLESLKNLGLADKILSEANDMSTIALYNPDENGHIRRTDRIPDTLPGISRYHQVVLHQGRIE
RHILDSIAEISDTRIKVERPLIPEKMEIDSSKAEDPEAYPVTMTLRYMSDHESTPLQFGHKTE
NSLFHSNLQTQEEEDANYRLPEGKEAGEIETVHCKYVIGCDGGHWSVRRTLGFEMIXVTE

KFSKDERVFIAGDACHTHSPKAGQGMNTSMMDTYNLGWKLGLVLTGRAKRDILKTYEEE
RHAFQAALIDFDHQFSRLFSGRPAKDVADEMGVSMDFKEAFVKGNEFASGTAINYDE

>d1gpea1 c.3.1.2 (A:1-328,A:525-587) Glucose oxidase {*Penicillium amagasakiense*}

YLPAAQIDVQSSLLSDPSKVAGKTYDYIIAGGGTLTGLTVAAKLTENPKIKVLVIEKGFYESN
DGAIIEDPNAYGQIFGTTVDQNYLTVPLINNRTNNIKAGKGLGGSTLINGDSWTRPDKVQI
DSWEKVFGMEGWNWDMFEYMKKAEAAARTPTAAQLAAGHSFNATCHGTNGTVQSGA
RDNGQPWSPIMKALMNTVSALGVPVQQDFLCGHPRGVSMIMNNLDENQVRVDAARAW
LLPNYQRSNLEILTQOMVGKVLFKQTASGPQAVGVNFGTNKAVNFDVFAKHEVLLAAGS
AISPLILEYSGIGLKSVDLQANVTQLLDLPVGIXCSMMSRELGGVVDATAKVYGTQGLRVI
DGSIPPTQVSSHVMTIFYGMALKVADAILDDYAKSA

>d1b5qa1 c.3.1.2 (A:5-293,A:406-463) Polyamine oxidase {Maize (*Zea mays*)}

PRVIVVGAGMSGISAARKLSEAGITDLLILEATDHIGGRMHKTNFAGINVELGANWVEGV
NGGKMNPWPIVNSTLKLNRNFRSDFDYLAQNVYKEDGGVYDEDYVQKRIELADSVEEM
GEKLSATLHASGRDDMSILAMQRLNEHQPNPATPVDMMVVDYKFDYEFAPPRVTSLQ
NTVPLATFSDFGDDVYFVADQRGYEAUVYYLAGQYLKTDDKSGKIVDPRLQLNKVVREI
KYSPGGVTVKTEDNSVYSADYVMVSASLGLVQSDLIQFKPKLPTWKVRAIYQFXWPVGV
NRYEYDQLRAPVGRVYFTGEHTSEHYNGYVHGAYLSGIDSAEILINCAQKKMC

>d1f8ra1 c.3.1.2 (A:4-319,A:433-486) L-amino acid oxidase {Malayan pit viper (*Calloselasma rhodostoma*)}

RNPLAECFQENDYEEFLEIARNGLKATSNPKHVIVVGAGMAGLSAAYVLAGAGHQVTVL
EASERPGGRVRYTYRNEEAGWYANLGPMLRPEKHRIVREYIRKFDLRLNEFSQENDNAWY
FIKNIRKKVGEVKKDPGLLKYPVKPSEAGKSAGQLYEESLGKVVEELKRTNCSYILNKYD
TYSTKEYLIKEGDLSPGAVDMIGDLLNEDSGYYVSFIESLKHDDIFAYEKRFEIVDGMMDK
LPTAMYRDIQDKVHFNAQVIKIQQNDQKVTVVYETLSKETPSVTADYVIVCTTSRAVRLIK
FNPPLPKKAHALRSVXFPTYQFQHFSDPLTASQGRIYFAGEYTAQAHGWIDSTIKSGLRA
ARDVNLASEN

>d1gosa1 c.3.1.2 (A:4-289,A:402-500) Monoamine oxidase B {Human (*Homo sapiens*)}

KCDVVVVGGGISGMAAAKLLHDSGLNVVLEARDRVGGRTYTLRNQKVKYVDLGGSY
VGPTQNRILRLAKELGLETYKVNEVERLIHHVKGKSYPRGPFPPVWNPITYLDHNNFWR
TMDDMGREIPSDAPWKAPLAEEDWNMTMKELLDKLCWTESAKQLATLFVNLCVTAETH
EVSALWFLWYVKQCGGTTRIISTTNGGQERKFVGGSGQVSERIMDLLGDRVKLERPVIYID
QTRENVLVETLHHEMYEAKYVISAIPPTLGMKIHFNPLPMMRNQMITRVXFPPGILTQYG
RVLRQPVDRIYFAGTETATHWSGYMEGAVEAGERAAAREILHAMGKIPEDEIWQSEPEVD
VPAQPITTTFLERHLPSVPGLLRLLGLTT

>d1chua2 c.3.1.4 (A:2-237,A:354-422) L-aspartate oxidase {*Escherichia coli*}

NTLPEHSCDVLIIGSGAAGLSLALRLADQHQVIVLSKGPVTEGSTFYAQGGIAAVFDETDSDI
DSHVEDTLIAGAGICDRHAVEFVASNARSCVQWLIDQGVLFDTIQPNGEESYHLTREGG
HSHRRILHAADATGREVETTLVSKALNHPNIRVLERTNAVDLIVSDKIGLPGTRRVVGAWV
WNRNKETVETCHAKAVVLATGGASKVYQYTTNPDISSGDGIAMAWRAGCRVANXCGGV
MVDDHGRTDVEGLYAIGEVSYTGLHGANRMASNSLLECLVYGWSAAEDITRRMPYAHDI
STLPPW

>d1fuma2 c.3.1.4 (A:1-225,A:358-442) Fumarate reductase flavoprotein subunit {*Escherichia coli*}

QTFQADLAIVGAGGAGLRAAIAAAQANPNAKIALISKVYPMRSHTVAAEGGSAAVAQDH
DSFEYHFHDTVAGGDWLCEQDVVDYFVHHCPTEMTQLELWGPCWSRRPDGSVNVRRFG

GMKIERTWFAADKTGFHMLHTLFQTSLQFPQIQRFDEHFVLDILVDDGHVRGLVAMNMM
EGTLVQIRANAVVMATGGAGRVYRYNTNGGIVTGDGMGMALSHGVPLRDXMGGIETDQ
NCETRIKGLFAVGECSSVGLHGANRLGSNSLAELVVFGRLAGEQATERAATAGNGNEAAI
EAQAAGVEQRLKDLVNQ

>d1qlaa2 c.3.1.4 (A:1-250,A:372-457) Fumarate reductase flavoprotein subunit {Wolinella
succinogenes}

MKVQYCDSLVIGGGLAGLRAAVATQQKGLSTIVLSLIPVKRSHSAAAQGGMQASLGNSK
MSDGDNEDLHFMDTVKGSDWGCQKVARMFVNTAPKAIRELAAWGVPWTRIHKGDRM
AIINAQKTTITEEDFRHGLIHSRDFGGTKKWRTCYTADATGHTMLFAVANECLKLGVSIQD
RKEAIALIHQDGKCYGAVVRDLVTGDIIAYVAKGTLIATGGYGRIYKNTTNAVVCCEGTGTA
IALETGIAQLGNXMGGIRTDIRGEAKLKGFLSAGEAACWDMHGFNRLGGNSVSEAVVAG
MIVGEYFAEHCANTQVDLETKTLEKFKVKGQEAYMKSLVES

>d1d4ca2 c.3.1.4 (A:103-359,A:506-570) Flavocytochrome c3 (respiratory
fumarate reductase) {Shewanella putrefaciens}

KFVPVDADKAAQDKAIAAGVKETTDVVIIGSGGAGLAAAVSARDAGAKVILLEKEPIPGG
NTKLAAGGMNAAETKPQAKLGIEDKKQIMIDDTMKGGRNINDPELVKVLANNSSDSIDW
LTSMGADMTDVGRMGASVNRSHRPTGGAGVGHAHVAQVLWDNAVKRGTDIRLNSRVV
RILEDASGKVTGVLVKGEYTGYYVIKADAVVIAAGGFAKNNERVSKYDPKLKGFKATNH
PGATGDGLDVALQAGAATRDLEXMGGGLVIDTKAEVKSEKTGKPITGLYAAGEVTGGVHG
ANRLGGNAISDIVTYGRIAGASAAKFAKD

>d1jnra2 c.3.1.4 (A:2-256,A:402-502) Adenylylsulfate reductase A subunit {Archaeon
Archaeoglobus fulgidus}

VYYPKKYELYKADEVPTVEVETDILIIGGGFSGCGAAYEAAYWAKLGGLKVTLVEKAAVE
RSGAVAQGLSAINTYIDLTGRSERQNTLEDYVRYVTLDMMGLAREDLVADYARHVDGTV
HLFEKWGLPIWKTPDGKYVREGQWQIMIHGESYKPIIAEAAKMAVGEENIYERVFIKELLK
DNNDPNAVAGAVGFSVREPKFYVFKAKAVILATGGATLLFRPRSTGEAAGRTWYAIFDTGS
GYYMGLKAGAMLTQXAGFWVCGPEDLMPEEYAKLFLPKYNRMFTTVKGLFAIGDCAGA
NPHKFSSGSFTEGRIAAKAAVRFILEQKPNPEIDDAVVEELKKKAYAPMERFMQYKDLS

>d3grs_1 c.3.1.5 (18-165,291-363) Glutathione reductase {Human (Homo sapiens)}

VASYDYLVIIGGGSGGLASARRAAELGARAADVESHKLGGTCVNVGCVPKKVMWNTAVH
SEFMHDHADYGFPSCGKFNWRVIKEKRDAYVSRLNAIYQNNLTSHIEIIRGHAAFTSDP
KPTIEVSGKKYTAPHILIATGGMPSTPHEXRPNTKDLSLNKLGIQTDDKGHIIVDEFQNTN
VKGIYAVGDVCGKALLTPVAIAAGRKLALHRLFEYKEDSKLD

>d3grs_2 c.3.1.5 (166-290) Glutathione reductase {Human (Homo sapiens)}

SQIPGASLGITSDGFFQLEELPGRSVIVGAGYIAVEMAGILSALGSKTSLMIRHDKVLRSFDS
MISTNCTELENAGVEVLKFSQVKEVKKTLSGLEVSMVTAVPGRLPVMTMIPDVEDCLLWA
IG

>d1feca1 c.3.1.5 (A:1-169,A:287-357) Trypanothione reductase {Crithidia fasciculata}

SRAYDLVVIGAGSGGLEAGWNAASLHKKRVAVIDLQKHHGPPHYAALGGTCVNVGCVPK
KLMVTGANYSMDTIRESAGFGWELDRESVRPNWKALIAAKNKAVSGINDSYEGMFADTE
GLTFHQGFALQDNHTVLVRESADPNSAVLETLDTEYILLATGSWPQHLGIEXPVRSQTLQ
LEKAGVEVAKNGAIKVDAYSKTNDNIYAIGDVTDRVMLTPVAINEGAAFVDTVFANKPR
ATD

>d1feca2 c.3.1.5 (A:170-286) Trypanothione reductase {Crithidia fasciculata}

GDDLCSNEAFYLDEAPKRALCVGGGYISIEFAGIFNAYKARGGQVDLAYRGDMILRGFD
SELRKQLTEQLRANGINVRTHENPAKVTKNADGTRHVVFESGAEDYDVVMLAIGR

>d1h6va1 c.3.1.5 (A:10-170,A:293-366) Mammalian thioredoxin reductase {Rat
(Rattus norvegicus)}

SYDFDLIIIGGSGGLAAAKEAAKFDKKVMVLDFVTPPLGTNWGLGGTCVNVGCIPKKL
MHQAALLGQALKDSRNYGWKLEDTVKHDWEKMTESVQNHIGSLNWGYRVALREKKV
VYENAYGKFIGPHKIMATNNKGKEKVYSAERFLIATGERPRYLGIXRDSCTRTIGLETVGV
KINEKTGKIPVTDEEQTNVPYIYAIGDILEGKLELTPVAIQAGRLLAQRLYGGSTVKCD

>d1h6va2 c.3.1.5 (A:171-292) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}

PGDKEYCISDDLFSLPYCPGKTLVVGASYVALECAGFLAGIGLDVTVMVRSILLRGFDQD
MANKIGEHEHGIKFIKQFVPTKIEQIEAGTPGRLLKVTAKSTNSEETIEDEFNTVLLAVG

>d1vdc_1 c.3.1.5 (1-117,244-316) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}

LETHNTRLCIVGSGPAAHTAAIYAARAELKPLLFEWGMANDIAPGGQLTTTTDVENFPFGP
EGILGVELTDKFRKQSERFGTTIFTETVTKVDFSSKPFKLFTDSKAILADAVILAIGAVAKXG
HEPATKFLDGGVELDSDGYVVTKPGTTQTSVPGVFAAGDVQDKKYRQAITAAGTGCMAA
LDAEHYLQEI

>d1vdc_2 c.3.1.5 (118-243) Thioredoxin reductase {Mouse-ear cress (Arabidopsis thaliana)}

RLSFVGSGEVLGGFWNRGISACAVCDGAAPIFRNKPLAVIGGGDSAMEEANFLTKYGSKV
YIIHRRDAFRASKIMQQRALSNPKIDVIWNSSVVEAYGDGERDVLGGLKVKNVVTGDVS
DLKVSGLFFAI

>d1hyua1 c.3.1.5 (A:199-325,A:452-521) Alkyl hydroperoxide reductase subunit F (AhpF), C-
terminal domains {Salmonella typhimurium}

AEKRAAEALNKRDAYDVLIVGSGPAGAAAAYVSARKGIRTGLMGERFGGQVLDTVDIEN
YISVPKTEGQKLALGALKAHVSDYDVVIDSQSASKLVPAATEGGLHQIETASGAVLKARSII
IATGAKXLPNTHWLEGALERNRMGEIIIDAKCETSVKGVFAAGDCTTVPYKQIIATGEGA
KASLSAFDYLIRTKIA

>d1fl2a2 c.3.1.5 (A:326-451) Alkyl hydroperoxide reductase subunit F (AhpF), C-terminal domains
{Escherichia coli}

WRNMNVPGEDQYRTKGVTYCPHCDGPLFKGKRVAVIGGGNSGVEAAIDLAGIVEHVTLL
EFAPEMKADQVLQDKLRSLKNVDIILNAQTTEVKGDGSKVVGLEYRDRVSGDIHNIELAG
IFVQIGL

>d1nhp_1 c.3.1.5 (1-119,243-321) NADH peroxidase {Enterococcus faecalis}

MKVIVLGSSHGGEAVEELLNLHPDAEIQWYEKGDFISFLSAGMQLYLEGKVVDVNSVR
YMTGEKMESRGVNVFSNTEITAIQPKHQVTVKDLVSGEERVENYDKLIISPGAVPFELDX
GVRPNTAWLKGTLELHPNGLIKTDEYMRTSEPDVFAVGDATLIKYNPADTEVNIALATNAR
KQGRFAVKNLEEPVKPFP

>d1nhp_2 c.3.1.5 (120-242) NADH peroxidase {Enterococcus faecalis}

IPGKDLDNIYLMRGRQWAIKQKTVDPEVNNVVVIGSGYIGIEAAEAFAGKKTVIDI
LDRPLGVYLDKEFTDVLTEEMEANNITATGETVERYEGDGRVQKVVTDKNAYDADLVV
VAV

>d1d7ya1 c.3.1.5 (A:5-115,A:237-308) NADH-dependent ferredoxin reductase, BphA4
{Pseudomonas sp., KKS102}

ALKAPVVVLGAGLASVSFVAELRQAGYQGLITVVGDEAERPYPDRPPLSKDFMAHGDAEK
IRLDCKRAPEVEWLLGVTAQSFDPAHTVALSDGRTLTPYGTLLATGAAPRAXVLANDAL

ARAAGLACDDGIFVDAYGRITTCPDVYALGDVTRQRNPLSGRFERIETWSNAQNQGIABAR
HLVDP

>d1d7ya2 c.3.1.5 (A:116-236) NADH-dependent ferredoxin reductase, BphA4 {*Pseudomonas* sp.,
KKS102}

LPTLQGATMPVHTLRTLEDARRIQAGLRPQSRLIVGGGVIGLELAATARTAGVHVSLVET
QPRLMSRAAPATLADFFVARYHAAQGVDLRFERSVTGSVDGVVLLDDGTRIAADMVVVGI
G

>d1lv1_1 c.3.1.5 (1-150,266-335) Dihydrolipoamide dehydrogenase {*Pseudomonas putida*}
QQTIQTLLIIGGGPGGYVAAIRAGQLGIPTVLVEGQALGGTCLNIGCIPSKALIHVAEQFHQ
ASRFTEPSPLGISVASPRLDIGQSVAWKDGIVDRLTTGVAALLKKHGVKVVHGWAKVLDG
KQVEVDGQRIQCEHLLLATGSSSVLPXRRPRTKGFNLECLDLKMNGAAIAIDERCQTSM
HNVWAIGDVAGEPMLAHRAMAQGEMVAEIIAGKARRFE

>d1lpfa2 c.3.1.5 (A:159-277) Dihydrolipoamide dehydrogenase {*Pseudomonas*
fluorescens}

PAPLSDDIIVDSTGALEFQAVPKKLGVIGAGVIGLELGSVWARLGAEVTVLEALDKFLPAA
DEQIAKEALKVLTQGLNIRLGARVTASEVKKKQVTVTFTDANGEQKETFDKLIVAVG

>d1ojt_1 c.3.1.5 (117-275,401-470) Dihydrolipoamide dehydrogenase {*Neisseria meningitidis*}
GSADA EYDVVVLGGPGGYSAFAAADEGLKVAIVERYKTLGGVCLNVGCIPSKALLHN
AAVIDEVRHLAANGIKYPEPELDIDMLRAYKDG VVSRLTGGLAGMAKSRKVDVIQGDGQ
FLDPHLEVSLTAGDAYEQAAPTGEKKIVAFKNCIIAAGSRXAPNGKLISA EKAGVAVTDR
GFIEVDKQMRNTNPHIYAIGDIVGQPM LAHKAVHEGHVAAENCAGHKAYFD

>d1ojt_2 c.3.1.5 (276-400) Dihydrolipoamide dehydrogenase {*Neisseria meningitidis*}
VTKLPFIPEDPRIIDSSGALALKEVPGKLLIIGGGIIGLEMGT VYSTLGSRLDV VEMMDGLM
QGADRDLVKVWQKQNEYRFDNIMVNTKTVAVEPKEDGVYVTFEGANAPKEPQRYDAVL
VAAGR

>d1jeha1 c.3.1.5 (A:1-160,A:283-355) Dihydrolipoamide dehydrogenase {*Baker's yeast*
(*Saccharomyces cerevisiae*)}

TINKSHDVVIIGGGPAGYVAAIKAAQLGFNTACVEKRGKLG GTCLNVGCIPSKALLNNSHL
FHQMHTAQKRGIDVNGDIKINVANFQKAKDDAVKQLTG GIELLFKKNKVTTYKNGSF
EDET KIRVTPVDGLEGT VKEDHILDVKNII VATGSEVTPFXVGRRPYIAGLGA EKIGLEV DK
RGRLVIDDQFNSKFPHIKVVG DVTFGPMLAHKAE EEGIAAV EMLKTGHGHVN

>d1dxa2 c.3.1.5 (A:153-275) Dihydrolipoamide dehydrogenase {*Garden pea (Pisum sativum)*}
SLPGVTIDEKKIVSSTGALALSEIPK KLVVIGAGYIGLEMGSVWGRIGSEVTVVEFA SEIVPT
MDAEIRKQFQRSLEKQGMKF KLT KVVGVDTSGDGVKLTVEPSAGGEQTII EADVVLVS
A

>d1fda1 c.3.1.5 (A:1-114,A:256-327) Flavocytochrome c sulfide dehydrogenase, FCSD,
flavin-binding subunit {*Purple phototrophic bacterium (Chromatium vinosum)*}

AGRKV VVVGGGTGGATAAKYIKLADPSIEVT LIEPNTDY YTCYLSNEVIGGDRKLESIKHG
YDGLRAHGIQVVHDSATGIDPDKKLVKTAGGA EFGYDRCV VAPGIELIYDKIEXQRAGKIA
QIAGLTNDAGWCPVDIKTFESSIHKG IHVIGDASIANPMPKSGYSANSQGVAAA AVVLL
KGEE

>d1fda2 c.3.1.5 (A:115-255) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding
subunit {*Purple phototrophic bacterium (Chromatium vinosum)*}

GYSEEAAAKLPHAWKAGEQTAILRKQLEDMADGGTVVIAPPAAPFRCPGPYERASQVAY

YLKAHKPMSKVIIIDSSQTFQSKQSQFSKGWERLYGFGTENAMIEWHPGPDSAVVKVDGGE
MMVETAFGDEFKADVNLIPP

>d1djna3 c.4.1.1 (A:341-489,A:646-729) Trimethylamine dehydrogenase, middle domain
{Methylophilus methylotrophus, w3a1}

DIRVCIGCNVCISRWEIGGPPMICTQNATAGEEYRRGWHPEKFRQTKNKDSVLIVGAGPSG
SEAARVLMESGYTVHLTDIAEKIGGHLNQVAALPGLGEWSYHRDYRETQITKLLKKNKE
SQLALGQKPMATADDVLQYGADKVIIATGAXSECTLWNLKARESEWAENDIKGIYLGDA
EAPRLIADATFTGHRVAREIEEANPQIAIPYKRETIAGWTPHMPGGNFKIEYKV

>d1cjca2 c.4.1.1 (A:6-106,A:332-460) Adrenodoxin reductase of mitochondrial p450
systems {Cow (Bos taurus)}

TPQICVVGSGPAGFYTAQHLLKHHSRAHVDIYEKQLVPFGLVRFVAPDHPEVKNVINTFT
QTARSDRCAFYGNVEVGRDVTQELQDAYHAVVLSYGAEDXKSRPIDPSVPFDPKLGVV
PNMEGRVVDVPGLYCSGWVKRGPTGVITTTMTDSFLTQILLQDLKAGHLPSGPRPGSAFI
KALLDSRGVWPVSFSDWEKLDAAEEVSRGQASGKPREKLLDPQEMLRLLGH

>d1h7wa4 c.4.1.1 (A:184-287,A:441-532) Dihydropyrimidine dehydrogenase,
domain 2 {Pig (Sus scrofa)}

EAYSAKIALLGAGPASISCASFLARLGYSITIFEKQEYVGGLSTSEIPQFRLPYDVVNFEIEL
MKDLGVKIIICGKSLSENEITLNTLKEEGYKAAFIGLPEXVLRDPKVKEALSPIKFNRWDL
PEVDPETMQTSEPWFAGGDIVGMANTTVESVNDGKQASWYIHKYIQAQYGASVSAKPE
LPLFYTPVDLVD

>d1an9a1 c.4.1.2 (A:1-194,A:288-340) D-amino acid oxidase, N-terminal domain {Pig (Sus scrofa)}

MRVVVIGAGVIGLSTALCIHERYHSLVQLPDVKVYADRFTPFTTTDVAAGLWQPYTSEPSN
PQEANWNQQTFFNYLLSHIGSPNAANMGLTPVSGYNLFREAVDPYWKDMVLGFRKLTPR
ELDMFPDYRYGWFNSTLILEGRKYLQWLTERLTERGVKFFLRKVESFEEVARGGADVIINC
TGVWAGVLQPDPLXQVRLEREQLRFGSSNTEVIHNYGHGGYGLTIHWGCALEVAKLFGK
VLEERNLL

>d1c0pa1 c.4.1.2 (A:999-1193,A:1289-1361) D-amino acid oxidase, N-terminal domain
{Yeast (Rhodotorula gracilis)}

LMMHSQKRVVVLGSGVIGLSSALILARKGYSVHILARDLPEDVSSQTFASPWAGANWTPF
MTLTDGPRQAKWEESTFKKWVELVPTGHAMWLKGTRRFAQNEDGLLGHWYKDITPNY
RPLPSSECPPGAIGVTYDLSVHAPKYCQYLARELQKLGFERRTVTSLEQAFDQADLVV
NATGLGAKSIAGIDDQAXRGGPRVEAERIVLPLDRTKSPLSLGRGSARAAKEKEVTLVHAY
GFSSAGYQQSWGAAEDVAQLVDEAFQRYHG

>d1tml_ c.6.1.1 (-) Cellulase E2 {Thermomonospora fusca, strain yx}

NDSPFYVNPNMSSAEWVRNNPNDPRTPVIRDRIASVPQGTWFAHHNPGQITGQVDALMS
AAQAAGKIPILVVYNAPGRDCGNHSSGGAPSHSAYRSWIDEFAAGLKNRPAYIIVEPDLISL
MSSCMQHVVQEVLETMAYAGKALKAGSSQARIYFDAGHSAWHSPAQMASWLQQADISN
SAHGATNTSNYRWTADEVAYAKAVLSAIGNPSLRAVIDTSRNGNGPAGNEWCDPSGRAIG
TPSTTNTGDPMIDAFLWIKLPGEADGCIAGAGQFVPQAAYEMAIAA

>d1qjwa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Trichoderma reesei, Cel6a}

ATYSGNPFVGVTPWANAYYASEVSSLAIPSLTGAMATAAAVAKVPSFMWLDTLDKTPLM
EQTLADIRTANKNGGNYAGQFVVFDPDRDCAALASNGEYSIADGGVAKYKNYIDTIRQI
VVEYSDIRTLVIEPDSLNLVTNLGTPKCANAQSAYLECIYAVTQLNLPNVAMYLDAGH
AGWLGWANQDPAAQLFANVYKNASSPRALRGLATNVANYNGWNITSPPSYTQGNVY

NEKLYIHAIGPLLANHGWSNAFFITDQGRSGKQPTGQQQWGDWCNVIGTGFGIRPSANTG
DSLSDSFVWVKPGGECGTSDSSAPRFDSHCALPDALQPAPQAGAWFQAYFVQLLTNAN
PSFL

>d1dysa_ c.6.1.1 (A:) Cellobiohydrolase II (Cel6) {Humicola insolens, Cel6b}

GNPFSGRITLLVNSDYSSKLDQTRQAFLSRGDQTNAAKVKYVQEKVGTFFYWISNIFLLRDI
DVAIQNARAANKARGENPIVGLVLYNLPDRDCSAGESSGELKLSQNGLNRYKNEYVNPFAQ
KLKAASDVQFAVILEPDAIGNMVTGTSAFCRNARGPQQEAIGYAISSLQASHIHLYLDVAN
GGWLGWADKLEPTAQEVATILQKAGNNAKIRGFSSNVSNYPYSTSNPPPYTSGSPSPDES
RYATNIANAMRQRGLPTQFIIDQSRVALSGARSEWGQWCNVNPAGFGQPFTTNTNPNVD
AIVWVKPGGESDGQCGMGGAPAAAGMWFDAYAQMLTQNAHDEIA

>d1e8ca1 c.98.1.1 (A:3-87) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}
RNLRLDLLAPWVPDAPSRLREMTLDSRVAAAGDLFVAVVGHQADGRRYIPQAIAQGVAAI
IAEAKDEATDGEIREMHGVPVIYLS

>d1gg4a3 c.98.1.1 (A:1-81) UDP-murNac-tripeptide D-alanyl-D-
alanine-adding enzyme MurF {Escherichia coli}

MISVTLSQLTDILNGELQGADITLDAVTTDTRKLTGCLFVALKGERFDAHDFADQAKAGG
AGALLVSRPLDIDLPQLIVK

>d1igra1 c.10.2.5 (A:1-149) L1 and L2 domains of the type 1 insulin-like growth factor receptor
{Human (Homo sapiens)}

EICGPGIDIRNDYQQKRLNCTVIEGYLHILLISKAEDYRSYRFPKLTVITEYLLLFRVAGL
ESLGDLPNLTIVIRGWKLFYNYALVIFEMTNLKDIGLYNLRNITRGAIRIEKNADLCYLSTV
DWSLILDAVSNNYIVGNKPPKECG

>d1igra2 c.10.2.5 (A:300-478) L1 and L2 domains of the type 1 insulin-like growth factor receptor
{Human (Homo sapiens)}

KVCEEEKKTKTIDSVTSAQMLQGCTIFKGNLLINIRRGNNIASELENFMGLIEVVTGYVKIR
HSHALVSLSLKLNRLILGEEQLEGNYSFYVLDNQNQLQQLWDWDHRNLTIKAGKMYFAF
NPKLCVSEIYRMEEVTGKGRQSKGDINTRNNGERASCESDVDDDDKEQKLISEEDLN

>d1jj2k_ c.12.1.1 (K:) Ribosomal protein L15 (L15p) {Archaeon Haloarcula
marismortui}

TSKKKRQRGSRTHGGGSHKNRRGAGHRGGRGDAGRDKHEFHNHEPLGKSGFKRPQKVQ
EEAATIDVREIDENVTLAADDVAEVEDGGFRVDVRDVVEEADDADYVKVLGAGQVRH
ELTLIADDFSEGAREKVEGAGGSVELTDLGEERQ

>d1jj2n_ c.12.1.1 (N:) Ribosomal protein L18e {Archaeon Haloarcula marismortui}

SKTNPRLSSLIADLKSAARSSGGAVWGDVAERLEKPRRTHAEVNLGRIERYAQEDETUVV
PGKVLGSGVLQKDVTVAAVDFSGTAETKIDQVGEAVSLEQAIENNPEGSHVRVIR

>d1h4xa_ c.13.2.1 (A:) Anti-sigma factor antagonist SpoIIaa {Bacillus sphaericus}

AFQLEMVTRETIVIRLFGELDHHAQEIRAKISTAIFQGAVTTIWNFERLSFMDSSGVGLV
LGRMRELEAVAGRTILLNPSPTMRKVVFQFSLGPWMMDATEEEAIDRV

>d1lauz_ c.13.2.1 (-) Anti-sigma factor antagonist SpoIIaa {Bacillus subtilis}

SLGIDMNVKESVLCIRLTGELDHHTAETLKQKVTQSLEKDDIRHIVLNLEDLSFMDSSGLG
VILGRYKQIKQIGGEMVVCALSPAVKRLFDMSGFLKIRFEQSEQQALLTLGVAS

>d1fc6a4 c.14.1.2 (A:78-156,A:249-463) Photosystem II D1 C-terminal processing protease
{Algae (Scenedesmus obliquus)}

VTSEQLLFLEAWRAVDRAVVDKSFNGQSWFKLRETYLKKEPMDRRAQTYDAIRKMLAVL

DDPFTRFLEPSRLAALRRGTXKVTINPVTFTTCSNVAAAALPPGAAKQQLGYVRLATFNSN
TTAAAQQAFTELSKQGVAGLVLDIRNNGGGLFPAGVNVARMMLVDRGDLVLIADSQGIRDI
YSADGNSIDSATPLVVLVNRGTASASEVLGALKDSKRGLIAGERTFGKGLIQTVVDLSDG
SGVAVTVARYQTPAGVDINKIGVSPDVQLDPEVLPTDLEGVCRVLGSDAAPRLF

>d1k32a4 c.14.1.2 (A:680-762,A:854-1061) Tricorn protease {Archaeon Thermoplasma acidophilum}

SSIHEEFLQMYDEAWKLARDNYWNEAVAKEISERIYEKYRNLVPLCKTRYDLSNVIVEMQ
GEYRTSHSYEMGGTFTDKDPFRSXDDRFIRYSWVEANRRYVHERSKGTIGYIHIPDMGM
MGLNEFYRLFINESSYQGLIVDVRFNNGGGFVSQLIIEKLMNKRIGYDNPRRGTLSPYPTNS
VRGKIIAITNEYAGSDGDIFSFSFKKLGLGKLIGTRTWGGVVGITPKRRLIDGTVLTQPEFAF
WFRDAGFGVENYGVDPDVEIEYAPHDYLSGKDPQIDYALIEELRN

>d1j7xa_ c.14.1.2 (A:) Interphotoreceptor retinoid-binding protein IRBP {African clawed frog (Xenopus laevis)}

DPSVTHVLHQLCDILANNYAFSERIPTLLQHLPNLDYSTVISEEDIAAKLNYELQSLTEDPR
LVLKSKTDTLVMPGDSIQAENIPEDEAMLQALVNTVFKVSILPGNIGYLRFDQFADVSVA
KLAPFIVNTVWEPITITENLIIDLRNVGGSSTAVPLLLSYFLDPETKIHFLTLHNRQQNSTD
EVYSHPKVLGKPYGSKKGVYVLTSHQTATAAEFAYLMQSLSRATIIGEITSGNLMHSHKVF
PFGDTQLSVTPPIINFIDSNGDYWLGGGVVPDAIVLADEALDKAKEIIAFHPPLA

>d1nzya_ c.14.1.3 (A:) 4-Chlorobenzoyl-CoA dehalogenase {Pseudomonas sp., strain CBS-3}
MYEAIGHRVEDGVAEITIKLPRHRNALSVKAMQEVTDALNRAEEDDSVGAVMITGAEDA
FCAGFYLRPIPLDKGVAGVRDHFRIAALWWHQMIHKIIRVKRPVLAANGVAAGGGLGISL
ASDMAICADSAKFVCAWHTIGIGNDTATSYSLARIVGMRRAMELMLTNRTLYPEEAKDW
GLVSRVYPKDEFREVAWKVARELAAAPTHLQVMAKERFHAGWMQPVEECTEFEIQNVIA
SVTHPHFMPCLTRFLDGHRADRPQVELPAGV

>d1ey3a_ c.14.1.3 (A:) Enoyl-CoA hydratase (crotonase) {Rat (Rattus norvegicus)}
FQYIITEKKGKNSSVGLIQLNRPKALNALCNGLIEELNQALETFEEDPAVGAIVLTGGEKAF
AAGADIKEMQNRTFQDCYSKGFLSHWDHITRIKKPVIAAVNGYALGGGCELAMMCDIYA
GEKAQFGQPEILLGTIPGAGGTQRLTRAVGKSLAMEMVLTGDRISAQDAKQAGLVSKIFPV
ETLVEEAIQCAEKIANNSKIIVAMAKESVNAAFEMTLTEGNKLEKKLFYSTFATDDRREGM
SAFVEKRKANFKDH

>d1dcia_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Rat (Rattus norvegicus)}

AYESIQVTSAQKHVLHVQLNRPEKRNAMNRAFWRELVECFQKISKDSDCRAVVVSGAGK
MFTSGIDLMDMASDILQPPGDDVARIWYLRDLISRYQKTFTVIEKCPKPVIAAIHGGCIGG
GVDLISACDIRYCTQDAFFQVKEVDVGLAADVGTLQRLPKVIGNRSLVNELTFTARKMMA
DEALDSGLVSRVFPDKDVMLNAAFALAADISSKSPVAVQGSKINLIYSRDHSVDES LDYM
ATWNMSMLQTQDIKSVQAAMEKKDSKSITFSKL

>d1hnua_ c.14.1.3 (A:) Dienoyl-CoA isomerase (delta3-delta2-enoyl-CoA isomerase) {Baker's yeast (Saccharomyces cerevisiae)}

NEKISYRIEGPFFIIHLINPDNLNALEGEDYIYLGELLELADRNRDVYFTIIQSSGRFFSSGAD
FKGIAKAQGGDTNKYPSETSKWVSNFVARNVYVTDAFIKHSHKVLICCLNGPAIGLSAALV
ALCDIVYSINDKVYLLYPFANLGLITEGGTTVSLPLKFGTNTTYECLMFNKPFPKYDIMCEN
GFISKNFNMPSNAEAFNAKVLEELREKVKGlyLPSCLGMKKLLKSNHIDAFNKAANSVEV
NESLKYWVDGEPLKRFRQ

>d1hzda_ c.14.1.3 (A:) AUH protein {Human (Homo sapiens)}

EDELVRHLEEEENRGIVVLGINRAYGKNSLSKNLIKMLSKAVDALKSDKKVRTIIIRSEVPG
 IFCAGADLKERAKMSSEVGPVFSKIRAVINDIANLPVPTIAAIDGLALGGGLELALACDIR
 VAASSAKMGLVETKLAIPGGGGTQRLPRAIGMSLAKELIFSARVLDGKEAKAVGLISHVL
 EQNQEGDAAYRKALDLAREFLPQGPVAMRVAKLAINQGMEVDLVTGLAIEEACYAQTIPT
 KDRLEGLLAFKEKRPPRYKGE

>d1ef8a_ c.14.1.3 (A:) Methylmalonyl CoA decarboxylase {Escherichia coli}

MSYQYVNVVTINKVAVIEFN YGRKLNALSKVFIDDLMQALSDLNRPEIRCILRAPSGSKV
 FSAGHDIHELPSGGRDPLSYDDPLRQITRMIQKFKPKIISMVEGSVWGGAFEMIMSSDLIIA
 ASTSTFSMTPVNLGVPYNLVGIHNLTRDAGFHIVKELIFTASPITAQRALAVGILNHVVEVE
 ELEDFTLQMAHHISEKAPLAIAVIKEELRVLGAEHTMNSDEFERIQGMRRAVYDSEDYQEG
 MNAFLEKRKPNFVGH

>d1jnxx1 c.15.1.3 (X:1649-1757) Breast cancer associated protein, BRCA1 {Human (Homo sapiens)}

RMSMVVSGLTPEEFMLVYKFARKHHITLTNLITEETTHVVMKTDAEFVCERTLKYFLGIAG
 GKWVVS YFWVTQSIKERKMLNEHDFEVRGDVVNGR NHQGPKRARES QD

>d1jnxx2 c.15.1.3 (X:1758-1859) Breast cancer associated protein, BRCA1 {Human (Homo sapiens)}

RKIFRGLEICCYGPFTNMPTDQLEWMVQLCGASVVKELSSFTLGTGVHPVVVQPDWTE
 DNGFHAIGQMCEAPVVTREWVLDSVALYQCQELDTYLIPQIP

>d1in1a_ c.15.1.2 (A:) DNA ligase III alpha {Human (Homo sapiens)}

GSADETL CQTKVLLDIFTGVRLYLPPSTPDFSRLRRYFVAFDGLVQEFDMTSATHVLGSR
 DKNPAAQQVSPEWIWACIRKRRVLAPC

>d1dgtb3 c.15.1.2 (B:2582-2660) NAD⁺-dependent DNA ligase, domain 4 {Thermus filiformis}

EEVSDLLSGLTFVLTGELSRPREEVKALLGRLGAKVTDSVSRKTSYLVVGENPGSKLEKAR
 ALGVAVLTEEEFWRFLKE

>d1di0a_ c.16.1.1 (A:) Lumazine synthase {Brucella abortus}

TSFKIAFIQARWHADIVDEARKSFVAELA AKTGG SVEVEIFDVP GAYEIPLHAKTLARTGR
 YAAIVGA AFVIDGGIYDHDFVATAVINGMMQVQLETEVPVLSVVLTPHHFHESKEHHDF
 HAHFKVKGV EAAHAALQIVSERSRIAA

>d1c41a_ c.16.1.1 (A:) Lumazine synthase {Rice blast fungus (Magnaporthe grisea)}

GPTPQQHDGSALRIGIVHARWNETIIEPLLAGTKAKLLACGVKESNIVVQSVPGSWELPIA
 VQRLYSASQLQTPSSGPSLSAGDLLGSSTDTLTALPTTTASSTGPF DALIAIGVLIKGETMHF
 EYIADSVSHGLMRVQLDTGVPVIFGVLT VLTDDQAKARAGVIEGSHNHGEDWGLAAVEM
 GVRRRDWAAGKT

>d1c2ya_ c.16.1.1 (A:) Lumazine synthase {Spinach (Spinacia oleracea)}

MNELEGYVTKAQSFRAIVVARFNEFVTRRLMEGALDTFKKYSVNEDIDVVWVPGAYEL
 GVTAQALGKSGKYHAIVCLGAVVKGDTSHYDAVVNSASSGVLSAGLNSGVPCVFGVLTC
 DNMDQAINRAGGKAGNKGAE SALTAIEMASLFEHHLK

>d1ejba_ c.16.1.1 (A:) Lumazine synthase {Baker's yeast (Saccharomyces cerevisiae)}

AVKGLGKPDQVYDGSKIRVGIIHARWNRVIIDALVKGAIERMASLGVEENNIIETVPGSYE
 LPWGTKRFVDRQAKLGKPLDVVIPIGVLIKGSTMHFEYISDSTTHALMNLQEKVDMPVIF

GLLTCMTEEQALARAGIDEAHSMHNGEDWGAAAVEMAVKFGKNAF

>glibc.1 c.17.1.1 (A:,B:) Interleukin-1beta converting enzyme (a cysteine protease) {Human (Homo sapiens)}

GNVKLCSLEEAQRIWKQKSAEIYPIMDKSSRTRLALICNEEFDSIPRRTGAEVDITGMTML
LQNLGYSVDVKKNLTASDMTTELEAFAHRPEHKTSDSTFLVFMHSHGIREGICGKKHSEQV
PDILQLNAIFNMLNTKNCPSLKDKPKVIIIQACRGDSPGVVWFKDXAIKKAHIEKDFIAFCS
STPDNVSWRHPTMGSVFIGRLIEHMQEYACSCDVEEIFRKVRFSFEQPAGRAQMPTTERTVT
LTRCFYLFPGH

>d1flja_ c.17.1.1 (A:) Caspase-7 {Human (Homo sapiens)}

YQYNMNFELKLGKCIINNKNFDKVTGMGVRNGTDKDAEALFKCFRSLGFDVIVYND CSC
AKMQDLLKKASEEDHTNAACFACILLSHGEENVYIGKDGVTPIKDLTAHFRGDRSKTLL
KPKLFFIQACRGTELDGDIQADSGPINDTDANPRYKIPVEADFLFAYSTVPGYYSWRSPGR
GSWFVQALCSILEEHGKDLEIMQILTRVNDVARHFESQSDDPHFHEKKQIPCVVSMLTKE
LYFS

>d1jxqa_ c.17.1.1 (A:) Caspase-9 {Human (Homo sapiens)}

MGALESRLGNADLAYILSMEPCGHCLINNVCRESGLRTRTGSNIDCEKLRRRFSSLHF
MVEVKGDLTAKKMLALLELARQDHGALDCCVVVILSHGCQASHLQFPGAVYGTGDCP
VSVEKIVNIFNGTSCPSLGGKPKLFFIQACGGEQKDHGFVASTSPEDESPGSNPEPATPF
QEGLRTFDQLDAISSLPTSDIFVSYSFTPGFVSWRDPKSGSWYVETLDDIFEQWAHSEDL
QSLLLRVANAVSVKGIYKQMPGCFNFLRKKLFFKTS

>d1dmga_ c.22.1.1 (A:) Ribosomal protein L4 {Thermotoga maritima}

AQVDLLNVKGEKVGTLISDFVFNIDPNYDVMWRYVDMQLSNRRAGTASTKTRGEVSG
GGRKPWPQKHTGRARHGSIRSPIWRHGGVVGPKPRDWSKKLNNKMKKLALRSALS VK
YRENKLLVLDLKLKLPKTKSLKEILQNLQLSDKKT LIVLPWKEEGYMNVKLSGRNLPDV
KVIIADNPNSKNKEKAVRIDGLNVFDMLKYDYLVLTRDMVSKIEEVLG

>d1jj2c_ c.22.1.1 (C:) Ribosomal protein L4 {Archaeon Haloarcula marismortui}

MQATIYDLGNTDGEVDLPDVFETPVRSDLIGKAVRAAQANRKQDYGSDEYAGLRTPAES
FGSGRGQAHVPKLDGRARRVPQAVKGRSAHPPKTEKDRSLDLNDRERQLAVRSALAATA
DADLVADRGHEFDRDEVVVVSDDFEDLVKTQEVVSLLEALDVHADIDRADETKIKAGQ
GSARGRKYYRPASILFVTSDEPSTAARNLAGADVATASEVNTEDLAPGGAPGRLTVFTESA
LAEVAER

>d1jbea_ c.23.1.1 (A:) CheY protein {Escherichia coli}

ADKELKFLVDDFSTMRIRVNLLKELGFNNVEEAEDGVDALNKLQAGGYGFVISDWN
MPNMDGLELLKTIRADGAMSALPVLMTAEAKKENIIAAAQAGASGYVVKPFTAATLEE
KLNKIFEKLG

>d1tmy_ c.23.1.1 (-) CheY protein {Thermotoga maritima}

GKRVLIVDDAAFMRMMLKDIITKAGYEVAGEATNGREAVEKYKELKPDIVTMDITPEM
NGIDAIKEIMKIDPNAKIIVCSAMGQQAMVIEAIKAGAKDFIVKPFQPSRVVEALNKVS

>d1a04a2 c.23.1.1 (A:5-142) Nitrate/nitrite response regulator (NARL), receiver domain {Escherichia coli}

EPATILLIDHPLMRTGVKQLISMAPDITVVGEASNGEQGIELAESLDPDLILLDLNMPGMN
GLETLDKLRKSLSGRIVVFSVSNHEEDVVTALKRGADGYLLKDMEPEDLLKALHQAAA
GEMVLSEALTPVLAASL

>d1Intr_ c.23.1.1 (-) NTRC receiver domain {Salmonella typhimurium}

MQRGIVWVDDDSSIRWVLERALAGAGLTCTTFENGNEVLAALASKTPDVLLSDIRMPG
MDGLALLKQIKQRHPMLPVIIMTAHSDLDAAVSAYQQGAFDYLPKPFIDEAVALVERAIS
HYQE

>d1dbwa_ c.23.1.1 (A:) Transcriptional regulatory protein FixJ, receiver domain {Rhizobium
meliloti}

MQDYTVHIVDDEEPVRKSLAFMLTMNGFAVKMHQSAEAFAPDVRNGVLVTDLRMP
DMSGVELLRNLGDLKINIPSIVITGHGDVPMAVEAMKAGAVDFIEKPFEDTVIIAIERASE
HLV

>d1qkka_ c.23.1.1 (A:) Transcriptional regulatory protein DctD, receiver domain {Sinorhizobium
meliloti}

PSVFLIDDDRDLRKAMQQTLELAGFTVSSFASATEALAGLSADFAGIVISDIRMPGMDGLA
LFRKILALDPLDPMILVTGHGDIPMAVQAIQDGAYDFIAKPFAADRLVQSARRAEKRRLV
MENRSLRRAAEAAASEGL

>d1dz3a_ c.23.1.1 (A:) Sporulation response regulator Spo0A {Bacillus stearothermophilus}
SIKVCIAADDNRELVSLLDEYISSQPDMEVIGTAYNGQDCLQMLEEKRPDILLDDIIMPHLDG
LAVLERIRAGFEHQPNVIMLTAFGQEDVTKKAVELGASYFILKPFDMENLAHHIRQVYGKT

>d1nat_ c.23.1.1 (-) Sporulation response regulator Spo0F {Bacillus subtilis}
NEKILIVDDQYGIRILLNEVFNKEGYQTFQAANGLQALDIVTKERPDLVLLDMKIPGMDGI
EILKRMKVIDENIRVIIMTAYGELDMIQESKELGALTHFAKPFIDEIRDAVKKYLPL

>d1a2oa1 c.23.1.1 (A:1-140) Methylesterase CheB, N-terminal domain {Salmonella typhimurium}
MSKIRVLSVDDSSALMRQIMTEIINSHSDMEMVATAPDPLVARDLIKKFNPVDVLTLDVEMPR
MDGLDFLEKLMRLRPMVVMVSSLTGKGSEVTLRALELGAIDFVTKPQLGIREGMLAYSE
MIAEKVRTAARARIAAHKP

>d1kgsa2 c.23.1.1 (A:2-123) PhoB receiver domain {Thermotoga maritima}
NVRVLVVEDERDLADLITEALKKEMFTVDVCYDGEEGMYMALNEPFDVVILDIMLPVHD
GWEILKSMRESGVNTPVLMALTALSDVEYRVKGLNMGADDYLPKPFDLRELIARVRALIRR
KSE

>d1leuca2 c.23.4.1 (A:131-306) Succinyl-CoA synthetase, alpha-chain, C-terminal domain {Pig
(Sus scrofa)}
NCPGVINPGECKIGIMPGHIIHKKGRIGIVSRSGTLTYEAVHQTTQVGLGQSLCVGIGGDPFN
GTDFTDCLIEFLNDPATEGIILIGEIGGNAEENAAEFLKQHNSGPKSKPVVSFIAGLTAPPGR
RMGHAGAIAGGKGGAKEKITALQSAGVVVSMSPAQLGTTIYKEFEKRKML

>d1jkjb1 c.23.4.1 (B:239-388) Succinyl-CoA synthetase, beta-chain, C-terminal domain
{Escherichia coli}
DPREAQAAQWELNYVALDGNIGCMVNGAGLAMGTMDIVKLHGGEPANFLDVGGGATK
ERVTEAFKIILSDDKVKAVLVNIFGGIVRCDLIADGIIIGAVAEVGVNVPVVVRLEGNNALG
AKKLADSGLNIIAAKGLTDAAQQVVAAVEGK

>d2fcr_ c.23.5.1 (-) Flavodoxin {Chondrus crispus}
KIGIFFSTSTGNTTEVADFIGKTLGAKADAPIDVDDVTDPAQALKDYDLLFLGAPTWNTGAD
TERSGTSWDEFLYDKLPEVDMKDLPVAIFGLGDAEGYPDNFCDAIEEIHDCFAKQGAKPV
GFSNPDDYDYEEKSVRDGKFLGLPLDMVNDQIPMEKRVAGWVEAVVSETGV

>d1f4pa_ c.23.5.1 (A:) Flavodoxin {Desulfovibrio vulgaris}
PKALIVYGSTTGNTTEYTAETIARELADAGYEVDSDRAASVEAGGLFEGFDLVLLGCSTWG
DDSIELQDDFIPLFDSLEETGAQGRKVACFGCGDSSWEYFCGAVDAIEEKLKLNLGAEIVQD

GLRIDGDPRAARDDIVGWAHDVRGAI

>d1ag9a_ c.23.5.1 (A:) Flavodoxin {Escherichia coli}

AITGIFFGSDTGNTENIAKMIQKQLGKDVADVHDIKSSKEDLEAYDILLGLIPTWYYGEA
QCDWDDFFPTLEEIDFNGKLVALFGCGDQEDYAEYFCDALGTIRDIIEPGATIVGHWPTA
GYHFEASKGLADDDHFVGLAIDEDRQPELTAERVEKWVKQISEELHLDEILNA

>d5nul__ c.23.5.1 (-) Flavodoxin {Clostridium beijerinckii}

MKIVYWSGTGNTTEKMAELIAKGIIESGKDVNTINVSDVNIDELLNEDILILGCSAMTDEVL
EESEFEPFIEEISTKISGKKVALFGSYGWGDGKWMRDFEERMNGYGCVVVETPLIVQNEP
DEAEQDCIEFGKKIANI

>d1bvyf_ c.23.5.1 (F:) FMN-binding domain of the cytochrome P450bm-3 {Bacillus megaterium}

NTPLLVLYGSNMGTAEGTARDLADIAMSKGFAPQVATLDSHAGNLPREGAVLIVTASYNG
HPPDNAKQFVDWLDQASADEVKGVRYSVFGCGDKNWATTYQKVPAFIDETLAAKGAEN
IADRGEADASDDFEGTYEEWREHMWSDVAAYFNL

>d1e5da1 c.23.5.1 (A:251-402) Rubredoxin oxygen:oxidoreductase (ROO), C-terminal domain
{Desulfovibrio gigas}

PTNKVVIFYDSMWHSTTEKMARVLAESFRDEGCTVKLMWCKACHHSQIMSEISDAGAVIV
GSPTHNNGILPYVAGTLQYIKGLRPQNKIGGAFGSFGWSGESTKVLAEWLTGMGFDMPAT
PVKVKNVPTHADYEQLKTMAQTIARALKAKLAA

>d1bmta2 c.23.6.1 (A:741-896) Methionine synthase, C-terminal domain {Escherichia coli}

EQGKTNGKMVIATVKGDVHDIGKNIVGVVLQCNNEYEIVDLGVMVPAEKILRTAKEVNAD
LIGLSGLITPSLDEMNVNAKEMERQGFTIPLLIGGATTSKAHTAVKIEQNYSGPTVYVQNAS
RTVGVVAALLSDTQRDDFVARTRKEYETVRIQHGR

>d1fmfa_ c.23.6.1 (A:) Glutamate mutase, small subunit {Clostridium tetanomorphum}

MEKKTIVLGVIGSDCHAVGNKILDHSFTNAGFNVVNIGVLSSQEDFINAAIETKADLICVSS
LYGQGEIDCKGLREKCD EAGLKGKILFVGGNIVVGKQNWPDVEQRFKAMGFDRVYPPGT
SPETTIADMKEVLGVE

>d7reqa2 c.23.6.1 (A:561-728) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta
subunits {Propionibacterium freudenreichii, subsp. shermanii}

AQIRTISGVYSKEVKNTPEVEEARELVEEFQAEGRPRILLAKMGQDGHDRGQKVIATAY
ADLGFDVDVGPLFQTPEETARQAVEADVHVVGVSLLAGGHLTLVPALRKELDKLGRPDILI
TVGGVIPEQDFDELKRDGAVEIYTPGTVIPESAISLVKKLRASLDA

>d7reqb2 c.23.6.1 (B:476-638) Methylmalonyl-CoA mutase C-terminal domains of alpha and beta
subunits {Propionibacterium freudenreichii, subsp. shermanii}

TKPFPAPARKGLAWHRDSEVFEQLMDRSTSVSERPKVFLACLGTTRDFGGREGFSSPVW
HIAGIDTPQVEGGTTAEIVEAFKKSGAQVADLCSSAKVYAQQGLEVAKALKAAAGAKALYL
SGAFKEFGDDAAEA EKLIDGRLFMGMDVVDTLSSTL DILGVAK

>d1cex__ c.23.9.1 (-) Cutinase {Fungus (Fusarium solani), subsp. pisi}

RTTRDDLINGNSASCADVIFIYARGSTETGNLGTLP SIANLES AFGKDG VWIQGVGGAY
RATLGDNALPRGTSSAAIREMLGLFQQANTKCPDATLIAGGYSQGAALAAASIEDLDSAIR
DKIAGTVLFGYTKNLQNRGRIPNYPADRTKVFCNTGDLVCTGSLIVAAPHLAYGPDARGP
APEFLIEKVRVAVRGS

>d1g66a_ c.23.9.1 (A:) Acetylxy lan esterase {Penicillium purpurogenum}

SCPAIHVFGARETTASPGYGSSSTVVNGVLSAYPGSTAEAINYPACGGQSSCGGASYSSSSVA
QGIAAVASAVNSFNSQCPSTKIVLVGYSQGGEIMDVALCGGGDPNQGYTNTAVQLSSSAVN

MVKAAIFMGDPMFRAGLSYEVGTCAAGGFDQRPAGFSCPSAAKIKSYCDASDPYCCNGS
NAATHQGYGSEYGSQALAFVKSCLG

>d2naca2 c.23.12.1 (A:1-147,A:336-374) Formate dehydrogenase {Pseudomonas sp., strain 101}

AKVLCVLYDDPVDGYPKTYARDDLKIDHYPGGQTLTPKAIDFTPGQLLSVSGELGLR
KYLESNHGTLLVVTSDKDGPDVFERELVDADVVISQPFWPAYLTPERIAKAKNLKLALTAG
IGSDHVDLQSAIDRNVTVAEVTYCNSXTTLTAQARYAAGTREILECFFEGRPIDEYLIVQG
GALA

>d1qp8a2 c.23.12.1 (A:1-82,A:264-302) Putative formate dehydrogenase {Archaeon Pyrobaculum aerophilum}

MELYVNFELPPEAEEELRKYFKIVRGGDLGNVEAALVSRITAEELAKMPRLKFIQVVTAGL
DHLPWESIPPHVTVAGNAGSNXGYGNERVWRQMVMEAVRNLITYATGGRPRNIAKREDY
IG

>d1dxy_2 c.23.12.1 (1-100,300-330) D-2-hydroxyisocaproate dehydrogenase {Lactobacillus casei}

MKIIAYGARVDEIQYFKQWAKDTGNTLEYHTEFLDENTVEWAKGFDGINSLQTTTPYAAGV
FEKMHAYGIKFLTIRNVGTDNIDMTAMKQYGIRLSNVPAYXTETAVHNMVYFSLQHLVDF
LTKGETSTEVTG

>d1gdha2 c.23.12.1 (A:2-100,A:292-321) D-glycerate dehydrogenase {Hyphomicrobium methylovorum}

KKKILITWPLPEAAMARARESYDVIAHGDDPKITIDEMIETAKSVDALLITLNEKCRKEVID
RIPENIKCISTYSIGFDHIDLDAACKARGIKVGNAPHGXATQAREDMAHQANDLIDALFGGA
DMSYALA

>d1psda2 c.23.12.1 (A:7-107,A:296-326) Phosphoglycerate dehydrogenase {Escherichia coli}

EKDKIKFLLVEGVHQALESRLAAGYTNI EFHKGALDDEQLKESIRDAHFGLRSRTHLTE
DVINAAEKLVAIGCFICIGTNQVDLDA AAKRGIPVFNAPFSXSTQEAQENIGLEVAGKLIKYS
DNGSTLSAVN

>d2dlda2 c.23.12.1 (A:1-103,A:301-337) D-lactate dehydrogenase {Lactobacillus helveticus}

MTKVFAAIRKDEEPFLNEWKEAHKDIDVDYTDKLLTPETAKLAKGADGVVVYQQLDYT
ADTLQALADAGVTKMSLRNVGVDNIDMDKAKELGFQITNVPVYSXYTTHAVRNMVVK
AFNNNLKLINGEKPDPSPVALNKNKF

>d1pjca2 c.23.12.2 (A:1-135,A:304-361) L-alanine dehydrogenase {Phormidium lapideum}
MEIGVPKEIKNQEFRVGLSPSSVRTLVEAGHTVFIETQAGIGAGFADQDYVQAGAQQVPSA
KDAWSREMVVKVKEPLPAEYDLMQKDQLLFTYLHLAAARELTEQLMRVGLTAIAYETVE
LPNRSPLPLTPMSIIXVPWTATQALNNSTLPYVVKLANQGLKALETDDALAKGLNVQAHR
LVHPAVQQVFPDLA

>d1f8ga2 c.23.12.2 (A:1-143,A:327-384) Nicotinamide nucleotide transhydrogenase dI component {Rhodospirillum rubrum}

MKIAIPKERRPGEDRVAISPEVVKLVGLGFEVIVEQGAGVGASITDDALTAAGATIASTAA
QALSQADV VVKVQRPMTAE EGTDEVALIKEGAVLMCHLGALTNRPVVEALTKRKITAYA
MELMPRISRAQSM DILSSQSNLXVAADASPLFAKNLLNFLT PHVDKDTKTLVMKLEDET
VSGTCVTRDGAIVHPALTGQGA

>d1gpma2 c.23.16.1 (A:3-207) GMP synthetase {Escherichia coli}
 ENIHKHRILILDFGSQYTQLVARRVRELGVYCELWAWDVTFAQIRDFNPSGILSGGPESTT
 EENSPRAPQYVFEAGVPVFGVCYGMQTMAMQLGGHVEASNEREFGYAQVEVVNDSALV
 RGIEDALTADGKPLLDVWMSHGDKVTAIPSDFITVASTESCPFAIMANEERFYGVQFHPE
 VTHTRQGMRLERFVRDICQCEAL

>d1a9xb2 c.23.16.1 (B:1653-1880) Carbamoyl phosphate synthetase, small subunit C-terminal domain {Escherichia coli}
 LNGMDLAKEVTTAEAYSWTQGSWTLTGGLPQAKKEDELPHFVVAYDFGAKRNILRMLVD
 RGCRLTIVPAQTS AEDVLKMNPDGIFLSNGPGDPAPCDYAITAIQKFLETDIPVFGICLGHQL
 LALASGAKTVKMKFGHHGGNHPVKDVEKNVVMITAQNHGFVAVDEATLPANLRVTHKSLF
 DGTLQGIHRTDKPAFSFQGNPEASPGPHDAAPLFDHFIELIEQYRKT

>d1qdlb_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Archaeon Sulfolobus solfataricus}
 MDLTLIIDNYDSFVYNIAQIVGELGSYPVIRNDEISIKGIERIDPRLIISP GPGTPEKREDIG
 VSLDVIKYL GK RTPILGVCLGHQAIGYAFGAKIRRARKVFH GKISNIILVNNSPLSLYYGIAK
 EFKATRYHSLVVDEVHRPLIVDAISAEDNEIMAIHHEEYPIYGVQFHPESVGTSLGYKILYN
 FLNRV

>d1i1qb_ c.23.16.1 (B:) Anthranilate synthase GAT subunit, TrpG {Salmonella typhimurium}
 ADILLDNIDSFTWNLADQLRTNGHN VVIYRNHIPAQTLIDRLATMKNPVLMLSPGPGVPS
 EAGCMPPELLRLRGKLP IIGICLGHQAIVEAYGGYVGQAGEILHGKATSIEHDGQAMFAGL
 ANPLPVARYHSLVGSNVPAGLTINAHFNGMVM AVRHDADRVC GFQFHPESILTTQGARLL
 EQTLAWAQK

>d1k9vf_ c.23.16.1 (F:) GAT subunit (or domain) of
 imidazoleglycerolphosphate synthase HisF {Thermotoga maritima}
 MRIGIISVPGNIMNLYRGVKRASENFEDVSIELVESPRNDLYDLLFIPGVGHFGEGRRLR
 ENDLIDFVRKHVEDERYVVG VCLGMQLLFEESEEAPGVKGLSLIEGNVVKLRSRRLPHM
 GWNEVIFKDTF PNGYYYFVHTYRAVCEEEHVLGTTEYDGEIFPSAVRKGRILGFQFHPEKS
 SKIGRKLLEKVIECSLSR

>d1jvna2 c.23.16.1 (A:-3-229) GAT subunit (or domain) of
 imidazoleglycerolphosphate synthase HisF {Baker's yeast (Saccharomyces cerevisiae), His7}
 GSHMPVVHVIDVESGNLQSLTNAIEHLGYEVQLVKSPKDFNISGTSRLILPGVGNYGHFVD
 NLFNRGFEKPIREYIESGKPIMGICVGLQALFAGSVESPKSTGLNYIDFKLSRFDDSEKPVPE
 IGWNSCIPSENLFGLDPYKRYFVHSFAAILNSEKKKNLENDGWKIAKAKYGSEEFIAAV
 NKNNIFATQFHPEKSGKAGLNV IENFLKQQSPPIPNYSAEEKELLMN

>d1que_2 c.25.1.1 (142-303) Ferredoxin reductase (flavodoxin reductase)
 {Cyanobacterium (Anabaena sp.), pcc 7119}
 LPDDPEANVIMLATGTGIAPMRTYLWRMFKDAERAANPEYQFKGFSWL VFGVPTTPNILY
 KEELEEIQKYPDNFRLTYAISREQKNPQGGRMYIQDRVAEHADQLWQLIKNQKTHTYIC
 GLRGMEEGIDAALSA AAKEGVTSWSDYQKDLKKAGRWHVETY

>d1fdr_2 c.25.1.1 (101-248) Ferredoxin reductase (flavodoxin reductase) {Escherichia coli}
 DEVPHCETLWMLATGTAIGPYLSILRLGKDLDRFKNLVLVHAARYAADLSYLPLMQELEK
 RYEGKLRIQTVVSRETAAGSLTGRIPALIESGELESTIGLPMNKETSHVMLCGNPQMVRDT

QQLLKETRQMTKHLRRRPGHMTAEHYW

>d1a8p_2 c.25.1.1 (101-258) Ferredoxin reductase (flavodoxin reductase) {Azotobacter vinelandii}

TSDLLPGKHLMLSTGTGLAPFMSLIQDPEVYERFEKVVLHGVVRQVNELAYQQFITEHLP
QSEYFGEAVKEKLIYYPTVTRESFHNQGRLTDLMRSGKLFEDIGLPPINPQDDRAMICGSPS
MLDESCEVLDGFGFLKISPRMGEPGDYLIERAFVEK

>d1qfja2 c.25.1.1 (A:98-232) NAD(P)H:flavin oxidoreductase {Escherichia coli}
RDDEERPMILIAGGTGFSYARSILLTALARNPNRDITIYWGGREEQHLYDLCELEALSLKHP
GLQVVPVVEQPEAGWRGRTGTVLTAVLQDHGTLAEHDIYIAGRFEMAKIARDLFCSERNA
REDRLFGDAFAFI

>d1ndh_2 c.25.1.1 (126-272) cytochrome b5 reductase {Pig (Sus scrofa), liver}
GKFAIRPDKKSSPVIKTVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLFANQTEKD
ILLRPELEELRNEHSARFKLWYTVDRAPEAWDYSQGFVNEEMIRDHLPPPEEEPLVLMCGP
PPMIQYACLPNLERVGHPKERCFAF

>d1jala3 c.25.1.4 (A:519-678) NADPH-cytochrome p450 reductase {Rat (Rattus norvegicus)}
RLPFKSTTPVIMVGP GTGIAPFMGFIQERAWLREQGKEVGETLLYYGCRSDEDYLYREEL
ARFHKDGALTQLNVAFSREQAHKVYVQHLLKRDREHLWKLIHEGGAHIYVAGDARNMA
KDVQNTFYDIVAEFGPMEHTQAVDYVKKLMTKGRYSLNVWS

>d1f20a2 c.25.1.4 (A:1233-1397) Neuronal nitric-oxide synthase FAD/NADP+ domain
{Rat (Rattus norvegicus)}

SFHLPRNPQVPCILVGP GTGIAPFRSFWQQRQFDIQHKGMNCPMVLVFGCRQSKIDHIYR
EETLQAKNKGVFRELYTAYSREPDRPKKYVQDVLQEQLAESVYRALKEQG GHIYVCGDV
TMAADV LKAIQRIMTQQGKLSEEDAGVFISRLRDDNRYHEDIFGV

>d1jila_ c.26.1.1 (A:) Tyrosyl-tRNA synthetase (TyrRS) {Staphylococcus aureus}

TNVLIEDLKWRGLIYQQTDEQGIEDLLNKEQVTLYCGADPTADSLHIGHLLPFLT LRRFQE
HGHRPIVLIGGGTGMIGDPSGKSEERVLQTEEQVDKNIEGISKQMHNIFEFGTDHGAVLVN
NRDWLGQISLISFLRDYGKHVG VNYMLGKDSIQSRLEHGISYTEFTYITILQAIDFGHLNRE
LNCKIQVGGSDQWGNITSGIELMRRMYGQTDAYGLTIPLVTKSDGKKFGKSESGAVWLD
AEKTSPYEFYQFWINQSDDEVIKFLKYFTFLGKEEIDRLEQSKNEAPHLREAQKTLAE EVT
KFIHGEDALNDAIRISQALF

>d1i6la_ c.26.1.1 (A:) Tryptophanyl-tRNA synthetase (TrpRS) {Bacillus stearothermophilus}
MKTIFSGIQPSGVITIGNYIGALRQFVELQHEYNCFIVDQHAI TVWQDPHEL RQNIRRLA
ALYLAVGIDPTQATLFIQSEVPAHAQA AAWMLQCIVYIGELERMTQFKEKSAGKEAVSAGLL
TYPPLMAADILLYNTDIVPVGEDQKQHIELTRDLAERFNKRYGELFTIPEARIPKVGARIMS
LVDPTKKMSKSDPNPKAYITLLDDAKTIEKKIKSAVTDSEGTIRYDKEAKPGISNLLNIYST
LSGQSIEELERQYEGKGYGVFKADLAQVVIETLRPIQERYHHWMESEELDRVLDEGA EKA
NRVASEMVRKMEQAMGLGR

>d1gtra2 c.26.1.1 (A:8-338) Glutaminyl-tRNA synthetase (GlnRS) {Escherichia coli}
TNFIRQIIDEDLASGKHTTVHTRFPPEPNGYLHIGHAKSICLNFGIAQDYKGQC NLRFDDTN
PVKEDIEYVESIKNDVEWLGFHWSGNVRYSSDYFDQLHAYAIELINKGLAYVDELTP EQIR
EYRGTLTQPGKNSPYRDRSVEENLALFEKMRAGGFEEGKACLR AKIDMASPFIVMRDPVL
YRIKFAEHHQTGNKWCIYPMYDFTHCISDALEGITHSLCTLEFQDNRRLYDWVLDNITIPV
HPRQYEF SRLNLEYTVMSKRKLNLLVTDKHVEGWDDPRMPTISGLRRRGYTAASIREFCK

RIGVTKQDNTIEMASLESCIREDLNEN

>d1gln_2 c.26.1.1 (1-305) Glutamyl-tRNA synthetase (GluRS) {Thermus thermophilus}

MVVTRIAPSPTGDPHVGTAYIALFNAYAWARRNGGRFIVRIEDTDRLARYVPGAEEERILAALK
WLGLSYDEGPDVAAPTGPYRQSERLPLYQKYAEELLKRGWAYRAFETPEELEQIRKEKGG
YDGRARNIPPEEAEERARRGEPHVIRLKVPRPGTTEVKDELRGVVVYDNQEIPDVVLLKS
DGYPTYHLANVDDHLMGVTDVIRAEELVSTPIHVLLYRAFGWEAPRFYHMPLLRNPD
KTKISKRKSHSTSLDWYKAEGFLPEALRNYLCLMGFSMPDGREIFTLEEFIQAFWERSVLG
GPVF

>d1a8h_2 c.26.1.1 (1-348) Methionyl-tRNA synthetase (MetRS) {Thermus thermophilus}

MEKVFYVTTPIYYVNAEPHLGHAYTTVVADFLARWHRLDGYRTFFLTGTDEHGETVYRA
AQAAGEDPKAFVDRVSGRFKRAWDLGLIAYDDFIRTTEERHKKVVQLVLKKVYEAGDIY
YGEYEGLYCVSCERFYTEKELVEGLCPIHGRPVERRKEGNYFFRMEKYRPWLQEYIQENP
DLIRPEGYRNEVLAMLAEPIDLSISRPKSRVPWGIPLPDENHVTVVWFDALLNYVSAL
DYPEGEAYRTFWPHAWHLIGKDILKPHAVFWPTMLKAAGIPMYRHLNVGGFLLGPDGRK
MSKTLGNVVDPFALLEKYGRDALRYLLREIPYGGDTPVSEEALRTRYEAD

>d1f4la2 c.26.1.1 (A:4-140,A:176-388) Methionyl-tRNA synthetase (MetRS) {Escherichia coli}

AKKILVTCALPYANGSIHLGHMLEHIQADVWVRYQRMRGHEVNFICADDAHGTPIMLKA
QQLGITPEQMIGEMSQEHQTDFAGFNISYDNYHSTHSEENRQLSELIYSRLKENGFIKNRTI
SQLYDPEKGMFLPDRFXVVSAGATPVMRDSEHFFFDLPSFSEMLQAWTRSGALQEYVANK
MQEWFESGLQQWDISRDPYFGFEIPNAPGKYFYVWLDAPIGYMGSFKNLCKDRGDSVS
FDEYWKKDSTAELYHFIGKDIFYFHSFWPAMLEGSNFRKPSNLFVHGYVTVNGAKMSK
SRGTFIKASTWLNHFDAADSLRYYYTAKLSSRIDDLNLEDVQVRNADIVNK

>d1ile_3 c.26.1.1 (1-197,387-641) Isoleucyl-tRNA synthetase (IleRS) {Thermus thermophilus}

MFKEVGEPNFPKLEEEVLAFWKREKIFQKSVENRKGGPRYTVYEGPPTANGLPHVGHQA
ARSYKDLFPYKTMRGYYAPRRAGWDTHGLPVELEVEKKLGLKSKREIEAYGIERFNQA
CRESVFTYEKEWEAFTERIAYWVDLEDAYATLEPTYIESIWWSLKNLFDRLGLLYRDHKVV
PYCPRCGTPLSSHEVALGYXPHCWRCSTPLMYATESWFIKNTLFKDELIRNNQEIHWVPP
HIKEGRYGEWLKNLVDWALSRLRYWGTPLPWVCQACGKEEAIGSFQELKARATKPLPEP
FDPHRPYVDQVELACACGGTMRRVPYVIDVWYDVGAMPFASLHYPFEHEEVFRESFPADF
IAEGIDQTRGWFNLSLHQLGVMLFGSIAFKNVICHGLILDEKGQKMSKSKGNVVDPDWDIR
KFGADALRWYIYVSAPPEADRRFGPNLVRETVRD

>d1ffya3 c.26.1.1 (A:1-200,A:395-644) Isoleucyl-tRNA synthetase (IleRS) {Staphylococcus aureus}

MDYEKTLMPKTDFFPMRGGLPNKEPQIQEKWDAEDQYHKALEKNKGNETFILHDGPPYA
NGNLHMGHALNKILKDFIVRYKTMQGFYAPYVPGWDTHGLPIEQALTKKGVDRKKMST
AEFREKCKEFALEQIELQKKDFRRLGVRGDFNDPYITLKPEYEEAAQIRIFGEMADKGLIYK
GKKPVYWSPSSSSLAEAEIEYXPHDWRTKKPVIFRATPQWFASISKVRQDILDAIENTNFK
VNWGKTRIYNMVRDRGEWVISRQRVWGVPLPVFYAENGEIIMTKETVNHVADLFAEHGS
NIWFEREAKDLLPEGFTHPGSPNGTFTKETDIMDVWFDGSSSHRGVLETRPELSFPADMYL
EGSDQYRGWFNSSITTSVATRGVSPYKFLLSHGFVMDGEGKKMSKSLGNVIVPDQVVKKQ
KGADIARLWVSSTDYLAADVRSDEILKQTSDD

>d1gaxa3 c.26.1.1 (A:1-189,A:343-578) Valyl-tRNA synthetase (ValRS) {Thermus thermophilus}

MDLPKAYDPKSVEPKWAEKWAKNPFVANPKSGKPPFVIFMPPPNVTGSLHMGHALDNSL

QDALIRYKMRMGFEAVWLPGTDHAGIATQVVVERLLLKEGKTRHDLGREKFLERVWQW
KEESGGTILKQLKRLGASADWSREAFTMDEKRSRAVRYAFSRYYHEGLAYRAPRLVNC
PRCETTLSDLEVEXTCSRCGTPIEYAFIPQWWLRMRPLAEEVLKGLRRGDIAFVPERWKK
VNMDWLENVKDWNIQRQLWWGHQIPAWYCEDCQAVNVPRPERYLEDPTSCEACGSPRL
KRDEDVFDTWFSALWPLSTLGWPEETEDLKAFYPGDVLVTGYDILFLWVSRMEVSGYH
FMGERPFKTVLLHGLVLDEKGQKMSKSGNVIDPLEMVERYGADALRFALIYLATGGQDI
RLDLRWLEMARNF

>d1f7ua2 c.26.1.1 (A:136-483) Arginyl-tRNA synthetase (ArgRS) {Baker's yeast
(*Saccharomyces cerevisiae*)}

SCKLVENKKVIIIEFSSPNIAKPFHAGHLRSTIIGGFLANLYEKLGWVIRMNYLGDWGWKQF
GLLAVGFERYGNEEALVKDPIHHLFDVYVRINKDIEEGDSIPLEQSTNGKAREYFKRMED
GDEEALKIWKRFRFESIEKYIDTYARLNKYDVYSGESQVSKESMLKAIDLFKEKGLTHED
KGAVLIDLTKFNKKGKAIQVQKSDGTTLYLTRDVGAAAMDREYKYHFDKMIYVIASQQDL
HAAQFFEILKQMGFEWAKDLQHVNFQGMVQGMSTRKGTVVFLDNILEETKEKMHEVMK
KNENKYAQIEHPPEEVADLVGISAVMIQDMQGKRINNYEFKWERMLSFE

>d1iq0a2 c.26.1.1 (A:97-466) Arginyl-tRNA synthetase (ArgRS) {*Thermus thermophilus*}

PFPRRPGVVLVEHTSVNPNKELHVGHLRNIALGDAIARILAYAGREVLVLNYIDDTGRQAA
ETLALRHVGLTWDGKEKYDHFAGRAYVRLHQDPEYERLQPAIEEVLHALERGELREEVN
RILLAQMATHALNARYDLLVWESDIVRAGLLQKALALLEQSPHVFRPREGKYAGALVM
DASVIPGLEDPPFVLLRSNGTATYYAKDIAFQFWKMGILEGLRFRPYENPYYPGLRTSAPE
GEAYTPKAEETINVVDVRQSHQALVRAALALAGYPALAEKAHHLAYETVLLRQMSG
RKGLAVSVDEVLEEATRRARAIVEEKNPDHPDKEEAARMVALGAIRFSMVKTEPKKQIDF
RYQEALSFE

>d1qja_ c.26.1.3 (A:) Phosphopantetheine adenylyltransferase {*Escherichia coli*}

KRAIYPGTDPITNGHIDIVTRATQMFHDVILAIASPSKKPMFTLEERVALAQQAHLGN
VEVVGFSDLMANFARNQHATVLIRGLRAVADFEYEMQLAHMNRHLMPELESVFLMPSKE
WSFISSSLVKEVARHQGDVTHFLPENVHQALMAKLA

>d1ej2a_ c.26.1.3 (A:) Nicotinamide mononucleotide (NMN) adenylyltransferase
{*Archaeon Methanobacterium thermoautotrophicum*}

MRGLLVGRMQPFHRGHLQVIKSILEEVDELIICIGSAQLSHSIRDPFTAGERVMMLTKALSE
NGIPASRYIIPVQDIECNALWVGHIKMLTPPFDRVYSGNPLVQRLFSEDGYEVTAPPLFYR
DRYSGTEVRRRMLDDGDWRSLLPESVVEVIDEINGVERIKHLA

>d1g8fa2 c.26.1.5 (A:169-389) ATP sulfurylase central domain {Baker's yeast (*Saccharomyces cerevisiae*)}

YPGLRKTPAQLRLEFQSRQWDRVAFQTRNPMHRAHRELTVRAAREANAKVLIHPVVGL
TKPGDIDHHTRVRYQEIHKRYPNGIAFLSLLPLAMRMSGDREAVWHAIIRKNYGASHFIV
GRDHAGPGKNSKGVDFYGPYDAQELVESYKHELDIEVVPFRMVITYLPDEDRYAPIDQIDT
TKTRTLNISGTELRRRLRVGGEIPEWFSYPEVVKILRESNP

>d1jhda2 c.26.1.5 (A:174-396) ATP sulfurylase central domain {unnamed symbiont of *Riftia pachyptila*}

PDTFRTAVEIRNEIKEHGWSKVVAQTRNPMHRAHEELCRMAMESLDADGVVVHMLLGK
LKKGDIPAPVRDAAIRTMAEVYFPNTVMVTGYGFDMLYAGPREAVLHAYFRQNMGATH
FIIGRDHAGVGDYYGAFDAQTIFDDEVPEGAMEIEIFRADHTAYSKKLNKIVMMRDVPDH
TKEDFVLLSGTKVREMLGQGIAPPPEFSRPEVAKILMDYYQSINS

>d1gpm1 c.26.2.1 (A:208-404) GMP synthetase, central domain {Escherichia coli}
WTPAKIIDDAVARIREQVGDDKVILGLSGGVDSSTAMLLHRAIGKNLTCVFVDNGLLRN
EAEQVLDMMFGDHFGLNIVHVPADRFLSALAGENDPEAKRKIIIGRVFVEVFDEEALKLED
VKWLAQGTIYPDVIESAASATGKAHVIKSHHNVGGLPKEMKMGLVEPLKELFKDEVRI
GLELGLPYDMLYRHPFP

>d1ih8a_ c.26.2.1 (A:) NH₃-dependent NAD⁺-synthetase {Bacillus subtilis}
SMQEKIMRELHVKPSIDPKQEIEDRVNFKQYVKKKTGAKGFVLGISGGQDSTLAGRLAQL
AVESIREEGGDAQFIAVRLPHGTQQDEDDAQLALKFIKPKDSWKFDIKSTVSAFSDQYQQE
TGDQLTDFNKGNVKARTRMIAQYAIGGQEGLLVLGTDHAAEAVTGFFTKYGDGGADLLP
LTGLTKRQGRITLLKELGAPERLYLKEPTADLLDEKPQQSDETELGISYDEIDDYLEGKEVS
AKVSEALEKRYSMTEHKRQVPASMFDDWWK

>d1ct9a1 c.26.2.1 (A:193-516) Asparagine synthetase B, C-terminal domain {Escherichia coli}
RDWFDYDAVKDNDVTDKNELRQALEDSSVKSHLMSDVPYGVLLSGGLDSSIISAITKKYAAR
RVEDQERSEAWWPQLHSFAVGLPGSPDLKAAQEVANHLGTVHHEIHFTVQEGDAIRDVI
YHIETYDVTITRASTPMYLMRSRIKAMGIKMLVLSGEGSDEVFGGYLYFHKAPNAKELHEE
TVRKLLALHMYDCARANKAMSAWGVEARVPFLDKKFLDVAMRINPQDKMCGNGKMEK
HILRECFAEYLPASVAWRQKEQFSDGVGYSWIDTLKEVAAQQVSDQQLETARFRFPYNTF
TSKEAYLYREIFEELFPLPSAAECVPG

>d1jgt1 c.26.2.1 (A:210-508) beta-Lactam synthetase {Streptomyces clavuligerus}
PGLSRRILPEGEAAVRAALEKAVAQRVTPGDTPLVVLSSGIDSSGVAACAHRAAGELDT
VSMGTDTSNEFREARAVVDHLRTRHREITPTTELLAQLPYAVWASESVDPDIIYLLPLTAL
YRALDGPERRILTGYGADIPLGGMHREDRLPALDITVLAHDMATFDGLNEMSPVLSTLAGH
WTHPHYWDREVLDDLVSLEAGLKRRHGRDKWVLRAAMADALPAETVNRPKLGVHEGS
GTTSSFSRLLLDHGVADRVEAKRQVVRELFDLTVGGGRHPSEVDTDDVVRSVADRT

>d1k92a1 c.26.2.1 (A:1-188) Argininosuccinate synthetase, N-terminal domain {Escherichia coli}
TTILKHLPGVQRIGIAFSGGLDTSALLWMRQKGAVPYAYTANLGQPDEEDYDAIPRRAM
EYGAENARLIDCRKQLVAEGIAAIQCGAFHNTTGGLTYFNTTPLGRAVTGTMLVAAMKED
GVNIWGDGSTYKGNDIERYFYGLLTNAELQIYKPWLDTFIDELGGRHEMSEFMACGF
DYKMSVEK

>d1dnpa2 c.28.1.1 (A:1-200) N-terminal domain of DNA photolyase {Escherichia coli}
TTHLVWFRQDLRLHDNLALAAACRNSSARVLALYIATPRQWATHNMSPRQAEILNAQLN
GLQIALAEKGIPLLFREVDDFVASVEIVKQVCAENSVTHLFYNYQYEVNERARDVEVERA
LRNVVCEGFDDSVILPPGAVMTGNHEMYKVFTPFKNWLVKRLREGMPECVAAPKVRSSG
SIEPSPSITLNYPRQSFDTAHF

>d1iqa2 c.28.1.1 (A:2-171) N-terminal domain of DNA photolyase {Thermus thermophilus}
GPLLVWHRGDLRLHDHPALLEALARGPVVGLVLDPNLKTTPRRRAWFLENVRALREA
YRARGGALWVLEGLPWKEVPEAARRLKAKAVYALTSHTPYGRYRDGRVREALPVPLHLL
PAPHLLPPDLPRAYRVYTPFSRLYRGAAPPLPPPEALPKGPEEGEIPREDPG

>d1qnf_2 c.28.1.1 (1-204) N-terminal domain of DNA photolyase {Anacystis
nidulans}
MAAPILFWHRRDLRLSDNIGLAAARAQSAQLIGLFCCLDPQILQSADMAPARVAYLQGCLQ
ELQQRYYQAGSRLLLLQGDPQHLIPQLAQQLQAEAVYWNQDIEPYGRDRDGQVAAALKT
AGIRAVQLWDQLLHSPDQILSGSGNPYSVYGPFWKNWQAQPKPTPVATPTLVDLSPEQLT
AIAPLLLSELPTLKLGLGFDWDGGF

>d1efva1 c.29.1.1 (A:20-207) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}
QSTLVIAEHANDSLAPITLNTITAATRLGGEVSCLVAGTKCDKVAQDLCKVAGIAKVLVAQ
HDVYKGLLPEELTPLILATQKQFNETHICAGASAFGKNLLPRVAAKLEVAPISDIIAIKSPDT
FVRTIYAGNALCTVKCDEKVKVFSVRGTSFDAAATSGGSASSEKASSTSPVEISEWLDQKL
TKS

>d1efvb1 c.29.1.1 (B:) Electron transfer flavoprotein, ETFP {Human (Homo sapiens)}
LRVLVAVKRVIDYAVKIRVKPDRTGVVTDGVKHSMNPFCEIAVEEAVRLKEKKLVKEVIAV
SCGPAQCQETIRTALAMGADRGHVEVPPAEERLGPLQVARVLAKLAEKEKVDLVLLGK
QAIDDDCNQTGQMTAGFLDWPQGTFASQVTLEGDKLKVEREIDGGLETLRLLKPAVVTA
DLRLNEPRYATLPNIMKAKKKKIEVIKPGDLGVDLTSKLSVISVEDPPQRTAGVKVETTEDL
VAKLKEIGRI

>d1efpa1 c.29.1.1 (A:2-184) Electron transfer flavoprotein, ETFP {Paracoccus denitrificans}
AVLLLGEVTNGALNRDATAKAVAAVKALGDVTVLCAGASAKAAAEAAKIAGVAKVLVA
EDALYGHRLAEPTAALIVGLAGDYSHIAAPATTDAKNVMRVAALLDVMVLSDVSAILDA
DTFERPIYAGNAIQVVKSKDAKKVFTIRTASFDAAGEGGTAPVTETAAAADPGLSSWVAD
EVAE

>d1mjha_ c.29.1.2 (A:) "Hypothetical" protein MJ0577 {Archaeon Methanococcus
jannaschii}

VMYKKILYPTDFSETAEIALKHVKAFKTLKAEEVILLHVIDEREIKKRDI FSLLLGVAGLNK
SVEEFENELKNKLTEEAKNKMENIKKELEDVGFKVKDIIVVGIPHEEIVKIAEDEGVDIIM
GSHGKTNLKEILLGSVTENVIKKSNKPVLVVKRNS

>d1jmva_ c.29.1.2 (A:) Universal stress protein A, UspA {Haemophilus influenzae}
MYKHILVAVDLSEESPILLKKAVGIAKRHDAKLSIIHVDVNFSDLYTGLIDVNMSMQDRIS
TETQKALLDLAESVDYPISEKLSGSGDLGQVLSDAIEQYDVDLLVTGHHQDFWSKLSMSST
RQVMNTIKIDMLVVPLRD

>d1dv1a2 c.30.1.1 (A:1-114) Biotin carboxylase (BC) subunit of acetyl-CoA
carboxylase {Escherichia coli}

MLDKIVIANRGEIALRILRACKELGIKTAVHSSADRD LKHVLLADETV CIGPAPSVKSYLN
IPAIISAAEITGAVAIHPGYGFLSENANFAEQVERS GFIFIGPKAETIRLMG

>d1gsoa2 c.30.1.1 (A:-2-103) Glycinamide ribonucleotide synthetase (GAR-syn). {Escherichia
coli}

EFMKVLVIGNGGREHALAWKAAQSPLVETV FVAPGNAGTALEPALQNVAIGVTDIPALLDF
AQNEKIDLTIVGPEAPLVKGVVDTFRAAGLKIFGPTAGAAQLEG

>d1b6ra2 c.30.1.1 (A:1-78) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK
{Escherichia coli}

MKQVCVLGNGQLGRMLRQAGEPLGIAVWPVGLDAEPAAVPFQQSVITAEIERWPETALTR
QLARHPAFVNRDVFPIIA

>d1eyza2 c.30.1.1 (A:2-112) Glycinamide ribonucleotide transformylase
PurT {Escherichia coli}

TLLGTALRPAATRVMLLGSGELGKEVAIECQRLGVEVIAVD RYADAPAMHVAHRSHVINM
LDGDALRRVVELEKPHYIVPEIEAIATDMLIQLEEEGLNVVPCARATKLTM

>d1a9xa3 c.30.1.1 (A:1-127) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia
coli}

MPKRTDIKSILILGAGPIVIGQACEFDYSGAQACKALREEGYRVINVNSNPATIMTDPEMAD

ATYIEPIHWEVVRKIIKERPD AVLPTMGGQTALNCALELERQGVLEEFVMTMIGATADAI
DKAE

>dliow_1 c.30.1.2 (1-96) D-Ala-D-Ala ligase {Escherichia coli, gene ddIB}

MTDKIAVLLGGTSAEREVSLNSGA AVLGLREGGIDAYPVDPK EVDVTQLKSMGFQKVFI
ALHGRGGEDGTLQGMLELMGLPYTGSGVMASALSMD

>dlehia1 c.30.1.2 (A:3-134) D-alanine:D-lactate ligase, VanA {Leuconostoc
mesenteroides, Ddl2}

KKRVALIFGGNSSEHDVSKRSAQNFYNAIEATGKYEIIVFAIAQNGFFLDTESSKKILALEDE
QPIVDAFMKTVDASDPLARIHALKSAGDFDIFFPVVHGNLGEDGTLQGLFKLLDKPYVGA
PLRGHAVSF

>d1e4ea1 c.30.1.2 (A:2-131) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}

NRIKVAILFGGCSEEHDSVKSAIEIAANINKEKYEPLYIGITKSGVWKMCEKPCA EWENE
NCYSAVLSPKMKMHGLLVKKNHEYEINHVDVAFSALHGKSGEDGSIQGLFELS GIPFVGC
DIQSSAICM

>d1poxa1 c.31.1.3 (A:183-365) Pyruvate oxidase {Lactobacillus plantarum}

YASANNYQTPLLPEPDVQAVTRLTQTLLAAERPLIYYGIGARKAGKELEQLSKTLKIPLMS
TYPAKGIVADRYPAYLGSANRVAQKPANEALAQADVVLVFGNNYPFAEVSKAFKNTRYFL
QIDIDPAKLGKRHKTDIAVLADAQKTLAAILAQVSERESTPWWQANLANVKNWRAYLAS
LED

>d1qpba1 c.31.1.3 (A:182-360) Pyruvate decarboxylase {Baker's yeast (Saccharomyces
cerevisiae)}

QTPIDMSLKPND AESEKEVIDTILVLIKDAKNPVILADACCSRH DVKAETKKLIDLTQFPAF
VTPMGKGSIDEQHPRYGGVYVGTLSKPEVKEAVESADLILSVGALLSDFNTG SFSYSYKT
KNIVEFHS DHMKIRNATFPGVQMKFVLQKLLTAIADAAKGYPVAVPARTPANA AVP

>d1zpdal c.31.1.3 (A:188-362) Pyruvate decarboxylase {Zymomonas mobilis}

EASDEASLNA AVDET LKFIANRDKVAVLVGSKLRAAGAE EAAVKFTDALGGAVATMAAA
KSFFPEENALYIGTSWGEVSYPGVEKTMKEADAVIALAPVFNDYSTTGWTDIPDPKKLV L
AEPRSVVVGIRFPSVHLKDYLTRLAQKVSKKTGSLDFFKSLNAGELKKAAPADPS

>d1bfd_1 c.31.1.3 (182-341) Benzoylformate decarboxylase {Pseudomonas
putida}

SVRLNDQDL DILVKALNSASNPAIVLGPDVDAANANADCVMLAERLKAPVWVAPSAPRC
PFPTRHPCFRGLMPAGIAAISQLLEGHDVVLVIGAPVFRYHQYDPGQYLKPGTRLISVTCDP
LEAARAPMGDAIVADIGAMASALANLVEESSRQLPTAAP

>d1jsca1 c.31.1.3 (A:280-460) Acetohydroxyacid synthase catalytic subunit {Baker's yeast
(Saccharomyces cerevisiae)}

AQDEFVMQSINKAADLINLAKKPVLYVGAGILNHADGPRLLKELSDRAQIPVTTTTLQGLG
SFDQEDPKSLDMLGMHGCATANLAVQNADLIIAVGARFDDRVTGNISKFAPEARRAAAEG
RGGIIHFEVSPKNINKVVQTQIAVEGDATTNLGKMMSKIFPVKERSEWFAQINKWKKEYP
Y

>d1licia_ c.31.1.5 (A:) AF1676 sir2 homolog {Archaeon Archaeoglobus fulgidus}

GSHHHHHHGHSHMDEKLLKTIAESKYLVALTGAGVSAESGIPTFRGKDGLWNRYRPEELAN
PQAFAKDPEKVWKWYAWRMEKVFNAQPNKAHQAF AELERLGV LKCLITQNVDDLHERA
GSRNVIHLHGSLRVVRCTSCNNSFEVESAPKIPLPKCDKCGSLLRPGVVWFGEMLPPDVL
DRAMREVERADVIVAGTS AVVQPAASLPLIVKQRGGAIIINPDETPLTPIADYSLRGKAG

EVMDELVRHVRKALS

>d1j8fa_ c.31.1.5 (A:) Sirt2 histone deacetylase {Human (Homo sapiens)}

GEADMDFLRNLFSQTLSSLGSQKERLLDELTLLEGVARYMQSERCRRVICLVGAGISTSAGIP
DFRSPSTGLYDNLEKYHLPYPEAIFEISYFKKHPEPFFALAKELYPGQFKPTICHYFMRLLK
DKGLLLRCYTNIDTLERLIGLEQEDLVEAHGTFYTSCHCVSASCRHEYPLSWMKEKIFSEV
TPKCEDCQSLVKPDIVFFGESLPARFFSCMQSDFLKVDLLVMGTSLQVQPFASLISKAPLS
TPRLINKEKAGQSDPFLGMIMGLGGGMDFDSSKKAYRDVAWLGECDQGCLALAEELGW
KKELEDLVRREHASIDAQS

>d1fsz_1 c.32.1.1 (23-231) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}

SPEDKELLEYLQQTAKITVVGCGGAGNNTITRLKMEGIEGAKTVAINTDAQQLIRTKAD
KKILIGKKLTRGLGAGGNPKIGEEAAKESAEIKAAIQSDSMVFITCGLGGGTGTGSAPVV
AEISKKIGALTVAVVTLPFVMEGKVRMKNNAMEGLERLKQHTDTLVVIPNEKLFEIVPNMP
LKLAFAKVADEVLINAVKGLVELITKDGL

>d1tuba1 c.32.1.1 (A:1-245) Tubulin alpha-subunit {Pig (Sus scrofa)}

MRECISIHVGQAGVQIGNACWELYCLEHGIQPDGQMPSDKTIGGGDDSFNTFFSETGAGK
HVPRAVFDLEPTVIDEVRTGTYRQLFHPEQLITGKEDAANNYARGHYTIGKEIIDLVLDRI
RKLADQCTGLQGFSVFHSFGGGTSGSFTSLLMERLSVDYGKKSKEFSIYPAPQVSTAVVE
PYNSILTTHTTLEHSDCAFMVDNEAIYDICRRNLDIERPTYTNLNLRLIGQIVSSITASLRFD

>d1im5a_ c.33.1.2 (A:) Pyrazinamidase/nicotinamidase {Archaeon Pyrococcus horikoshii}

PEEALIVVDMQRDFMPGGALPVPPEGDKIIPKVNEYIRKFKEKGALIVATRDWHPENHISFR
ERGGPWPRHCVQNTPGAEFVVDLPEDAVIISKATEPDKEAYSGFEGTDLAKILRNGNVKR
VYICGVATEYCVRATALDALKHGFVYLLRDAVKGIKPEDEERALEEMKSRGIKIVQF

>d1yaca_ c.33.1.2 (A:) YcaC {Escherichia coli}

TKPYVRLDKNDAAVLLVDHQAGLLSLVRDIEPDKFKNNVLALGDLAKYFNLPTILTTSAE
TGPNGPLVPELKAQFPDAPYIARPGNINAWDNEDFVKAVKATGKKQLIAGVVTEVCVAFP
ALSAIEEGFDVFVVTASGTFNEITRHSWDRMSQAGAQLMTWFGVACELHRDWRNDIA
GLATLFSNHIPDYRNLMTSYDTLT

>d1e20a_ c.34.1.1 (A:) Halotolerance protein Hal3 {Mouse-ear cress (Arabidopsis thaliana)}

RKPRVLLAASGSVAAIKFGNLCHCFTEWAEVRAVVTKSSLHFLDKLSLPQEVTLTYDEDE
WSSWNKIGDPVLHIELRRWADVLVIAPLSANTLGKIAGGLCDNLLTCIIRAWDYTKPLFVA
PAMNTLMWNNPFTERHLLSLDELGITLIPPIKKRLACGDYGNNGAMAEPSTIYSTVRLFWES
QAH

>d1g5qa_ c.34.1.1 (A:) Epidermin modifying enzyme (peptidyl-cysteine decarboxylase) EpiD
{Staphylococcus epidermidis}

MYGKLLICATASINVININHYIVELKQHFDEVNLFSPSSKNFINTDVLKLFCDNLYDEIKDP
LLNNINIVENHEYILVLPASANTINKIANGICDNLLTTVCLTGYQKLFIFPNMNIRMWGNPF
LQKNIDLLKNNDVKVYSPDMNKSFEISSGRYKNNITMPNIENVLNFVLN

>d1ig3a2 c.100.1.1 (A:10-178) Thiamin pyrophosphokinase, catalytic domain {Mouse (Mus musculus)}

HSSGLVPRGSHMEHAFTPLEPLLPTGNLKYCLVVLNQPLDARFRHLWKKALLRACADGG
ANHLYDLTEGERESFLPEFVSGDFDSIRPEVKEYYTKKGCDLISTPDQDHTDFTKCLQVLQ
RKIEEKELQVDVIVTLGGLGGRFDQIMASVNTLQATHITPVPIIIQK

>d1ig0a2 c.100.1.1 (A:3-223) Thiamin pyrophosphokinase, catalytic domain {Baker's yeast (Saccharomyces cerevisiae)}

EECIENPERIKIGTDLINIRNKMNLKELIHPNEDENSTLLILNQKIDIPRPLFYKIWKHLHDLKV
CADGAANRLYDYLDDDETLRIKYLPNYIIGDLSLSEKVYKYRKNKVTIKQTTQYSTDF
TKCVNLISLHFNSPEFRSLISNKDNLQSNHGIELEKGIHTLYNTMTESLVFSKVTPISLLALG
GIGGRFDQTVHSITQLYTLSENASYFKLCYMTF

>d1f75a_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {*Micrococcus luteus*}
NINAAQIPKHIAIIMDGNGRWAKQKKMPRIKGHYEGMQTVRKITRYASDLGVKYLTLYAF
STENWSRPKDEVNYLMKLPGDFLNTFLPELIEKNVKVETIGFIDDLPDHTKKAVLEAKEKT
KHNTGLTLVFALNYGGRKEIISAVQLIAERYKSGEISLDEISETHFNEYLFATANMPDPELLIR
TSGEERLSNFLIWQCSYSEFVFIDEFWPDFNEESLAQCISIQNR

>d1jp3a_ c.101.1.1 (A:) Undecaprenyl diphosphate synthase {*Escherichia coli*}
LPAHGCRHVAIIMDGNGRWAKKQGKIRAFGHKAGAKSVRRVSAANNGIEALTLYAFSS
ENWNRPAQEVSALEMELFVWALDSEVKSLSHRHNVRLRIIGDTSRFNSRLQERIRKSEALTAG
NTGLTLNIAANYGGRWDIVQGVRLAEKVQQGNLQPDQIDEEMLNQHVCMHLEAPVDL
VIRTGGEHRISNFWLWQIAYAELYFTDVLWPDFDEQDFEGALNAFANRE

>d1pvda2 c.36.1.1 (A:2-181) Pyruvate decarboxylase {*Baker's yeast (Saccharomyces cerevisiae)*}
SEITLGKYLFERLKQVNVNTVFGPLPGDFNLSLLDKIYEEVEGMRWAGNANELNAAYAADG
YARIKGMSCIITTFGVGELSALNGIAGSYAEHVGVLHVVGVPSSISHTLNGDFTVFHRMS
ANISETTAMITDIATAPAEIDRCIRTTYVTQRPVYLGLPANLVDLNVPAKLL

>d1pvda3 c.36.1.1 (A:361-556) Pyruvate decarboxylase {*Baker's yeast (Saccharomyces cerevisiae)*}
ASTPLKQEWMMWNQLGNFLQEGDVVIAETGTSAFGINQTTFPNNTYGISQVLWGSIGFTTG
ATLGAFAAAEIDPKKRVLFIGDGSLLQTLVQEISTMIRWGLKPYLFVLNNDGYTIEKLIHGP
KAQYNEIQGWDHLSLLPTFGAKDYETHRVATTGEWDKLTQDKSFNDNSKIRMIEIMLPVF
DAPQNLVKQAKLT

>d1zpda2 c.36.1.1 (A:2-187) Pyruvate decarboxylase {*Zymomonas mobilis*}
SYTVGTYLAERLVQIGLKHFAVAGDYNLVLLDNLLLKNMEQVYCCNELNCGFSAEGY
ARAKGAAAAVTYSVGALSAFDAIGGAYAENLPVILISGAPNNNDHAAGHVLHHALGKT
DYHYQLEMAKNITAAAEAIYTPEEAPAKIDHVIKTALREKKPVYLEIACNIASMPCAAPGP
ASALFND

>d1zpda3 c.36.1.1 (A:363-566) Pyruvate decarboxylase {*Zymomonas mobilis*}
APLVNAEIRARQVEALLTPNTTVIAETGDSWFNAQRMKLPNGARVEYEMQWGHIGWSVPA
AFGYAVGAPERRNILMVGDSFQLTAQEVQMVRLKLPVIFLINNYGYTIEVMIHDGPYN
NIKNWDYAGLMEVFNGNGGYDSGAAGLKAKTGGELAEAIKVALANTDGPTLIECFIGR
EDCTEELVKWGRVAAANSRKPVNK

>d1poxa2 c.36.1.1 (A:9-182) Pyruvate oxidase {*Lactobacillus plantarum*}
TNILAGAAVIKVLEAWGVDHLYGIPGGSINSIMDALSAERDRIHYIQVRHEEVGAMAAAA
DAKLTGKIGVCFGSAGPGGTHLMNGLYDAREDHVPVLALIGQFGTTGMNMDTFQEMNE
NPIYADVADYNVTAVNAATLPHVIDEAIIRRAYAHQGVAVVQIPVDLPWQQISAEDW

>d1poxa3 c.36.1.1 (A:366-593) Pyruvate oxidase {*Lactobacillus plantarum*}
KQEGPLQAYQVLRVANKIAEPDAIYSIDVGDLNANRHLKLTPSNRHITSNLFATMGVGIP
GAIAAKLNYPERQVFNLAGDGGASMTMQDLVTQVQYHLPVINVVFTNCQYGFIDEQED
TNQNDFIGVEFNDIDFSKIADGVHMQAFRVNKIEQLPDVFEQAKAIAQHEPVLIDAVITGD
RPLPAEKLRLDSAMSSAADIEAFKQRYEAQDLQPLSTYLKQFGLDD

>d1bfd_2 c.36.1.1 (2-181) Benzoylformate decarboxylase {*Pseudomonas putida*}
ASVHGTTYELLRRQGIDTVFGNPGSNELPFLKDFPEDFRYILALQEACVVGIADGYAQASR

KPAFINLHSAAGTGNAMGALSNAWNSHSPLIVTAGQQTRAMIGVEALLTNVDAANLPRPL
VKWSYEPASAAEVPHAMSRAIHMASMAPQGPVYLSVPYDDWDKDADPQSHHLFDRHVS
S

>d1bfd_3 c.36.1.1 (342-524) Benzoylformate decarboxylase {*Pseudomonas putida*}

EPAKVDQDAGRLHPETVFDLNDMAPENAIYLNSTTTAQMWQRLNMRNPGSYYFCA
AGGLGFALPAAIGVQLAEPERQVIAVIGDGSANYSISALWTAAQYNIPTIFVIMNNGTYGAL
RWFAGVLEAENVPGLDVPGLDFRALAKGYGVQALKADNLEQLKGSLQEALSAKGPVLIE
VSTV

>d1jsca2 c.36.1.1 (A:83-270) Acetohydroxyacid synthase catalytic subunit {*Baker's yeast (Saccharomyces cerevisiae)*}

PDMDTSFVGLTGGQIFNEMMSRQNVDTVFGYPGGAILPVYDAIHNSDKFNFVLPKHEQG
AGHMAEGYARASGKPGVVLVTSGPGATNVVTPMADAFADGIPMVVFTGQVPTSAIGTDA
FQEADVVGISRSCTKWNVMVKSVEELPLRINEAFEIATSGRPGPVLVDLPKDVTAAILRNPI
PTKTTLPS

>d1jsca3 c.36.1.1 (A:461-648) Acetohydroxyacid synthase catalytic subunit {*Baker's yeast (Saccharomyces cerevisiae)*}

AYMEETPGSKIKPQTVIKKLSKVANDTGRHVIVTTGVGQHQMWAAQHWTWRNPHTFITS
GGLGTMGYGLPAAIGAQVAKPESLVIDIDGDASFNMTLTELSSAVQAGTPVKILILNNEEQ
GMVTQWQSLFYEHRYSHTHQLNPDFIKLAEAMGLKGLRVKKQEELDAKLKEFVSTKGPV
LLEVEVDKK

>d1gpua1 c.36.1.2 (A:3-337) Transketolase, TK {*Baker's yeast (Saccharomyces cerevisiae)*}

QFTDIDKLAVSTIRILAVDTVSKANS GHGAPLGMAPAAHVLWSQMRMNPTNPDWINRDR
FVLSNGHAVALLYSMLHLTGYDLSIEDLKQFRQLGSRTPGHPEFELPGVEVTTGPLGQGISE
AVGMAMAQANLAATYNKPGFTLS DNYTYVFLGDGCLQEGISSEASSLAGHLKLGNLIAIY
DDNKITIDGATSISFDEDVAKRYEAYGWEVLYVENGNEDLAGIAKAIQA KLSKDKPTLIK
MTTITIGYGLHAGSHSVHGAPLKADDVKQLKSKFGFNPDKSFVVPQEVYDHYQKTILKP
GVEANNKWNKLFSEYQKKFPELGAELARRLSGQ

>d1gpua2 c.36.1.2 (A:338-534) Transketolase, TK {*Baker's yeast (Saccharomyces cerevisiae)*}

LPANWESKLPTYTAKDSAVATRKLS ETVLEDVYNQLPELIGGSADLTSPNLTRWKEALDFQ
PPSSSGSNYSGRYIRYGIREHAMGAIMNGISAFGANYKPYGGTFLNFVSYAAGAVRLSALS
GHPVIWVATHDSIGVGEDGPTHQPIETLAHFRSLPNIQVWRPADGNEVSAAYKNSLESKHT
PSIIALSRQNLQPQL

>d1dtwa1 c.36.1.3 (A:) Branched-chain alpha-keto acid dehydrogenase {*Human (Homo sapiens)*}

PQFPGASAEFIDKLEFIQPNVISGIPIYRVMDRQGGIINPSEDPHLPKEKVLKLYKSMTLLNT
MDRILYESQRQGRISFYMTNYGEEGTHVGSAAALDNTDLVFGQYREAGVLMYRDYPLEL
FMAQCYGNISDLGKGRQMPVHYGCKERHFVTISSPLATQIPQAVGAAYA AAKRANANRVVI
CYFGEGAASEGDAHAGFNFAATLECPHFFCRNNGYAISTPTSEQYRGDGIAARGPGYGIMS
IRVDGNDVFAVYNATKEARRRAVAENQPFLIEAMTYRIGHHSTSDDSSAYRSVDEVNYWD
KQDHPISRLRHLYLLSQGWWDDEEQEKAWRKQSRRKVM EAFEQAERKPKPNPNLLFSDVY
QEMPAQLRKQQESLARHLQTYGEHYPLDHFDDK

>d1qs0a1 c.36.1.3 (A:) 2-oxoisovalerate dehydrogenase, E1B {*Pseudomonas*}

putida}

NEYAPLRLHVPEPTGRPGCQTDFSYLRLNDAGQARKPPVDVDAADTADLSYSLVRVLDEQ
GDAQGPWAEDIDPQILRQGMRAMLKTRIFDSRMVVAQRQKKMSFYMQSLGEEAIGSGQA
LALNRTDMCFPTYRQQSILMARDVSLVEMICQLLSNERDPLKGRQLPIMYSVREAGFFTIS
GNLATQFVQAVGWAMASAIKGDTKIASAWIGDGATAESDFHTALTFAHVYRAPVILNVVN
NQWAISTFQAIAGGESTTFAGRGVGCGLASLRVDGNDVFVAVYAASRWAAERARRGLGPSLI
EWVITYRAGPHSTSDPSKYRPADDWSHFPLGDPIARLKQHLLIKIGHWSEEEHQATTAEFE
AAVIAAQKEAEQYGTLANGHIPSAASMFEDVYKEMPDHLRRQRQEL

>d1qs0b1 c.36.1.3 (B:2-205) 2-oxoisovalerate dehydrogenase, E1B {Pseudomonas putida}

ATTTMTMIQALRSAMDVMLERDDNVVYVGQDVGYFGGVFRCTEGLQTKYGKSRVFDAP
ISESGIVGTAVGMGAYGLRPVVEIQFADYFYPASDQIVSEMARLRYRSAGEFIAPLTRMPC
GGGIYGGQTHSQSPEAMFTQVCGLRTVMPSNPYDAKGLLIASIECDDPVIFLEPKRLYNGP
FDGHHDRPVTWPWSKHPHSAVPDG

>d1keka1 c.36.1.4 (A:2-258) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

GKKMMTTDGTATAHVAYAMSEVAAIYPITPSSTMGEEADDWAAQGRKNIFGQTLTIREM
QSEAGAAGAVHGALAAGALTTTFTASQGLLLMIPNMYKISGELLPGVFHVTARIAAAHAL
SIFGDHQDIYAARQTGFAMLASSSVQEAHDMALVAHLAAIESNVPFMHFFDGFRTSHEIQK
IEVLDYADMASLVNQKALAEFRAKSMNPEHPHVRGTAQNPDIYFQGREANPYYLKVPGI
VAEYMQKVASLTGRSY

>d1keka2 c.36.1.4 (A:786-1232) Pyruvate-ferredoxin oxidoreductase, PFOR, domains I and VI {Desulfovibrio africanus}

VKSEVLPRDSLKGSQFQEPLMEFSGACSGCGETPYVRVITQLFGERMFIANATGCSSIWGA
SAPSMFYKTNRLGQGPWAGNSLFEDAAEYGFGMNMSMFARRTHLADLAAKALES DASG
DVKEALQGWLAGKNDPIKSKEYGDKLKKLLAGQKDGLLGQIAAMSDLYTKKSVWIFGG
DWAYDIGYGGLDHVLASGEDVNVFVMDTEVYSNTGGQSSKATPTGAVAKFAAAGKRT
GKKDLARMVMTYGYVYVATVSMGYSKQQLKVLKEAESFPGPSLVIAYATCINQGLRKG
MGKSQDVMNTAVKSGYWPLFRYDPRLLAAQGKNPFQLDSKAPDGSVEEFLMAQNRFVL
DRSFPEDAKRLRAQVAHELDVRFKELEHMAATNIFESFAPAGGKADGSVDFGEGAECFTR
DDTPMMARPDSGEACDQNRAGTSEQQGDLSKRTKK

>d1gky__ c.37.1.1 (-) Guanylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SRPIVISGPSGTGKSTLLKKLFAEYPDSFGFSVSSTTRTPRAGEVNGKDYNFVSVDEFKSMI
KNNEFIEWAQFSGNYYGSTVASVKQVSKSGKTCILDIDMQGVKSVKAIPELNARFLFIAPP
SVEDLKKRLEGRGTETETESINKRLSAAQAELAYAETGAHDKVIVNDDLKAYKELKDFIF
AEK

>d1kgda_ c.37.1.1 (A:) Guanylate kinase-like domain of Cask {Human (Homo sapiens)}

HMRKTLVLLGAHGVGRRHIKNTLITKHPDRFAYPIPHTTTRPPKKDEENGKNYYFVSHDQM
MQDISNNEYLEYGSHEDAMYGTKLETIRKIHEQGLIAILDVEPQALKVLR TAEFAPFVVFIA
APTITPGLNEDESLQRLQKESDILQRTYAHYFDLTIINNEIDETIRHLEEAVELVC

>d1kja2 c.37.1.1 (A:526-724) Guanylate kinase-like domain of Psd-95 {Rat (Rattus norvegicus)}

VTQMEVHYARPIILGPTKDRANDDLLSEFPDKFGSCVPHTTRPKREYEIDGRDYHFVSSR
EKMEKDIQAHKFIEAGQYN SHLYGTSVQSVREVAEQGKHCILDVSANAVRRLQAHLHPI
AIFIRPRSLNVLEINKRITEEQARKAFDRATKLEQEFTECFSAIVEGDSFEEIYHKVKRVIED

LSGPYIWVPARERL

>d1ukz_ c.37.1.1 (-) Uridylate kinase {Baker's yeast (*Saccharomyces cerevisiae*)}

PAFSPDQVSVIFVLGGPGAGKGTQCEKLVKDYSFVHLSAGDLLRAEQGRAGSQYGELIKN
CIKEGQIVPQEITLALLRNAISDNVKANKHKFLIDGFPRKMDQAISFERDIVESKFILFFDCP
EDIMLERLLERGKTSGRSDDNIESIKKRFNTFKETSMPVIEYFETKSKVVRVRCDRSVEDV
YKDVQDAIRDSL

>d1deka_ c.37.1.1 (A:) Deoxynucleoside monophosphate kinase {Bacteriophage T4}

MKLIFLSGVKRSKGDTTADFIMSNYSVKYQLAGPIKDALAYAWGVFAANTDYPCLTRKE
FEGIDYDRETNLNLTKLEVITIMEQAFCYLNGKSPIKGVFVFDDEGKESVNFVAFNKITDVI
NNIEDQWSVRRLMQALGTDLIVNNFDRMYWVKLFALDYLDKFNNGYDYYIVPDTRQDH
EMDAARAMGATVIHVVRPGQKSNDRTHITEAGLPIRDGDLVITNDGSLEELFSKIKNTLKVL

>d1j90a_ c.37.1.1 (A:) Deoxyribonucleoside kinase {Fruit fly (*Drosophila melanogaster*)}

TQPFTVLIEGNISGKTTYLNHFEKYKNDICLLTEPVEKWRNVNGVNLLELMYKDPKKW
AMPFQSYVTLTMLQSHTAPTNNKKLKIMERSIFSARYCFVENMRRNGSLEQGMYNLTLEEW
YKFIEESIHVQADLIHYLRSTSPEVAYERIRQRARSEESCVPLKYLQELHELHEDWLIHQRRPQ
SCKVLVLDADLNLE

>d1jaga_ c.37.1.1 (A:) Deoxyguanosine kinase {Human (*Homo sapiens*)}

GPRRLSIEGNIAGVKSTFVKLLTKTYPEWHVATEPVATWQNIQAAGNQKACTAQLGNLLD
MMYREPARWSYTFQTSFSLRLKVQLEPFPEKLLQARKPVQIFERSVYSDRYIFAKNLFEN
GSLSDIEWHIYQDWHFLLWEFASRITLHGFIYQASPVCLKRLYQRAREEEKGIELAYLE
QLHGQHEAWLIHKTTKLHFEALMNIPVLVLDVNDDFSEEVTKQEDLMREVNTFVKNL

>d1ckea_ c.37.1.1 (A:) CMP kinase {*Escherichia coli*}

AIAPVITIDGPSGAGKGTLCMAAEALQWHLLDSGAIYRVLALAAALHHHVDVASEDALVP
LASHLDVRFVSTNGNLEVILEGEDVSGEIRTQEVANAASQVAAPRVREALRRQRAFREL
PGLIADGRDMGTVVFPDAPVKIFLDASSEERAHRRMLQLQVKGFSVNFERLLAEIKERDD
RDRNRAVAPLVPAADALVLDSTTLSIEQVIEKALQYARQKLALA

>d1e2ka_ c.37.1.1 (A:) Thymidine kinase {Herpes simplex virus type 1, different strains}

MPTLLRVYIDGPHGMGKTTTTQLLVALGSRDDIVYVPEPMTYWRVLGASETIANIYTTQH
RLDQGEISAGDAAVVM TSAQITMGMPYAVTDAVLAPHIGGEAGSSHAPPPALTLIFDRHPI
AALLCYPAAARYLMGSMTPQAVLAFVALIPPTLPGTNIVLGALPEDRHIDRLAKRQRPGERL
DLAMLAAIRRVYGLLANTVRYLQCGGSWREDWGQLSGTAVPPQGAEPQSNAGPRPHIGD
TLFTLFRAPPELLAPNGDLYNVFAWALDVLA KRLRSMHVFILDYDQSPAGCRDALLQLTSG
MVQTHVTTGPSIPTICDLARTFAREMGE

>d1nksa_ c.37.1.1 (A:) Adenylate kinase {Archaeon *Sulfolobus acidocaldarius*}

MKIGIVTGIPGVGKSTVLAKVKEILDNQGINNKIINYGDFMLATALKLG YAKDRDEMRLKS
VEKQKKLQIDAAKGIAEEARAGGEGYLFIDTHAVIRTPSGYLPGLPSYVITEINPSVIFLLEA
DPKIILSRQKRDTTRNRNDYSDES VILETINFARYAATASAVLAGSTVKVIVNVEGDPSIAA
NEIIRSMK

>d2ak3a1 c.37.1.1 (A:0-124,A:162-225) Adenylate kinase {Cow (*Bos taurus*), mitochondrial izozyme-3}

GASARLLRAAIMGAPGSGKGTVSSRITKHFELKHLSSGDLLRDNMLRGTEIGVLAKTFIDQ
GKLIPDDVMTRLVLHELKNLTQYNWLLDGFPRTPQA EALDRAYQIDTVINLNVPFVFIKQ
RLTXDRPETVVKRLKAYEAQTEPVLEYYRKKGVLETFSGTETNKIWP HVYAFLQTKLPQR

SQETSVTP

>d1ak2_1 c.37.1.1 (14-146,177-233) Adenylate kinase {Cow (Bos taurus), mitochondrial izozyme-2}

PKGVRVAVLLGPPGAGKGTQAPKLAKNFCVCHLATGDMLRAMVASGSELGKKLKATMDA
GKLVSDVMVLELIEKNLETPPCKNGFLLDGFPRTVRQAEMLDDLMEKRKEKLDVIEFSIP
DSLLIRRITGRLIHXSDDNKKALKIRLEAYHTQTTPLEVEYYSKRGHSAIDASQTPDVVFASI
LAAFSKATS

>d1zaka1 c.37.1.1 (A:3-127,A:159-222) Adenylate kinase {Maize (Zea mays)}

ADPLKVMISGAPASGKGTQCELIKTKYQLAHISAGDLLRAEIAAGSENGKRAKEFMEKGQ
LVPDEIVVNMVKERLRQPDAQENGWLLDGYPRSYSQAMALETLEIRPDTFILLDVPDELL
VERVVXFDDETEKVKLRLETYYQNIESLLSTYENIIVKVQGDATVDVFAKIDELLGSILEK
KNEMVSST

>d1tmka_ c.37.1.1 (A:) Thymidylate kinase {Baker's yeast (Saccharomyces cerevisiae)}

GRGKLILIEGLDRTGKTTQCNILYKKLQPNCKLLKFPERSTRIGGLINEYLTDDSFQLSDQAI
HLLFSANRWEIVDKIKKDLLEGKNIVMDRYVYSGVAYSAAKGTNGMDLDWCLQPDVGL
LKPDLTLFLSTQDVDNNAEKSGFGDERYETVKFQEKVKQTFMKLLDKEIRKGDESITVD
VTNKGIQEVEALIWQIVEPVLSTHIDHDKFSFF

>d4tmka_ c.37.1.1 (A:) Thymidylate kinase {Escherichia coli}

RSKYIVIEGLEGAGKTTARNVVVETLEQLGIRDMVFTREPGGTQLAEKLRSLLLDIKSVGD
EVITDKAEVLMFYAARVQLVETVIKPALANGTWVIGDRHDLSTQAYQGGGRGIDQHMLA
TLRDAVLGDFRPDLTLYLDVTPEVGLKRARARGELDRIEQESFDFFNRTRARYLELAAQD
KSIHTIDATQPLEAVMDAIRTTVTHWVKEL

>d1g3ua_ c.37.1.1 (A:) Thymidylate kinase {Mycobacterium tuberculosis}

MLIAIEGVLDGAGKRTLVEKLSGAFRAAGRSVATLAFPRYGQSVAAADIAAEALHGEHGDLA
SSVYAMATLFLDRAGAVHTIQGLCRGYDVVILDRYVASNAAYSAARLHENAAGKAAAW
VQRIEFARLGLPKPDWQVLLAVSAELAGERSRGRAQRDPGRARDNYERDAELQQRTGAV
YAEALAAQGWGGRWLTVVGADVDPGRLAATLA

>d1g8fa3 c.37.1.15 (A:390-511) ATP sulfurylase C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

PRPKQGFSIVLGNLSLTVSREQLSIALSTFLQFGGGRYKIFEHNNKTELLSLIQDFIGSGSG
LIIPDQWEDDKDSVVGKQNVYLLDTSSSADIQLESADEPISHIVQKVVLFLDNGFFVF

>d1i2da3 c.37.1.15 (A:391-573) ATP sulfurylase C-terminal domain {Fungus (Penicillium chrysogenum)}

PRATQGFTIFLTGYMNSGKDAIARALQVTLNQQGGRSVSLLLGDTVRLHLSSELGFTREDR
HTNIQRIAFVATELTRAGAAVIAAPIAPYEESRKFAVDASQAGSFFLVHVATPLEHCEQSDK
RGIYAAARRGEIKGFTGVDDPYETPEKADLVVDFSKQSVRSIVHEILVLESQGFLERQ

>d1aqua_ c.37.1.5 (A:) Estrogen sulfotransferase {Mouse (Mus musculus)}

EYYEVFGEFRGVLMDKRFTKYWEDVEMFLARPDDLVIATYPKSGTTWISEVVYMIYKEG
DVEKCKEDAFNRIPLYECRNEDLINGIKQLKEKESPRIVKTHLPPKLLPASFWCKNCKMIY
LCRNAKDVAVSYYYFLLMITSYPNPKSFSEFVEKFMQGQVPYGSWYDHVKAWWEKSKN
SRVLFMFYEDMKEDIRREVVKLIEFLERKPSAELVDRIIQHTSFQEMKNNPSTNYTMMPEE
MMNQKVSPFMRKGIIGDWKNHFPALRERFDEHYKQQMKDCTVKFRME

>d1efha_ c.37.1.5 (A:) Hydroxysteroid sulfotransferase {Human (Homo sapiens)}

DFLWFEGIAFPTMGFRSETLRKVRDEFVIRDEDVIILTYPKSGTNWLAEILCLMHSGDAK
WIQSVPIWERSPWVESEIGYTALSETESPRLFSSHLPIQLFPKSFSSKAKVIYLMRNPRDVL
VSGYFFWKNMKFIKKPKSWEEYFEWFQCQGTVLYGSWFDHIHGWMPMREEKNFLLS
YEELKQDTGRTEIKICQFLGKTLEPEELNLILKNSSFQSMKENKMSNYSLLSVDYVVDKAQLL
RKGVS GDWKNHFTVAQAEDFDKLFQEKMA DLPRKLAAALE

>d1lnsta_ c.37.1.5 (A:) Heparan sulfate N-deacetylase/N-sulfotransferase domain {Human (Homo sapiens)}

DPLWQDPCEDKRHKDIWSKEKTCDRFPKLLIIGPQKTGTALYLFLGMHPDLSSNYPSSSET
FEEIQFFNGHNYHKGIDWYMEFFPIPSNTTSDFYFEKSANYFDSEVAPRRAAALLPKAKVL
TILINPADRAYSWYQHQRADDDPVALKYTFHEVITAGSDASSKLRLALQNRCLVPGWYATHI
ERWLSAYHANQILVLDGKLLRTEPAKVMDMVQKFLGVTNTIDYHKTLAFDPKKGFWCQL
LEGGKTKCLGKSKGRKYPEMDLDSRAFLKDYYRDHNIELSKLLYKMGQTLPTWLREDLQ

>d1fmja_ c.37.1.5 (A:) Retinol dehydratase {Fall armyworm (Spodoptera frugiperda)}

PFPHYEFRELNPEEDKLVKANLGAFTTYVKLGPKGYMVYRPYLKDAANIYNMPLRPTDV
FVASYQRS GTTMTQELVWLIENDLNFEAAKTYMSLRYIYLDGFMIDPEKQEEYNDILPN
PENLDMERYLGLLEYSSRPGSSLLAAVPPTEKRFVKTHLPLSLMPPNMLD TVKMVYLARD
PRDVAVSSFHARLLYLLNKQSNFKDFWEMFHRGLYTLTPYFEHVKEAWAKRHPNMFLF
LFYEDYLDKDLPGCIARIADFLGKKLSEEQIQLRCEHLNFEKFKNNGAVNMEDYREIGILAD
GEHFIRKKGKAGCWRDYFDEEMTKQAEKWIKDNLKDTDLRYPNM

>d1a7j_ c.37.1.6 (-) Phosphoribulokinase {Rhodobacter sphaeroides}

SKKHPIISVTGSSGAGTSTVKHTFDQIFRREGVKAVSIEGDAFHRFNRA DMKAELDRRYAA
GDATFSHF SYEANELKELERVFREYGETGQGRTRTYVHDDAEAARTGVAPGNFTDWRDF
DSDSHLLFYEGLHGAVVNSEVNIAGLADLKIGVVPVINLEWIKIHRDRATRGTTEAVTD
VILRRMHAYVHCIVPQFSQTDINFQRPVVDTSNPFIARWIPTADESVVVIRFNPRGIDFPY
LTSMIHGSWMSRANSIVVPGNKLDLAMLQILTLPLIDRVVRESKV

>d1lesma_ c.37.1.6 (A:) Pantothenate kinase PanK {Escherichia coli}

QTLMTPYLQFDRNQWAALRDSVPMTLSEDEIARLKGINEDLSLEEVAEIYLP LSRLLNFYIS
SNLRRQAVLEQFLGTNGQRIPYIISIAGSVAVGKSTTARVLQALLSRWPEHRRVELITTDGFL
HPNQVLKERGLMKKKGFPE SYDMHRLVKFVSDLKSGV PNV TAPVYSHLIYDVIPDGDKT
VVQPDILILEGLNVLQSGMDYPHDPHHVFVSDFVDFSIYVDAPEDLLQTWYINRFLKFRE
GAFTDPDSYFHNYAKLTKEEAIKTAMTLWKEINWLNKQNILPTRERASLILTKSANHAVE
EVR LRK

>d1cl1ya_ c.37.1.8 (A:) Rap1A {Human (Homo sapiens)}

MREYKLVVLGSGGVGKSALT VQFVQGIFVEKYDPTIEDSYRKQVEVDCQQCMLEILDTA
GTEQFTAMRDLYMKNGQG FALVYSITAQSTFNDLQDLREQILRVKDTEDVPMILVGNKCD
LEDERVVGKEQGQN LARQWCNCAFLESSAKSKINVNEIFYDLVRQINR

>d3raba_ c.37.1.8 (A:) Rab3a {Rat (Rattus norvegicus)}

NFDYMFKILIIGNSSVGKTSFLFRYADDSFTPAFVSTVGIDFKVKTIYRNDKRIKLQIWDTA
GQERYRTITTAYYRGAMGFILMYDITNEESFNAVQDWSTQIKTYSWDNAQVLLVGNKCD
MEDERVVSSERGRQLADHLGFEFFEASAKDNINVKQTFERLVDVICEK

>d1byua_ c.37.1.8 (A:) Ran {Dog (Canis familiaris)}

EPQVQFKLVLVGDGGTGKTTFVKRHLTGFEFEKKYVPTLGVEVHPLVFHTNRGPIKFNVD
TAGQEKFGGLRDGYIQAQCAIMFDVTSRVTYKNVPNWHRDLVRVCENIPIVLCGNKVD
IKDRKVKAKSIVFHRKKNLQYYDISAKSNYNFEKPFLWLARKLIGDPNLEFVAMPALAPPE

VVMDPALAAQYEHDLVAQTT

>d1hura_ c.37.1.8 (A:) ADP-ribosylation factor {Human (Homo sapiens), ARF1}

GNIFANLFKGLFGKKEMRILMVGLDAAAGKTTILYKLLGEIVTTIPTIGFNVETVEYKNISF
TVWDVGGQDKIRPLWRHYFQNTQGLIFVVDSDNRERVNEAREELMRMLAEDELRLDAVL
LVFANKQDLPNAMNAAEITDKLGLHSLRHRNWYIQATCATSGDGLYEGLDWLSNQLRNQ
K

>d1f6ba_ c.37.1.8 (A:) SAR1 {Chinese hamster (Cricetulus griseus)}

SSVLQFLGLYKKTGKLVFLGLDNAGKTTLLHMLKDDRLGQHVPTLHPTSEELTIAGMTFT
TFDLGGHIQARRVWKNYLPAINGIVFLVDCADHERLLESKEELDSLMTDETIANVPILILGN
KIDRPEAISEERLREMFGLYGQTTGKGSVSLKELNARPLEVFMCSVLKRQGYGEGFRWM
AQYID

>d2ngra_ c.37.1.8 (A:) CDC42 {Human (Homo sapiens)}

MQTIKCVVVG DGAVGKTCLLISYTTNFKPSEYVPTVFDNYAVTVMIGGEPYTLGLFDTAG
QEDYDRLRPLSYPTDVLVCFSVSPSSFENVKEKWVPEITHHCPKTPFLLVGTQIDLRD
DPSTIEKLAKNKQKPITPETAEKLRDLKAVKYVECSALTQKGLKNVFDEAILAALEPPEP
KKSRRCVLL

>d1ek0a_ c.37.1.8 (A:) Ypt51 {Baker's yeast (Saccharomyces cerevisiae)}

VTSIKLVLLGEAAVGKSSIVLRFVSNDFEAENKEPTIGAAFLTQRTINEHTVKFEIWDTAGQ
ERFASLAPMYRNAQAALVVYDVTKPQSFIAKRWVKELHEQASKDIIIALVG NKIDMLQ
EGGERKVAREEGEKLAEKGLFFETS AKTGENVNDVFLGIGEKIPLK

>d1h65a_ c.37.1.8 (A:) Chloroplast protein translocon GTPase Toc34 {Garden pea (Pisum sativum)}

VREWSGINTFAPATQTKLLELLGNLQKEDVNSLTILVMGKGGVGKSSTVNSIIGERVVSISP
FQSEGPRPVMVSRSRAGFTLNIIDTPGLIEGGYINDMALNIIKSFLDKTIDVLLYVDRLDA
YRVDNLDKLVAKAITDSFGKGIWNKAIVALTHAQFSPPDGLPYDEFFSKRSEALLQVVRSG
ASLKKDAQASDIPVVLIENTSGRCNKNDSDKVL PNGIAWIPHLVQTITEVALNKSESIFVDK
NLIDKLAAAD

>d1bof_2 c.37.1.8 (10-60,182-354) Transducin (alpha subunit) {Rat (Rattus norvegicus)}

KAAVERSKMIDRNREDGEKAAREVKLLLLGAGESGKSTIVKQMKIIHEAGXTGIVETHF
TFKDLHFKMFDVGGQRSEKRWIHC FEGVTAIIFCVALS DYDLVLAEDEEMNRMHESMK
LFDSICNNKWFTDTSIILFLNKKDLFEKIKKSPLTICYPEYAGSNTYEEAAAYIQCQFEDLN
KRKDTKEIYTHFTCATDTKNVQVFDAVTDVVIKNNLKDCGLF

>d1exma3 c.37.1.8 (A:3-212) Elongation factor Tu (EF-Tu), N-terminal (G) domain {Thermus thermophilus}

GEFIRTKPHVNVGTIGHVDHGKTTLTAALTFVTAAENPNVEVKDYGDIDKAPEERARGITI
NTAHVEYETAKRHYSHVDCPGHADYIKNMITGAAQMDGAILVVSADGPMPTREHILL
ARQVGVPYIVFMNKVDMVDDPELLDLVEMEVRDLLNQYEFPGDEVVPVIRGSALLALEQ
MHRNPKTRRGENEWVDKIWELLD AIDEYIPT

>d1f60a3 c.37.1.8 (A:2-240) Elongation factor eEF-1alpha, N-terminal (G) domain {Baker's yeast (Saccharomyces cerevisiae)}

GKEKSHINVVIGHVDSGKSTTTGHLIYKCGGIDKRTIEKFEKEAAELGKGSFKYAWVLD
KLKAERERGITIDIALWKFETPKYQVTVIDAPGHRDFIKNMITGTSQADCAILIIAGGVGEF
EAGISKDGQTREHALLAFTLGVRQLIVAVNKMDSVKWDESRFQEIVKETS NFIKKVGYNP
KTVPFVPISGWNGDNMIEATTNAPWYKGWEKETKAGVVKGKTLLEAIDAIEQPSRPT

>d1dar_2 c.37.1.8 (1-282) Elongation factor G (EF-G), N-terminal (G) domain {Thermus

thermophilus}

MAVKVEYDLKRLRNIGIAAHIDAGKTTTTERILYYTGRIHKIGEVHEGAATMDFMEQERE
RGITITAAVTTCTFWKDHRIIIDTPGHVDFTIEVERSMRVLGDGAIVVFDSSQGVPEQSETVW
RQAEKYKVPRIAFANKMDKTGADLWLVRTMQLGARPVVMQLPIGREDTFSGIIDVLR
MKAYTYGNDLGTDIRIPIPEEYLDQAREYHEKLVEVAADFDENIMLKYLEGEEPTTEELV
AAIRKGTIDLKITPVFLGSALKNKGVLQLLDAVVDYLP

>d1g7sa4 c.37.1.8 (A:1-227) Initiation factor IF2/eIF5b, N-terminal (G) domain {Archaeon
Methanobacterium thermoautotrophicum}

MKIRSPIVSVLGHVDHGKTTLLDHIRGSAVASREAGGITQHIGATEIPMDVIEGICGDFLKK
FSIRETLPLFFIDTPGHEAFTTLRKRGGALADLAILVDINEGFKPQTQEALNILRMYRTPF
VVAANKIDRIHGWRVHEGRPFMETFSKQDIQVQKLDTKVYELVGLKHEEGFESERFDRV
TDFASQVSIIPISAITGEGIPPELLTMLMGLAQQYLREQLKIE

>d1lega1 c.37.1.8 (A:4-182) GTPase Era, N-terminal domain {Escherichia coli}

DKSYCGFIAIVGRPNVGKSTLLNKLLGQKISITSRKAQTTRHRIVGIHTEGAYQAIYVDTPG
LHMEEKRAINRLMNKAASSIGDVELVIFVVEGTRWTPDDEMVLNKLREGKAPVILAVNK
VDNVQEKADLLPHLQFLASQMNFLDIVPISAETGLNVDTIAAIVRKHLPEATHHFPE

>d1f5na2 c.37.1.8 (A:7-283) Interferon-induced guanylate-binding protein 1 (GBP1), N-terminal
domain {Human (Homo sapiens)}

MTGPMCLIENTNGRLMANPEALKILSAITQPMVVVAIVGLYRTGKSYLMNKLAKKKKGFS
LGSTVQSHTKGIWMWCVPHPKKPGHILVLLDTEGLGDVEKGDNDQNDWIFALAVLLSSTF
VYNSIGTINQQAMDQLYYVTELTHRIRSKSPDENENEVEDSADFVSFFPDFVWTLRDFSL
DLEADGQPLTPDEYLTYSKLKKGTSQKDETFNLPRLCIRKFFPKKKCFVDRPVHRRKLA
QLEKLQDEELDPEFVQQVADFCSYIFSNSKTKTLS

>d1jwyb_ c.37.1.8 (B:) Dynamin G domain {Slime mold (Dictyostelium discoideum)}

DQLIPVINKLQDVFNLTGSDPLDLPQIVVVGSSGKSSVLENIVGRDFLPRGSGIVTRRPLI
LQLTHLPIADDGSQTQEWGEFLHKPNDMFYDFSEIREEEIIRDTDRMTGKNKGISAQPINLKI
YSPHVVNLTLDLPGITKVPVGDQPTDIEQQIRRMVMAYIKKQNAIIVAVTPANTDLANS
ALQLAKEVDPEGKRTIGVITKLDLMDKGTDAVEVLTGRVIPLTLGFIGVINRSQEDIIAKKS
IRESLKSEILYFKNHPIYKSIANRSGTAYLSKTLNKLMMFHIRDTPDLKVKVSKMLS

>d2mysa2 c.37.1.9 (A:4-33,A:80-843) Myosin S1, motor domain {Chicken (Gallus gallus), pectoral
muscle}

DAEMAAFGEAAPYLKSEKERIEAQNKPFDXMNPPKYDKIEDMAMMTHLHEPAVLYNL
KERYAAWMIYTYSGLFCVTVPYKWLVPYNPKVVLAYRGKKRQEAPPHIFSISDNAYQF
MLTDRENQSILITGESGAGKTVNTKRVIQYFATIAASGEKKKEEQSGKMQGTLEDQIISANP
LLEAFGNAKTVRNDNSSRFGKFIRIHFGATGKLASADIETYLLEKSRVTFQLPAERSYHIFY
QIMSNKKPELIDMLLITNPYDYHYVSEGEITVPSIDDQEELMATDSIDILGFSADKTAIY
KLTGAVMHYGNLKFQKQREEQAEPDGTVEADKAAYLMGLNSAELLKALCYPRVGVGN
EAVTKGETVSEVHNSVGALAKAVYEKMLFWMVIRINQQLDTKQPRQYFIGVLDIAGFEIF
DFNSFEQLCINFTNEKLQQFFNHMFVLEQEEYKKEGIEWEFIDFGMDLAACIELIEKPMG
IFSILEEECMFPKATDTSFKNKLYDEHLGKSNNFQKPKPAKGKAEAHFSLVHYAGTVDYNI
SGWLEKNKDPLNETVIGLYQKSSVKTLALLFATYGGAEAGGGGKKGKGGKSSSFQTVSA
LFRENLNKLMANLRSTHPIFVRCIIPNETKTPGAMEHELVHLQLRCNGVLEGIRICRKGFP
SRVLYADFKQRYRVLNASAIPEGQFMDSKKASEKLLGGGDVDHTQYAFGHTKVFFKAGL
LGLLEEMRDDKLAIEITATQARCRGFLMRVEYRAMVERRESIFCIQYNVRSFMNVKHWP

WMKLFFKIKPLLK

>g2kin.1 c.37.1.9 (A.;B:) Kinesin {Rat (*Rattus norvegicus*)}

ADPAECSIKVMCRFRPLNEAEILRGDKFIPKFKGEETVVIGQGKPYVFDRLPNTTQEQV
YNACAKQIVKDVLEGYNGTIFAYGQTSSGKTHTMEGKLHDPQLMGIIPIAHDFDHIYSM
DENLEFHIKVSFYFEIYLDKIRDLLDVSKTNLAVHEDKNRVPYVKGCTERFVSSPEEVMDVI
DEGKANRHVAVTNMNEHSSRSHSIFLINIKQENVETEEKLSGKLYLVDLAGSEKVVXAKNIN
KSLSALGNVISALAEGTKTHVPYRDSKMTRILQDSDLGNCRTTIVICCSPSVFNEAETKSTL
MFGQRAKTIKNTVSVNLELTAEEWKKKYEKEKE

>d1i6ia_ c.37.1.9 (A:) Kinesin {Mouse (*Mus musculus*), kif1a}

GASVKVAVRVRPFNSREMSRDSKCIQMSGSTTTIVNPKQPKETPKSFSFDYSYWSHTSPED
INYSQKQVYRDIGEEMLQHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQGGIIPQLC
EDLFSRINDTTNDNMSYSVEVSMEIYCERVRDLLNPKNKGNLRVREHPLLGPYVEDLSK
LAVTSYNDIQDLMDSGNKARTVAATNMNETSSRSHAVFNIFTQKRHDAETNITTEKVS
KISLVDLAGSERADSTGAKGTRLKEGANINKSLTTLGKVISALAEEMDSGPNKNKKKKKTDFIP
YRDSVLTWLLRENLGNSRTAMVAALSPADINYDETLSTLRYADRAKQIRNTVSVNHHHH
H

>d1ii6a_ c.37.1.9 (A:) Kinesin {Human (*Homo sapiens*), mitotic kinesin eg5}

GKNIQVVVRCRPFNLAERKASAHSIVECDPVRKEVSVRTGGLADKSSRKTYTFDMVFGAS
TKQIDVYRSVVCPIILDEVIMGYNCTIFAYGQTGTGKTFTMEGERSPNEEYTWEEDPLAGIIP
RTLHQIFEKLTDNGTEFSVKVSLLEIYNEELFDLLNPSSDVSERLQMFDDPRNKRGVIIKGL
EEITVHNKDEVYQILEKGAAKRTTAATLMNAYSSRSHSVSVTIHMKETTIDGEELVKIGK
LNLVDLAGSENIGRSGAVDKRAREAGNINQSLTLGRVITALVERTPHVPYRESKLTRILQD
SLGGRTRTSIIATISPASLNLEETLSTLEYAHRAKNILNKPEV

>d2ncda_ c.37.1.9 (A:) Kinesin motor Ncd (non-claret disjunctional) {Fruit fly (*Drosophila melanogaster*)}

LRQRTEELLRCNEQQAAAELETCKEQLFQSNMERKELHNTVMDLRGNIRVFCRIRPPLESEE
NRMCCWTYHDESTVELQSIDAQAKSKMGQQIFSFDQVFHPLSSQSDIFEMVSPLIQSALD
GYNICIFAYGQTGSGKTYTMDGVPESVGVIPRTVDLLFDSIRGYRNLGWEYEIKATFLEIYN
EVLYDLLSNEQKDMEIRMAKNNKNDIYVSNITEETVLDPNHLRHLMTAKMNRATASTA
GNERSSRSHAVTKLELIGRHAEKQEISVGSINLVDLAGSESPKTSTRMTETKNINRSLSELT
NVILALLQKQDHIPYRNSKLTHLLMPSLGGNSKTLMFINVSPFQDCFQESVKSRLFAASVN
SC

>d1byi_ c.37.1.10 (-) Dethiobiotin synthetase {*Escherichia coli*}

SKRYFVTGTDTEVGKTVASCALLQAAKAAGYRTAGYKPVASGSEKTPEGLRNSDALALQ
RNSSLQLDYATVNPYTFAEPTSPHIISAEGRPIESLVMSAGLRALEQQADWVLVEGAGGW
FTPLSDTFTFADWVTQEQLPVILVVGKLGKINHAMLTAVIQHAGLTLAGWVANDVTPP
GKRHAHEYMTTLTRMIPAPLLGEIPWLAENPENAAATGKYINLALL

>d1dj3a_ c.37.1.10 (A:) Adenylosuccinate synthetase, PurA {Bread wheat (*Triticum aestivum*)}

ADRVSSLSNVSGVLGSQWGDEGKGKLVLDVLA PRFDIVARCQGGANAGHTIYNSEGKKFA
LHLVPSGILHEGTLCVVGNGAVIHVPGFFGEIDGLQSNVSCDGRILVSDRAHLLFDLHQT
VDGLREAEANSFIGTTRKGIGPCYSSKVTRNGLRVCDLRHMDTFGDKLDVLFEDAAARF
EGFKYSKGM LKEEVERYKKFAERLEPFIADTVHVLNESIRQKKKILVEGGQATMLDIDFGT
YPFVTSSSPSAGGICTGLGIAPRVIGDLIGVVKAYTTTRVGSGPFPTTELLGEEGDVLRKAGME
FGTTTGRPRRCGWLDIVALKYCCDINGFSSNLTKLDVLSGLPEIKLGVSYNQMDGEKLG

SFPGDLDTLEQVQVNYEVLPGWDSDISSVRSYSELPQAARRYVERIEELAGVPVHYIGVGP
GRDALIYK

>d1eg7a_ c.37.1.10 (A:) Formyltetrahydrofolate synthetase {*Moorella thermoacetica*}

DIEIAQAAKMKPMELARGLGIQEDEVLYGKYKAKISLDVYRRLKDKPDGKLILVTAITP
TPAGEGKTTTTSVGLTDALARLGKRVMLVCLREPSLGPSFGIKGGAAGGGYAQVVPMEDINL
HFTGDIHAVTYAHNLLAAMVDNHLQQGNVLNIDPRITWRRVIDLNERALRNIVIGLGKK
ANGVPRETGFDISVASEVMACLCCLASDLMDLKERFSRKVVGYTYDGKPVTAGDLEAQGS
MALLMKDAIKPNLVQTLNTPAFIHGGPFANIAHGCNSIIATKTALKLADYVVTAGFGAD
LGAEKFYDVKCRYAGFKPDATVIVATVRALKMHGGVPSKDLATENLEALREGFANLEKHI
ENIGKFGVPAVVAINAFPTDTEAELNLLYELCAKAGAEVALSWAKGGEGGLELARKVLQT
LESRPSNFHVLYNLDLSIKDKIAKIATEIYGADGVNYTAEADKAIQRYESLGYGNLPVMA
KTQYSFSDDMTKLGRPRNFTITVREVRLSAGGRLIVPITGAIMTMPGLPKRPAACNIDIDA
DGVITG

>d1fp6a_ c.37.1.10 (A:) Nitrogenase iron protein {*Azotobacter vinelandii*}

AMRQCAIYGKGGIGKSTTTQNLVAALAEMGKKVMIVGCDPKADSTRILHLSKAQNTIME
MAAEAGTVEDLEEDVLKAGYGGVKCVESGGPEPGVGCAGRGVITAINFLEEAGAYEDD
LDFVFYDVLGDVVCGGFAMPIRENKAQEIIYIVCSGEMMAMYAANNISKGIVKYANSQSV
RLGGGLICNSRNTDREDELIILANKLGTQMIHFVPRDNVVRRAEIRRMVTIEYDPKAKQA
DEYRALARKVVVDNKLIVPNPITMDELEELLMEFGIMEVEDESIVGKTAEV

>d1iona_ c.37.1.10 (A:) Cell division regulator MinD {Archaeon *Pyrococcus horikoshii*}

MTRIISIVSGKGGTGKTTVTANLSVALGEMGRKVLAVDGDLTMANLSLVLGVDVNDNLH
DVLGADAKLEDAYMTQFENVYILPGAVDWEHVIKADPRKLPEVIKSLKGKYDFILIDCPA
GLQLRAMSAMLGEEAILVTNPEISCLTDTMKVGMVLKKAGLAILGFILNRYGRSERDIPP
EAAQDVM DVPLLA VIPEDPVIREGTLEGIPAVKYKPESKGAQAFIKLAEV DKL AGIKAKI

>d1j8mf2 c.37.1.10 (F:87-297) GTPase domain of the signal sequence recognition protein Ffh {Archaeon *Acidianus ambivalens*}

DKEPKVIPDKIPYVIMLVGVQGTGKTTTAGKLAYFYKKKGFKVGLVGADVYRPAALEQL
QQLGQQIGVPVYGEPGEKDVVGIAKRGVEKFLSEKMEIIIVDTAGRHGYGEEAALLEEMK
NIYEAIKPDEVTLVIDASIGQKAYDLASKFNQASKIGTIIITKMDGTAKGGGALSAAVATGA
TIKFIGTGEKIDELEVFNPRRFVARLHHHH

>d1fts_2 c.37.1.10 (285-495) GTPase domain of the signal recognition particle receptor FtsY {*Escherichia coli*}

PLNVEGKAPFVILMVG VNGVGKTTTIGKLARQFEQQGKSVMLAAGDTFRAAAVEQLQV
WGQRNNIPVIAQHTGADSASVIFDAIQAAKARNIDVLIADTAGRLQNKSHLMEELKKIVR
VMKKLDVEAPHEVMLTIDASTGQNAVSQAKLFHEAVGLTGITLTKLDGTAKGGVIFSVAD
QFGIPIRYIGVGERIEDLRPFKADDFIEALFAR

>d1ihua1 c.37.1.10 (A:1-296) Arsenite-translocating ATPase ArsA {*Escherichia coli*}

MQFLQNIPPYLFFTGKGGVGKTSISCATAIRLAEQGKRVLLVSTD PASNVGQVFSQTIGNTI
QAIASVPGLSALEIDPQAAAQQYRARI VDP IKGVL PDDV VSSINEQLSGACTTEIAAFDEFT
GLLT DASLLTRFDHIIFDTAPTGHTIRLLQLPGAWSSFIDSNPEGASCLGPMAGLEKQREQY
AYAVEALSDPKRTRLVLVARLQKSTLQEVARTHLELAAIGLKNQYLVINGVLPKTEAANDT
LAAAIWEREQEALANLPADLAGLPTDTLFLQPVNMVGVSALSRLSTQP

>d1ihua2 c.37.1.10 (A:308-586) Arsenite-translocating ATPase ArsA {*Escherichia coli*}

QRPDIPSLSALVDDIARNEHGLIMLMGKGGVGKTTMAAAIAVRLADMGFVHLLTSDPAA
HLSMTLNGSLNNLQVSRIDPHEETERYRQHVLETKGKELDEAGKRLLEEDLRSPCTEEIAV
FQAFSRVIREAGKRFVMDTAPTGHTLLLLDATGAYHREIAKKMGEKGHFTTPMMLLQD
PERTKVLLVTLPETTPVLEAANLQADLERAGIHPWGWIIINNSLSIADTRSPLLRMRAQQEL
PQIESVKRQHASRVALVPVLASEPTGIDKLKQLAGHHH

>d1g19a1 c.37.1.11 (A:1-269) RecA protein, ATPase-domain {Mycobacterium tuberculosis}

MTQTPDREKALELAVAQIEKSYGKGSVMRLGDEARQPISVIPTGSIALDVALGIGGLPRGR
VIEIYGPESSGKTTVALHAVANAQAAGGVAAFIDAEHALDPDYAKKLGVDTSLLVSQPDT
GEQALEIADMLIRSGALDIVVIDSVAALVPRAELEGEMGDSHVGLQARLMSQALRKMTG
ALNNSGTTAIFINQLRDKIGVMFGSPETTTGGKALKFYASVRMDVRRVETLKDGTNAVGN
RTRVKVVKNKCLAPFKQAEFDILYGKGI

>d1crla_ c.37.1.11 (A:) Gene 4 protein (g4p, DNA primase), helicase domain {Bacteriophage T7}
MRERIREHLSSEESVGLLFSGCTGINDKTLGARGGEVIMVTSGSGMGKSTFVRQQALQWG
TAMGKKVGLAMLEESVEETAEDLIGLHNRVRLRQSDSLKREIIENGKFDQWFDELFGNDT
FHLYDSFAEAETDRLLAKLAYMRSGLGCDVIILDHISIVVSASGESDERKMIDNLMTKLKG
FAKSTGVVLVVICHKLPDKGKAHEEGRPVSITDLRGSGALRQLSDTHIALERNQQGDMF
NLVLRILKCRFTGDTGIAGYMEYNKETGWLEPSSY

>d1g8ya_ c.37.1.11 (A:) Hexameric replicative helicase repA {Escherichia coli, plasmid rsf1010}

ATHKPINILEAFAAAPPPLDYVLPNMVAGTVGALVSPGGAGKSMLALQLAAQIAGGPDLL
EVGELPTGPVIYLPADPPTAIHHRLHALGAHLSAEERQAVADGLLIQPLIGSLPNIMAPEW
FDGLKRAAEGRRLMVLDTLRRFHIEENASGPMAQVIGRMEIAAADTGCSIVFLHHASKG
AAMMGAGDQQQASRGSSVLVDNIRWQSYLSSMTSAEAEWGVDDDQRRFFVRFVGSKA
NYGAPFADRWFRRHGGVVKPA

>d1e9ra_ c.37.1.11 (A:) Bacterial conjugative coupling protein TrwB {Escherichia coli}

VGQGEFGGAPFKRFLRGTRIVSGGKLKRMTRKAKQVTVAGVPMPRDAEPRHLLVNGAT
GTGKSVLLRELAYTGLLRGDRMVIVDPNGDMLSKFGRDKDIILNPYDQRTKGWSFFNEIR
NDYDWQRYALSVPVPRGKTDEAEWASYGRLLLRETAKKLALIGTPSMRELFWHTTIATFD
DLRGFLEGTLAESLFAGSNEASKALTSARFVLSDKLPEHVTMPDGFIRSLEDPNNGNL
FITWREDMGPALRPLISAWVDVVCTSLSLPEEPKRRWLFIDELASLEKLASLADALTKGR
KAGLRVVAGLQSTSQLDDVYGVKEAQTLRASFRSLVVLGGSRTDPKTNEDMSLSLGEHE
VERDRYSKNTGKHHSTGRALERVREVRVMPAEIANLPDLTAYVGFAGNRPIAKVPLEIKQF
ANRQPAFVEGT

>d1e79a3 c.37.1.11 (A:95-379) Central domain of alpha and beta subunits of F1 ATP synthase {Cow (Bos taurus)}

VDVPVGEELLGRVVDALGNAIDGKGPIGSKARRRVGLKAPGIIPRISVREPMQTGIKAVDS
LVPIGRGQRELIIGDRQTGKTSIAIDTIINQKRFNDGTDEKKKLYCIYVAIGQKRSTVAQLVK
RLTDADAMKYTIVVSATASDAAPLQYLAPYSGCSMGEYFRDNGKHALIHYDDLKQAVAY
RQMSLLLRPPGREAYPGDVFYLSRLLERA AKMNDAFGGGSALTALPVIETQAGDVSAYI
PTNVISITDGQIFLETIFYKGIRPAINVGLSVSRVGSAAQ

>d1fx0b3 c.37.1.11 (B:98-377) Central domain of alpha and beta subunits of F1 ATP synthase {Spinach (Spinacia oleracea), chloroplast}

LSVPVGGPTLGRIFNVLGEPVDNLRPVDTRTTSPIHRSAPAFQTQLDTKLSIFETGIKVVNLLA

PYRRGGKIGLFGGAGVGKTVLIMELINNIKAHGGVSVFGGVGERTREGNDLYMEMKES
GVINEQNIAESKVALVYGQMNEPPGARMRVGLTALTMAEYFRDVNEQDVLLFIDNIFRFV
QAGSEVSALLGRMPSAVGYPQTLSTEMGSLQERITSTKEGSITSIQAVYVPADDLTD PAPAT
TFAHLDATTVLSRGLAAKGIYPAVDPLDSTSTMLQP

>d1cbua_ c.37.1.11 (A:) Adenosylcobinamide kinase/adenosylcobinamide phosphate
guanylyltransferase CobU {Salmonella typhimurium}

MILVTGGARSGKSRHAEALIGDAPQVLYIATSQILDDMAARIQHKKDGRPAHWRTAECW
RHLDTLITADLAPDDAILLECITTMVTNLLFALGGENDPEQWDYAAMERAIDDEIQILIAAC
QRCPAKVVLVTNEVGMGIVPENRLARHFRDIAGRVNQR LAAADEVWLVSIGGVKIK

>d1g64b_ c.37.1.11 (B:) ATP:corrinoid adenosyltransferase CobA {Salmonella
typhimurium}

QQRQQKVKDRVDARVAQAQEERGIIIVFTGNGKGKTTAAFGTAARAVGHGKNVGVVQFI
KGTWPNGERNLLEPHGVEFQVMATGFTWETQNREADTAACMAVWQH GKRLADPLLD
MVVLDELTYMVAYDYLPLEEVISALNARPGHQTVIITGRGCHRDILD LADTVSELRPVKH
AFDAGVKAQMIDY

>d1b0ua_ c.37.1.12 (A:) ATP-binding subunit of the histidine permease {Salmonella typhimurium}

NKLHVIDLHKRYGGHEVLKGVSLQARAGDVISIIGSSSGSKSTFLRCINFLEKPSGAIIVN
GQNINLVRDKDGQLKVADKNQLRLLRTRLTVMVFQHFNLWSHMTVLENVMEAPIQVLGLS
KHDARERALKYLA KVGIDERAQGKYPVHLSGGQQQRVSIARALAMEPDVLLFDEPTSAL
DPELVGEVLRIMQQ LAEEGKTMVVVTHEMGMFARHVSSHVIFLHQGKIEEEGDPEQVFGNP
QSPRLQQFLKGS LKKLEH

>d1g6ha_ c.37.1.12 (A:) MJ1267 {Archaeon Methanococcus jannaschii}

TMEILRTENIVKYFGFEKALDGVSSISVNKGDVTLIIGPNGSGKSTLINVITGFLKADEGRVY
FENKDITNKEPAELYHYGIVRTFQTPQPLKEMTVLENLLIGEICPGESPLNSLFYKKWIPKEE
EMVEKAFFKILEFLKLSHLYDRKAGELSGGQMKLVEIGRALMTNPKMIVMDEPIAGVAPGL
AHDIFNHVLELKAKGITFLIIEHRLDIVLNYIDHLYVMFNGQIIAEGRGEEIKNVLSDPKV
VEIYIGE

>d1jj7a_ c.37.1.12 (A:) Peptide transporter Tap1, C-terminal ABC domain {Human (Homo sapiens)}

GLLTPLHLEGLVQFDVSFAYPNRPDVLVLQGLTFTLRPGEV TALVGPNGSGKSTVAALLQ
NLYQPTGGQLLLDGKPLPQYEHRYLHRQVA AVGQEPQVFGRSLQENIAYGLTQKPTMEEI
TAAAVKSGAHSFISGLPQGYDTEVDEAGSQLSGGQRQAVALARALIRKPCVLILDDATSAL
DANSQLQVEQLLYESPERYSRSVLLITQHLSLVEQADHILFLEGGAI REGGTHQQLMEKKG
CYWAMVQA

>d1g2912 c.37.1.12 (1:1-240) Maltose transport protein MalK, N-terminal domain
{Archaeon Thermococcus litoralis}

MAGVRLVDVWKVFG EVTAVREMSLEVKDGEFMILLGPSGCGKTTTLRMIAGLEEPSRGQI
YIGDKLVADPEKGIFVPPKDRDIAMV FQS YALYPHMTVYDNIAFPLKLRKVPRQEIDQVRV
EVAELLGLTELLNRKPRELSGGQRQRVALGRAIVRKPVFLMDEPLSNLDAKLVRMR AE
LKKLQRQLGVTTIYVTHDQVEAMTMGDRIAVMNRGV LQQV GSPDEVYDKPANTFVAGFI

>g1ii8.1 c.37.1.12 (A,B:) Rad50 {Archaeon Pyrococcus furiosus}

MKLERVTVKNFRSHSDTVVEFKEGINLIIGQNGSGKSSLLDAILVGLYWPLRIKDIKKDEFT
KVGARDTYIDLIFEKDGTKYRITRRFLKGYSSGEIHAMKRLVGNEWKHVTEPSSKAISAF
MEKLIPYNIFLNAIYIRQGQIDAILESDEAREKV VREVLNLDKFETAYKKLSELKKTINNR IK
EYRDILARTEXRERVKKEIKDLEKAKDFT EELIEKVKKYKALAREAAALSKIGELASEIFA EF

TEGKYSEVVVRAEENKVRLFVVWEGKERPLTFLSGGERIALGLAFRLAMSLYLAGEISLLI
LDEPTPYLDEERRRKLITIMERYLKKIPQVILVSHDEELKDAADHVIRISLENGSSKVEVVS

>d1e69a_ c.37.1.12 (A:) Smc head domain {Thermotoga maritima}

MRLKKLYLKGFKSFGRPSLIGFSDRVTAIVGPNGSGKSNIIDAIKWVFGESKKELRASEKF
DMIFAGSENLPAGSAYVELVFEENGEEITVARELKRTGENTYYLNGSPVRLKDIRDRFAGT
GLGVDFYSIVGQGQIDRIVNASPEELRLESSKHPTSLVPRGSYQRVNESFNRFISLLFFGGEG
RLNIVSEAKSILDAGFEISIRKPGRRDQKLSLLSGGEKALVGLALLFALMEIKPSPFYVLDE
VDSPLDDYNAERFKRLLENKSKHTQFIVITHNKIVMEAADLLHGVMTMVNGVSAIVPVEV

>d1qhla_ c.37.1.12 (A:) Cell division protein MukB {Escherichia coli}

RGKFRSLTLINWNGFFARTFDLDELVTTLSSGGNGAGKSTTMAAFVTALIPDLTLLHFRNTT
EAGATSGSRDKGLHGKLGKAGVCYSMLDTINSRHQRVVVGVRLLQQVAGRDRKVDIKPFAI
QGLPMSVQPTQLVTETLNERQARVLPLNELKDKLEAMEGVQFKQFNSITDYHSLMFDLGI
IARRLSASDRSKFYRLIEASLYGGISSAITRSLRDYLLPEN

>d1e3ma2 c.37.1.12 (A:567-800) DNA repair protein MutS, the C-terminal domain {Escherichia coli}

YTCPTFIDKPGIRITEGRHPVVEQVLNEPFIANPLNLSPQRRMLITGPNMGGKSTYMRQTA
LIALMAYIGSYVPAQKVEIGPIDRIFTRVGAADDLASGRSTFMVEMTETANILHNATEYSLV
LMDEIGRGTSTYDGLSLAWACAENLANKIKALTFLATHYFELTQLPEKMEGVANVHLDAL
EHGDTIAFMHSVQDGAASKSYGLAVAALAGVPKEVIKRARQKLRELEIS

>g1qhh.1 c.37.1.13 (A;B;C;D:) DEXX box DNA helicase {Bacillus stearothermophilus, PcrA}

MNFLSEQLLAHLNKEQQEAVRTTEGPLLIMAGAGSGKTRVLTHRIAYLMAEKHVAPWNIL
AITFTNKAAREMRERVQSLGGAEDVWISTFHSMCVRLRRDIDRIGINRNFISILDPTDQL
SVMKTILKEKNIDPKKFEPRTILGTISAANKNELLPEQFAKRXYEYKVVSDVYQEYQQRLL
RNHSLDFDDLIMTTIQLFDRVPDVLHYYQYKFQYIHIDEYQDTNRAQYTLVKKLAERFQNI
CAVGADADQSIYRWGADIQNILSFERDYPNAKVILLEQNYRSTKRILQAANEVIEHNVNRK
PKRIWTENPEGKPILYYEAMNEADEAQFVAGRIREAVERGERRYRDFAVLYRTNAQSRVM
EEMLLKANIPYQIVGGLKFYDRKEIKDILAYLRVIANPDDDLSSLRIINVPKRGIGASTIDXL
FEALGELEMIGLGAKAAGALAAFRSQLEQWTQLQEYVSVTELVEEVLDKSGYREMLKAE
RTIEAQSRLENLDEFLSVTKHFENVSDDKSLIAFLTDLALISXGDAVMLMTLHAAKGLEFP
VVFLIGMEEGIFPHNRSLEDDDEMEEERRLAYVGITRAEEELVLTS AQMRTLFGNIQMDPP
SRFLNEIPAHLLETASR

>d1uaaa2 c.37.1.13 (A:308-640) DEXX box DNA helicase {Escherichia coli, RepD}

YGAEKVLSSANNEEHEAERVGTGELIAHHFVNKTQYKDYAILYRGNHQSRVFEKFLMQNRI
PYKISGGTSFFSRPEIKDLLAYLRVLTPDDDS AFLRIVNTPKREIGPATLKKLGEWAMTRN
KSMFTASFDMGSLQTLSGRGYEALTRFTHWLAEIQRLAEREPIAAVRDLIHGMDYESWLY
ETSPSPKAAEMRMKNVNQLFSWMTEMLEGSELDEPMTLTQVVTRFTLRDMMERGESEE
ELDQVQLMTLHASKGLEFPYVYVMVGMEEGFLPHQSSIDEDNIDEERRLAYVGITRAQKEL
TFTLCKERRQYGELVRPEPSRFLLELPQDDLIW

>d1hv8a1 c.37.1.13 (A:3-210) Putative DEAD box RNA helicase {Archaeon Methanococcus jannaschii}

VEYMNFNELNLSNINLNAIRNKGFEKPTDIQMKVIPLFLNDEYNIVAQARTGSGKTASFAIP
LIELVNENNGIEAIIPTRELAIQVADEIESLKGNKNLKIAKIYGGKAIYPQIKALKNANIVV
GTPGRILDHINRGTLNLKNVKYFILDEADEMLNMGFIKDVEKILNACNKDKRILLFSATMP
REILNLAKKYMGDYSFIKAKI

>d1gm5a3 c.37.1.13 (A:286-549) RecG helicase domain {Thermotoga maritima}
ETLPERILEKRKLLGVKDAYYGMHFPKTFYHLEKARERLAYEELFVLQLAFQKIRKEREK
HGGIPKKIEGKLAEFEIKSLPFLKLTNAQKRAHQEIRNDMISEKPMNRLLQGDVSGSKTVVA
QLAILDNYEAGFQTAFMVPTSILAIQHYRRTVESFSKFNIHVALLIGATTPESEKIKSGLRN
GQIDVVIGTHALIQEDVHFKNLGLVIIDEQHRFGVKQREALMNKGKMGVDTLVMSATPIPRS
MALAFYGDLDVTVIDEMPP

>d1gm5a4 c.37.1.13 (A:550-755) RecG helicase domain {Thermotoga maritima}
GRKEVQTMLVPMDRVNEVYEFVRQEVMRGGQAFIVYPLIEESDKLVKSAVEMYEYLSK
EVFPEFKLGLMHGRLSQEEKDRVMLEFAEGRYDILVSTTVIEVGIDVPRANVMVIENPERF
GLAQLHQLRGRVGRGGQEAYCFLVVGDVGEEAMERLRFRTLNTDGFKIAEYDLKTRGPG
EFFGVKQHGLSGFKVADLYRDLKLEW

>d1fuka_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IKQFYVNVEEEYKYECCLTDLYDSISVTQAVIFCNTRRKVEELTTKLRNDKFTVSAIYSDLP
QQERDTIMKEFRSGSSRILISTDLLARGIDVQQVSLVINYDLPANKENYIHRIGRGGRFGRK
GVAINFVTNEDVGAMRELEKFYSTQIEELPSDIATLLN

>d1qdea_ c.37.1.13 (A:) Initiation factor 4a {Baker's yeast (Saccharomyces cerevisiae)}

IQTNYDKVVYKFDDMELDENLLRGVFGYGFEEPSAIQQRAIMPIEGHDVLAQAQSGTGK
TGTFISIAALQRIDTSVKAPQALMLAPTRELALQIQKVVMAAFHMDIKVHACIGGTSFVE
DAEGLRDAQIVVGTPGRVFDNIQRRRFRTDKIKMFILDEADEMLSSGFKEQIYQIFTLLPPT
TQVVLLSATMPNDVLEVTTKFMRNPVRILV

>d1d9xa1 c.37.1.13 (A:2-414) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}
EGRFQLVAPYEPQGDQPQAIKLVLDGLRRGVKHQTLLGATGTGKTFTISNVIAQVNKPTLV
IAHNKTLAQQLYSELKEFFPHNAVEYFVSYYDYYQPEAYVPQTDITYIEKDAKINDEIDKLR
HSATSALFERRDVIIVASVSCIYGLGSPEEYRELVVSLRVGMEIERNALLRRLVDIQYDRNDI
DFRGTFVRVGDVVEIFPASRDEHCIRVEFFGDEIERIRAEVDALTGKVLGEREHVAIFPASHF
VTREEKMRLAIQNIEQELEERLAELEAQAQGLLEAQRLEQRTRYDLEMMREMFGFCSGIENY
SRHLALRPPGSTPYTLLDYFPDDFLIIVDESHVTLPQLRGMYNDRARKQVLVDHGFRLPS
ALDNRPLTFEEFEQKINQIYVSATPGPYELEHSPGVVEQIIRP

>d1d9xa2 c.37.1.13 (A:415-595) Nucleotide excision repair enzyme UvrB {Bacillus caldotenax}
TGLLDPTIDVRPTKGQIDDLIGEIRERVERNERTLVTTLTKKMAEDLTDYLKEAGIKVAYLH
SEIKTLERIEIIRDLRLGKYDVLVGINLLREGLDIPEVSLVAILDADKEGFLRSERSLIQTIGRA
ARNANGHVIMYADTITKSMEIAIQETKRRRAIQEEYNRKHGIVPRTVKKEIRDV

>d1jr3a2 c.37.1.13 (A:3-242) gamma subunit of DNA polymerase III, N-domain {Escherichia coli}
YQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAKG
LNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRFKV
YLIDEVHMLSRHSFNALLKTLEEPPEHVKFLLATTDPPQKLPVTILSRCLQFHLKALDVEQIR
HQLEHILNEEHIAHEPRALQLLARAEEGSLRDALSLTDQAIASGDGQVSTQAVSAMLG

>d1a5t_2 c.37.1.13 (1-207) delta prime subunit of DNA polymerase III, N-domain {Escherichia coli}

MRWYPWLRPDFEKLVASQAGRGHHALLIQALPGMGDDALIYALSRYLLCQQPQGHKSC
GHCRCQMLMQAGTHPDYYTLAPEKGKNTLGVDAVREVTEKLNEHARLGGAQVWVTD
AALLTDAAANALLKTLEPPAETWFFLATREPERLLATLRSRCRLHYLAPPEQYAVTWLS

REVTMSQDALLAALRLSAGSPGAALALFQG

>d1jr3d2 c.37.1.13 (D:1-211) delta subunit of DNA polymerase III, N-domain {Escherichia coli}
MIRLYPEQLRAQLNEGLRAAYLLLGNPDLLLQESQDAVRQVAAAQGFEHHHTFSIDPNTD
WNAIFSLCQAMSLFASRQTLLLLLPENGPNAINEQLLTLTGLLHDDLLLVIRGNKLSKAQ
ENAAWFTALANRSVQVTCQTPEQAQLPRWVAARAKQLNLELDDAANQVLCYCYEGNLL
ALAQALERLSLLWPDGKLTLPVEQAVNDAAH

>d1iqpa2 c.37.1.13 (A:2-232) Replication factor C {Archaeon Pyrococcus furiosus}
SEEIREVKVLEKPWVEKYRPQRLLDDIVGQEHIVKRLKHVYKTGSMPHLLFAGPPGVGKTT
AALALARELFGENWRHNFLELNASDERGINVIREKVKEFARTKPIGGASFKIIFLDEADALT
QDAQQALRRTMEMFSSNVRFILSCNYSSKIIPIQSRCAIFRFRPLRDEDIKRLRYIAENEG
LELTEEGLQAILYIAEGDMRRRAINILQAAAALDKKITDENVMVAS

>d1hqca2 c.37.1.13 (A:5-242) Holliday junction helicase RuvB {Thermus thermophilus}
ALRPKTLDEYIGQERLKQKLRVYLEAAKARKEPLEHLLLFPGPLGKTTLAHVIAHELGV
NLRVTSGPAIEKPGDLAAILANSLEEGDILFIDEIHRLSRQAEHLYPAMEDFVMDIVIGQGP
AARTIRLELPRFTLIGATTRPGLITAPLLSRFGIVEHLEYTPEELAQGVMRDARLLGVRITE
EAALEIGRRSRGTMRVAKRLFRRVRDFAQVAGEEVITRERALEALAALGLDE

>d1fnna2 c.37.1.13 (A:1-276) CDC6, N-domain {Archaeon Pyrobaculum aerophilum}
AIVVDDSVFSPSYVPKRLPHREQQLQQLDILLGNWLRNPGHHYPRATLLGRP GTGKTVTL
RKLWELYKDKTARFVYINGFIYRNFTAIIGEIARSLNIPFRRGLSRDEFLALLVEHLRERD
LYMFLVLDDAFNLAPDILSTFIRLGQEADKLGA FRIALVIVGHND AVLNNLDPSTRGIMGK
YVIRFSPYTKDQIFDILLDRAGLAEGSYSEDILQMIADITGAQTPLDTNRGDARLAIDIL
YRSAYAAQQNGRKHIAPEDVRKSSKEVLFG

>d1d2na_ c.37.1.13 (A:) Hexamerization domain of N-ethylmaleimide-sensitive fusion (NSF) protein {Chinese hamster (Cricetulus griseus)}
EDYASYIMNGIIKWGDPVTRVLDDGELLVQQTKNSDRTPLVSVLLEGPPHSGKTALAAKIA
EESNFPFIKICSPDKMIGFSETAKCQAMKKIFDDAYKSQ LSCVVVDDIERLLDYVPIGPRFS
NLVLQALLVLLKKAPPQGRKLLIIGTTSRKDV LQEMEMLNAFSTTIHVPNIATGEQLLEAL
ELLGNFKDKERTTIAQQVKGKKVWIGIKLLMLIEMSLQMDPEYRVKFLALLREEGASPLD

>d1e32a2 c.37.1.13 (A:201-458) Membrane fusion atpase p97, D1 domain {Mouse (Mus musculus)}
VGYDDVGGCRKQLAQIKEMVELPLRHPALFKAIGVKPPRGILLYGPPGTGKT LIARAVANE
TGAFFFLINGPEIMSKLAGESSENLKAFEEAEKNAPAIIFIDELDAIAPKREKTHGEVERRI
VSQLLTLM DGLKQRAHVIVMAATNRPN SIDPALRRFGRFDREVDIGIPDATGRLEILQIHTK
NMKLADDVDLEQVANETHGHVGADLAALCSEAALQAIRKKMDLIDLEDETIDAEVMNS
LAVTMDDFRWALSQ

>d1g6oa_ c.37.1.13 (A:) Hexameric traffic ATPase, HP0525 {Helicobacter pylori}

LSAEDKKFLEVERALKEAALNPLRHATEELFGDFLK MENITEICYNGNKV VVWLKNNGE
WQPFVDVRDRKAFSLSRMLMHFARCCASF KKKTIDNYENPILSSNLANGERVQIVLSPVTVN
DETISISIRIPSKTTYPHSFEEQGFYNLLDNKEQAISAIKD GIAIGKNVIVCGGTGSGKTTYI
KSIMEFIPKEERIISIEDTEEIVFKHHKNYTQLFFGGNITSADCLKSCLMRPDR IILGELRSS
EAYDFYNVLC SGHGKGTLTTLHAGSSEAFIRLANMSSSNSAARNIKFESLIEGFKDLIDMIV
HINHHKQCDEFYIK

>d1ht1e_ c.37.1.13 (E:) HslU {Escherichia coli}

HSEMTPREIVSELDKHIIGQDNAKRSVAIALRNRWRRMQLNEELRHEVTPKNILMIGPTGV
GKTEIARRLAKLANAPFIKVEATKFTEVGYVGKEVDSIIRDLTDAAVKMVRVQAIEKNRYR
AEELAEERILDVLIPPAKNNWGQTEQQQEPSAARQAFRKKLREGQLDDKEIEIDLAAAPM
GVEIMAPPGMEEMTSQLQSMFQNLGGQKQKARKLKIKDAMKLLIEEEAAKLVNPEELKQ
DAIDAVEQHGIVFIDEIDKICKRGESSGPDVSREGVQRDLLPLVEGCTVSTKHGMVKT DHI
LFIASGAFQIAKPSDLIPELQGR LPIRVELQALTTSDFERILTEPNASITVQYKALMATEGVNI
EFTDSGIKRIAEEAAWQVNESTENIGARRLHTVLERLMEEISYDASDLSGQNITIDADYVSK
HLDALVADEDLSRFIL

>d1g8pa_ c.37.1.13 (A:) ATPase subunit of magnesium chelatase, BchI {Rhodobacter capsulatus}
RPVFPFSAIVGQEDMKLALLLTAVDPGIGGVLVFGDRGTGKSTAVRALAALLPEIEAVEGCP
VSSPNVEMIPDWATVLSTNVIRKPTPVVDLPLGVSEDRVVGALDIERAISKGEKAFEPGLL
ARANRGYLYIDECNLLDHIVDLLLDVAQSGENVVERDGLSIRHPARFVLVGSGNPEEGDL
RPQLLDRFGLSVEVLSPRDVETRVEVIRRRD TYDADPKAFLEEW RPKDMDIRNQILEARE
RLPKVEAPNTALYDCAALCIALGSDGLRGELTLRSARALAALEGATAVGRDHLKRVATM
ALSHRLRRDPLDEAGSTARVARTVEETLP

>d1a1va1 c.37.1.14 (A:190-325) HCV helicase domain {Human hepatitis C virus (HCV), different
isolates}
PPAVPQSFQVAHLHAPTSGSKSTKVPAAYAAQGYKVLVLNPSVAATLGFGAYMSKAHGVD
PNIRTGVRTITTGSPITYSTYGKFLADGGCSGGAYDIIICDECHSTDATSILGIGTVLDQAETA
GARLVVLATATP

>d1cu1a3 c.37.1.14 (A:326-631) HCV helicase domain {Human hepatitis C virus (HCV), different
isolates}
PGSVTVPHPNIEEVALSNTGEIPFYGKAIPIEAIRGGRHLIFCHSKKKCDELA AKLSGLGINA
VAYYRGLDVSVIPTIGDVVVVATDALMTGYTGDFDSVIDCNTCVTQTVDFSLDPTFTIETT
TVPQDAVSRSQRRGRTGRGRRGIYRFVTPGERPSGMFDSSVLCECYDAGCAWYELTPAET
SVRLRAYLNTPLPVCQDHLEFWESVFTGLTHIDAHFLSQTQAGDNFPYLVAYQATVCA
RAQAPPPSWDQMWKCLIRLKPTLHGPTPLLYRLGAVQNEVT LTHPITKYIMACMSADLEV
VT

>d1gkub1 c.37.1.16 (B:1-250) Helicase-like "domain" of reverse gyrase {Archaeon Archaeoglobus
fulgidus}
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAASLCLFPEDFLLKEFVEFFRKC VGEPR
AIQKMWAKRILRKESFAATAPTGVGKTSFGLAMSLFLALKGKRCYVIFPTSLLVIQAAETIR
KYAEKAGVGTENLIGYYHGRIPKREKENFMQNLRNFKIVITTTQFLSKHYRELGHFDFIFV
DDVDAILKASKNVDKLLHLLGFHYDLKTKSWVGEARGCLMVSTATAKKGKKAELFRQL
LNFDIGSSRIT

>d1gkub2 c.37.1.16 (B:251-498) Helicase-like "domain" of reverse gyrase {Archaeon
Archaeoglobus fulgidus}
VRNVEDVAVNDESISTLSSILEKLGTGGIYARTGEEAEEIYESLKNKFRIGIVTATKKGDYE
KFVEGEIDHLIGTAHYYGTLVRGLDLPERIRFAVFVGCPSFRVTIEDIDSLSPQMVKLLAYLY
RNVDEIERLLPAVERHIDEVREILKKVMGKERPQAKDVVVREGEVIFPDLRTYIQGSGRTS
RLFAGGLTKGASFLLEDSELSAFIERAKLYDIEFKSIDEVDFEKL SRELDES RDRYRRR

>d1dbia_ c.41.1.1 (A:) Thermostable serine protease {Bacillus sp., AK.1}
WTPNDTY YQGYQYGPQNTYTDYAWDVTKGSSGQEIAVIDTGVDYTHPDL DGKVIKGYD
FVDNDYDPMDLNNHGTHVAGIAAAETNNATGIAGMAPNTRILAVRALDRNGSGT LSDIA

DAIIYAADSGAEVINLSLGCDCHTTTTLENAVNYAWNKGSVVVAAGNNGSSTTFEPASYE
NVIAVGAVDQYDRLASFSNYGTWVDVVAPGVDIVSTITGNRYAYMSGTSMASPHVAGLA
ALLASQGRNNIEIRQAIEQTADKISGTGTYFKYGRINSYNAVTY

>d1ic6a_ c.41.1.1 (A:) Proteinase K {Fungus (*Tritirachium album*), strain limber}

AAQTNAPWGLARISSTSPGTSTYYYDESAGQGSCVYVIDTGIEASHPEFEGRAQMVKTTY
YSSRDGNGHGHGTHCAGTVGSRTYGVAKKTQLFGVKVLDDNGSGQYSTIAGMDFVASDKN
NRNCPKGVVASLSLGGGYSSSVNSAAARLQSSGVMVAVAAGNNNADARNYSPASEPSVC
TVGASDRYDRRSSFSNYGSVLDIFGPGTDILSTWIGGSTRSISGTSMATPHVAGLAAYLMTL
GKTTAASACRYIADTANKGDLSNIPFGTVNLLAYNNYQA

>d1nocb_ c.43.1.1 (B:) Chloramphenicol acetyltransferase {*Escherichia coli*}

ITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAFCLKTVKKNKHKFYPAFIHILAR
LMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETFSSLWSEYHDDFRQFLHIYSQDV
ACYGENLAYFPKGFNIENMFFVSANPWVSFTSFDLNVANMDNFFAPVFTMGKYTQGDKV
LMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQG

>d1eaf_ c.43.1.1 (-) Dihydrolipoamide acetyltransferase {*Azotobacter vinelandii*}

IPPIPPVDFAKYGEIEEVPMTRLMQIGATNLHRSWLNVPHTVQFESADITELEAFRVAQKAV
AKKAGVKLTVLPLLLKACAYLLKELPDFNSSLAPSGQALIRKKYVHIGFAVDTPDGLLPV
IRNVDQKSLQLAAEAAELAEKARSKKLADAMQACFTISSLGHHGGTAFTPIVNAPEVA
ILGVSKASMQPVWDGKAFQPRMLPLSLSYDHRVINGAAAARFTKRLGDLLADIRAILL

>d1e2o_ c.43.1.1 (-) Dihydrolipoamide succinyltransferase {*Escherichia coli*}

ARSEKRVPMTRLRKRVAERLLEAKNSTAMLTTFNEVNMKPIMDLRKQYGEAFEKRHGIRL
GFMSFYVKAVVEALKRYPEVNASIDGDDVVYHNYFDVSMVSTPRGLVTPVLRDVTDLG
MADIEKKIKELAVKGRDGKLTVEDLTGGNFTITNGGVFGSLMSTPIINPPQSAILGMHAIKD
RPMVAVNGQVEILPMMYLALSVDHRLIDGRESVGFLVTIKELLEDPTRLLLDV

>d1d1qa_ c.44.1.1 (A:) Tyrosine phosphatase {*Baker's yeast (Saccharomyces cerevisiae)*}

IEKPKISVAFIALGNFCRSPMAEAIKHEVEKANLENRFNKIDSFGTSNYHVGESPDHRTVSI
CKQHGVKINHKGKQIKTKHFDEYDYIIGMDESNNLKKIQPEGSKAKVCLFGDWNTND
GTVQTIIEDPWYGDIDQDFEYNFKQITYFSKQFLKKEL

>d1jl3a_ c.44.1.1 (A:) Arsenate reductase ArsC {*Bacillus subtilis*}

NKIIYFLCTGNSCR SQMAEGWAKQYLGDEWKVYSAGIEAHGLNPNAV KAMKEVGIDISN
QTSDIIDSDILNNADLVVTL CGDAADKCPMTPPHVKREHWGFDDPARAQGTEEEKWAFFQ
RVRDEIGNRLKEFAETGK

>d1vhra_ c.45.1.1 (A:) VH1-related dual-specificity phosphatase, VHR {*Human (Homo sapiens)*}

SVQDLNDLLSDGSGCYSLPSQPCNEVTPRIYVGNASVAQDIPKLQKLGITHVLNAAEGRSF
MHVNTNANFYKDSGITYLGKANDTQEFNLSAYFERAADFIDQALAQKNGRVLVHCREG
YSRSPTLVIAYLMMRQKMDVKSALSIVRQNREIGPNDGFLAQLCQLNDRLAKEGKLKP

>d1mkp_ c.45.1.1 (-) Mapk phosphatase Pyst1 (mkp3) {*Human (Homo sapiens)*}

ASFPVEILPFLYLGC AKDSTNLDVLEEFGIKYILNVTPNLPLNFENAGEFKYKQIPISDHS
QNLSQFFPEAISFIDEARGKNCGLVHSLAGISRSVTVTVAYLMQKLNL SMNDAYDIVKM
KKSNI SPN FNFMGQLLDFERTL

>d1d5ra2 c.45.1.1 (A:14-187) Phosphoinositide phosphatase Pten (Pten tumor suppressor), N-terminal domain {*Human (Homo sapiens)*}

RRYQEDGFDLDTYIYPNIIAMGFPAERLEGVYRNNIDDVVRFLDSKHKNHYKIYNLCAER
HYDTAKFNCRVAQYPFEDHNPPQLELIKPFCELDLQWLSEDDNHVAAIHCKAGKGRTGV
MICAYLLHRGKFLKAQEALDFYGEVTRDKKGVTIPSQRRYVYYYSYLLKNHLD
>d1i9sa_ c.45.1.1 (A:) mRNA capping enzyme, triphosphatase domain {Mouse (Mus musculus)}
KIPPRWLNCPRRGQPVAGRFLPLKTMGLGPRYDSQVAEENRFHPSMLSNYLKSLSKVMSLL
VDLTNTRSFYDRNDIEKEGIKYIKLQCKGHGECPTTENTETFIRLCERFNERSPPELIGVHCT
HGFNRTGFLICAFLEKMDWSIEAAVATFAQARPPGIYKGDYKELFRRYGDIEEAPPPVL
PDWCFEDED
>d1fpza_ c.45.1.1 (A:) Kinase associated phosphatase (kap) {Human (Homo sapiens)}
TPIHISWLSLSRVNCSQFLGLCALPGCKFKDVRRNVQKDTEELKSCGIQDIFVFCTRGEISK
YRVPNLLDLYQQCGIITHHHPIADGGTPDIASCCEIMEELTTCLKNYRKTLIHSYGGGLGRSC
LVAACLLLYLSDTISPEQAIDSLRDLRGSGAIQTIKQYNYLHEFRDKLAAHL
>d1leoa_ c.45.1.2 (A:) Tyrosine phosphatase {Human (Homo sapiens), 1B}
EMEKEFEQIDKSGSWAAIYQDIRHEASDFPCRVAKLPKNKNRNRVYRDVSPFDHSRIKLHQE
DNDYINASLIKMEEAQRSYILTQGPLPNTCGHFWEMVWEQKSRGVVMLNRVMEKGSLLK
CAQYWPQKEEKEMIFEDTNLKLTLISEDIKSYTTRQLELENLTTQETREILHFHYTTWPD
FGVPESPASFLNFLFKVRESGSLSPHGPVVVHSSAGIGRSGTFCLADTCLLLMDKRKDPSS
VDIKKVLEMRKFRMGLIQTADQLRFSYLAVIEGAKFIMGDSSVQDQWKELSHED
>d2shpa1 c.45.1.2 (A:219-525) Tyrosine phosphatase {Human (Homo sapiens), shp-2}
TRINAAEIESRVRELSKLAETTDKVKQGFWEFETLQQQECKLLYSRKEGQRQENKNKNR
YKNILPFDHTRVVLHDGDPNEPVSDYINANIIMPEFETKCNNSPKPKSYIATQGCLQNTVN
DFWRMVVFQENSRVIVMTTKEVERGKSKCVKYWPDEYALKEYGVMRVRNVKESAAHDY
TLRELKLSKVGGQNTERTVWQYHFRTWPDHGVPSDPGGVLDLFLEEVHHKQESIMDAGPV
VVHCSAGIGRTGTFIVIDILIDIIREKGVDCDIDVPKTIQMVRSSQRSGMVQTEAQYRSIYMA
VQHYIETL
>d1jlina_ c.45.1.2 (A:) Tyrosine phosphatase {Mouse (Mus musculus), ptp-sl/br7}
GSPREKVAMEYLQSASRVLRSQLRDVVASSHLLQSEFMEIPMNFVDPKEIDIPRHGTKNR
YKTILPNPLSRVCLRPKNITDSLSTYINANYIRGYSGKEKAFIATQGPMINTVNDFWQMWW
QEDSPVIVMITKLKEKNEKCVLYWPEKRGYIGKVEVLVTGVTECDNYTIRNLVLKQGSHT
QHVKHYYWYTSWPDHKTPDSAQPLLQLMLDVEEDRLASEGRGPVVVHCSAGIGRTGCFIA
TSIGCQQLKEEGVVDALSIVCQLRVDRGGMVQTSEQYEFVHHALCLFESRLSPETV
>d1lypta_ c.45.1.2 (A:) Tyrosine phosphatase {Yersinia enterocolitica}
PEARAELSSRLTTLRNLTAPATNDPRYLQACGGEKLNFRDIQCRRQTAVRADLNANYIQV
GNTRTIACQYPLQSQLESHFRMLAENRTPVLAVLASSSEIANQRFGMPDYFRQSGTYGSIT
VESKMTQQVGLGDGIMADMYTLTIREAGQKTISVPVVHVGNWPDQTAVSSEVTKALASL
VDQTAETKRNMYESKGSSAVADDSKLRPVIHCRAVGRTAQLIGAMCMNDSRNSQLSVE
DMVSQMRVQRNGIMVQKDEQLDVLIKLAEGQGRPLLNS
>d1g4us2 c.45.1.2 (S:297-539) SptP tyrosine phosphatase, catalytic domain {Salmonella
typhimurium}
PQTMSGPTLGLARFAVSSIPINQQTQVKLSDGMPVPVNTLTDFDGKPVALAGSYPKNTPDAL
EAHMKMLLEKECSCLVLTSEDQMQAQQLPPYFRGSYTFGEVHTNSQKVSSASQGEAID
QYNMQLSCGEKRYTIPVLHVKNWPDHQPLPSTDQLEYLADRVKNSNQNGAPGRSSSDKH
LPMIHCLGGVGRTGTMAAALVLKDNPHSNLEQVRADFRDSRNNRMLEDASQFVQLKAM
QAQLLM

>d1laral c.45.1.2 (A:1307-1623) RPTP Lar {Human (Homo sapiens)}

MITDLADNIERLKANDGLKFSQEYESIDPGQQFTWENSNLEVNKPKNRYANVIAYDHSRVI
 LTSIDGVPGSIDYINANYIDGYRKQNAIATQGGLPETMGDFWRMVWEQRTATVMMTRL
 EESRVKCDQYWPARGTETCGLIQVTLTDELATYTVRTFALHKSGSSEKRELRQFQFM
 AWPDHGVPEYPTPILAFLLRRVKACNPLDAGPMVVHCSAGVGRTGCFIVIDAMLERMKHE
 KTVDIYGHVTCMRSQRNYMVQTEDQYVFIHEALLEAATCGHTEVPARNLYAHIQKLGQV
 PPGESVTAMELEFKLLASS

>d1qb0a_ c.46.1.1 (A:) CDC25b {Human (Homo sapiens)}

DHRELIGDYSKAFLLQTVDGKHQDLKYISPETMVALLTGKFSNIVDKFVIVDCRYPYEEYEG
 GHIKTAVNPLERDAESFLLKSPIAPCSLDKRVILIFHCEFSSEGRPMCRFIRERDRAVNDY
 PSLYYPEMYILKGGYKEFFPQHNFCEPQDYRPMNHEAFKDELKTFRLKTRSWA

>d1hzma_ c.46.1.1 (A:) Erk2 binding domain of Mapk phosphatase mkp-3 {Human (Homo sapiens)}

MIDTLRPVPFASMAISKTVAWLNEQLELGNRLLLMDCRPQELYESSHIESAINVAIPGIM
 LRRLQKGNLPPVRLFTRGEDRDRFTRRCGTDTVVLYDESSSDWNENTGGESLLGLLKK
 LKDEGCRAFYLEGGFSKFQAEFSLHCETNLDGS

>d1rhs_1 c.46.1.2 (1-149) Rhodanese {Cow (Bos taurus)}

VHQVLYRALVSTKWLAESVRAGKVGPGRLVLDASWYSPGTREARKEYLERHVP GASFFD
 IEECRDKASPYEVMPLSEAGFADYVGSLSNDTHVVVYDGDDLGSFYAPRVWWMFRVF
 GHRTVSVLNGGFRNLKEGHPVTSEPSRPEP

>d1rhs_2 c.46.1.2 (150-293) Rhodanese {Cow (Bos taurus)}

AIFKATLNRSLKTYEQVLENLESKRFQLVDSRAQGRYLGTQPEPDAVGLDSGHIRGSVN
 MPFMNFLTEDGFEEKSPEELRAMFEAKKVDLTPLIATCRKGV TACHIALAAYLCGKPDVAI
 YDGSWFEFHRRAPPETWVSQGGK

>d1e0ca1 c.46.1.2 (A:1-135) Sulfurtransferase {Azotobacter vinelandii}

MDDFASLPLVIEPADLQARLSAPELIIVDLTSAARYAEGHIPGARFVDPKRTQLGQPPAPGL
 QPPREQLESFLGELGHRPEAVYVVYDDEGGGWAGRFIWLDDVIGQQRYHYLNGGLTAWL
 AEDRPLSREL PAPA

>d1e0ca2 c.46.1.2 (A:136-271) Sulfurtransferase {Azotobacter vinelandii}

GGPVALSLHDEPTASRDYLLGRLGAADLAIWDARSPQEYRGEKVLA AKGGHIPGAVNFE
 WTAAMDPSRALRIRTDIAGRLEELGITPDKEIVTHCQTHHRSGLTYLIAKALGYPRVKGYA
 GSWGEGWGNHPDTPVEL

>d2trxa_ c.47.1.1 (A:) Thioredoxin {Escherichia coli}

SDKIIHLTDDSFDTDV LKADGAILVDFWAEWCGPCKMIAPILDEIADEYQGKLTVAKL NID
 QNPGTAPKYGIRGIPTLLL FKNGEVAATKVGALSKGQLKEFLDANLA

>d1ep7a_ c.47.1.1 (A:) Thioredoxin {Chlamydomonas reinhardtii}

GGSVIVIDSKAAWDAQLAKGKEEHKPIVVDFTATWCGPCKMIAPLFETLSNDYAGKVIFL
 KVDVDAVA AAEAAAGITAMPTFHVYKDGVKADDLVGASQDKLKALVAKHAAA

>d1f9ma_ c.47.1.1 (A:) Thioredoxin {Spinach (Spinacia oleracea), thioredoxin F}

MEAIVGKVTEVNKDTFWPIVKAAGDKPVVLD MFTQWCGPCKAMAPKYEKLAE EYLDVI
 FLKLD CNQENKTLAKELGIRVVPTFKILKENS VVG EVTGAKYDKLLEAIQAARS

>d1laba_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Bacteriophage T4}

MFKVYGYDSNIHKCGPCDNAKRLLT VKKQPF EFIMPEKGVFDDEKIAELLTKLGRDTQI
 GLTMPQVFAPD GSHIGGFDQLREYFK

>d1qfna_ c.47.1.1 (A:) Glutaredoxin (Thioltransferase) {Escherichia coli}

MQTVIFGRSGCPYSVRAKDLAEKLSNERDDFQYQYVDIRAEGITKEDLQQKAGKPVETVP
QIFVDQQHIGGYTDFAAWVKENLDA

>d1kte_ c.47.1.1 (-) Glutaredoxin (Thioltransferase) {Pig (*Sus scrofa*)}

AQAFVNSKIQPGKVVFVFIKPTCPFCRKTQELLSQLPFKEGLLEFVDITATSDTNEIQDYLQQ
LTGARTVPRVFIGKECIGGCTDLESMHKRGELLTRLQQVGAVK

>d1h75a_ c.47.1.1 (A:) Glutaredoxin-like NRDH-redoxin {*Escherichia coli*}

MRITIYTRNDCVQCHATKRAMENRGFDFFEMINVDRVPEAAEALRAQGFRQLPVVIAGDLS
WSGFRPDMINRLHPAP

>d1fo5a_ c.47.1.1 (A:) MJ0307, thioredoxin/glutaredoxin-like protein {Archaeon *Methanococcus jannaschii*}

MSKVKIELFTSPMCPHCPAAKRVVEEVANEMPDAVEVEYINVMENPQKAMEYGIMAVPTI
VINGDVEFIGAPTKEALVEAIKKRL

>d1iloa_ c.47.1.1 (A:) MTH985, a thioredoxin {Archaeon *Methanobacterium thermoautotrophicum*}

MMKIQIYGTGCANCQMLEKNAREAVKELGIDAEFEKIKEMDQILEAGLTALPGLAVDGEL
KIMGRVASKEEIKKILS

>d1gh2a_ c.47.1.1 (A:) Thioredoxin-like protein, N-terminal domain {Human (*Homo sapiens*)}

VGVKPVGSDPDFQPELSGAGSRLAVVKFTMRGCGPCLRIAPAFSSMSNKYPQAVFLEVDV
HQCQGTAAATNNISATPTFQFFRNKVRIDQYQGADAVGLEEKIKQHLE

>d1bjx_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (*Homo sapiens*)}

AATTLPDGAAAESLVESSEVAVIGFFKDVESDSAKQFLQAAEAIDDIPFGITSNSDVFSKYQ
LDKDGVVLFKKFDEGRNNFEGETKENLLDFIKHNQLPLVIEFTEQTA

>d1mek_ c.47.1.2 (-) Protein disulfide isomerase, PDI {Human (*Homo sapiens*)}

DAPEEEDHVLVLRKSNFAEALAAHKYLLVEFYAPWCGHCKALAPEYAKAAGKLKAEGSE
IRLAKVDATEESDLAQYGVRGYPTIKFFRNGDTASPKYTAGREADDIVNWLKKRTGPA
A

>d1a8l_1 c.47.1.2 (1-119) Protein disulfide isomerase, PDI {Archaeon *Pyrococcus furiosus*}

MGLISDADKKVIKEEFFSKMVNPVKLIVFVRKDHQCQYCDQLKQLVQELSELTDKLSYEIV
DFDTPEGKELAKRYRIDRAPATTITQDGKDFGVRYFGLPAGHEFAAFLEDIVDVSREET

>d1a8l_2 c.47.1.2 (120-226) Protein disulfide isomerase, PDI {Archaeon *Pyrococcus furiosus*}

NLMDETKQAIRNIDQDVRILVFVTPTCPYCPLAVRMAHKFAIENTKAGKGKILGDMVEAIE
YPEWADQYNVMAVPKIVIQVNGEDRVEFEGAYPEKMFLEKLLSALS

>d1hyua3 c.47.1.2 (A:1-102) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {*Salmonella typhimurium*}

MLDTNMKTQLRAYLEKLTKPVELIATLDDSAKSAEIKELLAEIAELSDKVTFKEDNTLPVR
KPSFLITNPGSQQGPRFAGSPLGHEFTSLVLALLWTGGHPS

>d1hyua4 c.47.1.2 (A:103-198) Alkyl hydroperoxide reductase subunit F (AhpF), N-terminal domain {*Salmonella typhimurium*}

KEAQSLEQIRDIDGDFEFETYYSLSCHNCPDVVQALNLMAVLNPRIKHTAIDGGTFQNEI
TERNVMGVPVAVFVNGKEFGQGRMTLTEIVAKVDTG

>d1a8y_1 c.47.1.3 (3-126) Calsequestrin {Rabbit (*Oryctolagus cuniculus*)}

GLDFPEYDGVDRVINVNAKNYKNVFKKYEVALLYHEPPEDDKASQRQFEMEELILELA
AQVLEDKGVGFGLVDSEKDAAVAKKLGLTEEDSIYVFKEDEVIEYDGEFSADTLVEFLLD

VLEDP

>d1a8y_2 c.47.1.3 (127-228) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
VELIEGERELQAFENIEDEIKLIGYFKNKDSEHYKAFKEAAEEFHPYIPFFATFDSKVAKKLT
LKLNEIDFYEAFMEEPVTIPDKPNSEEEIVNFVEEHRRS

>d1a8y_3 c.47.1.3 (229-347) Calsequestrin {Rabbit (Oryctolagus cuniculus)}
TLRKLKPESMYETWEDDMDGIHIVAFEEADPDGYEFLEILKSVAQDNTDNPDLIIWIDP
DDFPLLVPYWEKTFDIDLSAPQIGVVNVTADSVWMEMDDEEDLPSAEELEDWLEDVL

>d1glqa2 c.47.1.5 (A:1-78) Glutathione S-transferase {Mouse (Mus musculus), class pi}
PPYTIVYFPVRGRCEAMRMLLADQGQSWKEEVVTIDTWMQGLLKPTCLYGQLPKFEDGD
LTLYQSNAILRHLGRSLGL

>d1gtua2 c.47.1.5 (A:1-84) Glutathione S-transferase {Human (Homo sapiens), class mu}
PMILGYWDIRGLAHAIRLLLEYTDSSYEKKYTMGDAPDYDRSQWLNEKFGLGLDFPNL
PYLIDGAHKITQSNAILCYIARKHN

>d1gsea2 c.47.1.5 (A:2-80) Glutathione S-transferase {Human (Homo sapiens), class alpha (a1-1)}
AEKPKLHYFNARGKMESTRWLLAAAGVEFEKKFIKSAEDLDKLRNDGYLMFQQVPMVEI
DGMKLVQTRAILNYIASKYN

>d1ljra2 c.47.1.5 (A:1-79) Glutathione S-transferase {Human (Homo sapiens), class theta}
MGLELFLDLVSQPSRAVYIFAKKNGIPELRTVDLVKGQHSKEFLQINSLGKLPTLKDGD
FILTESSAILIYLSCKYQ

>d1pd212 c.47.1.5 (1:1-75) Glutathione S-transferase {Rat (Rattus norvegicus), class sigma}
MPNYKLLYFNMGRGAEIIRYIFAYLDIKYEDHRIEQADWPKIKPTLPFGKIPVLEVEGLTLH
QSLAIARYLTKNT

>d2gsq_2 c.47.1.5 (1-75) Glutathione S-transferase {Squid (Ommastrephes sloani pacificus), class sigma}
PKYTLHYFPLMGRAELCRFVLAAGHEEFTDRVVEMADWPNLKATMYSNAMPVLDIDGT
KMSQSMCIARHLAREFG

>d1eema2 c.47.1.5 (A:5-102) Glutathione S-transferase {Human (Homo sapiens), class omega}
SARSLGKGSAPGPVPEGSIRIYSMRFCFAERTRLVLKAKGIRHEVININLKNKPEWFFKK
NPFGLVPVLENSQGQLIYESAITCEYLDEAYPGKKL

>d1fw1a2 c.47.1.5 (A:5-87) Glutathione S-transferase {Human (Homo sapiens), class zeta}
KPILYSYFRSSCSWRVRIALALKGIDYKTPINLIKDGGQQFSKDFQALNPMKQVPTLKIDG
ITIHQSLAIIYEETRPTPR

>d1gnwa2 c.47.1.5 (A:2-85) Glutathione S-transferase {Mouse-ear cress (Arabidopsis thaliana)}
GIKVFHGHPASIATRRVLIALHEKNLDFELVHVELKDGEHKKEPFLSRNPFGQVPAFEDGDL
KLFESRAITQYIAHRYENQGTNL

>d1a0fa2 c.47.1.5 (A:1-80) Glutathione S-transferase {Escherichia coli}
MKLFYKPGACSLASHITLRESGKDFTLVSVLDLMKKRLENGDDYFAVNPKGQVPALLDD
GTLLEGVAIMQYLADSVPR

>d1g7oa2 c.47.1.5 (A:1-75) Glutaredoxin 2 {Escherichia coli}
MKLYIYDHCPYCLKARMIFGLKNIPVELHVLLNDDAETPTRMVGQKQVPILQKDDSRYM
PESMDIVHYVDKLDGK

>d1k0dd2 c.47.1.5 (D:99-200) Yeast prion protein ure2p, nitrogen regulation fragment {Baker's yeast (Saccharomyces cerevisiae)}
YSRITKFFQEQLPGLGYTLFSHRSA PNGFKVAIVLSELGFHYNTIFLDFNLGEHRAPEFVSVN

PNARVPALIDHGMNLSIWESGAILLHLVNKYYKETGNPL

>d1k0ma2 c.47.1.5 (A:6-91) Chloride intracellular channel 1 (cltc1) {Human (Homo sapiens)}
PQVELFVKAGSDGAKIGNCPFSQRLFMVLWLKGVTFNVTTVDTKRRTETVQKLCPPGEL
PFLLYGTEVHTDTNKIEEFLEAVLCP

>d1gp1a_ c.47.1.10 (A:) Glutathione peroxidase {Cow (Bos taurus)}
RTVYAFSARPLAGGEPFNLSSLRGKVLLIENVASLXGTTVRDYTQMNDLQRRLLGPRGLVV
LGFPNCQFGHQENAKNEEILNCLKYVRPGGGFEPNFMLEKCEVNGEKAHPLFAFLREVL
PTPSDDATALMTDPKFITWSPVCRNDVSWNFELVGPDPGVVRRYSRRFLTIDIEPDIETL
LSQ

>d1i5ga_ c.47.1.10 (A:) Tryparedoxin II {Crithidia fasciculata}
SGLKKFFPYSTNVLKGAADIALPSLAGKTVFFYFSASWCPPSRAFTPQLIDFYKAHAEEKK
NFEVMLISWDESAEDFKDYAKMPWLALPFEDRKGMEFLTTFGFDVKSIPITLVGVEADSG
NIITTQARTMVVKDPEAKDFPWP

>d1qmva_ c.47.1.10 (A:) Thioredoxin peroxidase 2 (thioredoxin peroxidase B, 2-cys
peroxiredoxin) {Human (Homo sapiens)}
SGNARIGKPAPDFKATAVVDGAFKEVKLSYKGYVVLFFYPLDFTFVAPTEIIAFSNRAE
DFRKLGCSEVLGVSVDSQFTHLAWINTPRKEGGLGPLNIPLADVTRRLSEYGVLTDEGI
AYRGLFIIDGKGVLRQITVNDLPVGRSVDEALRLVQAFQYTDEHGEVCPAGWKPGSDTIK
PNVDDSKYFSKH

>d1hd2a_ c.47.1.10 (A:) Peroxiredoxin 5 {Human (Homo sapiens)}
APIKVGDAIPAVEVFEGEPGNKVNLAELFKGKKGVLFGVPGAFTPGCSKTHLPGFVEQAE
ALKAKGVQVVAACLSVNDAFVTGEWGRAHKAEGKVRLLADPTGAFGKETDLLLLDDSLVSI
FGNRRLKRFSMVVQDGIVKALNVEPDGTGLTCSLAPNIISQL

>d1prxa_ c.47.1.10 (A:) HorF6 peroxidase {Human (Homo sapiens)}
LLGADVAPNFEANTTVGRIRFHDFLGDSWGILFSHPRDFTPVCTTELGRAAKLAPEFAKRN
VKLIASIDSVEDHLAWSKDINAYNSEEPTEKLFPPIIDDRNRELAILLGMLDPAEKDEKGM
PVTARVVVFVFGPKKKLKSILYPATTGRNFDEILRVVISLQLTAEKRVATPVDWKDGDSVM
VLPTIPEEEAKKLFPGKVFTKELPSGKKYLRYPQP

>d1kyga_ c.47.1.10 (A:) Alkyl hydroperoxide reductase AhpC {Salmonella
typhimurium}
SLINTKIKPFKNQAFKNGEFIEVTEKDTEGRWSVFFFYPADFTFVCPTTELGDVADHYEELQ
KLGVDVYSVSTDTHFTHKAHSSSETIAKIKYAMIGDPTGALTRNFDNMREDEGLADRAT
FVVDPPQGIIQAIEVTAEGIGRDASDLLRKIKAAQYVAHPGEVCP

>d1jfua_ c.47.1.10 (A:) Membrane-anchored thioredoxin-like protein TlpA, soluble domain
{Bradyrhizobium japonicum}
TGDPACRAAVATAQKIAPLAHGEVAALTMASAPLKLPLDAFEDADGKPKKLSDFRGKTLL
VNLWATWCVPCRKEMPALDELQGLSGPNFEVVAINIDTRDPEKPKTFLKEANLTRLGYF
NDQKAKVFQDLKAIGRALGMPTSVLVDPPQGCEIATAGPAEWASEDALKLIRAATG

>d1foha3 c.47.1.10 (A:462-662) Phenol hydroxylase, C-terminal domain {Soil-living yeast
(Trichosporon cutaneum)}
NLVTDKKSSKQELAKNCVVGTRFKSQPVVRHSEGLWMHFGDRLVTDGRFRIIVFAGKAT
DATQMSRIKKFSAYLDSSENSVISLYTPKVSDRNSRIDVITIHSCHRDDIEMHDFPAPALHPK
WQYDFIYADCDSWHHPKSYQAWGVDETGAHVVRPDGYTSLVTDLEGTAIEDRYFS
GILVEPKEKSGAQTEADWTKS

>d1a49a3 c.49.1.1 (A:396-530) Pyruvate kinase, C-terminal domain {Rabbit (*Oryctolagus cuniculus*)}

ELARSSSHSTDLMEAMAMGSVEASYKCLAAALIVLTESGRSAHQVARYRPRAPIIAVTRN
HQTARQAHLYRGIFPVVCKDPVQEAWAEDVDLRVNLAMNVGKARGFFKKGDVVIVLTG
WRPGSGFTNTMRVVPVP

>d1pkla3 c.49.1.1 (A:358-498) Pyruvate kinase, C-terminal domain {*Leishmania mexicana*}

NEYVFFNSIKKLQHIPMSADEAVCSSAVNSVYETKAKAMVVLSNTGRSARLVAKYRPNCP
IVCVTTRLQTCRQLNITQGVESVFFDADKLGHDEGKEHRVAAGVEFAKSKGYVQTGDYC
VVIHADHKVKGYANQTRILLVE

>d1a3wa3 c.49.1.1 (A:367-500) Pyruvate kinase, C-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}

DMRNCTPKPTSTTETVAASAAVFEQKAKAIIVLSTSGTTPRLVSKYRPNCPHILVTRCPRA
ARFSHLRYGVFPFVFEKEPVSDDVEARINFGIEKAKEFGILKKGDTYVSIQGFKAGAG
HSNTLQVSTV

>d1e0ta3 c.49.1.1 (A:354-470) Pyruvate kinase, C-terminal domain {*Escherichia coli*}

ITEAVCRGAVETAEKLDAPLIVVATQGGKSARAVRKYFPDATILALTNEKTAHQVLVLSKG
VVPQLVKEITSTDDFYRLGKELALQSGLAHKGDVVVMVSGALVPSGTTNTASVHVL

>d1e79g_ c.49.2.1 (G:) ATP synthase (F1-ATPase), gamma subunit {Cow (*Bos taurus*)}

ATLKDITRRLKSIKNIQKITKSMKMVAAAKYARAERELKPARVYGVGSLALYEKADIKTPE
DKKKHLIIGVSSDRGLCGAIHSSVAKQMKSEANLAAAGKEVKIIGVGDKIRSILHRTHSD
QFLVTFKEVGRRPPTFGDASVIALELLNSGYEFDEGSIIFNFRSVISYKTEEKPIFSLDTISS
AESMSIYDDIDADVLRNYQEYSLANIIYSLKESTTSEQSARMTAMDNASKNASEMIDKLT
LTFNRTRQAVITKELIEIISGAAAL

>d1fs0g_ c.49.2.1 (G:) ATP synthase (F1-ATPase), gamma subunit {*Escherichia coli*}

KITKAMEMVAASKMRKSQDRMAASRPYAETMRKVIGHLAHGNLEYKHPYLEDRDVKRV
GYLVVSTDRGLCGGLNINLFKKLLAEMKTTWTDKGVQCDLAMIGSKGVSSFFNSVGGNVV
AQVTGMGDNPSLSELIGPVKVMLQAYDEGRLDKLYIVSNKFINTMSQVPTISQLLPLPASD
DDDLKHKSWDYLYEPDPKALLDTLLRRYVESQVYQGVVENLASEQAARMVAMK

>d1kmma1 c.51.1.1 (A:326-424) Histidyl-tRNA synthetase (HisRS), C-terminal domain {*Escherichia coli*}

DPVVDIYLVASGADTQSAAMALAERLRDELPGVKLMTNHGGGNFKKQFARADKWGARV
AVVLGESEVANGTAVVKDLRSGEQTAVAQDSVA AHLRTLLG

>d1qe0a1 c.51.1.1 (A:326-420) Histidyl-tRNA synthetase (HisRS), C-terminal domain {*Staphylococcus aureus*}

IEENLDLFIVTMGDQADRYAVKLLNHLRHNGIKADKDYLRKIKGQMKQADRLGAKFTI
VIGDQELENNKIDVKNMTTGESETIELDALVEYFKK

>d1h4vb1 c.51.1.1 (B:326-421) Histidyl-tRNA synthetase (HisRS), C-terminal domain {*Thermus thermophilus*}

EKGPDLYLIPLTEEAVAEAFYLAEALRPRLRAEYALAPRKPAKGLEEALKRGAAAFAGFLGE
DEL RAGEVTLKRLATGEQVRLSREEVPGYLLQALG

>d1atia1 c.51.1.1 (A:395-505) Glycyl-tRNA synthetase (GlyRS), C-terminal domain {*Thermus thermophilus*}

QLAPIKVAVIPLVKNRPEITEYAKRLKARLLALGLGRVLYEDTGNIGKAYRRHDEVGTPFAV
TVDYDTIGQSKDGTTRLKDTVTVRDRDTMEQIRLHVDELEGFLRERLRW

>d1qf6a1 c.51.1.1 (A:533-642) Threonyl-tRNA synthetase (ThrRS), C-terminal domain {Escherichia coli}

FPTWLAPVQVVIMNITDSQSEYVNELTQKLSNAGIRVKADLRNEKIGFKIREHTLRRVPYM
LVCGDKEVESGKVAVRTRRGKDLGSMDEVIEKLQQEIRSRLKQLEE

>d1hc7a1 c.51.1.1 (A:277-403) C-terminal domain of ProRS {Thermus thermophilus}

RGLVLPRLAPIQVVIVPIYKDESRERVLEAAQGLRQALLAQGLRVHLDLDRDQHTPGYKF
HEWELKGVFPFRVELGPKDLEGGQAVLASRLGGKETPLAALPEALPGKLDAFHEELYRRA
LAFREDH

>d1g5ha1 c.51.1.1 (A:343-469) The aaRS-like accessory subunit of mitochondrial polymerase gamma, C-terminal domain {Mouse (Mus musculus)}

RKVLKLHPCLAPIKVALDVGKGPTVELRQVCQGLLNELLENGISVWPGYSETVHSSLEQL
HSKYDEMSVLFVSVLTETTLLENGLIQLRSRDTTMKEMMHISKLRDFLVKYLASASNVAAL
LDHHHHH

>d1cfr_ c.52.1.7 (-) Restriction endonuclease Cfr10I {Citrobacter freundii}

MDIISKSGEGNKYTINSAIAFVAYASHIDINTTEFSKVLSGLRDFINDEAIRLGGKISDGSFNK
CNGDWYEWLIGIRAEFFLESETNFIVVKMPNATSFDVMSIYKSCLSEFIYDLRSKLSLNNV
NLITSNPDFSII DIRGRREELKSMLKDISFSNISLSTISEIDNLYKNFIDYAELEHIKSFLSVKTT
FRPDRRLQLAHEGSLMKALYTHLQTRTWTINPTGIRYYAAATSIGNADVIGLKT VATHSITD
VKSLPQSAVDEIFKINSVLDVDSCLSHIL

>d1knva_ c.52.1.7 (A:) Restriction endonuclease Bse634I {Bacillus stearothermophilus}

NLTNSNCVEEYKENGKTKIRIKPFNALIELYHHQTPTGSIKENLDKLENYVKDVVKAKGL
AIPTSGAFSNTRGTWFEVMIAIQSWNYRVKRELNDYLIKMPNVKTFDFRKIFDNETREKL
HQLEKSLTHKQQVRLITSNPDLLIRQKDLIKSEYNLPINKLTHENIDVALTLFKDIEGKCK
WDSL VAGVGLKTSLRPDRRLQLVHEGNILKSLFAHLKMRYWNPKAEFKYYGASSEPVSK
ADDDALQTAATHIVNVNSTPERAVDDIFSLTSFEDIDKMLDQIIKK

>d1gefa_ c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Pyrococcus furiosus}

MYRKGAQAERELIKLLEKHGFVVR SAGSKKVDLVAGNGKKYLCIEVKVTKKDHLVVGK
RDMGR LIEFSRRFGGIPVLAVKFLNVGWR FIEVSPKIEKFVFTPSSGVSLEVLLGIQKTLE

>d1hh1a_ c.52.1.18 (A:) Archaeal Holliday junction resolvase Hjc {Archaeon Sulfolobus solfataricus}

SAVERNIVSRLRDKGFAVVRAPASGSKRKDPIPDIIALKNGVIL IEMKSRKDIEGKIYVRRE
QAEGLIEFARKSGGSLFLGVKKPGVLKFIPFEKLRR TETGNYVADSEIEGLDLEDLVRLVEA
KISRTLD

>d1tfr_2 c.53.1.2 (12-180) T4 RNase H {Bacteriophage T4}

KEGICLIDFSQIALSTALVNFPDKEKINLSMVRHLILNSIKFNVKKA KTLGYTKIVLCIDNAK
SGYWRRDFAYYYKKNRGKAREESTWDWEGYFESSHKVIDELKAYMPYIVMDIDKYEAD
DHIAVLVKKFSLEGHKILIISSDGDFTQLHKYPNVKQWSPMHKKWVKI

>d1bgxt2 c.53.1.2 (T:1-173) 5' to 3' exonuclease domain of DNA polymerase {Thermus aquaticus}

MRGMLPLFEPKGRVLLVDGHHLAYRTFHALKGLTTSRGEPVQAVYGFAKSLLKALKEDG
DAVIVVFDKAPSFRHEAYGGYKAGRAPT PEDFPRQLALIKELVDLLGLARLEVPGYEAD
DVLASLAKKAEKEGYEVRLTADKDLYQLLSDRIHVLHPEGYLITPAWLWEKYG

>d1xo1a2 c.53.1.2 (A:19-185) T5 5'-exonuclease {Bacteriophage T5}

RRNLMIVDGTNLGFRFKHNNSKKPFASSYVSTIQSLAKSYSARTTIVLGDKGKSVFRLEHL
PEYAGNRDEKYAQRTEEEKALDEQFFEY LKDAFELCKTTFTFTIRGVEADDMAAYIVKLI

GHLYDHVWLISTDGDWDTLLTDKVSRSFTTRREYHLRDMYEHNN

>d1b43a2 c.53.1.2 (A:1-219) Fen-1 nuclease {Archaeon *Pyrococcus furiosus*}

GVPIGEIIIPRKEIELENLYGKKIAIDALNAIYQFLSTIRQKDGTPLMDSKGRITSHLSGLFYRT
INLMEAGIKPVYVFDGEPPEFKKKELEKRREAREEAEEKWREALEKGEIEEARKYAQRAT
RVNEMLIEDAKKLLLELMGPIVQAPSEGEAQAAAYMAAKGSVYASASQDYDSLFGAPRLV
RNLITITGKRKLPGKNVYVEIKPELIILEEVLKELK

>d1ekja_ c.53.2.1 (A:) beta-carbonic anhydrase {Pea (*Pisum sativum*)}

EASERIKTGFLHFKKEKYDKNPALYGELAKGQSPPFMVFACSDSRVCPSHVLDFQPGAEFV
VRNVANLVPPYDQAKYAGTGAAIEYAVLHLKVSNIIVIGHSACGGIKGLLSFPFDGTYSTD
FIEEWVKIGLPAKAKVKAQHGDAPFAELCTHCEKEAVNASLGNLLTYPFVREGLVNKTLA
LKGGYYDFVKGSFELWGLEFGLSSTFSV

>d1g5ca_ c.53.2.1 (A:) beta-carbonic anhydrase {Archaeon *Methanobacterium thermoautotrophicum*}

IIKDILRENQDFRFRDLSDLKHSPKLCIITCMD SRLIDLLERALGIGRGDAKVIKNAGNIVDD
GVIRSAAVAIYALGDNEIIIVGHTDCGMARLDEDLIVSRMRELGVEEEVIENFSIDVLNPVG
DEEENVIEGVKRLKSSPLIPESIGVHGLIIDINTGRLKPLYLDE

>d1ddza1 c.53.2.1 (A:84-325) beta-carbonic anhydrase {Red alga (*Porphyridium purpureum*)}

VMSDLEKKFIELEAKLVAQPAGQAMPGKSNIFANNEAWRQEMLKQDPEFFNRLANGQSPE
YLWIGCADSRVPANQLLDLPAGEVFVHRNIANQCIHSDISFLSVLQYAVQYLKVKHILVCG
HYGCGGAKAALGDSRLGLIDNWLRRHVRMNAKYLDKCKDGDDEELNRLIELNVLEQ
VHNVCATSIVQDAWDAGQELTVQGVVYGVGDGKLRLDLGVVNSSDDISKFYRTKSDSG
ALKAG

>d1hjoa1 c.55.1.1 (A:3-188) Heat shock protein 70kDa, ATPase fragment {Human (*Homo sapiens*)}

KAAAIGIDLGTTYSCVGVFQHGKVEIANDQGNRTTPSYVAFTDTERLIGDAAKNQVALNP
QNTVFDARLIGRKFQDPVVQSDMKHWPQVINDGDKPKVQVSYKGETKAFYPEEISSM
VLTMKKEIAEAYLGYPTNAVITVPAYFNDSQRQATKDAGVIAGLNVLRINEPTAAAAYG
LDRT

>d1dkgd2 c.55.1.1 (D:186-383) Heat shock protein 70kDa, ATPase fragment {*Escherichia coli*, gene dnaK}

GNRTIAVYDLGGGTFDISIIEIDEVDGEKTFEVLATNGDTHLGGEDFDSRLINYLVEEFKKD
QGIDLRNDPLAMQRLKEAAEKAKIELSSAQQTVDNLPYITADATGPKHMNIKVTRAKLES
LVEDLVNRSIELLKVALQDAGLSVSDIDDVILVGGQTRMPMVQKKVAEFFGKEPRKDVNP
DEAVAIGA AVQGGVLT

>d1d4xa2 c.55.1.1 (A:147-375) Actin {Nematode (*Caenorhabditis elegans*)}

RTTGVVLDSGDGVTHTVPIYEGYALPHAILRLDLAGRDLDYLMKILTERGYSFTTTAEREI
VRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITVGNERFRCPEAMFQPSFLGM
ESAGIHETSYNSIMKCDIDIRKDLYANTVLSGGTMMYPGIADRMQKEITALAPSTMKIKIAP
PERKYSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHRKCF

>d1jcfa1 c.55.1.1 (A:1-140) Prokaryotic actin homolog MreB {*Thermotoga maritima*}

MLRKDIGIDLGTANTLVFLRGKGIVVNESVIAIDSTTGEILKVGLEAKNMIGKTPATIKAIR
PMRDGVIADYTVLVMLRYFINKAKGGMNLFKPRVVIGVPIGITDVERRAILDAGLEAGA
SKVFLIEEPMAAAIGSN

>d1jcfa2 c.55.1.1 (A:141-336) Prokaryotic actin homolog MreB {*Thermotoga*

maritima}

LNVEEPSGNMVDIGGGTTEVAVISLGSIVTWESIRIAGDEMDEAIVQYVRETYRVAIGERT
AERVKIEIGNVFPSKENDELETTVSGIDLSTGLPRKLTCLKGGEVREALRSVVVAIVESVRTT
LEKTPPELVSDIIERGIFLTGGGSLLRGLDTLLQKETGISVIRSEEPLTAVAKGAGMVLDKVN
ILKKLQGAG

>d1k8ka1 c.55.1.1 (A:3-160) Actin-related protein 3, Arp3 {Cow (Bos taurus)}

GRLPACVVDCGTGYTKLGYAGNTEPQFIIPSCIAIKESAKVGDQAQRRVMKGVDDLDFFIG
DEAIEKPTYATKWPIRHGIVEDWDLMERFMEQVIFKYLRAEPEDHYFLLTEPPLNTPENRE
YTAEIMFESFNVPGLYIAVQAVLALAASWTSRQVGE

>d1k8ka2 c.55.1.1 (A:161-418) Actin-related protein 3, Arp3 {Cow (Bos taurus)}

RTLGTVIDSGDGVTHVIPVAEGYVIGSCIKHIPIAGRDITYFIQQLLRDREVGIPPEQSLETA
KAVKERYSYVCPDLVKEFNKYDTDGSKWIKQYTGINAISKKEFSIDVGYERFLGPEIFFHPE
FANPDFTQPISEVVDEVIQNCPIDVRRPLYKNIVLSGGSTMFRDFGRRLQRDLKRTVDARL
KLSEELSGGRLKPKPIDVQVITHHMQRVAVWFGGSMMLASTPEFYQVCHTKKDYEEIGPSIC
RHNPVFGVMS

>d1e4ft1 c.55.1.1 (T:7-199) Cell division protein FtsA {Thermotoga maritima}

TVFYTSIDIGSRYIKGLVLGKRDQEWELAFSSVKSRLDEGEIKDAIAFKESVNTLLKELE
EQLQKSLRSDVFISFSSVSFEREDTVIERDFGEEKRSITLDILSEMQSEALEKLKENGKTPLH
IFSKRYLLDDERIVFNPLDMKASKIAIEYTSIVVPLKVYEMFYNFLQDTVKSPFQLKSSLVS
TAEGVL

>d1e4ft2 c.55.1.1 (T:200-390) Cell division protein FtsA {Thermotoga maritima}

TTPEKDRGVVVVNLGYNFTGLIAYKNGVPIKISYVPVGMKHVIKDVSAVLDTSFEESERLII
THGNAVYNDLKEEEIQYRGLDGNTIKTTTAKKLSVIIHARLREIMSKSKKFFREVEAKIVEE
GEIGIPGGVVLTTGGGAKIPRINELATEVFKSPVRTGCIYANSRPSIINADEVANDPSFAAFAFG
NVFA

>d1g99a1 c.55.1.2 (A:1-156) Acetate kinase {Archaeon Methanosarcina thermophila}

MKVLVINAGSSSLKYQLIDMTNESALAVGLCERIGIDNSIITQKKFDGKKLEKLTDLPTHKD
ALEEVVKALTDDEFGVIKDMGEINAVGHRVVHGGEKFTTSALYDEGVEKAIKDCFELAPL
HNPPNMMGISACAEIMPGTPMVIVFDTAHFHTMP

>d1g99a2 c.55.1.2 (A:157-398) Acetate kinase {Archaeon Methanosarcina thermophila}

PYAYMYALPYDLYEKHGVRKYGFHGTSHKYVAERAALMLGKPAEETKIITCHLNGGSSIT
AVEGGKSVETSMGFTPLEGLAMGTRCGSIDPAIVPFLMEKEGLTTREIDTLMNKKSGVLG
VSGLSNDFRDLDEAASKGNRKAELALEIFAYKVKKFFIGEYSAVLNGADAVVFTAGIGENSA
SIRKRILTGLDGIGIKIDDEKNKIRGQEIDISTPDAKVRVFIPTNEELAIARETKEIVET

>d1ig8a1 c.55.1.3 (A:18-224) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}

DVPKELMQQIENFEKIFTVPTETLQAVTKHFISELEKGLSKKGGNIPMIPGWVMDFPTGKE
SGDFLAIDLGGTNLRVVLVKLGGDRTFDTTQSKYRLPDAMRTTQNPDELWEFIADSLKAFI
DEQFPQGISEPIPLGFTFSFPASQNKINEGILQRWTKGFDIPNIENHDVVPMLQKQITKRNIPI
EVVALINDTTGTLVASYYTDP

>d1ig8a2 c.55.1.3 (A:225-486) Hexokinase {Baker's yeast (Saccharomyces cerevisiae), pII}

ETKMGVIFGTGVNGAYYDVCSDIEKLQGKLSDDIPPSAPMAINCEYGSFDNEHVVLPRTK
YDITIDEESPRPGQQTFEKMSSGYLGEILRLALMDMYKQGFIFKNQDLSKFDKPFVMDT
SYPARIEEDPFENLEDTDDLQNEFGINTTVQERKLIRRLSELIGARAARLSVCGIAAICQKR

GYKTGHIAADGSVYNRYPGFKEKAANALKDIYGTQTSLDDYPIKIVPAEDGSGAGAAVI
AALAQKRIAEGKSVGIIGA

>d1czan2 c.55.1.3 (N:223-465) Mammalian type I hexokinase {Human (Homo sapiens)}
HCEVGLIIGTGTNACYMEELRHIDLVEGDEGRMCINTEWGAFGDDGSLEDIRTEFDRAIDA
YSLNPGKQLFEKMOVSGMYLGELVRLILVKMAKEGLLFEGRITPELLTRGKFNTSDVSAIEK
NKEGLHNAKEILTRLGVEPSDDDCVSVQHVTIVSFRSANLVAATLGAILNRLRDNKGTPR
LRTTVGVDGSLYKTHPQYSRRFHKTLRRLVPDSDVRFLLESSESGSGKGAAMVTAVAYRLAE

>d1bg3a1 c.55.1.3 (A:1-222) Mammalian type I hexokinase {Rat (Rattus norvegicus)}
MIAAQLLAYYFTELKDDQVKKIDKYLAMRLSDEILIDILTRFKKEMKNGLSRDYNPTASV
KMLPTFVRSIPDGSEKGDFFALDLGGSSFRILRVQVNHEKNQNVSMESSEIYDTPENIVHSGS
TQLFDHVADCLGDFMEKKKIKDKKLPVGFTFSFPCRQSKIDEAVLITWTKRFKASGVEGA
DVVKLLNKAIKKRGDYDANIVAVVNDTVGTMMTCGYDDQ

>d1bu6o1 c.55.1.4 (O:3-253) Glycerol kinase {Escherichia coli}
KKYIVALDQGTSSRAVMDHDANIISVSQREFEQIYPKPGWVEHDPMEIWAQSSSTLVEV
LTKADISSQIAAIGITNQRETTIVWEKETGKPIYNAIVWQCRRTAEICEHLKRDGLEDYIRS
NTGLVIDPYFSGTKVKWILDHVEGSRERARRGELLFGTVDTWLIWKMTQGRVHVTDYTN
ASRTMLFNIHTLDWDDKMLEVLDIPREMLPEVRRSSEVYGQTNIGGKGGTRIPISGIAGDQ
QAALFGQ

>d1bu6o2 c.55.1.4 (O:254-499) Glycerol kinase {Escherichia coli}
LCVKEGMAKNTYGTGCFMLMNTGEKAVKSENGLLTTIACGPTGEVNYALEGAVFMAGA
SIQWLRDEMKLINDAYDSEYFATKVQNTNGVYVPAFTGLGAPYWDPYARGAIFGLTRG
VNANHIIRATLESIAAYQTRDVLEAMQADSGIRLHALRVDGGAVANNFLMQFSQDILGTRVE
RPEVREVTALGAAYLAGLAVGFWQNLDELQEKAVIEREFPRGIETTERNYRYAGWKKAVK
RAMAWEEH

>d1chma1 c.55.2.1 (A:2-156) Creatinase {Pseudomonas putida}
QMPKTLRIRNGDKVRSTFSAQEYANRQARLRAHLAAENIDAAIFTSYHNINYYSDFLYCSF
GRPYALVVTEDDVISISANIDGGQPWRRTVGTDNIVYTDWQRDNYFAAIQQALPKARRIGI
EHDHLNLQNRDKLAARYPDAELVDVAAACMRMR

>d1az9_1 c.55.2.1 (1-176) Aminopeptidase P {Escherichia coli}
SEISRQEFQRRRQALVEQMMPGSAALIFAAPEVTRSADSEYPYRQNSDFWYFTGFNEPEAV
LVLIKSSDTHNHSVLFNRVRDLTAEIWFGRRLGQDAAPEKLGVDRALAFSEINQQLYQLL
NGLDVVYHAQGEYAYADVIVNSALEKLRKGSRQNLTPATMIDWRPVVHEMRLFK

>d1jl1a_ c.55.3.1 (A:) RNase H (RNase HI) {Escherichia coli}
KQVEIFTAGSALGNPMPGGYGAILRYRGREKTFSAGYTRTTNNRMELMAAIVALEALKEH
AEVILSTDSQYVRQGITQWIHNWKKRGWKTADKKPVKNVDLWQRLDAALGQHQIKWE
WVKGHAGHPENERADELARAAAMNPTLEDTGYQVE

>d1leka_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Methanococcus jannaschii}
MIIIGIDEAGRPVLGPMVVCFAFAIEKEREELKKLGVKDSKELTKNKRAYLKKLLENLGY
VEKRILEAEEINQLMNSINLNDIEINAFSKVAKNLIEKLNIRDDEIEIYIDACSTNTKKFEDSF
KDKIEDIIKERNLNIIAEHKADAKYPVVSAAIIAKAERDEIIDYKKIYGDIGSGYPSDP
KTIKFLEDYFKKHKKLPDIARTHWTCKRILDKSKQT

>d1i39a_ c.55.3.1 (A:) Class II ribonuclease H (RNase HII) {Archaeon Archaeoglobus fulgidus}
MKAGIDEAGKGCVIGPLVVAGVACSDERLRKLGVKDSKKLSQGRREELAEIIRKICRTE
VLKVSPENLDERMAAKTINEILKECYAEIILRLKPEIAYVDSPPVIPERLSRELEEITGLRVVA

EHKADEKYPLVAAASIIAKVEREREIERLKEKFGDFGSGYASDPRTREVLKEWIASGRIPSC
VRMRWKTVSNLRQK

>d1c9ra1 c.55.3.1 (A:430-558) HIV RNase H (Domain of reverse transcriptase)
{Human immunodeficiency virus type 1}

EKEPIVGAETFYVDGAANAATKLKGAGYVTNKGRQKVPLTNTTNQKTELQAIYLALQD
SGLEVNIVTDSQYALGIIQAQDPKSESELVNQIIEALIKKEAVYLAWVPAHAGIGGNAAVDA
LVSAGIAA

>d1c0ma2 c.55.3.2 (A:49-216) Retroviral integrase, catalytic domain {Rous sarcoma virus (RSV,
avian sarcoma virus)}

GVNPRGLGPLQIWQTDFTLEPRMAPRSWLAVTVDASSAIVVTQHGRVTSVAVQHHWATA
IAVLGRPKAIKTDNGSCFTSKSTREWLARWGIAHTTGIPGNSQGQAMVERANRLKDRIR
VLAEGDGMKRIPTSKQGELLAKAMYALNHKERGENTKTPIQKHWRP

>d1c6va_ c.55.3.2 (A:) Retroviral integrase, catalytic domain {Simian immunodeficiency virus}

NSDLGTWQMDCTHLEGKIVIVAVHVASGFIEAEVIPQETGRQTALFLLKLAGRWPITHLHT
DNGANFASQEVKMWAWWAGIEHTFGVPYNPQSQGVVEAMNHHLKNQIDRIREQANSVE
TIVLMAVHCMNHKRRGGIGDMTPAERLINMITTEQEIQFQ

>d1kfsa1 c.55.3.5 (A:324-518) Exonuclease domain of prokaryotic DNA polymerase {Escherichia
coli}

MISYDNYVTILDEETLKAWIAKLEKAPVFAFDTETDSLNDNISANLVGLSFAIEPGVAAYIPVA
HDYLDAPDQISRERALELLKPLLEDEKALKVGQNLKYDRGILANYGIELRGIAFDTMLES
YILNSVAGRHDMSLAERWLKHKTITFEEIAGKGKNQLTFNQIALEEAGRYAAEDADVT
LQLHLKMWPDLQK

>d1qta1 c.55.3.5 (A:293-422) Exonuclease domain of prokaryotic DNA polymerase {Thermus
aquaticus}

ALEEAPWPPPEGAFVGVLSRKEPMWADLLALAAARGGRVHRAPEPYKALRDLKEARGL
LAKDLSVLALREGLGLPPGDDPMLLAYLLDPSNTTPEGVARRYGGEWTEEAGERAALSER
LFANLWGRLEG

>d1xwl_1 c.55.3.5 (297-468) Exonuclease domain of prokaryotic DNA polymerase {Bacillus
stearothermophilus, newly identified strain as yet unnamed}

AKMAFTLADRVTEMLADKAALVVEVVEENYHDAPIVGIAVVNEHGRFFLRPETALADP
QFVAWLGDETKKKSMFDSKRAAVALKWKGIELCGVSFDLLAAYLLDPAQGVDDVAAA
AKMKQYEAVRPDEAVYGKGAKRAVPDEPVLAEHLVRKAAAIWELERPFLDELRRN

>d1t7pa1 c.55.3.5 (A:1-210) Exonuclease domain of T7 DNA polymerase {Bacteriophage T7}

MIVSDIEANALLESVTKFHCGVIYDYSTAIEYVSYPDSFGAYLDALEAEVARGGLIVFHNG
HKYDVPALTKLAKLQLNREFHLPRENCIDTLVLSRLIHSNLKDTDMGLLRSGKLPGALEA
WGYRLGEMKGEYKDDFKRMLEEQGEYVDGMEWWNFNEEMMDYNVQDVVVTKALL
EKLLSDKHYFPPEIDFTDVGYTTFWSES

>d1ih7a1 c.55.3.5 (A:1-375) Exonuclease domain of family B (archaeal and phage) DNA
polymerases {Bacteriophage RB69}

MKEFYLTVEQIGDSIFERYIDSNGRERTREVEYKPSLFAHCPESQATKYFDIYGKPCTRKLF
ANMRDASQWIKRMEDIGLEALGMDDFKLAYLSDTYNYEIKYDHTKIRVANFDIEVTSPDG
FPEPSQAKHPIDAITHYDSIDDRFYVFDLLNSPYGNVEEWSIEIAAKLQEQQGGDEVPSIID
KIIYMPFDNEKELLMEYLNFWQQKTPVILTGWNVESFDIPYVYNRIKNIFGESTAKRLSPH
RKTRVKVIENMYGSREITLFGISVLDYIDLYKKFSFTNQPSYSLDYISEFELNVGKLKYDGP

ISKLRESNHQRYISYNIIDVYRVLQIDAKRQFINLSLDMGYAYAKIQISVFSPIKTWDAIIFNS
LKE

>d1tgoa1 c.55.3.5 (A:1-347) Exonuclease domain of family B (archaeal and phage) DNA polymerases {Archaeon *Thermococcus gorgonarius*}

MILDTDYITEDGKPVIRIFKKENGFEFKIDYDRNFEPYIYALLKDDSAIEDVKKITAERHGGT
VRVVRAEKVKKKFLGRPIEVWKLYFTHPQDVPARDKIKEHPAVVDIYEYDIPFAKRYLIDK
GLIPMEGDEELKMLAFDIETLYHEGEEFAEGPILMISYADEEGARVITWKNIDLPHYVDVVST
EKEMIKRFLKVVEKDPDVLITYNGDNFDFAYLKKRSEKLGVKFILGREGSEPKIQRMGD
RFAVEVKGRIHFDLYPVIRRTINLPTYTLEAVYEAIFGQPKEKVYAEIEAQAWETGEGLERV
ARYSMEDAKVTYELGKEFFPMEAQLSRLVGQSLWDVSRS

>d1fxa_ c.55.3.5 (A:) Exonuclease I {*Escherichia coli*}

QSTFLFHDYETFGTHPALDRPAQFAAIRTDFSEFNVIGEPEVFYCKPADDYLPQPGAVLITGIT
PQEARAKGENEAFAARIHSLFTVPKTCILGYNNVRFDDEVTRNIFYRNFYDPYAWSWQH
DNSRWDLDDVMRACYALRPEGINWPENDDGLPSFRLEHLTKANGIEHSNAHDAMADV
ATIAMAHLVKTRQPRFLDYLFTHRNKHKLMALIDVPQMKPLVHVSGMFGAWRGNTSWV
APLAHPENRNAVIMVDLAGDISPILLESDTLRERLYTAKTDLGDNAAPVKLVHINKC
PVLAQANTLRPEDADRLGINRQHCLDNLILRENQVREKVVAIFAEAEFPTPSDNVDAQL
YNGFFSDADRAAMKIVLETEPRNLPALDITFVDKRIEKLLFNRYARNFPGLTDYAEQQRW
LEHRRQVFTPEFLQGYADELQMLVQQYADDKEKVALLKALWQYADEIVEH

>d1jj2m_ c.55.4.1 (M:) Ribosomal protein L18 (L18p) {Archaeon *Haloarcula marismortui*}

ATGPRYKVPMMMMREARTDYHQRLRLKSGKPRLVARKSNKHVRAQLVTLGPNGDDTLA
SAHSSDLAEYGWEAPTGNMPSAYLTGLLAGLRAQEAGVEEAVLDIGLNSPTPGSKVFAIQ
EGAIDAGLDIPHNDVLDWQRTRGAHIAEYDEQLEEPLYSGDFDAADLPEHFDELRETL
LDGDIEL

>d1fjgk_ c.55.4.1 (K:) Ribosomal protein S11 {*Thermus thermophilus*}

KRQVASGRAYIHASYNNTIVTITDPDGNPITWSSGGVIGYKGSRKGPYAAQLAALDAAK
KAMAYGMQSVDVIVRGTGAGREQAIRALQASGLQVKSIVDDTPVPHNGCRPKKKFRKAS

>d1ewqa3 c.55.6.1 (A:121-266) DNA repair protein MutS, domain II {*Thermus aquaticus*}

LLQESLLPREANYLAAIATGDGWGLAFLDVSTGEFKGTVLKSKSALYDELFRHRPAEVL
APELLENGAFLDEFKRFRPVMLEAPFEPEGEGLALRRARGALLAYAQRTQGGALSQP
RFYDPGAFMRLPEATLRALEVFEPL

>d1e3ma3 c.55.6.1 (A:117-269) DNA repair protein MutS, domain II {*Escherichia coli*}

GTISDEALLQERQDNLLAAIWQDSKGFYATLDISSGRFRLSEPADRETMAAELQRTNP
AE LLYAEDFAEMSLIEGRRGLRRRPLWEFEIDTARQQLNLQFGTRDLVGFGVENAPRGLCAA
GCLLQYAKDTQRTTLPHIRSITMEREQDSIIM

>d1sfe_2 c.55.7.1 (12-92) Ada DNA repair protein {*Escherichia coli*}

LAVRYALADCELGRCLVAESERGICAILLGDDDATLISELQQMFPAADNAPADLMFQQHVR
EVIASLNQRDTPLTLPLDIR

>d1qnta2 c.55.7.1 (A:6-91) O6-alkylguanine-DNA alkyltransferase {Human (*Homo sapiens*)}

EMKRTTLDSPGLKLELSGCEQGLHEIKLLGKGTSAADAVEVPAPAAVLGGPEPLMQCTAW
LNAYFHQPEAIEEFPVPALHHPVFQQ

>d1mgta2 c.55.7.1 (A:1-88) O6-alkylguanine-DNA alkyltransferase {Archaeon

Pyrococcus kodakaraensis}

MLSVEKFRVGERVVWIGVIFSGRVQGI AFADRGTLMKRIHDLAEHLGKRGVSISLDVQPS
DYPEKVFVKVLIGELDNASFLRELSFEG

>d1ulb_ c.56.2.1 (-) Purine nucleoside phosphorylase, PNP {Human (Homo sapiens)}

MENGYTYEDYKNTAEWLLSHTKHPQVAIICGSGLGGLTDKLTQAQIFDYSEIPNFPSTV
PGHAGRLVFGFLNGRACVMMQGRFHMIEGYPLWKVTFPVRVFHLLGVDTLVVTNAAG
GLNPKFEVGDIMLIRDHINLPGFSGQNPLRGPNDRFGDRFPAMSDAYDRTMRQRALSTW
KQMGEQRELQEGTYVMVAGPSFETVAECRVLQKLGADAVGMSTVPEVIVARHCGLRVFG
FSLITNKVIMDYESLEKANHEEVLAAGKQAAQKLEQFVSILMASIPLPKAS

>d1k9sa_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Escherichia coli}

ATPHINAEMGDFADVLM PGDPLRAKYIAETFLEDAREVNNVRGMLGFTGT YKGRKISV
MGHGMGIPSCSIYTKELITDFGVKKIIRVGSCGAVLPHVKLRD VVIGMGACTDSKVNRI
KDHDFAAIADFD MVRNAVDAAKALGIDARVGNLFSADLFYSPDGEMFDVMEKYGILGVE
MEAAGIYGVAAEFGAKALTICTVSDHIRTHTTAAERQTTFNDMIKIALESVLLGDK

>d1qe5a_ c.56.2.1 (A:) Purine nucleoside phosphorylase, PNP {Cellulomonas sp.}

PPLDDPATDPFLVARAAADHIAQATGVEGHDMALVLGSGWGGAELLGEVVAEVP THEIP
GFSSVTRSIRVERADG SVRHALVLGSRTHLYEGKGVRAVVHGVRTAAATGAETLILTNGCG
GLNQEWGAGTPVLLSDHINTARSPLEGPTFVDLTDVYSPRLRELAHRVDPTLPEGVYAQF
PGPHYETPAEVRMAGILGADLVGMSTTLEAIAARHCGLEVLGVSLVTNLAAGISPTPLSHA
EVIEAGQAAGPRISALLADIAKR

>d1k3fa_ c.56.2.1 (A:) Uridine phosphorylase {Escherichia coli}

MSKSDVFHGLTKNDLQ GATLAIVPGDPDRVEKIAALMDKPVKLASHREFTTWRAELDG
KPVIVCSTGIGGPSTSI AVEELAQLGIRTFRLIGTTGAIQPHINVGDVLVT TASVRLDGASLH
FAPLEFFAVADFECTTALVEAAKSIGATTHVGTASSDTFYPGQERYDTYSGRVVRHFKGS
MEEWQAMGVMNYEMESATLLTMCASQGLRAGMVAGVIVNRTQQEIPNAETMKQTESH
AVKIVVEAARRLL

>d1cb0a_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Human (Homo sapiens)}

AVKIGIIGGTGLDDPEILEGRTEKYVDTPFGKPSDALILGKIKNVDCVLLARHGRQHTIMPS
KVNYQANIWALKEEGCTHVIVTTACGSLREEIQPGDIVIIDQFIDRTTMRPQSFYDGS HSCA
RGVCHIPMAEPFCPKTREVLIETAKKLGLRCHSKGTMVTIEGPRFSSRAESFMFRTWGADV
INMTTVPEVVLAKEAGICYASIAMATDYDCWKEHEEAVSVDRV LKTLKENANKAKSLLLT
TIPQIGSTEWSETLHNLKNMAQFSVLLP

>d1je0a_ c.56.2.1 (A:) 5'-deoxy-5'-methylthioadenosine phosphorylase {Archaeon Sulfolobus solfataricus}

PVHILAKKGEVAERVLVVGDPGRARLLSTLLQNPKLTNENRGFLVYT GKYNGETVSIATH
GIGGPSIAIVLEELAMLGANVFIRYGTGALVPYINLGEYIIVTGASYNQGG LFYQYLRDNA
CVASTPDFELTNKLVT SFSKRNLKYYYVGNVFSSDAFYAEDEEFVKKWSSRGNI AVEMECA
TLFTLSKVKGWKSATVLVSDNLAKGGIWITKEELEKSVMDGAKAVLDTLTS

>d1a2za_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {Archaeon Thermococcus litoralis}

MKKVLITGFEPFGGDSKNPTEQIAKYFDRKQIGNAMVYGRVLPVSVKRATIELKRYLEEIK
PEIVINLGLAPTYSNITVERIAVNIIDARIPDNDGYQPIDEKIEEDAPLAYMATLPVRAITKTL
RDNGIPATISYSAGTYLCNYVMFKTLHFSKIEGYPLKAGFIHVPYTPDQVVNKFFLLGKNT
PSMCLEAEIKAIELAVKVS LDYLEKDRDDIKIPL

>d1auga_ c.56.4.1 (A:) Pyrrolidone carboxyl peptidase (pyroglutamate aminopeptidase) {*Bacillus amyloliquefaciens*}

MEKKVLLTGFDPFGETVNPSWEAVKRLNGAAEGPASIVSEQVPTVFYKSLAVLREAIKK
HQPDIIICVGQAGGRMQITPERVAINLNEARIPDNEGNQPVGEDISQGGPAAYWTGLPIKRI
VEEIKKEGIPAAVSYTAGTFVCNHLFYGLMDEISRHHPHIRGGFIHIPYIPEQTLQKSAPSL
LDHITKALKIAAVTAAVHEDDIETG

>d1pca_1 c.56.5.1 (1-308) Carboxypeptidase A {Pig (*Sus scrofa*)}

ARTTSTFNATYHTLEEIYDFMDILVAEHPALVSKLQIGRSYEGRPYVLKFSTGGSNRPAIW
IDSGIHSREWITQASGVWFAKKITENYGQNSSFTAILDSMDIFLEIVTNPNGFAFTHSDNRL
WRKTRSKASGSLCVGSDSNRNWDAGFGGAGASSSPCAETYHGKYPNSEVEVKSITDFVK
NNGNIKAFISIHYSQLLLYPYGYKTQSPADKSELNQIAKSAVAALKSLYGTSYKYGSIIITVI
YQASGGVIDWTYNQGIKYSFSFELRDTGRRGFLLPASQIIPTAQETWLALLTIMEHTLNN

>d1h8la2 c.56.5.1 (A:4-304) Carboxypeptidase D, catalytic domain {Crested duck (*Lophonetta specularioides*)}

QAVQPVDFRHHHFSMEIFLRRYANEYPSITRLYSVGKSVELRELYVMEISDNPGIHEAGEP
EFKYIGNMHGNEVVGRELLLNLEIYLCKNFGTDPEVTDLVQSTRIHIMPSMNPDGYESQ
EGDRGGTVGRNNSNNYDLNRNFPDQFFQVTDPPQPETLAVMSWLKTYPFVLSANLHGG
LVVNYPFDDDEQGAIIYSKSPDDAVFQQLALSYSKENKKMYQGSPCKDLPTTEYFPHGITN
GAQWYNVPGGMQDWNYLNTNCFEVTIELGCVKYPKAEELPKYWEQNRRLQFIKQVH
R

>d1amp_ c.56.5.4 (-) Aminopeptidase {*Aeromonas proteolytica*}

MPPITQQATVTAWLPQVDASQITGTISSLESFTNRFYTTTSGAQASDWIASEWQALSASLP
NASVKQVSHSGYNQKSVVMTITGSEAPDEWIVIGGHLSTIGSHTNEQSVAPGADDDASG
IAAVTEVIRVLSENNFQPKRSIAFMAYAAEEVGLRGSQDLANQYKSEGKNVVSALQLDMT
NYKGSAQDVVFITDYTDSNFTQYLTQLMDEYLPSTYGFDTGCGYACSDHASWHNAGYPA
AMPFESKFNDYNPRIHTTQDTLANSPTGSHAKKFTQLGLAYAIEMGSATG

>d1qq9a_ c.56.5.4 (A:) Aminopeptidase {*Streptomyces griseus*}

APDIPLANVKAHLTQLSTIAANNNGGNRAHGRPGYKASVDYVKAKLDAAGYTTTLQQFTS
GGATGYNLIANWPGDPNKVLMAGAHLDVSSGAGINDNGSGSAAVLETALAVSRAGYQ
PDKHLRFWWGAEELGLIGSKFYVNNLPSADRSKLAGYLNFDMIGSPNPGYFVYDDDPVI
EKTFKNYFAGLNVPTETEGDGRSDHAPFKNVGVVPGGLFTGAGYTKSAAQAQKWGGT
AGQAFDRCYHSSCDLSNINDTALDRNSDAAAHAIWTLSS

>d1cg2a1 c.56.5.4 (A:26-213,A:327-414) Carboxypeptidase G2, catalytic domain {*Pseudomonas* sp., strain rs-16}

QKRDNVLFQAATDEQPAVIKTLEKLVNIETGTGDAEGIAAAGNFLEAELKNLGFTVTRSKS
AGLVVGDNIVGKIKGRGGKNLLLSHMDTVYLKILAKAPFRVEGDKAYGPGIADDDKGG
NAVILHTLKLKEYGVRDYGTITVLFNTDEEKSGFSRDLIQEEAKLADYVLSFEPTSAGD
EKLSLGTXFNAGEGGKKLVDAVAYYKEAGGTGLGVEERTGGGTDAAYAALSGKPVIESL
GLPGFGYHSDKAEYVDISAIPRRLYMAARLIMDLGAG

>d1di6a_ c.57.1.1 (A:) MogA {*Escherichia coli*}

ATLRIGLVSISDRASSGVYQDKGIPALEEWLTSALTTPFELETRLIPDEQAIIETLCELVDEM
SCHLVLTGGTGPARRDVTPDATLAVADREMPGFGEQMRQISLHFVPTAILS RQVGVIRKQ
ALILNLPQGPKSIKETLEGVKDAEGNVVHVGIFASVPYCIQLLEGPYVETAPEVVAEFRPKS
ARR

>d1jlja_ c.57.1.1 (A:) Gephyrin N-terminal domain {Human (Homo sapiens)}
HQIRVGVLTVSDSCFRNLAEDRSGINLKDLVQDPSLLGGTISAYKIVPDEIEEIKETLIDWCD
EKELNLILTGGTGAFPRDVTPEATKEVIEREAPGMALAMLMGSLNVTPLGMLSRPVCGR
GKTLIINLPGSKKGSQECFQFILPALPHAIDLLRDAIVKVKEVHD

>d1bgva2 c.58.1.1 (A:1-194) Glutamate dehydrogenase {Clostridium symbiosum}
SKYVDRVIAEVEKKYADEPEFVQTVEEVLSSLGPVVDAHPEYEEVALLERMVIPERVIEFR
VPWEDDNGKVHVNTGYRVQFNGAIGPYKGGRLRFAPSVNLSIMKFLGFQAFKDSLTTLP
MGGAKGGSDFDPNGKSDREVMRFCQAFMTELYRHIGPDIDVPAGDLGVGAREIGYMYG
QYRKIVGGFYNGVLTG

>d1gtma2 c.58.1.1 (A:3-180) Glutamate dehydrogenase {Archaeon Pyrococcus furiosus}
ADPYEIVIKQLERAAQYMEISEEALFLKRPQRIVEVTIPVEMDDGSVKVFTGFRVQHNWA
RGPTKGGIRWHPEETLSTVKALAAWMTWKTAVMDLPYGGGKGGIIVDPKKLSDREKERL
ARGYIRAIYDVISPYEDIPAPDVYTNPQIMAWMMDEYETISRRTPAFGIITGKPLSI

>d1hwx2 c.58.1.1 (A:1-208) Glutamate dehydrogenase {Cow (Bos taurus)}
ADREDDPNFFKMVEGFFDRGASIVEDKLVEDLKTRQTQEQRNRVRGILRIKPCNHVLSL
SFPIRRDDGSWEVIEGYRAQHSHQRTPCGGIRYSTDVSVDVKALASLMTYKCAVVDVP
FGGAKAGVKINPKNYTDEDLEKITRRFTMELAKKGFIPGVDVPAPNMSTGEREMSWIAD
TYASTIGHYDINAHACVTGKPISQGGI

>d1leha2 c.58.1.1 (A:1-134) Leucine dehydrogenase {Bacillus sphaericus}
MEIFKMEKYDYEQLVFCQDEASGLKAVIAIHDTTLGPALGGARMWTYNAAAAIEDAL
RLARGMTYKNAAAGLNLGGGKTVIIGDPFADKNEDMFALGRFIQGLNGRYITAEDVGT
TVDDMDLIHQETDYVT

>d1clda2 c.58.1.1 (A:1-148) Phenylalanine dehydrogenase {Rhodococcus sp., M4}
SIDSALNWDGEMTVTRFDAMTGAHFVIRLDSTQLGPAAGGTRAAQYSNLADALTDAGKL
AGAMTLKMAVSNLPMGGGKSVIALPAPRHSIDPSTWARILRIHAENIDKLSGNYWTGPDV
NTNSADMDTLNDTTEFVFGRSLERGGAGS

>d1a4ia2 c.58.1.2 (A:2-126) Tetrahydrofolate
dehydrogenase/cyclohydrolase {Human (Homo sapiens)}
APAEILNGKEISAQIRARLKNQVTQLKEQVPGFTPRLAILQVGNRDDSPLYINVKLKAAEEI
GIKATHIKLPRTTTESEVMKYITSLNEDSTVHGFLVQLPLDSENSINTEEVINAIAPKDVVDG

>d1edza2 c.58.1.2 (A:3-148) Tetrahydrofolate
dehydrogenase/cyclohydrolase {Baker's yeast (Saccharomyces cerevisiae)}
KPGRTILASKVAETFNTEIINNVEEYKKTHNGQGPLLVGFLANNDPAAKMYATWTQKTSSES
MGFRYDLRVIEDKDFLEEAIIQANGDDSVNGIMVYFPVFGNAQDQYLQVVCKEKDVEG
LNHVYYQONLYHNVRYLDKENRLKSIL

>d2uaga2 c.59.1.1 (A:298-437) UDP-N-
acetylmuramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}
GLPHRFEEVLEHNGVRWINDSKATNVGSTEAAALNGLHVDGTLHLLGGDGKSADFSPLA
RYLNGDNVRLYCFGRDGAQLAALRPEVAEQTETMEQAMRLLAPRVQPGDMVLLSPACAS
LDQFKNFEQRGNEFARLAKELG

>d1e8ca2 c.59.1.1 (A:338-497) UDP-N-acetylmuramyl tripeptide synthetase MurE
{Escherichia coli}
VCGRMEVFTAPGKPTVVVDYAHTPDALQALQAARLHCAGKLWCVFSGCGGDRDKGKR
PLMGAIAEEFADVAVVTDDNPRTEEPRAIINDILAGMLDAGHAKVMEGRAEAVTCAVMQ

AKENDVVLVAGKGHEDYQIVGNQRLDYS DRVTVARLLGVIARSH

>d1gg4a1 c.59.1.1 (A:313-447) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

VPGR LFP IQLAENQLLLDDSYNANVGSM TAAVQVLAEMP GYRVLVVG DMAELGA ESEAC
HVQVGEAAKAAGIDRVLSVGKQSHAISTASGVGEHFADKTALITRLKLLIAEQQVITILVK
GSRSAAMEEVVRALQ

>d1fzta_ c.60.1.1 (A:) Phosphoglycerate mutase {Yeast (Schizosaccharomyces pombe)}

MTTEAAPNLLVLTRHGESEWNKLNLTGWKDPALSETGIKEAKLGGERLKS RGYKFDIAF
TSALQRAQKTCQIILEEVGEPNLETIKSEKLNERYYGDLQGLNKDDARKK WGAEQVQIW
RRSYDIAPPNGESLKD TAERVLPYYKSTIVPHILKGEKVLIAAHGNSLRALIMDLEGLTGDQ
IVKRELATGVPIVYHLDKDGKYVSKELIDN

>d1e58a_ c.60.1.1 (A:) Phosphoglycerate mutase {Escherichia coli}

AVTKLVLRHGESQWNKENRFTGWYDVDLSEKGVSEAKAAGKLLKEEGYSFDFAYTSVL
KRAIHTLWNVLDEL DQAWLPVEKSWKLN ERHYGALQGLNKAETA EKYGDEQVKQWRR
GFAVTPPELT KDDERYPGHDP RYAKLSEKELPLTESALTIDRVIPYWN ETILPRMKSGERVI
IAAHGNSLRALVKYLDNMSEEEILELN IPTGVPLVYEFDENFKPLKRY YLGNAD EIAAKAA
AVANQ GK

>d1ebba_ c.60.1.1 (A:) Broad specificity phosphatase YhfR {Bacillus stearothermophilus}

ATTLYLTRHGETKWNVERRMQGWQDSPLTEKGRQDAMRLGKRLEAVELAAIYTSTSGRA
LETAEIVRGGRLPIYQDERLREIHLGDWEGKTHDEIRQMDPIAFDHFQAPHLYAPQRGE
RFCDVQQRAL EAVQSIVDRHEGETVLIVTHGVVLKTLMAAFKDTPLDHLWSPPYMYGTS
VTIIEVDGGTFHVAVEGDVSHIE

>d1ihp_ c.60.1.3 (-) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus ficuum}

SCDTV DQGYQCFSETSHLWGQYAPFFSLANESVISPEVPAGCRVTFAQVLSRHGARYPTDS
KGKKYSALIEEIQQNATTFDGKYAFLKTYNYS LGADDLTPFGEQELVNSGIKFYQRYESLT
RNIVPFIRSSGSSRVIASGKKFIEGFQSTKLKD PRAQPGQSSPKIDV VISEASSNNTLDPGTC
TVFEDSELADTVEANFTATFVPSIRQRL ENDL SGVTLTDTEVTYLMDMCSFDTISTSTVDT
KLSPFCDLFTHDEWINYDYLQSLKKYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDDT
SSNHTLDSSPATFPLNSTLYADFSHDNGIISILFALGLYNGTKPLSTTTVENITQTDGFSSAWT
VPFASRLYVEMMQCQAEQEPLVRVLVND RVVPLHGCPVDALGRCTRDSFVRGLSFARSG
GDWAECFA

>d1qfxa_ c.60.1.3 (A:) Phytase (myo-inositol-hexakisphosphate-3-phosphohydrolase) {Aspergillus niger}

KQFSQEFRDGYSILKH YGGNGPYSERVSYGIARDPPTSCEVDQVIMVKRHGERYPSPSAG
KDIEEALAKVYSINTTEYKGD LAFLNDW TYYPNECYNAETTSGPYAGLLDAYNHGND
YKARYGHLWNGETVVPFFSSGYGRVIETARKFGEFFGYNYSTNAALNIISESEVMGADS
LTPTCDTDNDQTTCDNLTYQLPQFKVAAARLNSQNPGMNLTASDVYNLMVMASFELNAR
PFSNWINAFTQDEWVSFGYVEDLNYYYCAGPGDKNMAAVGAVYANASLTLLNQGPKEA
GSLFFNFAHDTNITPIL AALGVLIPNEDLPLDRVAFGNPY SIGNIVPMGGH LTIERLSCQATA
LSDEGTYVRLVLNEAVLPFNDCTSGPGYSCPLANYTSILNKNLPDYTTTCNV SASYPQYLS
FWWNYNTTTELNYRSSPIACQEGDAMD

>d1dkla_ c.60.1.3 (A:) Phytase (myo-inositol-

hexakisphosphate-3-phosphohydrolase) {Escherichia coli}
 SEPELKLESVVIVSRHGVRAPTKATQLMQDVTPDAWPTWPVKLGWLTPRGGELIAYLGH
 YQRQRLVADGLLAKKGCPQSGQVAIIADVDERTRKTGEAFAAGLAPDCAITVHTQADTSS
 PDPLFNPLKTGVCQLDNANVTDAILS RAGGSIA DFTGHRQTAFRELERVLNFPQSNLCLKR
 EKQDESCSLTQALPSELKVSADNVSLTGAVSLASMLTEIFLLQQAQGMPEPGWGRITDSHQ
 WNTLLSLHNAQFYLLQRTPEVARSRATPLLDLIK TALT PPHPQKQAYGVTLP TSVLFIAGHD
 TNLANLGGALELNWTLPGQPDNTPPGGELVFERWRRLSDNSQWIQVSLVFQTLQQMRDK
 TPLSLNTPPGEVKLTLAGCEERNAQGMCSLAGFTQIVNEARIPACSL
 >d1nula_ c.61.1.1 (A:) Xantine-guanine PRTase (XPRTase) {Escherichia coli}
 EKYIVTWDMLQIHARKLASRLMPSEQWKGIIVSRGGLVPGALLARELGIRHVDTVCISSY
 DHDNQRELKVLKRAEGDGEGFIVIDDLVDTGGTAVAI REMYPKAHFVTIFAKPAGRPLVDD
 YVVDIPQDTWIEQPWDMGVVFPVPPISGR
 >d1fsga_ c.61.1.1 (A:) Hypoxantine-guanine-xanthine PRTase {Toxoplasma gondii}
 GSHMASKPIEDYGKGKGRIEPMYIPDNFTFYNADDFLVPPHCKPYIDKILLPGGLVKDRVEK
 LAYDIHRTYFGEELHIICILKSGRGFFNLLIDYLATIQKYSGRESSVPPFFEHYVRLKSYQND
 NSTGQLTVLSDDL SIFRDKHVLIVEDIVDTGFTLTEFGERLKAVGPKSMRIATLVEKRTDRS
 NSLKGFVGF SIEDVWIVGCCYDFNEMFRDFDHVAVLSDAARKKFEK
 >d1ecfa1 c.61.1.1 (A:250-492) Glutamine PRPP amidotransferase, C-terminal domain
 {Escherichia coli}
 NPCLFEYVYFARPDSFIDKISVYSARVNMGT KLGEKIAREWEDLDIDVVIPIPETSCDIALEI
 ARILGKPYRQGFVKNRYVGRTFIMPGQQLRRKSVRRKLNANRAEFRDKNVLLVDD SIVR
 GTTSEQUIEMAREAGAKKVYLASAAPEIRFPNVYGIDMPSATELIAHGREVDEIRQIIGADG
 LIFQDLNDLIDAVRAENPDIQQFECSVFNGVYVTKDVDQGYLDFLDTLRNDDAKAVQRQ
 >d1dqna_ c.61.1.1 (A:) Guanine PRTase {Giardia lamblia}
 MICSVTGKPKVDVLSTFFKDRNDVLESEVKKFHLLATFEECKALAADTARRMNEYKDV
 AEPVTLVALLTGAYLYASLLTVHLTFPYTLHFVKVSSYKGRQESVVFDEEDLKQLKEKRE
 VVLIDEYVDSGHTIFS IQEQIKHAKICSCFVKDVDAIKKHSALADTKMFYGYTPMPKGSW
 LIGFGLDDNGLRRGWAHLFDINLSESEVTEFRRLTEHIKGLNINGVNRY
 >d1tcla_ c.61.1.1 (A:) Hypoxanthine PRTase {Trypanosoma cruzi}
 YEFAEKILFTEEEIRTRIKEVAKRIADDYKKGKGLRPYVNPLVLISVLKGSFMFTADLCRALC
 DFNVPVRMEFICVSSYGEGLTSSGQVRMLLDTRHSIEGHHVLIVEDIVDTALTNLNLYHMY
 FTRRPASLKT VVLLDKREGRRVPFSADYVVANIPNAFVIGYGLDYDDTYREL RDIVVLRPE
 >d1qb7a_ c.61.1.1 (A:) Adenine PRTase {Leishmania donovani}
 PFKEVSPNSFLDDSHALSQLLKKS YRWYSPVFS PRNVPRFADVSSITESPETLKAIRDFLV
 QRYRAMSPAPTHILGFDARGFLFGPMIAVELEIPFVLMRKADKNAGLLIRSEPYEKEYKEA
 APEVMTIRYGSIGKGSRVVLIDDLATGGTALSGLQLVEASDAVVVEMVSILSIPFLKAAEK
 IHSTANSRYKDIKFISLLSDDALTEENCGDSKNYTGPRVLSCGDVLAEPH
 >d1g2qa_ c.61.1.1 (A:) Adenine PRTase {Baker's yeast (Saccharomyces cerevisiae)}
 MPIASYAQELKLALHQYPNFPSEGILFEDFLPIFRNPGLFQKLIDAFKLHLEEA FPEVKIDYI
 VGLESRGFLFGPTLALALGVGFVPVRKAGKLPGECKATYEKEYGSDLFEIQKNAIPAGSN
 VIIVDDIIATGGSAAAAGELVEQLEANLLEYNFMELDFLKGRSKLNAPVFTLL
 >d1loroa_ c.61.1.1 (A:) Orotate PRTase {Escherichia coli}
 MKPYQRQFIEFALSQVLKFGFETLKSGRKSPYFFNAGLFNTGRDLALLGRFYAEALVDS
 GIEFDLLFGPAYKGIPIATTTAVALAEHHDLDLPYCFNRKEAKDHGEGGNLVGSALQGRVM

LVDDVITAGTAIRESMEIIQANGATLAGVLISLDRQERGRGEISAIQEVERDYNCKVISIITLK
DLIAYLEEKPEMAEHLAAVKAYREEFGV

>d1a3c__ c.61.1.1 (-) Uracil PRTase {Bacillus subtilis}

QKAVILDEQAIRRALTRIAHEMIERNKGMNNCILVGIKTRGIYLAKRLAERIEQIEGNPVTV
GEIDITLYRDDLSKKTSNDEPLVKGADIPVDITDQKVILVDDVLYTGRTVRAGMDALVDVG
RPSSIQLAVLVDRGHRELPIRADYIGKNIPTSKSEKVMVQLDEVQNDLVAIYEN

>d1bd3a_ c.61.1.1 (A:) Uracil PRTase {Toxoplasma gondii}

QEEILQDIITRFPNVVLMKQTAQLRAMMTIIRDKETPKKEEFVIFYADRLIRLLIEEALNELPF
QKKEVTTPLDVSYHGVSFYSKICGVSIVRAGESMESGLRAVCRGVRIGKILIQRDETTAEP
KLIYEKLPADIRERWVMLLDPMCATAGSVCKAIEVLLRLGVKEERIIFVNILAAPQGIERVF
KEYPKVRMVTAAVDICLNSRYIYVPGIGDFGDRYFGTM

>d1dkra1 c.61.1.2 (A:8-166) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}

NLKIFSLNSNPELAKEIADIVGVQLGKCSVTRFSDGEVQINIEESIRGCDCYIIQSTSDPVNE
HIMELLIMVDALKRASAKTINIVIPYYGYARQDRKARSREPITAKLFANLLETAGATRVIAL
DLHAPQIQGFFDIPIDHLMGVPILGEYFEGKNLE

>d1dkra2 c.61.1.2 (A:167-316) Phosphoribosylpyrophosphate synthetase {Bacillus subtilis}

DIVIVSPDHGGVTRARKLADRLKAPIAIDKRRPRPNVAEVMNIVGNIEGKTAILIDDIIDTA
GTITLAANALVENGAKEVYACCTHPVLSGPAVERINNSTIKELVVTNSIKLPEEKKIERFKQ
LSVGPLLAEAHVRVHEQQSVSYLFS

>d1lfaa_ c.62.1.1 (A:) Integrin CD11a/CD18 (Leukocyte function associated antigen-1,
LFA-1) {Human (Homo sapiens)}

GNVDLVFLFDGSMQLPDEFQKILDFMKDVMKKLSNTSYQFAAVQFSTSYKTEFDFSDYV
KRKDPDALLKHVKHMLLLTNTFGAINYVATEVFREELGARPDATKVLIIITDGEATDSGNI
DAAKDIIRYIIGIGKHFQTKESQETLHKFASKPASEFVKILDTFEKLKDLFTTELQKKIYVIE

>d1atza_ c.62.1.1 (A:) von Willebrand factor A3 domain {Human (Homo sapiens)}

QPLDVILLLDGSSSFASYFDEMKSFAKAFISKANIGPRLTQVSVLQYGSITTIDVPWNVVP
EKAHLLSLVDVMQREGGPSQIGDALGFAVRYLTSEMHHGARGASKAVVILVTDVSVDSVD
AAADAARSNRVTVFPIGIGDRYDAAQLRILAGPAGDSNVVKLQRIEDLPTMVTLGNSFLH
KL

>d1fnsa_ c.62.1.1 (A:) von Willebrand factor A1 domain {Human (Homo sapiens)}

MYCSRLLDLVFLLDGSSRLSEAEFEVLKAFVVDMMERLRVSQKWVRVAVVEYHDGSHAY
IGLKDRKRPSSELRRIASQVKYAGSQVASTSEVLKYTLFQIFSKIDRPEASRIALLLMASQEPQ
RMSRNFVRYVQGLKKKKVIVIPVGIGPHANLKQIRLIEKQAPENKAFVLSSVDELEQQRDE
IVSYLCDLAPEAP

>d1ido__ c.62.1.1 (-) Integrin CR3 (CD11b/CD18, Mac-1), alpha subunit {Human (Homo sapiens)}

DSDIAFLIDGSGSIIPHDFRRMKEFVSTVMEQLKKSCTLFSLMQYSEEFRIHFTFKEFQNNP
NPRSLVKPITQLLGRTHATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDV
IPEADREGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREK

>d1aoxa_ c.62.1.1 (A:) Integrin alpha2-beta1 {Human (Homo sapiens)}

SCPSLIDVVVVCDESNSIYPWDAVKNFLEKFVQGLDIGPTKTQVGLIQYANNPRVVFNLNT
YKTKEEMIVATSQTSQYGGDLTNTFGAIQYARKYAYSAASGGRRSATKVMVVVTDGESH
DGSMLKAVIDQCNHDNLRFGIAVLGYLNRNALDTKNLIKEIKAIASIPTERYFFNVSDEAA
LLEKAGTLGEQIFSIEGGT

>d1jv2b2 c.62.1.1 (B:107-354) Integrin beta A domain {Human (Homo sapiens)}

VEDYPVDIYYLMDLSYSMKDDLWSIQNLGTLKATQMRKLTSNLRIGFGAFVDKPVSPYM
YISPPEALENPCYDMKTTCLPMFGYKHVLTLDQVTRFNEEVKKQSVSRNRDAPEGGFDA
IMQATVCDEKIGWRNDASHLLVFTTDAKTHIALDGRLAGIVQPNDBGQCHVGSDNHYSAS
TTMDYPSLGLMTEKLSQKNINLIFAVTENVVNLQNYSELIPGTTVGVLSDSSNVLQLIV
DAYGKIRSK

>d1poia_ c.63.1.1 (A:) Glutaconate-CoA transferase alpha {Acidaminococcus fermentans}

SKVMTLKDIAIAKYVHSGDHIALGGFTTDRKPYAAVFEILRQGITDLTGLGGAAGGDWDM
LIGNGRVKAYINCYTANSVGTNVSRFRKWFEAGKLTMEDYSQDVIYMMWHAAALGLP
FLPVTLMQGSGLTDEWGISKEVRKTLDKVPDDKFKYIDNPFPKGEKVAVVPVQVDVAIH
AQQASPDGTVRIWGGKFQDVDIAEAAKYTIVTCEEIISDEEIRRDPTKNDIPGMCVDAVVL
APYGAHPSQCYGLYDYDNPFLKVYDKVSKTQEDFDAFCKEWVFDLKDHDDEYLNKLGAT
RLINLKVVPGGLGYHIDMTKE

>d1poib_ c.63.1.1 (B:) Glutaconate-CoA transferase beta {Acidaminococcus fermentans}

DYTNNTNKEMQAVTIAKQIKNGQVVTVTGTLPLIGASVAKRVYAPDCHIIVESGLMDCSP
VEVPRSVGDLRFMAHCGCIWPNVRFVGFENEYLHKANRLIAFIGGAQIDPYGNVNSTSIG
DYHHPKTRFTGSGGANIATYSNTIIMMQHEKRRFMNKIDYVTSPGWIDGPGGRERLGLP
GDVGPQLVVTDKGILKFDEKTKRMYLAAYYPTSSPEDVLENTGFDLDVSKAVELEAPDPA
VIKLIREIDPGQAFIQVP

>d1jka_ c.65.1.1 (A:) Glycinamide ribonucleotide transformylase, GART {Escherichia coli}

MNIVVLISGNGSNLQAIIDACKTNKIKGTVRVAVFSNKADAFGLERARQAGIATHTLIASAF
DSREAYDRELIHEIDMYAPDVVVLGAFMRILSPAFVSHYAGRLLNIHPSLLPKYPGLHTHR
QALENGDEEHGTSVHFVTDELDDGGPVILQAKVPVFAGDSEDDITARVQTQEHAIFYPLVISW
FADGRLKMHENAAWLDGQRLPPQGYA

>d1fnta2 c.65.1.1 (A:1-206) Methionyl-tRNA^{met} formyltransferase {Escherichia coli}

SESLRIIFAGTPDFAARHLDALLSSGHNVVGVFTQPDPAAGRGKKLMPSPVKVLAEEKGLP
VFQPVSLRPQENQQLVAELQADVMVVVAYGLILPKAVLEMPRLGCINVHGSLLPRWRGAA
PIQRSLWAGDAETGVTIMQMDVGLDTGDMLYKLSCPITAEDTSGTLYDKLAELGPQGLITT
LKQLADGTAKPEVQDETLVTYAEK

>d1fp1d2 c.66.1.12 (D:129-372) Chalcone O-methyltransferase {Alfalfa (Medicago sativa)}

RGYLASFSTFLCYPALLQVWMNFKEAVVDEIDLFKNVHGVTKYEFMGKDKKMNQIFN
KSMVDVCATEMKRMLEIYTGFEGLSTLVDVGGGSGRNLELIISKYPLIKGINFDLPQVIENA
PPLSGIEHVGGDMFASVPQGDAMILKAVCHNWSDEKCFEFLSNCHKALSPNGKVIIIEFILP
EEPNTSEESKLVSTLDNLMFITVGGRETEREKQYEKLSKLSGFSKFQVACRAFNSLGVMIFY
K

>d1fp2a2 c.66.1.12 (A:109-352) Isoflavone O-methyltransferase {Alfalfa (Medicago sativa)}

LCLAPMVECVLDPTLSGSYHELKKWIYEEDTLFGVTLGSGFWDFLDKNPEYNTSFNDA
MASDSKLINLALRDCDFVFDGLESIVDVGGGTGTTAKIICETFPKLCIVFDRPQVVENLSG
SNNLTYVGGDMFTSIPNADAVLLKYILHNWTDKDCRLKKCKEAVTNDGKRKGVTHIDM
VIDKKKDENQVTQIKLLMDVNMALCLNGKERNEEEWKCLFIEAGFQHYKISPLTGFLSLIEI
YP

>d1dl5a1 c.66.1.7 (A:1-213) Protein-L-isoaspartyl O-methyltransferase

{*Thermotoga maritima*}

MREKLFWILKKYGVSDHIAKAFLEIPREEFLTKSYPLSYVYEDIVLVSYDDGEEYSTSSQPS
LMALFMEWVGLDKGMRVLEIGGGTGYNAAVMSRVVGEKGLVVSVEYSRKICEIAKRN
ERLGIENVIFVCGDGYGVPEFSPYDVIFVTVGVDVETWFTQLKEGGRVIVPINLKLSR
RQPAFLFKKKDPYLVGNYKLETRFITAGGNLG

>d1jg1a_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Archaeon *Pyrococcus furiosus*}
EKELYEKWMRTVEMLKAEGIIRSKEVERAFLKYPRYLSVEDKYKKYAHIDEPLPIPAGQTV
SAPHMVAIMLEIANLKPGMNILEVGTGSGWNAALISEIVKTDVYTIERIPELVEFAKRNLER
AGVKNVHVILGDGSKGFPPKAPYDVIIVTAGAPKIEPLIEQLKIGGKLIIPVGSYHLWQEL
LEVRKTKDGIKIKNHGGVAFVPLIGEYGWK

>d1kr5a_ c.66.1.7 (A:) Protein-L-isoaspartyl O-methyltransferase {Human (*Homo sapiens*)}
ASHSELIHNLRKNGIIKTDKVFVEMLATDRSHYAKCNPYMDSPQSIGFQATISAPMHAYA
LELLFDQLHEGAKALDVGSGSGILTACFARMVGCTGKVGIDHIKELVDDSVNNVRKDDP
TLLSSGRVQLVVGDRMGYAEAPYDAIHVGAAAPVVPQALIDQLKPGGRLILPVGPAGG
NQMLEQYDKLQDGSIKMKPLMGVIYVPLTDKEKQWSR

>d3mag_ c.66.1.9 (-) Polymerase regulatory subunit VP39 {*Vaccinia virus*}
MDVVSLDKPFMYFEEIDNELDYEPESANEVAKKLPYQGQLKLLLGELFFLSKLQRHGILD
GATVVYIGSAPGTHIRYLRDHFYNLGVIIKWMLIDGRHHDPIILNGLRDVTLVTRFVDEEYL
RSIKKQLHPSKIILISDVRSKRGNESTADLLSNYALQNVMSILNPVASSLKWRCPPDQ
WIKDFYIPHGKMLQPFAPSYSAEMRLLSIYTGEMRLTRVTKSDAVNYEKKMYLNLKIV
RNKVVVNFDPNQEYDYFHMVFMLRTVYCNKTFPTTKAKVLFLQQSIFRFLNIP

>d1yub_ c.66.1.9 (-) rRNA methyltransferase {*Streptococcus pneumoniae*, Ermam}
MNKNIKYSQNFLTSEKVLNQIIKQLNLKETDTVYEIGTGKGHLTTKLAKISKQVTSIELDSH
LFNLSSSEKLKLNTRVTLIHQDILQFQFPNKQRYKIVGNIPYHLSTQIIKKVVFESRASDIYLIV
EEGFYKRTLDIHRTLGLLLHTQVSIQQLKLPACFHPKPKVNSVLIKLTRHTTDVPDKYW
KLYTYFVSKWVNREYRQLFTKNQFHQAMKHAKVNNLSTITYEQVLSIFNSYLLFNGRK

>d1i4wa_ c.66.1.9 (A:) Transcription factor sc-mtTFB {Baker's yeast (*Saccharomyces cerevisiae*)}
PIPGIKDISKLKFFYGFKYLWNPTVYNKIFDKLDLTKTYKHPEELKVLDPYGVGIQSAIFY
NKYCPRQYSLLEKRSSLYKFLNAKFEGSPLQILKRDPYDWSTYSNLIDEERIFVPEVQSSDH
INDKFLT VANVTGEGSEGLIMQWLSCIGNKNWLYRFGKVKMLLWMPSTTARKLLARPGM
HSRSKCSVVREAFTDTKLIAISDANELKGFDSQCIEEWDPIFSAAEIWPTKGKPIALVEMD
PIDFDFDNDWDYVTRHLMILKRTPLNTVMDSLGHGGQQYFNSRITDKDLLKKCPIDLTN
DEFIYLTCLFMEWPFPK

>d6mhta_ c.66.1.10 (A:) DNA methylase HhaI, coenzyme-binding domain {*Haemophilus haemolyticus*}

MIEIKDKQLTGLRFIDLFAGLGGFRLALESCGAECVYSNEWDKYAQEVYEMNFGKEKPEGD
ITQVNEKTIPDHDILCAGFPCQAFSISGKQKGFEDSRGTLFFDIARIVREKKPKVFMENVK
NFASHDNGNTLEVVKNTMNELDYSFHAKVLNALDYGIPQKRERIYMICFRNDLNINQNFQF
PKPFELNTFVKDLLLLPDSEVEHLVIDRKDLVMTNQEIEQTTPKTVRLGIVGKGGQGERIYS
TRGIAITLSAYGGGIFAKTGGYLVNGKTRKLHPRECARVMGYPDYKVPSTSQAYKQFG
NSVVINVLQYIAYNIGSSLNFKPY

>d1g38a_ c.66.1.10 (A:) DNA methylase TaqI, coenzyme-binding domain {*Thermus aquaticus*}
VETPPEVVDFMVSLAEAPRGGRVLEPACAHGPFLRAFREAHGTGYRFVGVEIDPKALDLP
PWAEGILADFLWEPGEAFDLILGNPPYGIVGEASKYPIHVFKAVKDLYKKAFSTWKGKY

NLYGAFLEKAVRLLKPGGVLVFFVVPATWLVLEDFALLREFLAREGKTSVYYLGEVFPQKK
VSAVVIRFQKSGKGLSLWDTQESGFTPILWAEYPHWEGEIIRFETEETRKLEISGMPLGD
LFHIRFAARSPEFKKHPAVRKEPGPGLVPVLTGRNLKPGWVDYEKNHSGLWMPKERAKEL
RDFYATPHLVVAHTKGRVVAAWDERAYPWREEFHLLPKEGVRLDPSSSLVQWLNSEAMQ
KHVRTLYRDFVPHLTLRMLERLPVRREYGFHT

>d1dcta_ c.66.1.10 (A:) DNA methylase HaeIII, coenzyme-binding domain {Haemophilus aegyptius}

MNLISLFSGAGGLDLGFQKAGFRIICANEYDKSIWKTYESNHS AKLIKDISKISSDEFKPC
DGIIGPPCQSWSEGGSLRGIDDPKGKLFYEYIRILKQKKPIFFLAENVKGMMMAQRHNKAV
QEFIQEFDNAGYDVHIILLNANDYGVAQDRKRVFYIGFRKELNINYLPPPHLIKPTFKDVI
WDLKDNPIPALDKNKTNGNKCIPNHEYFIGSYSTIFMSRNRVRQWNEPAFTVQASGRQC
QLHPQAPVMLKVSKNLNKFVEGKEHLYRRLTVRECARVQGFDDFIFHYESLNDGYKMI
GNAVPPVNLAYEIAKTIKSAL

>d2dpma_ c.66.1.10 (A:) DpnM DNA adenine methyltransferase {Streptococcus pneumoniae}

TLQPFTKWTGGKRQLLPVIRELIPKTYNRYFEPFVGGGALFFDLAPKDAVINDFNAELINC
YQKIKDNPQELIEILKVHQEYNSKEYYDLRSADRDERIDMMSEVQRAARILYMLRVNFN
GLYRVNSKNQFNVPYGRYKNPKIVDEELISAISVYINNNQLEIKVGDFEKAIVDVRTGDFV
YFDPPYIPLSETSAFTSYTHEGFSFADQVRLRDAFKRLSDTGAYVMLSNSSSALVEELYKDF
NIHYVEATRTNGAKSSSRGKISEIIVTNYEK

>d1g55a_ c.66.1.10 (A:) DNMT2 {Human (Homo sapiens)}

EPLRVLELYSGVGGMHHALRESCIPAQVVAIDVNTVANEVYKYNFPHTQLLAKTIEGITL
EEFDRLSFDMLMSPPCQPFTRIGRQGDMDTSRTNSFLHILDILPRLQKLPKYILLENVKGF
EVSSTRDLIQTIENTCGFYQEFLSPTS LGIPNSRLRYFLIAKLQSEPLPFQAPGQVLMFEP
KIEIHRKNQQDSDSL SVKMLKDFLEDDTDVNQYLLPPKSLLRYALLLDIVQPTCRRSVCFTK
GYGSYIEGTGSVLQTAEDVQVENIYKSLTNLSQEEQITKLLILKLRYFTPKEIANLLGFPPEF
GFPEKITVKQRYRLLGNSLNVHVVAKLILYE

>d1booa_ c.66.1.11 (A:) m.PvuII N4 cytosine-specific DNA methyltransferase {Proteus vulgaris}

NFGKKPAYTTSNGSMYIGDSLELLESFPEESISLVMTSPPFALQRKKEYGNLEQHEYVDWF
LSFAKVVNKKLPDGSFVVDFFGAYMKGVPARSIYNFRVLIRMIDEVGFFLAEDFYWFNP
SKLPSPIEWVNKRKIRVKDAVNTVWWFSKTEWPKSDITKVLAPYSDRMKKLIEDPDKFYT
PKTRPSGHDIGKSFSKDNNGSIPPNLLQISNSESNGQYLANCKLMGIKAHPARFPAKLPEFFI
RMLTEPDDLVDIFGGSNTTGLVAERESRKWISFEMKPEYVAASAFLDNNISEEKITDIY
NRILNGESLDLNSI

>d1eg2a_ c.66.1.11 (A:) m.RsrI N6 adenosine-specific DNA methyltransferase {Rhodobacter sphaeroides}

GTTRHVYDVCDCLDTLAKLPDDSVQLIICDPPYNIMLADWDDHMDYIGWAKRWLAEEAE
RVLSPTGSIAIFGGLQYQGEAGSGDLISIISHMRQNSKMLLANLIWNYPNGMSAQRFFANR
HEEIAWFAKTKKYFFDLDAVREPYDEETKAAYMKDKRLNPESVEKGRNPTNVWRMSRL
NGNSLERVGHPTQKPAVIERLVRALSHPGSTVLDFAGSGVTARVAIQEGRNSICTDAAPV
FKEYYQKQLTFLQDDGLIDKARSYEIVEGAANFGAALQR

>d1ajsa_ c.67.1.1 (A:) Aspartate aminotransferase, AAT {Pig (Sus scrofa), cytosolic form}

APPSVFAEVPQAQPVLVFKLIADFREDPDPRKVN LGVGAYRTDDCQPWVLPVVRKVEQRI

ANNSSLNHEYLPILGLAEFRTCASRLALGDDSPALQEKRVGGVQSLGGTGALRIGAEFLAR
WYNGTNNKDTPVYVSSPTWENHNGVFTTAGFKDIRSYRYWDTEKRGLDLQGFLSDLEN
APEFSIFVLHACAHNPTGTDPTPEQWKQIASVMKRRFLFPFFDSAYQGFASGNLEKDAWAI
RYFVSEGFELFCAQSFSKNFGLYNERVGNLTVVAKEPDSILRVLSQMOKIVRVTSNPPAQ
GARIVARTLSDPELFHEWTGNVKTMADRILSMRSELRARLEALKTPGTWNHITDQIGMFS
FTGLNPKQVEYLINQKHIYLLPSGRINMCGLTTKNLDYVATSIHEAVTKIQ

>d2ay1a_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Paracoccus denitrificans}
MLGNLKPQAPDKILALMGEFRADPRQGKIDLVGVYKDATGHTPIMRAVHAAEQRMLET
ETTKTYAGLSGEPEFQKAMGELILGDGLKSETTATLATVGGTGALRQALELARMANPDLR
VVFSDPTWPNHVSIMNFMGLPVQTYRYFDAETRGVDFEGMKADLAAKKGDMVLLHG
CCHNPTGANLTLTDQWAEIASILEKTGALPLIDLAYQGFGDGLEEDAAGTRLIASRIPEVLIA
ASCSKNFGIYRERTGCLLALCADAATRELAQGAMAFLNRQTYSFPPFHGAKIVSTVLTTPPE
LRADWMAELEAVRSGMLRLREQLAGELRDLSGSDRFGFVAEHRGMFSRLGATPEQVKRI
KEEFGIYMGVDSRINIAGLNDNTIPILARAIIEVGV

>d3tata_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Escherichia coli}
MFQKVDAYAGDPILTLMERFKEDPRSDKVNLSIGLYYNEDGIIPQLQAVAEAEARLNAQPH
GASLYLPM EGLNLCYRHAIAPLLFGADHPVLKQQRVATIQTGGSGALKVGADFLKRYFPE
SGVWVSDPTWENHVAIFAGAGFEVSTYPWYDEATNGVRFNDLLATLKTLPARSIVLLHPC
CHNPTGADLTNDQWDVAVIEILKARELIPFLDIAYQGFGAGMEEDAYAIRAIASAGLPALVSN
SFSKIFSLYGERVGGLSVMCEDAEAAAGRVLGQLKATVRRNYSSPPNFGAQVVAVLNDEA
LKASWLAEEVEEMRTRILAMRQELVKVLSTEMPERNFDYLLNQRGMFSYTGLSAAQVDRL
REEFGVYLIASGRMCVAGLNTANVQRVAKAFAAVM

>d1gdea_ c.67.1.1 (A:) Aromatic aminoacid aminotransferase, AroAT {Archaeon Pyrococcus horikoshii}

ALSDRLELVSASEIRKLFDAAGMKDVISLGIGEPDFDTPQHIKEYAKEALDKGLTHYGPNI
GLLELREAI AEKLLKQNGIEADPKTEIMVLLGANQAFLMGLSAFLKDGEVLIPTPAFVS
YAPAVILAGGKPVVEPTYEEDEFRLNVDELKKYVTDKTRALIINSPCNPTGAVLTKKDLEEIA
DFVVEHDLIVISDEVYEHFIYDDARHYSIASLDGMFERTITVNGFSKTFAMTGWRLGFVAA
PSWIIERMVKFQMYNATCPVTFIQYAAAKALKDERSWKAVEEMRKEYDRRRKLVWKRL
NEMGLPTVKPKGAFYIFPRIRDGTGLTSKKFSELMLKEARVAVVPGSAFGKAGEGYVRISYA
TAYEKL EAMDRMERVLKERKLV

>d1bw0a_ c.67.1.1 (A:) Tyrosine aminotransferase (TAT) {Trypanosoma cruzi}

WDVSM SNHAGLVFNPIRTVSDNAKPSPSPKPIIKLSVGDPTLDKNLLTSAAQIKKLKEAIDS
QECNGYFPTVGSPEAREAVATWWRNSFVHKEELKSTIVKDNVVLCSGGSHGILMAITAICD
AGDYALVPQPGFPHYETVCKAYGIGMHFYNCRPENDWEADLDEIRRLKDDKTKLLIVTNP
SNPCGSNFSRKHVEDIVRLAEELRLPLFSDEIYAGMVFKGKDPNATFTSVADFETTVPVIL
GGTAKNLVVPGWRLGWLLYVDPHGNGPSFLEGLKRVGMLVCGPCTTVVQAALGEALLNT
PQEHL DQIVAKIEESAMYLYNHIGECIGLAPTMPRGAMYLMSRIDLEKYRDIKTDVEFFEK
LLEEENVQVLPGTIFHAPGFTRLTTTRPVEVYREAVERIKAFCQRHAA

>d1fg7a_ c.67.1.1 (A:) Histidinol-phosphate aminotransferase {Escherichia coli}

TVTITDLARENVRNLTPYQSARRLGGNGDVWLNANEYPTAVEFQLTQQTNLNRYPECQPKA
VIENYAQYAGVKPEQVLVSRGADEGIELLIRAFCEPGKDAILYCPPTYGMYSVSAETIGVEC
RTVPTLDNWQLDLQGISDKLDGVKV VYVCSNNPTGQLINPQDFRTLLELTRGKAIVVAD
EAYIEFCPQASLAGWLAEYPHLAILRTL SKAFALAGLRGFTLANEEVINLLMKVIAPYPLS

TPVADIAAQALSPQGIVAMRERVAQIIAEREYLIAALKEIPCVEQVFDSETNYILARFKASSA
VFKSLWDQGIILRDQNKQPSLSGCLRITVGTREESQRVIDALRAEQV

>d1kusa_ c.67.1.1 (A:) L-threonine-O-3-phosphate decarboxylase CobD {Salmonella enterica}
HGGNIREPATVLGISPDQLLDFSANINPLGMPVSVKRALIDNLDCIERYPDADYFHLHQAL
ARHHQVPASWILAGNGETESIFTVASGLKPRRAMIVTPGFAEYGRALAQSGCEIRRWSLRE
ADGWQLTDAILEALTPDLDCFLCTPNNPTGLLPERPLLQAIADRCCKSLNINLILDEAFIDFI
PHETGFIPALKDNPHIWVLRSLTKFYAIPGLRLGYLVNSDDAAMARMRRQQMPWSVNAL
AALAGEVALQDSAWQQATWHWLREEGARFYQALCQLPLLTVYPGRANYLLLRCEREDID
LQRRLLTQRILIRSCANYPGLDSRYRVAIRSAAQNERLLAALRNVLGTIAP

>d1jg8a_ c.67.1.1 (A:) Low-specificity threonine aldolase {Thermatoga maritima}
MIDLRSDTVTKPTEEMRKAMAQAEVGDDVYGEDPTINELERLAAETFGKEAALFVPSGT
MGNQVSIMAHTQRGDEVILEADSHIFWYEVGAMAVLSGVMHPVPGKNGAMDPDDVRK
AIRPRNIHFPRTSLIAIENTHNRSGGRVPLENIKEICTIAKEHGINVHIDGARIFNASIASGVP
VKEYAGYADSVMFCLSKGLCAPVGSVVVGDRDFIERARKARKMLGGGMRQAGVLAAA
GIIALTKMVDRLKEDHENARFLALKLKEIGYSVNPEDVKTNMVILRTDNLKVNAGHFIEA
LRNSGVLANAVSDTEIRLVTHKDVSRNDIEEALNIFEKLFKFS

>d1cl1a_ c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Escherichia coli}
KLDTQLVNAGRSKKYTLGAVNSVIQRASSLVFDSVEAKKHATRNRANGELFYGRRGTLTH
FSLQQAMCELEGGAGCVLFPCGAAVANSILAFIEQGDHVLMTNTAYEPSQDFCSKILSKL
GVTTSWFDPLIGADIVKHLQPNTKIVFLESPGSITMEVHDVPAIVAARSVPDAIIMIDNT
WAAGVLFKALDFGIDVSIQAATKYLVGHS DAMIGTAVCNARCWEQLRENAYLMGQMVD
ADTAYITSRGLRTLGVRLRQHHESSLKVAEWLAEHPQVARVNHPALPGSKGHEFWKRDF
GSSGLFSFVLKKKLNNNEELANYLDNFSLSMAYSWGYESLILANQPEHIAAIRPQGEIDFS
GTLIRLHIGLEDVDDLIADLDAGFARIV

>d1libja_ c.67.1.3 (A:) Cystathionine beta-lyase, CBL {Thale cress (Arabidopsis thaliana)}
ASVSTLLVNLDNKFDPFDAMSTPLYQTATFKQPSAIENGPYDYTRSGNPTRDALESLLAKL
DKADRAFCFTSGMAALSAVTHLIKNGEEIVAGDDVYGGSDRLLSQVVPRSGVVVKRVNT
TKLDEVAAAIGPQTKLVWLESPTNPRQQISDIRKISEMAHAQGALVLVDNSIMSPVLSRPLE
LGADIVMHSATKFIAGHS DVMAGVLAVKGEKLAKEVYFLQNSEGSGLAPFDCWLCLRGI
KTMALRIEKQQENARKIAMYLSSHPRVKKVYYAGLPDHPGHHLHFSQAKGAGSVFSFITG
SVALSKHLVETTKYFSIAVSFGSVKSLISMPCFMSHASIPAEVREARGLTEDLVRIAGIEDV
DDLISDLIAFKTFPL

>d1cs1a_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Escherichia coli}
RKQATIAVRSGLNDDEQYGCVPPIHLSSTYNFTGFNEPRAHDYSRRGNPTRDVVQRALA
ELEGGAGAVLTNTGMSAIHLVTTVFLKPGDLLVAPHDCYGGSYRLFDSLAKRGCYRVLFV
DQGDEQALRAALAEKPKLVLVESPSNPLLRVVDIAKICHLAREVGAVSVVDNTFLSPALQN
PLALGADLVLHSC TKYLNHSDVVAGVVIKDPDVVTELAWWANNIGVTGGAFDSYLLL
RGLRTLVP RMELAQRNAQAIVKYLQTQPLVKKLYHPSLPENQGHEIAARQQKGFGAMLSF
ELDGDEQTLRRFLGGLSLFTLAESLGGVESLISHAATMTHAGMAPEARAAAAGISETLLRIS
TGIEDGEDLIADLENGFRAANKG

>d1qgna_ c.67.1.3 (A:) Cystathionine gamma-synthase, CGS {Common tobacco (Nicotiana tabacum)}
MKYASFLNSDGSAIHAGERLGRGIVTDAITTPVVNTSAYFFNKTSSELIDFKEKRRASFEYG
RYGNPTTVVLEEKISALEGAESTLLMASGMCASTVMLLALVPAGGHIVTTTDCYRKTRIFI

ETILPKMGITATVIDPADVGALELALNQKKVNLFFTESPTNPFLRCVDIELVSKLCHEKGAL
VCIDGTFATPLNQKALALGADLVLHSATKFLGGHNDVLAGCISGPLKLVSEIRNLHHILGG
ALNPNAAYLIIRGMKTLHLRVQQQNSTALRMAEILEAHPKVRHVYYPGLQSHPEHHIAKK
QMTGFGGAVSFEVDGDLTTAKFVDALKIPYIAPSGGCESIVDQPAIMSYWDLSDRAK
YGIMDNLVRFSFGVEDFDDLKADILQALDSI

>d1e5ea_ c.67.1.3 (A:) Methionine gamma-lyase, MGL {Trichomonas vaginalis}

ERMTPATACIHANPQKDQFGAAIPPIYQTSTFVFDNCQQGGRNFAGQESGYIYTRLGNPTV
SNLEGKIAFLEKTEACVATSSGMGAIAATVLTILKAGDHLISDECLYGCTHALFEHALTKFG
IQVDFINTAIPGEVKKHMKPNTKIVYFETPANPTLKIIDMERVCKDAHSQEGVLVIADNTFC
SPMITNPVDFGVDVVVHSATKYINGHTDVVAGLICGKADLLQQIRMVGIKDITGSVISPHD
AWLITRGLSTLNIRMKAESENAEKVAEYLKSHPAVEKVYYPGFEDHEGHDIKKQMRMY
GSMITFILKSGFEGAKKLLDNLKLITLAVSLGGCESLIQHPASMTHAVVPKEEREAAAGITDG
MIRLSVGIEDADELIADFKQGLDALLR

>d1d2fa_ c.67.1.3 (A:) Modulator in mal gene expression, MalY {Escherichia coli}

LLPFTISDMDFATAPCIIEALNQRLMHGVFGYSRWKNDEFLLAAIAHWFSTQHYTAIDSQTV
VYGPSVIYMVSELIRQWSETGEGVVIHTPAYDAFYKAIEGNQRTVMPVALEKQADGWFC
DMGKLEAVLAKPECKIMLLCSPQNPTGKVWTCDELEIMADLCERHGVVISDEIHMDMV
WGEQPHIPWSNVARGDWALLTSGSKSFNIPALTGAYGIIENSSSRDAYLSALKGRDGLSSPS
VLALTAHIAAYQQGAPWLDALRIYLDNLTYIADKMNAAPFELNWQIPQSTYLAWLDRP
LNIDDNALQKALIEQEKVAIMPGYTYGEEGRGFVRLNAGCPRSKLEKGVAGLINAIRAVR

>d1c7na_ c.67.1.3 (A:) Cystalyisin {Treponema denticola}

MIYDFTTKISRKNLGLKWDLMYSQNPEVGNEVVPLSVADMEFKNPPELIEGLKKYLD
VLGYTGPTTEYKKTVKKWMKDRHQWDIQTWDIINTAGVVPVAVFNAVREFTKPGDGVIIIT
PVYYPFFMAIKNQERKIIECELLEKDGYYTIDFQKLEKLSKDKNNKALLFCSPHNPVGRV
WKKDELQKIKDIVLKSDDLMLWSDEIHFDLIMPGYEHTVFQSIDEQLADKTITFTAPSKTFNI
AGMGMSNIIKNPDIRERFTKSRDATSGMPFTTLGYKACEICYKECGKWLDGCIKVIDKNQ
RIVKDFFEVNHPEIKAPLIEGTYLQWIDFRALKMDHKAMEEFMIHKAQIFFDEGYIFGDGG
IGFERINLAAPSSVIQESLERLNKALKDLK

>d1eg5a_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Thermotoga maritima}

MRVYFDNNATTRVDDRVLLEEMIVFYREKYGNPNSAHGMGIEANLHMEKAREKVAKVLG
VSPSEIFFTSCATESINWILKTVAEFTFEKRKRRTIITPIEHKAVLETMKYLSMKGFKVKYVPV
DSRGVVKLEELEKLVDDEDTFLVSIMAAANNEVGTIQPVEDVTRIVKKKNKETLVHVDVAVQT
IGKIPFSLEKLEVDYASFSAHKFHGPKGVGITYIRKGVPIRPLIHGGGQERGLRSGTQNPVGI
VGAARAMEIAVEELSEAAKHMEKLRSLVSGLMNLGAHIITPLEISLPNTLSVSFPNIRGST
LQNLLSGYGIYVSTSSACTSKDERLRHVLDAMGVDRRIAQGAIRISLCKYNTTEEEVDYFL
KKIEEILSFL

>d1jf9a_ c.67.1.3 (A:) NifS-like protein/selenocysteine lyase {Escherichia coli}

IFSVDKVRADFPVLSREVNGLPLAYLDSAASAQKPSQVIDAEAEFYRHGYAAVHRGIHTLS
AQATEKMENVRKRASLFINARSAEELVFVRGTTEGINLVANSWGNSNVRAGDNIIISQMEH
HANIVPWQMLCARVGAELRVIPLNPDGTLQLETPLTLFDEKTRLLAITHVSNVLGTENPLA
EMITLAHQHGAKVLVDGAQAVMHHPVDVQALDCDFYVFSGHKLYGPTGIGILYVKEALL
QEMPPWEGGGSMIATVSLSEGTTWTKAPWRFEAGTPNTGGIIGLGALEYVSALGLNNIA
EYEQNLMHYALSQLESVPDLTLYGPQNRLGVIAFNLGKHHAYDVGSFLDNYGIAVRTGHH
CAMPLMAYYNNVPAMCRASLAMYNTHEEVDRLVTGLQRIHRLLG

>d1elua_ c.67.1.3 (A:) Cystine C-S lyase {Synechocystis sp.}

QFPGLANKTYFNFGGQGILPTVALEAITAMYGYLQENGPFSIAANQHIQQLIAQLRQALAE
TFNVDPNITITITDNVTTGCDIVLWGLDWHQGDEILLTDCEHPGIIAIVQAIAARFGITYRFFP
VAATLNQGDAAAVLANHLGPKTRLVILSHLLWNTGQVLPLAEIMAVCRRHQGNYPVRVL
VDGAQSAGSLPLDFSRLVDYYAFTGHKWFAGPAGVGGLYIHGDCLGEINPTYVGWRSIT
YGAKGEPTGWAEGGKRFEVATSAYPQYAGLLAALQLHQRQGTAEERYQAICQRSEFLWR
GLNQLPHVHCLATSAPQAGLVSTVDSPLGHRIVQKLEEQRIYLRITADPDCIRACCHYIT
DEEEINHLLARLADFGP

>d2dkb_ c.67.1.4 (-) Dialkylglycine decarboxylase {Pseudomonas cepacia}

LNDDATFWRNARHHLVRYGGTFEPMIERAKGSFVYDADGRAILDFTSGQMSAVLGHCHP
EIVSVIGEYAGKLDHLFSEMLSRPVVDLATRLANITPPGLDRALLSTGAESNEAAIRMAK
LVTGKYEIVGFAQSWHGMTGAAASATYSAGRKGVGPAAVGSFAIPAPFTYRPRFERNGAY
DYLAELDYAFDLIDRQSSGNLAAAFIAEPILSSGGIILPDGYMAALKRKCEARGMLLILDEA
QTGVGRTGTMFACQRDGVTPDILTSLKTLGAGLPLAAIVTSAAIEERAHELGYLFYTTHVS
DPLPAAVGLRVLDVVQRDGLVARANVMGDRRLRRGLLDLMEFDCIGDVRGRGLLLGVEI
VKDRRTKEPADGLGAKITRECMNLGLSMNIVQLPGMGGVFRIAPPLTVSEDEIDLGLSLLG
QAIERAL

>d2gsaa_ c.67.1.4 (A:) Glutamate-1-semialdehyde aminomutase (aminotransferase)
{Synechococcus sp., strain GR6}

FKTIKSDEIFAAAQKLMPGGVSSPVRAFKSVGGQPIVFDRVKDAYAWDVDGNRYIDYVGT
WGPAICGHAHPEVIEALKVAMEKGTSFGAPCALENVLAEMVNDAPSIEMVRFVNSGTEA
CMAVLRMLRAYTGRDKIIFEGCYHGHADMFLVKAGSGVATLGLPSSPGVPKKTANTLT
TPYNDLEAVKALFAENPGEIAGVILEPIVGNSGFIVPDAGFLEGLREITLEHDALLVFDEVM
TGFRAYGGVQEKFGVTPDLTTLGKIIGGGLPVGAYGGKREIMQLVAPAGPMYQAGTSLG
NPLAMTAGIKTLELLRQPGTYEYLDQITKRLSDGLLAIAQETGHAACGGQVSGMFGFFFT
EGPVHNYEDAKKSDLQKFSRFHRGMLEQGIYLAPSQFEAGFTSLAHEEDIDATLAAART
VMSAL

>d2oata_ c.67.1.4 (A:) Ornithine aminotransferase {Human (Homo sapiens)}

GPPTSDDIFEREYKYGAHNYHPLPVALERGKGIYLWDVEGRKYFDLSSYSAVNQGHCHP
KIVNALKSQVDKLTLSRAFYNNVLGEYEEYITKLFNYHKVLPMTGVEAGETACKLAR
KWGYTVKGIQKYKAKIVFAAGNFWGRTLSAISSSTDPTSVDGFGPFMPGFDIIPYNDLPAL
ERALQDPNVAAFMVEPIQGEAGVVVPDPGYLMGVRELCTRHQVLFIADIEQTGLARTGR
WLAVDYENVRPDIIVLLGKALSGGLYPVSAVLCDDIMLTIKPGEHGSTYGGNPLGCRVAIA
ALEVLEENLAENADKLGILRNELMKLPDVTAVRGKGLLNAIVIKETKDWDWAKVCL
RLRDNGLLAKPTHGDIIRFAPPLVIKEDELRESIEIINKTILSF

>d1gtxa_ c.67.1.4 (A:) 4-aminobutyrate aminotransferase, GABA-
aminotransferase {Pig (Sus scrofa)}

FDYDGPLMKTEVPGPRSRELMKQLNIIQNAEAVHFFCNYEESRGNYLVDVDGNRMLDLY
SQISSIPIGYSHPALVKLVQQPQNVSTFINRPALGILPPENFVEKLRESLLSVAPKGMSQLITM
ACGSCSNENAFKTIFMWYRSKERGQSFAFSKEELETMINQAPGCPDYSILSFMGAFHGRT
MGCLATTHSKAIHKIDIPSFWDPIAPFPRLKYPLEEFVKENQQEEARCLEEVEDLIVKYRKK
KKTVAGIIVEPIQSEGDNHASDDFFRKLDRDISRKHGCAFLVDEVQTGGGSTGKFWAHEH
WGLDDAADVMTFSKKMMTGFFHKEEFRPNAPYRIFNTWLGDPSKNLLLAEVINIIRE
DLLSNAAHAGKVLLTGLLDLQARYPQFISRVGRGTFCSDTPDESIRNKLISIARNKGVM

LGCGDKSIRFRPTLVFRDHHHLFLNIFSDILADFK

>d1bt4a_ c.67.1.4 (A:) Phosphoserine aminotransferase, PSAT {*Bacillus circulans*, subsp. *alkalophilus*}

SERAYNFNAGPAALPLEVLERAQAEFVDYQHTGMSIMEMSHRGAVYEAVHNEAQARLLA
LLGNPTGYKVLFIQGGASTQFAMIPMNFLKEGQTANYVMTGSWASKALKEAKLIGDTHV
AASSEASNYMTLPKLQEIQLDNAAYLHLTSNETIEGAQFKAFPDTGSVPLIGDMSSDILSR
PFDLNQFGLVYAGAQNKLGPSTVTVVIVREDLVAESPKHLPTMLRYDTYVKNNSLYNTTP
SFGIYMVNEVLKWIEERGGLGVQQANRKKASLIYDAIDQSGGFYRGCVDVDSRSDMNI
TFRLASEELEKEFVKASEQEGFVGLKGHRVGGGLRASIYNAVPHYESCEALVQFMEHFKRS
RG

>d1ejia_ c.67.1.4 (A:) Serine hydroxymethyltransferase {Mouse (*Mus musculus*)}

MADRDATLWASHEKMLSQPLKSDAEVYSIIKKESNRQRVGLELIASENFASRAVLEALGS
SLNNKYSEGYPGQRYGGTEFIDELEMLCQKRALQAYHLDPQCWGVNVQPYSGSPANFA
VYTALVEPHGRIMGLDLPDGGHLTHGFMTDKKKISATSIFFESMPYKVYPETGYINYDQLE
ENASLFHPKLIIAGTSCYSRNLDYARLRKIADDNGAYLMADMAHISGLVAAGVVPSPFEHC
HVVTTTTHTKTLRGCRAGMIFYRKGVRSVDPKTGKETYYELESINSVFPGLQGGPHNHA
IAGVAVALKQAMTTEFKIYQLQVLANCRALSDALTELGYKIVTGGSDNHLILMDLRSGKT
DGGRAEKVLEACSIACNKNTCPGDKSALRPSGLRLGTPALTSRGLLEEDFQKVAHFIHRGI
ELTLQIQSHMATKATLKEFKELAGDEKIQSAVATLREEVENFASNFSPLPLPDF

>d1b9ha_ c.67.1.4 (A:) 3-amino-5-hydroxybenzoic acid synthase (AHBA synthase)
{*Amycolatopsis mediterranei*}

KAPEFPAPQYDDAERNGLVRALQGGQWWRMGGDEVNSFEREFAAHHGAHALAVTN
GTHALELALQVMGVPGTEVIVPAFTFISSQAQRLGAVTPVDVDAATYNLDPEAVAA
AVTPRTKVIMPVHMAGLMADMDALAKISADTGVPLLQDAAHAHGARWQGRVGELEDSI
ATFSFQNGKLMTAGEGGAVVFPDGETEKYETAFLRHSCGRPRDDRRYFHKIAGSNMRLNE
FSASVLRALRLDEQIAVRDERWTLLSRLGAIDGVVPQGGDVRADRNSHYMAMFRIP
GLTEERRNALVDRLVEAGLPAAFAFRAIYRTDAFWELGAPDESVDIAIARRCPNTDAISSDC
VWLHHRVLLAGEPELHATAEIIADAVARA

>d1fc4a_ c.67.1.4 (A:) 2-amino-3-ketobutyrate CoA ligase {*Escherichia coli*}

GSHMRGEFYQQLTNDLETARAEGLFKEERIITSAAQQADITVADGSHVINFCANNYLGLAN
HPDLIAAAKAGMDSHGFGMASVRFIGTQDSHKELEQKLAFLGMEDAILYSSCFDANG
GLFETLLGAEDAIIISDALNHASIIDGVRLCKAKRYRYANNDMQELEARLKEAREAGARHV
LIATDGVFSMDGVIANLKGVCDDLADKYDALVMVDDSHAVGFVGENGRGSHEYCDVMGR
VDIITGTGKALGGASGGYTAARKEVVEWLRQSRPYLFSNSLAPAIVAASIKVLEMVEA
GSELRDRLWANARQFREQMSAAGFTLAGADHAIIPVMLGDAVVAQKFARELQKEGIYVT
GFFYPVVPKGQARIRTQMSAAHTPEQITRAVEAFTRIGKQLGVIA

>d1bs0a_ c.67.1.4 (A:) PLP-dependent acyl-CoA synthase (8-amino-7-oxonanoate synthase, AONS) {*Escherichia coli*}

SWQEKINAALDARRAADALRRRYPVAQGAGRWLVADDRQYLNFSNDYLGLSHHPQIIR
AWQQGAEQFGIGSGSGHVSIGYSVVHQALEEELAEWLGYSRALLFISGFAANQAVIAAM
MAKEDRIAADRLSHASLLEAASLSPSQLRRFAHNDVTHLARLLASPCPGQMMVTEGVFS
MDGDSAPLAEIQQVTQQHNGWLMVDDAHGTGVIGEQQGRGSCWLQKVKPELLVVTFGK
GFGVSGAAVLCSSTVADYLLQFARHLIYSTSMPPAQAQALRASLAVIRSDEGDARREKLAA
LITRFRAGVQDLPFTLADSCSAIQPLIVGDNSRALQLAEKLRQQGCWVTAIRPPTVPAGTA

RLRLTLTAAHEMQDIDRLLEVLHGNG

>d1qj5a_ c.67.1.4 (A:) Adenosylmethionine-8-amino-7-oxononanoate aminotransferase, BioA {*Escherichia coli*}

MTTDDLAFDQRHILHPYTSMTSPLPVYPVVS AEGCELILSDGRRLVDGMSSWWAAIHGYN
HPQLNAAMKSQIDAMSHVMFGGITHAPAIELCRKLVAMTPQPLECVFLADSGSVAVEVAM
KMALQYWQAKGEARQRFLTFRNGYHGDTFGAMSVCDPDNSMHSLWKGYLPENLFAPAP
QSRMDGEWDERDMVGFARLMAAHRHEIAAVIIEPIVQGAGGMRMYHPEWLKRIRKICDR
EGILLIADEIATGFGRTGKLFACEHAEIAPDILCLGKALTGGTMTLSATLTTREVAETISNGE
AGCFMHGPTFMGNPLACAAANASLAILESGDWQQQVADIEVQLREQLAPARDAEMVAD
VRVLGAIGVVETTHPVNMAALQKFFVEQGVWIRPFGKLIYLMPPYIILPQQLQRLTAAVNR
AVQDETFFCQ

>d1b8ga_ c.67.1.4 (A:) 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) {*Apple (Malus domestica)*}

MLSRNATFNSHGQDSSYFLGWQEYEKNPYHEVHNTNGHIIQMGLAENQLCFDLLESWLAK
NPEAAAFKKNGESIFAELALFQDYHGLPAFKKAMVDFMAEIRGNKVTFDPNHLVLTAGAT
SANETFIFCLADPGEAVLIPTPYYPGFDRDLKWRTGVEIVPIHCTSSNGFQITETALEEAYQE
AEKRNLRVKGVLVTNPSNPLGTTMTRNELYLLLSFVEDKGIHLISDEIYSGTAFSSPSFISVM
EVLKDRNCENSEVWQRVHVVSLSKDLGLPGFRVGAIYSNDDMVVAAATKMSSFGLVS
SQTQHLLSAMLSDKKLTKNYIAENHKRLKQRQKKLVSGLQKSGISCLNGNAGLFCWVDM
RHLLRSNTFEAEMELWKKIVYEVHLNISPGSSSCHCTEPGWFRVCFANLPERTLDLAMQRL
KAFVG

>d1i52a_ c.68.1.13 (A:) 4-diphosphocytidyl-2-c-methylerythritol (CDP-me) synthase (YgbP) {*Escherichia coli*}

HLDVCAVVAAGFGRRMQTECPKQYLSIGNQTILEHSVHALLAHPRVKRVVIAISPGDSRF
AQLPLANHPQITVVDGGDERADSVLAGLKAAGDAQWVLVHDAARPCLHQDDLARLLAL
SETSRTGGILAAPVRDTMKRAEPGKNIAIAHTVDRNGLWHALTPQFFPRELLHDCLTRALN
EGATITDEASALEYCGFHPQLVEGRADNIKVTRPEDLALAEFYLTR

>d1h7ea_ c.68.1.13 (A:) CMP:2-keto-3-deoxy-manno-octonic acid (CMP-KDO)synthetase, KdsB {*Escherichia coli*}

SKAVIVIPARYGSSRLPGKPLLDIVGKPMIQHVYERALQVAGVAEVWVATDDPRVEQAVQA
FGGKAIMTRNDHESGTDRLVEVMHKVEADIIYNLQGDEPMIRPRDVETLLQGMRDDPALP
VATLCHAIASAAEAAEPSTVKVVVNTRQDALYFSRSPIPYPRNAEKARYLKHVGIYAYRRDV
LQNYSQLPESMPEQAESLEQLRLMNAGINIRTFEVAATGPGVDTPACLEKVRALMAQELA
ENA

>d1jyka_ c.68.1.13 (A:) CTP:phosphocholine cytidylyltransferase LicC {*Streptococcus pneumoniae*}

EIRVKAIILAAGLGTRLRPLTENTPKALVQVNQKPLIEYQIEFLKEKGINDIIIVGYLKEQFD
YLKEYGVRLVFNDKYADYNNFYSLYLVKEELANSYVIDADNYLFKNMFRNDLTRSTYF
SVYREDCTNEWFLVYGDDYKVQDIIVDSKAGRILSGVSFWDAPTAEKIVSFIDKAYVSGEF
VDLYWDNMVKDNIKELDVYVEELEGNISYEIDSVQDYRKLEEILK

>d1maaa_ c.69.1.1 (A:) Acetylcholinesterase {*Mouse (Mus musculus)*}

EDPQLLVVRGGQLRGIRLKAPGGPVSAFLGIPFAEPPVGSRRFMPPEPKRPWSGVLDATT
FQNVCYQYVDTLYPGFEGTEMWNPNNRELSCLYLVNWPYPRPASPTPVLIWIYGGGFY
SGAASLDVYDGRFLAQVEGAVLVSMNYRVGTGFLALPGSREAPGNVGLLDQRLALQW
VQENIAAFGGDPMSVTLFGESAGAASVGMHILSLPSRSLFHRAVLQSGTPNGPWATVSAG

EARRRATLLARLVGCPPGGAGGNDTELIACLRTRPAQDLVDHEWHVLPQESIFRFSFVPVV
DGDFLSDTPEALINTGDFQDLQVLVGVVKDEGSYFLVYGVPGFSGDNESLISRAQFLAGV
RIGVPQASDLAAEAVVLHYTDWLHPEDPHTLRDAMSAVVGDHNVVCPVAQLAGRLAAQ
GARVYAYIFEHRASLTWPLWMGVPHGYEIEFIFGLPLDPSLNYTTEERIFAQRLMKYWTN
FARTGDPNDPRDRKSPQWPPYTAAQQYVSLNLKPLEVRRGLRAQTCAFWNRFLPKLLS
AT

>d1dx4a_ c.69.1.1 (A:) Acetylcholinesterase {Fruit fly (*Drosophila melanogaster*)}

DRLVVQTSSGPVRGRSVTVQGREGVHVYTGIPYAKPPVEDLRFRKPVPAEPWHGVLDATGL
SATCVQERYEYFPGFSGEEIWNPNNTNVSEDCLYINVWAPAKARLRHGRGANGGEHPNGK
QADTDHLIHNGNPQNTTNGLPILIWIYGGGFMGTGSATLDIYNADIMAAVGNVIVASFQYRV
GAFGFLHLAEMPSEFAEEAPGNVGLWDQALAIRWLKDNAHAFGGNPEWMTLFGESAGS
SSVNAQLMSPVTRGLVKRGMMSGTMNAPWSHMTSEKAVEIGKALINDCNCNASMLKT
NPAHVMSCMRSVDAKTISVQQWNSYSGILSFPSAPTIDGAFLPADPMTLMKTADLKDYDI
LMGNVRDEGTYFLLYDFIDYFDKDDATALPRDKYLEIMNNIFGKATQAEREAIIFQYTSWE
GNPGYQNQQQIGRAVGDHFFTCPTNEYAQAALERGASVHYYYFTHRTSTSLWGEWMGV
LHGDEIEYFFGQPLNNSLQYRPVERELGKRMLSAVIEFAKTGNPAQDGEWPNFSKEDPV
YYIFSTDDKIEKLARGPLAARCSFWNDYLPKVRSW

>d2bce__ c.69.1.1 (-) Bile-salt activated lipase (cholesterol esterase) {Cow (*Bos taurus*)}

AKLGSVYTEGGFVEGVNKKLSLFGDSVDIFKGIPFAAAPKALEKPERHPGWQGTAKAKSF
KKRCLQATLTQDSTYGNEDCLYLNIVVPQGRKEVSHDLPMIWIYGGAFLMGASQGANF
LSNYLYDGEEIATRGNVIVVTFNYRVGPLGFLSTGDSNLPNGYGLWDQHMAIAWVKRNE
AFGGDPDNITLFGESAGGASVSLQTLSPYNKGLIKRAISQSGVGLCPWAIQQDPLFWAKRI
AEKVGCPVDDTSKMAGCLKITDPRALTLAYKLPLGSTEYPKLHYLSFVPVIDGDFIPDDPV
NLYANAADVYIAGTNDMDGHLFVGMDVPAINSNKQDVTEEDFYKLVSGLTVTKGLRG
ANATYEVYTEPWAQDSSQETRKKTMVDLETDLFLIPTKIAVAQHKSHAKSANTYTYLFSQ
PSRMPIYPKWMGADHADDLQYVFGKPFATPLGYRAQDRTVSKAMIAWNTNFARTGDPNT
GHSTVPANWDPYTLEDDNYLEINKQMDSNSMKLHLRTNYLQFWTQTYQALPTVTSAGA
SLLPPEDNSQASPVPPADNSGAPTEPSAGDSEVAQMPVVIGF

>d1qe3a_ c.69.1.1 (A:) Thermophilic para-nitrobenzyl esterase (PNB esterase) {*Bacillus subtilis*}

THQIVTTQYGKVKGTTENGTVHKWKGIPYAKPPVGQWRFKAPEPEVWEDVLDATAYGPI
CPQPSDLLSLSYTELPRQSEDCLYVNVFAPDTPSQNLPMVMVWIHGGAFYLGAGSEPLYDGS
KLAAQGEVIVVTLNYRLGPFGFLHLSSFDEAYSNDLGLLDQAAALKWVRENISAFGGDPD
NVTVFGESAGGMSIAALLAMPAAKGLFQKAIMESGASRTMTKEQAASTAAFLQVLGIN
ESQLDRLHTVAAEDLLKAADQLRIAENIFQLFFQPALDPKTLPEEPEKSIAEGAASGIPL
LIGTTREDEGYLFFTPDSVDVHSQETLDAALEYLLGKPLAEKAADLYPRSLESQIHMMTDLLF
WRPAVAYASAQSHYAPVWMYRFDWHPEKPPYNKAFHALELPFVFGNLDGLERMAKAEIT
DEVKQLSHTIQSAWITFAKTGNPSTEAVNWPAYHEETRETVIDDSEITIENDPESEKRQKLF

>d1jkma_ c.69.1.2 (A:) Carboxylesterase {*Bacillus subtilis*, brefeldin A esterase}

PGRLGDESSGPRTDPRFSPAMVEALATFGLDAVAAAPPVSASDDLPTVLAAVGASHDGFQ
AVYDSIALDLPTDRDDVETSTETILGVDGNEITLHVFRPAGVEGVLPGLVYTHGGGMILT
TDNRVHRRWCTDLAAAGSVVVMVDFRNAWTAEGHHPFSGVEDCLAAVLWVDEHRESL
GLSGVVVQGESGGGNLAIATTLAKRRGRDLAIDGVYASIPYISGGYAWDHERRLTEPSL
VENDGYFIENGGMALLVRAYDPTGEHAEDPIAWPYFASEDELRLPFPVAVNELDPLRD
EGIAFARRLARAGVDVAARVNIGLVHGADVIFRHWLPAALESTVRDVAGFAADRRLR

>d1jjia_ c.69.1.2 (A:) Carboxylesterase {Archaeon *Archaeoglobus fulgidus*}
MLDMPIDPVYYQLAEYFDSLPKFDQFSSAREYREAINRIYEERNRQLSQHERVERVEDRTI
KGRNGDIRVRVYQQKPDSPVLVYYHGGGFVICSIESHDALCRRIARLSNSTVVSVDYRLAP
EHKFPAAVYDCYDATKWVAENAEELRIDPSKIFVGGDSAGGNLAAAVSIMARDSGEDFIK
HQILIYPVNVFVAPTPSLLEFGEGLWILDQKIMSWFSEQYFSREEDKFNPLASVIFADLENLP
PALIITAEDPLRDEGEVFGQMLRRAGVEASIVRYRGVLHGFINYYPVLKAARDAINQIAA
LLVFD

>d1jjfa_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase z {*Clostridium thermocellum*}
SLPTMPPSGYDQVRNGVPRGQVVNISYFSTATNSTRPARVYLPPGYSKDKKYSVLYLLHGI
GGSENDWFEGGGRANVIADNLIAEGKIKPLIIVTPNTNAAGPGIADGYENFTKDLLNSLIP
YIESNYSVYTDREHRAIAGLSMGGGQSFNIGLTNLDKFAYIGPISAAPNTYPTNERLFPDGGK
AAREKLKLLFIACGTNDSLIGFGQRVHEYCVANNINHVYWLIQGGGHDFNVWKPLWNF
LQMADEAGLTRD

>d1gkla_ c.69.1.2 (A:) Feruloyl esterase domain of the cellulosomal xylanase y {*Clostridium thermocellum*}
SFKYESAVQYRPAPDSYLNPCPQAGRIVKETYTGINGTKSLNVYLPYGYDPNKKYNIFYL
MHGGGENENTIFSNDVKLQNILDHAIMNGELEPLIVVTPTFNGGNCTAQNFYQEFRQNVIP
FVESKYSTYAESTTPQGIAASRMHRGFGGFAMGGLTTWYVMVNCLDYVAYFMPLSGDY
WYGNSPQDKANSIAEAINRSGLSKREYFVFAATGSEDIAYANMNPQIEAMKALPHFDYTS
DFSKGNFYFLVAPGATHWWGYVRHYIYDALPYFFHELEHHHHHHH

>g1wht.1 c.69.1.5 (A:,B:) Serine carboxypeptidase II {Wheat (*Triticum vulgaris*)}
GHAADRIARLPQPAVDFDMYSGYITVDEGAGRSLFYLLQEAPEDAQPAPLVLWLNGGPG
CSSVAYGASEELGAFRVKPRGAGLVLENYRWNKVANVFLDSPAGVGFSYTNSTSSDIYTS
GDNRTAHD SYAFLAKWFERFPHYKYRDFYIAGESYAGHYVPELSQLVHRSKNPVINLKGF
MVGNGLIIDDYHDYVGTTFEFWWNHGIVSDDTYRRLKEACLHDSFIHPSPACDAATDVATA
EQGNIDMYSLYTPVCNIXSYDPCTERYSTAYYNRRDVQMALHANVTGAMNYTWATCSDT
INTHWHDA PRSMLPIYRELIAAGLRIWVFGSDTDAVVPLTATRYSIGALGLPTTTTSWYPWY
DDQEVGGWSQVYKGLTLVSVRGAGHEVPLHRPRQALVLFQYFLQGKPMPGQ

>d1cpy_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (*Saccharomyces cerevisiae*)}
KIKDPKILGIDPNVTQYTGYPDVEDEDKHFFFWTFESRNDPAKDPVILWLNGGPGCSSLTG
LFFALGPSSIGPDLKPIGNPYSWNSNATVIFLDQPVNVGFSYSGSSGVSNTVAAGKDVYNF
LELFFDQFPEYVNBKGQDFHAGASYAGHYIPVFASEILSHKDRNFNLTSVLIGNGLTDPLTQ
YNYEPMACGEGGEPVLPSEECSAMEDSLERCLGLIESCYDSQSVWSCVPATYCNNAQ
LAPYQRTGRNVYDIRKDCEGGNLCYPTLQDIDDYLNQDYVKEAVGAEVDHYESC�FDIN
RNFLFAGDWMKPYHTAVTDLLNQDLPILVYAGDKDFICNWLGNKAWTDVLPWKYDEEF
ASQKVRNWTASITDEVAGEVKSYPKHFTYLRVFNGGHMVPFDVPEALSMVNEWIHGGFS
L

>d1lac5_ c.69.1.5 (-) Serine carboxypeptidase II {Baker's yeast (*Saccharomyces cerevisiae*)},
kex1(delta)p}
LPSSEYKVAYELLPGLSEVPDPSNIPQMHAGHIPLRSEDADEQDSSDLEYFFWKFTNND
NGNVDRPLIWLNGGGPGCSSMDGALVESGPFRVNSDGKLYLNEGSWISKGDLLFIDQPTGT
GFSVEQNKDEGKIDKNKFDEDELDVTKHFMDFLENYFKIFPEDLTRKIILSGESYAGQYIPF
FANAILNHNKFSKIDGDTYDLKALLIGNGWIDPNTQSLSYLPFAMEKKLIDESNPNFKHLT

NAHENCQNLINSASTDEAAHFSYQECENILNLLLSYTRESSQKGTADCLNMYNFNLKDSY
PSCGMNWPKDISFVSKFFSTPGVIDSLHLDSDKIDHWKECTNSVGTKLSNPISKPSIHLLPG
LLESGIEIVLFNGDKDLICNNKGVLDTIDNLKWGGIKGFSDDAVSFDWIHKSKSTDDSEEF
GYVKYDRNLTFVSVYNASHMVPFDKSLVSRGIVDIYSNDVMIIDNNGKNVMITT

>d1ivya_ c.69.1.5 (A:) Human 'protective protein', HPP {Human (Homo sapiens)}

APDQDEIQRLPGLAKQPSFRQYSGYLKSSGSKHLHYWFVESQKDPENSPVVLWLNGGPG
CSSLDGLLTEHGPFLVQPDGVTLEYNPYSWNLIANVLYLESPAGVGFSYSDDKFYATNDTE
VAQSNFEALQDFFRLPEYKNNKLFLTGESYAGIYIPTLAVLVMQDPSMNLQGLAVGNGLS
SYEQNDNSLVYFAYYHGLLGNRLWSSLQTHCCSQNKCNFYDNKDLECVTNLQEVARIVG
NSGLNIYNLYAPCAGGVPSHFRYEKDTVVVQDLGNIFTRLPLKRMWHQALLRSGDKVRM
DPPCTNTTAASYLNNPYVRKALNIPEQLPQWDMCNFLVNLQYRRLYRSMNSQYLKLLSS
QKYQILLYNGDVDMACNFMGDEWFVDSL NQKMEVQRRPWLVKYGDSGEQIAGFVKEFS
HIAFLTIKGAGH MVPTDKPLAAFTMFSRFLNKQPY

>d1b6g_ c.69.1.8 (-) Haloalkane dehalogenase {Xanthobacter autotrophicus}

MVNAIRTPDQRFSNLDQYPFSPNYLDDLPGYPGLRAHYLDEGNSDAEDVFLCLHGEPTW
SYLYRKMI PVFAESGARVIAPDFFGFGKSDKPVDEEDYTTEFHRN FLLALIERLDLRNITLV
VQDWGGFLGLTLPADPSRFKRLIIMNACLMTDPVTQPAFSAFVTQPADGFTAWKYDLVT
PSDLRLDQFMKRWAPTLTEAEASAYAAPFPDTSYQAGVRKFPKMVAQRDQACIDISTE AIS
FWQNDWNGQTFMAIGMKDKLLGPDVMYPMKALINGCPEPLEIADAGHFVQEFGEQVAR
EALKHFAETE

>d1cv2a_ c.69.1.8 (A:) Haloalkane dehalogenase {Sphingomonas paucimobilis, UT26, LinB}

GAKPFGEKKFIEIKGRRMAYIDEGTGDPILFQHGNPTSSYLWRNIMPHCAGLGRLIACDLIG
MGDSDKLDPSGPERYAYAEHRDYLDALWEALDLGDRVVLVVDWGSALGFDWARRHRE
RVQGIAYMEAIAMPIEWADFPEQDRDLFQAFRSQAGEELVLQDNVFVEQVLPGLILRPLSE
AEMAAYREPFLAAGEARRPTLSWPRQIPIAGTPADVVAIARDYAGWLSESPKLFINAEPG
ALTTGRMRDFCARTWPNQTEITVAGAHFIQEDSPDEIGAAIAAFVRRRLPA

>d1ek1a2 c.69.1.11 (A:226-544) Mammalian epoxide hydrolase, C-terminal domain {Mouse (Mus musculus)}

LPVPCNPNDVSHGYVTVKPGIRLHFVEMGSGPALCLCHGFPESWFSWRYQIPALAQAGFR
VLAIDMKGYGDSSSPPEIEEYAMELLCKEMVTFLDKLGIPQAVFIGHDWAGVMVWNMAL
FYPERVRAVASLNTPFMPDPDVSPMKVIRSIPVFNYQLYFQEPGVAEAELEKNMSRTFKSF
FRASDETGFIAVHKATEIGGILVNTPEDPNLSKITTEEEIEFYIQQFKKTGFRGPLNWYRNTE
RNWKWSCKGLGRKILVPALMVTAEKDIVLRPEMSKNMEKWIPFLKRGHIEDCGHWTQIE
KPTEVNQILIKWLQTE

>d1ehya_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Agrobacterium radiobacter}

AIRRPEDFKHYEVQLPDVKIHYVREGAGPTLLLLHGWPGFWWWSKVIGPLAEHYDVIV
PDLRGFGDSEKPDNLDSKYSLDKAADDQAALLDALGIEKAYVVGHDFAAIVLHKFIRKY
SDRVIKAAIFDPIQPDFGPVYFGLGHVHESWYSQFHQLDMAVEVVGSSREVCKKYFKHFF
DHWSYRDELLTEEELEVHVDNCMKPDNIHGGFNYYRANIRPDAALWTDLDHTMSDLPV
TMIWGLGDTCPYAPLIEFVPKYYSNYTMETIEDCGHFLMVEKPEIAIDRIKTAFR

>d1qo7a_ c.69.1.11 (A:) Bacterial epoxide hydrolase {Aspergillus niger}

KAFKFPSSASISPNPFTVSIPDEQLDDLKTLVRLSKIAPPTYESLQADGRFGITSEWLTTMR
EKWLSEFDWRPFPEARLNSFPQFTTEIEGLTIHFAALF SEREDAVPIALLHGWPGSFVEFYPIIL

QLFREEYTPETLPFHLVPSLPGYTFSSGPPLDKDFGLMDNARVVDQLMKDLGFGSGYIIQ
GGDIGSFVGRLLGVGFDACKAVHLNLCAMRAPPEGPSIESLSAAEKEGIARMEKFMTDGL
AYAMEHSTRPSTIGHVLSSSPIALLAWIGEKYLQWVDKPLPSETILEMVSLYWLTESFPRAI
HTYRETTPTASAPNGATMLQKELYIHKPFGFSFFPKDLCVPVRSWIATTGNLVFFRDHAEG
GHFAALERPRELKTDLTAFVEQVW

>d1brt__ c.69.1.12 (-) Bromoperoxidase A2 {*Streptomyces aureofaciens*}

PFITVGQENSTSIDLYYEDHGTGQPPVLIHGFPLSGHSWERQSAALLDAGYRVITYDRRGF
GQSSQPTTGYYDFTFAADLNTVLETLDLQDAVLVGFSTGTGEVARYVSSYGTARIAKVAF
LASLEPFLKTDNDPDGAAPQEFFDGIVA AVKADRYAFYTGFFNDFYNLDENLGRITSEE
VRNSWNTAASGGFFAAAAAPTWTYDFRADIPRIDVPALILHGTGDRTLPIENTARVFHKA
LPSAEYVEVEGAPHGLLWTHAEVNTALLAFLAK

>d1a8q__ c.69.1.12 (-) Bromoperoxidase A1 {*Streptomyces aureofaciens*}

PICTTRDGVEIFYKDWGQGRPVVFIHGWPLNGDAWQDQLKAVVDAGYRGIAHRRGHG
HSTPVWDGYDFDTFADDLNDLLDLDLRDVTLVASHMGGGELARYVGRHGTGRLRS AVL
LSAIPPVMIKSDKNPDGVPDEVFDALKNGVLTERSQFWKDTAEGFFSANRPGNKVTQGNK
DAFWYMAAQTIIEGGVRCVDAFGYTDFTEDLKKFDIPTLVVHGDDQVVPIDATGRKSA
QIIPNAELKVYEGSSHGIA MVPGDKEKFNRLLEFLNK

>d1thta__ c.69.1.13 (A:) Myristoyl-ACP-specific thioesterase {*Vibrio harveyi*}

QCKTIAHVLRVNNQELHVWETPPKENVPFKNNTILIASGFARRMDHFAGLAEYLTNGF
HVFYRDSLHHVGLSSGSIDEFTMTTGKNSLCTVYHWLQTKGTQNI GLIAASLSARVAYEVI
SDLELSFLITAVGVNLRDTLEKALGFDYLSLPIDELPNDLDFEGHKL GSEVFVRDCFEHH
WDTLDSTLDKVANTSVPLIAFTANNDDWVKQEEVYDMLAHIRTGHCKLYSLLGSS HDLG
ENLVVLRNFYQSVTKAAIAMDGGSLEIDVDFIEPDFEQLTIATVNERRLKA EIENRTPEMA

>d1ei9a__ c.69.1.13 (A:) Palmitoyl protein thioesterase 1 {*Cow (Bos taurus)*}

DPPAPLPLVIWHGMGDSCCNPLSMGAIKKMVEKKIPGIHVLSLEIGKTLREDVENSFFLNV
NSQVTTVCQILAKDPKLQGGYNAMGFSQGGQFLRAVAQRCPSPPMVN LISVGGQH QGVF
GLPRCPGESSHICDFIRKTLNAGAYNKAIQERLVQAEYWH DPIREDIYRNHSIFLADINQER
GVNESYKKNLMALKKFVMVKFLNDTIVDPVDSEWFGFYRSGQAKETIPLQESTLYTQDR
LGLKAMDKAGQLVFLALEGDHLQLSEEWFYAH IIPFLE

>d1auoa__ c.69.1.14 (A:) Carboxylesterase {*Pseudomonas fluorescens*}

MTEPLILQPAKPADACVIWLHGLGADRYDFMPVAEALQESLLTTRFVLPQAPTRPVTINGG
YEMPSWYDIKAMSPARSISLEELEVS AKMVTDLIEAQKRTGIDASRIFLAGFSQGGAVVFH
TAFINWQGPLGGVIALSTYAPTFGDELELSASQQRIPALCLHGQYDDVVQ NAMGRSAFEH
LKSRGVTVTWQEYPMGHEVLPQEIH DIGAWLAARLG

>d1fj2a__ c.69.1.14 (A:) Acyl protein thioesterase 1 {*Human (Homo sapiens)*}

MDPEFMSTPLPAIVPAARKATAAVIFLHGLGDTGHGWAEAFAGIRSSH IKYICPHAPVRPVT
LNMNVAMPSPWFDIIGLSPDSQEDES GIKQAAENIKALIDQEVKNGIPSNRIILGGFSQGGAL
SLYTALTQKLAGVTALSCWLPLRASFPQGPIGGANRDISILQCHGDCDPLVPLMFGSLTV
EKLKTLVNPANVTFKTYEGMMHSSCQ QEMMDVKQFIDKLLPPI

>d1tca__ c.69.1.17 (-) Triacylglycerol lipase {*Yeast (Candida antarctica)*, form b}

LPSGSDPAFSQPKSVLDAGLTCQGASPSVSKPILLVPGTGTGPQS FDSNWIPLSTQLGYTP
CWISPPPFMLNDTQVNTEYMVNAITALYAGSGNNKLPVLTWSQGG LVAQWGLTFFPSIRS
KVDRLMAFAPDYKGTVLAGPLDALAVSAPSVWQQTTGSALT TALRNAGGLTQIVPTTNLY
SATDEIVQPQVSNSPLDSSYLFNGKNVQAQAVCGPLFVIDHAGSLTSQFSYVVGRSALRST

TGQARSADYGITDCNPLPANDLTPEQKVAAAALLAPAAAAIVAGPKQNCEPDLMPYARPF
AVGKRTCSGIVTP

>d3tgl__ c.69.1.17 (-) Triacylglycerol lipase {Rhizomucor miehei}

GIRAATSQEINELTYTTLSANSYCRTVIPGATWDCIHCDATEDLKIIKTWSTLIYDTNAMV
ARGDSEKTIYIVFRGSSSIRNWIADLTFVPVSYPVSGTKVHKGFLDSYGEVQNELVATVLD
QFKQYPSYKVAVTGHSLGGATVLLCALDLYQREEGLSSSNLFLYTQGGQPRVGDPAFANYV
VSTGIPYRRTVNERDIVPHLPPAAFGFLHAGEEYWITDNSPETVQVCTSDLETSDCSNSIVP
FTSVLDHLSYFGINTGLCT

>d1tia__ c.69.1.17 (-) Triacylglycerol lipase {Penicillium camembertii}

DVSTSELDQFEFWVQYAAASYEADYTAQVGDKLSCSKGNCPEVEATGATVSYDFSDSTI
TDTAGYIAVDHTNSAVVLAFRGSYSVRNWADATFVHTNPGLCDGCLAELGFWSWKLV
RDDIIKELKEVVAQNPNYELVVVGHSLGAAVATLAATDLRGKGYPYSAKLYAYASPRVGNA
ALAKYITAQGNFRFTHTNDPVPKLPLLSMGYVHVSPEYWITSPNNATVSTSDIKVIDGDV
SFDGNTGTGLPLLTDFEAHIWYFVQVDAGKG

>d1thg__ c.69.1.17 (-) Type-B carboxylesterase/lipase {Fungus (Geotrichum candidum),
ATCC 34614}

EAPTAVLNGNEVISGVLEGKVDTFKGIPFADPPLNDLRFKHPQPFTGSYQGLKANDFSAC
MQLDPGNSLTLLDKALGLAKVIPEEFRGPLYDMAKGTVMNEDCLYLNVRPAGTKPDA
KLPVMVWIYGGAFVYGSSAAYPGNSYVKESINMGQPVVVFSINYRTGPFGLGGDAITAE
GNTNAGLHDQRKGLEWVSDNIANFGGDPDKVMIFGESAGAMSVAHQLIAYGGDNTYNG
KKLFHSAILQSGGPLPYHDSSSVGPDISYNRFAQYAGCDTSASANDTLECLRSKSSSVLHD
AQNSYDLKDLFGLLPQFLGFGPRPDGNIIPDAAYELFRSGRYAKVPYISGNQEDEGTAFAP
VALNATTPHVKKWLQYIFYDASEASIDRVLSLYPQTL SVGSPFRTGILNALTPQFKRVAI
LSDMLFQSPRRVMLSATKDVNRWTYLSTHLHNLVPFLGTFHGNELIFQFNVNIGPANSYLR
YFISFANHDPNVGTNLLQWDQYTDEGKEMLEIHMTDNVMRTDDYRIEGISNFETDVNL
YG

>d1i6wa__ c.69.1.18 (A:) Lipase A {Bacillus subtilis}

HNPVVMVHGIGGASFNFAGIKSYLSVQGWSRDKLYAVDFWDKTGTNYNNGPVLSRFVQK
VLDETGAKKVDIVAHSMGGANTLYYIKNLDGGNKVANVVTLGGANRLTTGKALPGTDPN
QKILYTSIYSSADMIVMNYLSRLDGARNVQIHGVGHIGLlySSQVNSLIKEGLNGGGQNTN

>d4lipd__ c.69.1.18 (D:) Lipase {Burkholderia cepacia (formerly Pseudomonas cepacia)}

DNYAATRYPIILVHGLTGTDKYAGVLEYWYGIQEDLQQRGATVYVANLSGFQSDDGPNR
GEQLLAYVKTVLAATGATKVNLVGHSQGGLTSRYVAAVAPDLVASVTTIGTPHRGSEFADF
VQGVLAYDPTGLSSTVIAAFVNVFGILTSSSNNTNQDALAALKTLTTAQAATYNQNYPSA
GLGAPGSCQTGAPTETVGGNTHLLYSWAGTAIQTISVFGVTGATDTSTIPLVDPANALDPS
TLALFGTGTVMVNRGSGQNDGVVSKCSALYGQVLSTSYKWNHLDEINQLLGVRGANAE
DPVAVIRTHANRLKLAGV

>d1ex9a__ c.69.1.18 (A:) Lipase {Pseudomonas aeruginosa}

STYTQTKYPIVLAHGMLGFDNILGVDYWFGIPSALRRDGAQVYVTEVSQLDTSEVRGEQL
LQQVEEIVALSQPKVNLIGHSHGGPTIRYVAAVRPDLIASATSVGAPHKGSdTADFLRQIP
PGSAGEAVLSGLVNSL GALISFLSSGSTGTQNSLGSLESLNSEGAARFNAKYPQGIPTSACG
EGAYKVNGVSYYSWSGSSPLTNFLDPSDAFLGASSLTFKNGTANDGLVGTCSHLGMVIR
DNYRMNHLDEVNQVFGLTSLFETSPVSVYRQHANRLKNASL

>d2masa__ c.70.1.1 (A:) Inosine-uridine nucleoside N-ribohydrolase, IU-NH {Crithidia fasciculata}

AKKIILDCDPGLDDAVAILLAHGNPEIELLAITTVVGNQTLAKVTRNAQLVADIAGITGVPI
AAGCDKPLVRKIMTAGHHGESGMGTVAYPEAFKKNKVDERHAVNLIIDLVMSEPKTITLV
PTGGLTNIAAARLEPRIVDRVKEVVLMMGGGYHEGNATSVAEFNIIDPEAAHIVFNESWQ
VTMVGLDLTHQALATPPILQRVKEVDTNPARFMLEIMDYTKIYQSNRYMAAAAVHDP
AVAYVIDPSVMTTERVPVDIELTGKLTGMTVADFRNPRPEHCHTQVAVKLDFEKFVWGLVL
DALERIGDP

>d1hoza_ c.70.1.1 (A:) Inosine-adenosine-guanosine preferring nucleoside hydrolase
{Trypanosoma vivax}

GSAKNVVLDDHGNLDDFVAMVLLASNTEKVRLLIGALCTDADCFVENGFNVTGKIMCLM
HNNMNLPLFPIGKSAATAVNPFKEWRCLAKNMDDMPILNIPENVELWDLKAENEKEYEG
QQLLADLMNSEEKVTICVTGPLSNVAWCIDKYGEKFTSKVEECVIMGGAVDVRGNVFLP
STDGTAEWNIYWDPAKTVFGCPGLRRIMFSLDSTNTVPVRSPYVQRFGEQTNFLLSILV
GTMWAMCTHCELLRDGDGYAWDALTAAYVVDQKVANVDPVPIDVVVDKQPNEGATV
RTDAENYPLTFVARNPEAEFFLDMLLSARAC

>d1ra9_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Escherichia coli}

MISLIAALAVDRVIGMENAMPWNLADLAWFKRNTLDKPVIMGRHTWESIGRPLPGRKNI
ILSSQPGTDDRVTWVKSVDIAACGDVPEIMVIGGGGRVYEQLPKAQKLYLTHIDAEVEG
DTHFPDYEPDDWESVFSEFHDADAQNSHSYCFEILERR

>d3dfr_ c.71.1.1 (-) Dihydrofolate reductase, prokaryotic type {Lactobacillus casei}

TAFLWAQNRNGLIGKDGHLPPWHLDDLHYFRAQTVGKIMVVGRRTYESFPKRPLPERTN
VVLTHQEDYQAQGAVVVDVAADFAYAKQHLDELVIAGGAQIFTAFKDDVDTLVTRL
AGSFEQDGTKMIPLNWDDFTKVSSRTVEDTNPALHTHTYEVWQKKA

>d1df7a_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Mycobacterium tuberculosis}

MVGLIWAQATSGVIGRGDIPWRLPEDQAHFREITMGHTIVMGRRTWDSLPAKVRPLPGR
RNVVLSRQADFMASGAEVVGSLEEALTSPEWVIGGGQVYALALPYATRCEVTEVDIGLP
REAGDALAPVLDETWRGETGEWRFSRSLRYRLYSYHRS

>d1d1ga_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Thermotoga maritima}

AKVIFVLAMDVSGKIASVESWSSFEDRKNFRKITTEIGNVVMGRITFEEIGRPLPERLNVV
LTRRPKTSNNPSLVFFNGSPADVVKFLEGKGYERVAVIGGKTVFTEFLREKLVDLFTVTEP
YVFGKGIPFFDEFEGYFPLKLLERMRLNERGTLFLKYSVE

>d1vdra_ c.71.1.1 (A:) Dihydrofolate reductase, prokaryotic type {Haloferax volcanii}

ELVSVAALAENRVIGRDGELPWPSIPADKKQYRSRIADDPVVLGRTTFESMRDDLPGSAQI
VMSRSERSFSVDTAHRAASVEEAVDIAASLDAETAYVIGGAAIYALFQPHLDRMVLSRVPG
EYEGDTYYPEWDAAEWELDAETDHEGFTLQEWVRS

>d8dfr_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Chicken (Gallus gallus)}

VRSLNSIVAVCQNMIGIGKDGNLPPWPLRNEYKYFQRMTSTSHVEGKQNAVIMGKKTWFS
IPEKNRPLKDRINIVLSRELKEAPKGAHYLSKSLDDALALLDSPELKSKVDMVWVVGTA
YKAAMEKPINHRLFVTRILHEFESDTFFPEIDYKDFKLLTEYPGVPADIQEEDGIQYKFEVY
QKSV

>d1dyr_ c.71.1.1 (-) Dihydrofolate reductases, eukaryotic type {Fungus (Pneumocystis carinii)}

NQKSLTLIVALTTSYGIGRSNSLPWKLKKEISYFKRVTSFVPTFDSFESMNVVLMGRKTW
ESIPLQFRPLKGRINVVITRNESSLGNGIHSKSLDHALELLYRTYGSESSVQINRIFVIGG
AQLYKAAMDHPKLDRIATIIYKDIHCDVFFPLKFRDKEWSSVWKKKEHSDLESWVGTK
VPHGKINEDGFDYEFEMWTRDL

>d1aoea_ c.71.1.1 (A:) Dihydrofolate reductases, eukaryotic type {Yeast (Candida albicans)}
MLKPNVAIIVAALKPALGIGYKGKMPWRLRKEIRYFKDVTTRTTKPNTRNAVIMGRKTWE
SIPQKFRPLPDRLNIILSRSYENEIIDDNIHASSIESSLNLVSDVERVFIIGGAEIYNELINNSLV
SHLLITEIEHPSPEIEMDTFLKFPLESWTKQPKSELQKFVGDTVLEDDIKEGDFTYNYTLW
TRK

>d1ekqa_ c.72.1.2 (A:) Hydroxyethylthiazole kinase (THZ kinase, ThiK) {Bacillus subtilis}
MDAQSAAKCLTAVRRHSPLVHSITNNVVNTNFTANGLLALGASPMAYAKEEVADMAKIA
GALVLNIGTLSKESVEAMIIAGKSANEHGVPVILDPVGAGATPFRTESARDIIREVRLAAIR
GNAAEIAHTVGVTDWLIKGV DAGEGGGDIIRLAQQAAQKLNTVIAITGEVDVIADTSHVY
TLHNGHKLLTKVTGAGCLLTSVVGAFCAVEENPLFAAIAAIISSYGVAQAQLAAQQQTADKGP
GSFQIELLNKLSTVTEQDVQEWATIERV

>d1jxha_ c.72.1.2 (A:) 4-amino-5-hydroxymethyl-2-methylpyrimidine phosphate kinase
(HMP-phosphate kinase, ThiD) {Salmonella typhimurium}
MQRINALTIAGTDPSSGAGIQADLKTFSALGAYGCSVITALVAENTCGVQSVYRIEPDFVA
AQLDSVFSVDVRIDTTKIGMLAETDIVEAVAERLQRHHVRNVVLDTVMLAKSGDPLLSPSAI
ETLRVRLLPQVSLITPNLPEAAALLDAPHARTEQEMLAQGRALLAMGCEAVLMKGGHLE
DAQSPDWLFTREGEQRFSAAPRVNTKNTHGTGCTLSAALAALRPRHRSWGETVNEAKAW
LSAALAQADTLEVKGKIGPVHHFHAWW

>d1rkd_ c.72.1.1 (-) Ribokinase {Escherichia coli}
AGSLVVLGSINADHILNLQSFPPTGETVTGNHYQVAFGGKGANQAVAAGRSGANIAFIAC
GDDSIGESVRQQLATDNIDITPVSVIKGESTGVALIFVNGEGENVIGIHAGANAALSPALVE
AQRERIANASALLMQLESPLESVMAAAKIAHQNKTIVALNPAPARELPDELLALVDIITPNE
TEAEKLTGIRVENDEDAKAAQVLHEKGIRTVLITLGSRGVWASVNGEGQRPVPGFRVQAV
DTIAAGDTFNGALITALLEEKPLPEAIRFAHAAAAIAVTRKGAQPSVPWREEIDAFDRQR

>d1bx4a_ c.72.1.1 (A:) Adenosine kinase {Human (Homo sapiens)}
VRENILFGMGNPLLDISAVVDKDFLDKYS LKPNQILAEDKHKELFDELVKKFKVEYHAG
GSTQNSIKVAQWMIQQPHKAATFFGCIGIDKFGEILKRKAAEAHVDAHYEYQNEQPTGTC
AACITGDNRS LIANLAAANCYKKEKHL DLEKNWMLVEKARVCYIAGFFLT VSPESVLKVA
HHASENNRIFTLNLSAPFISQFYKESLMKVMPYVDILFGNETEAATFAREQGFETKDIKEIA
KKTQALPKMNSKRQRIVIFTQGRDDTIMATESEVTAFVLDQDQKEIIDTNGAGDAFVGGF
LSQLVSDKPLTECIRAGHYAASIIIRRTGCTFPEKPDFH

>d1dgya_ c.72.1.1 (A:) Adenosine kinase {Toxoplasma gondii}
GPMRVFAIGNPILDVAEVPSSFLDEFFLKRGDATLATPEQMRIYSTLDQFNPTSLPGGSAL
NSVRVVQKLLRKPGSAGYMGAI GDDPRGQVLKELCDKEGLATRFMVAPGQSTGTCAVLI
NEKERTLCTHLGACGSFRIPENWTTFASGALIFYATAYTLTATPKNALEVAGYAHGIPNAIFT
LNLSAPFCVELYKDAMQSLLLHTNILFGNEEEFAHLAKVHNLVAAEKVALSVANKEHAVE
VCTGALRLLTAGQNTGATKLVMTRGHNPVIAAEQTADGTVVVHEVGVPVVA AEKIVDT
NGAGDAFVGGFLYGLSQGKTVKQCIMCGNACAQDVIQHVGFSLSF

>d2uaga3 c.72.2.1 (A:94-297) UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase MurD {Escherichia coli}
DIELFCREAAPIVAITGSNGKSTVTTLVGEMAKAAGVNVGVGGNIGLPALMLLDDECEL
YVLELSSFQLETTSSLQAVAATILNVTEDHMDRYPFGLQQYRAAKLRIYENAKVCVVNAD
DALTMPIRGADERCVSFGVNMGDYHLNHQQGETWLRVKGEKVLNVKEMKLSGQHNYT
NALAALALADAAGLPRASSLKALTTFT

>d1e8ca3 c.72.2.1 (A:88-337) UDP-N-acetylmuramyl tripeptide synthetase MurE {Escherichia coli}

QLNERLSALAGRFYHEPSDNLRLVGVTGTNGKTTTTQLLAQWSQLLGEISAVMGTVGNG
LLGKVIPTENTTGSADVQHELAGLVDQGATFCAMEVSSHGLVQHRVAALKFAASVFTNL
SRDHLDYHGDMEHYEAAKWLLYSEHHCGQAIINADDEVGRRWLAKLPDAVAVSMEDHI
NPNCHGRWLKATEVNYHDSGATIRFSSSWGDEIESHLMGAFNVSNLLLALATLLALGYP
LADLLKTAARLQP

>d1gg4a4 c.72.2.1 (A:82-312) UDP-murNac-tripeptide D-alanyl-D-alanine-adding enzyme MurF {Escherichia coli}

DTRLAFGELAAWVRQQVPARVVALTGSSGKTSVKEMTAAILSQCGNTLYTAGNLNNDIGV
PMTLLRLTPEDYAVIELGANHQGEIAWTVSLTRPEAALVNNLAAHLEGFGSLAGVAKA
KGEIFSGLPENGIAIMNADNNDWLNWQSVIGSRKVWRFSPNAANSDFATNIHVTSHGTE
FTLQTPGSDVLLPLPGRHNIANALAAAALSMSVGATLDAIKAGLANLKA

>d1ed8a_ c.76.1.1 (A:) Alkaline phosphatase {Escherichia coli}

TPEMPVLENRAAQGDITAPGGARRLTGDQTAALRDSLSDKPAKNIILLIGDGMGDSEITAA
RNYAEGAGGFFKGIDALPLTGQYTHYALNKKTKGPDYVTDASAATAWSTGVKTYNGAL
GVDIHEKDHP TILEMAKAAGLATGNVSTAELQDATPAALVAHVTSRKCYGPSATSEKCPG
NALEKGGKGSITEQLLNARADVTLGGGAKTFAETATAGEWQGKTLREQAQARGYQLVSD
AASLNSVTEANQQKPLLGLFADGNMPVRWLGPATYHGNIDKPAVTCTPNPQRNDSVPTL
AQMTDKAIELLSKNEKGFFLQVEGASIDKQDHAANPCGQIGETVDLDEAVQRALEFAKKE
GNTLVIVTADHAHASQIVAPDTKAPGLTQALNTKDGAVMVMMSYGNSEEDSQEHTGSQRLRI
AAYGPHAANVVGLTDQTDLFYTMKAALGLK

>d1ew2a_ c.76.1.1 (A:) Alkaline phosphatase {Human (Homo sapiens)}

IIPVEENPDFWNREAAEALGAACKLQPAQTAAKNLIIFLDGDMGVSTVTAARILKGQKK
DKLGPEIPLAMDRFPYVALSKTYNVDKHVPDSGATATAYLCGVKGNFQTIGLSAAARFNQ
CNTTRGNEVISVMNRAKKAGKSVGVTTRVQHASPAGTYAHTVNRNWYSDADVPASA
RQEGCQDIATQLISNMDIDVILGGGRKYMFRMGTPDPEYPDDYSQGGTRLDGKNLVQEW
LAKRQGARYVWNRTELMQASLDPSVTHLMGLFEPGDMKYEIHRDSTLDPSLMEMTEAA
LRLLSRNPRGFFLFVEGGRIDHGHESRAYRALTETIMFDDAIERAGQLTSEEDTSLSVTAD
HSHVFSFGGYPLRGSSIFGLAPGKARDRKAYTVLLYGNPGYVLKDGARPDVTESESGSP
EYRQQSAVPLDEETHAGEDVAVFARGPQAHLVHGVQEQTFAHVMAFAACLEPYTACDL
APP

>d1auk__ c.76.1.2 (-) Arylsulfatase A {Human (Homo sapiens)}

RPPNIVLIFADDLGYGDLGCYGHPSSTTPNLDQLAAGGLRFTDFYVPVSLCTPSRAALLTG
RLPVRMGMYPGVLVPSSRGGLPLEEVTVAEVLAAARGYLTGMAGKWHLGVGPEGAFLPP
HQGFHRFLGIPYSHDQGPCQNLTCFPATPCDGGCDQGLVPIPLLANSVEAQPPWLPGLE
ARYMAFAHDLMAQAQRQDRPFPLYASHHHTYPQFSGQSFAERSGRGPFGLDLMELDAA
VGTLMTAIGDLGLEETLVIFTADNGPETMRMSRGGCSGLLRGCKGTTYEAGGVREPALAF
WPGHIAPGVTHELASSDLLPTLAALAGAPLPNVTLDFGLSPLLLGTGKSPRQSLFFYPS
YPDEVGRGVFAVRTGKYKAHFFTQGSASHTTADPACHASSSLTAHEPPLLYDLSKDPGENY
NLLGGVAGATPEVLQALKQLQLLKAQLDAAVTFGPSQVARGEDPALQICCHPGCTPRPAC
CHCP

>d1fsu__ c.76.1.2 (-) Arylsulfatase B (4-sulfatase) {Human (Homo sapiens)}

SRPPHLVFLADDLGWNDVGFHGSRIPTPHLDALAAGGVLLDNYYTQPLXTPSRSQLLTG

RYQIRTGLQHIIWPCQPSCVPLDEKLLPQLLKEAGYTTHMVGKWHLGMYRKECLPTRR
GFDTYFGYLLGSEDYYSHERCTLIDALNVTRCALDFRDGEEVATGYKNMYSTNIFTKRAI
ALITNHPPEKPLFLYLALQSVHEPLQVPEEYLKPYDFIQDKNRHHYAGMVSLMDEAVGNV
TAALKSSGLWNNTVFIFSTDNGGQTLAGGNNWPLRGRKWSLWEGGVRGVGFVASPLLK
QKGVKNRELIHISDWLPTLVKLARGHTNGTKPLDGFVDVWKTISEGSPSPRIELLHNIDPNF
VDSSPCPRNSMAPAKDDSSLPEYSAFNSTSVHAAIRHGNWKLLTGYPGCGYWFPPPSQYNV
SEIPSSDPPTKTLWLFDIDRDPEERHDLRSREYPHIVTKLLSRLQFYHKHSVPVYFPAQDPRC
DPKATGVWGPWM

>d1hdha_ c.76.1.2 (A:) Arylsulfatase B (4-sulfatase) {Pseudomonas aeruginosa}

KRPNFLVIVADDLGFSDIGAFGGEIATPNLDALAIAGLRLTDFHTASTCSPTRSMLLTGTDH
HIAGIGTMAEALTPELEGKPGYEGHLNERVVALPELLREAGYQTLMAGKWHLGKPEQTP
HARGFERSFSLLPGAANHYGFEPYDESTPRILKGTPALYVEDERYLDTLPEGFYSSDAFG
DKLLQYLKERDQSRPFFAYLPFSAPHWPLQAPREIVEKYRGRYDAGPEALRQERLARLKE
LGLVEADVEAHPVLALTREWEALEDDEERAKSARAMEVYAAMVERMDWNIGRVVDYLR
RQGELDNTFVLFMSDNGAEGALLEAFPKFGPDLLGFLDRHYDNSLENIGRANSYVWYGP
RWAQAATAPSRLYKAFTTQGGIRVPALVRYPRLSRQGAISHAFATVMDVPTLLDLAGVRH
PGKRWRGREIAEPRGRSWLWLSGETEAAHDENTVTGWELFGMRAIRQGDWKAVYLPA
PVGPATWQLYDLARDPGEIHDLDLADSQPGKLAELIEHWKRYVSETGVV

>d1e4bp_ c.74.1.1 (P:) L-fucose-1-phosphate aldolase {Escherichia coli}

MERNKLARQIIDTCLEMTRLGLNQGTAGQVSVRYQDGMLITPTGIPYEKLTESHIVFIDGN
GKHEEGKLPSSSEWRFHMAAYQSRPDANAVVHNHVAHCTAVSILNRSIPAIHYMIAAAGGN
SIPCAPYATFGTRELSEHVALALKNRKATLLQHHGLIACEVNLEKALWLAHEVEVLAQLYL
TTLAITDPVPVLSDEEIAVVLEKF

>d1jdia_ c.74.1.1 (A:) L-ribulose-5-phosphate 4-epimerase {Escherichia coli}

MLEDLKRQVLEANLALPKHNLVTLTWGNVSAVDRERGVFVIKPSGVDYSIMTADDMVVV
SIETGEVVEGAKKPSSDTPTHRLLYQAFPSIGGIVHTHSRHATIWAQAGQSIPATGTTHADY
FYGTIPCTRKMTDAEINGEYEWETGNVIVETFEKQGIDAAQMPGVLVHSHGPFPAWGKNA
EDAVHNAIVLEEYAYMGIFCRQLAPQLPDMQQTLLNKHYLRKH

>d1cnza_ c.77.1.1 (A:) 3-isopropylmalate dehydrogenase, IPMDH {Salmonella typhimurium}

MSKNYHIAVLPGDGIGPEVMAQALKVMDAVRSRFDMRITTSHYDVGGIAIDNHGHPLPK
ATVEGCEQADAILFGSVGGPKWENLPPESQPERGALLPLRKHFKLFSNLRPAKLYQGLEAF
CPLRADIAANGFDILCVRELTGGIYFGQPKGREGSGQYEKAFDTEVYHRFEIERIARIAFES
ARKRRRKVTSIDKANVLQSSILWREIVNDVAKTYPDVELAHMYIDNATMQLIKDPSQFDV
LLCSNLFGDILSDECAMITGSMGMLPSASLNEQGFGLYEPAGGSAPDIAGKNIANPIAQILS
LALLRLYSLDANDAATAIEQAINRALEEGVRTGDLARGAAVSTDEMGDIIARYVAEGV

>d1hqs_ c.77.1.1 (A:) Isocitrate dehydrogenase, ICDH {Bacillus subtilis}

MAQGEKITVSNGLNVPNNPIIPFIEGDGTGPDWNAASKVLEAAVEKAYKGEKKITWKE
VYAGEKAYNKTGEWLPAETLDVIREYFIAIKGPLTTPVGGGIRSLNVALRQELDLFVCLRP
VRYFTGVPSVPKRPEDTDMVIFRENTEDIYAGIEYAKGSEEVQKLISFLQNELNVNKIRFPE
TSGIGIKPVSEEGTSRLVRAAIDYAEHGRKSVTLVHKGNIMKFTEGAFKNWGYELAEKEY
GDKVFTWAQYDRIAEQKDAANKAQSEAEAAGKIIKDSIADIFLQQILTRPNEFDVVAT
MNLNGDYISDALAAQVGGIGIAPANINYETGHAIFEATHGTAPKYAGLDKVNPSVILSG
VLLLEHLGWNEAADLVIKSMEKTIASKVVTYDFARLMDGATEVKCSEFGEELIKNMD

>d1ekxa1 c.78.1.1 (A:1-150) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}
 ANPLYQKHISINDLSRDDNLVLATAAKLKANPQPELLKHKVIASCFEASTRTRLSFETS
 MHRLGASVVGFSANTSLSGKKGETLADTISVISTYVDAIVMRHPQEGAARLATEFSGNV
 PVLNAGDGSNQHPTQTLLDLFTIQETQG

>d1ekxa2 c.78.1.1 (A:151-310) Aspartate carbamoyltransferase catalytic subunit {Escherichia coli}
 RLDNLHVAMVGDLYGRTVHSLTQALAKFDGNRFYFIAPDALAMPQYILDMLDEKGIW
 SLHSSIEEVMAEVDILYMTRVQKERLDPSEYANVKAQFVLRASDLHNAKANMKVLHPLP
 RVDEIATDVKTPHAWYFQQAGNGIFARQALLALVLNRDLVL

>d2at2a2 c.78.1.1 (A:145-295) Aspartate carbamoyltransferase catalytic subunit {Bacillus subtilis}
 FKGLTVSIHGDIKHSRVARNAEVLTRLGARVLFSGPSEWQDEENTFGTYVSMDEAVESSD
 VVMLLRIQNERHQSAVSQEGYLNKYGLTVERAERMKRHAIIIMHPAPVNRGVEIDDSLVS
 EKSRIFFKQMKNGVFIRMAVIQCALQTNVVR

>d1dxha2 c.78.1.1 (A:151-335) Ornithine transcarbamoylase {Pseudomonas aeruginosa}
 KPLHDISYAYLGDARNNMGNSLLIGAKLGMDVRIAAPKALWPHDEFVAQCKKFAEESG
 AKLTLTEDPKEAVKGVDVHTDVWVSMGEPVEAWGERIKELLPYQVNMEIMKATGNPRA
 KFMHCLPAFHNSSETKVKGQIAEQYPNLANGIEVTEDVFESPYNIAFEQAENRMHTIKAILV
 STLADI

>d1otha1 c.78.1.1 (A:34-184) Ornithine transcarbamoylase {Human (Homo sapiens)}
 KVQLKGRDLLTLKNFTGEEIKYMLWLSADLKFRKQKGEYLPLLQGKSLGMIFEKRSTRT
 RLSTETGFALLGGHPCFLTQDIHLGVNESLTDARVLSSMADAVLARVYKQSDLDTLAKE
 ASIPIINGLSLDYHPIQILADYTLTQEHYS

>d1otha2 c.78.1.1 (A:185-354) Ornithine transcarbamoylase {Human (Homo sapiens)}
 SLKGLTSLWIGDGNLHLSIMMSAAKFGMHLQAATPKGYEPDASVTKLAEQYAKENGTK
 LLLTNDPLEAAHGGNVLTDTWISMGREEEKKKRLQAFQGYQVTMKTAKVAASDWTFLH
 CLPRKPEEVDDEVFYSRSLVFPEAENRKWTIMAVMVSLLDYSPQLQKPKF

>d1b74a1 c.78.2.1 (A:1-105) Glutamate racemase {Aquifex pyrophilus}
 MKIGIFDSGVGGLTVLKAIRNRYRKVDIVYLGDTARVPYGIRSKDTIIRYSLECAGFLKDKG
 VDIIIVACNTASAYALERLKKENVPVFGVIEPGVKEALKKSR

>d1b74a2 c.78.2.1 (A:106-252) Glutamate racemase {Aquifex pyrophilus}
 NKKIGVIGTPATVKSGAYQRKLEEGADVFAKACPLFAPLAEEGLLEGEITRKVVEHYLKE
 FKKGIDTLILGCTHYPLLKKEIKKFLGDAEVVDSSEALSLSLHNFIKDDGSSSLELFFTDLSP
 NLQFLIKLILGRDYPVKLAEGVF

>d1qopb_ c.79.1.1 (B:) Tryptophan synthase, beta-subunit {Salmonella typhimurium}
 TTLNPFYGFEGGMYVPQILMPALNQLEEFVSAQKDPEFQAQFADLLKNYAGRPTALTK
 CQNITAGTRTTLYLKREDLLHGGAHKTNQVLGQALLAKRMGKSEIIAETGAGQHGVASAL
 ASALLGLKCRIYMGAKDVERQSPNVFRMLMGAEVIPVHSGSATLKDACNEALRDWSGS
 YETAHYMLGTAAGPHPYPTIVREFQRMIGEETKAQILDKEGRLPDAVIACVGGGSNAIGM
 FADFINDTSVGLIGVEPGGHGIETGEHGAPLKHGRVGIYFGMKAPMMQTADGQIEESYSIS
 AGLDFPSVGPQHAYLNSIGRADYVSITDDEALEAFKTLRHEGIIPALESSHALAHALKMM
 REQPEKEQLLVNLSGRGDKDIFTVHDIL

>d1tdj_1 c.79.1.1 (5-335) Allosteric threonine deaminase N-terminal domain {Escherichia coli}

QPLSGAPEGAEYLRAVLRAPVYEEAAQVTPLQKMEKLSSRLDNVILVKREDRQPVHSFKLR
GAYAMMAGLTEEQKAHGVITASAGNHAQGVAFSSARLGVKALIVMPTATADIKVDAVRG
FGGEVLLHGANFDEAKAKAIELSQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHLDR
VFVPVGGGGLAAGVAVLIKQLMPQIKVIAVEAEDSACLKAALDAGHPVDLPRVGLFAEGV
AVKRIGDETFRLCQEYLDIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIAL
HNIRGERLAHILSGANVNFHGLRYVSERCELGE

>d1e5xa_ c.79.1.1 (A:) Threonine synthase {Mouse-ear cress (*Arabidopsis thaliana*)}
IETAVKPPHRTEDNIRDEARRNRSNAVNPFSAKYVPFNAAPGSTESYSLDEIVYRSRSGGLL
DVEHDMEALKRFDGAYWRDLFDSRVGKSTWPYGSVWSKKEWVLPEIDDDDIVSAFEG
NSNLFWAERFGKQFLGMNDLWVKHCGISHTGSFKDLGMTVLVSQVNRLRKMGRPVG
GCASTGDTSAALSAYCASAGIPSIVFLPANKISMAQLVQPIANGAFVLSIDTDFDGCMLKIR
EITAELPIYLANSLNSLRLEGQKTAAIEILQQFDWQVPDWVIVPGNLTGNIYAFYKGFKMC
QELGLVDRIPRMVCAQAANANPLYLHYKSGWKDFKPMTASTTFASAIQIDPVSIDRAVY
ALKKCNIGIVEEATEEELMDAMAQADSTGMFICPHTGVALTALFKLRNQGVIAPTDRTVVV
STAHGLKFTQSKIDYHSNAIPDMACRFSNPPVDVKADFGAVMDVLKSYLGSNTLTS

>d1f2da_ c.79.1.1 (A:) 1-aminocyclopropane-1-carboxylate deaminase {Yeast (*Hansenula saturnus*)}

AGVAKFAKYPLTFGPSPISNLNRLSQHLGSKVNVYAKREDCNSGLAFGGNKLRLKLEYIVPD
IVEGDYTHLVSIGGRQSNQTRMVAALAAKLGGKCVLIQEDWVPIPEAEKDVYNRVGNIEL
SRIMGADVRIEDGFDIGMRKSFANALQELEDAGHKPYPIPAGCSEHKYGGGLGFVGFAD
VINQEVELGIKFDKIVVCCVTGSTTAGILAGMAQYGRQDDVIAIDASFTSEKTKEQTLRIA
NNTAKLIGVEHEFKDFTLDTRFAYPCYGVNNEGTTIEAIRCAEQEGVLTDPVYEGKSMQGL
IALIKEDYFKPGANVLYVHLGGAPALSAYSSFFPTKTA

>d1jbqa_ c.79.1.1 (A:) Cystathionine beta-synthase {Human (*Homo sapiens*)}

WIRPDAPSRCWQLGRPASESPHHHTAPAKSPKILPDILKKIGDTPMVRINKIGKKFGLKCE
LLAKCEFFNAGGSVKDRISLRMIEDAERDGTLPKPGDTIIEPTSGNTGIGLALAAVRGYRCI
IVMPEKMSSEKVDVLRALGAEIVRTPTNARFDSPEHSVGVAVRLKNEIPNSHILDQYRNAS
NPLAHYDTTADAILQQCDGKLDMLVASVGTGGTITGIARKLKEKCPGCRIIGVDPEGSILAE
PEELNQTEQTTYEVEGIGYDFIPTVLDRTVVDKWFKSNDEEAFTFARMLIAQEGLLCGGSA
GSTVAVAVKAAQELQEGQRCVVILPDSVRNYMTKFLSDRWMLQKGF

>d1iata_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {Human (*Homo sapiens*)}

AALTRDPQFQKLQQWYREHRSELNLRRLFDANKDRFNHFSLTNTNHHILVDYSKNLVT
EDVMRMLVDLAKSRGVEAARERMFNGEKINYTEGRAVLHVALNRNNTPIVDGKDVMP
EVNKVLDKMKSFQQRVRSQDWKGYTGKTITDVINIGIGGSDLGPLMVTEALKPYSSGGPR
VWYVSNIDGTHIAKTLAQLNPESLFIASKTFTTQETITNAETAKEWFLQAAKDPSAVAKH
FVALSTNTTKVKEFGIDPQNMFEFWDWVGGRYSLSAIGLSIALHVGFDNFEQLLSGAH
WMDQHFRTPLEKNAPVLLALLGIWYINCFGCETHAMLPYDQYLHRFAAYFQQGDMESN
GKYITKSGTRVDHQTGPVWGEPTNGQHAFYQLIHQGTKMIPCDFLIPVQTQHPKGLH
HKILLANFLAQTEALMRGKSTEEARKELQAAGKSPEDLERLLPHKVFEGNRPTNSIVFTKL
TPFMLGALVAMYEHKIFVQGIIWDINSFDQWGVELGKQLAKKIEPELDGSAQVTSHDAST
NGLINFIKQQREARV

>d1c7qa_ c.80.1.2 (A:) Phosphoglucose isomerase, PGI {*Bacillus stearothermophilus*}
AISFDYSNALPFMQENELDYLFSEFVKAAHHMLHERKGPSSDFLGWVDWPIRYDKNEFSRI
KQAAERIRNHSDALVVIGIGGSYLGARAAIEALSHTFHNQMNDTTQIYFAGQNISSTYISHL

LDVLEGKDLINVISKSGTTTEPAIAFRIFRDYMEKKYGKEEARKRIYVTTDRTKGALKKL
ADQEGYETFVIPDNIGGRYSVLTAAGLLPIAVAGLNIDRMMEGAASAYHKYNNPDLLTNES
YQYAAVRNILYRKGAIELLVNYEPSLHYVSEWWKQLFGESEGKDQKGLFPASVDFTTDL
HSMGQYVQEGRRNIETVLHVKKPQIELTIQEDPENIDGLNFLAGKTLDEVNKKAFQGT
LAHVDGGVPNLIVELDEMNEYTFGEMVYFFEKACGISGHLLGVNPFDPQPGVEAYKKNMF
ALLGKPGFEDEKAALMKRL

>d1aa6_2 c.81.1.1 (1-564) Formate dehydrogenase H {Escherichia coli}

MKKVVTVCPYCASGCKINLVVDNGKIVRAEAAQGKTNQGTLCCLKGYGWDFINDTQILT
PRLKTPMIRQRGGKLEPVSWDEALNYVAERLSAIEKEYGPDAIQTGSSRGTGNETNYV
MQKFARAVIGTNNVDCCARVCHGPSVAGLHQSVGNAGMSNAINEIDNTDLVVFVGYNPA
DSHPIVANHVINAKRNGAKIIVCDPRKIETARIADMHIALKNGSNIALLNAMGHVIEEEENLY
DKAFVASRTEGFEEYRKIVEGYTPESVEDITGVSASEIRQAARMYAQAKSAAILWGMGVT
QFYQGVETVRSLSLAMLGTNLGKPHAGVNPVRGQNNVQGACDMGALPDTPGYQYV
KDPANREKFAKAWGVESLPAHTGYRISELPHRAAHGEVRAAYIMGEDPLQTDALSARV
AFEDLELVIVQDIFMTKTASAADVILPSTSWGEHEGVFTAADRGRFQRFFKAVERPKWDLKT
DWQIIEIATRMGYPMHYNNNTQEIWDELRLHCPDFYGATYEKMGELGFIQWPCRDTSDA
DQGTSYLFKEKFDTPNGLAQFFTCDWVA

>d1tmo_2 c.81.1.1 (5-631) Trimethylamine N-oxide reductase {Shewanella massilia}

NEDEWLTTGSHFGAFKMKRKNGVIAEVKPFDLDDKYPTDMINGIRGMVYNPSRVRYPMVR
LDLFLKGHKSNTHQRGDFRFRVVTWDKALTLFKHSLDEVQTQYGPSGLHAGQTGWTRAT
GQLHSSTSHMQRAVGMHGNVYKKIGDYSTGAGQTILPYVLGSTEVYAQGTSWPLILEHS
DTIVLWSNDPYKNLQVGWNAETHESFAYLAQLKEKVKQGKIRVISIDPVVTKTQAYLGCE
QLYVNPQTDVTLMLAIAHEMISKKLYDDKFIQGYSLGFEEFVPYVMGTDKGVAKTPEWA
APICGVEAHVIRDLAKTLVKGRQTQFMMGWCIQRQQHGEQPYWMAAVLATMIGQIGLPGG
GISYGGHYSSIGVPSSGAAAPGAFPRNLDENQKPLFDSSDFKGASSTIPVARWIDAILEPGK
TIDANGSKVVYPDIKMMIFSGNNPWNHHQDRNRMKQAFHKLECVVTVDVNWTTATCRFS
DIVLPACTTYERNIDIDVYGAYANRGILAMQKMVEPLFDSLSDFEIFTRFAAVLGKEKEYTR
NMGEMEWLETLYNECKAANAGKFEMPDFATFWKQGYVHFGDGEVWTRHADFRNDPEI
NPLGTPSGLIEIFSRKIDQFGYDDCKGHPTWMEKT

>d1g8ka2 c.81.1.1 (A:4-682) Arsenite oxidase large subunit {Alcaligenes faecalis}

NDRITLPPANAQRTNMTCHFCIVGCGYHVYKWPELEEGGRAPEQNALGLDFRKQLPPLAV
TLTPAMTNVTEHDGARYDIMVVPDKACVVNSGLSSTRGGKMASYMYTPTGDGKERLS
APRLYAADWVDTTWDHAMALYAGLIKKTLDKDGPQGVFFSCFDHGGAGGGGFENTWGT
GKLMFSAIQTPMVRIHNRPAYNSECHATREMIGELNNAYEDAQLADVIWSIGNNPYESQ
TNYFLNHWLPNLQGATTSSKKERFPNENFPQARIIFVDPRETPSVAIARHVAGNDRVLHLA
IEPGTDTALFNGLFTYVVEQGWIDKPFIEAHTKGFDDAVKTNRLSLDECSNITGVPVDMKL
RAAEWSYKPKASQPRTMHAYEKGIWGNNDNYVIQSALLDLVIATHNVGRRGTGCVRM
GGHQEGYTRPPYPGDKKIYIDQELIKGKGRIMTWWGCNNFQTSNNAQALREAILQRSIV
KQAMQKARGATTEEMVDVIYEATQNGGLFVTSINLYPTKLAEAAHMLPAAHPGEMNLT
SMNGERRIRLSEKFMPPGTAMADCLIAARIANALRDMYQKDGAEMAAQFEGFDWKT
EEDAFNDGFRRAGQPGAPIDSQGGSTGHLVTYDRLRKSNNNGVQLPVVSWDESKGLVG
TEMLYTEGKFDTDDGKAHFKPAPWNG

>d2napa2 c.81.1.1 (A:4-600) Dissimilatory nitrate reductase (NAP) {Desulfovibrio desulfuricans}

RPEKWVKGVCRYCGTGCGVLVGVDGKAVAIQGNPNHNAGLLCLKGSLLIPVLNSKER
VTQPLVRRHKGGKLEPVSWDEALDLMASRFRSSIDMYGPNSVAWYGSQCLTEESYVAN
KIFKGGFGTNNVDGNPRLCMASAVGGYVTSFGKDEPMGTYADIDQATCFFIIGSNTSEHP
VLFRRRIARRKQVEPGVKIIVADPRRTNTSRIADMHVAFRPGTDLAFMHMAWVIINEELDN
PRFWQRYVNFMDAEGKPSDFEGYKAFLENYRPEKVAEICRVPVEQIYGAARAFESAATM
SLWCMGINQRVQGVFANNLIHNLHLITGQICRPGATSFSLTGQPNACGGVRDGGALSHLLP
AGRAIPNAKHRAEMEKLWGLPEGRIAPEPGYHTVALFEALGRGDVKCMIICETNPAHTLP
NLNKVHKAMSHPESFIVCIEAFPDAVTLEYADLVLPAPFWCERDGVYGCGERYSLTEKAV
DPPGQCRPTVNTLVEFARRAGVDPQLVNFRNAEDVWNEWRMVSKGTTYDFWGMTRERL
RKESGLIWPCPSEDHPGTSLRYVRGQDPCVPADHPDRFFFYGKPDGRAVIWMRPAKG

>d1ad3a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (*Rattus norvegicus*)}

SISDTVKRAREAFNSGKTRSLQFRIQQLEALQRMINENLKSISGALASDLGKNEWTSYYEE
VAHVLEELDTTIKELPDWAEDEPVAKTRQTQQDDLYIHSEPLGVVLVIGAWNYPFNLTIQP
MVGAVAAGNAVILKPSEVSGHMADLLATLIPQYMDQNLVYLVKGGVPETTELLKERFDHI
MYTGSTAVGKIVMAAAKHLTPVTLELGGKSPCYVDKDCDLDVACRRIAWGKFMNSGQ
TCVAPDYILCDPSIQNQIVEKLKKSCLKDFYGEDAKQSRDYGRIINDRHFQRVKGLIDNQKV
AHGGTWDQSSRYIAPTILVDVDPQSPVMQEEIFGPVMPIVCVRSLEEAIQFINQREKPLALY
VFSNNEKVIKKMIAETSSGGVTANDVIVHITVPTLPFGGVGNSGMGAYHGKKSFEFESH
RSCLVKSLNNEEAHKARYPPSPA

>d1bi9a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Rat (*Rattus norvegicus*),
retinal type II}

MASLQLLPSPTPNLEIKYTKIFINNEWQNSSESGRVFPVCNPATGEQVCEVQEADKVIDDKA
VQAARLAFSLGSVWRRMDASERGRLLDKLADLVERDRATLATMESLNGGKPFLLQAFYID
LQGVIKTLRYYAGWADKIHGMTIPVDGDYFTFTRHEPIGVCGQIIPWNFPLLMFTWKIAPA
LCCGNTVVIKPAEQTPLSALYMGALIKEAGFPPGVVNILPGYGPTAGAAIASHIGIDKIAFT
GSTEVGKLIQEAAGRSNLKRVTLLELGGKSPNIFADADLDYAVEQAHQGVFFNQGCCTA
GSRIFVEESIYEEFVKRSVERAKRRIVGSPFDPTEEQGPQIDKKQYNKILELIQSGVAEGAKL
ECGGKGLGRKGFFIEPTVFSNVTDDMRIAKEEIFGPVQEILRFKTMDEVIERANNSDFGLV
AAVFTNDINKALMVSSAMQAGTVWINCYNALNAQSPFGGFKMSGNGREMGEFGLREYS
EVKTVTVKIPQKNS

>d1a4sa_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Baltic cod (*Gadus callarias*)}

AQLVDSMPASTGSVVVTDDLNYWGGRIKSKDGATTEPVFEPATGRVLCQMVP CGAEE
VDQAVQSAQAAYLKWSKMAGIERSVMLEAARIIRERRDNIKLEVINNGKTITEAEYDID
AAWQCIEYYAGLAPTLSGQHILPQGAFAYTRREPLGVCAGILAWNYPFMIAAWKCAPAL
ACGNAVVF KPSPMTPVTGVILAEIFHEAGVPVGLVNVVQGAETGSLCHHPNVAKVSFT
GSVPTGKKVMEMSAKTVKHVTLELGGKSPLLIFKDCELENAVRGALMANFLTQGGVCTN
GTRV FVQREIMPQFLEE VVKRTKAIVVGDPLLTETRMGGLISKPQLDKVLGFVAQAKKEG
ARVLCGGEPLTPSPDKLKNGYFMSPCVLDNCRDDMT CVKEEIFGPVMSVLPFDTEEEVLQ
RANNTTFGLASGVFTRDISRAHRVAANLEAGTCYINTYSISPVEVPFGGYKMSGFGRENG
QATVDYYSQLKTVIVEMGDVDSL

>d1euha_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {*Streptococcus mutans*}

TKQYKNYVNGEWKLSENEIKIYEPASGAELGSVPAMSTEEVDYVYASAKKAQPAWRALS
YIERAAYLHKVADILMRDKEKIGAILSKEVAKGYKSAVSEVVRTAEIINYAAEEGLRMEGE
VLEGGSFEEAASKKKIAVVRREPVLVLAISPFNYPVNLAGSKIAPALIAGNVIAFKPPTQGS

SGLLLAEAF AEAGLPAGVFNTITGRGSEIGDYIVEHQAVNFINFTGSTGIGERIGKMAGMRP
IMLELGGKDSAIVLEDADLELTAKNIIAGAFGYSGQRCTAVKRVLVMESVADELVEKIREK
VLALTIGNPEDDADITPLIDTKSADYVEGLINDANDKGATALTEIKREGNLICPILFDKVTTD
MRLAWEEPFGPVLPIIRVTSVEEAIEISNKSEYGLQASIFTNDFPRAFGIAEQLEVGTVHINN
KTQRGTDNFPFLGAKKSGAGIQGVKYSIEAMTTVKSVVFDIK

>d1ez0a_ c.82.1.1 (A:) Aldehyde reductase (dehydrogenase), ALDH {Vibrio harveyi}

TDNVFYATNAFTGEALPLAFPVHTEVEVNQAATAAAKVARDFRRLNNSKRASLLRTIASSEL
EARSDDIIRAHLETALPEVRLTGEIARTANQLRFLADVNSGSYHQAILDTPNPTRAPLPK
PDIRRQQIALGPVAVFGASNFPLAFSAAGGDTASALAAGCPVIVKGHTAHPGTSQIVAECIE
QALKQEQLPQAIFTLLQGNQRALGQALVSHPEIKAVGFTGSVGGGRALFNLAHERPEPIPF
YGELGAINPTFIFPSAMRAKADLADQFVASMTMGCGQFCTKPGVVFALNTPETQAFIETA
QSLIRQQSPSTLLTPGIRDSYQSQVVSRRGSDDGIDVTFSSQAESPCVASALFVTSSENWRKHP
AWEEEIFGPQSLIVVCENVADMLSLSEMLAGSLTATIHATEEDYPQVSQLIPRLEEIAGRLVF
NGWPTGVEVGYAMVHGGPYPASTHSASTSVGAETIHRWLRPVAYQALPESLLPDSLKAE
NPLEIARAVDGGKAA

>d1kfia1 c.84.1.1 (A:3-205) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

QVIPAPRVQVTQPYAGQKPGTSGLRKKVSEATQPNYLENFVQSIFNTLRKDELKPKNVLFV
GGDGRYFNRQAIFSIIRLAYANDISEVHVGQAGLMSTPASSHYIRKVNEEVGNCIGGIILTAS
HNPGGKEHGDGFIKFNVRTGAPAPEDFTDQIYTHTTKIKEYLTVDYEFKHNLDQIGVYK
FEGTRLEKSHFEVKVVD

>d1kfia2 c.84.1.1 (A:206-323) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

VQDYTQLMQKLFDFDLLKGLFSNKDFSFRFDGMHGVAGPYAKHIFGTLLGCSKESLLNCD
PSEDFGGGHPDPNLTYAHDLEVELLDIHKKKDVGTVPQFGAACDGDADRNMILGRQFFV

>d1kfia3 c.84.1.1 (A:324-443) Exocytosis-sensitive phosphoprotein, pp63/parafusin {Paramecium tetraurelia}

TPSDSLAVIAANANLIFKNGLLGAARSMPTSGALDKVAAKNGIKLFETPTGWKFFGNLMD
AGLINLCGEESFGTGSNHIREKDGIVAVLAWLTILAHKNKNTDHFVTVEEIVTQYWQQFG

>d1k2yx1 c.84.1.1 (X:5-154) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

KAPTLPASIFRAYDIRGVVGDTLTAETAYWIGRAIGSESLARGEPCVAVGRDGRLSGPELVK
QLIQGLVDCGCQVSDVGMVPTPVLYYAANVLEGKSGVMLTGAHNPPDYNGFKIVVAGET
LANEQIQALRERIEKNDLASGVGSVEQVD

>d1k2yx2 c.84.1.1 (X:155-258) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

ILPRYFKQIRDDIAMAKPMKVVDVDCGNGVAGVIAPQLIEALGCSVIPLYCEVDGNFPNHHHP
DPGKPENLKDLIAKVKAENADLGLAFDGDGDRVGVVTNTGTII

>d1k2yx3 c.84.1.1 (X:259-367) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

YPDRLLMLFAKDVVSRNPGADIIFDVKCTRRLLIALISGYGGRPVMWKTGHSLIKKKMKET
GALLAGEMSGHVFFKERWFGFDDGIYSAARLLEILSQDQRDSEHVFSAF

>d1k2yx4 c.84.1.1 (X:368-463) Phosphomannomutase/phosphoglucomutase {Pseudomonas aeruginosa}

PSDISTPEINITVTEDSKFAIIEALQRDAQWGEGNITTLDGVRVDYPKGWGLVRASNTTPVL
VLRFEADTEEELERIKTVFRNQLKAVDSSLPVPF

>d1fw8a_ c.86.1.1 (A:) Phosphoglycerate kinase {Baker's yeast (Saccharomyces cerevisiae)}

SKYSLAPVAKELQSLLGKDVTFNLDCVGPEVEAAVKASAPGSVILLENLRYHIEEEGSRKV
DGQKVKASKEDVQKFRHELSSLADVINDAFGTAHRAHSSMVGFDPQRAAGFLLEKEL
KYFGKALENPTRPFLAILGGAKVADKIQIDLNDKVDSEIIIGGGMAFTFKKVLNTEIGDS
IFDKAGAEIVPKLMEKAKAKGVEVVLVPDFIADAFSADANTKTVTDKEGIPAGWQGLDN
GPESRKLFAATVAKATIVWNGPPGVFEFEKFAAGTKALLDEVVKSSAAGNTVIIGGGDT
ATVAKKYGVTDKISHVSTGGGASLELLEGKELPGVAFLEKKSLSSKLSVQDLDLKD KRVF
IRVDFNVPLDGKKITSNQRIVAALPTIKYVLEHHPRYVVLASHLGRPNGERN

>d16pk_ c.86.1.1 (-) Phosphoglycerate kinase {Trypanosoma brucei}

EKKSINECDLKGKKVLIRVDFNVVPKNGKITNDYRIRSALPTLKKVLTEGGSCVLMShLGR
PKGIPMAQAGKIRSTGGVPGFQQKATLKPVAKRSELLLRPVTFAPDCLNAADVVS KMSP
GDVVLENVRFYKEEGSKKAKDREAMAKILASYGDVYISDAFGTAHRDSATMTGIPKILG
NGAAGYLMEKEISYFAKVLGNPPRPLVAIVGGAKVSDKIQLLDNMLQRIDYLLIGGAMAY
TFLKAQGSIGKSKCEESKLEFARSLLKKAEDRKVQVILPIDHVCHEFKAVDSPLITEDQN
IPEGHMALDIGPKTIEKYVQTIGKCKSAIWNGPMGVFEMVPYSGTFAIAKAMGRGTHEH
GLMSIIGGGDSASAAELSGEAKRMSHVSTGGGASLELLEGKTLPGVTVLDDK

>d1ygpa_ c.87.1.4 (A:) Glycogen phosphorylase {Baker's yeast (Saccharomyces cerevisiae)}

TRRLTGFLPQEIKSIDTMIPLLSRALWNKHQVKKFNKAEDFQDRFIDHVETTLARSLYNCD
DMVAYEAASMSIRDNLVIDWNKTQQKFTTRDPKRVYYLSLEFLMGRALDNALINMKIEDP
EDPAASKGKPREMIKGALDELGFKLEDVLDQEPDAGLGNGGLGRLAACFVDSMATEGIPA
WGYGLRYEYGIFAQKIIDGYQVETPDYWLNSGNPWEIERNEVQIPVTFYGYVDRPEGGKT
TLSASQWIGGERVLAVAYDFVPVPGFKTSNVNNLRLWQARPTTEFDLNKFNNGDYKNSVAQ
QQRAESITAVLYPNDNFAQGKELRLKQQYFWCAASLHDILRRFKKSKRPWTEFPDQVAIQ
LNDTHPTLAIVELQRVLDLEKLDWHEAWDIVTKTFAYTNHTVMQEALEKWPRRLFGHL
LPRHLEIYDINWFFLEDVAKKFPKDVDLLSRISIIENSPERQIRMAFLAIVGSHKVNGVVE
LHSELIKTTIFKDFIKFYGPSKFVNVTNGITPRRWLKQANPSLAKLISETLNDPTEEYLLDM
AKLTQLEKYVEDKEFLKKWNQVKLNNKIRLVDLIKKENDGVDIINREYLDLDFDMQVK
RIHEYKRQQLNVFGIYRYLAMKNMLKNGASIEEVARKYPRKVSIFGGKSAPGYMAKLII
KLINC'VADIVNNDSEIEHLLKVVFVADYNVSKAEIIPASDLSEHISTAGTEASGTSNMKFV
MNGGLIIGTVDGANVEITREIGEDNVFLFGNLSERVEELRYNHQYHPQDLPSSLDVLSYI
ESGQFSPENPNEFKPLVDSIKYHGDYYLVSDDFESYLATHELVDQEFHNQRSEWLKKS VLS
LANVGFFSSDRCIEEYS DTIWNVEPVT

>d1qm5a_ c.87.1.4 (A:) Maltodextrin phosphorylase (MALP) {Escherichia coli}

SQIFNDKQFQEALSRQWQRYGLNSAAEMTPRQWWLAVSEALAEMLRAPFAKPVANQ
RHVNYISMEFLIGRLTGNNLLNLGWYQDVQDSLKAYDINLTDLLEEEIDPALGNGGLGR
AACFLDSMATVGQSATGYGLNYQYGLFRQSFVDGKQVEAPDDWHRSNYPWFRHNEALD
VQVGIGGKVTKDGRWEPEFTITGQAWDLPPVGYRNGVAQPLRLWQATHAHPFDLTKFND
GDFLRAEQQGINAELTKVLYPNDNHTAGKKLRMLQQYFQCACSVADILRRHHLAGRKL
HELADYEVIQLNDTHPTIAIPELLRVLIDEHQMSWDDAWAITSKTFAYTNHTLMPEALERW
DVKLVKGLLPRHMQIINEINTRFKTLVEKTPWGDEKVVAKLAVVHDKQVHMANLCVVG

GFAVNGVAALHSDLVVKDLFPEYHQLWPNKFHNVTNGITPRRWIKQCNPALAALLDKSLQ
KEWANDLDQLINLEKFADDAKFRDQYREIKQANKVRLAEFVKVRTGIEINPQAIFDIQIKR
LHEYKRQHLNLLHILALYKEIRENPQADRVPRVFLFGAKAAPGYYLAKNIIFAINKVADVIN
NDPLVGDKLVVFLPDYCVSAAEKLIPAADISEQISTAGKEASGTGNMKLALNGALTGT
LDGANVEIAEKVGEENIFIFGHTVEQVKAILAKGYDPVKWRKKDKVLDAVLKELESGKYS
DGDKHAFDQMLHSIGKQGGDPYLVMAADFAAYVEAQKQVDVLYRDQEAWTRAAILNTAR
CGMFSSDRSIRDYQARIWQAKR

>d1ii2a1 c.91.1.1 (A:201-523) Phosphoenolpyruvate (PEP) carboxykinase
(ATP-oxaloacetate carboxy-liase) {Trypanosoma cruzi}

HLCMHASANVGKQGDVTVFFGLSGTGKTTLSADPHRNLIGDDEHVWTDGRGVFNIEGGC
YAKAIGLNPKEKDIYDAVRFGAVAENCVLDRKTGEIDFYDESICKNTRVAYPLSHIEGALS
KAIAGHPKNVIFLTNDAFGVMPPVARLTSQAQAMFWFVMGYTANVPGVEAGGTRTARPIFS
SCFGGPFLVRHATFYGEQLAEKMQKHNSRVWLLNTGYAGGRADRGAKRMPLRVTRAIID
AIHDGTLDRTEYEEYPGWGLHIPKYVAKVPEHLLNPRKAWKDVRQFNETSKELVAMFQES
FSARFAAKASQEMKSAVPRYVEFA

>d1khba1 c.91.1.1 (A:260-622) Cytosolic phosphoenolpyruvate carboxykinase (GTP-
hydrolysing) {Human (Homo sapiens)}

WLAEHMLVLGITNPEGEKKYLAAAFPSACGKTNLAMMNPSLPGWKVECVGDDIAWMKF
DAQGHLRAINPENGFFGVAPGTSVKTNPNAIKTIQKNTIFTNVAETSDGGVYWEIDEPLA
SGVTITSWKNKEWSSEDGEPCAHPNSRFTCPASQCPIIDAAWESPEGVPIEGIIFFGRRPAG
VPLVYEALSWQHGVFVGAAMRSEATAAAEHKGKIIIMHDPFAMRPFFGYNFGKYLAHWL
SMAQHPPAAKLPKIFHVNWFRKDKEGKFLWPGFGENSRVLEWMFNRIDGKASTKLTPIGYI
PKEDALNLKGLGHINMMELFSISKEFWDEVEDIEKYLVDQVNADLPCEIEREILALKQRI
SQM

>d1ayl_2 c.109.1.1 (1-227) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate
carboxy-liase) {Escherichia coli}

MRVNNGLTPQELEYGISDVHDIVYNPSYDLLYQEELDPSLTGYERGVLTNLGAVAVDTGI
FTGRSPKDKYIVRDDTTRDTFWWADKGKGKNDNKPLSPETWQHLKGLVTRQLSGKRLF
VVDAFCGANPDTRLSVRFITEVAWQAHFVKNMFIRPSDEELAGFKPDFIVMNGAKCTNPQ
WKEQGLNSENFAFNLTERMQLIGGTWYGGEMKKGMFSMMNYLLPLKG

>d1ii2a2 c.109.1.1 (A:2-200) Phosphoenolpyruvate (PEP) carboxykinase (ATP-oxaloacetate
carboxy-liase) {Trypanosoma cruzi}

PPTIHRNLLSPELVQWALKIEKDSRLTARGALAVMSYAKTGRSPLDKRIVDTDDVRENVD
WGKVNMLSEESFARVRKIAKEFLDTREHLFVVDCFAGHDERYRLKVRVFTTRPYHALF
MRDMLIVPTPEELATFGEPDYVIYNAGECKADPSIPGLTSTTCVALNFKTREQVILGTEYAG
EMKKGILTVMFELMPQMN

>d1khba2 c.109.1.1 (A:10-259) Cytosolic phosphoenolpyruvate carboxykinase (GTP-
hydrolysing) {Human (Homo sapiens)}

NLSAKVVQGSLSLPQAVREFLENNALCQPDHIHICDGSEEENGRLLGQMEEGILRRLK
KYDNCWLALTDPRDVARIESTVIVTQEQRDTVPIPKTGLSQLGRWMSEEDFEKAFNARF
PGCMKGRTMYVIPFSMGLSPLSKIGIELTDSPLYVASMRIIMTRMGTPVLEALGDGEFVK
CLHSVGCPLPLQKPLVNNWPCNPELTIAHLPRREIISFGSGYGGNSLLGKKCFALRMAS
RLAKEEG

>d1doza_ c.92.1.1 (A:) Ferrochelatase {Bacillus subtilis}

SRKKMGLLMAYGTPYKEEDIERYYYTHIRRGKRKPEPEMLQDLKDRYEAIIGGISPLAQITEQ
QAHNLEQHLNEIQDEITFKAYIGLKHIEPFIEDAVAEMHKDGITEAVSIVLAPHFSTFSVQSY
NKRAKEEA EKLGGLTITSVESWYDEPKFVTYWVDRVKETYASMPEDERENAMLIVSAHS
LPEKIKEFGDPYPDQLHESAKLIAEGAGVSEYAVGWQSEGNTDPWLGPDVQDLTRDLFE
QKGYQAFVYVPVGVFVADHLEVLYDNDYECKVVTDDIGASYRPEMPNAKPEFIDALATV
VLKKLGR

>d1hrka_ c.92.1.1 (A:) Ferrochelatase {Human (Homo sapiens)}

RKPKTGILMLNMGGPETLGDVHDFLLRLFLDRDLMTLP IQNKLAPFIAKRLTPKIQEQYRR
IGGGSPIKIWTSKQGEGMVKLLDELS PNTAPHKYYIGFRYVHPLTEEAIEEMERDGLERAIA
FTQYPQYSCSTTGSSLNAIYRYYNQVGRKPTMKWSTIDRWPTHLLIQCFADHILKELDHF
PLEKRSEVVILFSAHSLPMSV VNRGDPYPQEV SATVQKV MERLEYCNPYRLVWQSKVGP
MPWLGPQTDESIKGLCERGRKNILLVPIAFTSDHIETLYELDIEYSQVLAKECGVENIRRAE
SLNGNPLFSKALADLVHSHIQSNELCSKQLT LSCPLCVNPVCRETKSFFTSQL

>d1toaa_ c.92.2.2 (A:) Periplasmic zinc binding protein TroA {Treponema pallidum}
GKPLVVTIGMIADAVKNIAQGDVHLKGLMGP GVDPHLYTATAGDVEWLGNADLILYNG
LHLETKMGEVFSKLRGSRLVAVSETIPVSQRLSLEEAEFDPHVWFDVKLWSYSVKAVYE
SLCKLLPGKTREFTQRYQAYQQQLDKLDAYVRRKAQSLPAERRVLVTAHDAFGYFSRAYG
FEVKGLQGVSTASEASAHD MQELAAFIAQRKLPAIFI ESSIPHK NVEALRDAVQARGHV VQ
IGGELFSDAMGDAGTSEGTYVGMVTHNIDTIVAALAR

>d1psza_ c.92.2.2 (A:) Pneumococcal surface antigen PssA {Pneumococcus
(Streptococcus pneumoniae)}

KKDTTSGQKLKV VATNSIIADITKNIAGDKIDLHSIVPIGQDPHEYEPLPEDVKKTSEADLIF
YNGINLETGGNAWFTKLVENAKKTENKDYFAVSDGVDVIYLEGQNEKGKEDPHAWLNLE
NGIIFAKNIAKQLSAKDPNNKEFYEKNLKEYTDKLDKLDKESKDKFNKIPAEKKLIVTSEG
AFKYFSKAYGVPSAYIWEINTEEEGTPEQIKTLVEKLRQTKVPSL FVESSVDDRPMKTVSQ
DTNIPIYAQIFTDSIAEQGKEGDSYYSMMKY NLDKIAEGLAK

>d1mioa_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium
pasteurianum}

SENLKDEILEKYIPKTKKTRSGHIVIKTEETPNPEIVANTRTVPGIITARGCAYAGCKGVVMG
PIKDMVHITHGPIGCSFYTWGGRRFKSKPENG TGLNFNEYVFSTDMQESDIVFGGVNKLK
DAIHEAYEMFHPAAIGVYATCPVGLIGDDILAVAATASKEIGIPVHAFSCEGYKGVSQSAGH
HIANNTVMTDIIGKGNKEQKKYSINVLGEYNIGGDAWEMDRVLEKIGYHVNATLTGDATY
EKVQNADKADLNLVQCHRSINYIAEMMETKYGIPWIKCNFIGVDGIVETLRDMAKCFDDP
ELTKRTEEVIAEEIAAIQDDLDYFKEKLQGKTACLYVGGSRSH TYMNM LKSFGVDSL VAG
FEFAHRDDYEGREVIPTIKIDADSKNIPEITVTPDEQKYRVVIPEDKVEELKKAGVPLSSYG
GMMKEMHDGTILIDDMNHHDMEVVLEKLKPDMFFAGIKEKFVIQKGGVLSKQLHSYDY
NGPYAGFRGVVNF GHELVNGIYTPAWKMITPPWKKASSES

>d1miob_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Clostridium
pasteurianum}

LDATPKEIVERKALRINPAKTCQPVGAMYAALGIHNCLPHSHGSQGCCSYHRTVLSRHFKE
PAMASTSSFTEGASVFGGGSNIKTAVKNIFSLYNPDIIAVHTTCLSETLGDDLPTYISQMEDA
GSIPEGKLV IHTNTPSYV GSHVTGFANMVQGIVNYLSENTGAKNGKINVIPGFVGPADMRE
IKRLF EAMDIPYIMFPDTS GVL DGP TTGEYKMYPEGGTKIEDLKDTGNSDLTSLSGSYASD
LGAKTLEKKCKVPFKTLRTPIGVSATDEFIMALSEATGKEVPASIEEERGQLIDL MIDAQQY

LQGKKVALLGDPDEIIALSKFIIELGAIPKYVVTGTPGMKFQKEIDAMLAEAGIEGSKVKVE
GDFFDVHQWIKNEGVDLLISNTYGKFIAREENIPFVRFGFPIMDRYGHYYNPKVGYKGAIR
LVEEITNVILDKIERECTEEDFEVVR

>d2minb_ c.92.2.3 (B:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Azotobacter vinelandii}

SQQVDKIKASYPLFLDQDYKDMLAKKRDGFEEKYPQDKIDEVFQWTTTKEYQELNFORE
ALTVNPAKACQPLGAVLCALGFEKTMPIYVHGSQGCVAYFRSYFNRFREPVSVCVSDSMTE
DAAVFGGQQNMKDGQLQCKATYKPDMAIVSTTCMAEIVGDDLNAFINNSKKEGFIPDEFP
VPFAHTPSFVGSHVTGWDNMFEGIARYFTLKSMDKVVGSNKKINIVPGFETYLGFRVI
KRMLSEMGGVGYSLSDPEEVLDTPADGQFRMYAGGTTQEEMKDAPNALNTVLLQPWHL
EKTKKFVEGTWKHEVPKLNIPMGLDWTDEFLMKVSEISGQPIASLTKERGRLVDMMTDS
HTWLHGKRFALWGDPDFVMGLVKFLELGCEPVHILCHNGNKRWKKAVDAILAASPYG
KNATVYIGKDLWHLRSLVFTDKPDFMIGNSYGKFIQRDTLHKGKEFEVPLIRIGFPIFDRHH
LHRSTTLGYEGAMQILTTLVNSILERLDEETRGMQATDYNHDLVR

>d1qgua_ c.92.2.3 (A:) Nitrogenase iron-molybdenum protein, alpha and beta chains {Klebsiella pneumoniae}

TNATGERNLALIQEVLEVPETARKERRKHHMMVSDPKMKSVGKCHISNRKSQPGVMTVR
GCAYAGSKGVVFGPIKDMAHISHGPGVCGQYSRAGRNNYYTGVSGVDSFGTLNFTSDFQ
ERDIVFGGDKKLSKLIEMELLFPLTKGITIQSECPVGLIGDDISAVANASSKALDKPVIPVR
CEGFRGVSQSLGHHIANDVVRDWILNNREGQPFETTPYDVAIIGDYNIGGDWASRILLEE
MGLRVVAQWSGDGTLVEMENTPFVKLNLVHCYRSMNYIARHMEEKHQIPWMEYNFFGP
TKIAESLRKIADQFDDTIRANAEAVIARYEGQMAAIIAKYRPRLEGRKVLLYMGGLRPRHV
IGAYEDLGMEIIAAGYEFANHDDYDRTLPLDKEGTLLFDDASSYELEAFVKALKPDLIGSG
IKEKYIFQKMGVPFRQMHSWDYSGPYHGYDGFALFARDMDMTLNNPAWNELTAPWL

>d2dri_ c.93.1.1 (-) D-ribose-binding protein {Escherichia coli, strain k-12}

KDTIALVVSTLNNPFFVSLKDGAQKEADKLGYNLVVLDSSQNNPAKELANVQDLTVRGTKI
LLINPTDSDAVGNVAVKMANQANIPVITLDRQATKGEVVSIIASDNVLGGKIAGDYIAKKA
GEGAKVIELQGIAGTSAARERGEFGQAVAAHKFNVLASQPADFDRIKGLNVMQNLLTAH
PDVQAVFAQNDEMALGALRALQTAGKSDVMVVGFDGTPDGEKAVNDGKLAATIAQLPD
QIGAKGVETADKVLKGEKVQAKYPVDLKLVLVKQ

>d8abp_ c.93.1.1 (-) L-arabinose-binding protein {Escherichia coli}

NLKLGLFLVKQPEEPWFQTEWKFADKAGKDLGFEVIKIAVPDGEKTLNAIDSLAASGAKGF
VICTPDPKLGSIVAKARGYDMKVIIVDDQFVNAKGKPMDTVPLVMLAATKIGERQQQE
LYKEMQKRGWDVKESAVMAITANELDTARRRTTGSM DALKAAGFPEKQIYQVPTKSNDI
PGAFDAANSMLVQHPEVKHWLVGMNDSTVLGGVVRATEGQGFKAADIIIGINGVDAVSE
LSKAQATGFYGSLLPSPDVHGYKSSEMLYNWVAKDVEPPKFTEVTDVVLITRDNFKEELE
KKGLGGK

>d1rpja_ c.93.1.1 (A:) D-allose-binding protein {Escherichia coli}

AAEYAVVLKTLSPFWVDMKKGIEDEAKTLGVSVDFASPSEGDFQSQQLFEDLSNKNY
KGIAFAPLSSVNLVMPVARAWKKGIYLVNLDEKIDMDNLKKAGGNVEAFVTTDNVAVGA
KGASFIIDKLGAEGGEVAIIIEGKAGNASGEARRNGATEAFKKASQIKLVASQPADWDRIKA
LDVATNVLQRNPNIKAIYCANDTMAMGVAQAVANAGKTGKVLVVGTDGIPEARVMVEA
GQMTATVAQN PADIGATGLKLMVDAEKS GKVPLDKAPEFKLVDSILVTQ

>d2gbp_ c.93.1.1 (-) Galactose/glucose-binding protein {Escherichia coli}

ADTRIGVTIYKYDDNFMSVVRKAIEQDAKAAPDVQLLMNDSQNDQSKQNDQIDVLLAK
GVKALAINLVDPAAGTVIEKARGQNPVFFNKEPSRKALDSYDKAYYVGTDSKESGII
QGDLIAKHWAANQGWDLNKDGQIQFVLLKGEPGHPDAEARTTYVIKELNDKGIKTEQLQ
LDTAMWDTAQAKDKMDAWLSGPNANKIEVVIANNAMAMGAVEALKAHNKSSIPVFG
VDALPEALALVKSGALAGTVLNDANNQAKATFDLAKNLADGKGAADGTNWKIDNKVV
RVPYVGVDKDNLAEFSSK

>d1pea_ c.93.1.1 (-) Amide receptor/negative regulator of the amidase operon (AmiC)
{*Pseudomonas aeruginosa*}

PLIGLLFSETGVTADIERSQRYGALLAVEQLNREGGVGGRPIETLSQDPGGDPDRYRLCAE
DFIRNRGVRFLVGCYMSHTRKAVMPVVERADALLCYPTPYEGFEYSPNIVYGGPAPNQNS
APLAAYLIRHYGERVVFIGSDYIYPRESNHVMRHLRQHGDTVLEEIYIPLYPSDDDLQRA
VERIYQARADVVFSTVVGTTAELYRAIARRYGDGRRPPIASLTSEAEVAKMESDVAEGQ
VVVAPYFSSIDTPASRAFVQACHGFFPENATITAWAEAAWQTLGLGAAQAAGNWRVED
VQRHLYDIDIDAPQGPVVRVERQNNHSSLSSRIAEIDARGVFQVRWQSPEPIRPDPYVVVHN
LDDW

>d1jx6a_ c.93.1.1 (A:) Quorum-sensing signal (autoinducer-2) binding protein LuxP {*Vibrio
harveyi*}

GYWGYQEFLDEFPEQRNLTNALSEAVRAQPVPLSKPTQRPIKISVVYPGQQVSDYWVRNI
ASFEKRLYKLNINYQLNQVFTRPNADIKQQSLSLMEALKSKSDYLIFTLDTTRHRKFVEHV
LDSTNTKLILQNITTPVREWDKHQPFLYVGFDAEGSRELATEFGKFFPKHTYYSVLVYFSE
GYISDVRGDTFIHQVNRDNNFELQSAYYTKATKQSGYDAKASLAKHPDVFDFIACSTDV
ALGAVDALAELGREDIMINGWGGGSAELDAIQKGDLDITVMRMNDDTGIAMAEAIKWD
LEDKPVPTVYSGDFEIVTKADSPERIEALKKRAFRYS

>d1dbqa_ c.93.1.1 (A:) Purine repressor (PurR), C-terminal domain {*Escherichia coli*}

KSIGLLATSSEAAAYFAEIIIEAVEKNCQKGYTLILGNAWNLEKQRAYLSMMAQKRVDGL
LVMCSEYPELLAMLEEYRHIPMVVMDWGEAKADFTDAVIDNAFEGGYMAGRYLIERG
HREIGVIPGLERNTGAGRLAGFMKAMEEAMIKVPESWIVQGDFEPESGYRAMQQILSQP
HRPTAVFCGDMAMGALCAADEMGLRVPQDVSLIGYDNVRNARYFTPALTTHQPKDSL
GETAFNMLLDRIVKNKEEPQSIEVHPRIERRSVADGPFRDYRR

>d1tfa_ c.93.1.1 (A:) Lac-repressor (lacR) core (C-terminal domain) {*Escherichia coli*}

SLIGVATSSLALHAPSQIVAAIKSRADQLGASVVSMVERSVEACKAAVHNLLAQRVSG
LIINYPLDDQDAIAVEAACTNVPALFLDVSDQTPINSIIFSHEDGTRLGVEHLVALGHQQIAL
LAGPLSSVSARLRLAGWHKYLTRNQIPIAEREQDWSAMSGFQQTMLNEGIVPTAML
VANDQMALGAMRAITESGLRVGADISVVGYYDDTEDSSCYIPPLTTIKQDFRLLGQTSVDRL
LQLSQGQAVKGNQLLPVSLVKRKTTLAPNTQTASPRALADSLMQLARQVSRL

>d1byka_ c.93.1.1 (A:) Trehalose repressor, C-terminal domain {*Escherichia coli*}

SDKVVAIIVTRLDSLSLENLAVQTMPLAFYEQGYDPIMMESQFSPQLVAEHLGVLRKRRNIDG
VVLFGFTGITEEMLAHWQSSLVLLARDAKGFASVCYDDEGAIKILMQRLYDQGHRNISYL
GVPHSDVTTGKRRHEAYLAFCKAHKLHPVAALPGLAMKQGYENVAKVITPETTALLCAT
DTLALGASKYLQEQRIDTLQLASVGNTPLMKFLHPEIVTVDPGYAEAGRQAACQLIAQVT
GRSEPQQIIPATLS

>d2lbp_ c.93.1.1 (-) Leucine-binding protein {*Escherichia coli*}

DDIKVAVVGAMSGPIAQWGIMEFNAGAEQAIKDINAKGGIKGDKLVGVEYDDACDPKQAV
AVANKIVNDGIKYVIGHLCSSSTQPASDIYEDEGILMISPGATAPELTQRGYQHIMRTAGLDS

SQGPTAAKYILETVKPQRIAIHDKQQYGEGLARSVQDGLKAANANVFFDGITAGEKDFS
ALIARLKKENIDFVYYGGYYPEMGQMLRQARSVGLKTQFMGPEGVGNASLSNIAGDAAE
GMLVTMPKRYDQDPANQGIVDALKADKKDPSGPYVWITYAAVQSLATALERTGSDEPLA
LVKDLKANGANTVIGPLNWDEKGDLKGFDFGVFQWHADGSSTKAK

>d1dp4a_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Rat
(*Rattus norvegicus*)}

SDLTVAVVLPLTNTSYPSWARVGPVELALARVKARPDLLPGWTVRMVLGSSENAAGV
CSDTAAPLAAVDLKWEHSPAVFLGPGCVYSAAPVGRFTHWVRVPLLTAGAPALGIGVKDE
YALTTRTGPSHVKLGDFTALHRRRLGWEHQALVLYADRLGDDRPCFFIVEGLYMRVRERL
NITVNHQEFVEGDPDHYPKLLRAVRRKGRVIYICSSPDAFRNLMMLALNAGLTGEDYVFF
HLDVFGQSLKSAQGLVPQKPWERGDGQDRSARQAFQAAKIITYKEPDNPEYLEFLKQLKL
LADKKFNFTVEDGLKNIIPASFHDGLLLYVQAVTETLAQGGTVTDGENITQRMWNRSFQG
VTGYLKIDRNGDRDTSDFSLWMDPETGAFRVVLNNGTSQELMAVSEHKLYWPLGYPPP
DVPKCGF

>d1jdpa_ c.93.1.1 (A:) Hormone binding domain of the atrial natriuretic peptide receptor {Human
(*Homo sapiens*)}

EALPPQKIEVLVLLPQDDSYLFSLTRVRPAIEYALRSVEGNGTGRRLLPPGTRFQVAYEDSD
CGNRALFSLVDRVAAARGAKPDLILGPVCEYAAAPVARLASHWDLPLMSAGALAAGFQH
KDSEYSHLTRVAPAYAKMGEMMLALFRHHHWSRAALVYSDDKLERNICYFTLEGVHEVF
QEEGLHTSIYSFDETKDLDLEDIVRNIQASERVVIMCASSDTIRSIMLVHRHGMTSGDYAF
FNIELFNSSSYGDGSWKRGDKHDFEAKQAYSSLQTVTLRTVKPEFEKFSMEVKSSVEKQ
GLNMEDYVNMVFVEGFHDAILLYVLALHEVLRAGYSKKDGGKIIQQTWNRTFEGIAGQVSI
DANGDRYGDFSVIAMTDVEAGTQEVIGDYFGKEGRFEMRP

>d1ewka_ c.93.1.1 (A:) Metabotropic glutamate receptor subtype 1 {Rat (*Rattus norvegicus*)}

RSVARMDGDVIGALFSVHHQPPAEKVPERKCGEIREQYGIQRVEAMFHTLDKINADPVLL
PNITLGSEIRDSCWHSSVALEQSIEFIRDSLIRDEKDGLENRCLPDGQTLPPGRTKKPIAGVI
GPGSSSVAIQVQNLLQLFDIPQIAYSATSIDLSDKTLYKYFLRVVPSDTLQARAMLDIVKRY
NWTYVSAVHTEGNYGESGMDAFKELAAQEGLCIAHSDKIYSNAGEKSFRLLRLRLERL
PKARVVVCFCEGMTVRGLLSAMRRLGVVGEFSLIGSDGWADRDEVIEGYEVEANGGITIK
LQSPEVRSFDDYFLKLRLDTNTRNPWFPEFWQHRFQCRLPGHLENPNFKKVCTGNESLE
ENYVQDSKMGFVINAIYAMAHGLQNMHHALCPGHVGLCDAMKPIDGRKLLDFLIKSSFV
GVSGEVWFDEKGDAPGRYDIMNLQYTEANRYDYVHVGTWHEGVLNIDDYKI

>d1jeta_ c.94.1.1 (A:) Oligo-peptide binding protein (OPPA) {*Salmonella typhimurium*}

ADVPAQVQLADKQTLVRNNGSEVQSLDPHKIEGVPESNVSRDLFEGLLISDVEGHPSPGVA
EKWENKDFKVWTFHLRENAKWSGDGTPVTAHDFVYSWQRLADPNTASPYASYLQYGHIA
NIDDIIAGKKPATDLGVKALDDHTFEVTLSEPVYFYKLLVHPSVSPVPSAVEKFGDKWT
QPANIVTNGAYKLKNWVNERIVLERNPQYWDNAKTVINQVTYLPISSEVTDVNRYRSGE
IDMTYNNMPIELFQKLKKEIPNEVRVDPYLCTYYEINNQKAPFNDVRVRTALKLALDRDI
IVNKVKNQGDLPAYSYPYTDGAKLVEPEWFKWSQQKRNEEAKKLLAEAGFTADKPLT
FDLLYNTSDLHKKLAIASIWKKNLGVNVNLENQEWKTFDTRHQGTDFVARAGWCA
DYNEPTSFLNTMLSDDSSNNTAHYKSPAFDKLIADTLKVADDTQRSELYAKAEQQLDKDSAI
VPVYYYYVNARLVKPWVGGYTGKDPLDNIYVKNLIIKH

>d1pda_1 c.94.1.1 (3-219) Porphobilinogen deaminase
(hydroxymethylbilane synthase), N-terminal domain {*Escherichia coli*}

DNVLR IATRQSPLALWQAHYVKDKLMASHPGLVVELVPMVTRGDVILDTPLAKVGGKGL
FVKELEVALLENRADI AVHSMKDVPVEFPQGLGLVTICEREDPRDAFVSNNYDSL DALPA
GSIVGTSSLRRQCQLAERRPDLIRSLRGNVGTRLSKLDNGEYDAIILAVAGLKRLGLESRIR
AALPPEISLPVGGGAVGIECRLDDSR TRELLAAL

>d11st__ c.94.1.1 (-) Lysine-, arginine-, ornithine-binding (LAO) protein {Salmonella typhimurium}

ALPQTVRIGTDTTYAPFSSKDAKGEFIGFDIDLGNEMCKRMQVKCTWVASDFDALIPSLKA
KKIDAISSLSITDKRQQEIAFSKLYAADSRLIAAKGSP IQPTLES LKGKHVGV LQGSTQEA
YANDNWRTKGV DVVAYANQDLIYSDLTAGRLDAALQDEVAASEGFLKQPAGKEYAFAGP
SVKDKKYFGDGTGVGLRKDDTELKAAFDKALTEL RQDGT YDKMAKKYFDFNVYGD K

>d1sbp__ c.94.1.1 (-) Sulphate-binding protein {Salmonella typhimurium}

KDIQLLNVSYP TRELYEQYNKA FSAHWKQETGDNVVIDQSHGGSGKQATSVINGIEADT
VTLALAYDVNAIAERGRIDKNWIKRLPDD SAPYTSTIVFLVRKGNPKQIHDWNDLIKPGVS
VITPNPKSSGGARWNYLAAWGYALHHNNNDQAKAEDFVKALFKNVEVLDSGARGSTNT
FVERGIGDVLIAWENEALLATNELGKDKFEIVTPSESILAEPTVSVVDKVV EKKDTKAVAE
AYLKYLSP EGQEIAAKNFYRPRDADVAKKYDDAFPKLKLFTIDEVFGGWAKAQKD HFA
DGGTFDQISK

>d1ixh__ c.94.1.1 (-) Phosphate-binding protein {Escherichia coli}

EASLTGAGATFPAPVYAKWADTYQKETGNKVNYQGIGSSGGVKQIIANTVDFGASDAPLS
DEKLAQEGLFQFPTVIGGVVLAVNIPGLKSGELVLDGKTLGDIYLGKIKKWDDEAIAKLNP
GLKLPSQNI AVVRRADGSGTSFVFTSYLAKVNEEWKNNVGTGSTVKWPIGLGGKGN DGI
AAFVQRLPGAIGYVEYAYAKQNNLAYTKLISADGKPVSPTEENFANA AKGADWSKTFAQ
DLTNQKGEDAWPITSTTFILIHKDQKKPEQGTEVLKFFDWAYKTGAKQANDLDYASLPDS
VVEQVRAAWKTNIKDSSGKPLY

>d3mbp__ c.94.1.1 (-) D-maltodextrin-binding protein, MBP {Escherichia coli}

KIEEGKLV I WINGDKGYNGLA EVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIIF
WAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWD AVRYNGKLIAYPIAVEALS LIYNKDLL
PNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGKYDIKDV
GVDNAGAKAGLTFVLVDLIK NKMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKV
NYGVTVLP TFKGQPSKPFVGVLSAGINAASPNKELAKEFLENYLLTDEGLEAVNKDKPLG
AVALKS YEEELAKDPRIAATMENAQKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDEA
LKDAQTRITK

>d1elja_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Pyrococcus furiosus}

MKIEEGKVVIWHAMQPNELEV FQSLAE EYMALCPEVEIVFEQKPNLEDALKAAIPTGQGP
DLFIWAHDWIGKFAEAGLLEPID EYVTEDLLNEFAPMAQDAMQYKGHYALPFAAETVAI
IYNKEMVSEPPKTFDEMKAIMEKYYPANEKYGIAWPINAYFISAIAQAFGGYYFDDKTE
QPGLDKPETIEGFKFFFTEIWPYMAPTGDYNTQQSIFLEGRAPMMVNGPWSINDVKKAGI
NFGVVPLPPIIKDGKEYWPRPYGGVKLIYFAAGIKNKDAAWKFAKWLT TSESIKTLALEL
GYIPVLT KVLDDPEIKNDPVIYGFQGAVQHAYLMPKSPKMSAVWGGVDGAIN EILQDPQN
ADIEGILKKYQQEILNNMQ

>d1eu8a_ c.94.1.1 (A:) D-maltodextrin-binding protein, MBP {Archaeon Thermococcus litoralis}

IEEGKIVFAVGGAPNEIEYWKGVIAEF EK KYPGVTVELKRQATDTEQRRLDLVNALRGKSS
DPDVFLMDVAWL GQFIASGWLEPLDDYVQKDN YDLSVFFQSVINLADKQG GKLYALPVY
IDAGLLYYRKDLLEKYGYSKPPETWQELVEMAQKIQSGERETNP NFVWGFVWQGKQY EGL

VCDFVEYVYSNGGSLGEFKDGKWVPTLNKPENVEALQFMVDLIHKYKISPPNTYTEMTE
EPVRLMFQQGNAAFERNWPYAWGLHNADDSPVKGKVGVAPLPHFPGHKSAATLGGWHI
GISKYSDNKALAWEFVKFVESYSVQKGFAMNLGWNPNRVDVYDDPAVVSKSPHLKELRA
VFENAVPRPIVPYPQLSEIIQKYVNSALAGKISPQEALDKAQKEAEELVKQ

>d3thia_ c.94.1.1 (A:) Thiaminase I {*Paenibacillus thiaminolyticus*}

ITLKVAIYPYVPDPARFQAAVLDQWQRQEPGVKLEFTDWDSYSADPPDDLDPFVLDISIFLS
HFVDAGYLLPFGSQDIDQAEDVLPFALQGAKRNGEVYGLPQILCTNLLFYRKGDLDKIGQV
DNIYELYKKIGTSHSEQIPPPQNKGLLINMAGGTTKASMYLEALIDVTGQYTEYDLLPPLD
PLNDKVIRGLRLLINMAGEKPSQYVPEDGDAYVRASWFAQGSGRAFIGYSESMMRMGDY
AEQVRFKPISSAGQDIPLFYSDVSVNSKTAHPELAKKLANVMASADTVEQALRPQADG
QYPQYLLPARHQVYEALMQDYPIYSELAQIVNKPNSRVFRLGPEVRTWLKDAKQVLPEAL
G

>d1mrp_ c.94.1.1 (-) Ferric-binding protein {*Haemophilus influenzae*}

DITVYNGQHKEAATAVAKAFEQETGIKVTLSNGKSEQLAGQLKEEGDKTPADVIFYTEQTA
TFADLSEAGLLAPISEQTIQQTAKQGVPLAPKKDWIALSGRSRVVVDHTKLSEKDMEKS
VLDYATPKWKKGIGYVSTSGAFLEQVVALSKMKGDKVALNWLKGLKENGKLYAKNSVA
LQAVENGEPAAALINNYWYNLAKEKGVENLKSRLYFVRHQDPGALVSYSGAAVLKASK
NQAEAKQFVDFLASKKGQEALVAARAEYPLRADVVSFPNLEPYEKEAPVVSATTAQDK
EHAIKLIEEAGLK

>d1dpe_ c.94.1.1 (-) Dipeptide-binding protein {*Escherichia coli*}

KTLVYCSEGSPEGFNPQLFISGTTYDASSVPLYNRLVEFKIGTTEVIPGLAEKWEVSEDGKT
YTFHLRKGVKWHDNKEFKPTRELNADDVVFSFDRQKNAQNPYHKVSGGSYEYFEGMGL
PELISEVKKVDDNTVQFVLTRPEAPFLADLAMDFASILSKEYADAMMKAGTPEKLDLNP
GTGPFQLQQYQKDSRIRYKAFDGYWGTPQIDTLVFSITPDASVRYAKLQKNECQVMPYP
NPADIARMKQDKSINLMEMPGLNVGYLSYNVQKKPLDDVKVRQALTYAVNKDAIIKAVY
QGAGVSAKNLIPPTMWGYNDVQDYTYDPEKAKALLKEAGLEKGFSDLWAMPVQRPY
NPNARRMAEMIQADWAKVGVQAKIVTYEWGEYLKRAKDGEHQTVMMGWTGDNGDPD
NFFATEFSCAASEQGSNYSKWICYKPFEDLIQPARATDDHNRVELYKQAQVVMHDQAPA
LIIAHSTVFEPVRKEVKGYVVDPLGKHHFENVISIE

>d1pot_ c.94.1.1 (-) Spermidine/putrescine-binding protein PotD {*Escherichia coli*}

NNTLYFYNWTEYVPPGLLEQFTKETGIKVIYSTYESNETMYAKLKTYKDGAYDLVVPSTY
YVDKMRKEGMIQKIDKSKLTNFSNLDPDMLNKPFDPNNDYSIPYIWGATAIGVNGDAVDP
KSVTSWADLWKPEYKGSLLLTDAREVFQMALRKLGYSGNTTDPKEIEAAYNELKKLMP
NVAAFNSDNPANPYMEGEVNLGMIWNGSAFVARQAGTPIDVWPKEGGIFWMDSLAIPA
NAKNKEGALKLINFLRPDVAKQVAETIGYPTPNLAARKLLSPEVANDKTLYPDAETIKNG
EWQNDVGAASSIYEEYYQKLKAG

>d1a99a_ c.94.1.1 (A:) Putrescine receptor (PotF) {*Escherichia coli*}

QKTLHIYNWSDYIAPDTVANFEKETGIKVVDVFDSDNEVLEGKLMAGSTGFDLVVPSASF
LERQLTAGVFQPLDKSKLPEWKNLDPELLKLVAKHDPDNKFAMPYMWATTGIGYNVDKV
KAVLGENAPVDSWDLILKPENLEKLKSCGVSFLDAPEEVFATVLNLYLGKDPNSTKADDYT
GPATDLLLKLRPNIYFHSSQYINDLANGDICVAIGWAGDVWQASNRAKEAKNGVNVSFS
IPKEGAMAFFDVFAMPADAKNKDEAYQFLNYLLRPDVVAHISDHVFIYANANKAATPLVSA
EVRENPGIYPADVRAKLFTLVQDPKIDRVRTRAWTKVKSG

>d1wdna_ c.94.1.1 (A:) Glutamine-binding protein {*Escherichia coli*}

KLVVATDTAFVPFEFKQGDLYVGFVDLWAAIAKELKLDYELKPMDFSGIIPALQTKNVDL
ALAGITITDERKKAIDFSDGYYSGLLMVKANNNDVKSVDLDGKVVAVKSGTGSVDY
AKANIKTKDLRQFPNIDNAYMELGTNRADAVLHDTNPLYFIKTAGNGQFKAVGDSLEAQ
QYGIAPFKGSDELKDKVNGALKTLRENGTYNEIYKKWFGTEPK

>d1ftka_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Rat (*Rattus norvegicus*), GluR2}
KTVVVTILESPYVMMKKNHEMLEGNERYEGYCVDLAAEIAKHCGFKYKLTIVGDGKY
GARDADTKIWNGMVGELVYGADIAIAPLTITLVREEVIDFSKPFMSLGISIMIKKPGTDGN
PIESAEDLSKQTEIAYGTLDSGSTKEFFRRSKIADFDMWTYMRSAEPSVFRVTTAEGVAR
VRKSKGKYAYLLESTMNEYIEQRKPCDTMKVGGNLDKGYGIATPKGSSLGNVNLAVL
KLNEQGLLDKLNKWWYDKGEC

>d1ii5a_ c.94.1.1 (A:) Glutamate receptor ligand binding core {Synechocystis sp., GluR0}

GSAMALKVGVVGNPPFVYGEKNAAFSGISLDVWRAVAESQKWNSEYVRQNSISAGIT
AVAEGELDILIGPISVTPERAAIEGITFTQPYFSSGIGLLIPGTATPLFRSVGDLKNKEVAVVR
DTTAVDWANFYQADVRETNLTAITLLQKKQVEAVMFDRPALIYYTRQNPNLNLEVTEI
RVSLEPYGFVLKENSPLQKTINVEMLNLLYSRVIAEFTERWLG

>d1amf_ c.94.1.1 (-) Molybdate-binding protein, ModA {*Escherichia coli*}

GKITVFAAASLTNAMQDIATQFKKEKGVDVSSFASSTLARQIEAGAPADLFISADQKW
MDYAVDKKAIDTATRQTLGNSLVVAPKASVQKDFTIDSKTNWTSLLNGGRLAVGDPEH
VPAGIYAKEALQKLGAWDTLSPKLAPAEDVRGALALVERNEAPLGIVYGSDAVASKGVKV
VATFPEDSHKKVEYPVAVVEGHNNATVKAFYDYLKGPQAAEIFKRYGFTIK

>d1atg_ c.94.1.1 (-) Molybdate-binding protein, ModA {*Azotobacter vinelandii*}

ELKVVATATNFLTLEQLAGQFAKQTGHAVVISSGSSGPVYAQIVNGAPYNVFFSADEKSPE
KLDNQGFALPGSRFTYAIGKLVLSAKPGLVDNQGKVLGNGWRHIAISNPQIAPYGLAG
TQVLTHLGLLDKLTAQERIVEANSVGQAHSQTASGAADLGFVALAQIIQAAAKIPGSHWFP
PANYYEPIVQQAVITKSTAEKANAEQFMSWMKGPKAVAIKAAGYVLPQ

>d1al3_ c.94.1.1 (-) Cofactor-binding fragment of CysB {*Klebsiella aerogenes*}

TWPDKGSlyvatTHTQARYALPGVIKGFIERYPVSLHMHQGSPTQIAEAVSKGNADFAIA
TEALHLYDDLVMPLPCYHWNRSIVVTPEHPLATKGSVSIEELAQYPLVITYTFGFTGRSELDT
AFNRAGLTPRIVFTATDADVIKTYVRLGLGVGVIASMAVDPVSDPDLVKLDANGIFSHSTT
KIGFRRSTFLRSYMYDFIQRFAHLTRDVTDAVALRSNEDIEAMFKDIKLPEK

>d1i6aa_ c.94.1.1 (A:) Hydrogen peroxide-inducible genes activator OxyR, regulatory domain {*Escherichia coli*}

ETMSGPLHIGLIPTVGPYLLPHIIPMLHQTFPKLEMYLHEAQTHQLLAQLDSGKLDVILAL
VKESEAFIEVPLFDEPMLLAIEDHPWANREAVPMADLAGEKLLMLEDGHCLRDQAMGF
CFEAGADEDTFRATSLETLRNMVAAGSGITLLPALAVPPERKRDGVVYLPAIKPEPRRTIG
LVYRPGSPLRSRYEQLAEAIRARMDGHFD

>d1kwha_ c.94.1.1 (A:) Alginate-binding periplasmic protein AlgQ2 {*Sphingomonas* sp.}

KEATWVTDKPLTLKIHMHFRDKWVDENWPVAKESFRLTNVKLQSVANKAATNSQEQQF
NLMMASGDLDPDVGGDNLDKDKFIQYGQEGAFVPLNKLIDQYAPHIKAFFKSHPEVERAIK
APDGNIFYFIPYVPDGVVARGYFIREDWLKKNLKPQNIDELYTVLKAFKEKDPNGNGKA
DEVFPIDRHPDEVFRLVNFVGARSSGSDNYMDFYIDNGRVKHPWAETAFRDGMKHVAQ
WYKEGLIDKEIFTRKAKAREQMFGGNLGGFTHDWFASTMTFNEGLAKTVPGFKLIPIAPP
TNSKGQRWEEDSRQKVRPDGWAITVKNKNPVETIKFFDFYFSRPGRDISNFGVPGVTYDI

KNGKAVFKDSVLKSPQPVNNQLYDMGAQIPIGFWQDYDYERQWTTPEAQAGIDMYVKG
KYVMPGFEGVNM TREERA IYDKY WADV RTYMYEMGQAWVMGTDVDKTWDEYQRQ
LKLRLGLYQVLQMMQQAYDRQYKN

>d1cb6a2 c.94.1.2 (A:1335-1691) Lactoferrin {Human (Homo sapiens)}

EEEVAARRARVVWCAVGEQELRKCNQWSGLSEGSVTCSSASTTEDCIALVLKGEADAMS
LDGGYVYTAGKCGLVPVLAENYKSQQSSDPDPCVDRPVEGYLAVAVRRSDTSLTWNS
VKGKKSCHTAVDRTAGWNIPMGLLFNQGTGCKFDEYFSQSCAPGSDPRS NL CALCIGDEQ
GENKCVPSNERYYG YTGAFRCLAENAGDVAFVKDVTVLQNTDGNNNEAWAKDLKLA
DFALLCLDGKRKPVTEARSCHLAMAPNHAVVSRMDKVERLKQVLLHQAKFGRNGSDC
PDKFCLFQSETKNLLFNDNTECLARLHGKTTYEKYLG PQYVAGITNLKKCSTSPLEACEF
LRK

>d1dot_1 c.94.1.2 (1-334) Ovotransferrin {Duck (Anas platyrhynchos)}

APPKTTVRWCTISSAEEKKCN SLKDHMQQERVTLSCVQKATYLDCAISNNEADAISLDG
GQVFEAGLAPYKLP IAAEVYERSSGSTTSYYAVAVVKKGTDFMIKDLRGKTSCHTGLGR
SAGWNIPIGTLIHREDIEWEGIESGISEQAVAKFFSASCVP GATIEQKLCRQCKGDAKTKCL
RNGPYSGYSGAFQCLKDGKGDVAFVKHTTVQENAPEEKDEYELLCLDGSRQPVD SYKTC
NWARVA AHAVVARDDSKIDDIWSFLGMQAYSLGVDTTSD FHLFGPPGKKDPVLKDLLFK
DSAIMLKRVPELMDSQLYLGFEYYS AIQSLRKD

>d1afwa1 c.95.1.1 (A:25-293) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

KNSLLEKRPEDVVIVAANRSAIGKGFKGAFKDVNTDYLLYNFLNEFIGRFPEPLRADLNLIE
EVACGNVLNVGAGATEHRAACLASGIPYSTPFVALNRQCSSGLTAVNDIANKIKVGQIDIG
LALGVESMTN NYKNVNPLGMISSEELQKNREAKKCLIPMGITNENVAANFKISRKDQDEF
AANSYQKAYKAKNEGLFEDEILPIKLPDGSICQSDEGPRPNVTAESLSSIRPAFIKDRGTTTA
GNASQVSDGVAGVLLARRSVANQ

>d1afwa2 c.95.1.1 (A:294-417) Thiolase {Baker's yeast (Saccharomyces cerevisiae)}

LNLPLVGLRYIDFQTVGVPPEIMGVGPAYAI PKVLEATGLQVQDIDIFEINEAFAAQALYCIHK
LGIDLNKVNP RGGAI ALGHPLGCTGARQVATILRELKKDQIGVVSMCIGTGMGAAAI FIK

>d1qla1 c.95.1.1 (A:4-268) Biosynthetic thiolase {Zoogloea ramigera}

SIVIASAARTAVGSFN GAFANTPAHEL GATVISAVLERAGVAAGEVNEVILGQVLPAGEGQN
PARQAAMKAGVPQEATAWGMNQLCGSGLRAVALGMQ QIATGDASIIVAGGMESMSMAP
HCAHLRGGVKMGDFKMIDTMIKDGLTDAFYGYHMGTTAENVAKQWQLSRDEQDAFAVA
SQNKAEAAQKDGRFKDEIVPFIVKGRKGDITVDADEYIRHGATLDSMAKL RPAFDKEGTV
TAGNASGLNDGAAAALLMSEAEASRRG

>d1ek4a1 c.95.1.1 (A:1-253) Beta-ketoacyl-ACP synthase I {Escherichia coli}

MKRVVITGLGIVSSIGNNQEV LASLREGRSGITFSQELKD SGMRSHVWGNVKLDTTGLI
DRKVVRFMSDASIYAFLSMEQAIADAGLSPEAYQNNPRVGLIAGSGGGS PRFQVFGADAM
RGPRGLKAVGPYVVT KAMASGVSA CLATPFKIHGVNYSISSASATSAHCIGNAVEQIQLGK
QDIVFAGGGEE LCWEMACEFDAMGALSTKYNDTPEKASRTYDAHRDGFVIAGGGGMVV
VEELEHALARGAHI

>d1kas_1 c.95.1.1 (2-251) Beta-ketoacyl-ACP synthase II {Escherichia coli}

KRRVVVTGLGMLSPVGNTVESTWKALLAGQSGISLIDHFDTSAYATKFAGLVKDFNCEDII
SRKEQRKMDAFIQYGIVAGVQAMQDSGLEITEENATRIGAAIGSGIGGLGLIEENHTSLMN
GGPRKISPFVPSTIVNMVAGHLTIMYGLRGPSISIATACTSGVHNIGHAARI IAYGDADVM
VAGGAEKASTPLGVGGFGAARALSTRNDNPQAASRPWDKERDGFVLGDGAGMLVLEEY

EHAKKRG

>d1kas_2 c.95.1.1 (252-412) Beta-ketoacyl-ACP synthase II {Escherichia coli}
KIYAEVLGFGMSSDAYHMTSPENGAGAALAMANALRDAGIEASQIGYVNAHGTSTPAG
DKAEAQAVKTIFGEAASRVLSSTKSMTGHLLGAAGAVESIYSILALRDQAVPPTINLDNP
DEGCDLDFVPHEARQVSGMEYTLCSFGFGGTNGSLIFKKI

>d1hnja2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Escherichia coli}
ISTHLHADGSYGELLTLPNADRVNPENSIHLMAGNEVFKVAVTELAHIVDETLAANNLDR
SQLDWLVPHQANLRIISATAKKLGMSMDNVVVTLDHRHGNTSAASVPCALDEAVRDGRIK
PGQLVLLEAFGGGFTWGSALVRF

>d1hzpa1 c.95.1.1 (A:-10-174) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}

MTEIATTSGARSVGLLSVGAYRPERVVTNDEICQHIDSSDEWIYTRTGIKTRRFAADDESAA
SMATEACRRALSNAGLSAADIDGVIVTTNTHFLQTPPAAPMVAASLGAKGILGFDLSAGC
AGFGYALGAAADMIRGGGAATMLVVGTEKLSPTIDMYDRGNCFIFADGAAAVVVGETPF
QGI

>d1hzpa2 c.95.1.1 (A:175-317) Ketoacyl-ACP synthase III (FabH) {Mycobacterium tuberculosis}

GPTVAGSDGEQADAIRQDIDWITFAQNPSGPRPFVRLEGPAVFRWAAFKMGDVGRRAMD
AAGVRPDQIDVFVPHQANSRINELLVKNLQLRPDAVVANDIEHTGNTSAASIPLAMAELLT
TGAAKPGDLALLIGYGAGLSYAAQVVRM

>d1bi5a1 c.95.1.2 (A:1-235) Chalcone synthase {Alfalfa (Medicago sativa)}

MVSVSEIRKAQRAEGPATILAIGTANPANCVEQSTYPDFYFKITNSEHKTTELKEKFQRMCD
KSMIKRRYMYLTEEILKENPNVCEYMAPSLDARQDMVVVEVPRLGKEAAVKAIKEWGQP
KSKITHLIVCTTSGVDMPGADYQLTKLLGLRPYVKRYMMYQQGAFAGGTVLRRLAKDLAE
NNKGARVLVVCSEVTAVTFRGPSDTHLDSL VGQALFGDGAAALIVGSDPVPEIEKP

>d1ee0a2 c.95.1.2 (A:236-395) Pyrone synthase (PyS, chalcone synthase 2) {Gerbera hybrida}
AVERPIFEIVSTDQTLIPDEKAMKHLHREGGLTFQLHRDVPLMVAKNIENAAEKALSPLGI
TDWNSVFWMVHPGGRAILDQVERKLNKEDKLRASRHLVSEYGNLISACVLFIIDEVRKR
SMAEGKSTTGEGLDCGVLF GFGPGMTVETVVLRSVRVT

>d1aln_1 c.97.1.1 (1-150) Cytidine deaminase {Escherichia coli}

MHPRFQTAFAQLADNLQSALEPILADKYFPALLTGEQVSSLKSATGLDEDALAFALLPLAA
ACARTPLSNFNVGAIARGVSGTWYFGANMEFIGATMQQTVHAEQSAISHAWLSGEKALA
AITVNYTPCGHCRQFMNELNSGLDLRIHLP

>d1aln_2 c.97.1.1 (151-294) Cytidine deaminase {Escherichia coli}

GREAHALRDYLPDAFGPKDLEIKTLLMDEQDHGYALTGDALSQAAIAAANRSHMPYSKS
PSGVALECKDGRIFSGSYAENAAFNP TLPLQ GALILLNLKGYDYPDIQRAVLAEKADAPLI
QWDATSATLKALGCHSIDRVLLA

>d1fus__ d.1.1.1 (-) RNase F1 {Fusarium moniliforme}

ESATTCGSTNYSASQVRAAANAACQYYQNDDTAGSSTYPHTYNNYEGFDFPVDGPYQEF
PIKSGGVYTGGSPGADRVVINTNCEYAGAITHTGASGNNFVGCSGTN

>d1rtu__ d.1.1.1 (-) RNase U2 {Ustilago sphaerogena}

CDIPQSTNCGGNVYSNDDINTAIQGALDDVANGDRPDNYPHQYYXEASEDITLCCGSGPW
SEFPLVYNGPYYSRDNYVSPGPDRVIYQTNTGEFCATVTHTGAASYDGFTQCS

>d1goua__ d.1.1.1 (A:) Barnase/Binase {Bacillus intermedius}

AVINTFDGVADYLIRYKRLPNDYITKSQASALGWVASKGDLAEVAPGKSIGGDVFSNREGR
LPSAGSRTWREADINYVSGFRNADRLVYSSDWLIYKTTDHYATFTRIR

>d0rst_ d.1.1.1 (-) RNase St {*Streptomyces erythreus*}

QAPCGDTSGFEEVRLADLPPEATDTYELIEKGGPYYPEDGTVFENREGILPDCAEGYYHE
YTVKTPSGDDRGAARRFVVGDGGEYFYTEDHYESFRLTIVN

>d1de3a_ d.1.1.1 (A:) Ribotoxin {Fungus (*Aspergillus giganteus*), alpha-Sarcin}

AVTWTCLNDQKNPKTNKYETKRLLYNQKAESNSHHAPLSDGKTGSSYPHWFTNGYDG
DGKLPKGRTPIKFGKSDCDRPPKHSKDGNKTDHYLLEFPTFPDGHDKFDSKKPKENPG
PARVIYTYPNKVFCGIIAHTKENQGELKLCSH

>d1lsg_1 d.2.1.2 (1-144) Lysozyme {Chicken (*Gallus gallus*)}

MKVFGRCELAAAMKRHGLDNYRGYSLGNWVCAAKFESNFNTQATNRNTDGDSTDYGILQ
INSRWWCNDGRTPGSRNLCNIPCSALLSSDITASVNC AKKIVSDGNMNAWVAWRNRCK
GTDVQAWIRGCRLQQHHLGGAKQAGDV

>d1b9oa_ d.2.1.2 (A:) alpha-Lactalbumin {Human (*Homo sapiens*)}

KQFTKCELSQLLKDIDGYGGIALPELICTMFHTSGYDTQAIVENDESTEYGLFQISNKLWC
KSSQVPQSRNICDISCDKFLDDDDITDDIMCAKKILDIKGIDYWLAKALCTEKLQWLCEK
L

>d1qsaa2 d.2.1.6 (A:451-618) 70 kDa soluble lytic transglycosylase, SLT70 {*Escherichia coli*}

LAYNDLFKRYTSGKEIPQSYAMAIARQESAWNPKVKSPVGASGLMQIMPGTATHTVKMFS
IPGYSSPGQLLPETNINIGTSYLQYVYQQFGNNRIFSSAAYNAGPGRVRTWLGN SAGRID
AVAFVESIPFSETRGYVKNVLAYDAYRYFMGDKPTLMSATEWGRRY

>d1qusa_ d.2.1.6 (A:) 36 kDa soluble lytic transglycosylase, SLT35 {*Escherichia coli*}

MVEPQHNVMMQMGDFANNPNAQQFIDKMVNKHGFD RQQLQEILSQA KRLDSVLR LMD
NQAPTTSVKPPSGPNGAWLRYRKKFITPDNVQNGVFWNQYEDALNRAWQVYGPPEII
VGIIGVETRWGRVMGKTRILDALATLSFNYPRAEYFSGELETFLLMARDEQDDPLNLKG
SFAGAMGYGQFMPSSYKQYAVDFSGDGHINLWDPVDAIGSVANYFKAHGWVKGDQVAV
MANGQAPGLPNGFKTKYSISQLAAAGLTPQQPLGNHQQASLLRLDVGTGYQYWYGLPN
FYTITRYNHSTHYAMAVWQLGQAVALARVQ

>d1chka_ d.2.1.7 (A:) Endochitinase {*Streptomyces* sp., strain N174}

AGAGLDDPHKKEIAMELVSSAENSSLDWKAQYKYIEDIGDGRGYTGGIIGFCSGTGDMLE
LVQHYTDLEPGNILAKYLPALKKVNGSASHSGLGTPFTKDWATAAKDTVFQQAQNDERD
RVYFDPAVSQAKADGLRALGQFAYYDAIVMHGPGNDPTSFGGIRKTAMKKARTPAQGGD
ETTYLNGFLDARKAAMLTEAAHDDTSRVDTEQRVFLKAGNLDLNPPLKWKTYGDPYVIN
S

>d1qgia_ d.2.1.7 (A:) Endochitinase {*Bacillus circulans*}

ASPDDNFSPETLQFLRNNTGLDGEQWNNIMKLINKPEQDDL N WIKYYGYCEDIEDERGYT
IGLFGATTGGSRDTHPDGPDFKAYDAAGASNP SADGALKRLGINGKMKGSILEIKDSE
KVFCGKIKKLQNDAAWRKAMWETFYNVYIRYSVEQARQRGFTSAVTIGSFVDTALNQGA
TGGSDTLQGLLARGSSSNEKTFMKNFHAKRTL VVD TNKYNKPPNGKNRVKQWDTLVD
MGKMNLKNVDSEIAQVTDWEMK

>d1pcia_ d.3.1.1 (A:) Caricain (protease omega) {Papaya (*Carica papaya*)}

LTSTERLIQLFNSWMLNHNKFYENVDEKLYRFEIFKDNLNYIDETNKKNN SYWLGLNEFA
DLSNDEFNEKYVGLIDATIEQSYDEEFINEDIVNLPENVDWRKKGAVTPVRHQGSCGSC
WAFSAVATVEGINKIRTGKLVELSEQELVDCERRSHGCKGGYPPYALEYVAKNGIHLRSKY

PYKAKQGTCTRAKQVGGPIVKTSQVGRVQPNNEGNLLNAIAKQPVSVVVESKGRPFQLYK
GGIFEGPCGTKVDGAVTAVGYGKSGGKGYILIKNSWGTAWGEKGYIRIKRAPGNSPGVCG
LYKSSYYPTKN

>d3gcb__ d.3.1.1 (-) Bleomycin hydrolase {Baker's yeast (Saccharomyces cerevisiae), Gal6}

AFQGAMASSIDISKINSWNKEFQSDLTHQLATTVLKNYNADDALLNKTRLQKQDNRVFNT
VVSTDSTPVTNQKSSGRAWLFAATNQLRLNVLSELNLKEFELSQAYLFFYDKLEKANYFL
DQIVSSADQDIDSRLVQYLLAAPTEDGGQYSMFLNLVKKYGLIPKDLYGDLPYSTTASRK
WNSLLTTKLREFAETLRTALKERSADDSIIVTLREQMQREIFRLMSLFMDIPPVQPNEQFTW
EYVDKDKKIHTIKSTPLEFASKYAKLDPSTPVSLINDPRHPYGKLIKIDRLGNVLGGDAVIY
LNVNETLSKLVVKRLQNNKAVFFGSHTPKFMDKKTGVMDIELWNYPAGYNLPQQKAS
RIRYHESLMTHAMLITGCHVDETSKLPLRYRVENSWGKDSGKDGLYVMTQKYFEEYCFQI
VVDINELPKELASKFTSGKEEPIVLPIWDPMGALA

>d2cb5a_ d.3.1.1 (A:) Bleomycin hydrolase {Human (Homo sapiens)}

SSSGLNSEKVAALIQKLNSDPQFVLAQNVGTTHDLLDICLKRA TVQRAQHVFQHAVPQEG
KPITNQKSSGRSWIFSCLVNVMRLPFMKKLNIEEFESQSYLFFWDKVERCYFFLSAFVDTA
QRKEPEDGRLVQFLLMNPANDGGQWDMVLVNIVEKYGVIPKKCFPESYTTEATRRMNDIL
NHKMREFCIRLRNLVHSGATKGEISATQDVMMEEIFRVVCICLGNPPETFTWEYRDKDN
YEKIGPITPLEFYREHVKPLFNMEDKICLVNDPRPQHKNKLYTVEYLSNMVGGRTLYN
NQPIDFLKKMVAASIKDGEAVWFGCDVGKHFNSKLGSLDMNLYDHEL VFGVSLKNMNK
AERLTFGESLMTHAMTFTAVSEKDDQDGAFTKWRVENS WGEDHGHKG YLCMTDEWFSE
YVYEVVVD RKHVPEEVLAVLEQEPIILPAWDPMGALA

>d3pbh__ d.3.1.1 (-) (Pro)cathepsin B {Human (Homo sapiens)}

MRSRPSFHPLSDELVNYVNKRNTTWQAGHNFYNVDMSYLRKLCGTF LGGPKPPQRVMF
TEDLKLPA SFDAREQWPQCPTIKEIRDQGSCGSCWAFGAVEAISDRICHTNAHVSVEVSAE
DLLTCCGSMCGDGCNGGYPAEAWNFWTRKGLVSGGLYESHV GCRPYSIPPCEHHVNGSR
PPCTGEGDTPKCSKICEPGYSPTYKQDKHYGYNSYSVSNSEKDIMAEIYKNGPVEGA FSV
YSDFLLYKSGVYQHVTGEMMGHAI RILGWGVENGTPYWL VANSWNTDWGDNGFFKIL
RGQDHCGIESEVVAGIPRTD

>d1cs8a_ d.3.1.1 (A:) (Pro)cathepsin L {Human (Homo sapiens)}

SLTFDHSLEAQWTKWKAMHNRLYGMNEEGWRRAVWEKNMKMIELHNQEYREGKHSFT
MAMNAFGDMTSEEFRQVMNGFQNRKPRKGKVFQEPLFYEAPRSVDWREKGYVTPVKN
QGQCSCSWAFSATGALEGQMFRKTGRLISLSEQNLVDCSGPQGNEG CNGGLMDYAFQYV
QDNGGLDSEESYPYEATEESCKYNPKYSVANDAGFVDIPKQEKALMKAVATVGPISVAIDA
GHESFLFYKEGIYFEPDCSSEDMDHGVLVVG YGFESTESDNNKYWL VKNSWGEEWGMG
GYVKMAKDRRNHCGIASAASYPTV

>d1deua_ d.3.1.1 (A:) (Pro)cathepsin X {Human (Homo sapiens)}

RGQTCYRPLRGDGLAPLGRTTYPRPHEYLSPADLPKSWDWRNV DGVNYASITRNQHIPQY
CGSCWAHASTSAMADRINIKRKGAWPSTLLSVQNVIDCGNAGSCEGGNDLSVWDYAHQ
HGIPDETCNNYQAKDQECDKFNQCGTCNEFKECHAIRNYTLWRVGDYGSLSGREKMMMA
EIYANGPISCGIMATERLANYTGGIYAEYQDTTYINHVVSVAGWGISDGTEYWIVRNSWGE
PWGERGWLRIVTSTYKDGKGARYNLAIEEHCTFGDPIV

>d1cv8__ d.3.1.1 (-) Staphopain {Staphylococcus aureus}

NEQYVNKLENFKIRETQGNNGWCAGYTMSALLNATYNTNKYHAEAVMRFLHPNLQGQQ

FQFTGLTPREMIYFGQTQGRSPQLLNRMTTYNEVDNLTKNNGIAILGSRVESRNGMHAG
HAMAVVGNAKLNNNGQEVIIIWNPWDNGFMTQDAKNNVIPVSNGDHYQWYSSIIYGY
>d1dkia_ d.3.1.1 (A:) Streptococcal pyrogenic exotoxin B {Streptococcus
pyogenes}
LDKVNLGGEISGSNMYVYNISTGGFVIVSGDKRSPEILGYSTSGSFDVNGKENIASFMESY
VEQIKENKKLDSTYAGTAEIKQPVVKSLLDSKGIHYNQGNPYNLLTPVIEKVKPGEQSFVG
QHAATGSVATATAQIMKYHNYPNKGLKDYYTYTLSSNNPYFNHPKNLFAAISTRQYNWNNI
LPTYSGRESNVQKMAISELMADVGISVDMDYGPSSGSAGSSRVQRALKENFGYNQSVHQI
NRGDFSQDWEAQIDKELSQNPVYYQGVGKVGGHAFVIDGADGRNFYHVNWGWGG
VSDGFFRLDALNPSALGTGGGAGGFNGYQSAVVGIKP
>d1uch_ d.3.1.6 (-) Ubiquitin C-terminal hydrolase UCH-L3 {Human (Homo sapiens)}
RWLPLEANPEVTNQFLKQLGLHPNWQFVDVYGMPELLSMVPRPVCALLLPITEKYE
VFRTEEEKIKSQGQDVTSSVYFMKQTISNACGTIGLIHAIANNKDKMHFESGSTLKKFLE
ESVSMSPPEARARYLENYDAIRVTHETSAHEGQTEAPSIDEKVLDLHFIALVHVDGHLIELDG
RKPPPINHGETSDETLLEDAIEVCKKFMERDPDELRFNAIALSAA
>d1cmxa_ d.3.1.6 (A:) Ubiquitin C-terminal hydrolase UCH-L3 {Synthetic, based on
Saccharomyces cerevisiae sequence}
RAVVPIESNPEVFTNFAHKLGLKNEWAYFDIYSLTEPELLAFLPRPVKAIVLLFPINEDRKSS
TSQQITSSYDVIWFKQSVKNACGLYAILHSLSNNQSLLEPGSDLDNFLKSQSDTSSSKNRFD
DVTDDQFVLNVIKENVQTFSTGQSEAPEATADTNLHYITYVEENGIFELDGRLNSGLPYL
GKSDPTATDLIEQELVRVRVASYMENANEEDVLNFAMLGPGN
>d1avpa_ d.3.1.7 (A:) Human adenovirus 2 proteinase {Mastadenovirus H2}
MGSSEQELKAIVKDLGCGPYFLGTYDKRFPGFVSPHKLACAIVNTAGRETGGVHWMFAFA
WNPRSKTCYLFEPFGFSDQRLKQVYQFEYESLLRRSAIASSPDRCTITLEKSTQSVQGPNSA
ACGLFCCMFLHAFANWPQTPMDHNPTMNLITGVPSNMLNSPQVQPTLRRNQEQLYSFLE
RHSPYFRSHSAQIRSATSFCHLKNM
>d1euva_ d.3.1.7 (A:) Ulp1 protease C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}
GSLVPELNEKDDDQVQKALASRENTQLMNRDNIEITVRDFKTLAPRRWLNDTIIIEFFMKYI
EKSTPNTVAFNSFFYTNLSERGYQGVRRWMKRKKTQIDKLDKIFTPINLNQSHWALGIIDL
KKKTIGYVDSLNGPNAMSFALITDLQKYVMEESKHTIGEDFDLIHLDCPQPNGYDCGIY
VCMNTLYGSADAPLDFDYKDAIRMRRFIAHLILTALK
>d1h8xa_ d.5.1.1 (A:) Ribonuclease A (also ribonuclease B, S) {Cow (Bos taurus)}
KESAAAKFERQHMDSGNSPSSSSTYCNQMMRRRNMTQGRCKPVNTFVHEPLVDVQNVNC
FQEKVTCKNGQGNCYKSNSSMHITDCRLTNGSRYPNCAYRTSQKERHIIVACEGSPYVPV
HFDASVE
>d1bc4_ d.5.1.1 (-) Cytotoxic ribonuclease {Bullfrog (Rana catesbeiana)}
ENWATFQQKHIINTPIINCNTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVINMNVLST
TRFQLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP
>d1hi2a_ d.5.1.1 (A:) Eosinophil-derived neurotoxin (EDN) {Human (Homo sapiens)}
MKPPQFTWAQWFETQHINMTSQQCTNAMQVINNYQRRCKNQNTFLLTTFANVVNVCGN
PNMTCPSNKTRKNCHHSGSQVPLIHCNLTTPSPQNISNCRYAQTPANMFYIVACDNRDQRR
DPPQYPVVPVHLDRII
>d1agi_ d.5.1.1 (-) Angiogenin {Cow (Bos taurus)}
AQDDYRYIHFLTQHYDAKPKGRNDEYCFNMMKNRRLTRPCKDRNTFIHGNKNDIKAICE

DRNGQPYRGDLRISKSEFQITICKHKGGSSRPPCRYGATEDSRVIVVGCENGLPVHFDESFI
TPRH

>d1i4ma_ d.6.1.1 (A:) Prion protein domain {Human (Homo sapiens)}

GAVVGGLGGYMLGSAMSRPIIHFGSDYEDRYRENMHRYPNQVYYRPMDEYSNQNNFV
HDCVNITIKQHTVTTTTTKGENFTETDVKMMERVVEQMCITQYERESQAYY

>d1i17a_ d.6.1.1 (A:) Prion-like protein Doppel {Mouse (Mus musculus)}

RVAENRPGAFIKQGRKLDIDFGAEGNRYYAANYWQFPDGIYYEGCSEANVTKEMLVTSC
VNATQAANQAEFSREKQDSKLHQRVLWRLIKEICSAKHCDFWLERGAA

>d1mgas_ d.9.1.1 (A:) Melanoma growth stimulating activity (MGSA) {Human (Homo sapiens)}

ASVATELRQCQLQTLQGIHPKNIQSVNVKSPGPHCAQTEVIATLKNRKAACLNPPASPIVKKI
IEKMLNSDKSN

>d1lhuna_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Human (Homo sapiens), 1-beta}

APMGSDPPTACCFSTARKLPRNFVVDYYETSSLCSQPAVVFQTKRSKQVCADPSESWWQ
EYVYDLELN

>d1ha6a_ d.9.1.1 (A:) Macrophage inflammatory protein, MIP {Mouse (Mus musculus), ccl20/mip-
3a}

ASNYDCCLSYIQTPLPSRAIVGFTRQMADEACDINAIFHTKKRKSVCADPKQNWVKRAV
NLLSLRVKKM

>d1esra_ d.9.1.1 (A:) Monocyte chemoattractant protein-2 (MCP-2) {Human (Homo sapiens)}

EPDSVSIPITCCFNVINRKIPIQRLESYTRITNIQCPKEAVIFKTQRGKEVCADPKERWVRDS
MKHLDQIFQNLKP

>d1el0a_ d.9.1.1 (A:) CC chemokine I-309 {Human (Homo sapiens)}

SKSMQVPFSRCCFSFAEQEIPLRAILCYRNTSSICSNEGLIFKLKRGKEACALDTVGWVQR
HRKMLRHCPSKRK

>d1eiha_ d.9.1.1 (A:) Eotaxin-2 {Human (Homo sapiens)}

VVIPSPCCMFFVSKRIPENRVVSYQLSSRSTCLKAGVIFTTKKGQSCGDPKQEWVQRYM
KNLDAKQKKASPR

>d1j9oa_ d.9.1.1 (A:) Lymphotoxin {Human (Homo sapiens)}

VGSEVSDKRTCVSLLTQRLPVSRIKTYTITEGSLRAVIFITKRGLKVCADPQATWVRDVVRS
MDRKSNTNRNNMIQTKPTGTQOSTNTAVTLTG

>d1b2ta_ d.9.1.1 (A:) Chemokine domain of fractalkine {Human (Homo sapiens)}

MQHHGVTKCNITCSKMTSKIPVALLIHYQQNQASCGKRAIILETRQHRLFCADPKEQWVK
DAMQHLDRQAAALTRNG

>d1a15a_ d.9.1.1 (A:) Stromal cell-derived factor-1 (SDF-1) {Human (Homo sapiens)}

KPVSLSYRCPCRFFESHVARANVKHLKILNTPACALQIVARLKNNNRQVCIDPKLKWIEY
LEKALN

>d1g91a_ d.9.1.1 (A:) Myeloid progenitor inhibitory factor-1 (MPIF-1) {Human (Homo sapiens)}

MDRFHATSADCCISYTPRSIPCSLLESYFETNSECSKPGVIFLTKKGRRFCANPSDKQVQVC
MRMLKLDTRIKTRKN

>d1ap0_ d.9.2.2 (-) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}

HMVEEVLEEEEEYVVEKVLDRRVVKGKVEYLLKWKGFSDNTWEPEENLDCPDLIAE
FLQSQKTAHETDKS

>d1dz1a_ d.9.2.2 (A:) Modifier protein 1 (M31, HP1 beta) {Mouse (Mus musculus)}

HMKEESEKPRGFARGLEPERIIGATDSSGELMFLMKWKNSEADLVPAAKEANVKCPQVVI

SFYEERLTWH

>d1e0ba_ d.9.2.2 (A:) HP1 homologue SWI6 {Fission yeast
(Schizosaccharomyces pombe)}

QVENYDSWEDLVSSIDTIERKDDGTLEIYLTWKNGAISHHPSTITNKKCPQKMLQFYESHL

>d1g6za_ d.9.2.2 (A:) Histone methyltransferase clr4 chromo domain {Fission yeast
(Schizosaccharomyces pombe)}

ISSPKQEEYEYERIVDEKLDRNGAVKLYRIRWLNYSRSSDTWEPPENLSGCSAVLAEWKRR
KRRLKGSNS

>d1k9a_ d.10.1.3 (A:) Methyl-CpG-binding protein 2, MECP2 {Human (Homo sapiens)}

ASASPKQRRSIIRDRGPMYDDPTLPEGWTRKLKQRKSGRSAGKYDVYLINPQGKAFRSKV
ELIAYFEKVGDTSLDPNDFDTVTGRGSGSGC

>d1d9na_ d.10.1.3 (A:) Methylation-dependent transcriptional repressor MBD1/PCM1
{Human (Homo sapiens)}

MAEDWLDCPALGPGWKRREVFRKSGATCGRSDTYYSPTGDRIRSKVELTRYLGPACDLT
LFDKQGILCYPAPK

>d1k25a1 d.11.1.1 (A:632-692) Penicillin-binding protein 2x (pbp-2x), c-terminal domain
{Streptococcus pneumoniae}

TESSYAMPSIKDISPGELAEALRRNIVQPIVVGTTGKIKETSVEEGTNLAPNQVLLLSDK

>d1k25a2 d.11.1.1 (A:693-750) Penicillin-binding protein 2x (pbp-2x), c-terminal domain
{Streptococcus pneumoniae}

VEEIPDMYGWKKETAETFAKWLDIELEFEGSGSVVQKQDVRTNTAIKNIKKIKLTLGD

>d4rh_ d.13.1.1 (-) Histidine triad nucleotide-binding protein (HINT) {Rabbit (Oryctolagus
cuniculus)}

RPGGDTIFGKIIRKEIPAKIIFEDDQCLAFHDISPQAPTHFLVIPKKHISQISAAEDADESLLGH
LMIVGKKCAADLGLKKGYRMVVNEGSDGGQSVYHVHLHVLGGRQMNWPPG

>d1emsal d.13.1.1 (A:281-440) NIT-FHIT fusion protein, C-terminal domain {Nematode
(Caenorhabditis elegans)}

RSDLYTLHINEKSSSETGGLKFARFNIPADHIFYSTPHSFVFNLPVTDGHVLVSPKRVVPR
LTDLTAETADLFIVAKKVQAMLEKHHNVTSTTICVQDGKDAGQTVPHVHIHILPRRAGD
FGDNEIYQKLASHDKEPERKPRSNEQMAEEAVVYRNLM

>d1guqa1 d.13.1.2 (A:2-177) Galactose-1-phosphate
uridylyltransferase {Escherichia coli}

TQFNPVDHPHRRYNPLTGQWILVSPHRAKRPWQGAQETPAKQVLPADHPDCFLCAGNVR
VTGDKNPDYTGTYVFTNDFAALMSDTPDAPESHDPMLRCQSARGTSRVICFSPDHSKTLF
ELSVAALTEIVKTWQEQTAEKGKTYPVVQVFENKGAAMGCSNPHPGGQIWANSFLPN

>d1guqa2 d.13.1.2 (A:178-348) Galactose-1-phosphate
uridylyltransferase {Escherichia coli}

EAEREDRLQKEYFAEQSPMLVDYVQRELADGSRTVVETEHWLAVVPYWAAPFETLLL
PKAHVLRITDLTDAQRSDLALALKKLTSRYDNLFQCSFPYSMGWHGAPFNGEENQHWQL
HAHFYPPLRSATVRKFMVGYEMLAETQRDLTAEQAAERLRAVSDIHFRESGV

>d1k6za_ d.198.1.1 (A:) YopE chaperone SycE {Yersinia pestis}

SFEQAITQLFQQLSLSIPDTIEPVIGVKVGEFACHITEHPVGQILMFTLPSLDNNDKETLLS
HNIFSQDILKPILSWDEVGGHPVLWNRQPLNSLDNNSLYTQLEMLVQGAERLQTSSLISPP
RSFSHH

>d1jyoe_ d.198.1.1 (A:) Virulence effector SptP secretion chaperone SicP {Salmonella typhimurium}

LQAHQDIIANIGEKLGLPLTFDDNNQCLLLLSDIFTSIEAKDDIWLLNGMIPLSPVCGDSI
WRQIMVINGELAAANNEGTLAYIDAAETLLLIHAITDLTNTYHISQLESFVNQQEALKNILQ
EYAKV

>d1k3ea_ d.198.1.1 (A:) Secretion chaperone CesT {Escherichia coli}

MSSRSELLLEKFAEKIGISISFNENRLCSFAIDEIYYISLSDANDEYMMIYGVCCKFPTDNS
NFALEILNANLWFAENGOPYLCYEAGAQSLLLALRFPLDDATPEKLENEIEVVVKSMENL
YLVVHNQGITLENEHMKIEEISS

>d1k3sa_ d.198.1.1 (A:) Secretion chaperone SigE {Salmonella enterica}

MESLLNRLYDALGLDAPEDPELLIIDDGIQVYFNESDHTLEMCCPFMPLPDDILTQLHFLRL
NYTSAVTIGADADNTALVALYRLPQTSTEEALTGFELFISNVKQLKEHYA

>d1k8kf_ d.198.2.1 (F:) ARPC4 (20 kDa subunit) {Cow (Bos taurus)}

TATLRPYLSAVRATLQAALCLENFSSQVVERHNKPEVEVRSSKELLQPVITISRNEKEKVL
EGSINSVRVSIQVKADEIEKILCHKFMRFMMAENFFILRRKPVEGYDISFLITNFHTEQ
MYKHLVDFVIHFMEIDKEISEMKLSVNARARIVAEFFLKNF

>d1k8kd1 d.198.2.1 (D:1-120) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

MILLEVNNRIIEETLALKFENAAAGNKPEAVEVTFADFDGVLVHISNPNGDKTKVMVSISL
KFYKELQAHGADELLKRVYGSYLVNPESGYNVSLYDLENLPASKDSIVHQAGMLKRNC

>d1k8kd2 d.198.2.1 (D:121-284) ARPC2 (34 kDa subunit) {Cow (Bos taurus)}

FASVFEKYFQFQEEGKEGENRAVIHYRDETMVYESKKDRVTVVSTVFKDDDDVVIGK
VFMQEFKEGRRASHTAPQVLFHSHREPPELEKDTDAVGDNIGYITFVLFPRHTNASARDNT
INLIHTFRDYLHYHIKCSKAYIHTMRKAKTSDFLKVLRARPDA

>d1dar_3 d.14.1.1 (476-599) Elongation factor G (EF-G), domain IV {Thermus thermophilus}

VGKPQVAYRETITKPVDFEGKFIQRTGGRGQYGHVKIKVEPLPRGSGFEFVNAIVGGVIPK
EYIPAVQKGIEEAMQSGPLIGFPVVDIKVTLYDGSYHEVDSSEMAFKIAGSMAIKEAVQKG
DP

>d1fjge1 d.14.1.1 (E:74-154) Ribosomal protein S5, C-terminal domain {Thermus thermophilus}

GTIPHEIEVEFGASKIVLKPAAPGTGVIAGAVPRAILELAGVTDILTKEGSRNPINIAATME
ALRQLRTKADVERLRKG

>d1fjgi_ d.14.1.1 (I:) Ribosomal protein S9 {Thermus thermophilus}

EQYYGTGRRKEAVARVFLRPGNGKVTVNGQDFNEYFQGLVRAVALEPLRAVDALGRFD
AYITVRGGGKSGQIDAIKLGIARALVQYNPDYRAKLKPLGFLTRDARVVERKKYGGHKAR
RAPQYSKR

>d1b63a1 d.14.1.3 (A:217-331) DNA mismatch repair protein MutL {Escherichia coli}

GTAFLQALAEWQHGDLTLRGWVADPNHTTPALAEIQYCYVNGRMMRDRLINHAIRQA
CEDKLGADQQPAFVLYLEIDPHQVDVNVHPAKHEVRFHQSRVHDFIYQGVLSVLQ

>d1h7sa1 d.14.1.3 (A:232-365) DNA mismatch repair protein PMS2 {Human (Homo sapiens)}

GQKQLQSLIPFVQLPPSDSVCEEYGLSCSDALHNLFIYISGFISQCTHGVGRSSTDRQFFINR
RPCDPAKVCRLVNEVYHMYNRHQYPFVVLNISVDSECVDINVTDPKRQILLQEEKLLLAV
LKTSLIGMFDS

>d1e1a1 d.14.1.3 (A:221-392) DNA gyrase B {Escherichia coli}

GKAFVEYLNKNKTPIHPNIFYFSTEKDGIGVEVALQWNDGFQENIYCFTNNIPQRDGGTH

LAGFRAAMTRTLNAYMDKEGYSKKAKVSATGDDAREGLIAVSVKVPDPKFSSQTKDKL
VSSEVKSAVEQQMNELLA EYLLNPTDAKIVVGKIIDAARAREARRAREMT

>d1e3ha2 d.14.1.4 (A:3-151) Polynucleotide phosphorylase/guanosine pentaphosphate synthase
(PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}
NETHYAEVIDNGAFGTRTIRFETGRLARQAAGSAVAYLDDDTMVLSATTASKNPKDQLD
FFPLTVDVEERMYAAGKIPGSFFRREGRPSEDAILTCRLIDRPLRPSFKKGLRNEIQVVATIM
ALNPDHLYDVVAINAASASTQLAGLP

>d1e3ha3 d.14.1.4 (A:346-482) Polynucleotide phosphorylase/guanosine pentaphosphate synthase
(PNPase/GPSI), domains 1 and 4 {Streptomyces antibioticus}
TDIRTLAAEVEAIPRVHGSALFERGETQILGVTTLNMLRMEQQDLTSPVTRKRYMHNYN
FPPYSVGETGRVGSPKRREIGHGALAERAIVPVLPTREEFPYAIRQVSEALGSNGSTSMGSV
CASTMSLLNAGVPLK

>d1h72c1 d.14.1.5 (C:5-167) Homoserine kinase {Archaeon Methanococcus jannaschii}
MKVRVKAPCTSANLGVGFDVFGCLCKEYPDVIEVEAIDDKEIIIEVDDKNIPTDPDKNVAG
IVAKKMIDDFNIGKGVKITIKKGVKAGSGLGSSAASSAGTAYAINELFKLNLDKLLVDYA
SYGELASSGAKHADNVAPAIFGGFTMVNTNIEPLEVLHIPID

>d1fi4a1 d.14.1.5 (A:3-190) Mevalonate 5-diphosphate decarboxylase {Baker's yeast
(Saccharomyces cerevisiae)}
VYTASVTAPVNIATLKYWGKRDTKLNLPNTSSISVTLSQDDLRTLTAATAPEFERDTLWL
NGEPHSIDNERTQNCLRDRLRQLRKEMESKDASLPTLSQWKLHIVSENNFPTAAGLASSAA
GFAALVSAIAKLYQLPQSTSEISRIARKGSGSACRSLFGGYVAWEMGKAEDGHDSMAVQIA
DSSDWP

>d1c3ta_ d.15.1.1 (A:) Ubiquitin {Human (Homo sapiens)}
MQLFVKTLTGKTLTVELEPSDTVENLKAQIQDKEGIPPDQQLIFAGKQLEDGRTLSDYNL
QKESTIHLVLRRLGG

>d1a5r_ d.15.1.1 (-) SUMO-1 (smt3 homologue) {Human (Homo sapiens)}
GMSDQAEKPTEDLGDKKEGEYIKLVIGQDSSEIHFKVKMTTHLKKLKESYCQRQGV
MNSLRFLFEGQRIADNHTPKELGMEEEDVIEVYQEQTGGHSTV

>d1vcba_ d.15.1.1 (A:) Elongin B {Human (Homo sapiens)}
MDVFLMIRRHKTITFTDAKESSTVFELKRIVEGILKRPPDEQRLYKDDQLDDGKTLGECG
FTSQTARPQAPATVGLAFRADDTFEALCIEPFSSPPE

>d1h8ca_ d.15.1.2 (A:) Fas-associated factor 1, Faf1 {Human (Homo sapiens)}
NAEPVSKLRIRTPSGEFLERRFLASNKLQIVDFVASKGFPWDEYKLLSTFPRRDVTQLDPN
KSLLEVKLFPQETLFLEAKE

>d1i42a_ d.15.1.2 (A:) p47 {Rat (Rattus norvegicus)}
KASSILINEAEPTTNIQIRLADGGRLVQKFNHSHRISDIRLFIVDARPAMAATSFVLMTTFP
NKELADENQTLKEANLLNAVIVQRLT

>d1gc7a3 d.15.1.4 (A:1-87) Radixin {Mouse (Mus musculus)}
MPKPINVRVTMDAELEFAIQPNTTGKQLFDQVVKTVGLREVWFFGLQYVDSKGYSTWL
KLNKKVTQQDVKKENPLQFKFRAKFFPE

>d1gg3a3 d.15.1.4 (A:1-81) Erythroid membrane protein 4.1R {Human (Homo sapiens)}
MHCKVSLDDTVYECVVEKHAKGQDLLKRVCEHLNLEEDYFGLAIWDNATSKTWLDS
AKEIKKQVRGVPWNFTFNVKFYP

>d1c1yb_ d.15.1.5 (B:) c-Raf1 RBD {Human (Homo sapiens)}

SENTIRVFLPNKQRTVVNVNRNGMSLHDCMLKALKVRGLQPECCAVFRLLEHKGGKKARLD
WNTDAASLIGEELQVDFL

>d1raxa_ d.15.1.5 (A:) Ral guanosine-nucleotide exchange factor, RalGDS {Human (Homo sapiens)}

QQVGDCCIIRVSLDVDNGNMYKSILVTSQDKAPAVIRKAMDKHNLEEEEPEDYELLQILSD
DRCLKIPENANVFYAMNSTANYDFVLKKRTFT

>d1e8xa3 d.15.1.5 (A:142-321) Phosphoinositide 3-kinase (PI3K) {Pig (Sus scrofa)}

AASEETLAFQRQLNALIGYDVTDVSNVHDELEFTRRRRLVTPRMAEVAGRDPKLYAMHP
WVTSKPLPEYLLKKITNNCVFIVHRSTTSQTIKVSADDTPGTILQSFFTKMAKKKSLMDIP
ESQNERDFVLRVCGRDEYLVGETPIKNFQWVRQCLKNGEEIHLVLDTPPDALDEVKE

>d1i35a_ d.15.1.5 (A:) Protein kinase byr2 {Yest (Schizosaccharomyces pombe)}

CILRFIACNGQTRAVQSRGDYQKTLAIALKKFSLEDASKFIVCVSQSSRIKLITEEEFKQICF
NSSSPERDRLIIVPKEKPCPSFEDLRRSWEIE

>d1d4ba_ d.15.2.1 (A:) Cell death-inducing effector B (CIDE-B), N-terminal domain {Human (Homo sapiens)}

MEYLSALNPDDLRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATRQELLAK
ALETLLLVGLTLVLEEDGTAVDSEDFQLLEDDTCLMVLQSGQSWSPTRSGVLHHHHHHH

>d1c9fa_ d.15.2.1 (A:) Caspase-activated DNase (CAD), DFF40, N-terminal domain {Mouse (Mus musculus)}

MCAVLRQPKCVKLRLHSACKFGVAARSCQELLRKGCVRVFLPMPGSRCLYEDGTEVT
DDCFPGLPNDAAELLLLTAGETWHGYVSD

>d1f2ri_ d.15.2.1 (I:) Inhibitor of caspase-activated DNase (ICAD), DFF45, N-terminal domain {Mouse (Mus musculus)}

MELSRGASAPDPDDVRPLKPCLLRRNHSRDQHGVAASSLEELRSKACELLAIDKSLTPITL
VLAEDGTIVDDDDYFLCLPSNTKFVALACNEKWTYNDSD

>d1f0za_ d.15.3.2 (A:) Thiamin biosynthesis sulfur carrier protein ThiS {Escherichia coli}

MQILFNDQAMQCAAGQTVHELLEQLDQRQAGAALAINQQIVPREQWAQHIVQDGDQILL
FQVIAGG

>d1jsba_ d.15.3.2 (A:) Hypothetical protein MTH1743 {Archaeon Methanobacterium thermoautotrophicum}

MVIGMKFTVITDDGKKILESGAPRRIKDVLEGEIPIETVVVKKNGQIVIDEEEIFDGDIIIVI
RVIYGG

>d1frd_ d.15.4.1 (-) 2Fe-2S ferredoxin {Cyanobacterium (Anabaena sp.), pcc 7119 and 7120}

ASYQVRLINKKQDIDTTIEIDEETTILDGAEENGIELPFSGHSGSCSSCVGKVVEGEVDQSD
QIFLDDEQMGKGFALLCVTYPRSNCTIKTHQEPYLA

>d1doi_ d.15.4.1 (-) 2Fe-2S ferredoxin {Archaeon Haloarcula marismortui}

PTVEYLNVEVDDNGWDMYDDDVFGASDMDLDDDEDYGSLEVNEGEYILEAAEAQGY
DWPFGSCRAGACANCAAIVLEGDIDMDMQILSDEEVEDKNVRLTCIGSPDADEVKIVYNA
KHLDYLQNRVI

>d1e9ma_ d.15.4.1 (A:) Ferredoxin VI {Rhodobacter capsulatus}

AKIIFIEHNGTRHEVEAKPGLTVMEAARDNGVPGIDADCGGACACSTCHAYVDPWVDK
LPKALPTETDMIDFAYEPNPATSR LTCQIKVTSLLDGLVVHLPEKQI

>d1b9ra_ d.15.4.1 (A:) Terpredoxin {Pseudomonas sp.}

PRVVFIDEQSGEYAVDAQDGQSLMEVATQNGVPGIVAECGGSCVCATCRIEIEDAWVEIVG

EANPDENDLLQSTGEPMTAGTRLSCQVFIDPSMDGLIVRVPLPA

>d1ayfa_ d.15.4.1 (A:) Adrenodoxin {Cow (Bos taurus)}

KITVHFINDGETLTTKGKIGDSLDDVVQNNLDIDGFGACEGTLACSTCHLIFEQHIFEKL
EAITDEENDMLDLAYGLTDRSRLGCQICLTAKMDNMTVRVP

>d1feha2 d.15.4.2 (A:1-126) Fe-only hydrogenase, N-terminal domain {Clostridium pasteurianum}
MKTIINGVQFNTDEDTTILKFARDNNIDISALCFLNNCNNDINKCEICTVEVEGTGLVTAC
DTLIEDGMIINTNSDAVNEKIKSRISQLLDIHEFKCGPCNRRENCEFLKLVIKYKARASKPFL
P

>d1dgja2 d.15.4.2 (A:1-80) Aldehyde oxidoreductase, N-terminal domain {Desulfovibrio
desulfuricans}

METKTLIVNGMARRLLVSPNDLLVDVLRSQLQLTSVKVGCCKGQCGACTVILDGKVVRA
CIKMSRVAENASVTTLLEGIG

>d1fo4a2 d.15.4.2 (A:3-92) Xanthine oxidase, N-terminal domain {Cow (Bos taurus)}

ADELVFFVNGKKVVEKNADPETTLAYLRRKLGLRGTKLGCGECCGACTVMLSKYDR
LQDKIIHFSANACLAPICTLHHVAVTTVEGIG

>d1ffa2 d.15.4.2 (A:3-81) Carbonyl monooxygenase (CO) dehydrogenase iron-sulfur protein,
N-domain {Hydrogenophaga pseudoflava}

KKIITVNVNGKAQEKAVEPRTLLIHLREELNLTGAHIGCETSHCGACTVDIDGRSVKSCTH
LAVQCDGSEVLTVGLA

>d2pia_3 d.15.4.2 (224-321) Phthalate dioxygenase reductase, C-terminal domain
{Pseudomonas cepacia, db01}

SFGATNTNARENTPFTVRLSRSGTSFEIPANRSILEVLRDANVRVPSSCESGTCGSKTALCS
GEADHRDMVLRDDEKGTQIMVCVSRAKSAELVLDL

>d1fumb2 d.15.4.2 (B:1-105) Fumarate reductase iron-sulfur protein, N-terminal domain
{Escherichia coli}

AEMKNLKIEVVRYNPEVDTAPHSAPFYEVYPDATTSLLDALGYIKDNLAPDLSYRWSCR
AICGSCGMMVNNVPKLACKTFLRDYTDGMKVEALANFPIERDLVVD

>d1qlab2 d.15.4.2 (B:1-106) Fumarate reductase iron-sulfur protein, N-terminal domain {Wolinella
succinogenes}

MGRMLTIRVFKYDPQSAVSKPHFQEYKIEEAPSMTIFVLNMIRETYDPDLNFDVFCRAGIC
GSCGMMINGRPSLACRTLTDFEDGVITLLPLPAFKLIKDLSD

>d1jq4a_ d.15.4.2 (A:) Methane monooxygenase reductase N-terminal domain {Methylococcus
capsulatus}

MQRVHTITAVTEDGESLRFECRSDVDVITAALRQNIIFLMSSCREGGCATCKALCSEGDYDL
KGCSVQALPPEEEEEGLVLLCRTYPKTDLEIELPYTH

>d1ssn_ d.15.5.1 (-) Staphylokinase {Staphylococcus aureus}

SSSFDKGKYKKGDDASYFEPTGPYLMVNVTGVDSKGNELLSPHYVEFPIKPGTTLTKEKIE
YYVEWALDATAYKEFRVVELDPSAKIEVTYYDKNKKKEETKSFPITEKGFVVPDLSEHIKN
PGFNLITKVIEKK

>d1bmlc1 d.15.5.1 (C:12-148) Streptokinase {Streptococcus equisimilis}

SVNNSQLVSVAGTVEGTNQDISLKFFEIDLTSPAHGGKTEQGLSPKSKPFATDSGAMPH
KLEKADLLKAIQEQLIANVHSNDDYFEVIDFASDATITDRNGKVYFADKDGSVTLPTQPQV
EFLLSGHVRVRPYKE

>d1bmlc3 d.15.5.1 (C:285-372) Streptokinase {Streptococcus equisimilis}

DPFDRSHLKLFTIKYVDVNTNELLKSEQLLTASERNLDFRDLYDPRDKAKLLYNNLDAFGI
MDYTLTGKVEDNHDDTNRIITVYMGKR

>d1qqa_ d.15.5.1 (A:) Streptokinase {Streptococcus equisimilis}

IQNQAKSVDEYTVQFTPLNPDDDFRPLGLKLTLLKTLAIGDTITSQELLAQAQSILNKNH
PGYTIYERDSSIVTHDNDIFRTILPMDQEFTYRVKNREQAYRINKKSGLNNEINNTDLISEKY
YVLKKGEKPYDPFD

>d1esfa2 d.15.6.1 (A:121-233) Staphylococcal enterotoxin A, SEA {Staphylococcus aureus}

EEKKVPINLWLDGKQNTVPLETVKTNKKNVTQELDLQARRYLQEKYNLYNSDVFDGK
VQRGLIVFHTSTEPSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHIDIYLYTS

>d1i4pa2 d.15.6.1 (A:121-239) Staphylococcal enterotoxin C2, SEC2 {Staphylococcus aureus}

NHFDNGLQNVLRVYENKRNTISFEVQTDKKSVAQELDIKARNFLINKKNLYEFNSSPY
ETGYIKFIENNGNTFWYDMMPAPGDKFDQSKYLMMYNDNKTVDSSKSVKIEVHLTTKNG

>d3tss_2 d.15.6.1 (94-194) Toxic shock syndrome toxin-1 (TSST-1) {Staphylococcus aureus}

LPTPIELPLKVKVHKGDSPLKYWPKFDKKQLAISTLDFKIRHQLTQTHGLYRSSDKTGGY
WKITMNDGSTYQSDLSKKFEYNTEKPPINIDEIKTIEAEIN

>d1enfa2 d.15.6.1 (A:102-213) Staphylococcal enterotoxin H, SEH {Staphylococcus aureus}

EKLAQERVIGANVWVDGIQKETELIRTNNKNVTQELDIKIRKILSDKYKIYYKDSEISKGL
IEFDMKTTPRDYSFDIYDLKGENDYEIDKIYEDNKTLSDDISHIDVNLTY

>d1an8_2 d.15.6.1 (96-208) Streptococcal superantigen Spe-C {Streptococcus pyogenes}

NKVNHLKLLGNLFISGESQQNLNNKIILEKDIVTFQEIDFKIRKYLMDNYKIYDATSPYVSGR
IEIGTKDGKHEQIDLFDSNEGTRSDIFAKYKDNRIINMKNFSHFDIYLEK

>d1et9a2 d.15.6.1 (A:96-204) Streptococcal superantigen Spe-H {Streptococcus
pyogenes}

EKKEIKVPVNVWDKSKQQPPMFITVNPVKVTAQEVDIKVRKLLIKKYDIYNNREQKYSKG
TVTLDLNSGKDIVFDLYYFGNGDFNSMLKIYSNNERIDSTQFHVDVSIS

>d1eu3a2 d.15.6.1 (A:97-209) Streptococcal superantigen Smez-2 {Streptococcus
pyogenes}

TSIPKNIPVNLWINGKQISVPYNEISTNKTTVTAQEIDLKVRKFLIAQHQLYSSGSSYKSGRL
VFHTNDNSDKYSFDLFYVGYRDKESIFKVYKDNKSFNIDKIGHLDIEIDS

>d1pgx_ d.15.7.1 (-) Immunoglobulin-binding protein G, different constituent domains
{Streptococcus sp., group G}

ELTPAVTTYKLIVINGKTLKGETTTKAVIDAETAEKAFKQYANDNGVDGVWTYDDATKTFT
VTEMVTEVPVA

>d2ptl_ d.15.7.1 (-) Immunoglobulin light chain-binding domain of protein L {Peptostreptococcus
magnus}

ENKEETPETPETDSEEEVTIKANLIFANGSTQTAEFKGTFEKATSEAYAYADTLKKDNGEYT
VDVADKGYTLNIFAG

>d1k0ia2 d.16.1.2 (A:174-275) p-Hydroxybenzoate hydroxylase (PHBH) {Pseudomonas
aeruginosa}

LKVFERVYPFGWLGLLADTPPVSHELIYANHPRGFALCSQRSATRSQYYVQVPLSEKVED
WSDERFWTELKARLPSEVAEKLVTGPSLEKSIAPLRSFVVEP

>d1foha4 d.16.1.2 (A:241-341) Phenol hydroxylase {Soil-living yeast (Trichosporon cutaneum)}

GEQTDYIWGVLDVAPASNFPDIRSRAIHSAESGSIMIIPRENNLVRFYVQLQARAEEKGGRV
DRTKFTPEVVIANAKKIFHPYTFDVQQLDWFTAYHIGQR

>d1an9a2 d.16.1.3 (A:195-287) D-amino acid oxidase {Pig (*Sus scrofa*)}
LQPGRGQIIKVDAPWLKNFIITHDLERGIYNSPYIIPGLQAVTLGGTFQVGNWNEINNIQDH
NTIWEGCCRLPLETLKDAKIVGEYTGFRPVRP

>d1c0pa2 d.16.1.3 (A:1194-1288) D-amino acid oxidase {Yeast (*Rhodotorula gracilis*)}
AEPiRGQTVLVKSPCKRCTMDSSDPASPAYIIPRPGGEVICGGTYGVGDWDLSVNPETVQRI
LKHCLRLDPTISSDGTIEGIEVLRHNVGLRPAR

>d1el8a2 d.16.1.3 (A:218-321) Sarcosine oxidase {*Bacillus* sp., strain b0618}
LQPYRQVVGFFESDESKYSNDIDFPGMVEVPNGIYYGFPSFGGCGCLKLYHTFGQKIDPD
TINREFGVYPEDESNLRAFLEEYMPGANGELKRGAVCMYTKTL

>d1b5qa2 d.16.1.5 (A:294-405) Polyamine oxidase {Maize (*Zea mays*)}
DMAVYTKIFLKFPRKFWPEGKGREFFLYASSRRGYGVWQEFQYDPANVLLVTVTDE
ESRRIEQQSDEQTKAEIMQVLRKMFPKGKDVDPATDILVPRWWSDRFYKGTFSN

>d1f8ra2 d.16.1.5 (A:320-432) L-amino acid oxidase {Malayan pit viper (*Calloselasma rhodostoma*)}
HYRSGTKIFLTCTTKFWEDDGIHGGKSTTDLPSRFIYYPNHNFTNGVGVIIAYGIGDDANFF
QALDFKDCADIVFNDLSLIHQLPKKDIQSCYPSVIQKWSLDKYAMGGITT

>d1gosa2 d.16.1.5 (A:290-401) Monoamine oxidase B {Human (*Homo sapiens*)}
PLGSVIKCIYVYKEPFWRKKDYCGTMIIDGEEAPVAYTLDDTKPEGNYAAIMGFILAHKAR
KLARLTKEERLKKLCELYAKVLGSLEALEPVHYEEKNWCEEQYSGGCYTTY

>d1eqka_ d.17.1.2 (A:) Phytocystatin {Japanese rice (*Oryza sativa*), subsp. *japonica*, oryzacystatin-I}
MSSDGGPVLGGVEPVGNENDLHLVDLARFAVTEHNKKANSLLFEKLVSVKQQVAGTL
YYFTIEVKEGDACKLYEAKVWEKPWMDFKELQEFKPVDAASANA

>d1dvd__ d.17.1.2 (-) Cystatin A (stefin A) {Human (*Homo sapiens*)}
MIPGGLSEAKPATPEIQEIVDKVKPQLEEKTNETYGKLEAVQYKTQVVAGTNYYIKVRAG
DNKYMHLKVFKSLPGQNEDLVLTGYQVDKNKDDDELTF

>d1g96a_ d.17.1.2 (A:) Cystatin C {Human (*Homo sapiens*)}
VGGPMDASVEEEGVRRALDFAVGEYNKASNDMYHSRALQVVRARKQIVAGVNYFLDVE
LGRITCTKTQPNLNCNPFHDQPHLKRKAFCFSFIYAVPWQGTMTLSKSTCQDA

>d1oaca2 d.17.2.1 (A:91-185) Copper amine oxidase, domains 1 and 2 {*Escherichia coli*}
KRPHPLNALTAEIKQAVEIVKASADFKPNTRFTEISLLPPDKEAVWAFALENKPVDPQPRK
ADVIMLDGKHIIIEAVVDLQNNKLLSWQPIKDAHG

>d1oaca3 d.17.2.1 (A:186-300) Copper amine oxidase, domains 1 and 2 {*Escherichia coli*}
MVLDDDFASVQNIINNSEEFAAAVKKRGITDAKKVITPLTVGYFDGKDGLKQDARLLKVI
SYLDVGDGNYWAHPIENLVAVVDLEQKKIVKIEEGPVVPVPMPTARPFDRDRA

>d1ksia2 d.17.2.1 (A:6-98) Copper amine oxidase, domains 1 and 2 {Pea seedling (*Pisum sativum*)}
VQHPLDPLTKEEFLAVQTIVQNKYPISNNRLAFHYIGLDDPEKDHVLRVETHPTLVSIPIKIF
VVAIINSQTHEILINLRIRSIVSDNIHNGY

>d1ksia3 d.17.2.1 (A:99-206) Copper amine oxidase, domains 1 and 2 {Pea seedling (*Pisum sativum*)}
GFPILSVDEQSLAIKLPLKYPPFIDSVKKRGLNLSEIVCSSFTMGWFGEEKNVRTVRLDCFM
KESTVNIYVRPITGITIVADLDLMKIVEYHDRDIEAVPTAENTYQ

>d1av4_2 d.17.2.1 (9-96) Copper amine oxidase, domains 1 and 2 {*Arthrobacter globiformis*}

ASPFRLASAGEISEVQGILRTAGLLGPEKRIAYLGVLDPARGAGSEAEDRRFRVFIHDTVSGA
 RPQEVTVSVTNGTVISAVELDTAATG
 >d1av4_3 d.17.2.1 (97-211) Copper amine oxidase, domains 1 and 2 {Arthrobacter globiformis}
 ELPVLEEEFEVVEQLLATDERWLKALAARNLDVSKVRVAPLSAGVFHEYAEERGRRLRGL
 AFVQDFPEDSAWAHPVDGLVAYVDVVSKEVTRVIDTGVFPVPAEHGNYTDPELTG
 >d1a2va2 d.17.2.1 (A:18-115) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula
 polymorpha)}
 PARPAHPLDPLSTAEIKAATNTVKSIFAGKKISFNTVTLREPARKAYIQWKEQGGPLPPRLA
 YYVILEAGKPGVKEGLVDLASLSVIETRALETVQPI
 >d1a2va3 d.17.2.1 (A:116-236) Copper amine oxidase, domains 1 and 2 {Yeast (Hansenula
 polymorpha)}
 LTVEDLCSTEEVIRNDPAVIEQCVLSGIPANEMHKVYCDPWTIGYDERWGTGKRLQQALV
 YYRSEDEDSQYSHPLDFCPIVDTEEEKKVFIDIPNRRRKVSKHKHANFYPPKHMIEKVGAM
 R
 >d1ouna_ d.17.4.2 (A:) Nuclear transport factor-2 (NTF2) {Rat (Rattus norvegicus)}
 GDKPIWEQIGSSFIQHYYQLFDNDRTQLGAIYIDASCLTWEGQQFQGKAAIVEKLSSLPFQ
 KIQHSITAQDHQPTPDSCIISMVVGQLKADEDPIMGFHHQMFLKNINDAWVCTNDMFRLA
 LHNH
 >d1jkga_ d.17.4.2 (A:) NTF2-related export protein 1 (p15) {Human (Homo sapiens)}
 ASVDFKTYVDQACRAAEFVNYYTTMDKRRRLLSRLYMGATATLVWNGNAVSGQESLS
 EFFEMLPSSFEQISVVDQCPVHDEATPSQTTVLVVICGSVKFEGNKQRDFNQNFILTAQASP
 SNTVWKIASDCFRFQDWAS
 >d1jkgb_ d.17.4.2 (B:) NTF2-like domain of Tip associating protein, TAP {Human (Homo sapiens)}
 APPCKGSYFGTENLKSLLVHFLQQYYAIYDSGDRQGLLDAYHDGACCSLSIPFIPQNPARSS
 LAEYFKDSRNVKKLKDPTLRFLLKHTRLNVVAFLNELPKTQHDVNSFVVDISAQTSTLL
 CFSVNGVFKEVDGKSRDSLRAFTRTFIAPASNSGLCIVNDEL FVRNASSEEIQRAFAMPAP
 TP
 >d1qiga_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI
 {Comamonas testosteroni and Pseudomonas testosteroni}
 MNTPEHMTAVVQRYVAALNAGDLGDGIVALFADDATVENPVGSEPRSGTAAIREFYANSLK
 LPLAVELTQEVRAVANEAAFAFIVSFEYQGRKTVVAPIDHFRFNGAGKVSMRALFGEKNI
 HAGA
 >d1ea2a_ d.17.4.3 (A:) Delta-5-3-ketosteroid isomerase, steroid delta-isomerase, KSI
 {Pseudomonas putida}
 NLPTAQEVQGLMARFIELVDVGDIQVQMYADDATVEDPFGQPPIHGREQIAAFYRQGLG
 GGKVRACLTGPVRASHNGCGAMPFRVEMVWNGQPCALDVIDVMRFDEHGRIQTMQAY
 WSEVNLSV
 >d3frua2 d.19.1.1 (A:1-178) Fc (IgG) receptor, alpha-1 and alpha-2 domains {Rat (Rattus
 norvegicus)}
 AEPRLPLMYHLAAVSDLSTGLPSFWATGWLGAQQYLTYNLNRQEADPCGAWIWENQVS
 WYWEKETTDLKSKEQLFLEAIRTLNENQINGTFTLQGLLGCCLAPDNSSLPTAVFALNGEEF
 MRFNPRTGNWSGEWPETDIVGNLWMKQPEAARKESEFLTSCPERLLGHLERGRQNLEW
 >d1cd1a2 d.19.1.1 (A:7-185) CD1, alpha-1 and alpha-2 domains {Mouse (Mus musculus)}
 NYTFRCLQMSSFANRSWSRTDSVVWLGLDLQTHRWSNDSATISFTKPWSQGKLSNQQWEK

LQHMFQVYRVSFTRDIQELVKMMSPKEDYPIEIQLSAGCEMYPGNASESFLHVAFQGKYV
VRFWGTSWQTVPGAPSWLDLPIKVLNADQGTSATVQMLLNDTCPLFVRGLLEAGKSDLE
K

>d1jk8a2 d.19.1.1 (A:2-84) MHC class II, N-terminal domains of alpha and beta chains {Human (Homo sapiens), HLA-DQ8}

VADHVASYGVNLYQSYGPSGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFAL
TNIAVLKHNLNIVIKRSNSTAATN

>d1fnga2 d.19.1.1 (A:1-81) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

IKEEHTIIQAEFYLLPDKRGEFMFDGDEIFHVDIEKSETIWRLEEFKAFASFEAQGALANI
AVDKANLDVMKERSNNTN

>d1i3rb2 d.19.1.1 (B:1-120) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), I-EK}

GKKVITAFNEGLKGGGSLVGGGSGGGSRPWFLEYCKSECHFYNGTQVRLLVRYFYN
LEENLRFDSDVGEFRAVTELGRPDAENWNSQPEFLEQKRAEVDTVCRHNYEIFDNFLVPR
R

>d1k8ia2 d.19.1.1 (A:11-92) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

QNHTFRHTLFCQDGIPNIGLSETYDEDELFSFDFSQNTRVPRLPDFAEWAQGQGDASAI
DKSFCEMLMREVS PKLEGQIP

>d1k8ib2 d.19.1.1 (B:1-94) MHC class II, N-terminal domains of alpha and beta chains {Mouse (Mus musculus), H2-DM}

GFVAHVESTCVLNDAGTPQDFTYCVSFNKDLLACWDPDVGKIVPCEFGVLSRLAEIISN
ILNEQESLIHRLQNLQDCATHTQPFWDVLTHRTR

>d1i4fa2 d.19.1.1 (A:1-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), HLA-A2.1}

GSHSMRYFFTSVSRPGRGEPRFIAVG YVDDTQFVRFDSDAASQRMEPRAPWIEQEGPEY
WDGETRKVKAHSQTHRVDLGLRGYYNQSEAGSHTVQRMYGCDVGS DWRFLRGYHQYA
YDGKDYIALKEDLRSWTAADMAAQTTKHKWEAAHVAEQLRAYLEGTCVEWLRRYLEN
GKETLQR

>d1de4a2 d.19.1.1 (A:4-181) MHC class I, alpha-1 and alpha-2 domains {Human (Homo sapiens), hemochromatosis protein Hfe}

RSHSLHYLFMGASEQDLGLSLFEALGYVDDQLFVFYDHESRRVEPRTPWVSSRISSQMW
LQLSQSLKGWDHMFVTDFWTIMENHNHSHKESHTLQVILGCEMQEDNSTEGYWKYGYDG
QDHLEFCPDTLDWRAAEPRAWPTKLEWERHKIRARQN RAYLERDCPAQLQLLELGRGV
LD

>d1zaga2 d.19.1.1 (A:5-183) Zinc-alpha-2-glycoprotein, ZAG {Human (Homo sapiens)}

DGRYSLTYIYTGLSKHVEDVPAFQALGSLNDLQFFRYNSKDRKSQPMGLWRQVEGMEDW
KQDSQLQKAREDIFMETLKDIVEYYNDSNGSHVLQGRFGCEIENNRSSGAFWKYYYD
GKDYIEFNKEIPAWVPFDPAAQITKQKWEAEVPVYVQRAKAYLEEECPATLRKYLKYSKNILDR

>d1hyrc2 d.19.1.1 (C:0-180) MHC I homolog {Human (Homo sapiens), Mic-a}

MEPHSLRYNLTVLSWDGVSQSGFLTEVHLDGQPFLRCDRQKCRAKPQGQWAEDVLGNK
TWDRETRDLTGNGKDLRMTLAHIKDQKEGLHSLQEIRVCEIHEDNSTRSSQHFYYDGE
LFSQNLETKEWTMPQSSRAQTLAMNVRNFLKEDAMKTKTHYHAMHADCLQELRRYLKS

GVVLRR

>d1kcg_ d.19.1.1 (C:) Class I MHC-related molecule Ulbp3 {Human (Homo sapiens)}

DAHSLWYNFTIIHLPRHGQQWCEVQSQVDQKNFLSYDCGSDKVLSMGHLEEQLYATDAW
GKQLEMLREVGQRLRLELADTELEDFTPSGPLTLQVRMSCECEADGYIRGSWQFSFDGRK
FLLFDSNNRKWTVVHAGARRMKEKWEKDSGLTTFFKMVSMRDCKSWLRDFLMHRKKR
LE

>d1jfm_ d.19.1.1 (A:) NK cell ligand RAE-1 beta {Mouse (Mus musculus)}

DAHSLRCNLTIKDPTPADPLWYEAKCFVGEILILHLSNINKTMTSGDPGETANATEVKKCLT
QPLKNLCQKLNRNKVSNTKVDTHKTNGYPHLQVTMIYPQSQGRTPSATWEFNISDSYFFTF
YTENMSWRSANDESGVIMNKWKDDGEFVKQLKFLIHECSQKMDEFKQSKEK

>d2ucz_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae),
ubc7}

SKTAQKRLKELQQLIKDSPPGIVAGPKSENNIFIWDCLIQPPDTPYADGVFNAKLEFPKD
YPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKILLSVMSM
LSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

>d1jata_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Baker's yeast (Saccharomyces cerevisiae),
ubc13}

AASLPKRIKETELVSDPVPGITAEPHDDNLRYFQVTIEGPEQSPYEDGIFELELYLPDDYP
MEAPKVRFLTkiYHPNIDRLGRICLDVLKTNWSPALQIRTVLLSIQALLASPNPNPLANDV
AEDWIKNEQGAKAKAREWTKLYAKKKP

>d1j7da_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), mms2}

GVKVPRNFRLLLEELEGQKGVGDGTVSWGLEDDEDMTLTRWTGMIIGPPRTNYENRIYSL
KVECGPKYPEAPPSVRFVTKINMNGINNSSGMVDARSIPVLAKWQNSYSIKVVLQELRRL
MMSKENMKLPQPPEGQTYNN

>d1c4zd_ d.20.1.1 (D:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubch7}

SRRLMKELEEIRKCGMKNFRNIQVDEANLLTWQGLIVPDNPPYDKGAFRIEINFPAEYPFK
PPKITFKTKIYHPNIDEKGVCLPVISAENWKPATKTDQVIQSLIALVNDPQPEHPLRADLA
EEYSKDRKKFCKNAEEFTKKY

>d1u9aa_ d.20.1.1 (A:) Ubiquitin conjugating enzyme {Human (Homo sapiens), ubc9}

LNMSGIALSRLAQERKAWRKDHPFGFVAVPTKNPDGTMNLMNWECAIPGKKGTWEGG
LFLKRLMLFKDDYPSSPPKCKFEPPLFHPNVYPSGTVCLSILEEDKDWRPAITIKQILLGIQEL
LNEPNIQDPAQAEAYTIYCQNRVEYEKRVRAQAKKFAPS

>d2e2c_ d.20.1.1 (-) Ubiquitin conjugating enzyme {Clam (Spisula solidissima), E-2C}

MTTSKERHSVSKRLQQELRTLMSGDPGITAFPDGDNLFKWVATLDGPKDTVYESLKYKL
TLEFPSDYPYKPPVVKFTTPCWHPNVDQSGNICLDILKENWTASYDVRTILLSLQSLGEP
NNASPLNAQAADMWSNQTEYKKVLHEKYKTAQSDK

>d1bwza1 d.21.1.1 (A:1-130) Diaminopimelate epimerase {Haemophilus influenzae}

MQFSKMHGLGNDVVDGVTQNVFFTPETIRRLANRHCGIGFDQLLIVEAPYDPELDFHY
RIFNADGSEVSQCGNGARCFARFVTLKGLTNKKDISVSTQKGNMVLTVKDMNQIRVNMG
EPIWEPAKIPF

>d1bwza2 d.21.1.1 (A:131-274) Diaminopimelate epimerase {Haemophilus influenzae}

TANKFEKNYILRTDIQTVLCGAVSMGNPHCVVQVDDIQTANVEQLGPLLESHERFPERVN
AGFMQIINKEHIKLRVYERGAGETQACGSGACA AVAVGIMQGLLNNNVQVDLPGGSLMIE
WNGVGHPYMTGEATHIYDGFITL

>d1h6ra_ d.22.1.1 (A:) Green fluorescent protein, GFP {Jellyfish (*Aequorea victoria*)}

SKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLTCLKFIVTTGKLPVPWPTLVT
TFAYGLQCFAYPDHMKRHDFFKSAMPEGYVQERTIFFKDDGNYKTRAEVKFEGDTLVN
RIELKGIDFKEDGNILGHKLEYNNSHCYIVADKQKNGIKVNFKIRHNIEDGSVQLADHY
QQNTPIGDGPVLLPDNHLYCYQSALS KDPNEKRDHMLLEFVTAAGITH

>d1ggxa_ d.22.1.1 (A:) Red fluorescent protein (fp583 or dsred(clontech)) {Coral (*Discosoma* sp.)}

VIKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKLKVTKGGPLPFAWDILSPQFQ
YGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFIYKVKFIG
VNFPSDGPVMQKKTMGWEASTERLYPRDGV LKGEIHKALKLKDGGHYLVEFKSIYMAK
KPVQLPGY YVDSKLDITSHNEDYTIVEQYERTEGRHHLFL

>d2pil_ d.24.1.1 (-) Pilin {Gc (*Neisseria gonorrhoeae*)}

FTLIELMIVIAIVGILAAVALPAYQDYTARAQVSEAILLAEGQKSAVTEYYLNHGKWPENNT
SAGVASPPSDIKGKYVKEVEVKNGVV TATMLSSGVNNEIKGKLSLWARRENGSVKWF
GQPVTRTDDDTVADAKDGKEIDTKHLPSTCRDNFDAK

>d1hpwa_ d.24.1.1 (A:) Pilin {*Pseudomonas aeruginosa*}

ALEGTEFARAQLSEAMTLASGLKTKVSDIFSQDGSCPANTAATAGIEKDTDINGKYVAKVT
TGGTAAASGGCTIVATMKASDVATPLRGKTLTLTLGNADKGSYTWACTSNADNKYLPKTC
QTATTTTP

>d1dzoa_ d.24.1.1 (A:) Pilin {*Pseudomonas aeruginosa*, type IV pilin, pak pilin}

GTEFARSEGASALASVNPLKTTVEEALSRGWSVKSGTGTEDATKKEVPLGVAADANKLG
TIALKPDPADGTADITLFTMGAGPKNKGKIITLRTAADGLWKCTSDQDEQFIPKGC SR

>d1rot_ d.26.1.1 (-) FKBP59-I, N-terminal domain {Rabbit (*Oryctolagus cuniculus*)}

GVDISPKQDEGV LKVIKREGTGTETPMIGDRVFVHYTGWLLDGTKFDSSLDRKDKFSFDL
GKGEVIKAWDIAVATMKVGELCRITCKPEYAYGSAGSPPKIPP NATLVFEVELFEFKG

>d1pina2 d.26.1.1 (A:45-163) Mitotic rotamase PIN1, domain 2 {Human (*Homo sapiens*)}

GKNGQGEPARVRC SHLLVKHSQSRPSSWRQEKITRTKEEALELINGYIQIKSGEEDFESL
ASQFSDCSSAKARGDLGAFSRGQM QKPFEDASFALRTGEMSGPVFTDSGIHIL RTE

>d1eq3a_ d.26.1.1 (A:) Parvulin {Human (*Homo sapiens*), hpar14}

NAVKVRHILCEKHGKIMEAMEKLKSGMRFNEVAAQYSEDKARQGGDLGWMTRGSMVG
PFQEAAAFALPVSGMDKPVFTDPPVKTKFGYHIIMVEGRK

>d1fd9a_ d.26.1.1 (A:) Macrophage infectivity potentiator protein (MIP) {*Legionella pneumophila*}

TDKDKLSYSIGADLGKNFKNQGIDVNPEAMAKGMQDAMSGAQLALTEQQMKDVLNKF
QKDLMAKR TAEFNKKADENKVGAEFLTENKNKPGVVVLPSGLQYKVINSGNGVKPGK
SDTVTVEYTGRLIDGTVFDSTEKTGKPATFQVSQVIPGWTEALQLMPAGSTWEIYVPSGLA
YGRPSVGGPIGPNETLIFKIHLISVKKS

>d1edqa3 d.26.3.1 (A:444-516) Chitinase A {*Serratia marcescens*}

YGRGWTGVNGYQNNIPFTGTATGPVKGTWENGIVDYRQIAGQFMSGEWQYTYDATAEA
PYVFKPSTGDLITFD

>d1goia3 d.26.3.1 (A:292-379) Chitinase B {*Serratia marcescens*}

YGRAFKGVSGGNGGQYSSHSTPGEDPYPSTDYWLVGCEECVRDKDPRIAS YRQLEQMLQ
GNYGYQRLWNDKTKTPYLYHAQNGLFVTY

>d1d2ka2 d.26.3.1 (A:293-354) Chitinase 1 {*Fungus (Coccidioides immitis)*}

YGRAFASTDGIGTSFNGVGGGSWENGWVDYKDMPQQGAQVTELEDIAASYSYDKNKRY
LISY

>d1e9la2 d.26.3.1 (A:267-336) Chitinase-like lectin ym1 {Mouse (Mus musculus)}

YGHTFILSDPSKTGIGAPTISTGPPGKYTDESGLLAYEYVCTFLNEGATEVWDAPQEVPIA
YQGNNEWVGY

>d1qcsa2 d.31.1.1 (A:86-201) C-terminal domain of NSF-N, NSF-Nc {Hamster (Cricetus
griseus)}

DKAKQCIGTMTIEIDFLQKKNIDSNPYDTDKMAAEFIQQFNNQAFSVGQQLVFSFNDKLF
GLLVKDIEAMDPSILKGEPASGKRQKIEVGLVVGNSQVAFEKAENSSLNLIGKAKT

>d1cr5a2 d.31.1.1 (A:108-210) C-terminal domain of NSF-N, NSF-Nc {Baker's yeast
(Saccharomyces cerevisiae), sec18p}

SGKQSYLGSIDIDISFRARGKAVSTVFDQDELAKQFVRCYESQIFSPTQYLIMEFQGHFFDL
KIRNVQAIDLGDIEPTSAVATGIETKGILTKQTQINFFKGR

>d1cz4a2 d.31.1.1 (A:92-185) C-terminal domain of VAT-N, VAT-Nc {Archaeon Thermoplasma
acidophilum}

TEIAKKVTLAPIIRKDQRLKFGEGIEEYVQRALIRRPMLQDNISVPGLTLAQGTGLLFKVV
KTLPSKVPVEIGEETKIEIREEPASEVLEEGG

>d1e32a3 d.31.1.1 (A:107-200) Membrane fusion atpase p97 domain 2, P97-Nc {Mouse (Mus
musculus)}

DVKYGKRIHVLPIDDTVEGITGNLFEVYLKPYFLEAYRPIRKGDIFLVRGGMRAVEFKVVE
TDPSPYCIVAPDTVIHCEGEPIKREDEEESLNE

>d1qipa_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Human (Homo sapiens)}

GGLTDEAALSCCSDADPSTKDFLLQQTMLRVKDKPKSLDFYTRVLGMTLIQKCDFPIMKF
SLYFLAYEDKNDIPKEKDEKIAWALSARKATLELTHNWGTEDDETQSYHNGNSDPRGFGHI
GIAVPDVYSACKRFEELGVKFVKKPDDGKMKGLAFIQDPDGYWIEILNPKNMATLM

>d1f9za_ d.32.1.1 (A:) Glyoxalase I (lactoylglutathione lyase) {Escherichia coli}

MRLHTMLRVGDLQRSIDFYTKVLGMKLLRTSENPEYKYSLAFVGYGPETEEAVIELTYN
WGVDKYELGTAYGHIALSVDNAEACEKIRQNGGNVTREAGPVKGGTTVIAFVEDPDGY
KIELIEEKDAGRGLGN

>d1qtoa_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Streptomyces
verticillus}

MVKFLGAVPVLTAVDVPANVSFWVDTLGFEKDFGDRDFAGVRRGDIRLHISRTEHQIVAD
NTSAWIEVTPDALHEEWARAVSTDYADTSGPAMTPVGESPA GREFAVRDPAGNCVHFTA
GE

>d1ecsa_ d.32.1.2 (A:) Bleomycin resistance protein, BRP {Klebsiella pneumoniae}

TDQATPNLPSRDFDSTAAFYERLGFIVFRDAGWMILQRGDLMLEFFAHPGLDPLASWFS
CCLRLDDLAEFYRQCKSVGIQETSSGYPRIHAPELQGWGGTMAALVDPDGTLLRLIQNEL

>d1gdga1 d.32.1.3 (A:1-132) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Pseudomonas sp.}

SIERLGYLGFVAVKDVPAWDHFLTKSVGLMAAGSAGDAALYRADQRAWRIAVQPGELDDL
AYAGLEVDDAAALERMADKLRQAGVAFTRGDEALMQQRKVMGLLCLQDPFGLPLEIYY
GPAEIFHEPFLPSAP

>d1han_2 d.32.1.3 (133-289) 2,3-Dihydroxybiphenyl dioxygenase (DHBD, BPHC enzyme)
{Burkholderia cepacia (formerly Pseudomonas cepacia)}

AVSGFLTGEQGLGHFVRCVPDSKALAFYTDVLGFQLSDVIDMKMGPDVTVPAYFLHCN
ERHHTLAIAAFPLPKRIHHFMLEVASLDDVGFAFDRVDADGLITSTLGRHTNDHMSFYAS
TPSGVEVEYGWSARTVDRSWVVVRHDSPPSMWGHKSVR

>d1mpya1 d.32.1.3 (A:1-145) Catechol 2,3-dioxygenase
(metapyrocatechase) {Pseudomonas putida, mt2}

MNKGVMRPGHVQLRVLDMSKALEHYVELLGLIEMDRDDQGRVYLKAWTEVDKFSVLV
READEPGMDFMGFKVVDLALRQLERDL MAYGCAVEQLPAGELNSCGRVRVFQAPSGH
HFELYADKEYTGKWGLNDVNPEAWPRDLKG

>d1mpya2 d.32.1.3 (A:146-307) Catechol 2,3-dioxygenase
(metapyrocatechase) {Pseudomonas putida, mt2}

MAAVRFDHALMYGDELPATYDLFTKVLGFYLAQVLDENGTRVAQFLSLSTKAHDVAFIH
HPEKGRLHHVSFHLETWEDLLRAADLISMTDTSIDIGPTRHGLTHGKTIYFFDPSGMRNEV
FCGGDYNYPDHKPVTTTQDLGKAIFYHNRILNERFMTVLT

>d1cxa1 d.32.1.3 (A:4-153) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas
fluorescens}

YENPMGLMGFEFIEFASPTPGTLEPIFEIMGFTKVATHRSKNVHLYRQGEINLILNNEPNSIA
SYFAAEHGSPVCGMAFRVKDSQKAYNRALELGAQPIHIDTGPMELNLPKIGGAPPLYLI
DRFGEGSSIIDIDFVYLEGVERNVPV

>d1cxa2 d.32.1.3 (A:154-356) 4-hydroxyphenylpyruvate dioxygenase, HppD {Pseudomonas
fluorescens}

AGLKVIDHLTHNVYRGRMVYWANFYEKLFNFREARYFDIKGEYTGLTSKAMSAPDGMIR
IPLNEESSKGAGQIEEFLMQFNQEGIQHVAFLTDDLVTWDALKKIGMRFMFTAPPDTYYE
MLEGRLPDHGEPVDQLQARGILLDGSSVEGDKRLLQIFSETLMGPVFFEFIQKRGDDGFG
EGNFKALFESIERDQVRRGVLAT

>d1b3ob2 d.37.1.1 (B:112-159) Type II inosine monophosphate dehydrogenase
{Human (Homo sapiens)}

QGFITDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRVLGIIS

>d1jr1a3 d.37.1.1 (A:178-232) Type II inosine monophosphate dehydrogenase
{Chinese hamster (Cricetulus griseus)}

IMTKREDLVVAPAGITLKEANEILQRSKKGKLPVNNENDELVAIIARTDLKKNRD

>d1zfja2 d.37.1.1 (A:95-158) Type II inosine monophosphate dehydrogenase
{Streptococcus pyogenes}

NGVIIDPFFLTPEHKVSEAEELMQRYRISGVPIVETLANRKLVGIIITNRDMRFISDYNAPISE
H

>d1zfja3 d.37.1.1 (A:159-220) Type II inosine monophosphate dehydrogenase
{Streptococcus pyogenes}

MTSEHLVTAAGVTDLETAERILHEHRIEKLPLVDNSGRLSGLITIKDIEKVIEFPAAKDEF

>d1c8ua1 d.38.1.3 (A:2-115) Thioesterase II (TesB) {Escherichia coli}
SQALKNLLTLLNLEKIEGLFRGQSEDLGLRQVFGGQVVGQALYAAKETVPEERLVHSFHS
YFLRPGDSKKPIIYDVETLRDGNFSARRVAAIQNGKPIFYMTASFQAPEAGF

>d1c8ua2 d.38.1.3 (A:116-286) Thioesterase II (TesB) {Escherichia coli}

EHQKTMPSPAPDGLPSETQIAQSLAHLPPVLKDKFICDRPLEVRPVEFHNPLKGHVAEP
HRQVWIRANGSVDDLRVHQYLLGYASDLNFLPVALQPHGIGFLEPGIQIATIDHSMWFHR
PFNLNEWLLYSVESTSASSARGFVRGEFYTDQGVVLVASTVQEGVMRNHN

>d1egl__ d.40.1.1 (-) Eglin C {Leech (*Hirudo medicinalis*)}
TEFGSELKSFPEVVGKTVDQAREYFTLHYPQYDVYFLPEGSPVTLDLRYNRVRVFYNPGT
NVVNHVPHVG

>d1ypci_ d.40.1.1 (I:) Chymotrypsin inhibitor CI-2 {Barley (*Hordeum vulgare*)}
MKTEWPELVGKSVAAAKKVILQDKPEAQIIVLPVGTIVTMEYRIDRVRLFVDKLDNIAQVP
RVG

>d1dwma_ d.40.1.1 (A:) Trypsin inhibitor LUTI {Flax (*Linum usitatissimum*)}
SRRCPGKNAWPELVGKSGNMAAATVERENRNHAIVLKEGSAMTKDFRCDRVWVIVND
HGVVTSVPHIT

>d1dgia3 d.41.1.1 (A:194-310) Aldehyde oxidoreductase, domain 3 {*Desulfovibrio desulfuricans*}
EFGADAALRMPENTLHLALAQAQVSHALIKGIDTSEAEKMPGVYKVLTHKDVKGKNRIT
GLITFPTNKGDGWERPILNDSKIFQYGDALAIVCADSEANARAAAQKVKFDLELLPEY

>d1fo4a3 d.41.1.1 (A:537-694) Xanthine oxidase, domain 5 (?) {Cow (*Bos taurus*)}
KLDPTYTSATLLFQKHPPANIQLFQEVPNGQSKEDTVGRPLPHLAAAMQASGEAVYCDDI
PRYENELFLRLVTSTRAHAKIKSIDVSEAQKVPGFVCFLSADDIPGSNETGLFNDETTFVAKD
TVTCVGHIIIGAVVADTPEHAERAAHVVKVTYEDLPA

>d1jrob1 d.41.1.1 (B:2-123) Xanthine dehydrogenase chain B, N-terminal domain
{*Rhodobacter capsulatus*}
SVGKPLPHDSARAHVTGQARYLDDLPCPANTLHLAFLGLSTEASAAITGLDLEPVRESPGVI
AVFTAADLPHDNDASPAPSPEPVLATGEVHFVVGQPIFLVAATSHRAARIAARKARITYAPR

>d1ffvb1 d.41.1.1 (B:7-146) Carbon monoxide (CO) dehydrogenase molybdoprotein,
N-domain {*Hydrogenophaga pseudoflava*}
DAEARELAGMGASRLRKEDARFIQKGKGYVDDIKMPGMLHMDIVRAPIAHGRIKKIH
KDAALAMPGVHAVLTAEDLKPLKLHWMPTLAGDVAAVLADEKVHFQMQEVAIVIADDR
YIAADAVEAVKVEYDELPVVIDP

>d1qapa2 d.41.2.1 (A:8-129) Quinolinic acid
phosphoribosyltransferase, N-terminal domain {*Salmonella typhimurium*}
DDRRDALLERINLDIPAAVAQALREDLGGEVDAGNDITAQLLPADTQAHATVITREDGVFC
GKRWVEEVFIQLAGDDVRLTWHVDDGDAIHANQTVFELQGPVRLTGERTALNFVQTL
SG

>d1qpoa2 d.41.2.1 (A:2-116) Quinolinic acid
phosphoribosyltransferase, N-terminal domain {*Mycobacterium tuberculosis*}
GLSDWELAAARAAIARGLDEDLRYGPDVTTLATVPASATTTASLVTREAGVVAGLDVALL
TLNEVLGTNGYRVLDREVEDGARVPPGEALMTLEAQTRGLLTAERTMLNLVGHLSG

>d2tpt_3 d.41.3.1 (336-440) Thymidine phosphorylase {*Escherichia coli*}
TAMLTAKAVYADTEGFVSEMDTRALGMVAVMGGGRRQASDTIDYSVGFTDMARLGDQV
DGQRPLAVIHAKDENNWQEAQAKAVKAAIKLADKAPESTPTVYRRISE

>d1brwa3 d.41.3.1 (A:331-433) Pyrimidine nucleoside phosphorylase {*Bacillus stearothermophilus*}
KAAVTSTVTAAADGYVAEMAADDIGTAAMWLGAQAKKEDVIDLAVGIVLHKKIGDRV
QKGEALATIHSNRPDVLDVKEKIEAAIRLSPQVPARPLIYETIV

>d1buoa_ d.42.1.1 (A:) Promyelocytic leukemia zinc finger (PLZF) protein BTB domain {Human
(*Homo sapiens*)}
MGMIQLQNPSHPTGLLCKANQMRLAGTLCDDVIMVDSQEFHAHRTVLACTSKMFEILFH
RNSQHYTLDFLSPKTFQQILEYAYTATLQAKAEDLDDLLYAAEILEIEYLEEQCLKMLETIQ

>d1vcbb_ d.42.1.1 (B:) Elongin C {Human (Homo sapiens)}
MYVKLISSDGHEFIVKREHALTS GTIKAMLSGPGQFAENETNEVNFREIPSHVLSKVCMYF
TYKVRYSNSTEIPFPIAPEIALELLMAANFLDC

>d1hv2a_ d.42.1.1 (A:) Elongin C {Baker's yeast (Saccharomyces cerevisiae)}
MSQDFVTLVSKDDKEYEISRSAAMISPTLKAMIEGPFRESKGRIELKQFDSHILEKAVEYLN
YNLKYSGVSEDDDEIPEFEIPTMSLELLLAADYLSI

>d1tlda_ d.42.1.2 (A:) Shaker potassium channel {California sea hare (Aplysia californica)}
ERVVINVSGLRFETQLKTLNQFPD TLLGNPQKRNRYYDPLRNEYFFDRNRPSFDAILYFYQ
SGGRLRRPVNVPLDVFSEEIKFYELGENAFERYREDEGF

>d3kvt_ d.42.1.2 (-) akv3.1 voltage-gated potassium channel {California sea hare (Aplysia californica)}
ENRVIINVGGIRHETYKATLKKIPATRLSRLTEGMLNYDPVLNEYFFDRHPGVFAQIINYR
SGKLHYPTDVCGPLFEEELFWGLDSNQVEPCCWMTYTAHR

>d1fs1b2 d.42.1.2 (B:2-68) Cyclin A/CDK2-associated p45, Skp1 {Human (Homo sapiens)}
PSIKLQSSDGEIFEVDVEIAKQSVTIKTMLEDLGMDPVPLPNVNAAILKKVIQWCTHHKDD

>d1efub2 d.43.1.1 (B:140-282) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}
DVLGSYQHGARIGVLVAAKGADEELVKHIAMHVAASKPEFIKPEDVSAEVVEKEYQVQL
DIAMQSGKPKEIAEKMVEGRMKKFTGEVSLTGQPFVMEPSKTVGQLLKEHNAEVTGFIRF
EVGEGIEKVETDFAAEVAAMSKQS

>d1efub4 d.43.1.1 (B:55-139) Elongation factor Ts (EF-Ts), dimerisation domain {Escherichia coli}
VAADGVIKTKIDGNYGIILEVNCQTDFVAKDAGFQAFADKVLDAAVAGKITDVEVLKAQF
EEERVALVAKIGENINIRRVAALEG

>d1tfe_ d.43.1.1 (-) Elongation factor Ts (EF-Ts), dimerisation domain {Thermus thermophilus}
AREGIIGHYIHHNQRVGVLVELNCETDFVARNELFQNLAKDLAMHIAMMNPRYVSAEEIP
AEELEKERQIYIQAALNEGKPQQAIEKIAEGRLKKYLEEVVLLEQPFVKDDKVVKELIQQ
AIAKIGENIVRRFCRFELGA

>d1kkca2 d.44.1.1 (A:98-213) Mn superoxide dismutase (MnSOD) {Aspergillus fumigatus}
EKSGGGKIDQAPVLKAAIEQRWGSFDKFKDAFN TLLGIQGS GWGLVTDGPKGKLDIT
TTHDQDPVTGAAPVFGVDMWEHAYYLQYLNDKASYAKGIWNVINWAEAEENRYIAGDK

>d1isaa2 d.44.1.1 (A:83-192) Fe superoxide dismutase (FeSOD) {Escherichia coli}
NAGGEPTGKVAEAI AASFGSFADFKAQFTDAAIKNFGSGWTWLVKNSDGKLAIVSTSNAG
TPLTTDATPLLTVDVWEHAYYIDYRNARPGYLEHFWALVNWEFVAKNLAA

>d1coja2 d.44.1.1 (A:91-212) Fe superoxide dismutase (FeSOD) {Aquifex pyrophilus}
GGKGEPSEALKKKIEEDIGGLDACTNELKAAAMAFRGWAILGLDIFSGRLV VNGLD AHN V
YNLTGLIPLIVIDTYEHAYYVDYKNKRPPYIDAFFKNINWDVVNERFEKAMKAYEALKDFI
K

>d1b06a2 d.44.1.1 (A:93-210) Fe superoxide dismutase (FeSOD) {Archaeon Sulfolobus acidocaldarius}
PAGKGGGKPGGALADLIDKQYGSFDRFKQVFSESANSLPGSGWTVLYYDNESGNLQIMT
VENHFMNHIAELPVILIVDEFEHAYYLQYKNKRGDYLN AWWNVVNWD DAEKRLQKLYN
K

>d1di2a_d.50.1.1 (A:) Double-stranded RNA-binding protein A, second dsRBD {Xenopus laevis}
 MPVGS LQELAVQKGWRLPEYTVAQESGPPHKREFTITCRVET FVETGSGT SKQVAKRVAA
 EKLLTKFKT

>d1ekza_d.50.1.1 (A:) Staufen, domain III {Fruit fly (Drosophila melanogaster)}
 MDEGDKKSPISQVHEIGIKRNM TVHFV LREEGPAHMKNFITACIVGSIVTEGEGNGKKVS
 KKRAAEKMLVELQKL

>d1qu6a1_d.50.1.1 (A:1-90) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}
 GSHMEMAGDLSAGFFMEELNTYRQKQG VVLKYQELPNSGPPHRRFTFQVIIDGREFPEG
 EGRSKKEAKNAAAKLAVEILNKEKKAVSPL

>d1qu6a2_d.50.1.1 (A:91-179) dsRNA-dependent protein kinase pkr {Human (Homo sapiens)}
 LLTTTNSSEGLSMGNYIGLINRIAQKKRLTVNYEQCASGVHGPEGFHYKCKMGQKEYSIG
 TGSTKQEAQQLAAKLAYLQILSEETGSGC

>d1ec6a_d.51.1.1 (A:) Neuro-oncological ventral antigen 2, nova-2, KH3 {Human (Homo sapiens)}
 MKELVEI AVPENLVGAILGKGGKTLVEYQELTGARIQISKKG EFLPGTRNRRVTITGSPAAT
 QAAQYLISQRVTYEQGVRASNPQKV

>d1vig_d.51.1.1 (-) Vigilin, KH6 {Human (Homo sapiens)}
 INRMDYVEINIDHKFHRHLIGKSGANINRIKDQYKVSVRIPDSEKSNLIRIEGDPQGVQQA
 KRELLELAS

>d2fmr_d.51.1.1 (-) Fragile X protein, KH1 {Human (Homo sapiens)}
 ASRFHEQFIVREDLMGLAIGTHGANIQQARKVPGVTAIDLDEDTCTFHIYGEDQDAVKKA
 RSFLE

>d1khma_d.51.1.1 (A:) HnRNP K, KH3 {Human (Homo sapiens)}
 GSPNSYGD LGGPIITTQVTIPKDLARSIIGKGGQRIKQIRHESGASIKIDEPLEGSEDRIITITG
 TQDQIQNAQYLLQNSVKQYSGKFF

>d1klga_d.51.1.1 (A:) RNA splicing factor 1 {Human (Homo sapiens)}
 TRVSDKVMIPQDEYPEINFVGLLIGPRGNTLKNIEKECNAKIMIRGKGSVKEGKVGRKDG
 QMLPGEDEPLHALVTANTMENVKKAVEQIRNILKQGIETPEDQNDLRKMQLRELARLNGT
 LR

>d3proc1_d.52.1.1 (C:6-85) Alpha-lytic protease prodomain {Lysobacter enzymogenes}
 PQLKFAMQRDLGIFPTQLPQYLQTEKLARTQAAA IEREFGAQFAGSWIERNEDGSFKLVAA
 TSGARKSSTLGGVEVRNVR

>d3proc2_d.52.1.1 (C:86-163) Alpha-lytic protease prodomain {Lysobacter enzymogenes}
 YSLKQLQSAMEQLDAGANARVKGVS KPLDGVQSWYVDPRSNAV VVKVDDGATDAGVD
 FVALSGADSAQVRIESSPGKL

>d1fjgc1_d.52.3.1 (C:2-106) Ribosomal protein S3 N-terminal domain {Thermus thermophilus}
 GNKIHPIGFRLGITRDWESRWYAGKKQYRHLLLEDQRI RGLLEKELYSAGLARVDIERAAD
 NVAVTVHVAKPGVVIGRGGGERIRV LREELAKLTGKNVALNVQEV

>d1legaa2_d.52.3.1 (A:183-295) GTPase Era C-terminal domain {Escherichia coli}
 DYITDRSQRFMASEIIREKLMRFLGAELPYSVTVEIERFVSNERGGYDINGLILVEREGQKK
 MVIGNKGAKIKTIGIEARKDMQEMFEAPVHLELWVKVKSGWADDERALRSL

>d1hh2p3_d.52.3.1 (P:277-344) Transcription factor NusA, C-terminal domains {Thermotoga
 maritima}
 DDPKQLIANALAPATVIEVEILDKENKAARVLVPPTQLSLAIGKGGQNARLAAKLTGWKID
 IKPIMNL

>d1k0ra2 d.52.3.1 (A:184-262) Transcription factor NusA, C-terminal domains {Mycobacterium tuberculosis}

THPNLVRKLFSLVPEIADGSVEIVAVAREAGHRSKIAVRSNVAGLNAKGACIGPMGQVRV
NVMSELSGEKIDIIDYDD

>d1e3ha4 d.52.3.1 (A:579-632) Polynucleotide phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domain 6 {Streptomyces antibioticus}

APRIITVKIPVDKIGEVIGPKRQMINQIQEDTGAEITIEDDGTIYIGAADGPAA

>d1hh2p4 d.202.1.1 (P:1-126) Transcription factor NusA, N-terminal domain {Thermotoga maritima}

MNIGLLEALDQLEEEKGISKEEVIPILEKALVSAYRKNFGNSKNVEVVIDRNTGNIKVYQL
LEVVEEVEDPATQISLEEAKKIDPLAEVGSIVKKELNVKNFGRIAAQTAKQVLIQRIRELEK
EKQ

>d1k0ra4 d.202.1.1 (A:-4-99) Transcription factor NusA, N-terminal domain {Mycobacterium tuberculosis}

VSRRHNMNIDMAALHAIEVDRGISVNELLETIKSALLTAYRHTQGHQTDARIEIDRKTGVVR
VIARETDEAGNLISEWDDTPEGFGRIAATTARQVMLQRFDAE

>d1onea2 d.54.1.1 (A:1-141) Enolase {Baker's yeast (Saccharomyces cerevisiae)}

AVSKVYARSVYDSRGNPTVEVELTTEKGVFRSIVPSGASTGVHEALEMRDGDKSKWMGK
GVLHAVKNVNDVIAPAFVKANIDVKDQKAVDDFLISLDGTANKSKLGANAILGVSLAASR
AAAAEKNVPLYKHLADLSKSKT

>d1ec7a2 d.54.1.1 (A:5-137) D-glucarate dehydratase {Escherichia coli}

FTTPVVTEMQVIPVAGHDSMLMNLSGAHAPFFTRNIVIIKDNSGHTGVGEIPGGEKIRKTL
EDAIPLVVGKTLGEYKNVLTIVRNTFADRDAGGRGLQTFDLRTTIHVVTGIEAAMLDDL
GQHLGVNVASLLG

>d1fhua2 d.54.1.1 (A:1-99) O-succinylbenzoate synthase {Escherichia coli}

MRSAQVYRWQIPMDAGVVLRDRRLKTRDGLYVCLREGEREWGGEISPLPGFSQETWEEA
QSVLLAWVNNWLAGDCELPQMPSVAFGVSCALAEITDLP

>d1muca2 d.54.1.1 (A:4-130) Muconate-lactonizing enzyme (cis muconate cycloisomerase) {Pseudomonas putida}

ALIERIDAIIVDLPTIRPHKLAMHTMQQQTLVVLRVRCSDGVEGIGEATTIGGLAYGYESPE
GIKANIDAHLPALIGLAADNINAAMLKLDKLA KGNTFAKSGIESALLDAQGKRLGLPVS
ELLGG

>d2mnr_2 d.54.1.1 (3-132) Mandelate racemase {Pseudomonas putida}

EVLITGLRTRAVNVPLAYPVHTAVGTVGTAPLVLIDLATSAGVVGHSYLFAYTPVALKSLK
QLDDMAAMIVNEPLAPVSLEAMLAKRFCLAGYTGLIRMAAAGIDMAAWDALGKVHET
PLVKLLGANAR

>d1jpdx2 d.54.1.1 (X:-2-113) L-Ala-D/L-Glu epimerase {Escherichia coli}

GSHMRTVKVFEEAWPLHTPFVIARGSRSEARVVVVELEEEGIKGTGECTPYPRYGESDAS
VMAQIMSVVPQLEKGLTREELQKILPAGAARNALDCALWDLAARRQQQSLADLIGI

>d1jpm2 d.54.1.1 (A:1-125) L-Ala-D/L-Glu epimerase {Bacillus subtilis}

MKIIRIETSRIAVPLTKPFKTALRTVYTAESVIVRITYDSGAVGWGEAPPTLVITGDSMDSIES
AIHHVLKPALLGKSLAGYEAILHDIQHLLTGNMSAKAAVEMALYDGWAQMCGLPLYQML
GG

>d1kca2 d.54.1.1 (A:1-160) beta-Methylaspartase {Clostridium tetanomorphum}

MKIVDVLCTPGLTGIFYFDDQRAIKKGAGHDGFTYTGSTVTEGFTQVRQKGESISVLLVLE
DGQVAHGDCAAVQYSGAGGRDPLFLAKDFIPVIEKEIAPKLIGREITNFKPMAEEFDKMTV
NGNRLHTAIRYGITQAILDAVAKTRKVTMAEVIRDEYNP

>d1bxea_ d.55.1.1 (A:) Ribosomal protein L22 {Thermus aquaticus, subsp. Thermus thermophilus}
MEAKAIARYVRISPRKVRVLVVDLIRGKSLEEARNILRYTNKRGAYFVAKVLESAAANAVN
NHDMLEDRLYVKAAYVDEGPALKRVLPRARGRADIKKRTSHITVILGEK

>d1jj2q_ d.55.1.1 (Q:) Ribosomal protein L22 {Archaeon Haloarcula marismortui}
GISYSVEADPDTTAKAMLRERQMSFKHSAIAREIKGKTAGEAVDYLEAVIEGDQPVPFKQ
HNSGVGHKSKVDGWDAGRYPEKASKAFLDLLENVGNADHQGFDGEAMTIKHVAAHK
VGEQQGRKPRAMGRASAWNSPQVDVELILEEP

>d1h6ha_ d.189.1.1 (A:) p40phox NADPH oxidase {Human (Homo sapiens)}
AVAQQLRAESDFEQLPDDVAISANIADIEEKRGTSHFVVFVIEVKTKGGSKYLIYRRYRQFH
ALQSKLEERFGPDSKSSALACTLPTLPAKVYVGVKQEIEMRIPALNAYMKSLLSLPVWV
LMDEDVRIFFYQSPYDSEQVP

>d1gd5a_ d.189.1.1 (A:) p47phox NADPH oxidase {Human (Homo sapiens)}
GSMGDTFIRHIALLGFEKRFVPSQHYVYMFLVKWQDLSEKVYRRFTEIYEFHKTLEMF
PIEAGAINPENRIIPHLPAKWFQDGRQAAENRQGTLECYCSTLMSLPTKISRCPHLLDFFKV
RPDDLKLP

>d1vjw_ d.58.1.4 (-) Ferredoxin {Thermotoga maritima}
MKVRVDADACIGCGVCENLCPDVFQLGDDGKAKVLQPETDLPCAADAADSCPTGAISVE

>d1fxra_ d.58.1.4 (A:) Ferredoxin I {Sulfate-reducing bacteria (Desulfovibrio africanus)}
ARKFYVDQDECIACESCVEIAPGAFAMDPEIEKAYVKDVEGASQEEVEEAMDTCPVQCIH
WEDE

>d1iqza_ d.58.1.4 (A:) Ferredoxin {Bacillus thermoproteolyticus}
PKYTIVDKETCIACGACGAAAPDIYDYDEGGIAYVTLDNQGIVEVPDILIDDMMDAFEG
CPTDSIKVADEPFDDGPNKFE

>d1jb0c_ d.58.1.4 (C:) Photosystem I iron-sulfur protein PsaC {Synechococcus elongatus}
AHTVKIYDTCIGCTQCVRACPTDVLEMVPWDGCKAGQIASSPRTEDCVGCKRCETACPTD
FLSIRVYLGAETTRSMGLAY

>d1feha3 d.58.1.5 (A:127-209) Fe-only hydrogenase, second domain {Clostridium pasteurianum}
KDKTEYVDERSKSLTVDRKCLLCGRVCVNACGKNTETYAMKFLNKGKTIIGAEDKCF
DDTNCLLCGQCIIACPVAALSEKS

>d1hfe12 d.58.1.5 (L:2-86) Fe-only hydrogenase larger subunit, N-domain {Desulfovibrio desulfuricans}
SRTVMERIEYEMHTPDPKADPDKLHFVQIDEAKCIGCDTCSQYCPTAAIFGEMGEPHSIPHI
EACINCGQCLTHCPENAIYEAQS

>d1keka5 d.58.1.5 (A:669-785) Pyruvate-ferredoxin oxidoreductase, PFOR, domain V {Desulfovibrio africanus}

TSQFEKRGVAINVPQWVPENCICQNCQCAFVCPHSAILPVLAKKEELVGAPANFTALEAKGK
ELKGYKFRIQINTLDCMGCNCADICPPKEKALVMQPLDTQRDAQVPNLEYAARIP

>d1h7wa5 d.58.1.5 (A:845-1017) Dihydropyrimidine dehydrogenase, C-terminal domain {Pig (Sus scrofa)}

ELQGWGQSPGTESHQKGKPVPRIAELMGKKLPNFGPYLEQRKKIIAEEKMRLKEQNAA
 FPPLERKPFIPKKPIPAIKDVGKALQYLGTFGELSNIEQVVAVIDEEMCINCGKCYMTCNDS
 GYQAIQFDPETHLPTVTDCTGCTLCLSVCPIIDCIRMVSRTTPYEPKRGL

>d1jnrb_ d.58.1.5 (B:) Adenylylsulfate reductase B subunit {Archaeon Archaeoglobus fulgidus}
 PSFVNPEKCDGCKALERTACEYICPNDLMTLDKEKMKAYNREPDMCWECYSCVKMCPQ
 GAIDVRGYVDYSPLGGACVPMRGTSDIMWTVKYRNGKVLRFKFAIRTPWGSIQPFEGFP
 EPTEEALKSELLAGEPEIIGTSEFPQVKKKA

>d1pca_2 d.58.3.1 (4A-99A) Procarboxypeptidase A {Pig (Sus scrofa)}
 KEDFVGHQVLRISVDDEAQVQKVKELEDLEHLQLDFWRGPARPGFPIDVRVPFPSIQAVK
 VFLEAHGIRYTIMIEDVQLLLDEEQEQMFASQGR

>d1nsa_2 d.58.3.1 (7A-95A) Procarboxypeptidase B {Pig (Sus scrofa)}
 FEGEKVFRVNVEDENDISELHELASTRQIDFWKPDSTQIKPHSTVDFRVKAEDILAVEDFL
 EQNELQYEVLINNLRSVLEAQFDSVSR

>d1spbp_ d.58.3.2 (P:) Subtilisin prosegment {Bacillus amyloliquefaciens}
 EKKYIVGFKQTMSTMSAAKKKDVISEKGGKVQKQFKYVDAASATLNEKAVKELKKDPS
 VAYVEEDHVAHAY

>d1itpa_ d.58.3.2 (A:) Proteinase A inhibitor 1, POIA1 {Oyster mushroom (Pleurotus ostreatus)}
 GSAGKFIVIFKNDVSEDKIRETKDEVIAEGGTITNEYNMPGMKGFAGELTPQSLTKFQGLQ
 GDLIDSIEEDGIVTTQ

>d1hal_1 d.58.7.1 (8-92) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
 EPEQLRKLFIGGLSFETTDESLSHFEGWGTLDTCVVMRDPNTRSRGFGFVYATVEEVD
 AAMNARPHKVDGRVVEPKRAVSRE

>d2up1a2 d.58.7.1 (A:99-190) Nuclear ribonucleoprotein A1, RNP A1, UP1 {Human (Homo sapiens)}
 GAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKIEVIEIMTDRGSGKKRGFAFVTFFDDHDSV
 DKIVIQKYHTVNGHNCEVRKALSKQEMASAS

>d1fht_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}
 AVPETRPNHTIYINNLNEKIKKDELKKSLEYAIFSQFGQILDILVSRSLKMRGQAFVIFKEVSS
 ATNALRSMQGFPFYDKPMRIQYAKTDSIIAKMKGTTFVERDRKREKRKPKSQE

>d2u1a_ d.58.7.1 (-) Splicesomal U1A protein {Human (Homo sapiens)}
 MAPAQPLSENPPNHILFTNLPEETNELMLSMLFNQFPGFKEVRLVPGRHDIAFVEFDNEV
 QAGAARDALQGFKITQNNAMKISFAKK

>d1u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}
 ARRLYVGNIPFGITEEAMMDFFNAQMRLGGLTQAPGNPVLAVQINQDKNFAFLEFRSVDE
 TTQAMAFDGIIFQGQSLKIRRPHDYQPLPG

>d2u2fa_ d.58.7.1 (A:) Splicing factor U2AF 65 KDa subunit {Human (Homo sapiens)}
 AHKLFIGGLPNYLNDQVKELLTSFGPLKAFNLVKDSATGLSKGYAFCEYVDINVTDAQIA
 GLNGMQLGDKLLVQRASVGAKNA

>d1sxl_ d.58.7.1 (-) Sex-lethal protein {Drosophila melanogaster}
 MSYARPGGESIKDTNLYVTNLPRTITDDQLDTIFGKYGSIVQKNILRDKLTGRPRGVAFVRY
 NKREEAQEAISALNNVIPEGGSQPLSVRLAEEHGK

>d1d8za_ d.58.7.1 (A:) Hu antigen C (Huc) {Mouse (Mus musculus)}
 MDSKTNLIVNYLPQNMTQDEFKSLFGSIGDIESCKLVRDKITGQSLGYGFVNYS DPNDAD
 KAINTLNGLKLQTKTIKVSYPSSASIR

>d1cvja1 d.58.7.1 (A:11-90) Poly(A)-binding protein {Human (Homo sapiens)}
ASLYVGDLHPDVTEAMLYEKFSPAGPILSIRVCRDMITRRSLGYAYVNFQQPADAERALDT
MNFDDVIKGPVRIMWSQRD

>d1cvja2 d.58.7.1 (A:91-179) Poly(A)-binding protein {Human (Homo sapiens)}
PSLRKSGVGNIFIKNLDKSIDNKALYDTFSAFGNILSCKVVCDENGSKGYGFVHFETQEAA
ERAIEKMNGMMLNDRKV FVGRFKSRKER

>d1qm9a1 d.58.7.1 (A:1-110) Polypyrimidine tract-binding protein {Human (Homo sapiens)}
MGNSVLLVSNLNPervTPQSLFILFGVYGDVQRVKILFNKKENALVQMADGNQAQLAMS
HLNGHKLHGKPIRITLSKHQNVQLPREGQEDQGLTKDYGNSPLHRFKKPGS

>d1qm9a2 d.58.7.1 (A:111-198) Polypyrimidine tract-binding protein {Human (Homo sapiens)}
KNFQNIFFPSATLHLSNIPPSVSEEDLKVLFFSSNGGVVKGKFFQKDRKMALIQMGSVEEA
VQALIDLHNHDLGENHHLRVFSKSTI

>d1fj7a_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}
GSHMLEDPVEGSESTTPFNLFIGNLNPNKSVAELKVAISELFAKNDLAVVDVRTGTNRKFG
YVDFESAEDLEKALELTGLKVFGNEIKLEKPKGRDGTGRC

>d1fjca_ d.58.7.1 (A:) Nucleolin {Golden hamster (Mesocricetus auratus)}
SHMLEDPCTSKKVRAARTLLAKNLSFNITEDELKEVFEDALEIRLVSQDGKSKGIAYIEFKS
EADAENLEEKQGAIEDGRSVSLYYTGEKGGTRG

>d1h6kx_ d.58.7.1 (X:) CBP20, 20KDa nuclear cap-binding protein {Human (Homo sapiens)}
KSCTLYVGNLSFYTTTEEQIYELFSKSGDIKKIIMGLDKMTACGFCFVEYYSRADAENAMRY
INGTRLDDRIIRTDWDAG

>d1dbda_ d.58.8.1 (A:) Papillomavirus-1 E2 protein {Bovine papillomavirus type 1}
RRTTNDGFHLLKAGGSCFALISGTANQVKCYRFRVKKNHRHRYENCTTTWFTVADNGAE
RQGQAQILITFGSPSRQDFLKHVPLPPGMNISGFTASLDF

>d1a7ge_ d.58.8.1 (E:) Papillomavirus-1 E2 protein {Human papillomavirus type 31}
ATTPIIHLKGDANILKCLRYRLSKYKQLYEQVSSTWHWTCTDGKHKNIAIVTLTYISTSQRD
DFLNTVVIPNTVSVSTGYMTI

>d1b3ta_ d.58.8.1 (A:) Epstein barr virus nuclear antigen-1 (ebna1) {Epstein-Barr virus}
KGGWFGKHRGQGGSNPKFENIAEGLRALLARSHVERTTDEGTWVAGVFVYGGSKTSLYN
LRRGTALAIPQCRLTPLSRLPFGMAPGPGPQPGPLRESIVCYFMVFLQTHIFAEVLKDAIKD
LVMTKPAPTCNIRVTVCSEDDGVDLP

>d1bwva2 d.58.9.1 (A:7-149) Ribulose 1,5-bisphosphate carboxylase-
oxygenase {Galdieria partita}
RIKNSRYESGVIPYAKMGYWNPDYQVKD TDVLALFRVTPQPGVDPIEAAA VAGESSTAT
WTVVWTDLLTAADLYRAKAYKVDQVPNNPEQYFAYIAYELDLFEEGSIANLTASIIGNVFG
FKAVKALRLEDMRLPLAYLKTFQ

>d5rub2 d.58.9.1 (A:2-137) Ribulose 1,5-bisphosphate carboxylase-oxygenase
{Rhodospirillum rubrum}
DQSSRYVNLALKEEDLIAGGEHVLCA YIMKPKAGYGYVATAAHFAAESSTGTNVEVCTTD
DFTRGVDALVYEVDARELTKIAYPVALFDRNITDGKAMIASFLTLTMGNNQGMGDVEYA
KMHDFFVPEAYRALFD

>d1dar_4 d.58.11.1 (600-689) Elongation factor G (EF-G), domains III and V {Thermus
thermophilus}
VILEPIMRVEVTTPEEYMGDVIGDLNARRGQILGMEPRGNAQVIRAFVPLAEMFGYATDL

RSKTQGRGSFVMFFDHYQEVPKQVQEKLIK

>d1fma4 d.58.11.1 (A:404-482) Elongation factor G (EF-G), domains III and V {Thermus thermophilus}

VPEPVIDVAIEPKTKADQEKLSQALARLAEEDPTFRVSTHPETGQTIISGMGELHLEIIVDRL
KREFKVDANVGKPQVA

>d1b64__ d.58.12.1 (-) Guanine nucleotide exchange factor (GEF) domain from elongation factor-1 beta {Human (Homo sapiens)}

MLVAKSSILLDVKPWDDETDMAKLEECVRSIQADGLVWGSSKLVPGYGIKKLQIQCVVE
DDKVGTDMLLEEQITAFEDYVQSM DVAAFNKI

>d1gh8a_ d.58.12.1 (A:) aEF-1beta {Archaeon Methanobacterium thermoautotrophicum}

MGDVVATIKVMPESPVDLEALKKEIQERIPEGTELHKIDEEPIAFGLVALNVMVVGDAE
GGTEAAEESLSGIEGVSNIETDVRRLM

>d1fa0a1 d.58.16.1 (A:352-523) Poly(A) polymerase, C-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

NDFFFRYKFYLEITAYTRGSDEQHLKWSGLVESKVRLLVMKLEVLAGIKIAHPFTKPFESS
YCCPTEDDYEMIQDKYGSHKTETALNALKLVTDENKEEESIKDAPKAYLSTMYIGLDFNIE
NKKEKVDIHIPCTEFVNLCSFNEDYGDHKVFNLALRFVKG YDLPDEVFD

>d1f5aa1 d.58.16.1 (A:365-498) Poly(A) polymerase, C-terminal domain {Cow (Bos taurus)}

PNFFQKYKHYIVLLASAPTEKQRLEWVGLVESKIRILVGSLEKNEFITLAHVNPQSFPAPKE
NPDKEEFRTMWVIGLVFKKTENSENLSVDLT YDIQSFTDTVYRQAINSKMFEVDMKIAAM
HVKRKQLHQLLP

>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)}

AREVILAVHGMTCSACTNTINTQLRALKGVTCKDISLVTNECQVTYDNEVTADSIKEIIEDC
GFDCEILRDS

>d1aw0__ d.58.17.1 (-) Menkes copper-transporting ATPase {Human (Homo sapiens)}

LTQETVINIDGMTCNQSCVQSIEGVISKKPGVKSRVSLANSNGTVEYDPLLTSPETLRGAIED
MGFDATLSD

>d1cc8a_ d.58.17.1 (A:) ATX1 metallochaperone protein (ATOX1) {Baker's yeast (Saccharomyces cerevisiae)}

AEIKHYQFNVVMTCSGCSGAVNKVLTKLEPDVSKIDISLEKQLVDVYTTLPYDFILEKIKK
TGKEVRSGKQL

>d1cpza_ d.58.17.1 (A:) Copper chaperone {Enterococcus hirae}

AQEFSVKGMSCNHCVARIEEAVGRISGVKKVKVQLKKEKAVVKFDEANVQATEICQAIN
ELGYQAEVI

>d1k0va_ d.58.17.1 (A:) Copper chaperone {Bacillus subtilis, CopZ}

MEQKTLQVEGMSQCQHCVKAVETSGELDGVS AVHVNLEAGKVDVSFDADKVS VKDIAD
AIEDQGYDVAKIEGR

>d1qupa2 d.58.17.1 (A:2-73) Copper chaperone for superoxide dismutase, N-terminal domain {Baker's yeast (Saccharomyces cerevisiae)}

TTNDTYEATYAIPMHCENCVNDIKACLKNVPGINSLNFDIEQQIMSVESVAPSTIINTLRNC

GKDAIIRGA

>d1gmua2 d.58.38.1 (A:71-138) Urease metallochaperone UreE, C-terminal domain
{Klebsiella aerogenes}

DEEVSVVRCDPFFMLAKACYALGNRHVPLQIMPGELEHYHHDHVLDDMLRQFGLTVTFG
QLPFEPEAGA

>d1leara2 d.58.38.1 (A:75-142) Urease metallochaperone UreE, C-terminal domain
{Bacillus pasteurii}

LEKVYVIKQTMQEMGKMAFEIGNRHTMCIIEDDEILVRYDKTLEKLIDEVGVSYEQSERR
FKEPFKY

>d1tdj_2 d.58.18.2 (336-423) Allosteric threonine deaminase C-terminal domain
{Escherichia coli}

QREALLAVTIPEEKGSFLKFCQLLGGRSVTEFNRYFADAKNACIFVGVRLSRGLEERKEIL
QMLNDGGYSVVDLSDDDEMAKLHVRYMV

>d1tdj_3 d.58.18.2 (424-514) Allosteric threonine deaminase C-terminal domain
{Escherichia coli}

GGRPSHPLQERLYSFEFPESPGALLRFLNTLGTYWNISLFHYRSHGTDYGRVLA AFELGDH
EPDFETRLNELGYDCHDETNNPAFRFFLAG

>d1dqaal d.58.20.1 (A:587-703) NAD-binding domain of HMG-CoA reductase
{Human (Homo sapiens)}

GMTRGPVVRLPRACDSAEVKAWLETSEGFVAVIKEAFDSTSRFARLQKLHTSIAGRNLRIYRF
QSRSGDAMGMNMISKGTEKALSKLHEYFPQMILAVSGNYCTDKKPAAINWIEGRG

>d1qaxal d.58.20.1 (A:111-220) NAD-binding domain of HMG-CoA reductase
{Pseudomonas mevalonii}

LMHAQVQIVGIQDPLNARLSLLRRKDEIIELANRKDQLLNSLGGGCRDIEVHTFADTPRGP
MLVAHLIVDVRDAMGANTVNTMAEAVAPLMEAITGGQVRLRILSNLADL

>d1azsa_ d.58.29.1 (A:) Adenylyl cyclase VC1, domain C1a {Dog (Canis familiaris)}

DMMFHKIIYIQKHDNVSI LFADIEGFTSLASQCTAQELVMTLNELFARFDKLA AENHCLRIKI
LGDCYYCVSGLPEARADHAHCCVEMGMDMIEAISLVREMTGVNVNMRVGIHSGRVHCG
VLGLRKWQFDVWSNDVTLANHMEAGGKAGRIHITKATLSYLN GDYEVEPGCGGERNAY
LKEHSIETFLIL

>d1azsb_ d.58.29.1 (B:) Adenylyl cyclase IIC1, domain C2a {Rat (Rattus norvegicus)}

HQSYDCVCVMFASIPDFKEFYTESDVNKEGLECLRLNEIADFDLLSKPKFSGVEKIKTI
GSTYMAATGLSAIPSQEHAQEPERQYMHIGTMVEFAYALVGKLD AINKHSFNDFKLRVGI
NHGPVIAGVIGA QKPQYDIWGNTVNVASRMDSTGVLDKIQVTEETSLILQTLGYTCTCRGI
INVKGKGD LKTYFVNT

>d1fx2a_ d.58.29.1 (A:) Receptor-type monomeric adenylyl cyclase {Trypanosome (Trypanosoma
brucei), different isoform}

NNNRAPKEPTDPVTLIFTDIESSTALWAAHPDLM PDAVA AHHRMVRS LIGRYKCYEVKTV
GDSFMIASKSPFAAVQLAQELQLCFLHHDWGTNALDDSYREFEEQRAEGECEYTPPTAHM
DPEVYSRLWNGLRVRVGIHTGLCDIRHDEVTKGYDYYGRTPNMAARTESVANGGQVLM T
HAAYMSLSAEDRKQIDVTALGDVALRGVSDPVKMYQLNTVPSRNFAALRLDREYFD

>d1e6ya2 d.58.31.2 (A:1002-1283) Alpha chain {Archaeon Methanosarcina barkeri}

AADIFSKFKKDM EVKFAQEFGSNKQTGGDITDKTAKFLRLGPEQDPRKVEMIKAGKEIAE
KRGIAFYNPMMHSGAPLGQRAITPYTISGTDIVCEPDDLHYVNNAAMQQMWD DIRRTCIV

GLDMAHETLEKRLGKEVTPETINHYLEVLNHAMPGAADVQEMMVETHPALVDDCYVKV
FTGDDALADEIDKQFLIDINKEFSEEQAAQIKASIGKTSWQAIHIPTIVSRITDGAQTSRWA
AMQIGMSFISAYAMCAGEAAVADLSFAAKHAALVSMGEMPLA

>d1hbn2 d.58.31.2 (B:2-188) Beta chain {Archaeon Methanobacterium thermoautotrophicum}
AKFEDKVDLYDDRGNLVEEQVPLEALSPLRNPAIKSIVQGIKRTVAVNLEGIEENALKTAKV
GGPACKIMGRELDLDIVGNAESIAAAKEMIQVTEDDDTNVELLGGGKRALVQVPSARFD
VAAEYSAAPLVATATAFVQAIINEFDVSMYDANMVKA AVLGRYPQSVEYMGANIATMLDIP
QKLEGP

>d1e8ga1 d.58.32.1 (A:274-560) Vanillyl-alcohol oxidase {Fungus (Penicillium
simplicissimum)}

GGYQSYLITLPKDGDLKQAVDIIRPLRLGMALQNVPTIRHILLDA AVLGDKRSYSSRTEPLS
DEELDKIAKQLNLGRWNFYGALYGPEPIRRVLWETIKDAFSAIPGVKFYFPEDTPENSVLR
VRDKTMQGIPTYDELKVIDWLPNGAHLFFSPIAKVSGEDAMMQYAVTKKRCQEAGLDFI
GTFTVGMREMHIVCIVFNKKDLIQKRKVQWLMRTLIDDCAANGWGEYRTHLAFMDQI
METYNWNNSSFLRFNEVLKNAVDPNGIAPGKSGVWPSQYSHVTWKL

>d1dqa1 d.58.32.1 (A:243-521) Flavoprotein subunit of p-cresol methylhydroxylase
{Pseudomonas putida}

PVFKPFEVIFEDEADIVEIVDALRPLRMSNTIPNSVVIASLWEAGSAHLTRAQYTTPEGHT
PDSVIKQMOKDTGMGAWNLYAALYGTQEVDVNWKIVTDVFKKLKGGRIVTQEEAGDT
QPFKYRAQLMSGVPNLQEFGLYNWRGGGSMWFAPVSEARGSECKKQAAMAKRVLHK
YGLDYVAEFIVAPRDMHHVIDVLYDRTNPEETKRADACFNELLDEFEKEGYAVYRVNTRF
QDRVAQSYGPVKRKLHAIKRAVDPNNILAPGRSGIDLNNDF

>d1fra1 d.58.33.1 (A:1-148)
Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon
Methanopyrus kandleri}

MEINGVEIEDTFAEAFEAKMARVLITAASHKWAMIAVKEATGFGTSVIMCPAEAGIDCGYV
PPEETPDGRPGVTIMIGHNDEDELKEQLLDRIGQCVMTAPTASAFDAMPEAEKEDEDRVG
YKLSFFGDGYQEEDELGRKVKWIPVV

>d1fra2 d.58.33.1 (A:149-296)
Formylmethanofuran:tetrahydromethanopterin formyltransferase {Archaeon
Methanopyrus kandleri}

EGEFIVEDSFGITTGVAGGNFYIMAESQPAGLQAAEAAVDAIKGVEGAYAPFPGGIVASASK
VGSKQYDFLPASTNDAYCPTVEDNELPEGVKCVYEIVINGLNEEAVKEAMRVGIEAACQQ
PGVVKISAGNFGGKLGQYIEHLHDLF

>d1qda1 d.58.34.1 (A:2-180) Formiminotransferase domain of formiminotransferase-
cyclodeaminase. {Pig (Sus scrofa)}

SQLVECVPNFSEGKNQEVIDAISRAVAQTPGCVLLDVDSGPSTNRTVYTFVGRPEDVVEGA
LNAARAAAYQLIDMSRHHGEHPRMGALDVCPFIPVRGVMTDECVRCAQAFGQRLAEELG
VPVYLYGEAARTAGRQSLPALRAGEYEALPEKLKQAEWAPDFGPSAFVPSWGATVAGAR
K

>d1qda2 d.58.34.1 (A:181-326) Formiminotransferase domain of formiminotransferase-
cyclodeaminase. {Pig (Sus scrofa)}

FLLAFNINLLSTREQAHRIALDLREQGRGKDQPGRLKKVQAIGWYLDEKNLAQVSTNLLD
FEVTGLHTVFEETCREAQELSLPVVGSQVLGLVPLKALLDAAAFYCEKENLFLQDEHRIR

LVVNRLGLDSLAPFKPKERIIEYLV

>d1dj0a1 d.58.35.1 (A:7-114) Pseudouridine synthase I {Escherichia coli}

PPVYKIALGIEYDGSKYYGWQRQNEVRSVQEKLEKALSQVANEPITVFCAGRTDAGVHG
TGQVVHFETTALRKDAAWTLGVNANLPGDIAVRWVKTPDDFHARFSAT

>d1dj0a2 d.58.35.1 (A:115-270) Pseudouridine synthase I {Escherichia coli}

ARRRYRIIYNHRLRPAVLKSGVTHFYEPLDAERMHRAAQCLLGENDFTSFRAVQCQSRT
WRNVMHINVTRHGPYVVVDIKANAFVHHMVRNIVGSLMEVGAHNQPESWIAELLA
AKDRTLAAATAKAEGLYLVAVDYPDRYDLPKPPMGPLFLAD

>d1k8wa1 d.58.35.2 (A:9-73) Pseudouridine synthase II TruB {Escherichia coli}

MDINGVLLLDKPQGMSSNDALQKVKRIYNANRAGHTGALDPLATGMLPICLGEATKFSQ
YLLDS

>d1k8wa2 d.58.35.2 (A:74-312) Pseudouridine synthase II TruB {Escherichia coli}

KRYRVIARLGQRTDTSADGQIVEERPVTFSAEQLAAALDTFRGDIEQIPSMYSALKYQGK
KLYEYARQGIEVPREARPITVYELLFIRHEGNELELEIHCSKGTYIRTIIDDLGEKLGCAHV
IYLRRLAVSKYPVERMVTLEHLRELVEQAEQQDIPAAELLDPLLMPMDSPASDYPVVNLPL
TSSVYFKNGNPVRTSGAPLEGLVRVTEGENGKFIGMGEIDDEGRVAPRRLVVEY

>d1aop_1 d.58.36.1 (81-145) Sulfite reductase, domains 1 and 3 {Escherichia coli}

LLRCRLPGGVITTKQWQAIDKFAGENTIYGSIRLTNRQTFQFHGILKKNVKPVHQMHLHSV
GLDAL

>d1aop_2 d.58.36.1 (346-425) Sulfite reductase, domains 1 and 3 {Escherichia coli}

IGWVKGIDDNWHLTLFIENGRILDYPARPLKTGLLEIAKIHKGDFRITANQNLIIAGVPESEK
AKIEKIAKESGLMNAVT

>d1bxya_ d.59.1.1 (A:) Prokaryotic ribosomal protein L30 {Thermus thermophilus}

MPRLKVKLVKSPIGYPKDQKAALKALGLRRLQQERVLEDTPAIRGNVEKVAHLVRVEVVE

>d1jj2v_ d.59.1.1 (V:) Archaeal L30 (L30a) {Archaeon Haloarcula marismortui}

MHALVQLRGEVNMHTDIQDTLEMLNIHHVNHCTLPETDAYRGMVAKVNDVFAFGEPSQ
ETLETVLATRAEPLEGDADVDDEWVAEHTDYDDISGLAFALLSEETTLREQGLSPTLRLHP
PRGGHDGVKHPVKEGGQLGKHDTEGIDDLLEAMR

>d2ifl_ d.64.1.1 (-) Eukaryotic translation initiation factor eIF-1 (SUI1) {Human (Homo sapiens)}

MRGSHHHHHHTDPMSAIQNLHSFDPFADASKGDDLLPAGTEDYIHIRIQQRNGRKTLLTV
QGIADDYDKKKLVKAFKKKFACNGTVIEHPEYGEVIQLQGDQRKNICQFLVEIGLAKDDQ
LKVHGF

>d1d1ra_ d.64.1.1 (A:) YciH {Escherichia coli}

KGDGVVRIQRQTSGRKGKGVCLITGVDLDDAELTKLAAELKKKCGCGGAVKDGVIQIG
DKRDLLKSLEAKGMKVLAGGLE

>d1f7ua3 d.67.2.1 (A:2-135) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Baker's yeast (Saccharomyces cerevisiae)}

ASTANMISQLKKLSIAEPAVAKDSDPDVNIVDLMRNYISQELSKISGVDSSLIFFPALEWTNT
MERGDLLIPIPLRIKGANPKDLAVQWAEKFCGDFLEKVEANGPFIQFFFPQFLAKLVIP
DILTRKEDYG

>d1iq0a3 d.67.2.1 (A:1-96) Arginyl-tRNA synthetase (ArgRS), N-terminal 'additional' domain {Thermus thermophilus}

MLRRALEEAIAQALKEMGVPVRLKVARAPKDKPGDYGVPPLFALAKELRKPPQAIAQELK

DRLLPPEFVEEAVPVGGYLNFRRLRTEALLREALRPKA

>d1j98a_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Bacillus subtilis}
VESFELDHNNAVAPYVRHCGVHKVGTGVDVGNKFDIRFCQPNKQAMKPDTHLEHLLAF
TIRSHAKEYDHFIDIIDISPMGCQTGYLVLVSGETTSAEIVDLLEDTMKEAVEITEIPAANEK
QCGQAKLHDLEGAKRLMRFWLSQDKEELLKVFG

>d1j6wa_ d.185.1.2 (A:) Autoinducer-2 production protein LuxS {Haemophilus influenzae}

LLDSFKVDHTKMNAVRIAKTMLTPKGDNITVFDLRFICIPNKEILSPKGIHTLEHLFAGFM
RDHLNGDSIEIIDISPMGCRTGFYMSLIGTPNEQKVSEAWLASMQDVLGVQDQASIPELNI
YQCGSYTEHSLEDAHEIAKNVIARGIGVNKNEDLSLDN

>d1hr6b2 d.185.1.1 (B:246-462) Mitochondrial processing peptidase (MPP) beta chain {Baker's yeast (Saccharomyces cerevisiae)}

GPLPVFCRGERFIKENTLPTTHIAIALEGVSWSPADYFVALATQAIVGNWDRAIGTGTNSPS
PLAVAASQNGSLANSYMSFSTSYADSLWGMIVTDSNEHNVRLIVNEILKEWKRIKSGKI
SDAEVNRAKAQLKAALLSLDGGSTAIVEDIGRQVVTTGKRLSPEEVFEQVDKITKDDIIM
WANYRLQNKPVSMVALGNTSTVPNVSYIEEKLNQ

>d1hr6a1 d.185.1.1 (A:14-233) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}

ARTDNFKLSSLANGLKVATSNTPGHFSALGLYIDAGSRFEGRNKLGCTHILDRLAFKSTEH
VEGRAMAETLELLGGNYQCTSSRENLMYQASVFNQDVGKMLQLMSETVRFPKITEQELQ
EQKLSAEYEIDEVWMKPELVLPPELLHTAAYSGETLGSPLICPRGLIPSISKYYLLDYRNKFY
TPENTVAAFVGVPEHEKAELTGKYLGDWQSTHPPITKK

>d1hr6a2 d.185.1.1 (A:234-470) Mitochondrial processing peptidase (MPP) alpha chain {Baker's yeast (Saccharomyces cerevisiae)}

VAQYTGGESCIPPAPVFGNLPelfHIQIGFEGLPIDHPDIYALATLQTLLGGGGSFSAGGPGK
GMYSRLYTHVLNQYYFVENCVAFNHSYSDSGIFGISLSCIPQAAPQAVEVIAQQMYNTFAN
KDLRLTEDEVSRANKQLKSSLLMNLESKLVELEDMDGRQVLMHGRKIPVNEMISKIEDLKP
DDISRVAEMIFTGNVNNAGNGKGRATVVMQGDGRGSFGDVENVLKAYGLGNSSS

>d1be3a1 d.185.1.1 (A:1-233) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}

TATYAQALQSVPETQVSQLDNGLRVASEQSSQPTCTVGWIDAGSRYESEKNNGAGYFVE
HLAFKGTKNRPGNALEKEVESMGAHLNAYSTREHTAYYIKALSKDLPKAVELLADIVQNC
SLEDSQIEKERDVILQELQENDTSMRDVVFNYLHATAFQGTPLAQSVGPSENVKLSRA
DLTEYLSRHYKAPRMVLAAGGLEHRQLDLAQKHFSGLSGTYDEDAVPTLSP

>d1be3a2 d.185.1.1 (A:234-446) Cytochrome bc1 core subunit 1 {Cow (Bos taurus)}

CRFTGSQICHREDGLPLAHVAIAVEGPGWAHPDNVALQVANAIIGHYDCTYGGGAHLSSPL
ASIAATNKLQSFQTFNICYADTGLLGAHFVCDHMSIDDMFVLQGGQWMRLCTSATESE
VLRGKNLLRNALVSHLDGTPVCEDIGRSLTYGRRIPLAEWESRIAEDARVVREVCSKY
FYDQCPAVAGFGPIEQLPDYNRIRSGMFWLRF

>d1ezva1 d.185.1.1 (A:27-239) Cytochrome bc1 core subunit 1 {Baker's yeast (Saccharomyces cerevisiae)}

AEVTQLSNGIVVATEHNPAHTASVGVVFGSGAANENPYNNGVSNLWKNIFLSKENSAAVAA
KEGLALSSNISRDFQSYIVSSLPGSTDKSLDFLNQSFQQKANLLSSSNFEATKKSVLKQVQ
DFEDNDHPNRVLEHLHSTAFQNTPLSLPTRGTLESLENLVVADLESFANNHFLNSNAVVG
TGNIKHEDLVNSIESKNLSLQTGTPVLKK

>d1ezva2 d.185.1.1 (A:240-456) Cytochrome bc1 core subunit 1 {Baker's yeast (*Saccharomyces cerevisiae*)}

KAAFLGSEVRLRDDTLPAWISLAVEGEPVNSPNYFVAKLAAQIFGSYNAFEPASRLQGIK
LLDNIQEYQLCDNFNFHLSYKDSGLWGFSTATRNVMTIDDLIHFTLKQWNRLTISVTDTE
VERAKSLLKLQLGQLYESGNPVNDANLLGAEVLIKGSKLSLGEAFKKIDAIVKDVKAWA
GKRLWDQDIAIAGTGQIEGLLDYMRIRSDMSMMRW

>d1be3b2 d.185.1.1 (B:236-439) Cytochrome bc1 core subunit 2 {Cow (*Bos taurus*)}

KAKYHGGEIREQNGDSLVHAALVAESAAGSAEANAFAFVLQHVLGAGPHVKRGSNATSSL
YQAVAKGVHQPFVDVSAFNASYSDSGLFGFYTISQAASAGDVIKAAYNQVKTIQAQGNLSNP
DVQAAKNKLKAGYLMSVESSEGLFDEVGSQLAAGSYTPPSTVLQQIDAVADADVINA
KKFVSGRKSMASGNLGHTPFIDEL

>d1bccb1 d.185.1.1 (B:18-235) Cytochrome bc1 core subunit 2 {Chicken (*Gallus gallus*)}

PPHPQDLEITKLPNGLVIASLENYSPGSTIGVFIKAGSRYENSSNLGTSHLLRLASSLTTKGA
SSFKITRGIEAVGGKLSVESTRENMAYTVECLRDDVEILMEFLNVTTAPEFRPWEVADLQ
PQLKIDKAVAFQNPQTHVIENTHAAAYRNALADSLYCPDYRIGKVTSVELHDFVQNHFTS
ARMALVGLGVSHPV LKNVAEQLLNIRGGLGLSGA

>d1ezvb1 d.185.1.1 (B:17-218) Cytochrome bc1 core subunit 2 {Baker's yeast (*Saccharomyces cerevisiae*)}

LTVSARDAPTKISTLAVKVHGGSRATKDGVAHLLNRFNFQNTNTRSALKLVRESELLGGT
FKSTLDREYITLKATFLKDDLPPYYVNALADVLYKTAFAKPHELTSVLPAARYDYAVAEQCP
VKSAEDQLYAITFRKGLGNPLLYDGVVERVSLQDIKDFADKVYTKENLEVSGENVVEADLK
RFVDESLLSTLPAGKSLVSK

>d1ezvb2 d.185.1.1 (B:219-368) Cytochrome bc1 core subunit 2 {Baker's yeast (*Saccharomyces cerevisiae*)}

SEPKFFLGEENRVRFIGDSVAAIGIPVNKASLAQYEVLANYLTSALSSELSGLISSAKLDKFTD
GGLFTLFVRDQDSAVVSSNIKKIVADLKKGKDLSPAINYTKLKNVQNESVSSPIELNFDV
KDFKLKGKFNYYVAVGDVSNLPYLDEL

>d1ejda_ d.68.2.2 (A:) UDP-N-acetylglucosamine enolpyruvyl transferase (EPT,
MurA, MurZ) {*Enterobacter cloacae*}

MDKFRVQGPTRLQGEVTISGAKNAALPILFAALLAEEPVEIQNVPKLKDIDTTMKLLTQLG
TKVERXGSVWIDASNVNFSAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCAIGARP
VDLHIFGLEKLGAIEKLEEGYVKASVNGRLKGAHIVMDKVSVGATVTIMSAATLAEGTTII
ENAAREPEIVDTANFLVALGAKISGQGTDRITIEGVERLGGGVYRVLPDRIETGTFLVAAAI
GGKIVCRNAQPDTLDAVLAKLREAGADIETGEDWISLDMHGKRPKAVTVRTAPHPAFPTD
MQAQFTLLNLVAEGTGVTETIFENRFMHVP E LIRMGAAHAEIESNTVICHGVEKLSGAQVM
ATDLRASASLVLAGCIAEGTTVVDRIYHIDRGYERIEDKLRLALGANIERVKGE

>d1g6sa_ d.68.2.2 (A:) 5-enol-pyruvyl shikimate-3-phosphate(EPSP) synthase {*Escherichia coli*}

MESLTLQPIARVDGTINLPGSKSVSNRALLLAALAHGKTVLTNLLDSDDVRHMLNALTAL
GVSYTLSADRTRCEIIGNGGPLHAEGALELFLGNAGTAMRPLAAALCLGSNDIVLTGEPR
MKERPIGHLVDALRLGGAKITYLEQENYPPRLQGGFTGGNVDDVDGSVSSQFLTALLMTA
PLAPEDTVIRIKGDLVSKPYIDITLNLMTKFTGVEIENQHYQQFVVKGGQSYQSPGYTLVEG
DASSASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATICWGDDYISCTRGE
NAIDMDMNHIPDAAMTIATAALFAKGTTLRNINWRVKETDRLFAMATELRKVGAEEVE
EGHDYIRITPPEKLNFAEIATYNDHRMAMCFSLVALSDTPVTILDPKCTAKTFPDYFEQLAR

ISQAA

>d1bwvs_ d.73.1.1 (S:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Galdieria partita}

VRITQGTFSFLPDLTDEQIKKQIDYMISKKLAIGIEYTNDIHPRNAYWEIWGLPLFDVTDPA
AVLFEINACRKARSNFYIKVVGFSSVRGIESTIISFIVNRPKHEPGFNLMRQEDKSRSIKYTIH
SYESYKPEDERY

>d1gk8i_ d.73.1.1 (I:) Ribulose 1,5-bisphosphate carboxylase-oxygenase {Chlamydomonas reinhardtii}

MVWTPVNNKMFETFSYLPPLTDEQIAAQVDYIVANGWIPCLEFAEADKAYVSNESAIRFG
SVSCLYYDNRYWTMWKLPMFGCRDPMQVLRREIVACTKAFPDAYVRLVAFDNQKQVQIM
GFLVQRP

>d1xxaa_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Escherichia coli}
LKNLVLDIDYNDVAVVIHTSPGAAQLIARLLDSLGAEGILGTIAGDDTIFTTPANGFTVKD
LYEAILELF

>d1b4ba_ d.74.2.1 (A:) C-terminal domain of arginine repressor {Bacillus stearothermophilus}

ALVDVFIKLDGTGNLLVLRTPGNAHAIGVLLDNLDWDEIVGTICGDDTCLIIICRTPKDAK
KVSNNQLLSML

>d1bdfa1 d.74.3.1 (A:2-52,A:179-232) RNA polymerase alpha {Escherichia coli}
QGSVTEFLKPRLVDIEQVSSTHAKVTLEPLERGFGLHTLGNALRAILLSSMPXPVERIAYNVE
AARVEQRTDLDKLVIEMETNGTIDPEEAIRRAATILAEQLEAFV

>d1i50c1 d.74.3.1 (C:3-41,C:173-268) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}

EEGPQVKIREASKDNVDFILSNVDLAMANSRRVMIAEIXAAAIEFEYDPWNKLKHTDYW
YEQDSAKEWPQSKNCEYEDPPNEGDPFDYKAQADTFYMNVESVGSIPVDQVVVRGIDTL
QKKVASILLALTQMDQD

>d1c0aa2 d.74.4.1 (A:288-420) Prokaryotic AspRS, insert domain {Escherichia coli}
NPMELTDVADLLKSVEFAVFAGPANDPKGRVAALRVPGGASLTRKQIDEYGNFVKIYGAK
GLAYIKVNERAKGLEGINSPVAKFLNAEIIEDILDRTAQAQDGMIFFGADNKKIVADAMGA
LRLKVGKDLGLT

>d1g51a2 d.74.4.1 (A:295-414) Prokaryotic AspRS, insert domain {Thermus thermophilus}

FGLELKEVGPLFRQSGFRVFQEAESVKALALPKALSRRKEVAELEEVAKRHKAQGLAWARV
EEGGFSGGVAKFLEPVREALLQATEARPGDTLLFVAGPRKVAATALGAVRLRAADLLGLK

>d1ewqa4 d.75.2.1 (A:1-120) DNA repair protein MutS, domain I {Thermus aquaticus}

MEGMLKGEGPGPLPPLLQQYVELRDQYPDYLLLFQVGDFYECFGEDAERLARALGLVLT
HKTSKDFTTPMAGIPLRAFEAYAERLLKMGFRLAVADQVEPAEEAEGLVRRREVTQLLTPGT

>d1e3ma4 d.75.2.1 (A:2-116) DNA repair protein MutS, domain I {Escherichia coli}
SAIENFDAHTPMMQQYLRLKAQHPEILLFYRMGDFYELFYDDAKRASQLLDISLTKRGAS
AGEPIPMAGIPYHAVENYLAKLVNQGESVAICEQIGDPATSKGPVERKVVIVTP

>d1iq4a_ d.77.1.1 (A:) Ribosomal protein L5 {Bacillus stearothermophilus}

MNRLKEKYLNEVVPALMSKFNYKSIMQVPKIEKIVINMGVGDAVQNPKALDSAVEELTLI
AGQRPVVTRAKKSIAGFRLRQGMPIGAKVTLRGERMYEFLDKLISVSLPRARDFRGVSKK

SFDGRGNYTLGIKEQLIFPEIDYDKVNVKVRGMDIVIVTTANTDEEARELLALLGMPFQK
>d1jj2d_ d.77.1.1 (D:) Ribosomal protein L5 {Archaeon Haloarcula marismortui}
FHEMREPRIEKVVVHMGIGHGGRDLANAEDILGEITGQMPVRTKAKRTVGEFDIREGDPI
GAKVTLRDEMAEEFLQTALPLAELATSQFDDTGNFSFGVEEHTEFPSQEYDPSIGIYGLDV
TVNLVRPGYRVAKRDKASRSIPTKHRLNPADAVAFIESTYDVEV
>d1fsz_2 d.79.2.1 (232-356) Cell-division protein FtsZ {Archaeon Methanococcus jannaschii}
INVDFAADV KAVMNNGGLAMIGIGESDSEKRAKEAVSMALNSPLLDVDIDGATGALIHVM
GPEDLTLEEAREVVATVSSRLDPNATIHWGATIDENLENTVRVLLVITGVQSRIEFTDTGLKR
KKL
>d1tuba2 d.79.2.1 (A:246-440) Tubulin alpha-subunit {Pig (Sus scrofa)}
GALNVDLTFEQTNLVPYPRGHFPLATYAPVISAEEKAYHEQLSVAEITNACFEPANQMVKCD
PRHGKYMACECLLYRGDVVPKDVNAAIATIKTKRTIQFVDWCPTGFKVGINYEPPTVPPG
DLAKVQRAVCMLSNTTAIAEAWARLDHKFDLMYAKRAFWHWYVGEGMEEGEFSEARED
MAALEKDYEYEEVGVDV
>d1tubb2 d.79.2.1 (B:246-437) Tubulin beta-subunit {Pig (Sus scrofa)}
GQLNADLRKLAVNMVFPRLHFFMPGFAPLTSRGSQQYRALTVPCLTQMMFQAKNMMAA
CDPRHGRYLTVAAVFRGRMSMKEVDEQMLNVQNKNSYFVEWIPNNVKTAVCDIPRGL
KMSATFIGNSTAIQELFKRISEQFTAMFRRKAFLHWYTGEGMDEMEFTEAESNMNDLVSE
YQQYQD
>d1ck9a_ d.79.3.1 (A:) Eukaryotic ribosomal protein L30 (L30e) {Baker's yeast
(Saccharomyces cerevisiae)}
APVKSQESINQKLALVIKSGKYTLGYKSTVKSLRQGKSKLIHAAANTPVLRKSELEYAMLS
KTKVYYFQGGNNELGTAVGKLFVRGVVSILEAGDSDLITTLA
>d1jj2f_ d.79.3.1 (F:) Ribosomal protein L7ae {Archaeon Haloarcula marismortui}
PVYVDFDVPADLEDDALEAVARDTGAVKKGTNETTKSIERGSAELVFVAEDVQPEEIV
MHIPELADEKGVPFIFVEQQDDLGHAAAGLEVGSAAAVTDAGAAATVLEEIADKVEELR
>d1e7ka_ d.79.3.1 (A:) Spliceosomal 15.5kd protein {Human (Homo sapiens)}
ADVNP KAYPLADAHLTKLLDLVQQSCNYKQLRK GANEATKTLNRGISEFVMAADAEP
LEIHLPLLCEDKNVPYVFVRSKQALGRACGVSRPVIACSVTIKEGSQLKQQIQSIQQSIER
LLV
>d1gd0a_ d.80.1.3 (A:) Microphage migration inhibition factor (MIF) {Human (Homo sapiens)}
PMFIVNTNVPRAVDPDGFLSELTQQLAQATGKPPQYIAVHVVPDQLMAFGGSSEPCALCSL
HSIGKIGGAQNRSYKLLCGLLAERLRISPDRVYINYYDMNAANVGWNNSTFALEHH
>d1dpta_ d.80.1.3 (A:) D-dopachrome tautomerase {Human (Homo sapiens)}
PFLELDTNLPANRVPAGLEKRLCAAAASILGKPADRVNVTVRPGLAMALSGSTEPCAQLSI
SSIGVVGTAEENRSHSAHFFFLTKELALGQDRILIRFFPLESWQIGKIGTVMTFL
>d1cf2o2 d.81.1.1 (O:139-303) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Archaeon Methanothermobacter thermophilus}
SCNTTGLCRTLKPLHDSFGIKKVRVIVRRGADPAQVSKGPINAIIPNPPKLPSHHGPDVKT
VLDINIDTMAVIVPTTLMHQHNVMVEVEETPTVDDIIDVFEDTPRVILISAEDGLTSTAEIME
YAKELGRSRNDLFEIPVWRESITVVDNEIYYMQAVHQESD
>d1ggaa2 d.81.1.1 (A:165-333) Glyceraldehyde-3-phosphate dehydrogenase
(GAPDH) {Trypanosoma brucei brucei, glycosome}
CTTNCLAPLVHVLVKEGFGISTGLMTTVHSYTATQKTVDGVSVDKDWRGGRAAALNIIPST

TGAAKAVGMVIPSTQGKLTGMAFRVPTADVSVVDLTFIATRDTSIKEIDAALKRASKTYM
KNILGYTDEELVSADFISDSRSSIYDSKATLQNNLPNERRFFKIVSWYD

>d1gl3a2 d.81.1.1 (A:134-354) Aspartate beta-semialdehyde dehydrogenase
{*Escherichia coli*}

NCTVSLMLMSLGGLFANDLVDWVSVATYQAASGGGARHMRRELLTQMGHLYGHVADELA
TPSSAILDIERKVTTLTRSGELPVDNFGVPLAGSLIPWIDKQLDNGQSREEWKGAETNKIL
NTSSVIPVDGLCVRVGALRCHSQAFTIKLKKDVS IPTVEELLA AHN PWAKVVPNDREITMR
ELTPAAVTGTLTTPVGRLRKLNMGPFLSAFTVGDQLLWG

>d1ebfa2 d.81.1.2 (A:151-340) Homoserine dehydrogenase {*Baker's yeast* (*Saccharomyces cerevisiae*)}

PIISFLREIIQTGDEVEKIEGIFSGTLSYIFNEFSTSQANDVKFSDVVKVAKKLGYTEPDPRDD
LNGLDVARKVTIVGRISGVEVESPTSFPVQSLIPKPLESVKSADEFLEKLSDYDKDLTQLKK
EAATENKVLRFIGKVVDATKSVSVGIEKYDYSHPFASLKGSDNVISIKTKRYTNPVVIQGA
GAG

>d1e5qa2 d.81.1.2 (A:125-391) Saccharopine reductase {*Rice blast fungus* (*Magnaporthe grisea*)}
LDPGIDHLYAIKTIEEVHAAGGKIKTFLSYCGGLPAPESSDNPLGYKFSWSSRGVLLALRNA
ASFYKDGKVTNVAGPELMATAKPYFIYPGFAFVAYPNRDSTPYKERYQIPEADNIVRGTLR
YQGFPQFIKVLVDIGFLSDEEQPFLKEAIPWKEATQKIVKASSASEQDIVSTIVSNATFESTE
EQKRIVAGLKWL GIFSDKKITPRGNALDTLCATLEEKMQFEEGERDLV MLQHKFEIENKD
GSRETRTSSLCEYGAPIGSGG

>d1f06a2 d.81.1.3 (A:119-268) Diaminopimelic acid dehydrogenase (DAPDH)
{*Corynebacterium glutamicum*}

WDPGMFSINRVYAAAVLAEHQQHTFWGPGLSQGHSDALRRIPGVQKAVQYTLPSEDALE
KARRGEAGDLTGKQTHKRQCFVVAADHERIENDIRTMPDYFVG YEVEVNFIDEATFDS
EHTGMPHGGHVITTGDTGGFNHTVEYILKLD

>d1dih_2 d.81.1.3 (131-240) Dihydrodipicolinate reductase {*Escherichia coli*}
VGVNVMLKLLEKAAKVMGDYTDIEII EAHHRHKVDAPSGTALAMGEAIAHALDKDLKD
CAVYSREGHTGERVPGTIGFATVRAGDIVGEHTAMFADIGERLEITHKASSR

>d1k5ha3 d.81.1.3 (A:126-274) 1-deoxy-D-xylulose-5-phosphate reductoisomerase
{*Escherichia coli*}

ESLVTGGRLFMDAVKQSKAQLLPVDSEHNAIFQSLPQPIQHN LGYADLEQNGVVSILLTGS
GGPFRETPLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIEARWLFNASASQ
MEVLIHPQSVIHSMVRYQDGSVLAQLGEP

>d1h6da2 d.81.1.5 (A:213-374) Glucose-fructose oxidoreductase {*Zymomonas mobilis*}
DPMNRAAVKLIRENQLGKLG MVTTDNSDVMDQNDPAQQWRLRREL AGGGS LMDIGIYG
LNGTRYLLGEEPIEVRAYTYS DPNDERFVEVEDRIIWQMRFRSGALSHGASSYSTTTTSRFS
VQGDKAVLLMDPATGY YQNLISVQTPGHANQSMMPQFIMPAN

>d1dpga2 d.81.1.5 (A:182-412,A:427-485) Glucose 6-phosphate dehydrogenase
{*Leuconostoc mesenteroides*}

KEMVQNIAALRFGNPIFDAAWN KDYIKNVQVT LSEVLGVEERAGYYDTAGALLDMIQNH
TMQIVGWLAMEKPESFTDKDIRAAKNAAFNALKIYDEAEVNKYFVRAQYGAGDSADFK
PYLEELDVPADSKNNTFIAGELQFDLPRWEGVPFYVRSGKRLAAKQTRVDIVFKAGTFNF
GSEQEAQEAVLSIIIDPKGAIELKLN AKSVEDAFNTRTIDLGWTVSDEDKKNTPXGSNFAD
WNGVSIWKFVDAISAVYTADKAPLETYKSGSMGPEASDKLLAANGDAWVFKG

>d1qkia2 d.81.1.5 (A:200-434,A:450-511) Glucose 6-phosphate dehydrogenase {Human (Homo sapiens)}

DHYLGKEMVQNLMLVLRFANRIFGPWIWNRDNIACVILTFKEPFGTEGRGGYFDEFGIIRDVM
 QNHLLQMLCLVAMEKPASTNSDDVRDEKVKVLKCISEVQANNVVLGQYVGNPDGEGEA
 TKGYLDDPTVPRGSTTATFAAVVLYVENERWDGVPFILRCGKALNERKAEVRLQFHDVAG
 DIFHQQCKRNELVIRVQPNEAVYTKMMTKKPGMFFNPEESELDTYGNRYKNVKLPXMH
 FVRSEDELLEAWRIFTPLLHQIELEKPKPIPIYIYGSRGPTADELMKRVGFQYEGTYKWVN

>d1ekga_d.82.2.1 (A:) C-terminal domain of frataxin {Human (Homo sapiens)}

LDETTYERLAEETLDSLAEFFEDLADKPYTFEDYDVSFGSGVLTVKLGDDLGTIVINKQT
 PNKQIWLSSPSSGPKRYDWTGKNWVYSHDGVSLHELLAAELTKALKTKLDLSSLAYS GK

>d1ew4a_d.82.2.1 (A:) CyaY {Escherichia coli}

MNDSEFHRLADQLWLTIEERLDDWDGSDIDCEINGGVLTITFENGSKIINRQEPLHQVW
 LATKQGGYHFDLKGDEWICDRSGETFWDLLEQAATQQAGETVSFR

>d1ewfa1 d.83.1.1 (A:1-217) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

VNPGVVVRISQKGLDYASQQGTAALQKELKRIKIPDYSDFSFIKHLGKGHYSFYSDIREF
 QLPSSQISMVNPVGLKFSISNANIKISGKWKAAQKRFLKMSGNFDLSIEGMSISADLKLGSNP
 TSGKPTITCSSSHINSVHVHISKSKVGWLIQLFHKIESALRNKMNSQVCEKVTNSVSSE
 LQPYFQTLPMVKIDSVAGINYLVAAPPATTA

>d1ewfa2 d.83.1.1 (A:218-456) Bactericidal permeability-increasing protein, BPI {Human (Homo sapiens)}

ETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHDRMVYLGLSDYFFNTAGLVYQEAGVL
 KMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFPNMKIQIHVSASTPPHLSVQPTGLTFYPA
 VDVQAFVLPNSALASLFLIGMHTTGSMEVSAESNRLVGELKLDRLLELKHNSNIGPFPPVE
 LLQDIMNYIVPILVLPVNEKLQKGFPLPTPARVQLYNVVLQPHQNFLFLGADV VYK

>d1e6ta_d.85.1.1 (A:) MS2 virus coat protein {Bacteriophage MS2}

ASNFTQFVLVDNGGTGDVTVAPSNFANGVAEWISSNSRSQAYKVTCSVRQSSAQNRKYTI
 KVEVPKVATQTVGGVELPVAAWRSYLNMEITPIFATNSDCELVKAMQGLLKDGNIPIPSAI
 AANS GIY

>d1qbea_d.85.1.1 (A:) Qbeta coat protein {Bacteriophage Qbeta}

AKLETVTGLNIGKDGKQTLVLNPRGVNPTNGVASLSQAGAVPALEKRVTVSVSQPSRNRK
 NYKVQVKIQNPTACTANGSCDPSVTRQAYADVTFSTQYSTDEERAFVRTELAALLASPLL
 IDAIDQLNPAY

>d1dwna_d.85.1.1 (A:) PP7 coat protein {Bacteriophage PP7}

SKTIVLSVGEATRTLTEIQSTADRQIFEEKVGPLVGRLRLTASLRQNGAKTAYRVNLKLDQA
 DVVDCSTSVCGELPKVRYTQVWSDVTIVANSTEASRKS LYDLTKSLVATSQVEDLVVNL
 VPLGR

>d1ej1a_d.86.1.1 (A:) Translation initiation factor eIF4e {Mouse (Mus musculus)}

KHPLQNRWALWFFKNDKSKTWQANLRLISKFDTVEDFWALYNHIQLSSNLMPGCDYSLF
 KDGI EPMWEDEKNKRGGRWLITLNKQQRSDLD RFWLETLLCLIGESFDDYSDDVCGAV
 VNVRAKGDKIAIWTTECENRDAVTHIGRVYKERLGLPPKIVIGYQSHADTATKSGSTTKNR
 FVV

>d1lap8__ d.86.1.1 (-) Translation initiation factor eIF4e {Baker's yeast (Saccharomyces cerevisiae)}

MSVEEVSKKFEENVSVDDTTATPKTVLSDSAHFVDVKHPLNTKWTLWYTKPAVDKSESWS

DLLRPVTSFQTVEEFWAIIQNIPEPHELPLKSDYHVFRNDVRPEWEDEANAKGGKWSFQL
 RGKGADIDELWLRLLAVIGETIDEDDSQINGVVLRSIRKGGNKFALWTKSEDKEPLLRIIG
 KFKQVLKLTDDGHLEFFPHSSANGRHPQPSITL
 >d1aoga3 d.87.1.1 (A:358-487) Trypanothione reductase {Trypanosoma cruzi}
 DHTRVASAVFSIPPIGTCGLIEEVASKRYEVVAVYLSSFTPLMHKVS GSKYKTFVAKIITNHS
 DGTVLGVHLLGDNAPEIIQGIGICLKLNAKISDFYNTIGVHPTSAEELCSMRTPSYYYVKGE
 KMEKP
 >d1h6va3 d.87.1.1 (A:367-499) Mammalian thioredoxin reductase {Rat (Rattus norvegicus)}
 YDNVPTTVFTPLEYGCCGLSEEKAVEKFGEENIEVYHSFFWPLEWTVPSRDNNKCYAKVI
 CNLKDNERVVGFHVLGPNAGEVTQGFAAALKCGLTKQQLDSTIGIHPVCAEIFTTLSVTKR
 SGGDILQSGCCG
 >d1nhp_3 d.87.1.1 (322-447) NADH peroxidase {Enterococcus faecalis}
 GVQGSSGLAVFDYKFASTGINEVMAQKLGKETKAVTVVEDYLMDFNPDQKQAWFKLVY
 DPETTQILGAQLMSKADLTANINAI SLAIQAKMTIEDLAYADFFFQPAFDKPWNIINTAALE
 AVKQER
 >d1d7ya3 d.87.1.1 (A:309-405) NADH-dependent ferredoxin reductase, BphA4 {Pseudomonas sp.,
 KKS102}
 TAPGYAELPWYWS DQGALRIQVAGLASGDEEIVRGEVSLDAPKFTLIELQKGRIVGATCV
 NNARDFAPLRLLAVGAKPDRAALADPATDLRKLAAA
 >d1lv_3 d.87.1.1 (336-458) Dihydrolipoamide dehydrogenase {Pseudomonas putida}
 PAAIAAVCFDPEVVVGKTPEQASQQLDCIVAQFPFAANGRAMSLESKSGFVRVARR
 DNHLILGWQAVGVAVSELSTAFAQSLEMGACLEDVAGTIHAHPTLGEAVQEAALRALGHA
 LHI
 >d1lpfa3 d.87.1.1 (A:349-472) Dihydrolipoamide dehydrogenase {Pseudomonas
 fluorescens}
 YDLIPSVIYTHPEIAWVGKTEQTLKAEGVEVNVGTFPFAASGRAMAANDTTGLVKVIADA
 KTDRVLGVHVIGPSAAELVQQAIGMEFGTSAEDLGMMVFSHPTLSEALHEAALAVNGH
 AIHIA
 >d1ojt_3 d.87.1.1 (471-598) Dihydrolipoamide dehydrogenase {Neisseria
 meningitidis}
 ARVIPGVAYTSPEVAWVGETELSAKASARKITKANFPWAASGRAIANGCDKPFTKLIFDAE
 TGRIIIGGIVGPNGGDMIGEVCLA IEMGCDAADIGKTIHPHPTLGESIGMAAEVALGTCTD
 LPPQKK
 >d1fcd3 d.87.1.1 (A:328-401) Flavocytochrome c sulfide dehydrogenase, FCSD, flavin-binding
 subunit {Purple phototrophic bacterium (Chromatium vinosum)}
 PGTPSYLNTCYSILAPAYGISVA AIYRPNADGSAIESVPDSSGGVTPVDAPDWVLEREVQYA
 YSWYNNIVHDTFG
 >d1ffvc1 d.87.2.1 (C:178-287) Carbon monoxide (CO) dehydrogenase flavoprotein, C-terminal
 domain {Hydrogenophaga pseudoflava}
 GTGWAYEKLKRKTGDWATAGCAVVMRKS GNTVSHIRIALTNVAPTALRAEAAEAALLGK
 AFTKEAVQAAADA AIAICEPAEDLRGDADYKTAMAGQMVKRALNAAWARCA
 >d1fo4a4 d.87.2.1 (A:415-531) Xanthine oxidase, domain 4 (?) {Cow (Bos taurus)}
 DEFFSAFKQASRREDDIAKVTCGMRVLFQPGSMQVKELALCYGGMADRTISALKTTQKQ
 LSKFWNEKLLQDVCAGLA EELSLSPDAPGGMIEFRRTLTL SFFKFYLTVLKKGKDS

>d1jroa3 d.87.2.1 (A:346-462) Xanthine dehydrogenase chain A, domain 4 {Rhodobacter capsulatus}

PGLRCYKLSKRFDQDISAVCGCLNLTGSKIETARIAFGGMAGVPKRAAAFEAALIGQDF
REDTIAAALPLLAQDFTPLSDMRASAAYRMNAAQAMALRYVRELSGEAVAVLEVMP

>d1mnma_ d.88.1.1 (A:) MCM1 transcriptional regulator {Baker's yeast (Saccharomyces cerevisiae)}

QKERRKIEIKFIENKTRRHVTFSKRKHGIMKKAFELSVLTGTQVLLLTVSETGLVYTFSTPK
FEPIVTQQEGRNLIQACLNAPDD

>d1legwa_ d.88.1.1 (A:) Mef2a core {Human (Homo sapiens)}

GRKKIQITRIMDERNRQVTFTKRKFGLMKKAYELSVLCDCEIALIIFNSSNKLQYASTDM
DKVLLKYTEY

>d1nox_ d.90.1.1 (-) NADH oxidase {Thermus thermophilus, HB8}

PVLDAKTAALKRRSIRRYRKDPVPEGLREILEAALRAPSAWNLPWRIVVVRDPATKRA
LREAAFGQAHVVEAPVVLVLYADLEDALAHLEDEVIHPGVQGERREAQKQAIQRAFAAMG
QEARKAWASGQSYILLGYLLLLLEAYGLGSVPMLGFDPERVRAILGLPSRAAIPALVALGY
PAEEGYPSHRLPLERVVLWR

>d1vfra_ d.90.1.1 (A:) Flavin reductase P (NADPH:FMN oxidoreductase) {Vibrio fischeri}

THPIIHDLENRYTSKKYDPSKKVSQEDLAVLLEALRLSASSINSQPWKFIVIESDAAKQRMH
DSFANMHQFNQPHIKACSHVILFANKLSYTRDDYDVVLSKAVADKRITEEQKEAAFASFKE
VELNCDENGEHKAWTKPQAYLALGNALHTLARLNIDSTTMEGIDPELLSEIFADELKGYE
CHVALAIGYHHPSEDYNASLPKSRKAFEDVITIL

>d1kqba_ d.90.1.1 (A:) Nitroreductase {Enterobacter cloacae}

DIISVALKRHSTKAFAASKKLTAEEAEKIKTLLQYSPSSTNSQPWHFIVASTEELGKARVAKS
AAGTYVFNERKMLDASHVVVFCATAMDDAWLERVVDQEEADGRFNTPEAKAANHKG
RTYFADMHRVDLKDQWMAKQVYLVNNGNLLGVGAMGLDAVPIEGFDAAILDEEFG
KEKGFTSLVVVPVGHHSVEDFNATLPKSRLPLSTIVTEC

>d1f5va_ d.90.1.1 (A:) Nitroreductase {Escherichia coli, oxygen-insensitive form}

MTPTIELICGHSIRHFTDEPISEAQREAIINSARATSSSSFLQCSSIIRITDKALREELVTLTGG
QKHVAQAAEFWVFCADFNRLQICPDAQLGLAEQLLLGVVDTAMMAQNALIAAESLGL
GGVYIGGLRNNEAVTKLLKLPQHVLPLFGLCLGWPADNPDLKPRLPASILVHENSYPQLD
KGALAQYDEQLAEYYLTRGSNNRRDTWSDHIRRTIIESRPFILDYHLHKQGWATR

>d1g12a_ d.92.1.12 (A:) Fungal zinc peptidase {Grifola frondosa}

TYNGCSSEQSALAAAASAAQSYVAESLSYLQTHAATPRYTTWFGSYISSRHSTVLQHYT
DMNSNDFSSYSFDCCTCTAAGTFAYVYPNRFGTVYLCGAFWKAPTGTDSQAGTLVHESS
HFTRNGGTKDYAYGQAAAKSLATMDPKAVMNADNHEYFSENNPAQS

>d1eb6a_ d.92.1.12 (A:) Fungal zinc peptidase {Aspergillus oryzae, deuterolysin}

TEVTDCKGDAESSLTALSNAAKLANQAEEAESGDESKFEEYFKTTDQQTRTTVAERLR
AVAKEAGSTSGGSTTYHCNDPYGYCEPNVLAYTLPSKNEIANCDIYYSELPLAQKCHAQ
DQATTTLHEFTHAPGVYQPGTEDLGYGYDAATQLSAQDALNNADSYALYANAIELKC

>d1ezm_ d.92.1.2 (-) Elastase {Pseudomonas aeruginosa}

AEAGGPGGNQKIGKYTYGSDYGPLIVNDRCEMDDGNVITVDMNSSTDDSKTTPFRFACPT
NTYKQVNGAYSPLNDAHFFGGVVFVKLYRDWFGTSPLTHKLYMKVHYGRSVENAYWDGT
AMLFGDGATMFYPLVSLDVAHEVSHGFTEQNSGLIYRGQSGGMNEAFSDMAGEAAEFY
MRGKNDFLIGYDIKKGSGALRYMDQPSRDGRSIDNASQYYNGIDVHHSSGVYNRAFYLL

ANSPGWDTRKAFEVFDANRYWTATSNYNSGACGVIRSAQNRNYSAADVTRAFSTVG
VTCP

>d1npc__ d.92.1.2 (-) Neutral protease {Bacillus cereus, strain dsm 3101}

VTGTNKVGTGKGVLDGDKSLNTTSLGSSYYLQDNTRGATIFTYDAKNRSTLPGTLWADA
DNVFNAAYDAAAVDAHYAGKTYDYKATFNRSINDAGAPLKSTVHYGSNNNAFW
NGSQMVYGDGDGVTFTSLSGGIDVIGHELTHAVTENSNNLIYQNESGALNEAISDIFGTLVE
FYDNRNPDWEIGEDIYTPGKAGDALRSMSPDKYGDPDHYSKRYTGSSDNGGVHTNSGII
NKQAYLLANGGTHYGVTVTGIGKDKLGAIIYRANTQYFTQSTTFSQARAGAVQAAADLY
GANSAEVAAVKQSFSAVGVN

>d1j7na1 d.92.1.14 (A:27-263) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}

ERNKTQEEHLKEIMKHIVKIEVKGEEAVKKEAAEKLLEKVPDVLMEYKAIGGKIYIVDG
DITKHISLEALSEDKKKIKDIYGKDALLHEHYVYAKEGYEPLVIQSSDYVENTEKALNV
YYEIGKILSRDILSKINQPYQKFLDVLNTIKNASDSGDQDLLFTNQLKEHPTDFSVEFLEQN
SNEVQEVFAKAFAYYIEPQHRDVLQLYAPEAFNYMDKFNEQEINLSLEELKDQR

>d1j7na2 d.92.1.14 (A:551-773) Anthrax toxin lethal factor, N- and C-terminal domains {Bacillus anthracis}

PKSKIDTKIQEAQLNINQEWKALGLPKYTKLITFNVHNRYASNIVESAYLILNEWKNNIQ
SDLIKKVTNYLVDGNRFRVFTDITLPNIAEQYTHQDEIYEQVHSGGLYVPESRSILLHGPSK
GVELRNDSEGFIEFGHAVDDYAGYLLDKNQSDLVTSKKFIDIFKEEGSNLTSYGRNTNEA
EFFAEAFRLMHSTDHAERLKVQKNAPKTFQFINDQIKFI

>d3btaa3 d.92.1.7 (A:1-546) Botulinum neurotoxin {Clostridium botulinum, serotype A}

PFVVKQFNKYKDPVNGVDIAYIKIPNVGQMOPVKAFKIHNKIWVIPERDFTNPEEGDLNPP
PEAKQVPVSYDYSTYLSTDNEKDNLYLKGVTCLFERIYSTDLGRMLLTSIVRGIPFWGGSTI
DTELKVIDTNCINVIQPDGSYRSEELNLVIIGPSADIIQFECKSFGHEVLNLTRNGYGSTQYI
RFSPDFTFGFEESLEVDTNPLLGGAGKFATDPAVTLAHELIHAGHRLYGIAINPNRVFKVNTN
AYYEMSGLEVSFEELRTFGGHDAKFIDSLQENEFRLYYNKFKDIASTLNKAKSIVGTTAS
LQYMKNVFKEKYLLSEDTSGKFSVDKLKFDKLYKMLTEIYTEDNFVKFFKVLNRKTYLN
FDKAVFKINIVPKVNYTIYDGFNLNNTNLAANFNGQNTNINNMNFTKLKNFTGLFEFYKLL
CVRGIITSKTKSLDKGYNKALNDLCIKVNNWDLFFSPSEDNFTNDLNKGEEITSNTNIEAA
EENISLDLIQYYLTFNFDNEPENISIENLSSDIIGQLELMPNIEFPNGKKYELDK

>d1epwa3 d.92.1.7 (A:1-533) Botulinum neurotoxin {Clostridium botulinum, serotype B}

PVTINNFNYNPIDNNNIIMMEPPFARGTGRYYKAFKITDRIWIIPERYTFGYKPEDFNKSS
GIFNRDVCEYYDPDYLNTNDKKNIFLQTMIKLFNRIKSKPLGEKLLEMIINGIPYLGDRRVP
LEEFNTNIASVTVNKLISNPGEVERKKGIFANLIIFGPGPVLNENETIDIGIQNHFAFREGFGG
IMQMKFCPEYVSFVNNVQENKGASIFNRRGYFSDPALILMHELIHVLHGLYGIKVDLPIV
PNEKKFFMQSTDAIQAEELYTFGGQDPSIITPSTDKSIYDKVLQNFRGIVDRLNKLVCISD
PNININIKNFKDKYKFVEDSEGKYSIDVESFDKLYKSLMFGFTETNIAENYKIKTRASYF
SDSLPPVKIKNLLDNEIYTIEEGFNISDKDMEKEYRGQNKAINKQAYEEISKEHLAVYKIQM
CKSVKAPGICIDVDNEDLFFIADKNSFSDDLKNERIEYNTQSNYIENDFPINELILDLDLIS
KIELPSENTESLTDNFVDVPVYEKQPAIKKIFTDE

>d1qba_4 d.92.2.1 (201-337) Bacterial chitinase, Domain 2 {Serratia marcescens}

SNADLQTLPAAGALRGKIVPTPMQVKVHAQDADLRKGVLDLSTLVKPAADVVSQRFALL
GVPVQTNGYPIKTDIQPGKFKGAMAVSGAYELKIGKKEAQVIGFDQAGVFYGLQSILSLVP

SDGSGKIATLDASDAPR

>d1jaka2 d.92.2.1 (A:8-150) beta-N-acetylhexosaminidase, N-terminal domain {Streptomyces plicatus}

DRKAPVRPTPLDRVIPAPASVDPGGAPYRITRGTHIRVDDREARRVGDYLA DLLRPATGY
RLPVTAHGHGGIRLRLAGGPYGDEGYRLDSGPAGVTITARKAAGLFHGVQTLRQLLPPAV
EKDSAQPGPWL VAGGTIEDTPR

>d1fhs__ d.93.1.1 (-) Growth factor receptor-bound protein 2 (GRB2) {Human (Homo sapiens)}
GIEMKPHPWFFGKIPRAKAEEMLSKQRHDGAFLIRESESAPGDFSLSVKFGNDVQHFKVL
RDGAGKYFLWVVKFNSLNELVDYHRSTSVSRNQIFLRDIEQVPQQPTYVQA

>d1mil__ d.93.1.1 (-) Shc adaptor protein {Human (Homo sapiens)}
GSQLRGEPWFH GKLSRREA EALLQLNGDFLVRESTTTTPGQYVLTGLQSGQPKHLLLVDPE
GVVRTKDH RFESVSH LISYHMDNHLPIISAGSELCLQQPVERKL

>d1pica__ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Human (Homo sapiens)}

GSPIPHHDEK TWNVGSSNRNKAENLLRGKRDGTFLVRESSKQGCYACSVVVDGEVKHCV
INKTATGYGFAEPYNLYSSLKELVLHYQHTSLVQHNDSLNVTLAYPVYAQQRR

>d1fu6a__ d.93.1.1 (A:) Phosphatidylinositol 3-kinase, p85-alpha subunit {Rat (Rattus norvegicus)}

GMNNNMSLQDAEWYWGDISREEVNEKL RDTADGTFLVRDASTKMHGDYTLTLRKGGN
NKSIFHRD GKYGFSDPLTFNSVVELINHYNESLAQYNPKLDVKLLYPVSKY

>d1lab2__ d.93.1.1 (-) Proto-oncogen tyrosine kinase {Human (Homo sapiens)}

GSGNSLEKHSWYHG PVS RNAAEYLLSSGINGSFLVRESESSPGQRSISLRYEGRVYHYRIN
TASDGKLYVSSES RFNTLAELVHHHSTVADGLITTLHY PAKRGIHRD

>d1a81a1 d.93.1.1 (A:9-137) Syk tyrosine kinase {Human (Homo sapiens)}

SANHL PFFFGNITREEAEDYLVQGGMSDGLYLLRQSRNYLGGFALSVAHGRKAHHTY TIER
ELNGTYA IAGGRTHASPADLCHYHSQESDGLVCLLKKPFNR PQGVQPKTGPFDLKENLIR
EYVKQ TWN

>d1a81a2 d.93.1.1 (A:138-262) Syk tyrosine kinase {Human (Homo sapiens)}

LQGQALEQAIISQKPQLEKLIATTAHEKMPWFH GKISREESEQIVLIGSKTNGKFLIRARDN
NGSYALCLLHEGKVLHYRIDKDKTGKLSIPEGKKFDTLWQLVEHYSYKADGLLRVLT VPC
QKI

>d2plda__ d.93.1.1 (A:) Phospholipase C-gamma-1 {Cow (Bos taurus)}

GSPGIHESKEWYHASLTRAQAEHMLMRVPRDGAFLVRKRNEPNSY AISFRAEGKIKHCRV
QQEGQTVMLGNSEFDSLVDLISYYEKHPLYRKMKLRYPINEENSS

>d1blk__ d.93.1.1 (-) P55 Blk protein tyrosine kinase {Mouse (Mus musculus)}

GSVAPVETLEVEKWFFRTISRKDAERQLLAPMNKAGSFLIRESESNKGAFSLSVKDITTQG
EVVKHYKIRSLDNGGYISPRITFPTLQALVQHYSKKGDGLCQKLTLP CVNLA

>d1jwoa__ d.93.1.1 (A:) Csk homologous kinase Chk {Human (Homo sapiens)}

LSLMPWFH GKISGQEAVQQLQPPEDGLFLVRESARHPGDYVLCVSFGRDVIHYRVLHRDG
HLTIDEAVFFCNLMDMVEHYSKDKGAICTKLVRPKRK

>d1bgl3 d.93.1.1 (A:576-716) STAT3b {Mouse (Mus musculus)}

ILALWNEGYIMGFISKERERAILSTKPPGTFLRFSESSKEGGVTFTWVEKDISGSTQIQSVE
PYTKQQLNNMSFAEIIIMGYKIMDATNILVSPLVYLYPDIPKEEAFGKYCRPESQEHPEADPG
SAAPYLKTKFICVTPF

>d2cbla3 d.93.1.1 (A:264-351) Cbl {Human (Homo sapiens)}
 THPGYMAFLTYDEVKARLQKFHHPGSYIFRLSCTRLGQWAIGYVTADGNILQTIPHNKPL
 FQALIDGFREGFYLPDGRNQNPDLTG

>d2shpa2 d.93.1.1 (A:2-110) Tyrosine phosphatase shp-2 {Human (Homo sapiens)}
 KSRRWFHPNITGVEAENLLLTRGVDGSFLARPSKSNPGDLTSLVRRNGAVTHIKIQNTGDY
 YDLYGGEKFATLAELVQYYMEHHGQLKEKNGDVIELKYPLNCADPTSE

>d1d4ta_ d.93.1.1 (A:) The Xlp protein Sap {Human (Homo sapiens)}
 MDAVAVYHGKISRETGEKLLLATGLDGSYLLRDSSEVPGVYCLCVLYHGYIYTYRVSQTE
 TGSWSAETAPGVHKRYFRKIKNLISAFQKPDQGIVIPQYPVEK

>d1ptf_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Enterococcus faecalis}
 MEKKEFHIVAETGIHARPATLLVQTASKFNSDINLEYKGKSVNLKSIMGVMSLGVGQGSD
 VTITVDGADEAEGMAAIVETLQKEGLA

>d1opd_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Escherichia coli}
 MFEQEVTTITAPNGLHTRPAAQFVKEAKGFTSEITVTSNGKSASAKDLFKLQTLGLTQGTVV
 TISAEGEDEQKAVEHLVKLMAELE

>d1pch_ d.94.1.1 (-) Histidine-containing phosphocarrier protein (HPr) {Mycoplasma capricolum}
 AKFSAITDKVGLHARPASVLAKEASKFSSNITHANEKQGNLKSIMNVMAMAIKTGTEITI
 QADGNDADQAIQAIKQTMIDTALIQQ

>d1g9za_ d.95.2.1 (A:) DNA endonuclease I-CreI {Chlamydomonas reinhardtii}
 NTKYNKEFLLYLAGFVDGDGSIIAQIKPNQSYKFKHQLSLTFQVTQKTQRRWFCLKVDEI
 GVGYYVRDRGSVSDYILSEIKPLHNFLTQLQPFLKLKQKQANLVLKIIQLPSAKESPDKFLE
 VCTWVDQIAALNDSKTRKTTSETVRAVL

>d1b24a1 d.95.2.1 (A:7-99) I-dmoI {Archaeon Desulfurococcus mobilis}
 VSGISAYLLGLIIGDGGLYKLKYKGNRSEYRVVITQKSENLKQHIAPLMQFLIDELNVKSK
 IQIVKGDTRYELRVSSKKLYYYFANMLERIR

>d1b24a2 d.95.2.1 (A:100-179) I-dmoI {Archaeon Desulfurococcus mobilis}
 LFNMRQIAFIKGLYVAEGDKTLKRLRIWNKNKALLEIVSRWLNNLGVRNTIHLDDHRHG
 VYVLNISLRDRIKFVHTILS

>d1dfaa2 d.95.2.2 (A:181-298) PI-SceI {Baker's yeast (Saccharomyces cerevisiae)}
 PILYENDHFFDYMQKSKFHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTE
 YAEKLNLCAYKDRKEPVAKTVNLYSKVVRGNGIRNNLNTENPLWDAIVGLGFLKD

>d1dfaa3 d.95.2.2 (A:299-415) PI-SceI {Baker's yeast (Saccharomyces cerevisiae)}
 GVKNIPLSFLSTDNIGTRETFLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGLVSLARSLGLVV
 SVNAEPAKVDMNGTKHKISYAIYMSGGDVLLNVLSKAGSKKFRPAPAAFARE

>d1dq3a3 d.95.2.2 (A:129-226) PI-Pfui intein {Archaeon Pyrococcus furiosus}
 PDGEDYKFIFDYWLAGFIAGDGCDFKYHSHVKGHEYIYDRLRIYDYRIETFEIINDYLEKT
 FGRKYSIQKDRNIYYIDIKARNITSHYKLLEGIDNG

>d1dq3a4 d.95.2.2 (A:227-335) PI-Pfui intein {Archaeon Pyrococcus furiosus}
 IPPQILKEGKNAVLSFIAGLFDAEGHVSNNKPGIELGMVKNRLIEDVTHYLNALGIKARIREK
 LRKDGIDYVLHVEEYSSLLRFYELIGKNLQNEEKREKLEKVLNSNHKG

>d1a8ra_ d.96.1.1 (A:) GTP cyclohydrolase I {Escherichia coli}
 PLSKEAALVHEALVARGLETPLRPPVHEMDNETRKSIIAGHMTEIMQLLNLDLADDSLM
 ETPHRIAKMYVDEIFSGLDYANFPKITLIENKMKVDEMVTVRDITLTSTCESHFVTIDGKAT
 VAYIPKDSVIGLSKINRIVQFFAQRPQVQERLTQQILIALQTLLGTNNVAVSIDAVHYCVKAR

GIRDATSATTTTSLGGLFKSSQNTRHEFLRAVRHHN

>d1is8a_ d.96.1.1 (A:) GTP cyclohydrolase I {Rat (*Rattus norvegicus*)}

RPRSEEDNELNLPNLAAAYSSILRSLGEDPQRQGLLKPWRAATAMQFFTKGYQETISDVL
NDAIFDEHDDEMIVVKDIDMFSMCEHHLVPFVGRVHIGYLPNKQVLGLSKLARIVEIYSRR
LQVQERLTKQIAVAITEALQPAGVGVVIEATHMCMVMRGVQKMNSKTVTSTMLGVFRED
PKTREEFLTLIRS

>d1dhn_ d.96.1.3 (-) 7,8-dihidroneopterin aldolase {*Staphylococcus aureus*}

MQDTIFLKGMRFYGYHGALSAENEIGQIFKVDVTLKVDLSEAGRTDNVIDTVHYGEVFEE
VKSIMEGKAVNLLLEHLAERIANRINSQYNRMETKVRITKENPPIPGHYDGVGIEIVRENK

>d1b9la_ d.96.1.3 (A:) 7,8-dihidroneopterin triphosphate epimerase {*Escherichia coli*}

AQPAAIIRIKNLRRTFIGIKEEEINNRQDIVINVTIHYPADKARTSEDINDALNYRTVTKNII
QHVENNRFSLLEKLTQDVLDIAREHHWVTYAEVEIDKLHALRYADSVSMTLSWQR

>d1uox_1 d.96.1.4 (1-136) Urate oxidase (uricase) {*Aspergillus flavus*}

SAVKAARYGKDNVRVYKVHKDEKTGVQTVYEMTVCVLLGEIETSYTKADNSVIVATDSI
KNTIYITAKQNPVTPPELFGSILGTHFIEKYNHIIHAAHVNIIVCHRWTRMDIDGKPHPHSFIR
DSEEKRNQVDVVE

>d1uox_2 d.96.1.4 (137-295) Urate oxidase (uricase) {*Aspergillus flavus*}

GKGIDIKSSSLGTLVKSTNSQFWGFLRDEYTTLKETWDRILSTDVDATWQWKNFSGLQE
VRSHVPKFDATWATAREVTLKTFAEDNSASVQATMYKMAEQILARQQLIETVEYSLPNKH
YFEIDLSWHKGLQNTGKNAEVFAPQSDPNGLIKCTVGRS

>d1e3ha5 d.101.1.1 (A:152-262) Polynucleotide
phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5
{*Streptomyces antibioticus*}

FSGPIGGVRVALIRGQWVAFPTHTELEDAVFDMMVAGRVLEDGDVAIMMVEAEATEKTIQ
LVKDGAEPTEEVVAAGLDAAKPFIKVLCKAQADLAAKAAKPTGEFPVFLD

>d1e3ha6 d.101.1.1 (A:483-578) Polynucleotide
phosphorylase/guanosine pentaphosphate synthase (PNPase/GPSI), domains 2 and 5
{*Streptomyces antibioticus*}

APVAGIAMGLISQEINGETHYVALTDILGAEDAFGDMDFKVAGTKEFVTALQLDTKLDGIP
ASVLAAALKQARDARLHILDVMMEAITPDEMSPN

>d1seta2 d.104.1.1 (A:111-421) Seryl-tRNA synthetase (SerRS) {*Thermus thermophilus*, strain
hb27}

VGGEANREIKRVGGPPEFSFPPLDHVALMEKNGWWEPRISQVSGSRSYALKGDLALYEL
ALLRFAMDFMARRGFLPMTLPSYAREKAFLGTGHFPAYRDQVWIAAETDLYLTGTAEVVL
NALHSGEILPYEALPLRYAGYAPAFRSEAGSFGKDVRGLMRVHQFHKVEQYVLTEASLEA
SDRAFQELLENAAEILRLLELPYRLVEVATGDMGPGKWRQVDIEVYLPSEGRYRETHSCSA
LLDWQARRANLRYRDPEGRVRYAYTLNNTALATPRILAMLENHQLQDGRVRVPQALIPY
MGKEVLEPCG

>d1e1oa2 d.104.1.1 (A:161-502) Lysyl-tRNA synthetase (LysRS) {*Escherichia coli*, gene
lysU}

DQEVRYRQRYLDLIANDKSRQTFVVRSKILAAIRQFMVARGFMEVETPMMQVIPGGASAR
PFITHHNALDLDMYLRIAPELYLKRLVVGGFERVFEINRNFRNEGIVSRHNPEFTMMELYM
AYADYHDIELTESLFRTLAQEVLGTTKVITYGEHVDFGKPFKLTMR EAIKKYRPETDM
ADLDNFDAAKALAEISGITVEKSWGLGRIVTEIFDEVAEHLIQPTFITEYPAEVSPLARRN

DVNPEITDRFEFFIGGREIGNGFSELNDAEDQAERFQEQVNAKAAGDDEAMFYDEDYVTA
LEYGLPPTAGLGIGIDRMIMLFTNSHTIRDVILFPAMRP

>d1qe0a2 d.104.1.1 (A:1-325) Histidyl-tRNA synthetase (HisRS) {Staphylococcus aureus}

MIKIPRGTDILPEDSKKWRYIENQLDELMTFYNYKEIRTPIFESTDLFARGVGDSTDVVQK
EMYTFKDKGDRSITLPEGTAAVRSYIEHKMQGNPNQPIKLYYNGPMFRYERKQKGRYR
QFNQFGVEAIGAENPSVDAEVLAMVMHIYQSFGCLKHLKLVINSVGDMASRKEYNEALVK
HFEPIVHEFCSDCQSRLHTDPMRILDCKVDRDKEAIKTAPRITDFLNEESKAYYEQVKAYL
DDLGIPTYTEDPNLVRGLDYTHHTAFELMMDNPNYDGAITTLCGGGRYNGLLELLDGPSET
GIGFALSIERLLLALEEEIEILD

>d1atia2 d.104.1.1 (A:1-394) Glycyl-tRNA synthetase (GlyRS) {Thermus thermophilus}

AASSLDELVALCKRRGFIFQSSEIYGGLQGVYDYGPLGVELKNNLKQAWWRRNVYERDD
MEGLDASVLTHRLVLHYSGHEATFADPMVDNRITKKRYRLDHLLEKEQPEEVLKRLYRAM
EVEEENLHALVQAMMQAPERAGGAMTAAGVLDPASGEPGDWTPPRYFNMMFQDLRGP
RGGRGLLAYLRPETAQGIFVNFKNVLDATSRKLGFGIAQIGKAFRNEITPRNFIFRVREFEQ
MEIEYFVRPGEDEYWHRYWVEERLKWQEMGLSRENLPYQQPPESSAHYAKATVDILY
RFPHGSLELEGIAQRTDFDLGSHTKDQEALGITARVLRNEHSTQRLAYRDPETGKWFVPY
VIEPSAGVDRGVLALLAEFTREELPNGEERIVLKLKP

>d1qf6a4 d.104.1.1 (A:242-532) Threonyl-tRNA synthetase (ThrRS) {Escherichia coli}

RDHRKIGKQLDLYHMQEEAPGMVFWHNDGWTIFRELEVFRSKLKEYQYQEVKGPFMM
DRVLWEKTGHWDNYKDAMFTTSSENREYCIKPMNCPGHVQIFNQGLKSYRDLPLRMAE
FGSCHRNEPSGSLHGLMRVRGFTQDDAHIFCTEEQIRDEVNGCIRLVYDMYSTFGFEKIVV
KLSTRPEKRIGSDEMWDRAEADLAVALEENNIPFEYQLGEGAFYGPKEFTLYDCLDRAW
QCGTVQLDFSLPSRLSASYVGEDNERKVPVMIHRAILGSMERFIGILTEEFAGF

>d1eova2 d.104.1.1 (A:205-557) Aspartyl-tRNA synthetase (AspRS) {Baker's yeast (Saccharomyces cerevisiae)}

PILLEDASRSEAEAEAAGLPVVNLDTRLDYRVIDLRTVTNQAIFRIQAGVCELFREYLATK
KFTEVHTPKLLGAPSEGGSSVFVETVYFKGKAYLAQSPQFNKQQLIVADFERVYEIGPVFRA
ENSNTHRHMTFTGLDMEMAFEEHYHEVLDTLSELFVIFSELPKRFAHEIELVRKQYPVE
EFKLPKDGKMOVRLTYKEGIEMLRAAGKEIGDFEDLSTENEKFLGKLVRDKYDTDFYILDK
FPLEIRPFYTMPDPANPKYSNSYDFFMRGEEILSGAQRIHDHALLQERMKAHGLSPEDPGL
KDYCDGFSYGCPHAGGGIGLERVVMFYLDLKNIRRASLFPRDPKRLRP

>d1g51a3 d.104.1.1 (A:105-294,A:415-580) Aspartyl-tRNA synthetase (AspRS) {Thermus thermophilus}

TPPFPVDAGWRGEEKEASEELRLKYRYLDLRRRRMQENLRLRHRVIKAIWDFLDREGFV
QVETPFLTKSTPEGARDFLVPYRHEPGLFYALPQSPQLFKQMLMVAGLDYFQIARCFRDE
DLRADRQPDFTQLDLEMSFVEVEDVLELNERLMAHVFREALGVELPLPFPRLSYEEAMER
YGSCKPDLRXREGFRFLWVDFPLLEWDEEEEAWTYMHHPFTSPHPEDLPLLEKDPGRV
RALAYDLVLNGVEVGGGSIRIHDPRQLARVFRLLGIGEEEQREKFGFFLEALEYGAPPHGG
IAWGLDRLLALMTGSPSIREVIAFPKNKEGKDPLTGAPSPVPEEQRLRELGLMVVRP

>d1jja_ d.104.1.1 (A:) Phenyl-tRNA synthetase (PheRS) alpha subunit, PheS {Thermus thermophilus and (Thermus aquaticus)}

RVDVSLPGASLFSGGLHPITLMERELVEIFRALGYQAVEGPEVESEFFNFDALNIPEHHPAR
DMWDTFWLTGEGFRLEGPLGEEVEGRLLLRTHHTSPMQVRYMVAHTPPFRIVVPGRVFRFE

QTDATHEAVFHQLEGLVVGEGIAMAHKGAIIYELAQALFGPDSKVRFQPVYFPFVEPGAQ
FAVWWPEGGKWLELGGAGMVHPKVQAVDAYRERLGLPPAYRGVTGFAFGLGVERLAM
LRYGIPDIRYFFGGRLKFLEQFKGVL

>d1jjcb5 d.104.1.1 (B:475-681) Phenyl-tRNA synthetase (PheRS) beta subunit, PheT, central domain {Thermus thermophilus (Thermus aquaticus)}

ALPAFFPAPDNRGVEAPYRKEQRLREVLSSGLGFQEVYTYSFMDPEDARRFRLDPPRLLLL
NPLAPEKAALRTHLFPGLVRVLKENLDLDRPERALLFEVGRVFREREETHLAGLLFGEGV
GLPWAKERLSGYFLLKGYLEALFARLGLAFRVEAQAFPLHPGVSGRVLVEGEEVGFLGA
LHPEIAQELELPPVHLFELRLPLDPKP

>d1hc7a2 d.104.1.1 (A:5-276) Prolyl-tRNA synthetase (ProRS) {Thermus thermophilus}

KGLTPQSQDFSEWYLEVIQKAELADYGPVRGTIVVRPYGYAIWENIQVLD RMFKETGHQ
NAYFPLFIPMSFLRKEAEHVEGFSPELAVVTHAGGEELEEPLAVRPTSETVIGYMWSKWIR
SWRDLPQLLNQWGNVVRWEMRTRPFLRTSEFLWQEGHTAHATREEAEEVRRMLSIYAR
LAREYAAIPVIEGLKTEKEKFAGAVYTTTIEALMKDGKALQAGTSHYLG ENFARAFDIKFQ
DRDLQVKYVHTTSWGLSWRFIGAIIMTHGDD

>d1g5ha2 d.104.1.1 (A:41-330) The aaRS-like accessory subunit of mitochondrial polymerase gamma, N-terminal domain {Mouse (Mus musculus)}

EALVDLCRRRHFLSGTPQQLSTAALLSGCHARFGPLGVELRKNLASQWWSSMVVFREQV
FAVDSLHQEPGSSQPRDSAFRLVSPESIREILQDREPSKEQLVAFLENLLKTSGKLRATLLHG
ALEHYVNCLDLVNRKLPFGLAQIGVCFHPVSNSNQTPSSVTRVGEKTEASLVWFTPTRTSS
QWLDFWLRHRLWLWRKFAMSPSNFSSADCQDELGRKGSKLYYSFPWGKEPIETLWNLG
DQELLHTYPGNVSTIQGRDGRKNVPCVLSVSGDVDLGTLAYLYDSFQL

>d12asa_ d.104.1.1 (A:) Asparagine synthetase {Escherichia coli}

AYIAKQRQISFVKSHFSRQLEERLGLIEVQAPILSRVGDGTQDNLSGAEKAVQVKVKALPD
AQFEVVHSLAKWKRQTLGQHDFSAGEGLYTHMKALRPDEDRLSPLHSVYVDQWDWER
VMGDGERQFSTLKSTVEAIWAGIKATEAAVSEEFGLAPFLPDQIHVHSQELLSRYPD LDA
KGRERAIKDLGAVFLVGIGGKLSDGHRHDVRAPDYDDWSTPSELGHAGLNGDILVWNP
VLEDAFELSSM GIRVDADTLKHQLALTGDEDRLLELWHQALLRGEMPQTIGGGIGQSRLT
MLLLQLPHIGQVQAGVWPAAVRESVPSLL

>d1qtsa2 d.105.1.1 (A:825-938) Alpa-adaptin AP2, C-terminal subdomain {Mouse (Mus musculus)}

FFQPTEMASQDFFQRWKQLSNPQQEVQNIFKAKHPMDTEITKAKIIGFGSALLEEVDPNPA
NFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKDTVSQRLCELLSEQF

>d1e42a2 d.105.1.1 (A:825-937) Beta2-adaptin AP2, C-terminal subdomain {Human (Homo sapiens)}

LFVEDGKMERQVFLATWKDIPNENELQFQIKECHLNADTVSSKLQNNNVYTIKR NVEG
QDMLYQSLKLTNGIWILAELRIQPGNPNTLSLKCRAPEVSQYIYQVYDSILKN

>d1c44a_ d.106.1.1 (A:) Sterol carrier protein 2 (SCP2) {Rabbit (Oryctolagus cuniculus)}

SSAGDGFKANLVFKEIEKKLEEEGEQFVKKIGGIFAFKVKDGP GGKEATWVVDVKNKGKS
VLPNSDKKADCTITMADSDLLALMTGKMNPQSAFFQGKLKITGNMGLAMKLQNLQLQP
GKAKL

>d1ikta_ d.106.1.1 (A:) SCP2-like domain of MFE-2 {Human (Homo sapiens)}

LQSTFVFEEIGRRLKDIGPEVVKVNAVFEWHITKGGNIGAKWTIDLKSGSGKVYQGP AK
GAADTTIILSDEDFMEVVLGKLDPQKAFFSGRLKARGNIMLSQKLQMILKDYAKL

>d1b87a_ d.108.1.1 (A:) Aminoglycoside 6'-N-acetyltransferase {Enterococcus faecium}

MIISEFDRNNPVLKDQLSDLLRLTWPEEYGDSSAEVEEMMNPERIAVAAVDQDELVGFIG
 AIPQYGITGWELHPLVVESSRRKNQIGTRLVNYLEKEVASRGGITIYLGTTDDLHGTTLSTQ
 DLYEHTFDKVASIQNLREHPYEFYEKLGKIVGVLPNANGWDKPDIMAKTIIPRPS
 >d1bo4a_ d.108.1.1 (A:) Aminoglycoside 3-N-acetyltransferase {Serratia marcescens}
 GIIRTCRLGPDQVKSMRAALDLFGREFGDVATYSQHQPDSYLGNNLLRSKTFIALAAFDQE
 AVVGALAAAYVLPKFEQPRSEIYIYDLAVSGEHRRQGIATALINLLKHEANALGAYVIYVQA
 DYGDPAVALYTKLG
 >d1ygha_ d.108.1.1 (A:) Catalytic domain of GCN5 histone acetyltransferase
 {Baker's yeast (Saccharomyces cerevisiae)}
 KIEFRVNNNDNTKENMMVLTGLKNIFQKQLPKMPKEYIARLVYDRSHLSMAVIRKPLTVV
 GGITYRPFDKREFAEIVFCAISSTEQVRGYGAHLMNHLKDYVRNTSNIKYFLTYADNYAIG
 YFKKQGFTKEITLDSIWMGYIKDYEGGTLMQCSMLPRIRYLD
 >d1qsma_ d.108.1.1 (A:) Histone acetyltransferase HPA2 {Baker's yeast (Saccharomyces
 cerevisiae)}
 DNITVRFTENDKEGWQRLWKSQYDFYEVSPDDLDDFNFRFLDPNIMWAAVAVESS
 EKIIGMINFFNHMTTWDFDKIYINDLYVDENSrvKGAGGKLIQFVYDEADKLGTPSVYW
 CTDESNHRAQLLYVKVGYKAPKILYKRKGY
 >d1bob_ d.108.1.1 (-) Histone acetyltransferase HAT1 {Baker's yeast (Saccharomyces
 cerevisiae)}
 FKPETWTSSANEALRVSIVGENAVQFSPLFTYPIYGDSEKIYGYKDLIIHLAFDSVTFKPYV
 NVKYSAKLGDDNIVDVEKKLSFLPKDDVIVRDEAKWVDCFAERKTHNLSDFEKEVSE
 YSLNGEEFVVKSSLVDDFARRMHRRVQIFSLFIEAANYIDETDPSWQIYWLLNKKTKEL
 IGFVTYKYWHYLGAKSFDEDIDKKFRAKISQFLIPPYQNKGHGSCLYEAIQSWLEDKSI
 TEITVEDPNEAFDDLDRNDIQRLRKLGYDAVFQKHSLSDEFLESSRSLKLEERQFNRL
 VEMLLLLNNS
 >d1fy7a_ d.108.1.1 (A:) Histone acetyltransferase ESA1 {Baker's yeast (Saccharomyces
 cerevisiae)}
 ARVRNLNRIIMGKYEIEPWYFSPYPIELTDEDFIYIDDFTLQYFGSKKQYERYRKKCTLRHP
 PGNEIYRDDYVSFFEIDGRKQRTWCRNLCLLSKLFLDHKTLYYDVPFLFYCMTRRDELG
 HHLVGYFSKEKESADGYNVACILTPQYQRMGYGKLLIEFSYELSKKENKVGSPKPLSDL
 GLLSYRAYWSDTLITLLVEHQKEITIDEISSMTSMTTDILHTAKTLNILRYYKGQHIIIFLNE
 DILDYRNRLKAKKRRTIDPNRLIWKPP
 >d1cjsa_ d.108.1.1 (A:) Serotonin N-acetyltransferase {Sheep (Ovis aries)}
 HTLPANEFRCCLTPEDAAGVFEIEREAFISVSGNCPLNLDEVQHFLTLCPELSLGWVFEGRV
 AFIIGSLWDEERLTQESLALHRPRGSAHLHALAVHRSFRQQGKGSVLLWRYLHHVGAQP
 AVRAVLMCEDALVPFYQRFQHPAGPCAIVVGSALTFTMHCSL
 >d1i12a_ d.108.1.1 (A:) Glucosamine-phosphate N-acetyltransferase GNA1 {Baker's yeast
 (Saccharomyces cerevisiae)}
 LPDGFYIRRMEEGDLEQVTETLKVLTTVGTITPESFCKLIKYWNEATVWVNDNEDKKIMQY
 NPMVIVDKRTETVAATGNIIERKIIHELGLCGHIEDIAVNSKYQGQGLGKLLIDQLVTIGFD
 YGCYKIILDCDEKNVKFYKCGFSNAGVEMQIRK
 >d1iica1 d.108.1.2 (A:34-218) N-myristoyl transferase, NMT {Baker's yeast (Saccharomyces
 cerevisiae)}
 AMKDHKFWRTQPVKDFDEKVVEEGPIDKPKTPEDISDKPLPLSSFEWCSIDVDNKKQLE

DVFLNENYVEDRDAGFRFNYTKEFFNWALKSPGWKKDWHIGVRVKETQKLVAFISAIP
VTLGVRGKQVPSVEINFLCVHKQLRSKRLTPVLIKEITRRVKNCDIWHALYTAGIVLPAPVS
TCR

>d1iica2 d.108.1.2 (A:219-455) N-myristoyl transferase, NMT {Baker's yeast (*Saccharomyces cerevisiae*)}

YTHRPLNWKKLYEVDFTGLPDGHTTEEDMIAENALPAKTKTAGLRKLKKEDIDQVFELFKR
YQSRFELIQIFTKEEFEHNFIDGEESLPLDKQVIFSYYVEQPDGKITDFFSFYSLPFTILNNTKY
KDLGIGYLYYYATDADFQFKDRFDPKATKALKTRLCELIYDACILAKNANMDVFNALTSQ
DNTLFLDDLKFGPGDGFNLFYLFNYRAKPITGGLNPDNSNDIKRRSNVGVVML

>d2vik__ d.109.1.1 (-) Villin, domain 1 (res. 1-126) {Chicken (*Gallus gallus*)}

VELSKKVTGKLDKTPGIQIWRIENMEMVPVPTKSYGNFYEGDCYVLLSTRKTGSGFSYN
IHYWLGNSSQDEQGAAYTTQMDEYLGSAVQVHREVQGHSETFRAYFKQGLIYKQG
GVASGMK

>d1svy__ d.109.1.1 (-) Severin, domain 2 {*Dictyostelium discoideum*}

EYKPRLLHISGDKNAKVAEVPLATSSLNSGDCFLLDAGLTIYQFNGSKSSPQEKNAAEVA
RAIDAERKGLPKVEVFCETDSDIPAEFWKLGGKGAIAAKH

>d1d0na2 d.109.1.1 (A:153-262) Gelsolin {Horse (*Equus caballus*)}

VPNEVVVQRLQVKGRVVRATEVPVSWESFNNGDCFILDLGNNIYQWCGSKSNRFERL
KATQVSKGIRDNERSGRAQVSVFEEGAPEAMLQVLGPKPTLPEATEDTVK

>d1d0na3 d.109.1.1 (A:263-383) Gelsolin {Horse (*Equus caballus*)}

EDAANRKLAKLYKVSNGAGPMVSVLADENPFAQGALRSEDCFILDHGKDGKIFVWKGK
QANMEERKAALKTASDFISKMDYPKQTQVSVLPEGGETPLFRQFFKNWRDPDQTEGLGL
AYL

>d1d0na4 d.109.1.1 (A:384-532) Gelsolin {Horse (*Equus caballus*)}

SSHIAHVERVPFDAATLHTSTAMAAQHGMDDDG TGQKQIWRVEGSNKVPVDPATYQGQFY
GGDSYIILYNRYHGSRQGQIYNWQGAQSTQDEVAASAILTAQLDEELGGTPVQSRVVQG
KEPAHLMSLFGGKPMIVYKGGTSREGGQTA

>d1d0na5 d.109.1.1 (A:533-628) Gelsolin {Horse (*Equus caballus*)}

PASTRLFQVRASSSGATRAVEIIPKAGALNSNDAFVLKTPSAAYLWVGAGASEAEKTGAQE
LLRVLRAQPQVAEGSEPDSFWEALGGKATYRTSP

>d1d0na6 d.109.1.1 (A:629-755) Gelsolin {Horse (*Equus caballus*)}

RLKDKKMDAHPPLRFACSNKIGRFVIEVPGEFMQEDLATDDVMLLDTWDQVFVWVGK
DSQDEEKTEALTSAKRYIDTDPAHRDRRTPTVVKQGFEPSPFVGWFLGWDDSYWSVDPL
DRALAEALAA

>d1cnua_ d.109.1.2 (A:) Cofilin (actin depolymerizing factor, ADF) {*Amoeba (Acanthamoeba castellanii)*, actophorin}

GIAVSDDCVQKFNELKLGHQHRYVTFKMNASNTEVVVEHVGGPNATYEDFKSQLPERDC
RYAIFDYEFQVDGGQRNKITFILWAPDSAPIKSKMMYTSTKDSIKKKLVGIQVEVQATDAA
EISEDAVSERAKKD

>d1hqz1_ d.109.1.2 (1:) Cofilin-like domain of actin-binding protein abp1p {Baker's yeast (*Saccharomyces cerevisiae*)}

LEPIDYTTHSREIDA EYLKIVRGSDPD TTWLIISPNAKKEYEPESTGSSFHDFLQLFDETKVQ
YGLARVSPPGSDVEKIIIGWCPDSAPLKTRASFAANFAAVANNLFKGYHVQVTARDEDDL
DENELLMKISNAAGA

>d1ak7__ d.109.1.2 (-) Dextrin {Human and pig (Homo sapiens) and (Sus scrofa)}
 TMITPSSGNSASGVQVADEVCRIFYDMKVRKCSTPEEIKKRKKAVIFCLSADKKCIIVEEGK
 EILVGDVGVTTITDPFKHFVGMLEPKDCRYALYDASFETKESRKEELMFFLWAPELAPLKSK
 MIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLGGSLIVAFEGCPV

>d1pne__ d.110.1.1 (-) Profilin (actin-binding protein) {Cow (Bos taurus)}
 AGWNAIDNLMADGTCQDAAIVGYKDSPSVWAAVPGKTFVNITPAEVGILVGKDRSSFFV
 NGLTLGGQKCSVIRDSLLQDGEFTMDLRTKSTGGAPT FNITVTMTAKTLVLLMGKEGVHG
 GMINKKCYEMASHLRRSQY

>d1ypra__ d.110.1.1 (A:) Profilin (actin-binding protein) {Baker's yeast (Saccharomyces cerevisiae)}
 SWQAYTDNLIGTGKVDKAVIYSRAGDAVWATSGGLSLQPNEIGEIVQGFDNPAGLQSNGL
 HIQGQKFMLLRADDRSIYGRHDAEGVVCVVRTKQTVIIAHYPPTVQAGEATKIVEQLADYLI
 GVQY

>d1cqa__ d.110.1.1 (-) Profilin (actin-binding protein) {Birch (Betula verrucosa)}
 SWQTYVDEHLMCDIDGQGEELAASAIVGHDGSVWAQSSSPQFKPQEITGIMKDFEEPGH
 LAPTGLHLGGIKYPMVIQGEAGAVIRGKKGSGGITIKKTGQALVFGIYEETVTPGQCNMNV
 ERLGDYLIDQGL

>d1ifqa__ d.110.4.1 (A:) Sec22b {Mouse (Mus musculus)}
 SVLLTMIARVADGLPLAASMQEDEQSGRDLQQYQSQAKQLFRKLNEQSPTRCTLEAGAM
 TFHYIIEQGV CYLVLC EAAPKKLAFAYLEDLHSEFDEQHGGKKVPTVSRPYSFIEFDTFIQK
 TKKLYI

>d1h8ma__ d.110.4.1 (A:) Synaptobrevin homolog 1 ykt6 {Baker's yeast (Saccharomyces cerevisiae)}
 MRIYYIGVFRSGGEKALELSEVKDLSQFGFFERSSVGQFMFFAETVASRTGAGERQSIEEG
 NYIGHVYARSEGICGVLITDKQYPVRPAYTLLNKILDEYLV AHPKEEWADV TETNDALKM
 KQLDTYISKYQDPSQADA

>d1cfe__ d.111.1.1 (-) Pathogenesis-related protein 1 (PR1) {Tomato (Lycopersicon esculentum), P14a}
 QNSPQDYLA VHNDARAQVGVGPMSWDANLASRAQNYANSRAGDCNLIHSGAGENLAK
 GGGDFTGRAAVQLWV SERPSYNYATNQCVGGKKCRHYTQV VWRNSVRLGCGRARCNN
 GWWFISCNYDPVGNWIGQRPY

>d1qnxa__ d.111.1.1 (A:) Insect allergen 5 (AG5) {Yellow jacket (Vespula vulgaris), Ves v 5}
 AEAEFN NYCKIKCLKGGVHTACKY GSLKPNCGNKVVS YGLTKQEKQDILKEHNDFRQK
 IARGLETRGNPGPQPPAKNMKNLVWNDELAYVAQVWANQCQYGHDTCDRVAKYQVGG
 NVALTGSTA AKYDDPVKLVKMWEDEVKDYNPKKKFSGNDFLKTGHYTQM VWANTKEV
 GCGSIKIYIQEKWHKH YLVCNYGPSGNFKNEELYQTK

>d1a6ja__ d.112.1.1 (A:) Nitrogen regulatory bacterial protein IIa-ntr {Escherichia coli}
 LQLSSVLNRECTRSRVHCQSKKRALEIISELA AKQLSLPPQVVF EAILTREKMGSTGIGNGI
 AIPHGKLEEDTLRAVG VVQLETPIAFDAIDNQPV DLLFALLVPADQTKTHLHTLSLVAKRL
 ADKTICRRLRAAQSD EELYQIITDTE

>d1a3aa__ d.112.1.1 (A:) Phosphotransferase IIa-mannitol {Escherichia coli}
 LFKLGAENIFLGRKAATKEEAIRFAGEQLVKG GGYVEPEYVQAMLDREKLTPTYLGESI AVP
 HGTVEAKDRVLKTGVVFCQYPEGVRFGE EDDIARLVIGIAARNNEHIQVITSLTNALDDE
 SVIERLAHTTSVDEVLELLAGRK

>d1mut__ d.113.1.1 (-) Nucleoside triphosphate pyrophosphorylase (MutT) {Escherichia coli}

MKKLQIAVGIIRNENNEIFITRRAADAHMANKLEFPGGKIEMGETPEQAVVRELQEEVGIT
PQHFSLEKLEYEFPDRHITLWFWLVERWEGEPWGKEGQPGEWMSLVGLNADDFPPANE
PVIAKLKRL

>d1g0sa_ d.113.1.1 (A:) ADP-ribose pyrophosphatase {Escherichia coli}

MLKPDNLPVTFGKNDVEIIARETLYRGFFSLDLYRFRHRLFNGQMSHEVRREIFERGHAAV
LLFPDPVRDEVVLIEQIRIAAYDTSETPWLLEMVAGMIEEGESVEDVARREAIEEAGLIVKR
TKPVLSFLASPGGTSSIMVGEVDATTASGIHGLADENEDIRVHVVSREQAYQWVEEGK
IDNAASVIALQWLQLHHQALKNEWA

>d1jkna_ d.113.1.1 (A:) Diadenosine tetraphosphate hydrolase {Narrow-leaved blue lupine (Lupinus angustifolius)}

GPLGSMDSPEGYRRNVGICLMNNDKKIFAASRLDIPDAWQMPQGGIDEGEDPRNAAIRE
LREETGVTSAEVIAEVPYWLTYDFPPKVREKLNIQWGS DWKGQAQKWFLFKFTGQDQEI
NLLGDGSEKPEFGEWSWVTPEQLIDLTVFEKKPVYKEVLSVFAPHL

>d1tsy_ d.117.1.1 (-) Thymidylate synthase {Lactobacillus casei}

MLEQPYLDLAKKVLDEGHFKPDRHTGTYSIFGHQMRFDLSKGFPLLTKKVPFGLIKSEL
LWFLHGD TNIRFLQHRNHIWDEWAFEKWKSDEYHGPDMTDFGHSRQKDPEFAAVYH
EEMAKFDDRVLHDDAFAAKYGD LGLVYGSQWRAWHTSKGDTIDQLGDVIEQIKTHPYSR
KLIVSAWNPEDVPTMALPPCHTLYQFYVNDGKLSLQLYQRSADIFLGVPFNIA SYALLTHL
VAHECGLEVGEFIHTFGDAHLYVNHL DQIKEQLSRTPRPAPTLQLNPDKHDIFDFDMKDIK
LLNYDPYPAIKAPVAV

>d1bkpa_ d.117.1.1 (A:) Thymidylate synthase {Bacillus subtilis}

TQFDKQYNSIIKDIINNGISDEEFVVRTKWSDGTPAHTLSVISKQMRFDNSEVPILT TTKV
AWKTAIKELLWIWQLKSNDVNDLNM MG VHIWDQWKQEDGTIGHAYGFQLGKKNRSLN
GEKVDQVDYLLHQLKNNPSSRRHITMLWNPDELDAMALTPCVYETQWYVKHGLHLEV
RARSNDMALGNPFNVFQYNVLQRMIAQVTGYELGEYIFNIGDCHVYTRHIDNLKIQMER
EQFEAPELWINPEVKDFYDFTIDDFKLINYKHGDKLLFEVAV

>d1f28a_ d.117.1.1 (A:) Thymidylate synthase {Pneumocystis carinii}

NAEEQQYLNLVQYIINHGEDRPDRGTGTLSVFAPSPLKFSLRNKTFPLLTTRKVFIRGVIEE
LLWFIRGETDSLKLREKNIHIWDANGSREYLD SIGLTKRQEGDLGPIYGFQWRHF GA EYID
CKTNYIGQGVDQLANIIQKIRTSPYDRRLILSAWNPADLEKMALPPCHMFCQFYVHIPSN
HRPELSCQLYQRSCDMGLGVFNIA SYALLTCMIAHVCDLDPGDFIHMVMDCHYKDHIE
ALQQQLTRSPRPFTLSLNRSITDIEDFTLDDFN IQNYHPYETIKMKMSI

>d1b5ea_ d.117.1.1 (A:) dCMP hydroxymethylase {Bacteriophage T4}

MISDSMTVEEIRLHLGLALKEKDFVVDKTGVKTIEIIGASFVADEPFIFGALNDEYIQRELE
WYKSKSLFVKDIPGETPKIWQQVASSKGEINSNYGWAIWSEDNYAQYDMCLAELGQNPD
SRRGIMIYTRPSMQFDYNKDGM SDFMCTNTVQYLIRDKKINAVVNMRSNDVVFGFRNDY
AWQKYVLDKLVSDLNAGDSTRQYKAGSIWNVGS LHVYSRHFYLV DHHWKTGETHISK
KDY

>d1axx_ d.120.1.1 (-) Cytochrome b5 {Rat (Rattus norvegicus)}

DKDVKYTTLEEIQKHKDSKSTWVILHHKVYDLTKFLEEHPGGEEVLREQAGGDATENFE
DVGHSTDARELSKTYIIGELHPDDRSKIAKPSETL

>d1cxya_ d.120.1.1 (A:) Cytochrome b558 {Ectothiorhodospira vacuolata}

TLPVFTLEQVAEHHSPDDCWMAIHGKVYDLTPYVPNHGPGAGMMLVWCGQESTEAWET
KSYGEPHSSLAARLLQRYLIGTL

>d1ltda2 d.120.1.1 (A:10-97) Flavocytochrome b2, N-terminal domain {Baker's yeast (*Saccharomyces cerevisiae*)}

KISPAEVAKHNKPDCCWVVINGYVYDLTRFLPNHPGGQDVIKFNAGKDVTAIFEPLHAPN
VIDKYIAPEKKLGPLQGSMPELVCPPY

>d1soxa2 d.120.1.1 (A:3-93) Sulfite oxidase, N-terminal domain {Chicken (*Gallus gallus*)}

SYPEYTREEVGRHRSPEERVVWTHGTDVFDVTDVDFVELHPGGPKILLAAAGGALEPFWALY
AVHGEPHVLELLQQYKVGELSPDEAPAAPDA

>d1eila2 d.122.1.2 (A:2-220) DNA gyrase B {*Escherichia coli*}

SNSSDSSSIKVLKGLDAVRKRPGMYIGDTHDGTGLHHMVFEVVDNAIDEALAGHCKEIIV
TIHADNSVSVQDDGRGIPTGIHPPEGVSAAEVIMTVLHAGGKFDDNSYKVSGGLHGVGV
VVNALSQKLELVIQREGKIHRQIYEHGVPQAPLAVTGETEKTGTMRVFWPSLETFTNVTEF
EYEILAKRLRELSFLDSGVSIRLRDKRDGKEDHFHYEG

>d1b63a2 d.122.1.2 (A:-2-216) DNA mismatch repair protein MutL {*Escherichia coli*}

SHMPIQVLPPQLANQIAAGEVVERPASVVKELVENS LDAGATRIDI DIERGGAKLIRIRDNG
CGIKKDELALALARHATSKIASLDDLEAIISLGFRGEALASISSVSRLTLTSRTAEQQEAWQA
YAEGRDMNVTVKPAHPVGTTLLEVLDFYNTPARRKFLRTEKTEFNHIDEIIRRIALARFD
VTINLSHNGKIVRQYRAVPEGGQKERRLGAIC

>d1h7sa2 d.122.1.2 (A:29-231) DNA mismatch repair protein PMS2 {Human (*Homo sapiens*)}

GQVVLSLSTAVKELVENS LDAGATNIDLKLDYGVDLIEVSDNGCGVEEENFEGLTLKHH
TSKIQEFADLTQVETFGFRGEALSSLCALSDVTISTCHASAKVGTRLMFDHNGKIIQKTPYP
RPRGTTVSVQQLFSTLPVRHKEFQRNIKEYAKMVQVLHAYCIISAGIRVSCTNQLGQGKR
QPVVCTGGSPSIKENIGSVF

>d1bxda_ d.122.1.3 (A:) Histidine kinase domain of the osmosensor EnvZ {*Escherichia coli*}

TGQEMPMEMADLNAVLGEVIAAESGYEREIETALYPGSIEVKMHPLSIKRAVANMVVNAA
RYGNGWIKVSSGTEPNRAWFQVEDDGP G I A P E Q R K H L F Q P F V R G D S A R T I S G T G L G L A I V
Q R I V D N H N G M L E L G T S E R G G L S I R A W L P V P V T R A Q G T T K E G

>d1i58a_ d.122.1.3 (A:) Histidine kinase CheA {*Thermotoga maritima*}

GSHMVPISFVFNRFPRMVRDLAKKMNKEVNFIMRGEDTELDRTFVEEIGEPLLHLLRNAI
DHGIEPKEERIAKKGKPIGTLILSARHEGNNVIEVEDDGRGIDKEKIIRKAIEKGLIDESKA
ATLSDQEILNFLVPGFSTKEKVSEVSGRGVGM DVVKNV VESLNGSISIESEKDKGTVTI
RLPLT

>d1id0a_ d.122.1.3 (A:) Histidine kinase PhoQ domain {*Escherichia coli*}

RELHPVAPLLDNLTALNKVYQRKGVNISLDISPEISFVGEQNDFVEVMGNVLDNACKYC
LEFVEISARQTDEHLYIVVEDDGP G I P L S K R E V I F D R G Q R V D T L R P G Q G V G L A V A R E I T E Q Y
EGKIVAGESMLGGARMEVIFGRQH

>d1gkza2 d.122.1.4 (A:186-378) Branched-chain alpha-ketoacid dehydrogenase kinase (BCK) {Rat (*Rattus norvegicus*)}

DFVGIICTRLSPKKIIEKWVDFARRLCEHKYGNAPRVRINGHVAARFPFIPMPLDYILPELLK
NAMRATMESHLDTPYNVPDVVITIANNDVDLIIRISDRGGGIAHKDLDRVMDYHFTTAEA
STQDPRISPLFGHLDMHSGGQSGPMHGFGLPTSRAYAEYLGGSLQLQSLQGIGTDVYL
RLRHIDGREE

>d1jm6a2 d.122.1.4 (A:1177-1366) Pyruvate dehydrogenase kinase {Rat (*Rattus norvegicus*), isozyme 2}

PKHIGSIDPNCVSDVVKDAYDMAKLLCDKYMASPDLEIQEVNATNATQPIHMOVVPSH
LYHMLFELFKNAMRATVESHESSLTPPIKIMVALGEEDLSIKMSDRGGGVPLRKIERLFSY
MYSTAPTPQPGTGGTPLAGFGYGLPISRLYAKYFQGDQLQFSMEGFGTDAVIYALKALSTDS
VERLPVY

>d1bola_ d.124.1.1 (A:) Ribonuclease Rh {*Rhizopus niveus*}

SSCSSTALSCSNSANSNDTCCSPEYGLVVLNMQWAPGYGPDNAFTLHGLWPDKCSGAYAPS
GGCDNRASSSIASVIKSKDSSLYNSMLTYWPSNQGNVFWWSHEWSKHGTCVSTYDPD
CYDNYEEGEDIVDYFQKAMDLSQYNVYKAFSSNGITPGGTYTATEMQSAIESYFGAKA
KIDCSSGTLSDVALYFYVRGRDITYVITDALSTGSCSGDVEYPTK

>d1dixa_ d.124.1.1 (A:) RNase LE {*Tomatoes (Lycopersicon esculentum)*}

ASGSKDFDFFYFVQQWPGSYCDTKQSCCYPTTGKPAADFGIHGLWPNNNDGTYPSCDP
NSPYDQSQISDLISSMQQNWPTLACPSGSGSTFWSEWEKHGTCAESVLTNQHAYFKKAL
DLKNQIDLLSILQGADIHPDGESYDLVNIRNAIKSAIGYTPWICNVQDQSGNSQLYQVYICV
DGSGLSIECPIFPGGKCGTSIEFPTF

>d1iqqa_ d.124.1.1 (A:) S3-RNase {*Japanese pear (Pyrus pyrifolia)*}

YDYFQFTQQYQLAVCNSNRTLCKDPPDKLFTVHGLWPSNMVGPDPSCPIKNIRKREKLL
EHQLEIHWPNVFDRTKNNLFWDKIEWMKHGSCGYPTIDNENHYFETVIKMYISKKQNVSRI
LSKAKIEPDGKKRALLDIENAIRNGADNKKPKLKCQKKGTTTELVEITLCSDKSGEHFIDC
PHPFEPISPHYCPTNNIKY

>d1g61a_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {*Archaeon Methanococcus jannaschii*}

MIIRKYFSGIPTIGVLALTTEEITLLPIFLDKDDVNEVSEVLETKCLQTNIGGSSLVGSLSVAN
KYGLLLPKIVEDEELDRIKNFLKENNLDLNEIISKNTALGNLILTNDKGALISPELKDFK
KDIEDSLNVEVEIGTIAELPTVGSNAVVTNKGCLTHPLVEDDELEFLKSLFKVEYIGKGTAN
KGTTSVGACIIANSKGAVVGGDTTGPELLIIEDALGL

>d1g62a_ d.126.1.1 (A:) Ribosome anti-association factor eIF6 (aIF6) {*Baker's yeast (Saccharomyces cerevisiae)*}

MATRTQFENSNEIGVFSKLTNTYCLVAVGGSENFYSAFEELGDAIPVHTTIAGTRIIGRMT
AGNRRGLLVPTQTTDQELQHLRNSLPDSVKIQRVEERLSALGNVICCNDYVALVHPDIDRE
TEELISDVLGVEVFRQTISGNILVGSYCSLSNQGLVHPQTSVQDQEELSSLLQVPLVAGTV
NRGSSVVGAGMVVNDYLAVTGLDTTAPELSVIESIFRL

>d1jdw_ d.126.1.2 (-) L-arginine: glycine amidinotransferase {*Human (Homo sapiens)*}

CPVSSYNEWDPLEEVIVGRAENACVPPFTIEVKANTYEKYWPFYQKQGGHYFPKDHLKK
AVAEIEEMCNILKTEGVTVRRPDIDWSLKYPDFESTGLYSAMPDILVVGNEIIEAPM
AWRSRFFEYRAYRSIIKDYFHRGAKWTTAPKPTMADELYNQDYPIHSVEDRHKLAAQGKF
VTTEFEPCFDAADFIRAGRDIFAQRSQVTNYLGIEWMRRHLAPDYRVHIISFKDPNPMHID
ATFNIIGPGIVLSNPDRPCHQIDLFKKAGWTIITPPTPIIPDDHPLWMSSKWLMSNVLMLE
KRMVVDANEVPIQKMFELGITTIVNIRNANSLGGGFHCWTCDVRRRGTLQSYLD

>d1bwda_ d.126.1.2 (A:) L-arginine: inosamine-phosphate amidinotransferase {*Streptomyces griseus*}

RSLVSVHNEWDPLEEVIVGTAVGARVPTADRSVFAVEYAGDYESQEIPSGAYPDRVLKET
EEELHVLAAELTKLGVTVRRPGPRDHSALIKTPDWETDGFHDYCPRDGLLSVGQTHIETPM
ALRSRFLESLAYKDLLLEYFASGSRWLSAPKPRLTDDSYAPQAPAGERLTDEEPVFDAANV
LRFGTDLLYLVSDSGNELGAKWLQSAVGDTYTVHPCRKLYASTHVDSTIVPLRPLVLTNP

SRVNDENMPDFLRSWENITCPELVDIGFTGDKPHCSVWIGMNLLVVRPDLAVVDRRQTAL
IRLLEKHGMNVLPQLTHSRTLGGGFHCATLDVRRRTGALETYQF

>d1chma2 d.127.1.1 (A:157-402) Creatinase, catalytic (C-terminal) domain {Pseudomonas putida}
MIKSAAEHVMIRHGARIADIGGAAVVEALGDQVPEYEVALHATQAMVRAIADTFEDVEL
MDTWTWFQSGINTDGAHNPVTTRKVNKGDILSLNCFPMIAGYYTALERTFLDHCSDDH
LRLWQVNVVEVHEAGLKLKPGARCSDIARELNEIFLKHDVLQYRTFGYGHSGFTLSHYYG
REAGLELREDIDTVLEPGMVVSMEPMIMLPEGLPGAGGYREHDILIVNENGAENITKFPY
GPEKNIR

>d1c22a_ d.127.1.1 (A:) Methionine aminopeptidase {Escherichia coli}
AISIKTPEDIEKMRVAGRLAAEVLEMIEPYVKPGVSTGELDRICNDYIVNEQHAVSACLG
HGYPKSVCSINEVVCHGIPDDAKLLKDGDIVNIDVTVIKDGFGHGDTSKMFIVGKPTIMGE
RLCRITQESLYLALRMVKPGINLREIGAAIQKFVEAEGFSVVREYCGHGIGQGFHEEPQVL
HYDSRETNVVLKPGMTFTIEPMVNAGKKEIRTMKDGWTVTKDRSLSAQYEHTIVVTDN
GCEILTLRKDDTIPAIISHD

>d1xgsa2 d.127.1.1 (A:1-194,A:272-295) Methionine aminopeptidase {Archaeon Pyrococcus
furiosus}

MDTEKLMKAGEIAKKVREKAIKLARPGMLLELAESIEKMIMELGGKPAFPVNLSINEIAA
HYTPYKGDTTVLKEGDYLIKIDVGVIDGFIADTAVTVRVGMEDELMEAAKEALNAAIS
VARAGVEIKELGKAIENEIRKRGFKPIVNLSGHKIERYKLHAGISIPNIYRPHDNYVLKEGD
VFAIEPFATIGAXRNGIVAQFEHTIIVEKDSVIVTTE

>d1b6a_2 d.127.1.1 (110-374,449-478) Methionine aminopeptidase {Human (Homo
sapiens)}

KVQTDPPSPICDLYPNGVFPKGQECEYPPTQDGRTAAWRTTSEEKKALDQASEEIWNDF
REAAEAHRQVRKYVMSWIKPGMTMIEICEKLEDCSRKLIKENGLNAGLAFPTGCSLNNC
AAHYTPNAGDTTVLQYDDICKIDFGTHISGRIIDCAFTVTFNPKYDTLLKAVKDATNTGIK
CAGIDVRLCDVGEAIQEVMESEYEVEIDGKTYQVKPIRNLNGHSIGQYRIHAGKTVPIVK
GEATRMEEGEVYAIETFGSTGKGVVXDIKGSYTAQFEHTILLRPTCKEVVSRGDDY

>d1az9_2 d.127.1.1 (177-440) Aminopeptidase P, C-terminal domain {Escherichia coli}
SPEEIAVLRAGEITAMAHTRAMEKCRPGMFEYHLEGEIHHEFNHRHGARYPSYNTIVGSGE
NGCILHYTENECMRDGDVLIDAGCEYKGYAGDITRTFPVNGKFTQAQREIYDIVLESLE
TSLRLYRPGTSILEVTGEVVRIMVSGLVKLGILKGDVDELIAQNAHRPFFMHGLSHWLGLD
VHDVG VYGQDRSRILEPGMVLTVEPGLYIAPDAEVPEQYRGIGIRIEDDIVITETGNENLTA
SVVKKPEEIEALMVAARKQ

>d1qnaa1 d.129.1.1 (A:17-115) TATA-box binding protein (TBP), C-terminal domain
{Arabidopsis thaliana}

HPSGIVPTLQNIVSTVNLDCKLDLKAIALQARNAEYNPKRFAAVIMRIREPKTALIFASGK
MVCTGAKSEDFSKMAARKYARIVQKLGFPAKFKDFKI

>d1qnaa2 d.129.1.1 (A:116-198) TATA-box binding protein (TBP), C-terminal domain
{Arabidopsis thaliana}

QNIVGSCDVKFPIRLEGLAYSHAAFSSYEPELFPGLIYRMKVPKIVLLIFVSGKIVITGAKMR
DETYKAFENIYPVLSEFRKI

>d1aisa1 d.129.1.1 (A:1-92) TATA-box binding protein (TBP), C-terminal domain
{Archaeon Pyrococcus woesei}

MVDMASKVKLRIENIVASVDLFAQLDLEKVLDCPNKYNPEEFPGIICHLDDPKVALLIFSS

GKLVVTGAKSVQDIERAVAKLAQKLKLSIGV

>d1aisa2 d.129.1.1 (A:93-181) TATA-box binding protein (TBP), C-terminal domain {Archaeon *Pyrococcus woesei*}

KFKRAPQIDVQNMVFSGDIGREFNLDVVALTLPNCEYEPEQFPGVIYRVKEPKSVILLFSSG
KIVCSGAKSEADAWAVRKLLRELDKY

>d1mpga2 d.129.1.2 (A:1-99) 3-Methyladenine DNA glycosylase II (gene *alkA* or *aidA*) {*Escherichia coli*}

MYTLNWQPPYDWSWMLGFLAARAVSSVETVADSYARSLAVGEYRGVVTAIPDIARHTL
HINLSAGLEPVAAECLAKMSRLFDLQCNPQIVNGALGRLG

>d1ko9a2 d.129.1.2 (A:12-135) 8-oxoguanine glycosylase {Human (*Homo sapiens*)}

GHRTLASTPALWASIPCPRSELRLDLVPSGQSFRWREQSPAHWSGVLADQVWTLTQTEEQ
LHCTVYRGDKSQASRPTPDELEAVRKYFQLDVTLAQLYHHWGSVDSHFQEVAQKFQGVRLRQ

>d1mxa_1 d.130.1.1 (1-102) S-adenosylmethionine synthetase {*Escherichia coli*}

AKHLFTSESVSEGHDPKIDQISDAVLDAILEQDPKARVACETYVKTGMVLVGGEITTSW
VDIEEITRNTVREIGYVHSDMGFDANSCAVLSAIGKQSPDI

>d1mxa_2 d.130.1.1 (108-231) S-adenosylmethionine synthetase {*Escherichia coli*}

RADPLEQGAGDQGLMFGYATNETDVLMPAPITYAHLVQRQAEVRKNGTLPWLRPDAKS
QVTFQYDDGKIVGIDAVVLSTQHSEEIDQKSLQEAVMEEIKPILPAEWLTSATKFFINPTGR
FV

>d1mxa_3 d.130.1.1 (232-383) S-adenosylmethionine synthetase {*Escherichia coli*}

IGGPMGDCGLTGRKIIVDITYGGMARHGGGAFSGKDPKVDRAAAYAARYVAKNIVAAGL
ADRCEIQVSYAIGVAEPTSIMVETFGTEKVPSEQTLTLLVREFFDLRPYGLIQMLDLLHPIYKE
TAAAYGHFGREHFPWEKTDKAQLLRDAAGLK

>d2pola1 d.131.1.1 (A:1-122) DNA polymerase III, beta subunit {*Escherichia coli*}

MKFTVEREHLKPLQQVSGPLGGRPTLPILGNLLQVADGTLSTGTDLMEMVARVALV
QPHEPGATTVPARKFFDICRGLPEGAEIAVQLEGERMLVRSGRSRLSTLPAADFPNLDD
W

>d2pola2 d.131.1.1 (A:123-244) DNA polymerase III, beta subunit {*Escherichia coli*}

QSEVEFTLPQATMKRLIEATQFSMAHQDVRYYLNGMLFETEGEELRTVATDGHRLAVCSM
PIGQSLPSHSVIVPRKGVIELMRMLDGGDNPLRVQIGSNNIRAHVGDFITSKLVDGRFPDY

>d2pola3 d.131.1.1 (A:245-366) DNA polymerase III, beta subunit {*Escherichia coli*}

RRVLPKNPDKHLEAGCDLLKQAFARAAILSNEKFRGVRLYVSENQLKITANNPEQEEAEEI
LDVTYSGAEMEIGFNVSYVLDVLNALKCENVRMMLTDSVSSVQIEDAASQSAAYVVM
MRL

>d1b77a1 d.131.1.2 (A:1-110) gp45 sliding clamp {Bacteriophage RB69}

MKLSKDTIAILKNFASINSGILLSQGKFIMTRAVNGTTYAEANISDEIDFDVALYDLNSFLSIL
SLVSDDAEISMHTDGNIKIADTRSTVYWPAADKSTIVFPNKPIQFP

>d1b77a2 d.131.1.2 (A:111-228) gp45 sliding clamp {Bacteriophage RB69}

VASVITEIKAEDLQQLLRVSRGLQIDTIAITNKDGKIVINGYNKVEDSGLTRPKYSLTLTDYD
GSNNFNFINMANMKIQPGNYKVMLWGAGDKVAAKFESSQVSYVIAMEADSTHDF

>d1dmla1 d.131.1.2 (A:29-169) UL42 {Human herpes virus type 1}

APCQVVLQGAELNGILQAFAPLRTSLDSSLVMGDRGILIHNTIFGEQVFLPLEHSQFSRYR
WRGPTAAFLSLVDQKRSLLSVFRANQYPDLRRVELAITGQAPFRTLVRQRIWTTTSDGEAVE

LASETLMKRELTSFVVLV

>d1dmla2 d.131.1.2 (A:170-319) UL42 {Human herpes virus type 1}

PQGTPDVQLRLTRPQLTKVLNATGADSATPTTFELGVNGKFSVFTTSTCVTFAAREEGVSS
STSTQVQILSNALTKAGQAAANAKTVYGENTHRTFSVVVDDDCSMRAVLRRRLQVGGGTLK
FFLTTPVPSLCVTATGPNAVSAVFLKPKQ

>d1plq_1 d.131.1.2 (1-126) Prolifirating cell nuclear antigen (PCNA) {Baker's yeast
(*Saccharomyces cerevisiae*)}

MLEAKFEEASLFKRIIDGFKDCVQLVNFQCKEDGIIAQAVDDSRVLLVSLEIGVEAFQEYRC
DHPVTLGMDLTSLSKILRCGNNTDTLTLIADNTPDSIILLFEDTKKDRIA EYSLKLMDIDAD
FL

>d1plq_2 d.131.1.2 (127-258) Prolifirating cell nuclear antigen (PCNA) {Baker's yeast
(*Saccharomyces cerevisiae*)}

KIEELQYDSTLSLPSEFSKIVRDLSQLSDSINIMITKETIKFVADGDIGSGSVIIKPFVDM EHP
ETSIKLEMDQPVDLTFGAKYLLDIIKGSSLSDRV GIRLSSEAPALFQFDLKSGFLQFFLAPKF
NDEE

>d1axca1 d.131.1.2 (A:1-126) Prolifirating cell nuclear antigen (PCNA) {Human (*Homo sapiens*)}

MFEARLVQGSILKKVLEALKDLINEACWDISSSGVNLQSMDSHVSLSVQLTLRSEGFDTYR
CDRNLAMGVNLTSMSKILKCAGNEDIITLRAEDNADTLALVFEAPNQEKVSDYEMKLMD
LDVEQL

>d1axca2 d.131.1.2 (A:127-255) Prolifirating cell nuclear antigen (PCNA) {Human (*Homo sapiens*)}

GIPEQEYSCVVKMPSGEFARICRDL SHIGDAVVISCAKDG VKFSASGELGNNGNIKLSQTSN
VDKEEEAVTIEMNEPVQLTFALRYLNFFTKATPLSSTVTLSMSADVPLVVEYKIADMGHLK
YYLAPKI

>d1ge8a1 d.131.1.2 (A:2-117) Prolifirating cell nuclear antigen (PCNA) {Archaeon *Pyrococcus furiosus*}

PFEIVFEGAKEFAQLIDTASKLIDEAAFKVTE DGISM RAMDPSRVVLIDLNLPS SIFSKYE VV
EPETIGVNL DHLKKILKRGKAKDTLILKKGEENFLEITIQTATRTFRVPLID

>d1ge8a2 d.131.1.2 (A:126-247) Prolifirating cell nuclear antigen (PCNA) {Archaeon
Pyrococcus furiosus}

PELPFTAKVVVLGEVLKDAVKDASLVSDSIKFIARENEFIMKAEGETQEVEIKLTLEDEGLL
DIEVQEETKSAYGVSYSMDVMKGLGKADEVTIKFGNEMPMQMEYYIRDEGRLTFL LAPR
V

>d1hlra4 d.133.1.1 (A:311-907) Aldehyde oxidoreductase {*Desulfovibrio gigas*}

MSGPAAAAEDAIEIHPGTPNVYFEQPIVKGEDTGPIFASADVTVEGDFYVGRQPHMPIEPD
VAFAYMGDDGKCYIHSKISIGVHLHLYMIAPGVGLEPDQLVLVANPMGGTFGYKFSPTSEA
LVAVAAMATGRP VHLYRYNYQQQQYTGKRSPWEMNVKFAAKKDGTLLAMESDWLV DH
GPYSEFGDLLTLRGAQFIGAGYNIPNIRGLGRTVATNHVWGS AFRGYGAPQSMFASECLM
DMLAEKLGMDPLELRYKNAYRPGDTNPTGQEPEVFSLPDMIDQLRPKYQA ALEKAQKES
TATHKKGVGISIGVYGSGLDGPDASEAWAELNADGTITVHTAWEDHGQGADIGCVGTAHE
ALRPMGVAPEKIKFTWPNTATTPNSGPSGGSREQVMTGN AIRVACENLLKACEKPGGGYY
TYDELKAADKPTKITGNWTASGATHCDAVTGLGKPFVVYMYGVFMAEVTVDVATGQTT
VDGMTLMADLGS LCNQLATDGQIYGGLAQGIGLALSEDFEDIKKHATLVGAGFPFIKQIPD

KLDIVYVNHPRPDGPFASGVGELPLTSPHAAIINAISATGVRIYRLPAYPEKVLEALKA
>d1fo4a5 d.133.1.1 (A:695-1332) Xanthine oxidase, C-terminal domain {Cow (Bos taurus)}
IITIEDAIKNSFYSGSELKIEKGLKKGFSEADNVVSGELYIGGQDHFYLETHCTIAIPKGEE
GEMELFVSTQNAMKTQSFVAKMLGVPVNRILVRVKRMGGGFGGKETRSTLVSVAVALAA
YKTGHPVRCMLDRNEDMLITGGRHPFLARYKVGFMKTGTIVALEVDHYSNAGNSRDLSH
SIMERALFHMDNCKIPNIRGTGRLOCKTNLSSNTAFRGFGGPQALFIAENWMSEVAVTCGL
PAEEVRWKNMYKEGDLTHFNQRLEGFSVPRCWDECLKSSQYYARKSEVDKFNKENCWK
KRGLCIPTKFGISFTVPFLNQAGALIHVYTDGSVLVSHGGTEMGQGLHTKMVQVASKAL
KIPISKIYISETSTNTVPNSSPTAASVSTDIYGQAVYEACQTILKRLEPFKKKNPDGSWEDW
VMAAYQDRVSLSTTGFYRTPNLGYSFETNSGNAFHYYFTYGVACSEVEIDCLTGDHKNLRT
DIVMDVGSSLNPAIDIGQVEGAFVQGLGLFTLEELHYSPEGSLHTRGPSTYKIPAFGSIPTF
RVSLLRDCPNKKAIYASKAVGEPPLFLGASVFFAIKDAIRAARAQHTNNNTKELFRLDSPAT
PEKIRNACVDKFTTLCVTGAPGNCKPWSLRV

>d1jrob2 d.133.1.1 (B:124-777) Xanthine dehydrogenase chain B, C-terminal domain
{Rhodobacter capsulatus}

PAITLDQALAADSRFEGGPVIWARGDVETALAGAAHLAEGCFEIGGQEHFYLEGQAALA
LPAEGGVVIHCSSQHPSEIQHKVAHALGLAFHDVRVEMRRMGGGFGGKESQGNHLAIAC
AVAARATGRPCKMRYDRDDDMVITGKRHDFRIRYRIGADASGKLLGADFVHLARCGWSA
DLSLPVCDRAMLHADGSYFVPALRIESHRLRTNTQSNTAFRGFGGPQGALGMERAIEHLA
RGMGRDPaelRALNFYDPPERGGLSAPSPPEPIATKKTQTTHYGGQEVADCVLGELVTRLQ
KSANFTTRRAEIAAWNSTNRTLARGIALSPVKFGISFTLTHLNQAGALVQIYTDGSVALNH
GGTEMGQGLHAKMVQVAAAVLGIDPVQVRITATDTSKVPNTSATAASSGADMNGMAVK
DACETLRGRLAGFVAAREGCAARDVIFDAGQVQASGKSWRFAEIVAAAYMARISLSATGF
YATPKLSWDRLRGQGRPFYFAYGAAITEVVIDRLTGENRILRTDILHDAGASLNPALDIGQ
IEGAYVQGAGWLTTEELVWDHCGRLMTHAPSTYKIPAFSDRPRIFNVALWDQPNREETIFR
SKAVGEPFPFLGISAFLALHDACAACGPHWPDLPATPEAVLAARRAEGR

>d1qj2b2 d.133.1.1 (B:147-809) Carbon monoxide (CO) dehydrogenase molybdo protein
{Pseudomonas carboxydovorans}

VDPFKAMEPDAPLLREDIKDKMTGAHGARKHHNHIFRWEIGDKEGTDATFAKAEVVS
MFTYHRVHPSPLETCQCVASMDKIKGELTLWGTFQAPHVIRTVVSLISGLPEHKIHVIAPDI
GGGFGNKVGAYSGYVCAVASIVLGVPVKWVEDRMENLSTTSFARDYHMTTELAATKD
GKILAMRCHVLADHGAFDACADPSKWPAGFMNICTGSYDMPVAHLAVDGVYTNKASGG
VAYRXSFRVTEAVYAIERIAETLAQRLEMDSADLRIKNFIQPEQFPYMAPLGWEYDSGNYP
LAMKKAMDTVGYHQLRAEQKAKQEAFAKRGRETREIMGIGISFFTEIVGAGPSKNCDILGVS
MFDSAEIRIHPTGSVIARMGTKSQGGGHETTYAQIIATELGIPADDIMIEEGNTDTAPYGLGT
YGRSTPTAGAAATAVAARKIKAKAQMIAAHMLEVHEGDLEWDVDRFRVKGLPEKFKTMK
ELAWASYNPPPNLEPGLEAVNYYDPPNMTYPFGAYFCIMDIDIDTGVAKTRRFYALDDCG
TRINPMIIEGQVHGGLTEAFAMGQEIYDEQGNVLGASFMDFLPTAVETPKWETDYTV
TPSPHHPIGAKGVGESPHVGGVPCFSNAVNDAYAFNLNAGHIQMPHDAWRLWKVGEQLGL
HV

>d1aop_3 d.134.1.1 (149-345) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4
{Escherichia coli}

NDMNRNVLCSTSNPYESQLHAEAYEWAKKISEHLLPRTRAYAEIWLDQEKVATTDEEPILG
QTYLPRKFKTTVVIPPQNDIDLHANDMNFVAIAENGKLVGFNLLVGGGLSIEHGNKKTYA

RTASEFGYLPLEHTLAVAEAVVTTQRDWGNRTDRKNAKTKYTLERVGVETFKAEVERRAGIKFEPIRPYEFTGRGDR

>dlaop_4 d.134.1.1 (426-570) Sulfite reductase hemoprotein (SiRHP), domains 2 and 4 {Escherichia coli}

PQRENSMACVSFPTCPLAMAEAEERFLPSFIDNIDNLMAKHGVSDEHIVMRVTGCPNGCGR
AMLAEVGLVGKAPGRYNLHLGGNRIGTRIPRMYKENITEPEILASLDELIGRWAKEREAGE
GFGDFTVRAGIIRPVLDPAARDLWD

>d1f0ia1 d.136.1.2 (A:6-263) Phospholipase D {Streptomyces sp.}

AATPHLDAVEQTLRQVSPGLEGDVWERTSGNKLDGSAADPSDWLLQTPGCWGDDKCAD
RVGTRKRLAKMTENIGNATRTVDISTLAPFPNGAFQDAIVAGLKESAAKGNLSLKVRILVGA
APVYHMGIPSKYRDKLTAKLGKAAENITLNVASMTTSKTAFSWNHSHKILVVDGQSALTG
GINSWKDDYLDTHPVSDVDLALTGPAAGSAGRYLDTLWTWTCNKNSNIASVWFAASGN
AGCMPTMHKDTNPKASPATG

>d1f0ia2 d.136.1.2 (A:264-514) Phospholipase D {Streptomyces sp.}

NVPVIAVGGLGVGIKDVDPKSTFRPDLPTASDTKCVVGLHDNTNADRDYDTVNPEESALR
ALVASAKGHIEISQQDLNATCPPLPRYDIRLYDALAAKMAAGVKVRIVSDPANRGAVGS
GGYSQIKSLSEISDTLRNRLANITGGQQAAKTAMCSNLQLATFRSSPNGKWADGHPYAQH
HKLVSVDSSFTFYIGSKNLYPSWLQDFGYIVESPEAAKQLDAKLLDPQWKYSQETATVDYAR
GICGA

>d1jy1a1 d.136.1.3 (A:145-350) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}

LEDPGEGQDIWDMLDKGNPFQFYLTRVSGVKPKYNSGALHIKDILSPLFGTLVSSAQFNYS
FDVDWLKQYPPEFRKKPILLVHGDKREKAHLHAQAKPYENISLCQAKLDIAFGTHHTK
MMLLLYEEGLRVVIHTSNLIHADWHQKTQGIWLSPLYPRIADGTHKSGESPTHFKANLISY
LTAYNAPSLKEWIDVIHKHDLSET

>d1jy1a2 d.136.1.3 (A:351-608) Tyrosyl-DNA phosphodiesterase TDP1 {Human (Homo sapiens)}

NVYLIGSTPGRFQGSQKDNWGHFRLKLLKDHASSMPNAESWPVVGQFSSVSGSLGADES
KWLCSEFKESMLTLGKESKTPGKSSVPLYLIYPSVENVRTSLEGYPAGGSLPYSIQTAEKQN
WLHSYFHKWSAETSGRSNAMPHIKTYMRSPDFSKIAWFLVTSANLSKAAWGALEKNGT
QLMIRSYELGVFLPSALGLDSFKVKQKFFAGSQEPMATFPVPYDLPPELYGSKDRPWIWN
IPYVKAPDTHGNMWVPS

>d1ckv__ d.137.1.1 (-) Soluble methane monooxygenase regulatory protein B {Escherichia coli}

MSVNSNAYDAGIMGLKGKDFADQFFADENQVVHESDTVVLVLKKSDEINTFIEEILLTDY
KKNVNPTVNVEDRAGYWWIKANGKIEVDCDEISELLGRQFNVDYFLVDVSSTIGRAYTL
GNKFTITSELMGLDRKLEDYHA

>d1g10a_ d.137.1.1 (A:) Toluene-4-monooxygenase catalytic effector protein {Pseudomonas mendocina}

STLADQALHNNNVGPIIRAGDLVEPVIETAEIDNPGKEITVEDRRAYVRIAAEGELILTRKTL
EEQLGRPFNMQELEINLASFAGQIQADEQIRFYFDKTM

>d1hqi__ d.137.1.1 (-) Phenol hydroxylase P2 protein {Pseudomonas sp., CF600}

MSSLVYIAFQDNDNARYVVEAIIQDNPHAVVQHHPAMIRIEAEKRLEIRRETVEENLGRAW
DVQEMLVDVITIGGNVDEDDDRFVLEWKN

>d1i94h_ d.140.1.1 (H:) Ribosomal protein S8 {Thermus thermophilus}

MLTDPIADMLTRIRNATRVYKESTEVPASRFKEILKILAREGFIKGYERVEVDGKPYLRIHL
KYGPRRQGPDRPEQVIKHIRRISRPGRRVYGVKEIPRVRRGLGAILSTPKGVLTDREAR

KLGVGGELICEVW

>d1i6ua_d.140.1.1 (A:) Ribosomal protein S8 {Archaeon Methanococcus jannaschii}
SLMDPLANALNHISNCERVGKKVYIKPASKLIGRVLKVMQDNGYIGEFEFIEDGRAGIFK
VELIGKINKCGAIKPRFPVKKFGYEKFEKRYLPARDFGILIVSTTQGVMSHEEAKKRGLGG
RLLAYVY

>d1rl6a1 d.141.1.1 (A:7-81) Ribosomal protein L6 {Bacillus stearothermophilus}
PIEIPAGVTVTNNGNTVTVKGPKGELTRTFHPDMTITVEGNVITVTRPSDEKHHRALHGTT
RSLLANMVEGVSKG

>d1rl6a2 d.141.1.1 (A:82-170) Ribosomal protein L6 {Bacillus stearothermophilus}
YEKALELVGVGYRASKQGKKLVLSVGYSHPVEIEPEEGLEIEVPSQTKIIVKGADKQRVGE
LAANIRAVRPPEPYKGKGIRYEGELVRL

>d1jj2e1 d.141.1.1 (E:1-79) Ribosomal protein L6 {Archaeon Haloarcula marismortui}
PRVELEIPEDVDAEQDHLDTVEGDNGSVTRRLWYPDIDVSDGDTVVIESDEDNAKTMS
TIGTFQSHIENMFHGVTEG

>d1jj2e2 d.141.1.1 (E:80-172) Ribosomal protein L6 {Archaeon Haloarcula marismortui}
WEYGMVEVFYSHFPMQVNVEGDEVVIENFLGEKAPRRTTIHGD TDVEIDGEELTVSGPDIE
AVGQTAADIEQLTRINDKDVRVFQDGVYITRKP

>d1gsa_2 d.142.1.1 (123-314) Glutathione synthetase {Escherichia coli}
NEKLFTAWFSDLTPETLVTRNKAQLKAFWEKHS DIILKPLDGMGGASIFRVKEGDPNLGVI
AETLTEHGTRYCMAQNYLPAIKDGD KRVLVVDGEPVPYCLARIPQGGETRGNLAAGGRG
EPRPLTESDWK IARQIGPTLKEKGLIFVGLDIIGDRLTEINVTSP TCIREIEAEFPVSITGMLM
DAIEARLQ

>d1iow_2 d.142.1.1 (97-306) D-ala-D-ala ligase {Escherichia coli, gene ddlB}
KLRSKLLWQGAGLPVAPWVALTRA EF EKGLSDKQLAEISALGLPVIVKPSREGSSVGMSK
VVAENALQDALRLAFQHDEEV LIEKWLSGPEFTVAILGEEILPSIRIQPSGTFYDYEA KFLS
DETQYFCPAGLEASQEANLQALVLKAWTTLGCKGWGRIDVMLDSDGQFYLL EANTSPG
MTSHSLVPMAARQAGMSFSQLVVRILELAD

>d1ehia2 d.142.1.1 (A:135-362) D-alanine:D-lactate ligase, VanA {Leuconostoc mesenteroides, Ddl2}
DKALT KELLTVNGIRNTKYIVDPESANNWSWDKIVAELGNIVFVKAANQGSSVGISRVT
NAE EYTEALSDSFQYDYKVLIEEAVNGARELEVGVIGNDQPLVSEIGAHTVPNQSGDGW
YDYN NKFVDNSAVHFQIP AQLSPEVTKEVKQMALDAYKVLNLRGEARMDFLLDEN NVP
YLGE PNTLPGFTNMSL FKR LWDYSDINNAKLVDMLIDYGFEDFAQNKKLS

>d1e4ea2 d.142.1.1 (A:132-342) D-alanine:D-lactate ligase, VanA {Enterococcus faecium}
DKSLTYIVAKNAGIATPAFWVINKDDRPVAATFTYPVFVKPARSGSSFGVKKVNSADELDY
AIESARQYDSKILIEQAVSGCEVGCAVLGNSAALVVG EVDQIRLQY GIFRIHQEVEPEKGSE
NAVITVPADLSAEERGRIQETVKKIYKTLGCRGLARVDMFLQDN GRIVLNEVNTLPGFTSY
SRYPRMMAAAGISLP ELIDRLIVLALK

>d1dv1a3 d.142.1.2 (A:115-330) Biotin carboxylase subunit of acetyl-CoA carboxylase {Escherichia coli}
DKVSAIAAMKKAGVPCVPGSDGPLGDDMDKNRAIAKRIGYPV IIKASGGGGGRGMRVVR
GDAELAQSISMTRAEAKAAFSNDMVYMEKYLENPRHVEIQVLADGQGNAIYLAERDCS

MQRRHQKVVEEAPAPGITPELRRYIGERCAKACVDIGYRGAGTFEFLFENGFEFYFIEMNTR
IQVEHPVTEMITGVDLIKEQLRIAAGQPLSIKQEEVHV

>d1gsoa3 d.142.1.2 (A:104-327) Glycinamide ribonucleotide synthetase (GAR-syn) {Escherichia coli}

SKAFTKDFLARHKIPTAEYQNFTEVEPALAYLREKGAPIVIKADGLAAGKGVIVAMTLEEA
EAAVHDMLAGNAFGDAGHRIVIEEFLDGEEASFIVMVDGEHVLPMATSQDHKRVGDKDT
GPNTGGMGAYSPAPVVTDDVHQRTMERIIWPTVKGMAAEGNTYTGFLYAGLMIDKQGNP
KVIEFNCRFGDLETQPIMLRMKSDLVELCLAACESKLDEKTSEWD

>d1b6ra3 d.142.1.2 (A:79-276) N5-carboxyaminoimidazole ribonucleotide synthetase, AIRC, PurK {Escherichia coli}

DRLTQKQLFDKLHLPTAPWQLLAERSEWPAVFDRLGELAIVKRRTGGYDGRGQWRLRAN
ETEQLPAECYGECIVEQGINFSGEVSLVGARGFDGSTVFYPLTHNLHQDGILRTSVAFPQAN
AQQQARAEEMLSAIMQELGYVGVMMAMECFVTPQGLLINELAPRVHNSGHWQTQNGASIS
QFELHLRAITDLPLPQPVV

>d1eyza3 d.142.1.2 (A:113-318) Glycinamide ribonucleotide transformylase PurT {Escherichia coli}

NREGIRRLAAEELQLPTSTYRFADSESLFREAVADIGYPCIVKPMSSSGKGQTFIRSAEQL
AQAWKYAQGGGRAGAGRVIVEGVVKFDFEITLLTVSAVDGVHFCAPVGHREQEDGDYRES
WQPQQMSPLALERAQEIARKVVLALGGYGLFGVELFVCGDEVIFSEVSPRPHDTGMVTLI
SQDLSEFALHVR AFLGLPVGGIRQY

>d1a9xa5 d.142.1.2 (A:128-402) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

DRRRFDVAMKKIGLETARSGIAHTMEEALAVAADVGFPCIRPSFTMGGSGGGIAYNREEF
EEICARGLDLSPTKELLIDESLIGWKEYEMEVRDKNDNCIIVCSIENFDAMGIHTGDSITV
APAQTLTDKEYQIMRNASMAVLREIGVETGGSNVQFAVNPKNRGLVIVEMNPRVSRSSALA
SKATGFPIAKVAAKLAVGYTLDELMNDITGGRTPASFEPSIDYVVTKIPRFNFEKFAGANDR
LTTQMKSVEVMAIGRTQQESLQKALRGL

>d1a9xa6 d.142.1.2 (A:677-935) Carbamoyl phosphate synthetase (CPS), large subunit {Escherichia coli}

RFQHAVERLKLKQPANATVTAIEMAVEKAKEIGYPLVVRAAMEIVYDEADLRRYFQTAVL
LDHFLDDAVEVDVDAICDGEMVLIGGIMEHIEQAGVHSGDSACSLPAYTSLSQEIQDVMRQ
QVQKLAFELQVRGLMNVQFAVKNNEVYLIEVNPRAARTVPFVSKATGVPLAKVAARVMA
GKSLAEQGVTKVIPPYYSVKEVVLFPNKFPGVDPLLGPENRSTGEVMGVGRTFAEFAK
AQLGS

>d1jkjb2 d.142.1.4 (B:1-238) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Escherichia coli}

MNLHEYQAKQLFARYGLPAPVGYACTTPREAEAAASKIGAGPWVVKCQVHAGGRGKAG
GVKVVNSKEDIRAFANWLGKRLVTYQTDANGQPVNQILVEAATDIAKELYLGAVVDRSS
RRVVFMASTEGGVEIEKVAEETPHLIHKVALDPLTGPMPLYQGRELAFKLGLEGKLVQQFT
KIFMGLATIFLERDLALIEINPLVITKQGDLCIDGKLGADGNALFRQPDIREMRDQSQE

>d1eucb2 d.142.1.4 (B:0-245) Succinyl-CoA synthetase, beta-chain, N-terminal domain {Pig (Sus scrofa)}

MVNLQEYQSKKLMSDNGVKVQRFFVADTANEALEAAKRLNAKEIVLKAQILAGGRGKG
VFSSGLKGGVHLTKDPEVVGQLAKQMIGYNLATKQTPKEGVKVNKMVAEALDISRETY

LAILMDRSCNGPVLVGSPQGGVDIEEVAASNPELIFKEQIDIIEGIKDSQAQRMAENLGFLG
PLQNQAADQIKKLYNLFLKIDATQVEVNPFGETPEGQVVCFDAKINFDDNAEFRQKDIFA
MDDKSEN

>d2hgsa2 d.142.1.6 (A:304-474) Eukaryotic glutathione synthetase {Human (Homo sapiens)}
TKKVQQELSRPGMLEMLLPQGPEAVARLRATFAGLYSLDVGEEGDQAIAEALAAPSRFVL
KPQREGGNNLYGEEMVQALKQLKDSEERASYILMEKIEPEPFENCLLRPGSPARVVQCIS
ELGIFGVYVRQEKTLMNKHVGHLLRTKAIEHADGGVAAGVAVLDNPYPV

>d2hgsa3 d.142.1.6 (A:3-201) Eukaryotic glutathione synthetase {Human (Homo sapiens)}
TNWGSLLQDKQQLEELARQAVDRALAEGVLLRTSQEPTSSEVVSYAPFTLFPSPVPSALLE
QAYAVQMDFNLLVDVAVSQNAAFLEQTLSSSTIKQDDFTARLFDIHKQVLKEGIAQTVFLGLN
RSDYMFQRSADGSPALKQIEINTISASFGLASRTPAVHRHVLSVLSKTKEAGKILSNPNPSK
GLALGIAKAWELYGS

>d1a0i_2 d.142.2.1 (2-240) ATP-dependent DNA ligase, N-terminal domain {Bacteriophage T7}
VNIKTNPFKAVSFVESAIKKALDNAGYLIAEIKYDGVGRNICVDNTANSYWLRSVSKTIPA
LEHLNGFDVRWKRLNDDRCFYKDGFMLDGELMVKGVDFTGSGLLRTKWTDTKNQE
FHEELFVEPIRKDKVPFKLHTGHLHIKLYAILPLHIVESGEDCDVMTLLMQEHVKNMPLPL
LQEYFPEIEWQAAESYEVYDMVELQQLYEQKRAEGHEGLIVKDPMCITYKRGKSGWWK
MK

>d1fvia2 d.142.2.1 (A:2-189) ATP-dependent DNA ligase, N-terminal domain {Chlorella virus,
PBCV-1}
AITKPLLAATLENIEDVQFPCLATPKIAGIRSVKQTQMLSRTFKPIRNSVMNRLLTPELLPEGS
DGEISIEGATFQDTTSAVMTGHKMYNAKFSYYWFDYVTDPLKKYIDRVEDMKNYITVH
PHILEHAQVKIIPVEINNITELLQYERDVLSKGFEGVMIRKPDGKYKFRSTLKEGILLK
MKQ

>d1blxa_ d.144.1.1 (A:) Cyclin-dependent PK (CDK, different isozymes) {Human (Homo sapiens)}
GLCRADQQYECVAEIGEGAYGKVFKARDLKNNGRFVALKRVRVQTGEEGMPLSTIREVAV
LRHLETFEHPNVVRLFDVCTVSRTDRETKLTLVFEHVDQDLTTYLDKVPEPGVPTETIKDM
MFQLLRGLDFLHSHRVHRDLKPQNILVTSSGQIKLADFGGLARIYSFQMALTSVVVTLWY
RAPEVLLQSSYATPVDLWSVGCIFAEMFRRKPLFRGSSDVDQLGKILDVIGLPGEEDWPRD
VALPRQAFHSSKSAQPIEFVTDIDELGKDLLKCLTFNPAKRISAYSALSHPYFQDLERCKE
N

>d1apme_ d.144.1.1 (E:) cAMP-dependent PK, catalytic subunit {Mouse (Mus musculus)}
SEQESVKEFLAKAKEDFLKKWETPSQNTAQLDQFDRIKTLGTGSFGRVMLVKHKESGNH
YAMKILDKQKVVKLKQIEHTLNEKRILQAVNFPFLVKLEFSFKDNSNLYMVMEYVAGGE
MFSHLRRIGRFAEPHARFYAAQIVLTFEYLHSLDLIYRDLKPENLLIDQQGYIQVTDGFAK
RVKGRWTLCGTPEYLAPEIILSKGYNKAVDWWALGVLIYEMAAGYPPFFADQPIQIYEKI
VSGKVRFPSPHFSSDLKDLLRNLLQVDLTKRFGNLKNGVNDIKNHKWFATTDWIAIYQRKV
EAPFIPKFKGPGDTSNFDDYEEEEIRVSINEKCGKEFTEF

>d1a06__ d.144.1.1 (-) Calmodulin-dependent protein kinase {Rat (Rattus norvegicus)}
WKQAEDIRDIYDFRDVLGTGAFSEVILAEDKRTQKLVAIKCIAKKALEGKEGSMENEIAVL
HKIKHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIVEKGFYTERDASRLIFQVLDAVKYL
HDLGIVHRDLKPENLLYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTPGYVAPEVLAQK
PYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPLYWDDISDSAKDFIRH
LMEKDPEKRFTCEQALQHPWIAGDTALDKNIHQSVSEQIKKNFAKSKWKQAFNATAVVR

HM

>d1ia8a_ d.144.1.1 (A:) Cell cycle checkpoint kinase chk1 {Human (Homo sapiens)}

AVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEA VAVKIVDMKRAVDCPENIKKEICINKM
LNHENVVKFYGHRREGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFFHQLMAGVVYL
HGIGITHRDIKPENLLDRLDNLKISDFGLATVFRYNNRERLLNKMCGTLPYVAPELLKRR
EFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKKTYLNPWKKIDSAPLAL
LHKILVENPSARITIPDIKKDRWYNKPLKKGAKRP

>d1phk__ d.144.1.1 (-) gamma-subunit of glycogen phosphorylase kinase (Phk) {Rabbit (Oryctolagus cuniculus)}

FYENYEPKEILGRGVSSVVRRCIHKPTCKEYAVKIIDVTGGGSFSAEEVQELREATLKEVDI
LRKVS GHPNIIQLKDTYETNTFFFLVFDLMKKGELFDYLTEKVTLSEKETRKIMRALLEVIC
ALHKL NIVHRDLKPENILLDDDMNIKLTDGFGSCQLDPGEKLREVC GTPSYLAPEIIEC SMN
DNHPGYGKEVDMWSTGVIMYTLLAGSPFWHRKQMLMLRMIMSGNYQFGSPEWDDYS
DTV KDLVSRFLVVQPQKRYTAEELAHPPFQQYV

>d1h8fa_ d.144.1.1 (A:) Glycogen synthase kinase-3 beta (Gsk3b) {Human (Homo sapiens)}

SKVTTTVVATPGQGPD RPQEVSYTDTKVIGNSGFGVVYQAKLCDSGELVAIKKVLQGKAFK
NRELQIMRKLDHCNIVRLRYFFYSSGEKKDEVYLNVLVDYVPETVYRVARHYSRAKQTL P
VIYVKLYMYQLFRSLAYIHSFGICHRDIKPQNLLLDPD TAVLKLCDFGSAKQLVRGEPNVS
YICSRYYRAPELIFGATDYTSSIDVWSAGCVLAELLGQPIFP GDSGVDQLVEIHKVLGTPTR
EQIREMNP NYTEFAFPQIK AHPWTKVFRPRTPEAIALCSRLL EYTP TARLTPLEACAH SFF
DEL RDPNVKLPNGRDTPALFNFTTQELSSNPPLATILIPPHARIQA

>d1tkia_ d.144.1.1 (A:) Titin, kinase domain {Human (Homo sapiens)}

KELYEKYMIAEDLGRGEFGIVHRCVETSSKKT YMAKFVKVKGTDQVLVKKEISILNIARH
RNILHLHESFESMEELVMIFEFISGLDIFERINTSA FELNEREIVSYVHQVCEALQFLHSHNIG
HFDIRPENI IYQTRRSSTIKIIEFGQARQLKPGDNFRLLFTAPEYYAPEVHQHDVVSTATDM
WSLGT LVYVLLSGINPFLAETNQ QIIENIMNAEYTFDEEAFKEISIEAMDFVDRLLV KERKS
RMTASEALQHPWLKQKIERVSTKVIRTLKHRRYYHTLIKKDLNMVVSAA RISC GGAIR SQ
KGVSVAKVKVASI

>d1koba_ d.144.1.1 (A:) Twitchin, kinase domain {California sea hare (Aplysia californica), twk43}

INDYDKFYEDIWKKYVPQPVEVKQGSVYDYYDILEELGSGAFGVVHRCVEKATGRVFVA
KFINTPYPLDKYTVKNEISIMNQLHHPKLINLHDAFEDKYEMVLILEFLSGGELFDRIAAED
YKMSEAEVINYMRQACEGLKHMHEHSIVHLDIKPENIMCETKKASSVKIIDFGLATKLP
DEIVKVT TATAEFAAPEIVDREPVG FYTDMWAIGVLGYVLLSGLSPFAGEDDLET LQNVKR
CDWEFDEDAFSSVSPEAKDFIKNLLQKEPRKRLTVHDALEHPWLKGDHSNLT SRIPSSRYN
KIRQKIKEKYADWPAPQPAIGRIANFSSLRKHRPQEYQIYDSYFDRKEAV

>d1jnk__ d.144.1.1 (-) c-jun N-terminal kinase (jnk3s) {Human (Homo sapiens)}

DNQFYSVEVG DSTFTVLKRYQNLKPIGSGAQGIVCAAYDAVLDRNVAIKKLSRPFQ NQTH
AKRAYRELVL MKCVNHKNII SLLNVFTPQKTLEEFQDVYLMELMDANLCQVIQMELDH
ERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVKS DCTLKILDFGLARTAGTSFM MTPYV
VTRY YRAPEVILGMGYKENVDIWSVGCIMGEMVRHKILFPGRDYIDQWNKVIEQLGTPC
PEFMKKLQPTVRNYVENRPKYAGLTFPKLFPDSLFPADSEHNKLKASQARDLLSKMLVIDP
AKRISVDDALQHPYINVWYDPAEVEAPPPQIYDKQLDEREHTIEEWKELIYKEVMN

>d1ckia_ d.144.1.1 (A:) Casein kinase-1, CK1 {Rat (Rattus norvegicus)}

MELRVGNRYRLGRKIGSGSFGDIYLGTDIAAGEEVAIKLECVKTKHPQLHIESKIYKMMQG
GVGIPTIRWCGAEGDYNVMVMELLGPSLEDLFNFCSRKFSLKTVLLADQMISRIEYIHSK
NFIHRDVKPDNFLMGLGKKGNLVYIIDFGLAKKYRDARTHQHIPPYRENKNLTGTARYASIN
THLGIEQSRDDLESGLGYVLMYFNLGSLPWQGLKAATKRQKYERISEKKMSTPIEVLCKG
YPSEFATYLNFCRSLRFDDKPDYSYLRQLFRNLFHRQGFSYDYVFDWNMLKFGASR

>d1a6o__ d.144.1.1 (-) Protein kinase CK2, alpha subunit {Maize (Zea mays)}

SKARVYADVNVLRPKEYWDYEALTQWGEQDDYEVVRKVGRGKYSEVFEGINVNNNE
KCIHKILKPVKKKKIKREIKILQNLCGGPNIVKLLDIVRDQHSKTPSLIFEYVNNTDFKVLYP
TLTDYDIRYYIYELLKALDYCHSQGIMHRDVKPHNVIMIDHELKRLRLIDWGLAEFYHPGK
EYNVRVASRYFKGPELLVDLQDYDYSLDMWSLGCMFAGMIFRKEPFFYGHNDHDLVKI
AKVLGTDGLNVYLNKYRIELDPQLEALVGRHSRKPWLKFMNADNQHLVSPEAIDFLDKL
LRYDHQERLTALEAMTHPYFQQVRAAENS

>d1b6cb_ d.144.1.1 (B:) Type I TGF-beta receptor R4 {Human (Homo sapiens)}

TTLKDLIYDMTTSGSGSGLPLLQRTIARTIVLQESIGKGRFGEVWRGKWRGEEVAVKIFSS
REERSWFREAIEYQTVMLRHENILGFIAADNKDNGTWTQLWLVS DYHEHGS LFDYLNRY
TVTVEGMIKLALSTASGLAHLHMEIVGTQGKPAIAHRDLKSKNILVKKNGTCCIADLGLAV
RHDSATDTIDIAPNHRVGTKRYMAPEVLDD SINMKHFESFKRADIYAMGLVFWEIARRCSI
GGIHEDYQLPYDLPSPDPSVEEMRKVVCEQKLRPNIPNRWQSCEALRVMAKIMREC WY
ANGAARLTALRIKKTLSQLSQEG

>d1f3mc_ d.144.1.1 (C:) pak1 {Human (Homo sapiens)}

SDEEILEKLRSIVSVGDPKKKYTRFEKIGQGASGTVYTAMDVATGQEVAIRQMNLQQQPK
KELIINEILVMRENKNPNIVNYLDSYLVGDELWVVM EYLAGGSLTDVVTETCMDEGQIAA
VCRECLQALEFLHSNQVIHRDIKSDNILLGMDG SVKLTDFG FCAQITPEQSKRSTMVGPY
WMAPEVVTRKAYGPKVDIWSLGIMAIEMIEGEPYLNENPLRALYLIATNGTPELQNPEKL
SAIFRDFLNRCLDM DVEKRGSAKELLQH QFLKIAKPLSSLTPLIAAAKEATK

>d1howa_ d.144.1.1 (A:) Skyp1 {Baker's yeast (Saccharomyces cerevisiae)}

FHPAFKGEPYKDARYILVRKLGWGHFSTVWLAKDMVNNTHVAMKIVRGDKVYTEAAED
EIKLLQRVNDADNTKEDSMGANHILKLLDHFHNHKGPNGVHVVMMVFEVLGENLLALIKKY
EHRGIPLIYVKQISKQLLLGLDYMHRRCGIIHTDIKPENVLMEIVDSPENLIQIKIADLGNAC
WYDEHYTNSIQTREYRSPEVLLGAPWGCGADIWSTACLIFELITGDFLFEPDEGHSYTKDD
DHIAQIIELLGELPSYLLRNGKYTRTFFNSRGLLRNISKLFKFWPLEDVLTEKYKFSKDEAKE
ISDFLSPMLQLDPRKRADAGGLVNHPWLKDTLGMEEIRVPDRELYGSGSDIPGWFEFEEVR

>d1vr2a_ d.144.1.2 (A:) Vascular endothelial growth factor receptor 2 (kdr) {Human (Homo sapiens)}

LPYDASKWEFPRDRLKLGKPLGRGAFGQVIEADAFGIDKTATCRTCRTVAVKMLKEGATHSEH
RALMSELKILIHIGHHLNVVNLLGACTKPGGPLMVIVEFCKFGNLSTYLRSKRNEFVPYKV
APEDLYKDFLTLEHLICYSFQVAKGMEFLASRCKIHRDLAARNILLSEKNVVKICDFGLAR
DIYKDPDYVRKGDARLPLKWMAPETIFDRVYTIQSDVWSFGVLLWEIFSLGASYPGVKI
DEEFCRRLKEGTRMRAPDYTTPEMYQTMDCWHGEPSQRPTFSELVEHLGNLLQANA

>d1ir3a_ d.144.1.2 (A:) Insulin receptor {Human (Homo sapiens)}

SSVFVPDEWEVSREKITLLRELQGSGFMVYEGNARDIIKGEAETRVAVKTVNESASLRER
IEFLNEASVMKGFTCHHVVRLLGVVSKGQPTLVVMELMAHGDLKSYLRSLRPEAENNP
RPPPTLQEMIQMAAEIADGMAYLNAKKFVHRDLAARNCMVAHDFTVKIGDFGMTRDIYE
TDYYRKGGKGLLPVRWMAPESLKDG VFTTSSDMWSFGVVLWEITSLAEQPYQGLSNEQ

VLKFVMDGGYLDQPDNCPERVTDLMRMCWQFNPKMRPTFLEIVNLLKDDLHPSFPEVSF
FHSEENK

>d1byga_d.144.1.2 (A:) C-terminal src kinase (csk) {Human (Homo sapiens)}

GWALNMKELKLLQTIGKGEFGDVMLGDYRGNKVAVKCIKNDAQAFLAEASVMTQLR
HSNLVQLLGVIVEEEKGGLYIVTEYMAKGSLVDYLRSGRSVLGGDCLLKFSLDVCEAMEY
LEGNFVHRDLAARNVLVSEDNVAKVSDFGLTKEASSTQDTGKLPVKWTAPEALREKKF
STKSDVWSFGILLWEIYSFGRVPYPRIPKDVVPRVEKGYKMDAPDGCPPAVYEVMKNCW
HLDAAMRPSFLQLREQLEHIKTHEL

>d1jpaa_d.144.1.2 (A:) ephb2 receptor tyrosine kinase {Mouse (Mus musculus)}

KIFIDPFTFEDPNEAVREFAKEIDISCVKIEQVIGAGEFGEVCSGHLKLPKREIFVAIKTLKS
GYTEKQRRDFLSEASIMGQFDHPNVIHLEGVVTKSTPVMITEFMENGSLDSFLRQNDGQF
TVIQLVGMLRGIAAGMKYLADMNYVHRDLAARNILVNSNLVCKVSDFGLSRFLEDDTSD
PTYTSALGGKIPRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYWDMTNQDVI
NAIEQDYRLPPPMDCPSALHQLMLDCWQKDRNHRPKFGQIVNTLDKMIRNPNSLKA

>d1fvra_d.144.1.2 (A:) Tie2 kinase {Human (Homo sapiens)}

PTIYPVLDWNDIKFQDVIGEGNFGQVLKARIKKDGLRMDAAIKRMKEYASKDDHRDFAG
ELEVLCCLGHHPNIINLLGACEHRGYLYLAIEYAPHGNLLDFLRKSRVLETDPAFAIANSTA
STLSSQQLLHFAADVARGMDYLSQKQFIHRDLAARNILVGENYVAKIADFGLSRGQEVYV
KKTMGRLPVRWMAIESLNSVYTTNSDVWSYGVLLWEIVSLGGTPYCGMTCAELYEKL
QGYRLEKPLNCDDEVYDLMRQCWREKPYERPSFAQILVSLNRMLEERKTYVNTTLYEKF
TYAGIDCSAE

>d1e8ga2 d.145.1.1 (A:6-273) Vanillyl-alcohol oxidase {Fungus (Penicillium
simplicissimum)}

EFRPLTLPPKLSLSDFNEFIQDIIRIVGSENVVEISSKDQIVDGSYMKPTHTHDPHVMDDQD
YFLASAIVAPRNVADVQSIVGLANKFSFPLWPISIGRNSGYGGAAPRVSGSVVLDMGKNM
NRVLEVNVEGAYCVVEPGVTYHDLHNYLEANNLRDKLWLDVDPDLGGGSVLGNAVERGV
GYTPYGDHWMHSGMEVVLANGELLRTGMGALPDPKRPETMGLKPEDQPWSKIAHLFP
YGFPGPYIDGLFSQSNMGIVTKIGIWLMPNP

>d1f0xa2 d.145.1.1 (A:9-273) D-lactate dehydrogenase {Escherichia coli}

NKAFLNELARLVGSSHLTDPAKTARYRKGRSGQGDALAVVFPGLLELWRVLKACVTA
DKIILMQAANTGLTEGSTPNGNDYDRDVVHISTLRDLKLHVLGKGEQVLAYPGTTLYSLEK
ALKPLGREPHSVIGSSCIGASVIGGICNNSGGSLVQRGPAYTEMSLFARINEDGKLTLVNHL
GIDLGETPEQILSKLDDDDRIKDDDVHRHDGRHAHDYDYVHRVRDIEADTPARYNADPDRLF
ESSGCAGKLAVFAVRLDTFEAE

>d1i19a2 d.145.1.1 (A:57-273) Cholesterol oxidase {Brevibacterium sterolicum}

VAPLPTPPNFPNDIALFQQAYQNWSKEIMLDATWVCSPKTPQDVVRLANWAHEHDYKIRP
RGAMHGWTPLTVEKGANVEKVILADTMTHLNGITVNTGGPVATVTAGAGASIEAIVTELQ
KHDLGWANLPAPGVLSIGGALAVNAHGAALPAVGQTTLPGHTYGSLSNLVTELTAVVWN
GTTYALETYQRNDPRITPLLTNLGRCFLTSTVMQAGPN

>d1luxy_1 d.145.1.2 (3-200) Uridine diphospho-N-
Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain {Escherichia
coli}

HSLKPWNTEFGIDHNAQHIVCAEDEQQLLNAWQYATAEGQPVLILGEGSNVLFLEDYRGTV
IINRIKGIEIHDEPDWYLVHVGAGENWHRLVKYTLQEGMPGLENLALIPGCVGSSPIQNIG

AYGVELQRVCA YVDSVELATGKQVRLTAKECRFGYRDSIFKHEYQDRFAIVAVGLRLPKE
WQPVLT YGDLTRLDPPT

>d1hska1 d.145.1.2 (A:15-208) Uridine diphospho-N-
Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
{Staphylococcus aureus}

NKDIYQALQQLIPNEKIKVDEPLKRYTYTKTGGNADFYITPTKNEEVQAVVKYAYQNEIPV
TYLGNGSNIIREGGIRGIVISLLSLDHIEVSDDAIAGSGAAIIDVSRVARDYALTGLEFACGI
PGSIGGAVYMNAGAYGGEVKDCIDYALCVNEQGS LIKLT TKELELDYRNSIIQKEHLVVLE
AAFTLAP

>d1qj2c2 d.145.1.3 (C:1-177) Carbon monoxide (CO) dehydrogenase flavoprotein, N-terminal
domain {Pseudomonas carboxydovorans}

MIPGSFDYHRPKSIADAVALLT KLGEDARPLAGGHSLIPIMKTRLATPEHLVDLRDIGDLVG
IREEGTDVVIGAMTTQHALIGSDFLA AKLPIRETSLLIADPQIRYMGTIGGNAANGDPGND
MPALMQCLGAAYELTGPEGARIVAARDYYQGAYFTAIEPGELLTAIRIPVPPT

>d1fo4a6 d.145.1.3 (A:192-414) Xanthine oxidase, domain 3 (?) {Cow (Bos taurus)}

SPSLFNPEEFMPLDPTQEPIFPPELLRLKDVPPKQLRFEGERV TWIQA STLKELLDLKAQHP
EAKLVVGNTEIGIEMKFKNQLFPMIICPAWIPELNAVEHGPEGISFGAACALSSVEKTLLEA
VAKLPTQKTEVFRGVLEQLRWFA GKQVKSVASLG GNIITASPISDLNPVFMASGTKLTIVSR
GTRRTVPMDH TFFPSYRK TLLGP EEILLSIEIPYSRE

>d1jroa4 d.145.1.3 (A:179-345) Xanthine dehydrogenase chain A, domain 3 {Rhodobacter
capsulatus}

PAFLPETS DALADWYLAHPEATLIAGGTDVSLWVTKALRDLPEVAFLSHCKDLAQIRETPD
GYGIGAGVTIAALRAFAEGPHPALAGLLRRFASEQVRQVATIGGNIANGSPIGDGP PALIAM
GASLT LRRGQERRRM PLEDF FLEYRKQDRRPGEFVESVTLPKSA

>d1luxy_2 d.146.1.1 (201-342) Uridine diphospho-N-
Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
{Escherichia coli}

VTPQQVFNAVCHMRTTKLPDPKVNGNAGAFFKNPVVSAETAKALLSQFPTAPNYPQADG
SVKLAAGWLIDQCQLKGMQIGGA AVHRQQALVLINEDNAKSE DVVQLAHHVRQKVGEK
FNVWLEPEVRFIGASGEVSAVETIS

>d1hska2 d.146.1.1 (A:209-317) Uridine diphospho-N-
Acetylenolpyruvylglucosamine reductase, MurB, C-terminal domain
{Staphylococcus aureus}

GKMTEIQAKMDDLTERRESKQPLEY PSCGSVFQRPPGHFAGKLIQDSNLQGHRIGGVEVS
TKHAGFMVNVDNGTATDYENLIHYVQKTVKEKFGIELNREVRIIG EHPK

>d1qr0a1 d.150.1.1 (A:1-101) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

MKIYGIYMDRPLSQEENERFMTFISPEKREKRRFYHKEDAHRTLLGDV LVRSVISRQYQL
DKSDIRFSTQEY GKPCIPDL PDAHFNISHSGRWVIGAFDS

>d1qr0a2 d.150.1.1 (A:102-228) 4'-Phosphopantetheinyl transferase SFP {Bacillus subtilis}

QPIGIDIEKTKPISLEIAKRFFSKTEYS DLLAKDKDEQTDYFYHLWSMKESFIKQEGKGLSL
PLDSFSVRLHQDGQVSIELPD SHSPCYIKTYEVDPGYKMAVCAAH PDPEDITMVS YEELL
RAAA

>d1ako__ d.151.1.1 (-) DNA-repair enzyme exonuclease III {Escherichia coli}

MKFVSFNINGLRARPHQLEAIVEKHQPDVIGLQETKVHDDMFPLEEVAKLGYNV FYHGQ

KGHYGVALLTKETPIAVRRGFPGDDEEAQRRIIMAEIPSLGNVTVINGYFPQGESRDHPIK
FPAKAQFYQNLQNYLETELKRDNPVLMGDMNISPTDLDIGIGEENRKRWLRTGKCSFLPE
EREWMDRMSWGLVDTRHANPQTADRFSWFDYRSKGFDDNRGLRIDLLLASQPLAEC
CVETGIDYEIRSMEKPSDHAPVWATFR

>d1hd7a_ d.151.1.1 (A:) DNA repair endonuclease Hap1 {Human (Homo sapiens)}

LYEDPPDQKTSPSGKPATLKICSWNVDGLRAWIKKKGLDWVKEEAPDILCLQETKCSENK
LPAELQELPGLSHQYWSAPSDKEGYSGVGLLSRQCPLKVSYGIGDEEHDQEGRVIVAEFDS
FVLVTAYVPNAGRGLVRLEYRQRWDEAFRKFLKGLASRKPLVLCGDLNVAHEEIDLRNPK
GNKKNAGFTPQERQGFGEELLQAVPLADSFRLYPNTPYAYTFWTYMMNARSKNVGWRL
DYFLLSHSLLPALCDSKIRSKALGSDHCPITLYLAL

>d2dnja_ d.151.1.1 (A:) Deoxyribonuclease I {Cow (Bos taurus)}

LKIAAFNIRTFGETKMSNATLASIYIVRIVRRYDIVLIQEVDRSHLVAVGKLLDYLNQDDPNT
YHYVVSEPLGRNSYKERYLFLFRPNKVSVDLTYQYDDGCESCND SFSREPAVVKFSSHS
TKVKEFAIVALHSAPSDAVAEINSLYDVYLDVQQKWHLNDVMLMGDFNADCSYVTSSQW
SSIRLRTSSTFQWLIPDSADTTATSTNCAYDRIVVAGSLLQSSVVPGSAAPFDFQAAYGLSN
EMALAISDHYPVEVTLT

>d1gdoa_ d.153.1.1 (A:) Glucosamine 6-phosphate synthase, N-terminal domain {Escherichia coli}
CGIVGAIAQRDVAEILLEGRLRLEYRGYDSAGLAVVDAEGHMTRLRRLGKVQMLAQAAE
EHPLHGGTGIAHTRWATHGEPSEVNAHPHVSEHIVVVHNGIENHEPLREELKARGYTFVS
ETDTEVIAHLVNWELKQGGTLREAVLRAIPQLRGAYGTVMDSRHPDTLLAARSGSPLVIG
LGMGENFIASDQLALLPVTRRFIFLEEGDIAEITRRSVNIFDKTGAEVKRQDIESNL

>d1gph12 d.153.1.1 (1:1-234) Glutamine PRPP amidotransferase, N-terminal domain
{Bacillus subtilis}

CGVFGIWGHEEAPQITYYGLHSLQHRGQEGAGIVATDGEKLTAKGQGLITEVFQNGELS
KVKGKGAIGHVRYATAGGGGYENVQPLLFRSQNNGSLALAHNGNLVNATQLKQQLENQ
GSIFQTSSDTEVLAHLIKRSGHFTLKDQIKNSLSMLKGAYAFLIMTETEMIVALDPNGLRPL
SIGMMGDAYVVASETCAFDVVGATYLREVEPGEMLIINDEGMKSERFSMNINRS

>d1ecfa2 d.153.1.1 (A:1-249) Glutamine PRPP amidotransferase, N-terminal domain
{Escherichia coli}

CGIVGIAGVMPVNQSIYDALTVLQHRGQDAAGIITIDANNCFRRLRKANGLVSDVFEARHM
QRLQGNMGIGHVRYPTAGSSSASEAQPFYVNSPYGITLAHNGNLNAHELKKLFEEKRR
HINTTSDSEILLNIFASELDNFRHYPLEADNIFAAIAATNRLIRGAYACVAMIIGHGMVAFRD
PNGIRPLVLGKRIDENRTEYMVASESVALDTLGFDFLRDVAPGEAIYITEEGQLFTRQCAD
NPVS

>d1ct9a2 d.153.1.1 (A:1-192) Asparagine synthetase B, N-terminal domain {Escherichia coli}

ASIFGVFDIKTDAVELRKKALELSRLMRHRGPDWSGIYASDNAILAHERLSIVDVNAGAQF
LYNQKQKTHVLAVNGEIYNHQALRAEYGDYQFQTGSDCEVILALYQEKGPFLDDLQGM
FAFALYDSEKDAYLIGRDHLGIIPLYMGYDEHGQLYVASEMKALVPVCRTIKEFPAGSYLW
SQDGEIRSYH

>d1jga2 d.153.1.1 (A:4-209) beta-Lactam synthetase {Streptomyces clavuligerus}

PVLPAAFGFLASARTGGGRAPGVFATRGSHTDIDTPQGERSLAATLVHAPSVAPDRAVARS
LTGAPTTAVLAGEIYNRDELLSVLPAGPAPEGDAELVLRLLERYDLHAFRLVNGRFATVVR
TGDRVLLATDHAGSVPLYTCVAPGEVRASTEAKALAAHRDPKGFPLADARRVAGLTGVY
QVPAGAVMDIDLGS GTAVTHRTWT

>d1ea0a3 d.153.1.1 (A:1-422) Alpha subunit of glutamate synthase, N-terminal domain {Azospirillum brasilense}

CGVGFIAAIDGKPRRSVVEKGIEALKAVWHRGAVDADGKTGDGAGIHVAVPQKFFKDHV
KVIGHRAPDNKLAVGQVFLPRISLDAQEACRCIVETEILAFGYIYGWRQVPINVDIIGEKA
NATRPEIEQIIVGNNKGVSDQFELDLYIIRRIEKAVKGEQINDFYICSLSARSIIYKGMFLA
EQLTTFYPDLLDERFESDFAIYHQRYSTNTFTWPLAQPFRLAHNGEINTVKGNNVNMW
AHETRMEHPAFGTHMQDLKPVIGVGLSDSGSLDTVFEVMVRAGRTAPMVKMMLVLPQAL
TSSQTTPDNHKALIQYCNSVMEPWDGPAALAMTDGRWVVGMDRNLRLPMRYTITTDG
LIIGGSETGMVKIDETQVIEKGRLPGEMIAVDLQSGKLYRDRELKDHLATLKPWDKWWQ
N

>g1gk9.1 d.153.1.2 (A:,B:) Penicillin acylase {Escherichia coli}

QSSSEIKIVRDEYGMPHIYANDTWHLFYGYGYVVAQDRLFQMEMARRSTQGTVAEVLGK
DFVKFDKDIRRNYWPDAIRAQIAALSPEDMSILQGYADGMNAWIDKVNTNPETLLPKQFN
TFGFTPKRWEPFDVAMIFVGTMANRFSdstSEIDNLALLTALKDKYGVSQGMVFNQLK
WLVNPSAPTTIAVQESNYPLKFNQQNSQTAXSNMWVIGKSKAQDAKAIMVNGPQFGWYA
PAYTYGIGLHGAGYDVTGNTPFAYPLVFGHNGVISWGSTAGFGDDVDIFAERLSAEKPG
YYLHNGKWKMLSRREETITVKNGQAETFTVWRTVHGNILQTDQTTQTAYAKSRAWDGK
EVASLLAWTHQMKAKNWQEWtQQAQKQALINWYYADVNGNIGYVHTGAYPDRQSGH
DPRLPVPGTGKWDWKGLLPFEMNPKVYNPQSGYIANWNNSPQKDYPASDLFAFLWGGA
DRVTEIDRLLEQKPRLTADQAWDVIRQTSRQDLNRLFLPTLQAATSGLTQSDPRRQLVET
LTRWDGINLLNDGKTWQQPGSAILNVWLTSMLKRTVVAVPMFDPKWYSASGYETTQ
DGPTGSLNISVGAKILYEAVQGDKSPIQAVDLFAGKPQQEVLAALEDTWETLSKRYGN
NVSNNWKTAMALTFRANNFFGVPQAAAEETRHAQAEYQNRGTENDMIVFSPTTSDRPVLA
WDVVAPGQSGFIAPDGTVDKHYEDQLKMYENFGRKSLWLTQDVEAHKESQEVLVHVR

>g1fm2.1 d.153.1.2 (A:,B:) Cephalosporin acylase {Brevundimonas diminuta}

QAPIAAYKPRSNEILWDGYGVPHIYGVDAPSAFYGYGWAQARSHGDNILRLYGEARGKG
AEYWGPDIYEQTTVWLLTNGVPERAQQWYAQQSPDFRANLDAFAAGINAYAQQNPDDISP
EVRQVLPVSGADVVAHAHRLMNFlyVASPGRTLGXSNswAVAPGKTANGNALLLQNP
SWTTDYFTYYEAHLVTPDFEIIYGATQIGLPVIRFAFNQRMGITNTVNGMVGATNYRLTLQ
DGGYLYDGQVRPFERRQASYRLRQADGSTVDKPLEIRSSVHGPVFERADGTAVAVRVAGL
DRPGMLEQYFDMITAHSFDDYEAAMARMQVPTFNIVYADREGTINYSFNGVAPKRAEGDI
AFWQGNVPGDSSRYLWTETHPLDDLPRVTNPPGGFVQNSNDPPWTPTWPVTYCPANHPS
YLAPQTPHSLRAQQSVRLMSENDDTLERFMALQFSHRAVMADRTLPLIPAALIDPDPEV
QAAARLLAAWDRDFTSDSRAALLFEEWARLFAGQNFAGQAAFATPWSLDKPVSTPYGVR
DPKAAVDQLRTAIANTKRKYGAIDRPFGDASRMILNDVNVPGAAGYGNLGSFRVFTWSD
PDENGIRTPVHGETWVAMIEFSTPVRAYGLMSYGNSRQPGTTHYSDQIERVSRADFRELL
RREQVEAAVQERTPFNF

>d1pma1_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Archaeon Thermoplasma acidophilum}

TTTVGITLKDAVIMATERRTMENFIMHKNGKKLFQIDTYTGMTIAGLVGDAQVLVRYMK
AELELYRLQRRVNMPiEAVATLLSNMLNqVKYMPYMVQLLVGGIDTAPHVFSIDAAGGSV
EDIYASTGSGSPFVYGVLESQYSEKMTVDEGVDLVIRAISSAKQRDSASGGMIDVAVITRK
DGYVQLPTDQIESRIRKLGLIL

>d1ryp1_ d.153.1.4 (1:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces

cerevisiae)}}
 QFNPHYGDNGGTILGIAGEDFAVLAGDTRNITDYSINSRYEPKVFDNIVMSANGFAADG
 DALVKRFKNSVKWYHFDHNDKKLSINSAARNIQHLLYGKRFFPYVHTIAGLDEDEGKGA
 VYSFDPVGSYEREQCRAAGAAASLIMPFLDNQVNFKNQYEPGTNGKVKKPLKYLVSVEEV
 IKLVRDSFTSATERHIQVGDGLEILIVTKDGVKREFYELKRD
 >d1ryp2_ d.153.1.4 (2:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces
 cerevisiae)}}
 TQQPIVTGTSVISMKYDNGVIAADNLGSYGSLLRFNNGVERLIPVGDNTVVGISGDISDMQ
 HIERLLKDLVTENAYDNPLADAEAELEPSYIFEYLATVMYQRRSKMNPLWNAIIVAGVQS
 NGDQFLRYVNLGVTYSSPTLATGFGAHMANPLLRKVVDRES DIPKTTVQVAEEAIVNAM
 RVLRYRDARSSRNFS LAIIDKNTGLTFKKNLQVENMKWDFAKDIKGYGTQKI
 >d1ryph_ d.153.1.4 (H:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces
 cerevisiae)}}
 LKKGEVSLGASIMAVTFKDG VILGADSRTTGTGAYIANRVTDKLRVHDKIWCCRS GSAAD
 TQAIADIVQYHLELYTSQYGTPSTETAASVFKELCYENKDNLTAGIIVAGYDDKNKGEVYT
 IPLGGSVHKLPYAIAGSGSTFIYGYCDKNFRENMSKEETVDFIKHSLSQAIKW DGS SGGVIR
 MVVLTAAGVERLIFYPDEYEQL
 >d1rypi_ d.153.1.4 (I:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces
 cerevisiae)}}
 TTIVGVKFNNGVVIAADTRSTQGPIVADKNC AKLHRISPKIWCAGAGTAADTEAVTQLIGS
 NIELHSLYTSREPRVVSALQMLKQHLFKYQGHIGAYLIVAGVDPTGSHLFSIHAHGSTDVG
 YYLSLGSGSLAAMAVLESHWKQDLTKEEAIKLASDAIQAGIWNDLGSGSNVDVCVMEIG
 KDAEYLRNYLT PNVREEKQKSYKFPRTTAVLKESIVNICD
 >d1rypj_ d.153.1.4 (J:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces
 cerevisiae)}}
 SDPSSINGGIVVAMTGKDCVAIACDLRLGSQSLGVS NKFEKIFHYGHVFLGITGLATDVTTL
 NEMFRYKTNLYKLKEERAIEPETFTQLVSSSLYERRFGPYFVG PVVAGINSKSGKPFIAGFD
 LIGCIDEAKDFIVSGTASDQLFGMCESLYEPNLEPEDLFETISQALLNAADR DALSGWGAV
 VYIIKKDEVVKRYLKMRQD
 >d1rypk_ d.153.1.4 (K:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces
 cerevisiae)}}
 MDIILGIRVQDSVILASSKAVTRGISVLKDSDDKTRQLSPHTLMSFAGEAGDTVQFAEYIQA
 NIQLYSIREDYELSPQAVSSFVRQELAKSIRSRPYQVNVLIGGYDKKKNKPELYQIDYLG
 KVELPYGAHGYSGFYTFSLLDHHRPDMTTEGLDLLKLCVQELEKRMPMDFKGVIVKI
 VDKDGIRQVDDFQAQ
 >d1rypl_ d.153.1.4 (L:) Proteasome beta subunit (catalytic) {Baker's yeast (Saccharomyces
 cerevisiae)}}
 TTTLAFRFQGGIIVAVDSRATAGNWWASQTVKR VIEINPFL LGTMAGGAADCQFWETWLG
 SQCRLHELREKERISVAAASKILSNLVYQYKGAGLSMGTMICGYTRKEGPTIYYVDSGT
 RLKGDIFCVGSGQT FAYGVLD SNYKWDLSVEDALYLGKRSILAAHRDAYS GGSVNLYH
 VTEDGWYIHGNH DVGELFWKVKEEESFN NVIG
 >d1rypa_ d.153.1.4 (A:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces
 cerevisiae)}}
 AGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVPDKLLDPTTVS

YIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKRMANLSQIYTQ
RAYMRPLGVILTFVSVDEELGPSIYKTDPAGYVVGKATATGPKQQEITTNLENHFKSKI
DHINEESWEKVVEFAITHMIDALGTEFSKNDLEVG VATKDKFFTLAENIEERLVAIAEQD
>d1rypb_d.153.1.4 (B:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

MTDRYSFSLTTFSPSGKLGQIDYALTAVKQGVTS LGIKATNGVVIA TEKKSSSPLAMSETLS
KVSLLTPDIGAVYSGMGPDYRVLV DKS RKVAHTSYKRIYGEYPPTKLLVSEVAKIMQEATQ
SGGVRPFGVSLLIAGHDEFNGFSLYQVDP SGSYFPWKATAIGKGSVAAKT FLEKRWNDEL
ELED AIIHALLTLKESVEGEFNGDTIELAII GDENPDLLGYTG IPTDKGPRFRKLTSQEINDRL
EAL

>d1rypc_d.153.1.4 (C:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GSSRRYSRTTIFSP EGRLYQVEYALE SISHAGTAIGIMASDGIVLAAERKVTSTLLEQDTSTE
KLYKLNDKIAVAVAGLTADAEILINTARIHAQNYLKTYNEDIPVEILVRRLSDIKQGYTQHG
GLRPFVGSFIYAGYDDRYGYQLYTSNPSGNYTGWKAISVGANTSAAQTLLQMDYKDDM
KVDDAIELALKTL SKTTDSSALTYDRLEFATIRKGANDGEVYQKIFKPQEIKDILVKTGIT

>d1rypd_d.153.1.4 (D:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GYDRALSIFSPDGHIFQVEYALEAVKRGTC AVGVKGKNCVVLGCERRSTLKLQDTRITPSK
VSKIDSHVVLSFSGLNADSRILIEKARVEAQSHRLTLEDPVTVEYLTRYVAGVQQRYTQSG
GVRPFGVSTLIAGFDPRDDEPKLYQTEPSGIYSSWSAQ TIGRNSKTVREFLEKNYDRKEPPA
TVEECVKLTVRSLLEV VQTGAKNIEITVVKPDS DIVALSSEEINQYVTQIEQEKEQE

>d1rype_d.153.1.4 (E:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

DRGVSTFSPEGRLFQVEYSLEAIKLGSTAIGIATKEGVVLGV EKRATSP LLES DSIEKIVEIDR
HIGCAMSGLTADARSMIEHARTAAVTHNLYYDEDINVESTQSVCDLALRFGE GASGEERL
MSRPFVGVALLIAGHDADDGYQLFHAEPSTFYRYNAKAIGSGSEGAQAELLNEWHSSSLTL
KEAELLVLKILKQVMEEKLDENNAQLSCITKQDGFKIYDNEKTAELIKELKEKEAAE

>d1rypf_d.153.1.4 (F:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

FRNNYDGDVTFTSPTGRLFQVEYALEAIKQGSVTVGLRSNTHAVLVALKRNADELSSYQK
KIIKCDEHMGSLAGLAPDARVLSNYLRQQCNYS SLVFN RKLAVERAGHLLCDKAQKNT
QSYGGRPYGVGLLIIGYDKSGAHLLEFQPSGNVT ELYGTAIGARSQGA KTYLERTLDTFIKI
DGNPDELIKAGVEAISQSLRDESLTVDNLSIAIVGKDTPFTIYDGEAVAKYI

>d1rypg_d.153.1.4 (G:) Proteasome alpha subunit (non-catalytic) {Baker's yeast (Saccharomyces cerevisiae)}

GTGYDLSNSVFSPDGRNFQVEYAVKAVENGTT SIGIKCNDGVVFAVEKLITSKLLVPQKNV
KIQVVD RHIGCVYSG LIPDGRHLVNRGEEAASF KKLYKTPIPIPAFADRLGQYVQAHTLY
NSVRPFGVSTIFGGVDKNGAHL YMLEPSGSYWG YKGAATGKGRQSAKAELEKLV DHHPE
GLSAREAVKQAAKIIYLAHEDNKEKDFELEISWCSLSETNGLHKFVKGDLLQE AIDFAQKE
IN

>d1ht1a_d.153.1.4 (A:) HslV (ClpQ) protease {Escherichia coli}

TTIVSVRRNGHVVIAGDGQATLGNTVMKGNVKKVRRLYNDKVIAGFAGGTADAFTLFEL
FERKLEMHQGH LVKAAVELAKDWRTDRMLRKLEALLAVADETASLIITGNGDVVQPEND

LIAIGSGGPYAQAAARALLENTLSAREIAEKALDIAGDICIYTNHFHTIEELSYK

>glapy.1 d.153.1.5 (A.;B:) Glycosylasparaginase

(aspartylglucosaminidase, AGA) {Human (Homo sapiens)}

SPLPLVVNTWPFKNATEAAWRALASGGSALDAVESGCAMCEREQCDGSVGFSGSPDELG
ETTL DAMIMDGT TMDVGAVGDLRRIKNAIGVARKVLEHTTHTLLVGESATTFAQSMGFN
EDLSTSASQALHSDWLARNCPNYWRNVIPDPSKYCGPYKPPXTIGMVVIHKTGHIAAGT
STNGIKFKIHGRVGDSPIPGAGAYADDTAGAAAATGNGDILMRFLPSYQAVEYMRRGEDP
TIACQKVISRIQKHFPEFFGAVICANVTGSYGAACNKLSTFTQFSFMVYNSEKNQPTEEKV
DCI

>g2gac.1 d.153.1.5 (A.;B:) Glycosylasparaginase

(aspartylglucosaminidase, AGA) {Flavobacterium meningosepticum}

NKPIVLSTWNFGLHANVEAWKVL SKGGKALDAVEKGVRLVEDDPTERSVGYGGRPDRD
GRVTLDACIMDENYNIGSVACMEHIKNPISVARAVMEKTPHVMLVGDGALEFALSQGFKK
ENLLTAESEKEWKELKTXCIGMIALDAQNLSGACTTSGMAYKMHGRVGDSPHAGLF
VDNEIGAATATGHGEEVIRTVGTHLVVELMNQGRTPQQACKEAVERIVKIVNRRGKNLKD
IQVGFIALNKKGEYGAYCIQDGFNFVHDQKGNRLETP

>d2bc2a_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacillus cereus}

TVIKNETGTISISQLNKNVWVHTELGSFNGEAVPSNGLVLNTSKGLVLVDSSWDDKLTKE
IEMVEKKFQKRVTDVITHAHADRIGGIKTLKERGIKAHSTALTAELAKKNGYEEPLGDLQ
TVTNLKFNGMKVETFYPGKGHTEDNIVVWLPQYNILVGGALVKSTSADLGNVADAYVN
EWSTSIENVLKRYRNINAVVPGHGEVGDGKGLLLHTLDLLK

>d1a7ta_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Bacteroides fragilis}

SVKISDDISITQLSDKVYTYVSLAEIEGWGMVPSNGMIVINNHQAALLDTPINDAQTEMLV
NWVTDSLHAKVTTFIPNHHWGDCIGGLGYLQKRGVQSYANQMTIDLAKEKGLPVEHGF
TDSLTVSLDGMPLQCYLGGGHATDNIVVWLPTENILFGGCMLKDNQTTSIGNISDADVT
AWPKTLDKVKAKFPSARYVVPGHGNYGGTELIEHTKQIVNQYIESTS

>d1smla_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Xanthomonas maltophilia}

EVPLPQLRAYTVDASWLQPMAPLQIADHTWQIGTEDLTALLVQTPDGAVLLDGGMPQMA
SHLLDNMKARGVTPRDLRLILLSHAHADHAGPVAELKRRTGAKVAANAESAVLLARGGS
DDLHFGDGITYPPANADRIVMDGEVITVGIVFTAHFMAHGHTPGSTAWTWTDRNGKPV
RIAYADSLAPGYQLQGNPRYPHLIEDYRRSFATVRALPCDVLLTPHPGASNWDYAAGAR
AGAKALTCKAYADAAEQKFDGQLAKETAG

>d1jjea_ d.157.1.1 (A:) Zn metallo-beta-lactamase {Pseudomonas aeruginosa, IMP-1}

SLPDLKIEKLDEGVYVHTSFEEVNGWGVVPKHGLVVLVNAEAYLIDTPFTAKDTEKLV
FWERGYKIKGSISSHFHSDSTGGIEWLNSRSIPTYASELTNELLKKDGKVQATNSFSGVNY
WLVKNKIEVFYPPGHTPDNVVWLPERKILFGGCFIKPYGLGNLGDANIEAWPKSAKLL
KSKYGKAKLVVPSHSEVGDA SLLKLTLEQAVKGLNESKK

>d4kbpa2 d.159.1.1 (A:121-432) Plant purple acid phosphatase, catalytic domain
{Kidney bean (Phaseolus vulgaris)}

QTGLDVPYTFGLIGDLGQSFDSTNTLSHYELSPKKGQTVLFGDLSYADRYPNHDNVRW
DTWGRFTERSVAYQPWIWTAGNHEIEFAPEINETEPFKPFSYRYHVPYEASQSTSPFWYSIK
RASAHIIVLSSYSAYGRGTPQYTWLKKELRKVKRSETPWLIVLMHSPLYNSYNHHFMEGE
AMRTKFEAWFVKYKVDVVFAGHVHAYERSERVSNIAYKITDGLCTPVKDQSAPVYITIGD
AGNYGVDSNMIQPQPEYSAFREASFGHGMFDIKNRTHAHFSWNRNQDGVAVEADSVWF

FNHRHWYPVDDST

>d1utea_d.159.1.1 (A:) Mammalian purple acid phosphatase {Pig (*Sus scrofa*)}

PTPILRFVAVGDWGGVPNAPFHTAREMANAKAIATTVKTLGADFILSLGDNFYFTGVHDA
KDKRFQETFEDVFSDSLNRNVPWHVLAGNHDHLGNVSAQIAYSKISKRWNFPSYYRLRF
KIPRSNVSVIAIFMLDVTVLCGNSDDFVSQQPERPRNLALARTQLAWIKKQLAAAKEDYVL
VAGHYVPVWSIAEHGPTHCLVKQLLPLLTTHKVTAYLCGHDHNLQYLQDENGGLGFVLSGA
GNFMDPSKKHLRKVPNGYLRHFHGAENSLGGFAYVEITPKEMSVTYIEASGKSLFKTKLP
RRA

>d1jk7a_d.159.1.3 (A:) Protein phosphatase-1 (PP-1) {Human (*Homo sapiens*)}

KLNIDSIIQRLLEVRGSKPGKNVQLQENEIRGLCLKSREIFLSQPILLELEAPLKICGDIHGQ
YYDLLRLFEYGGFPESNYLFLGDYVDRGKQSLETICLLLAYKIKYPENFFLLRGNEHCASI
NRIYGFYDECKRRYNIKLWKTFTDCFNCLPIAAIVDEKIFCCHGGLSPDLQSMEQIRRMRP
TDVPDQGLLCDLLWSDPKDVLGWGENDRGVSTFGAEVVAKFLHKHDLDLICRAHQV
VEDGYEFFAKRQLVTLFSAPNYCGEFDNAGAMMSVDETLMCSEFQILKPA

>d1auia_d.159.1.3 (A:) Protein phosphatase-2B (PP-2B, calcineurin A subunit) {Human (*Homo sapiens*)}

TDRVVKAVPFPPSHRLTAKEVFDNDGKPRVDILKAHLMKEGRLEESVALRIITEGASILRQE
KNLLDIDAPVTVCGDIHGQFFDLMLKLFVGGSPANTRYLFLGDYVDRGYFSIECVLYLWA
LKILYPKTLFLLRGNECRHLTEYFTFKQECKIKYSERVYDACMDAFDCLPLAALMNQQF
LCVHGGLSPEINTLDDIRKLDRFKEPPAYGPMCDILWSDPLEDFGNEKTQEHFTHNTVRGC
SYFYSPAVCEFLQHNNLLSILRAHEAQDAGYRMYRKSQTTGFPSLITIFSAPNYLDVYNN
KAAVLKYENNVMNIRQFNCSPPHYWLPNFMVFTWSLFPVGEKVTEMLNVNLNICSDDDE
LGSEEDGFDGATAAARKEVIRNKIRAIGKMARVFSVLREESESVLTLKGLTPTGMLPSGVL
SGGKQTLQSATVEAIEADEAIKGFSPQHKITSFEEAKGLDRINERMPPR

>d1g5ba_d.159.1.3 (A:) lambda ser/thr protein phosphatase {Bacteriophage lambda}
MRYYEKIDGSKYRNIVVVGDLHGCTNLMNKLDLTIGFDNKKDLLISVGDVDRGAENVE
CLELITFPWFRAVRGNHEQMMIDGLSERGNVNHVLLNNGGGWFFNLDYDKEILAKALAH
KADELPLIIELVSKDKKYVICHADYPFDEYEFGKPVHDHQQVIWNRERISNSQNGIVKEIKG
ADTFIFGHTPAVKPLKFANQMYIDTGAVFCGNLTLIQVQGA

>d1emsa2_d.160.1.1 (A:10-280) NIT-FHIT fusion protein, N-terminal domain {Nematode (*Caenorhabditis elegans*)}

MATGRHFIAVCQMTSDNDLEKNFQAAKNMIERAGEKKCEMVFLPECDFIGLNKNEQIDL
AMATDCEYMEKYRELARKHNIWLSLGGGLHHKDPSDAAHPWNTHLIIDSDGVTRAEYNK
LHLFDLEIPGKVRLMESEFSKAGTEMIPVDTPIGRLGLSICYDVRFPESLWNRKRGALL
SFPSAFTLNTGLAHWETLLRARAIENQCYVVAQAQTGAHNPKRQSYGHSMVVDPWGAV
VAQCSERVDMCFAEIDLSYVDTLREMOPVFSHR

>d1f89a_d.160.1.1 (A:) hypothetical protein yl85 {Baker's yeast (*Saccharomyces cerevisiae*)}

SASKILSQIKVALVQLSGSSPDKMANLQRAATFIERAMKEQPDTKLVVLPECFNSPYSTD
QFRKYSEVINPKEPSTSVQFLSNLANKFKIILVGGTIPELDPKTDKIYNTSIIFNEDGKLIDKH
RKVHLFDVDIPNGISFHESETLSPGEKSTTIDTKYGKFGVGICYDMRFPESLWNRKRGAF
AMIYPSAFNTVTGPLHWHLLARSRAVDNQVYVMLCSPARNLQSSYHAYGHSIVVDPRGKI
VAEAGEGEEIIYAELDPEVIESFRQAVPLTKQRRF

>d1qdla_d.161.1.1 (A:) Anthranilate synthase
aminodeoxyisochorismate synthase/lyase subunit, TrpE {Archaeon *Sulfolobus solfataricus*}

AMEVHPISEFASPFEVFKCIERDFKVAGLLESIGGPQYKARYSVIAWSTNGYLKIHDDPVNI
LNGYLKDLKLADIPGLFKGGMIGYISYDAVRFWEKIRDLKPAAEDWPYAEFFTPDNIIYD
HNEGKVYVNADLSSVGGCGDIGEFKVSFYDESLNKNSEYERIVSESLEYIRSGYIFQVVLRS
FYRYIFSGDPLRIYYNLRRINSPYMFYLFDEKYLIGSSPELLFRVQDNIVETYPAGTRPR
GADQEEDLKLELELMNSEKDKAHMLVLDLARNDLGKVCVPGTVKVPPELMEYVEKYSHV
QHIVSKVIGTLKKKYNALNVLSATFPAGTVSGAPKPMAMNIETLEEYKRGPYAGAVGFIS
ADGNAEFAIAIRTAFLNKELLRIHAGAGIVYDSNPESEYFETEHKLKALKTAIGVR

>d1i7qa_ d.161.1.1 (A:) Anthranilate synthase
aminodeoxyisochorismate synthase/lyase subunit, TrpE {Serratia marcescens}

TKPQLTLLKVQASYRGDPTTLFHQLCGARPATLLLESAEINDKQNLQSLVIDSALRITALG
HTVSVQALTANGPALLPLLDEALPPEVRNQARPNGRELTFPAIDAVQDEADARLSLSVFDA
LRTILTLVDSPADEREAVMLGGLFAYDLVAGFENLPALRQDQRCPDFCFYLAETLLVLDHQ
RGSARLQASVFSEQASEAQLQHRLEQLQAEQQPPPIPHQKLENMQLSCNQSDDEEYGA
VVSELQEAIRQGEIFQVVPSSRRFSLPCAPLGPYQTLKDNNPSPYMFFMQDDDFTLFGASP
ESALKYDAGNRQIEIYPAGTRPRGRRADGSLDLDLSRIELEMRTDHKELAEHMLVLDL
ARNDLARICQAGSRYVADLTQVDRYSFVMHLVSRVVGTLRADLDVLHAYQACMNMGTL
SGAPKVRAMQLIAALRSTRRGSYGGRVGYFTAVRNLDTCIVIRSAYVEDGHRVQAGAGV
VQDSIPEREADETRNKARAVLRAIATAHHAKEVF

>d1k0ga_ d.161.1.1 (A:) P-aminobenzoate synthase component I {Escherichia coli}
MKTLSPAVITLLWRQDAAEFYFSRLSHLPWAMLLHSGYADHPYSRFDIVVAEPICLTTLTFG
KETVVSESEKRTTTTDDPLQVLQQLVDRADIRPTHNEDLPFQGGALGLFGYDLGRRFESLP
EIAEQDIVLPDPAVGIYDWALIVDHQRHTVSLLSHNDVNARRAWLESQQFSPQEDFTLTS
DWQSNMTREQYGEKFRQVQEYLHSGDCYQVNLAQRFHATYSGDEWQAFQLNQANRA
PFSAFLRLEQGAILSLSPERFILCDNSEIQTRPIKGTLPRLPDPQEDSKQAVKLANSKDRAE
NLMIVDLMRNDIGRVAVAGSVKVPPELVVPEPFAVHHLVSTITAQLPEQLHASDLLRAAFP
GGSITGAPKVRAMEIIDELEPQRRNAWCGSIGYLSFCGNMDTSITIRTLTAINGQIFCSAGGG
IVADSQEEAEYQETFDKVNRIKQLEK

>d1mla2 d.162.1.1 (A:145-313) Malate dehydrogenase {Pig (Sus scrofa)}
VTTLDIVRANAFVAELKGLDPARVSVPIGGHAGKTIPLISQCTPKVDFPQDQLSTLTGRIQ
EAGTEVVKAKAGAGSATLSMAYAGARFVFSLV DAMNGKEGVVECSFVKSQETDCPYFST
PLLLGKKGIEKNLIGIKISPFEEKMIAEAIPELKASIKKGEEFVKNM

>d1civa2 d.162.1.1 (A:194-385) Malate dehydrogenase {Flaveria bidentis, chloroplast}
TRLDENRAKCQLALKAGVFYDKVSNVTIWGNHSTTQVPDFLNAKIHGIPVTEVIRDRKW
LEDEFTNMVQTRGGVLIKKWGRSSAASTAVSIVDAIRSLVTPTPEGDWSTGVYTNNGNPY
GIAEDIVFSMPCRSKGDGDYEFVKDVIFDDYLSKKIKKSEDELLAEKKCVAHLTGEGLAVC
DLPEDTMLPGEM

>d2hlp2 d.162.1.1 (A:163-330) Malate dehydrogenase {Archaeon Haloarcula
marismortui}

FGRLDSARFRYVLSEEFDAVPQNVEGTILGEHGDAQVPVFSKVRVDGTDPEFSGDEKEQ
LLGDLQESAMDVIERKGATEWGPARGVAHMVEAILHDTGRVLPASVKLEGEFGHEDTAF
GVPVRLGSNGVEEIVEWDLDDYEQDLMADAAEKLSDQYDKIS

>d1b8pa2 d.162.1.1 (A:159-329) Malate dehydrogenase {Aquaspirillum arcticum}
LRLDHNRLSQIAAKTGKPVSSIEKLFVWGNHSPTMYADYRYAQIDGASVKDMINDDAW
NRDTFLPTVGKRGAAIIDARGVSSAASAANAIDHIHDWVLGTAGKWTTMGIPSDGSYGI

PEGVIFGFPVTTENGEYKIVQGLSIDAFSQRINVTNLNELLEEQNGVQHLLG
 >d1gv0a2 d.162.1.1 (A:143-305) Malate dehydrogenase {Chlorobium tepidum}
 AGVLDSARFRSFIAMELGVSMDVTACVLGGHGDAMVPVVKYTTVAGIPVADLISAERIA
 ELVERTRTGGAIEIVNHLKQGSIFYSPATSVVEMVESIVLDRKRVLTCAVSLDGQYGIDGTF
 VGVVPVKLGKNGVEHIYEIKLDQSDLDLLQKSAKIVDENCCKML
 >d1hya2 d.162.1.1 (A:167-329) L-2-hydroxyisocaproate dehydrogenase, L-HICDH
 {Lactobacillus confusus}
 GTLLDTARMQRAVGEAFDLDPRSVSGYNLGEHGNSQFVAWSTVRVMGQPIVTLADAGDI
 DLAAIEEEARKGGFTVLNGKGYTSYGVATSAIRIAKAVMADAHAEVSVNRRDDMGMYL
 SYPAIIGRDGVLAETTLDTTDEQEKLQSRDYIQQRFDEIVDTL
 >d9lta2 d.162.1.1 (A:163-331) Lactate dehydrogenase {Pig (Sus scrofa)}
 SGCNLSARFRYLMGERLGVHPLSCHGWILGEHGDSSVPVWSGVNVAGVSLKNLHPELG
 TDADKEHWKAVHKEVVDSAYEVIKLGKGYTSAIGLSVADLAESIMKNLRRVHPISTMIKG
 LYGIKENVFLSVPCILGQNGISDVVKVTLTPEEEHLKKSADTLWGIQKELQF
 >d1ceqa2 d.162.1.1 (A:164-329) Lactate dehydrogenase {Malaria parasite (Plasmodium
 falciparum)}
 GGVLDSRLKYYISQKLNVCPRDVNAHIVGAHGNKMVLLKRYITVGGIPLQEFINNKLISD
 AELEAIFDRTVNTALEIVNLHASPYVAPAAAIEMAESYLKDLKKVLICSTLLEGQYGHSDI
 FGGTPVVLGANGVEQVIELQLNSEEKAKFDEAIAETKRMKALA
 >d1llc_2 d.162.1.1 (165-334) Lactate dehydrogenase {Lactobacillus casei}
 TSLDTARFRQSAEMVNVDAHSVHAYIMGEHGDTEFPVWSHANIGGVITAEWVKAHPEIK
 EDKLVKMFEDVRDAAYEIIKLGATFYGIATALARISKAILNDENAVLPLSVYMDGQYGIN
 DLYIGTPAVINRNGIQNILEIPLTDHEEESMQKSASQLKKVLTDAFAKNDI
 >d1llda2 d.162.1.1 (A:150-319) Lactate dehydrogenase {Bifidobacterium
 longum, strain am101-2}
 TNLDSARLRFLIAQQTGVNVKNVHAYIAGEHGDSEVPLWESATIGGVPMSDWTPLPGHDP
 LDADKREEIHQEVKNAAYKIINGKGATNYAIGMSGVDIIEAVLHDTNRILPVSSMLKDFHGI
 SDICMSVPTLLNRQGVNNTINTPVSDKELAALKRSAETLKETAQAQFGF
 >d1hyea2 d.162.1.1 (A:146-313) MJ0490, lactate/malate dehydrogenase {Archaeon
 Methanococcus jannaschii}
 LGTHLSLRFKVAIAKFFGVHIDEVRTRIIGEHDGSMVPLLSATSIGGIPIQKFERFKELPIDEI
 IEDVKTKEQIIRLKGSEFGPAAAILNVVRCIVNNEKRLTLTSAYVDGEFDGIRDVCIGVP
 VKIGRDGIEEVVSIELDKDEIIAFKSAEIIKKYCEEVKNL
 >d1aiha_ d.163.1.1 (A:) Integrase {Bacteriophage HP1}
 ETELAFLYERDIYRLLAECDNSRNPDLGLIVRICLATGARWSEAETLTQSQVMPYKITFTNT
 KSKKNRTVPISDELFDMLPKKRGRLFNDAYESFENAVLRAEIELPKGQLTHVLRHTFASHF
 MMNGGNILVLKEILGHSTIEMTMRYAHFAPSHLESVAVKFNPLSNPAQ
 >d1ae9a_ d.163.1.1 (A:) Integrase (Int) {Bacteriophage lambda}
 RSRLTADEYLKIYQAAESSPCWLRLAMELAVVTGQRVGDLCEMKWSDIVDGYLYVEQSK
 TGVKIAIPTALHIDALGISMKETLDKCKEILGGETIIASTRREPLSSGTVSRYFMRARKASGL
 SFEGDPPTFHELRSLSARLYEKQISDKFAQHLLGHKSDTMASQFRDDRGREWDKIEI
 >d1f44a2 d.163.1.1 (A:130-343) Cre recombinase {Bacteriophage P1}
 RAKQALAFERTDFDQVRSLMENS DRCDIRNLAFLGIAYNTLLRIAEIARIRVKDISRTDGG
 RMLIHIGRTKTLVSTAGVEKALSLGVTKLVERWISVSGVADDPNNYLFCRVRKNGVAAPS

ATSQLSTRALEGIFEATHRLIYGAKDDSGQRYLAWSGHSARVGAARDMARAGVSIPEIMQ
AGGWTNVNIVMNFIRNLDSETGAMVRLLEDGD

>d1a0p_2 d.163.1.1 (111-292) Recombinase XerD {*Escherichia coli*}

KDLSEAQVERLLQAPLIDQPLELRDKAMLEVLYATGLRVSELVGLTMSDISLRQGVVRVIG
KGNKERLVPLGEEAVYWLETYLEHGRPWLLNGVSDVLFPSQRAQQMTRQTFWHRIKHY
AVLAGIDSEKLSPHVLRHAFATHLLNHGADLRVVQMLLGHSDLSTTQIYTHVATERLRQL
HQ

>d1f0a2 d.163.1.1 (A:135-423) Flp recombinase {*Baker's yeast (Saccharomyces cerevisiae)*}

KGNSHSHKMLKALLSEGESIWEITEKILNSFEYTSRFTKTKTLYQFLFLATFINCGRFSDIKN
VDPKSFKLQVQKYLGVIIQCLVTETKTSVSRHIYFFSARGRIDPLVYLDEFLRNSEPVLRV
NRTGNSSSNKQEYQLKDNLVRSYNKALKKNAPYSIFAINGPKSHIGRHLMTSFLSMKG
LTELTNVVGNWSDKRASAVARTTYTHQITAIPDHYFALVSRYAYDPISKEMIALKDETNPI
EEWQHIEQLKGSAGSIRYPANGIISQEVLDYLSSYINRRI

>d1a3a1 d.163.1.2 (A:431-626,A:720-765) Eukaryotic DNA topoisomerase
I, catalytic core {*Human (Homo sapiens)*}

PSSRIKGEKDWQKYETARRLKKCVDKIRNQYREDWKSSEMKVVRQRAVALYFIDKLALRA
GNEKEEGETADTVGCCSLRVEHINLHPELDGQEYVVEFDLFGKDSIRYYNKVPVEKRVFK
NLQLFMENKQPEDDLFDRLNTGILNKHLDLMEGLTAKVFRTYNASITLQQQLKELTAPD
ENIPAKILSYNRANRAVXKLNYLDPRITVAWCKKWGVPIEKIYNKTQREKFAWAIDMADE
DYEYF

>d1a41__ d.163.1.2 (-) Eukaryotic DNA topoisomerase I, catalytic core {*Vaccinia virus*}

NAKRDRIFVRVYNVMKRINCFINKNIKKSSSTDSNYQLAVFMLMETMFFIRFGMKMYLKEN
ETVGLLTLLKNKHIEISPDEIVIKFVGKDKVSHEFVVHKSNRLYKPLLKLTDDSSPEEFLNFK
LSERKVYECIKQFGIRIKDLRTYGVNYTFLYNFWTNVKSISPLPSPKKLIALTIKQTAEVVG
HTPSISKRAYMATILEMVKDKNFLDVVSKTTFDEFLSIVVDHVKS

>d1cf5a_ d.165.1.1 (A:) Beta-momorcharin {*Bitter gourd (Momordica charantia)*}

DVNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLNLTSYAYETISVAID
VTNVYVVAYRTRDVSYYFFKESPPAYNILFKGTRKITLPYTGNYENLQTAHAKIRENIDLGL
PALSSAITTLFYNAQSAPSALLVLIQTAEAAARFKYIERHVAKYVATNFKPNLAIISLENQW
SALSKQIFLAQNQGGKFRNPVDLIKPTGQRFQVTNVDSVDVKGNIKLLLSNRASTADEN

>d1ce7a_ d.165.1.1 (A:) Mistletoe lectin I A-chain {*European mistletoe (Viscum album)*}

YERGDLDVTAQTTGAGYFSFITLLRDYVSSGSFSNAIPLLSQSGGGGEAGRFVLVELTNSG
GDGITVAIDVTNLYVVAYQAGSQSYFLSGPGGRHGFTGTTRSSLPFNGSYPDLEQYGGQR
KQIPLGIDQLIQSVTALKFPGSTRTGARSILILIQMISEAARFNIPILWRARQYINSGASFLPDV
YMLELETSWGQQSTQVQHSTDGVFNPNIALADPGGGVTLTNVRDVIAASLAIMLFVC

>d1d6aa_ d.165.1.1 (A:) Pokeweed antiviral protein alpha {*Pokeweed (Phytolacca americana)*}

VNTIYNVGSTTISKYATFLNDRNEAKDPSLKCYGIPMLPNTNTNPKYVLVELQGSNKKTI
TLMLRRNNLYVMGYSDPFETNKCRYHIFNDISGTERQDVETTLCPNANSRVSKNINFDSRY
PTLESKAGVKSRSQVQLGIQILDSNIGKISGVMSFTEKTEAEFLVAIQMVSEAAARFKYIEN
QVKTNFNRAFNPNPKVLNLQETWGKISTAIHDAKNGVLPKPLELVDASGAKWIVLRVDEI
KPDVALLNYVGGSCQTT

>d1qi7a_ d.165.1.1 (A:) Saporin So6 {*Common soapwort (Saponaria officinalis)*}

VTSITLDLVNPTAGQYSSFVDKIRNNVKDPNLKYGGTDIAVIGPPSKEKFLRINFQSSRGTV

SLGLKRDONLYVVAYLAMDNNTNVNRAYYFKSEITSAELTALFPEATTANQKALEYTEDYQSI
EKNAQITQGDKSRKELGLGIDLLLTMEAVNKKARVVKNEARFLIAIQMTAEVARFRYIQ
NLVTKNFPNKFSDSNKVIQFEVSWRKISTAIYGDANGVFNKDYDFGFGKVRQVKDLQM
GLLMYLGKPK

>d1ift__ d.165.1.1 (-) Ricin A-chain {Castor bean (*Ricinus communis*)}

YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRRHEIPVLPNRVGLPINQRFILVELSNHAEL
SVTLALDVTNAYVVGIRAGNSAYFFHPDNQEDAEATHLFTDVQNRYTFAFGGNYDRLE
QLAGNLRENIELGNGPLEEASALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT
RIRYNRRSAPDPSVITLENSWGRSLTAIQESNQGAFAPIQLQRRNGSKFSVYDVSVILIPIAL
MVYRCAPP

>d1hwma_ d.165.1.1 (A:) Ebulin A-chain {*Sambucus ebulus*}

IDYPSVSFNLAKSTTYRDFLKNLRDRVATGTYEVNGLPVLRRRESEVQVKNRFVLVRLT
NYNGDVTSAVDVTNLYLVAFSANGNSYFFKDATELQKSNLFLGTTQHTLSFTGNYDNLE
TAAGTRRESIELGPNPLDGAITSLWYDGGVARSLVLQIMVPEAARFRYIEQEVRRSLQQLT
SFTPNALMLSMENNWSSMSLEVQLSGDNVSPFSGTVQLQNYDHTPRLVDNFEELYKITGI
AILLFRCA

>d1f0la2 d.166.1.1 (A:1-187) Diphtheria toxin, N-terminal domain {*Corynebacterium diphtheriae*}
GADDVVDSSKSFVMENFSSYHGTPGYVDSIQKGIQPKSGTQGNYYDDDWKGFYSTDN
KYDAAGYSVDNENPLSGKAGGVVKVTYPGLTKVLALKVDNAETIKKELGLSLTEPLMEQ
VGTEEFIKRFGDGASRVVLSLPFAEGSSSVEYINNWEQAKALSVELEINFETRGRKGQDAM
YEYMAQACA

>d1ikpa2 d.166.1.1 (A:395-606) Exotoxin A, C-terminal domain {*Pseudomonas aeruginosa*}

PTGAEFLGDGGDVSFSTRGTQNWTVRLLQAHQRQLEERGYVVFVGYHGTFLAAQSIVFG
GVRARSQDLDAIWRGFYIAGDPALAYGYAQDQEPDARGRIRNGALLRVYVPRSSLPGFYR
TSLTLAAPEAAAGEVERLIGHPLPLRLDAITGPEEEGGRLETILGWPLAERTVVIPSAIPTDPR
NVGGDLDPSSIPDKEQAISALPDYASQPGK

>d1prta_ d.166.1.1 (A:) Pertussis toxin, S1 subunit {*Bordetella pertussis*}

DPPATVYRYDSRPPEDVFQNGFTAWGNNDNVLEHLTGRSCQVGSSNSAFVSTSSRRYTE
VYLEHRMQEAVEAERAGRGTGHFIGYIYEVADNNTFYGAASSYFEYVDYGDNAGRILA
GALATYQSEYLAHRRIPPENIRRVTRVYHNGITGETTTTEYSNARYVSQQTRANPNPYTSR
RSVASIVGTLVRMAPVVGACMARQAESSEAMAAWSEAGEAMVLVYYESIAYSF

>g1xtc.1 d.166.1.1 (A:,C:) Cholera toxin {*Vibrio cholerae*}

NDDKLYRADSRPPDEIKQSGGLMPRGQSEYFDRGTQMNNLYDHARGTQTGFVRHDDGY
VSTSISLRSAPHLVGQTILSGHSTYYLYVLATAPNMFNVNDVLGAYSPHPDEQEVSAALGGIP
YSQIYGWYRVHFGVLDEQLHRNRGYRDRYYSNLDIAPAADGYGLAGFPPEHRAWREEP
WIHHAPPGCGNAPRXSNTCDEKTQSLGVKFLDEYQSKVKRQIFSGYQSDIDTHNRIKDEL

>d1qslal d.166.1.1 (A:60-264) Vegetative insecticidal protein 2 (VIP2) {*Bacillus cereus*}

TDKVEDFKEDKEKAKEWKGKEKEWKLATEKGKMNNFLDNKNNDIKTNYKEITFSMAG
SFEDEIKDLKEIDKMFDTNLSNIIYKNVEPTTIGFNKSLTEGNTINSDAMAQFKEQFLD
RDIKFDSYLDTHLTAQQVSSKERVILKVTVPSPGKGSTTPTKAGVILNNSEYKMLIDNGYMV
HVDKVSQVVKKGVECLQIEGTLKK

>d1qsla2 d.166.1.1 (A:265-461) Vegetative insecticidal protein 2 (VIP2) {*Bacillus cereus*}

SLDFKNDINAEAHSWGMMKNYEEWAKDLTDSQREALDGYARQDYKEINNYLRNQGGSGN

EKLDAQIKNISDALGKKPIPENITVYRWCGMPEFGYQISDPLPSLKDFEEQFLNTIKEDKGY
MSTSLSSERLAAFGSRKIILRLQVPKGSTGAYLSAIGGFASEKEILLDKDSKYHIDKVTEVII
KGVKRYVVDATLLT

>d1g24a_ d.166.1.1 (A:) Exoenzyme c3 {Clostridium botulinum}

AYSNTYQEFTNIDQAKAWGNAQYKKYGLSKSEKEAIVSYTKSASEINGKLRQNKGVIN
PSNLIKQVELLDKSFNKMKT PENIMLFRGDDPAYLGTEFQNTLLNSNGTINKTAFEKAKAK
FLNKDRLEYGYISTSLMNVSQFAGRPITKFKVAKGSKAGYIDPISAFAGQLEMLLPRHSTY
HIDDMRLSSDGKQIIITATMMGTAINPK

>d1j7na3 d.166.1.1 (A:264-550) Anthrax toxin lethal factor, middle domain {Bacillus anthracis}

MLSRYEKWEKIKQHYQHWSDSLSEEGRLLKKLQIPIEPKKDDIIHLSLSEEKELLKRIQID
SSDFLSTEEKEFLKKLQIDIRDSLSEEEKELLNRIQVDSSNPLSEKEKEFLKKLKLDIQPYDI
NQRLQDTGGLIDSPSINLDVRKQYKRDIQNIDALLHQSIGSTLYNKIYLYENMNINNLTATL
GADLVDSTDNTKINRGIFNEFKKNFKYSSISNYMIVDINERPALDNERLKWRIQLSPDTRA
GYLENGKLILQRNIGLEIKDVQIIKQSEKEYIRIDAKVV

>d1chua3 d.168.1.1 (A:238-353) L-aspartate oxidase {Escherichia coli}

LEFNQFHPTALYHPQARNFLLTEALRGEGAYLKRDPDGRFMPDFDERGELAPRDIVARAID
HEMKRLGADCMFLDISHKPADFIRQHFPMIYEKLLGLGIDLTQEPVPIVPAAHYT

>d1fuma3 d.168.1.1 (A:226-357) Fumarate reductase flavoprotein subunit {Escherichia coli}

MEFVQYHPTGLPGSGILMTEGCRGEGGILVNKNGYRYLQDYGMGPETPLGEPKNKYMEL
GPRDKVSQAFWHEWRKGNTISTPRGDVVYDLRHLGEKKLHERLPFICELAKAYVGVDP
VKEPIVRPTAHYT

>d1e39a3 d.168.1.1 (A:360-505) Flavocytochrome c3 (respiratory fumarate reductase) {Shewanella frigidimarina}

QYIQAAPTL SVKGGVMVTEAVRGNGAILVNREGKRFVNEITTRDKASAAILAQTGKSAYL
IFDDSVRKSLSKIDKYIGLGVAPTADSLVKLGKMEGIDGKALTETVARYNSLVSSGKDTDFE
RPNLPRALNEGNYAIEVTPGVHH

>d1jnra3 d.168.1.1 (A:257-401) Adenylylsulfate reductase A subunit {Archaeon Archaeoglobus fulgidus}

FEHRFIPFRFKDGYGPVGAWFLFFKCKAKNAYGEEYIKTRAAELEKYKPYGAAQPIPTPLR
NHQVMLEIMDGNQPIYMHTEEALAEAGGDKKKLKHIEEAFEDFLDMTVSQALLWAC
QNIDPQEQPSEAAPAEPYIMGSHSGE

>d1qdda_ d.169.1.1 (A:) Lithostathine, inhibitor of stone formation {Human (Homo sapiens)}

QEAQTELPQARISCPEGTNAYRSYCYFNEEDRETWVDADLYCQNMNSGNLVSFLTQAEG
AFVASLIKESGTDDFNWIGLHDPKKNRAWHWSSGSLVSYKSWGIGAPSSVNP GYCVSLT
SSTGFQKWKDVPCEDKFSFVCKFKN

>d1b6e_ d.169.1.1 (-) CD94 {Human (Homo sapiens)}

CSCQEKWVG YRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSSSQQFYWI
GLSYSEEHTAWLWENGSA LSQYLFP SFETFN TKNCIAYNPNGNALDESCEDKNRYICKQQ
LI

>d1e87a_ d.169.1.1 (A:) CD69 {Human (Homo sapiens)}

SSCSEDWVG YQRKCYFISTVKRSWTS AQNACSEHGATLAVIDSEKDMNFKRYAGREEH
WVGLKKEPGHPWKWSNGKEFNW FNV TGSDKCVFLKNTEVSSMECEKNLYWICKNPY
K

>d1hya_ d.169.1.1 (A:) NK cell-activating receptor nkg2d {Human (Homo sapiens)}
 ESYCGPCPKNWICYKNNCYQFFDESKNWWYESQASCMSQNASLLKVYSKEDQDLLKLVKS
 YHWMGLVHIPTNGSWQWEDGSILSPNLLTIEMQKGDCALYASSFKGYIENCSTPNTYICM
 QRTV

>d1egia_ d.169.1.1 (A:) Macrophage mannose receptor, CRD4 {Human (Homo sapiens)}
 CPEDWGASSRTSLCFKLYAKGKHEKKTWFESRDFCRALGGDLASINNKEEQQTIWRLITA
 SGSYHKLFWLGLTYGSPSEGFTWSDGSPVSYENWAYGEPNNYQNVEYCGELKGDPTMS
 WNDINCEHLNNWICIQ

>d1c3aa_ d.169.1.1 (A:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis), flavocetin-A}
 DFDICPGWSAYDRYCYQAFSKPKNWEDAESFCEEGVKTSHLVSISSGEGDFVAQLVAEKI
 KTSFQYVWIGLRIQNKEQQCRSEWSDASSVNYENLVKQFSKKCYALKKGTELRTWFNVY
 CGTENPEVCKYTPEC

>d1c3ab_ d.169.1.1 (B:) Snake coagglutinin {Habu snake (Trimeresurus flavoviridis), flavocetin-A}
 GFCCPLGWSSYDEHCYQVFQQKMNWEDAEEKFCTQQHKGSHLVSFHSSEEVDVFTSKTFP
 ILKYDFVWIGLSNVWNECTKEWSDGTKLDYKAWSGGSDCIVSKTTDNQWLSMDCSSKY
 YVVCKFQA

>d2afpa_ d.169.1.1 (A:) Type II antifreeze protein {Sea raven (Hemitripterus americanus)}
 QRAGPNCPAGWQPLGDRCIYYETTAMTWALAETNCMKLGGLASIHSQEEHSFIQTLNA
 GVVWIGGSACLQAGAWTWSDGTPMNFERSWCSTKPDDVLAACCMQMTAAADQCWDDL
 PCPASHKSVCAMTF

>d1h8ua_ d.169.1.1 (A:) Eosinophil major basic protein {Human (Homo sapiens)}
 RYLLVRSLQTFSQAWFTCRRCYRGNLVSIHNFNINYRIQCSVSALNQGQVWIGGRITGSGR
 CRRFQWVDGSRWNFAYWAAHQPSRGGHCVALCTRGGYWRRACHLRLPFICSY

>d1qo3c_ d.169.1.1 (C:) NK cell receptor ly49a {Mouse (Mus musculus)}
 STVLDLQHTGRGDKVYWFYGMKCYFVMDRKTWSGCKQTCQSSSLSLKIDDEDEL
 KFLQLVVPDSCWVGLSYDNKKKDWAWIDNRPSKLALNTRKYNIRDGGCMLLSKTRLD
 NGNCDQVFICICGKRLD

>d1dv8a_ d.169.1.1 (A:) H1 subunit of the asialoglycoprotein receptor {Human (Homo sapiens)}
 CPVNWVEHERSCYWFSRSGKAWADADNYCRLEDAHLVVVTSWEEQKFVQHHIGPVNT
 WMGLHDQNGPWKWVDGTDYETGFKNWRPEQPDDWYGHGLGGGEDCAHFTDDGRWN
 DDVCQRPYRWVCETEL

>d1k9ja_ d.169.1.1 (A:) DC-SIGNR (DC-SIGN related receptor) {Human (Homo sapiens)}
 CRHCPKDWTFQGNCFMSNSQRNWHDSVTACQEVRAQLVVIKTAEQNFLQLQTSRSN
 RFSWMGLSDLNQEGTWQWVDGSPLSPSFQRYWNSGEPNNSGNEDCAEFSGSGWNDNRC
 DVDNYWICKKPAA

>d1g1sa1 d.169.1.1 (A:1-118) E-selectin {Human (Homo sapiens)}
 WTYHYSTKAYSWNISRKYCQNRYTDLVAIQNKNEIDYLNKVLPPYYSSYYWIGIRKNNKT
 WTWVGTKKALTNEAENWADNEPNKRNNEDCVEIYIKSPSAPGKWNDHECLKKKHALC
 Y

>d1fifa1 d.169.1.1 (A:105-226) Mannose-binding protein A, lectin domain {Rat (Rattus norvegicus)}

KKSGKKFFVTNHERMPFSKVKALCSELRGTVAI PRNAEENKAIQEVAKTS AFLGITDEVTE
GQFMYVTGGRLTYSNWKKDQPD DWYGHGLGGGEDCVHIVD NGLWNDDSCQRPYTAVC
EFPA

>d1byfa_ d.169.1.1 (A:) Lectin TC14 {Tunicate (Polyandrocarpa misakiensis)}
DYEILFSDETMNYADAGTYCQSRGMALVSSAMRDSTMVKAILAFTEVKGH DYWVGADN
LQDGAYNFLWNDGVSLPTDSLWSPNEPSNPQSWQLCVQIWSKYNLLDDVGC GGARRVI
CEKELD

>d1tn3__ d.169.1.1 (-) Tetranectin {Human (Homo sapiens)}
ALQTVCLKG TKVHMKCF LAFTQTKTFHEASEDCISRGGTLSTPQTGSENDALYEYLRQSV
GNEAEIWLGLNDMAAEGTWVDMTGARIA YKNWETEITAQPDGGKTENCAVL SGAANGK
WFDKRCRDQLPYICQFGIV

>d1prt2 d.169.1.2 (B:4-89) Pertussis toxin, S2/S3 subunits, N-terminal domain
{Bordetella pertussis}
GIVIPPQEQITQH GSPYGR CANKTRALTVAELRSGDLQEYLRHVTRGWSIFALYDGT YLG
GEYGGVIKDGTPGGAFDLKTTFCIM

>d1prea1 d.169.1.2 (A:2-84) Proaerolysin, N-terminal domain {Aeromonas hydrophila}
EPVYPDQLRLFSLGQGVCGDKYRPVNREEAQSVKSNIVGMMGQWQISGLANGWVIMGP
GYNGEIKPGTASNTWCYPTNPVTGE

>d1f00i3 d.169.1.3 (I:842-939) Intimin {Escherichia coli}
LIVPNMSKRVTYND AVNTCKNF GGKLPSSQNELENVFKAWGAANKYEYKSSQTIISWV
QQTAQDAKSGVASTYDLVKQNPLNNIKASESNAYATCVK

>d1cwva5 d.169.1.3 (A:887-986) Invasin {Yersinia pseudotuberculosis}
NRWIYDGG RSLVSSLEASRQCQGS DMSAVLESSRATNGTRAPDGT LWGEWGS LTAYSSD
WQSGEYWVKKTSTDFETMNMDTGALQPGPAYLA FPLCALSI

>d1jfeb1 d.171.1.1 (B:200-464) Fibrinogen C-terminal domains {Chicken (Gallus gallus), beta}
SPCVASCNIPVVS GRECEDIYRKGGGETSEMYIIQPD PFTTPYRVYCDMETDNGGWTLIQNR
QDGSVNFGRAWDEYKRGFGNIAKSGGKKYCDTPGEYWLGN DKISQLTKIGPTKVL IEME
DWN GDKVSALYGGFTIHNEG NKYQLSVSNYKGNAGNALMEGASQLYGENRTMTIHNG
MYFSTYDRDNDGWLTTDPRKQCSKEDGGGWWYNRCHAANPNGRYYWGGTYSW DMA
KHGTDDGIVWMNWKGSWYSMKKMSMKIKPYFPD

>d1jc9a_ d.171.1.1 (A:) Tachylectin 5a {Japanese horseshoe crab (Tachypleus tridentatus)}
DPTDCADILLNGYRSSGGYRIWPKSWMTVGTLNVYCDMETDGGGWTVIQRRGN YGNPS
DYFYKPWKNYKLGF GNIEKDFWLGNDRIFALTNRQNYMIRFDLKD KENDTRYAIYQDFW
IENEDYLYCLHIGNYSGDAGNSFGRHNGHNFSTIDKDHDTHETHCAQTYKGGW WYDRC
HESNLNGLYLNGEHSYADGIEWRAWKGYHYSLPQVEMKIRPVEF

>d1hya2 d.177.1.1 (A:119-416) Fumarylacetoacetate hydrolase, FAH, C-terminal domain {Mouse
(Mus musculus)}

ATIGDYTD FYSSRQHATNVGIMFRGKENALLPNWLHLPVGYHGRASSIVVSGTPIRRPMG
QMRPDNSKPPVYGACRLLDMELEMAFFVGPGNRFG EPIPKAHEHIFGMVLMNDWSAR
DIQQWEYVPLGPF LGKSF GTTISPWVVPMDALMPFVVPNPKQDPKPLPYLCHSQPYTFDI
NLSVSLKGEGMSQAATICRSNFKHMYWTMLQQLTHHSVNGCNLRPGDLLASGTISGSDP
ESFGSMLELSWKGT KAIDVGQGQTRTFLLDGDEV IITGHCQGDGYRVGFGQCAGKVL PAL

>d1i7oa1 d.177.1.1 (A:1-213) 4-hydroxyphenylacetate degradation bifunctional
isomerase/decarboxylase HpcE {Escherichia coli}

MKGTIFAVALNHRSQLDAWQEAFFQQSPYKAPPKTAVWFIKPRNTVIGCGEPIFPQGEKVL
SGATVALIVGKTATKVVREEDAAEYIAGYALANDVSLPEESFYRPAIKAKCRDGFCEPIGETVA
LSNVDNLTITYTEINGRPADHWNTADLQRNAAQLLSALSEFATLNPGDAILLGTGPQARVEIQP
GDRVRVLAEGFPPLNPPVDEREVTTRK

>d1i7oa2 d.177.1.1 (A:214-429) 4-hydroxyphenylacetate degradation bifunctional
isomerase/decarboxylase HpcE {Escherichia coli}

SFPTLPHPHGTLFALGLNYADHASELEFKPPEEPLVFLKAPNTLTGDNQTSVRPNNIEYMH
YEAELVVVIGKQARNVSEADAMDYVAGYTVCNDAIRDYLENYYRPNLRVKS RDGLTPM
LSTIVPKEAIPDPHNLT LRFTVNGELRQQGTTADLIFSVPFLIAYLSEFMTLNP GDMIATGTP
KGLSDVVP GDEVVVEVEGVGRLVNRIVSEETAK

>d1hw8a2 d.179.1.1 (A:441-586,A:704-861) Substrate-binding domain of HMG-CoA reductase
{Human (Homo sapiens)}

EPRPNEECLQILGNAEKGAKFLSDAEIIQLVNAKHIPAYKLETLIETHERGV SIRRQLLSKKL
SEPSSLQYLPYRDYNYSLVMGACCENVIGYMPIPVGVAGPLCLDEKEFQVPMATTEGCLV
ASTNRGCRAIGLGGGASSRVLADXKSVVCEAVIPAKVVREVLKTTTEAMIEVNINKNLVG
SAMAGSIGGYNAHAANIVTAIYIACGQDAAQNVGSSNCITLMEASGPTNEDLYISCTMP SI
EIGTVGGGTNLLPQQACLQMLGVQGACKDNPGENARQLARIVCGTVMAGELSLMAALA
AGH

>d1qaxa2 d.179.1.1 (A:4-110,A:221-428) Substrate-binding domain of HMG-CoA reductase
{Pseudomonas mevalonii}

DSRLPAFRNLSPAARLDHIGQLLGLSHDDVSLLANAGALPMDIANGMIENVIGTFELPYAV
ASNFGINGRDVLVPLVVEEPSIVAAASYMAKLARANGGFTTSSSAPXRLARAQVRITPQQL
ETA EFSGEAVIEGILDAYAF AAVDPYRAATHNKGIMNGIDPLIVATGNDWRAVEAGAHAYA
CRSGHYGSLTTWEKDNNHGLVGTLEMPMPVGLVGGATKTHPLAQLSLRILGVKTAQALA
EIAVAVGLAQNLGAMRALATEGIQRGHMALHARNIAVVAGARGDEV DWVARQLVEYHD
VRADRAVALLKQKRGQ

>d1bdfa2 d.181.1.1 (A:53-178) RNA polymerase alpha subunit {Escherichia coli}
GCAVTEVEIDGVLHEYSTKEGVQEDILEILLNLKGLAVRVQKDEVILT LNKSGIGPV TAA
DITHDGDVEIVKPQHVICHLTDENASISMRIKVQRGRGYVPASTRIHSEEDERPIGRLLVDA
CYS

>d1i50c2 d.181.1.1 (C:42-172) RPB3 {Baker's yeast (Saccharomyces cerevisiae)}
PTLAIDSVEVETNTTVLADEFIAHRLGLIPLQSM DIEQLEYSRDCFCEDHCDKCSVVLTLQA
FGESESTTNVYSKDLVIVSNLMGRNIGHPIIQDKEGNGVLICKLRKGQELKLT CVAKKGIA
KEHAKWGP

>d1ovaa_ e.1.1.1 (A:) Ovalbumin {Hen (Gallus gallus)}
GSIGAASMEFCFDVFKELKVHHANENIFYCPIAIMSALAMVYLGAKDSTR TQINKVVRFD
KLPGFGDSIEAQCGTSVNVHSSLRDILNQITKPNDVYSFSLASRLYAEERYPILPEYLQCVK
ELYRGGLEPINFQTAADQARELINSWVESQTNGIIRNVLQSSVDSQTAMVLVNAIVFKGL
WEKAFKDEDTQAMPFRVTEQESKPVQMMYQIGLFRVASMASEKMKILELPFASGTMSML
VLLPDEVSGLEQLESII NFEKLTEWTSNVMEERKIKVYLPRMKMEEKYNLT SVLMAMGI
TDVFSSANLSGISSAESLKISQAVHAAHAEINEAGREVVGSAEAGVDAASVSEEFRA DHP
FLFCIKHIATNAVLFFGRCVSP

>d1qlpa_ e.1.1.1 (A:) Antitrypsin, alpha-1 {Human (Homo sapiens)}
FNKITPNLA EFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGTKADTHDEILEGLNFNLT

EIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSEGLKLVDKFLEDVKKLYHSEAFVNF
GDTEEAKKQINDYVEKGTQGGKIVDLVKELDRDTVFALVNYIFFKGKWERPFVVDTEED
FHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNATAIFFLPDEGKLQHLENE
LTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGITKVFNSGADLSGVTEEAPLK
LSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSIPPEVKFNKPFVFLMIEQNTKSPLFMGKV
NPTQK

>d1e05i_ e.1.1.1 (I:) Antithrombin {Human (Homo sapiens)}

SPVDICTAKPRDIPMNPNCIYRSPEKKATEDEGSEQIPEATNRRVWELSKANSRFATTFYQ
HLADSKNDNDNIFLSPLSISTAFAMTKLGACNDTLQQLMEVFKFDTISEKTSQIHFFFAKL
NCRLYRKANKSSKLVSANRLFGDKSLTFNETYQDISELVYGAKLQPLDFKENAEQSRAAIN
KWVSNKTEGRITDVIPSEAINELTVLVLVNTIYFKGLWKSFKSPENTRKELFYKADGESCSA
SMMYQEGKFRYRRVAEGTQVLELPFKGDDITMVLILPKPEKSLAKVEKELTPEVLQEWLD
ELEEMMLVVMHMPRFRIEDGFSLEQLQDMGLVDLFSPEKSKLPGIVAEGRDDLYVSDAFH
KAFLEVNEEGSEAAASTAVVIAGRSLNPNRVTFKANRPFLVFIREVPLNTIIFMGRVANPCV

>d1a7ca_ e.1.1.1 (A:) Plasminogen activator inhibitor-1 {Human (Homo sapiens)}

HHPPSYVAHLASDFGVRVFQQAQASKDRNVFSPYGVASVLAMLQLTTGGETQQQIQA
AMGFKIDDKGMAPALRHLYKELMGPWNKDEISTTDAIFVQRDLKLVQGFMPHFFRLFRST
VKQVDFSEVERARFIINDWVKTHTKGMISNLLGKGAVDQLTRLVLVNALYFNGQWKTPFP
DSSTHRRRLFHKSDGSTVSVPMMAQTNKFNYTEFTTPDGHYYDILELPYHGDTLMSFIAAP
YEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPKFSLETEVDLRKPLENLGMTDMFR
QFQADFTSLSDQEPLHVAQALQVKIEVNESGTVESSSTAVIVSARMAPEEIIIMDRPFLFVV
RHNPTGTVLFGQVMEP

>d1by7a_ e.1.1.1 (A:) Plasminogen activator inhibitor-2 {Human (Homo sapiens)}

EDLCVANTLFALNLFKHLAKASPTQNLFLSPWSISSTMAMVYMGSRGSTEDQMAKVLQF
NEVGAAADKIHSSFRSLSSAINASTGNYLLESVNKLFGEKSASFREYIRLCQKYYSSEPQ
AVDFLECAEEARKKINSWVKTQTKGKIPNLLPEGSVDGDMVLVNAVYFKGKWKTPFE
KKLNGLYPFRVNSAQRTPVQMMYLREKLNIGYIEDLKAQILELPYAGDVSMFLLLPEADI
VSTGLELLESEITYDKLNKWTSKDKMAEDEVEVYIPQFKLEEHYELRSILRSMGMEDAFN
KGRANFSGMSERNDLFLSEVFHQAMVDVNEEGTEAAAGTGGVMTGRTGHGGPQFVADH
PFLFLIMHKITNCILFFGRFSSP

>g1jjo.1 e.1.1.1 (A:,C:,E:) Neuroserpin {Mouse (Mus musculus)}

TITEWSVNMYNHLRGTGEDENILFSPLSIALAMGMELGAXENQYVMKLANSFLVQNGF
HVNEEFLQMLKMYFNAEVNHVDFSQNVAVANSINKWVENYTNLSLLKDLVSPEDFDGVTN
LALINAVYFKGNWKSQFRPENTRTFSFTKDDSEVQIPMMYQQGEFYFGEFSDGSNEAGG
IYQVLEIPYEGDEISMMLALSREQEVPLATLEPLLKAQLIEEWANSVKKQKVEVYLPRFTVE
QEIDLKDKALGVTEIFIKDANLTAMSDKKELFLSKAVHKSCIEVNEEGSEAAAAASGMIAI
SXYPQVIVDHPFLYLIRNRKSGIILFMGRVMNPHH

>d1sek__ e.1.1.1 (-) Serpin K {Tobacco hawkmoth (Manduca sexta)}

GETDLQKILRESNDQFTAQMFSEVVKANPGQNVVLSAFSVLPPLGQLALASVGESHDELL
RALALPNDNVTKDVFADLNRGVRAVKGVDLKMASKIYVAKGLELNDDFAAVSRDVFSGE
VQNVDFVKSVEAAGAINKWVEDQTNRIKNLVDPDALDETTRSVLVNAIYFKGSWKDKF
NKERTMDRDFHVSKDKTIKVPTMIGKKDVRVYADVPELDAKMIEMSYEGDQASMIILPNQ
VDGITALEQKLKDPKALSRAEERLYNTEVEIYLPKFKIETTTDLKEVLSNMNIKKLFTPGA
ARLENLLKTESLYVDAAIQKAFIEVNEEGAEAAAAANAFKITTYSFHFVPKVEINKPFFFSL

KYNRNSMFSGVCVQP

>g1f0c.1 e.1.1.1 (A:,B:) Viral serpin crmA (cytokine response modifier protein) {Cowpox virus}
MDIFREIASSMKGENVFISPPSISSVLTIYYGANGSTAEQLSKYVEKEADKNKDDISFKSM
NKVYGRYSAVFKDSFLRKIGDNFQTVDFDTCRTVDANKCVDFITEGKINPLLDEPLSPDT
CLLAISAVYFKAKWLMPFEKEFTSDYPFYVSPTEMVDVSMMSMYGEAFNHASVKESFGN
FSIIELPYVGDTSMVVILPDNIDGLESIEQNLTDTNFKKWCDSMDAMFIDVHIPKFKVTGSY
NLVDALVKLGLTEVFGSTGDYSNMCNSDVSDAMIHKTYIDVNEEYTEAAAATCALVAD
CAXSTVTNEFCADHPFIYVIRHVDGKILFVGRYCSPTTN

>d1imva_ e.1.1.1 (A:) Riment epithelium-derived factor, PEDF {Human (Homo sapiens)}
TGALVEEEDPFFKVPVNKLAAAVSNFGYDLYRVRSSMSPTTNVLLSPLSVATALSALSIGA
DERTESIIHRLYYDLISSPDHGTYKELLDVTAPQKNLKSASRIVFEKKLRIKSSSFVAPLEK
SYGTRPRVLTGNPRLDLQEINNWWQAQMKGKLARSTKEIPDEISILLGVAHFKGQWVTK
FDSRKTSLDFYLDERTVRVPMMSDPKAVLRYGLDSDLCKIAQLPLTGSMSSIFFLPLKV
TQNLTLEESLTSEFIHDIDRELKTVQAVLTVPKLKLSYEGEVTKSLQEMKLQSLFDSPDFSK
ITGKPIKLTQVEHRAGFEWNEDGAGTTPSPGLQPAHLTFPLDYHLNQPFIFVLRDTRDTGAL
LFIGKILDPRGP

>d1es5a_ e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., K15}
KPTIAAVGGYAMNNGTGTTLYTKAADTRRSTGSTTKIMTAKVVLAQSNLNLDAKVTIQK
AYS DYVVANNASQAHLIVGDKVTVRQLLYGLMLPSGCDAAYALADKYGSGSTRAARVKS
FIGKMNTAATNLGLHNTHFDSFDGIGNGANYSTPRDLTKIASSAMKNSTFRTVVKTKAYT
AKTVTKTGSIRTMDTWKNTNGLLSSYSGAIGVKTGAGPEAKYCLVFAATRGGKTVIGTVL
ASTSIPARESDATKIMNYGFAL

>d1hvba_ e.3.1.1 (A:) D-ala carboxypeptidase/transpeptidase {Streptomyces sp., R61}
DLPAPDDTGLQAVLHTALSQGAPGAMVRVDDNGTIHQLSEGVADRATGRAITTTDRFRVG
SVTKSFSAVVLLQLVDEGKLDLDASVNTYLPGLLPDDRITVRQVMShRSGLYDYTNMFA
QTPVPGFESVRNKVFSYQDLITLSLKHGVTNAPGAAYSNTNFVAGMLIEKLTGHSVATE
YQNRIFTPLNLDTFYVHPDTPVIPGTHANGYLTPDEAGGALVDSTEQTVSWAQSAAGAVISS
TQDLDTFFSALMSGQLMSAAQLAQMQQWTTVNSTQGYGLGLRRRDLSCGISVYGHTGT
VQGYTYAFASKDGKRSVTALANTSNNVNLNTMARTLES AFCGKP

>d1ci9a_ e.3.1.1 (A:) Esterase EstB {Burkholderia gladioli}
AASLAARLDAVFDQALRERRLVGAIVARHGEILYRRAQGLADREAGRPMREDTLFRLA
SVTKPIVALAVLRLVARGELALDAPVTRWLPEFRPRLADGSEPLVTIHLLTHTSGLGYWL
LEGAGSVYDRLGISDGIDLRDFDLNLRRLASAPLSFAPGS GWQYSLALDVLGAVVERA
TGQPLAAAVDALVAQPLGMRDCGFVSAEPPERFAVPYHDGQPEPVRMRDGIEVPLPEGHGA
AVRFAPSRVFEPGAYPSGGAGMYGSADDVLRALAIRANPGFLPETLADAARRDQAGVG
AETRGPWGFGYLSAVLDDPAAAGTPQHAGTLQWGGVYGHSWFVDRALGLSVLLLTNT
AYEGMSGPLTIALRDAVYA

>d1g6aa_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PSE-4 carbenicillinase}
SKFQQVEQDVKAIEVSLSARIGVSVLDTQNGEYWDYNGNQRFPLTSTFKTIACAKLLYDA
EQGKVNPNSTVEIKKADLVITYSPVIEKQVGQAITLDDACFATMTTSDNTAANIILSAVGGP
KGVTDFLRQIGDKETRLDRIEPLNEGKLGLDRDTTTPKAIAS TLNKFLFGSALSEM NQKK
LESWMVNNQVTGNLLRSVLPAGWNIADKSGAGGFGARSITAVVWSEHQAPIHVSIIYLAQT
QASMEERNDAIVKIGHSIFDVYTS

>d1alq_ e.3.1.1 (-) beta-Lactamase, class A {Staphylococcus aureus}

SEPIVLVIFTNKNKSDKPNDKLISETAKSVMKEFAAGSKNAAKELNDLEKKYNAHIGVY
ALDTKSGKEVKFNSDKRFAYASTSKAINSAILLEQVPYNKLNKKVHINKDDIVAYSPILEKY
VGKDITLKALIEASMTYSDNTANNKIIKEIGGIKKVKQRLKELGDKVTNPVRYEIELNYYS
PKSKKDTSTPAAFGKTLNKLIIANGKLSKENKKFLLDMLNKNKSGDTLIKDGVPKDYKVA
DKSGQAITYASRNDVAFVYPK

>d1mfoa_ e.3.1.1 (A:) beta-Lactamase, class A {Mycobacterium fortuitum}

APIDDQLAELERRDNVLIGLYAANLQSGRRITHRPDEMFCSTFKGYVAARVLQMAEHG
EISLDNRVFDADALVPNSPVTEARAGAEMTLAELCQAALQRSNTAANLLKTIGGPAA
VTAFARVSGDERTRLDRWEVELNSAIPGDPRDTSTPAALAVGYRAILAGDALSPQGRGLE
DWMRANQTSSMRAGLPEGWTTADKTGSGDYGSTNDAGIAFGPDGQRLLVMMTRSQA
HDPKAENLRPLIGELTALVLPSSL

>d1e25a_ e.3.1.1 (A:) beta-Lactamase, class A {Pseudomonas aeruginosa, PER-1}

SPLLKEQIESIVIGKKATVGVAVWGPDDLEPLLNPFEKFPMQSVFKLHLAMLVLHQVDQG
KLDLNQTVIVNRAKVLQNTWAPIMKAYQGDEFSVPVQQLQYSVSHSDNVACDLLFELV
GGPAALHDYIQSMGIKETAVVANEAMHADDQVQYQNWTSMKGAAILKKFEQKTQLS
ETSQALLWKWMVETTTGPERLKGLLPAGTVVAHKTGTSQIKAGKTAATNDLGIILLPDGR
PLLAVFVKDSAESSERTNEAIIAQVAQTAYQFELKKLSAL

>d1dy6a_ e.3.1.1 (A:) beta-Lactamase, class A {Serratia marcescens, Sme-1}

NKSDAAAKQIKKLEEDFDGRIGVFAIDTGSNTFGYRSDEFPLCSSFKGLAAVLERVQ
QKKLDINQKVKEYESRDLEYHSPITTKYKSGMTLGDMSAALQYSDNGATNIIMERFLG
GPEGMTKFMRSIGDNEFRLDRWELELNTAIPGDKRDTSTPKAVANSLNKLALGNVLNAKV
KAIYQNWLGKNTTGDARIRASVPADWVVGDKTGSCGAYGTANDYAVIWPKNRAPLIVSI
YTTRKSKDDKHSDKTIAEASRIAIQAI

>d1ga0a_ e.3.1.1 (A:) AMPC beta-Lactamase, class C {Enterobacter cloacae, P99, cephalosporinase}

PVSEKQLAEVVANTVTPLMKAQSVPGMAVAVIYQGKPHYTYFGKADIAANKPVTPQTLFE
LGSISKTFTGVLGGDAIARGEISLDDPVTRYWPQLTGKQWQGIRMLDLATYTAGGLPLQV
PDEVTDNASLLRFYQNWQPQWKPQTTRYANASIGLFGALAVKPSGMPYEAMTTRVLK
PLKLDHTWINVPKAEAAHYAWGYRDGKAVRAVRVSPGMLDAQAYGVKTNVQDMANWV
MANMAPENVADASLKQGIALAQSRWRIGSMYQGLGWEMLNWPVEANTVVEGSDSKV
ALAPLPVAEVNPPAPPVKASWVHKTGSTGGFGSYVAFIPEKQIGIVMLANTSYPNPARVEA
AYHILEALQ

>d1k55a_ e.3.1.1 (A:) Class D beta-lactamase {Pseudomonas aeruginosa, OXA-10}

SITENTSWNKEFSAEAVNGVFVLCKSSSKSCATNDLARASKEYLPASTFKIPNAIIGLETGVI
KNEHQVFKWDGKPRAMKQWERDLTLRGAIQVSAVPVFQQIAREVGEVRMOKYLKKFSY
GNQNISGGIDKFWLEGQLRISAVNQVEFLESYLNKLSASKENQLIVKEALVTEAAPEYLV
HSKTGFSGVGTESNPGVAWWVGWVEKETEVYFFAFNMDIDNESKLPLRKSIPTKIMESEGI
IG

>d1k25a4 e.3.1.1 (A:264-631) Penicillin-binding protein 2x (pbp-2x), transpeptidase domain {Streptococcus pneumoniae}

TLSSPLQSFMETQMDAFLEKVKGYMTATLVSAKTGEILATTQRPTFNADTKEGITEDFV
WRDILYQSNYEPGSAMKVMTLASSIDNNTFPSGEYFNSSSELKIADATTRDWDVNEGLTTG
GMMTFLQGFAHSSNVGMSLLEQKMGDATWLDYLRKFKFGVPTRFGLTDEYAGQLPADNI
VSIAQSSFGQGISVTQTQMLRAFTAIANDGVMLEPKFISAIYDTNNQSVRKSQKEIVGNPVS

KEAASTTRNHMILVGTDPLYGTMYNHYTGKPIITVPGQNVAVKSGTAQIADEKNGGYLVG
STNYIFSAVTMNPAENPDFILYVTVQQPEHYSGIQLGEFATPILERASAMKESLNLQSPAKN
LDKVT

>d1hd8a2 e.3.1.1 (A:3-262) Penicillin-binding protein 5, N-terminal domain {Escherichia coli}
LNIKTMPGVPQIDAESYILIDYNSGKVLAEQNADVRRDPASLTKMMTSYVIGQAMKAGK
FKETDLVTIGNDAWATGNPVFKGSSLMFLKPGMQVPVSQLIRDINLQSGNDACVAMADFA
AGSQDAFVGLMNSYVNALGLKNTHFQTVHGLDADGQYSSARDMALIGQALIRDVPNEY
SIYKEKEFTFNGIRQLNRNGLLWDNSLNVGDIKTGHTDKAGYNLVASATEGQMRLISAVM
GGRTFKGREAESKKLLTWGFRF

>d1ei5a3 e.3.1.1 (A:3-335) D-aminopeptidase, N-terminal domain {Ochrobactrum
anthropi}

KFDTSALEAFVRHIPQNYKGPGGVVAVVKDGEVVLQHAWGFADLRTRTPMTLDTRMPIC
SVSKQFTCAVLLDAVGEPELLDDALEAYLDKFEDERPAVRDLCNNQSGLRDYWALSVLCG
ADPEGVFLPAQAQSLLRRLKTTHFEPGSHYSYCNGNFRILADLIEAHTGRTLVDILSERIFAP
AGMKRAELISDTALFDECTGYEGDTPVRGFLPATNRIQWMGDAGICASLNDMIAWEQFIDA
TRDDESGLYRRLSGPQTFKDGVAAPYGFLNLHETGGKRLTGHHGALRGWRCQRWHCA
DERLSTIAMFNFEGGASEVAFKLMNIALGVSSS

>d1hbza_ e.5.1.1 (A:) Catalase I {Micrococcus lysodeikticus}
TTPHATGSTRQNGAPAVSDRQSLTVGSEGPVVLHDTHLLETHQHFNRMNIPERRPHAKGSG
AFGEFEVTEDEVSKYTKALVFQPGTKTETLLRFSTVAGELGSPDTWRDVRGFALRFYTEEG
NYDLVGNNPTIFFLRDPMKFTHFIRSQKRLPDSGLRDATMQWDFWTNNPESAHQVTYLM
GPRGLPRTWREMNGYGSHTYLWVNAQGEKHWVKYHFISQQGVHNLNDEATKIAGENA
DFHRQDLFESIAKGDHPKWDLYIQAIPYEEGKTYRFNPFDLTKTISQKDYPRIKVGTLTLNR
NPKNHFAQIESAAFPSNTVPGIGLSPDRMLLGRAFAHDAQLYRVGAHVNLQPVNRPKN
AVHNYAFEGQMWDHTGDRSTYVPNSNGDSWSDDETGPVDDGWEADGTLTREAAQALRA
DDDDFGQAGTLVREVFSQERDDFVETVAGALKGVRQDVQARAFEYWKNVDATIGQRIE
DEVKRHEGDGIPGVEAGGEARI

>d1cf9a2 e.5.1.1 (A:27-597) Catalase II {Escherichia coli, HP11}
DSLAPEDGSHRPAAEPTPPGAQPTAPGSLKAPDTRNEKLNSLEDVRKGSSENALTTNQG
RIADDQNSLRAGSRGPTLLEDFILREKITHFDHERIPERIVHARGSAAHGYFQPYKSLSDIT
KADFLSDPNKITPVFVRSTCQGGAGSADTVRDIRGFATKFYTEEGIFDLVGNNPTIFFIQD
AHKFPDFVHAVKPEPHWAIPQGQSAHDTFWDYVSLQPETLHNVMWAMSDRGIPRSYRTM
EGFGIHTFRLINAEGKATFVRFWKPLAGKASLVWDEAQKLTGRDPDFHRRELWEAIEAG
DFPEYELGFQLIPEEDEFKDFDLDLPTKLIPEELVPVQRVGKMVLNRNPDNFFAENEQAA
FHPGHIVPGLDFTNDPLLQGRIFSXTDTQISRLGGPNFHEIPINRPTCPYHNFQRDGMHRM
GIDTNPANYEPNSINDNWPRETTPPGPKRGGFESYQERVEGNKVRERSPSFGEYYSHPLFW
LSQTPFEQRHIVDGFSFELSKVVRPYIRERVVDQLAHIDLTLAQAVAKNLGIELTDDQLNITP
PPDVNGLKKDPSLSLYAIPDGD

>d1buca2 e.6.1.1 (A:1-232) Butyryl-CoA dehydrogenase {Megasphaera elsdenii}
MDFNLTDIQQDFLKLHDFGEKKLAPTVDTERDHKGIYDKELIDELSLGITGAYFEEKYGG
SGDDGGDVLSYILAVEELAKYDAGVAITLSATVSLCANPIWQFGTEAQKEKFLVPLVEGTK
LGAFLTEPNAGTDASGQQTATKNDDGTYTLNGSKIFITNGGAADIYVFAMTDKSKGNH
GITAFILEDGTPGFTYGKKEDKMGIHTSQTMELVFQDVKVPAENMLGEE

>d1jqia2 e.6.1.1 (A:4-234) Butyryl-CoA dehydrogenase {Rat (Rattus norvegicus)}

VYQSVELPETHQMLRQTCRDFAEKELVPIAAQLDKEHLFPTSQVKKMGELGLLAMDVPE
ELSGAGLDYLAYSIALEEISRGCASTGVIMSVNNSLYLGPILKFGSSQQKQWITPFTNGDK
IGCFALSEPGNGSDAGAASTTAREEGDSWVLNGTKAWITNSWEASATVVFASDTRSRQNK
GISAFLVPMPTPGLTLGKKEDKLGIRASSTANLIFEDCRIPKENLLGEPG

>d1egda2 e.6.1.1 (A:10-241) Medium chain acyl-CoA dehydrogenase {Human (Homo sapiens)}
LGFSFEFTEQQKEFQATARKFAREEIIPVAAEYDKTGEYPVPLIRRAWELGLMNTHIPENCG
GLGLGTFDACLISEELAYGCTGVQTAIEGNSLGQMPIIIAGNDQQKKKYLGRMTEEPLMC
AYCVTEPGAGSDVAGIKTKAEKKGDEYIINGQKMWITNGGKANWYFLLARSDPDPKAPA
NKAFTGFIVEADTPGIQGRKELNMGQRCS DTRGIVFEDVKVPKENVLIGD

>d1ivha2 e.6.1.1 (A:6-241) Isovaleryl-coa dehydrogenase {Human (Homo sapiens)}
VDDAINGLSEEQRQLRQTMAKFLQEHLAPKAQEIDRSNEFKNLREFWKQLGNLGVLGITA
PVQYGGSGGLGYLEHVLVMEEISRASGAVGLSYGAHSNLCINQLVRNGNEAQKEKYLPKLI
SGEYIGALAMSEPNAGSDVVSMLKKAEEKGNHYILNGNKF WITNGPDADVLIVYAKTDL
AAVPASRGITAFIVEKGM PGFSTSKKLDKLGMRGSNTCELIFEDCKIPAANILGHEN

>d1spia_ e.7.1.1 (A:) Fructose-1,6-bisphosphatase {Spinach (Spinacia oleracea)}
AATQTKARTRSKYEIETLTGWLLKQPMAGVIDAELTIVLSSISLACKQIASLVQRAGISNLT
GIQGAVNIQGEDQKKLDVVSNEVFSSCLRSSGRTGIIASEEEDVPVAVEESYSGNYIVVFDP
LDGSSNIDAAVSTGSIFGIYSPNDECIVDSHDDESQLSAEEQRCVVNVCPGDNLLAAGY
CMYSSSVIFVLTIGKGVYAFTLDPMYGEFVLTSEKIQIPKAGKIYSFNEGNYKMWPDKLLK
YMDDLKEPGESQKPYSSRYIGSLVGDFHRTLTYGGIYGYPRDAKSKNGKLRLLYECAPMS
FIVEQAGGKGS DGHQRILDIQPTIEHQRVPLYIGSVEEVEKLEKYLA

>d2hhma_ e.7.1.1 (A:) Inositol monophosphatase {Human (Homo sapiens)}
WQECMDYAVTLARQAGEVVCEAIKNEMNVMLKSSPVDLVTATDQKVEKMLISSIKEKYP
SHSFIGEESVAAGEKSILTDNPTWIIDPIDGTTNFVHRFPFVAVSIGFAVNKKIEFGVVYSCVE
GKMYTARKGKGAF CNGQKLQVSQQEDITKSLLVTELGS SRTPETVRMVLSNMEKLF CIPV
HGIRSVGTAAVNMCLVATGGADAYYEMGIHCWDVAGAGIIVTEAGGVLM DVTGGPF DLM
SRRVIAANNRILAERIAKEIQVIPLQRDDE

>d1g0ha_ e.7.1.1 (A:) Archaeal inositol
monophosphatase/fructose-1,6-bisphosphatase {Archaeon Methanococcus jannaschii, MJ0109}
MKWDEIGKNIAKEIEKEILPYFGRKDKSYVVGTS PS GDETEIFDKISEDIALKYLKSLNVNI
VSEELGVIDNSSEWTVVIDPIDGSFN FINGIPFFAF C FGVFKNNEPYYGLTYEFLT KSFYEAY
KGKGAYLNGRKIKVKDFNPNNIVISYYP SKKIDLEKL RNKV KVRV RIFGAFGLEMCYVAKG
TLDAVFDVRPKVRAVDIASSYIICKEAGALITDENGDELKFDLNATDRLNIIIVANSKEMLDII
LDLL

>d1inp_ e.7.1.1 (-) Inositol polyphosphate 1-phosphatase {Cow (Bos taurus), brain}
MSDILQELLRVSEKAANIARACRQQT L FQLLIEEKKEGEKNKKFAVDFKTLADVLVQEVI
KENMENKFPGLGKKIFGEESNELTNDLGEKIIMRLGPTEEETVALLSKVLNGNKLASEALA
KV VHQDVFFSDPALDSVEINIPQDILGIWVDPIDSTYQYIKGSADITPNQGIFPSGLQCVTVL
IGVYDIQTGVPLMGVINQPFVSQDLHTRRWKGQCYWGLSYLGTNIHSLPPVSTRNSEA
QSQGTQNPSSSEGSCRFSVISTSEKETIKGALSHVCGERIFRAAGAGYKSLCVILGLADIYIF
SEDTTFKWDSCAAHAILRAMGGGMVDLKECLERNPDTGLDLPQLVYHVGNEGAAGVDQ
WANKGGLIAYRSEKQLETFLSRLLQHLAPVATHT

>d1kala_ e.7.1.1 (A:) 3';5'-adenosine bisphosphatase, PAP phosphatase {Baker's yeast
(Saccharomyces cerevisiae)}

ALERELLVATQAVRKASLLTKRIQSEVISHKDSTTITKNDNSPVTTG DYAAQTHIINAIKSNFP
DDKVVGEESSSGLSDAFVSGILNEIKANDEVYNKNYKKDDFLFTNDQFPLKSLEDVRQIID
FGNYEGGRKGRFWCLDPIDGTKGFLRGEQFAVCLALIVDGVVQLGCIGCPNLVLSSYGAQ
DLKGHESFGYIFRAVRGLGAFYSPSSDAESWTKIHVRHLKDTKDMITLEGVEKGHSSHDE
QTAIKNKLNISKSLHLDSQAKYCLLALGLADVYLRLPIKLSYQEKIWDHAAGNVIVHEAG
GIHTDAMEDVPLDFGNGRTLATKGVIASSGPRELHDLVVSTSCDVIQSR

>d1jp4a_ e.7.1.1 (A:) PIPase {Rat (*Rattus norvegicus*)}

HNVLMLRLVASAYSIAQKAGTIVRCVIAEGDLGIVQKTSATDLQTKADRMVQMSICSSLSR
KFKPLTHIGEEDLPPGEVDQELIEDGQSEEILKQPCPSQYSAIKEEDLVVWVDPVDGTKEYT
EGLLDNVTVLIGIAYEGKAIAGIINQPYNYQAGPDAVLGRTIWGVLGLGAFGFQLKEAPA
GKHIITTTTRSHSNKLVTDCAAMNPDNVLRVGGAGNKIIQLIEGKASAYVFASPGCKKWD
CAPEVILHAVGGKLTDIHGNPLQYDKEVKHMNSAGVLAALRNYEYYASRVPEVKSALIP

>d1kfsa2 e.8.1.1 (A:519-928) DNA polymerase I (Klenow fragment) {*Escherichia coli*}

HKGPLNVFENIEMPLVPVLSRIERNGVKIDPKVLHNHSEELTLRLAELEKKAHEIAGEEFNL
SSTKQLQTLFEKQGIKPLKKTTPGGAPSTSEEVLLEALDYPLPKVILEYRGLAKLKSTYTD
KLPLMINPKTGRVHTSYHQAVTATGRLSSTDPNLQNIPVRNEEGRRIRQAFIAPEDYVIVSA
DYSQIELRIMAHLSRDKGLLTAFAGKDIHRATAAEVFGLPLETVTSEQRSSAKAINFGLIY
GMSAFGLARQLNIPRKEAQKYMDLYFERYPGVLEYMERTRAQAKEQGYVETLDGRRLLY
PDIKSSNGARRAAAERAAINAPMQGTAADIHKRAMIAVDLQAEQPRVRMIMQVHDEL
VFEVHKDDVDVAVAKQIHQLMENCTRLDVPLLEVGSGENWDQAH

>d1t7pa2 e.8.1.1 (A:211-704) T7 phage DNA polymerase {Bacteriophage T7}

LEAVDIEHRAAWLLAKQERNGFPFDTKAIEELYVELAARRSELLRKLTTETFGSWYQPKGG
TEMFCHPRTGKPLPKYPRIKTPKVGIGFKPKNKAQREGREPCELDTREYVAGAPYTPVE
HVVFNPSRDHIQKKLQEAGWVPTKYTDKGAPVVDDEVLEGVRVDDPEKQAAIDLIKEY
LMIQKRIGQSAEGDKAWLRYVAEDGKIHGVSVPNGAVTGRATHAFPNAQIPGVRSPYGE
QCRAAFGAEHHLDGITGKPWVQAGIDASGLELRCLAHFMARFDNGEYAHEILNGDIHTK
NQIAAELPTRDNAKTFIYGFLYGAGDEKIGQIVGAGKERGKELKKKFLENTPAIAALRESIQ
QTLVESSQWVAGEQQVKWKRRWIKGLDGRKVHVRSPHAALNTLLQSAGALICKLWIIKT
EEMLVEKGLKHGWDGDFAYMAVHDEIQVGCRTTEEIAQVVIETAQEAMRWVGDHWNF
RCLLDTEGKMGPNWAICH

>d1ih7a2 e.8.1.1 (A:376-903) T4-like DNA polymerase {Bacteriophage RB69}

QNKVIPQGRSHPVQPYPGAFVKEIPNRYKYVMSFDLTSLYPSIIRQVNISPETIAGTFKVAP
LHDYINAVAERP SDVYSCSPNGMMYYKDRDGVVPTEITKVFNQRKEHKG YMLAAQRNG
EIIKEALHNP NLSVDEPLDVDRFDFSDEIKEKIKKLSAKSLNEMLFRAQRTEVAGMTAQI
NRKLLINSLYGALGNVWFRYYDLRNATAITTFGQMALQWIERKVNEYLNVCGTEGEAF
VLYGDTDSIYVSADKIIDKVGESKFRDTHNWVDFLDKFARERMEPAIDRGFREMCEYMN
NKQHLMFMDREAIAGPPLGSKGIGGFWTGKKRYALNVWDMEGTRYAEPKLKIMGLETQ
KSSTPKAVQKALKECIRRM LQEGEESLQEYFKEFEKEFRQLNYISIASVSSANNIAKYDVG
GFPGPKCPFHIRGILTYNRAIKGNIDAPQVVEGEKVYVLPLREGNPF GDKCIAWPSGTEITD
LIKDDVLHWMDYTVLLEKTFIKPLEGFTSAAKLDYEKKASLFDMFDF

>d1tgoa2 e.8.1.1 (A:348-773) T4-like DNA polymerase {Archaeon *Thermococcus gorgonarius*}

STGNLVEWFLLRKAYERNELAPNKPDERELARRRESYAGGYVKEPERGLWENIVYLD FR
LYPSIIITHNVSPDTLNREGCEEYDVAPQVGHKFCKDFPGFIPSL LGDLLEERQKVKKKMK

ATIDPIEKKLLDYRQRAIKILANSFYGYGYAKARWYCKECAESVTAWGRQYIETTIREIEE
KFGFKVLYADTDGFFATIPGADAETVKKKAKEFLDYINAKLPGLLELEYEGFYKRGFFVTK
KKYAVIDEEDKITTRGLEIVRRDWSEIAKETQARVLEAILKHGDVEEAVRIVKEVTEKLSK
YEVPPKLVIIYEQITRDLDYKATGPHVAVAKRLAARGIKIRPGTVISYIVLKSGSRIGDRAI
PFDEFDPAKHKYDAEYYIENQVLPAYERILRAFGYRKEDLRYQKTRQVGLGAWLKPKT

>d1k1sa_ e.8.1.5 (A:) DinB homolog (DBH) {Archaeon *Sulfolobus solfataricus*}

MIVIFVDFDYFFAQVEEVLNPQYKKGKPLVSVYSGRKTSGAVATANYEARKLGVKAGMP
IHKAMQIAPSAIYVPMRKPIYEAFSNRIMNLLNKHADKIEVASIDEAYLDVTNKVEGNFENG
IELARKIKQEILEKEKITVTVGVAPNKLAKIADKSKPNGLGVIRPTEVQDFLNELDIDEIPG
IGSVLARRLNELGIQKLRDILSKNYNELEKITGKAKALYLLKLAQNKYSEPVENKSKIPHG
RYLTLPYNTRDVKVILPYLKKAINAYNKVNGIPMRITVIAIMEDLDILSKGKKFKHGISID
NAYKVAEDLLRELLVRDKRRNVRRIGVKLDNIIN

>d1jiha_ e.8.1.5 (A:) DNA polymerase eta {Baker's yeast (*Saccharomyces cerevisiae*)}

MSKFTWKELIQLGSPSKAYESSLACIAHIDMNAFFAQVEQMRCGLSKEDPVVCVQWNSII
AVSYAARKYGISRMDTIQEALKKCSNLIHTAVFKKGEDFWQYHDGCGSWVQDPAKQIS
VEDHKVSLEPYRRESRKALKIFKSACDLVERASIDEVFLDLGRICFNMLMFDNEYELTGDL
KLKDALSNIREFIGGNYDINSHLPLIPEKIKSLKFEGDVFNPEGRDLITDWDVILALGSQ
VCKGIRDSIKDILGYTTSCGLSSTKNVCKLASNYKKPDAQTIVKNDCLLDFLDCGKFEITSF
WTLGGVLGKELIDVLDLPHENSIKHIRETWPDNAGQLKEFLDAKVKQSDYDRSTSNIDPL
KTADLAEKLFKLSRGRYGLPLSSRPVVKSMMSNKNLRGKSCNSIVDCISWLEVFCAELTS
RIQDLEQEYNKIVIPRTVSISLKTksyevyrksGPVAYKGINFQSHELLKVGKIFVTDLDIKG
KNKSYYPLTKLSMTITNFDII

>d1mml_ e.8.1.2 (-) MMLV reverse transcriptase {Moloney murine leukemia virus}

TWLSDFPQAWAETGGMGLAVRQAPLIPLKATSTPVSISKQYPMSQEARLGKPHIQRLLDQ
GILVPCQSPWNTPLLPVKKPGTNDYRPVQDLREVNRVEDIHPTVPNPYNLLSGLPPSHQ
WYTVLDLKDAFFCLRLHPTSQPLFAFEWRDPEMIGSQLTWTRLPPQGFKNSPTLFDEALH
RDLADFRIQHPDLILLQYVDDLLLAATSELDCCQGTRALLQTLGNLGYRASAKKAQICQK
QVKYLGYLEK

>d1c9rb1 e.8.1.2 (B:) HIV-1 reverse transcriptase {Human immunodeficiency virus type 1}

PISPIETVPVKLAPGMDGPKVKQWPLTEEKIKALVEICTEMEKEGKISKIGPENPYNTPVFAI
KKKDSTKWRKLVDFRELNKRRTQDFWEAALGIPHPAGLKKKKSVTVLDVGDAYFSVPLDE
DFRKYTAFTIPSINNETPGIRYQYNVLPQGWKGSPAIFQSSMTKILEPFKAQNPDIVIYQYID
DLYVGSdleigQHRTKIEELRQHLLRWGLTTPDKKHQKEPPFLWMGYELHPDKWAAAAA
AAAAAAAATVNDIQKLVGKLNWAAQIYPGIAAAALSAALAGTKALTAAPLTAAALEL
AANRAAAAAAAGVYYDPSKDLIAEIQQGQGWTYQIYQEPFKNLKTGKYARMRGAGH
TNDVKQLTEAVQKITTESIVIWGKTPKFKLPIQKETWETWWTEYWQATWIPEWEFVNTPP
LVALWYALE

>d1ldr_ e.8.1.4 (-) Viral RNA-dependent RNA-polymerase {Poliovirus type 1, strain Mahoney}

VGYPINAPSKTKLEPSAFHYVFEGVKEPAVLTKNDPRLKTDfEEAIFSKYVGNKITEVDEY
MKEAVDHYAGQLMSLDINTEQMCLDAMYGTDGLEALDLSTSAGYPYVAMGKKKRDIL
NKQTRDTKEMQKLLDTYGINLPLVTYVKDELRSKTKVEQGKSRLIEASSLNDsvAMRMA
FGNLYAAFHKNPGVITGSavgCDPDLFWSKIPVLMEEKLFAFDYTGyDASLPAWFEALK
MVLEKIGFGDRVDYIDYLNHSHHLYKNKTYCVKGGMPSGSGTSIFNSMINNLIIRTLKK

TYKGIDLDHLKMIAYGDDVIASYPHEVDASLLAQSGKDYGLTMTPADKSATFETVTWEN
VTFLKRFFRADEKYPFLIHPVMPMKEIHESIRWTKDPRNTQDHVRSLLCLLAWHNGEEYIN
KFLAKIRSVPIGRALLPEYSTLYRRWLSF

>d1c2pa_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Hepatitis C virus}

HHSYTWGTGALITPCAAEESKLPINALSNSLLRHHNMVYATTSSRAGLRQKKVTFDRLQVL
DDHYRDVLKEMKAKASTVKAKLLSVEEACKLTPPHSAKSKFGYGAKDVRNLSSKAVNHI
HSVWKDLEDTVTPIDTTIMAKNEVFCVQPEKGGRKPARLIVFPDLGVRVCEKMALYDV
VSTLPQVVMGSSYGFQYSPGQRVEFLVNTWKSCKNPMGFSYDTRCFDSTVTENDIRVEES
IYQCCDLAPEARQAIKSLTERLYIGGPLTNSKGQNCGYRRCRASGVLTTS CGNTLT CYLKA
SAACRAAKLQDCTMLVNGDDL VVICESAGVQEDAASLRAFTEAMTRY SAPP GPPQPEY
DLELITSCSSNVSAHDASGKRVYYLTRDPTT PLARAAWETARHTPVNSWLGNIIMYAPTL
WARMILMTHFFSILLAQE QLEKALDCQIYGACYSIEPLDLPQIIERLHGLSAFSLHSYSPGEI
NRVASCLRKLGVPLRVWRHRARSVRARLLSQGGRAATCGKYLFNWA V KTKLKLTPIPAA
SQLDLSGWV FVAGYSGGDIYHS

>d1khva_ e.8.1.4 (A:) Viral RNA-dependent RNA-polymerase {Rabbit hemorrhagic disease virus}

FCGEPIDYRGITAHRLVGAEP RPPVSGTRYAKVPGVPDEYKTGYR PANLGRSDPDSKSLM
NIAVKNLQVYQQEPKLDK VDEFIERAAADVLGYLRFLT KGERQANLNFKA AFNTLDLSTS
CGPFVPGKKIDHVKDGVMDQVLAKHLYKCSVANS GKALHHIYACGLKDEL RPLDKVK
EGKKRLLWGCDVG VAVCAA V FHNICYKLKMVARFGPIAVGVDMTSRDVDVIINNLT SK
ASDFLCLDYSKWDSTMSPCVVRLAIDILADCCEQTELT KSVVLT LKSHPM TILDAMIVQTK
RGLPSGMPFTSVINSICHWLLWSAAVYKSCAEI GLHCSNLYEDAPFYTYGDDGVYAMTPM
MVSLLPAIENLRDYGLSPTAADKTEFIDVCPLNKISFLKRTFELTDIGWVSKLDKSSILRQL
EWSKTTSRH MVIEETYDLAKEERG VQLEELQVAAA H GQEFFNFVCRELERQQAYTQFS
VYSYDAARKILADRR

>d1i50a_ e.29.1.1 (A:) RBP1 {Baker's yeast (Saccharomyces cerevisiae)}

VGQQYSSAPLRTVKEVQFGLFSPEEVRAISVAKIRFPETMDETQTRAKIGGLNDPRLGSIDR
NLKCQTCQEGMNECPGHFGHIDLAKPVFHVGFIAKIKK VCEVCMHCGKLLLDEHNELM
RQALAIKDSKKRFAAIWTLCKTKMVCETDVPSEDDPTQLVSRGGCGNTQPTIRKDGLKLV
GSWKKDRATGDADEPEL RVLSTEEILNIFKHISVKDFTSLGFNEVFSRPEWMILTCLPVPPP
PVRPSISFNESQRGEDDLTFKLADILKANISLETLEHNGAPHHAIEEAESLLQFHVATYMDN
DIAGQPQALQKSGRPVKSIRARLKGKEGRIRGNLMGKRVD FSARTVISGDPNLELDQVGV
PKSIAKTLTYPEVVTPYNIDRLTQLVRNGPNEHPGAKYVIRDSGDRIDLRYSKRAGDIQLQ
YGWKVERHIMDNDPVL FNRQPSLHKMSMMAHRVKVIPYSTFRLNLSVTSPYNADFDGDE
MNLHVPQSEETRAELSQLCAVPLQIVSPQSNKPCM GIVQDTLCGIRKLT LRDTFIELDQVL
NMLYWVPDWDGVIPTPAIIPKPLWSGKQILSVAIPNGIHLQRFDEGTLLSPKDNGMLIID
GQIFGVVEKKT V GSSNGLIHVVTREKGPQVCAKLFGNIQKV VNFWLLHNGFSTGIGDTI
ADGPTMREITETIAEAKKKVLDVTKEAQANLLTAKHGMTLRESFEDNVVRFLNEARDKA
GRLAEVNLKDLNNVKQMV MAGSKGSFINIAQMSACVQQSVEGKRIAFGFVDR TLP HFS
KDDYSPESKGFVENSYLRGLTPQEFFFHAMGGREGLIDTAVKTAETGYIQRRLVKALEDIM
VHYDNTTRNSLGNVIQFIYGEDGMDAAHIEKQSLDTIGGS DAAFEKRYRVDLLNTDHTLD
PSLLESGSEILGDLKLQVLLDEEYKQLVKDRKFLREVFDGEANWPLPVNIRRIIQAQQT
FHIDHTKPSDLTIKDIVLGVKDLQENLLVLRGKNEIIQNAQRDAVTLFCCLLSRLATRRVL
QEYRLTKQAFDWVLSNIEAQFLRSV VHPGEMVGVLAQAQSIGEPATQMTLNTFFHAGVASK
KVTSGVPRLKEILNVAKNMKTPSLTVYLEPGHAADQEQA KLIRSAIEHTTLKSVTIASEIYY

DPDPRSTVIPEDDEEIIQLHFSLLDEEAEQSFDQQSPWLLRLELDRAAMNDKDLTMGQVGER
IKQTFKNDLFVIWSEDNDEKLIIRCRVVRPKSLDAETEAEDHMLKKIENTMLENITLRGV
ENIERVVMKMYDRKVPSPPTGEYVKEPEWVLETDGVNLSEVMTVPGIDPTRIYTNSFIDIM
EVLGIEAGRAALYKEVYNVIASDGSYVNYRHMALLVDVMTTQGGTTSVTRHGFNRSTNG
ALMRCSFEETVEILFEAGASAELDDCRGVSENVILGQMAPIGTGAFDVMIDEESL

>dli6vc_e.29.1.1 (C:) RNA-polymerase beta {Thermus aquaticus}

KIKRFGRIREVIPLPLTEIQVESYKKALQADVPEKRENVGIQAAFKETFPIEEGDKGKGG
LVLDLFLEYRIGDPPFSQDECREKDLTYQAPLYARLQLIHKDTGLIKEDEVFLGHLPLMTED
GSFIINGADRVIVSQIHRSPGVYFTPDARPGRYIASIPLPKRGPWIDLEVEASGVVTMKVN
KRFKPLVLLLRVLGYDQETLVRELSAYGDLVQGLLDEAVLAMRPEEAMVRLFTLLRPGDP
PKKDKALAYLFGLLADPKRYDLGEAGRYKAEKLGVLGSLGRTLVRFEDGEFKDEVFLPTL
RYLFALTAGVPGHEVDDIDHLGNRRIRTVGELMADQFRVGLARLARGVRERMVMGSPDT
LTPAKLVNSRPLEAALREFFSRSQLSQFKDETNPSSLRHKRRISALGPGGLTRERAGFDVR
DVHRTHYGRICPVETPEGANIGLITSLAAYARVDALGFIRTPYRRVKNVGVVTEEVVYMTAS
EEDRYTIAQANTPLEGDRIATDRVARRRGEPVIVAPEEVEFMDVSPKQVFSLNTNLIPFLE
HDDANRALMGSNMQTQAVPLIRAQAPVMTGLEERVVRDSLAAALYAEEDGEVVKVDGT
RIAVRYEDGRLVHPLRRYARSNQGTAFDQRPRVRVGQRVKKGDLLADGPASEEGFLALGQ
NVLVAIMPFDGYNFEDAIVISEELLKRDFYTSIHIERYEIEARDTKLGPERRITRDIPHLSEAAL
RDLDEEGIVRIGAEVKPGDILVGRTSFKGEQEPSPEERLLRSIFGEKARDVKDTSLRVPPGE
GGIVVGRLRLRRGDPGVELKPGVREVVRVFVAQKRKLQVGDKLANRHGNKGVVAKILPV
EDMPHLPDGTVPDVILNPLGVPSRMNLGQILETHLGLAGYFLGQRYISPVFDGATEPEIKE
LLAEAFNLYFGKRQGEFGVDKREKEVLARAELGLVSPGKSPEEQLKELFDLGKVVLYD
GRTGEPFEGPIVVGQMFIMKLYHMVEDKMHARSTGPYSLITQQPLGGKAQFGGQRFEM
EVWALEAYGAAHTLQEMLTIKSDDIEGRNAAYQAIKGEDVPEPSVPESFRVLVKELQALA
LDVQTLDEKDNPDVDFEGL

>dli50b_e.29.1.2 (B:) RBP2 {Baker's yeast (Saccharomyces cerevisiae)}

FEDESAPITAEDSWAVISAFFREKGLVSQQLDNFQFVDYTLQDIICEDSTLILEQLAQHTTE
SDNISRKYEISFGKIYVTKPMVNESDGVTHALYPQEARLRNLTYSGLFVDVKKRTYEAD
VPGRELKYELIAEESEDDSESQKVFGRPLPIMLRSKNCYLSEATESDLYKLKECPFDMGGY
FIINGSEKVLIAQERSAGNIVQVFKAAPSPISHVAEIRSALEKGSRFISTLQVKLYGREGSS
ARTIKATLPYIKQDIPVIFRALGIIPDGEILEHICYDVNDWQMLEMLKPCVEDGFVIQDRE
TALDFIGRRGTALGIKKEKRIQYAKDILQKEFLPHITQLEGFESRKAFFLGYMINRLLLCAL
DRKDQDDRDFHFGKKRLDLAQLLQFLKTLFKKLTKDIFRYMQRTVEEAHDFNMKLAIN
AKTITSLKYALATGNWGEQKKAMSSRAGVSQVLNRYTYSSTLSHLRRTNTPIGRDGKLA
KPRQLHNTHWGLVCPAETPEGQACGLVKNLSCISVGTDPMPITFLSEWGMPELEDY
VPHQSPDATRVFVNGVWHGVHRNPARLMETLRTLRRKGDINPEVSMIRDIREKELKIFTD
AGRVYRPLFIVEDDES LGHKELKVRKGHIAKLMATEYQDIEGGFEDVEEYTWSSLLNEGL
VEYIDAEESSESILIAMQPEDLEPAEANEENDLDVDPKRIRVSHHATTFTHCEIHPSMILGVA
ASIIPFPDHNQSPRNTYQSAMGKQAMGVFLTNYNVRMDTMANILYYPQKPLGTTRAMEY
LKFRELPAQNIAVAIACYSYGNQEDSMIMNQSSIDRGLFRSLFFRSYMDQEKKYGMSITE
TFEKPQRTNLTLMKHGTYDKLDDGLIAPGVRVSGEDVIIGKTPISPDEEELGQRTAYHS
KRDASTPLRSTENGIVDQVLVTTNQDGLKFVKVRVRTTKIPQIGDKFASRHGQKGTIGITY
RREDMPFTAEGIVPDLINPHAIPSRMTVAHLIECLLSKVAALSGNEGDA SPFTDITVEGISK
LLREHGYQSRGFVEMYNGHTGKKLMAQIFFGPTYTQRLRHMVDDKI HARARGPMQVLT

RQPVEGRSRDGGRLRFGEEMERDCMIAHGAASFLKERLMEASDAFRVHICGICGLMTVIAKL
NHNQFECKGCDNKIDYQIHIPYAAKLLFQELMAMNITPRLYTDRSRDF

>d1i6vd_ e.29.1.2 (D:) RNA-polymerase beta-prime {Thermus aquaticus}

KEVRKVRIALASPEKIRWSYGEVEKPETINYRTLKPERDGLFDERIFGPIKDYEACCGKY
KRQRFEAKVCERCACAVEVTRSIVRRYMAHIELATPAAHIWVFKDVPSKIATLLDLSATELE
QVLYFNKYIVLDPKAAVLDAVPVEKRQLLTDXXXXXXXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXIDARMGAELQELLKELDLEKLERELLEEMKHPSRARRAKARKRLEVVR
AFLDSGNRPEWMILEAVPVLPPDLRPMVQVDGGRFATSDLNDLYRRLINRNNRLKKLLAQ
GAPEIIIRNEKRMLQEAVDAVIDNGRRGSPVTNPGSERPLRSLTDILSGKQGRFRQNLLGKR
VDYSGRSVIVVGPQLKLHQCGLPKRMALELFPKFLKKMEEKAFAPNVKAARRMLERQR
DIKDEVWDALEEVHKGVVLLNRAPTLHRLGIQAFQPVLEVGQSIQLHPLVCEAFNADFD
GDQMAVHVPLSSFAQAEARIQMLSAHNLLSPASGEPLAKPSRDIIILGLYYITQVRKEKKGA
GMAFATPEEALAAAYERGEVALNAPIVVAGRETSVGRLKFVFANPDEALLAVAHGLLDLQD
TVTTRYLGRRLETSPGRILFARIVGEAVGDEKVAQELIQMDVPQEKNLKDLYVQAFLRLG
MEKTARLLDALKYYGFTLSTTSGITIGIDDAVIPEEKQRYLEEADRKLQRQIEQAYEMGFLTD
RERYDQVIQLWTETTEKVTQAVFNNFEENYPFNPLYVMAQSGARGNPQQIRQLCGMRGL
MQKPSGETFEVPVRSSFREGLTVLEYFISSHGARKGGADTALRTADSGYLTRKLVDAHEI
VVREADCGTTNYSVPLFQMDEVTRTLRLRKRSDIESGLYGRVLAREVEALGRRLEEGRY
LSLEDVHFLIKAAEAGEVREVPRSPVLCQTRYGVCQKCYGYDLSMARPVSIGEAVGVVA
AESIGEPGTQLTMRFTHTGGVAVGTDITQGLPRVIELFEARRPKAKAVISEIDGVVRIEEGED
RLSVFVESEGFSKEYKLPKDARLLVKDGDYVEAGQPLTRGAIDPHQLLEAKGPEAVERYL
VDEIQKVYRAQGVKLHDKHIEIVVRQMLKYVEVTDPGDSRLLEGQVLEKWDVEALNER
LIAEGKVPVAVKPLLGMVTKSALSTKSWLSAASFQNTTHVLTEAAIAGKKDELIGLKENV
ILGRLIPAGTGSDFVRFTQVVDQRTLKAI

>d1jn3a_ e.9.1.1 (A:) DNA polymerase beta, catalytic (31 kD) fragment {Rat (Rattus norvegicus)}

DDTSSSINFLTRVTGIGPSAARKLVDEGIKTLEDLRKNEDKLNHHQRIGLKYFEDFEKRIPR
EEMLMQMDIVLNEVKKLDPEYIATVCGSFRRGAESSGDMVLLTHPNFTSESSKQPKLLH
RVVEQLQKVRFITDLSKGETKFMGVCQLPSENDENEYPHRRIDIRLIPKDQYYCGVLYFT
GSDIFNKNLRAHALEKGFTINEYTIRPLGVTGVAGEPLPVDSEQDIFDYIQWRYREPKDRSE

>d1jmsa2 e.9.1.1 (A:243-510) Terminal deoxynucleotidyl transferase {Mouse (Mus musculus)}

DERYKSFKLFTSVFGVGLKTAEKWFRMGFRTLSKIQSDKSLRFTQMOKAGFLYEDLVSC
VNRPEAEAVSMLVKEAVVTFLPDALVTMTGGFRRGKMTGHDVDFLITSPEATEDEEQQLL
HKVTDVFWKQQGLLLYCDILESTFEKFKQPSRKVDALDHFQKCFILKLDHGRVHSEKSGQ
QEGKGWKAIRVDLVMCPYDRRAFALLGWTGSRQFERDLRRYATHERKMMLDNHALYDR
TKRVFLEAESEEEIFAHLGLDYIEPWENA

>d1jaja_ e.9.1.1 (A:) DNA polymerase X {African swine fever virus}

MLTLIQGKKIVNHLRSRLAFEYNGQLIKILSKNIVAVGSLRREEKMLNDVDLLIIVPEKKLL
KHVLPNIRIKLSFSVKVCGERKCVLFIEWEKKTYQLDLFTALAEKPYAIFHFTGPVSYLI
RIRAAKKKKNYKLNQYGLFKNQTLVPLKITTEKELIKELGFTYRIPKKRL

>d1ecl_ e.10.1.1 (-) DNA topoisomerase I, 67K N-terminal domain {Escherichia coli}

GKALVIVESPAKAKTINKYLGSDYVVKSSVGHIRDLTSGSAAKKSADSTSTKTAKPKKPD
ERGA LVNRMGVDPWHNWEAHYEVLPGKEKVVSELKQLAEKADHIYLATDL DREGAIA
WHLREVIGGDDARYSRVVFNEITKNAIRQAFNKP GELNIDRVNAQQARRFMDRVVGYMV
SPLLWKKIARGLSAGRVQSVAVRLVVEREREIKAFVPEEFWEVDASTTTPSGEALALQVTH

QNDKPFPRPVNKEQTQAAVSLLEKARYSVLEREDKPTTSKPGAPFITSTLQQAASTRLGFGV
KKTMMMAQRLYEAGYITYMRTDSTNLSQDAVNMVRGYISDNFGKKYLPESPNQYASKG
NSQEAHEAIRPSDVNVMAESLKDMEADAQKLYQLIWRQFVACQMPAKYDSTTLTVGAG
DFRLKARGRILRFDGWTKVMPALRKGDEDRILPAVNKGDALTLVELTPAQHFTKPPARFSE
ASLVKELEKRGIGRPSTYASIISTIQDRGYVRVENRRFYAEKMGEIVTDRLEENFRELMNYD
FTAQMENSOLDQVANHEAEWKAVLDHFFSDFTQQLDKAEKDPEEGGMRPN

>d1i7da_ e.10.1.1 (A:) DNA topoisomerase III {Escherichia coli}

MRLFIAEKPSLARAIADVLPKPHRKGDFIECGNGQVVTWCIGHLLEQAQPDAYDSRYAR
WNLADLPVPEKWQLQPRPSVTKQLNVIKRFLEHASEIVHAGDPDREGQLLVDEVLDYLQ
LAPEKRQQVQRCLINDLNPAVERAIDRLRSNSEFVPLCVSALARARADWLYGINMTRAY
TILGRNAGYQGVLSVGRVQTPVLGLVVRDEEIEFVAKDFFEYKAHIVTPADERFTAIWQ
PSEACEPYQDEEGRLLHRPLAEHVNRISGQPAIVTSYNDKRESESAPLPFSLSALQIEAAK
RFGLSAQNVLDICQKLYETHKLITFPRSDCRYLPEEHFAGRHAVMNAISVHAPDLLPQPVV
DPDIRNRCWDDKKVDAHHAIPTARSSAINLTENEAKVYNLIARQYLMQFCPDAVFRKCVI
ELDIAGKGFVAKARFLAEAGWRTLLGSKERDEENDGTPLPVVAKGDELLCEKGEVVERQ
TQPPRHFTDATLLSAMTGIAFVQDKDLKKILRATDGLGTEATRAGHIELLFKRGFLTCKGR
YIHSTDAGKALFHSLPEMATRPDMTAHWESVLTQISEKQCRYQDFMQPLVGTLYQLIDQA
K RTPVRQFRGIVAP

>d1gkub3 e.10.1.1 (B:499-1054) Topoisomerase "domain" of reverse gyrase {Archaeon
Archaeoglobus fulgidus}

QEFDLIKPALFIVESPTKARQISRFFGKPSVKVLDGAVVYEIPMQKYVLMVTASIGHVVDLI
TNRGFHGVLVNGRFVPVYASIKRCRDCGYQFTEDRESCPKCGSENVDNSRSRIEALRKLA
HDAEFVIVGTDPDTEGEKIAWDLKNLLSGCGAVKRAEFHEVTRRAILEALESIRDVDENL
VKAQVVRRIEDRWIGFVLSQKLWERFNNRNL SAGRAQTLVLGWIIDRFQESRERRKIAIVR
DFDLVLEHDEEEFDLTIKLVEEREELRTPLPPYTTETMLSDANRILKFSVKQTMQIAQELFE
NGLITYHRTDSTRVSDVGQRIAKEYLGDGDFVGREWGEGSAHECIRPTRPLTRDDVQRLIQE
GVLVVEGLRWEHFALYDLIFRRFMASQCRPFKVVVKKYSIEFDGKTAEERIVRAEGRAY
ELYRAVWVKNELPTGTFRVKAEVKSVPKVLPFTQSEIIQMMKERGIGRPSTYATIVDRLFM
RNYVVEKYGRMIPTKL GIDVFRFLVRRYAKFVSEDRTDLESRMDAIERGELDYLKALED
MYAEIKSID

>d1bjt_ e.11.1.1 (-) DNA topoisomerase II, C-terminal fragment (residues 410-1202) {Baker's
yeast (Saccharomyces cerevisiae)}

RKSRITNYPKLEDANKAGTKEGYKCTLVLTEGDSALSLAVAGLAVVGRDYYGCYPLRGK
MLNVREASADQILKNAEIQAIIKIMGLQHRKKYEDTKSLRYGHLMMIMTDQDHDGSHIKG
LIINFLESSFLGLLDIQGFLLFITPIIKVSITKPTKNTIAFYNNMPDYEKWREEESHKFTWKQK
YYKGLGTSLAQEVREYFSNLDRLHLKIFHSLQGNDKDYIDLAFSKKKADDRKEWLRQYEP
GTVLDPTLKEIPISDFINKELILFSLADNIRSIPNVLDGFKPGQRKVLYGCFKKNLKSELKVA
QLAPYVSECTAYHHGEQSLAQTIIGLAQNFVGSNNIYLLLPNGAFGTRATGGKDAAYRYI
YTELNKLTRKIFHPADDPLYKYIQEDEKTVEPEWYLPILPMILVNGAEGIGTGWSTYIPFN
PLEIKNIRHLMNDEEELQMHPWFRGWTGTIEEIEPLRYRMYGRIEQIGDNVLEITELPART
WTSTIKEYLLLGLSGNDKIKPWIKDMEEQHDDNIKFIITLSPEEMAKTRKIGFYERFKLISPI
SLNMNMAFDPHGKIKKYNVNEILSEFYVVRLEYQYQKRKDHMSERLQWEVEKYSFQVKF
IKMIIIEKELTVTNKPRNAIQELENLGFPRFNKEGKPYGSPNDEIAEQINDVKGATSDEEDE
ESSHEDTENVINGPEELYGTIEYLLGMRIWSLTKERYQKLLKQKQEKETELNLLKLSAK

DIWNTDLKAFEVGYQEFLQRDAEARG

>d1ab4_ e.11.1.1 (-) DNA Gyrase A {Escherichia coli}

VGRALPDVRDGLKPVHRRVLYAMNVLGNDWNKAYKKSARVVGDVIGKYHPHGDSAVY
DTIVRMAQPFSLRYMLVDGQGNFGSIDGDSAAAMRYTEIRLAKIAHELMADLEKETVDFV
DNYDGTEKIPDVMPTKIPNLLVNGSSGIAVGMATNIPPHNLTEVINGCLAYIDDEDISIEGLM
EHIPGPDFPTAAIINGRRGIEEAYRTGRGKVYIRARAEVEVETIIVHEIPYQVNKARLIEKIAE
LVKEKRVEGISALRDESDKDGMRIVIEGEVVLNNLYSQTLQVVSFGINMVALHHGQPKIM
NLKDIIAAFVRHRREVVTTRTIFELRKARDRAHILEALAVALANIDPIELIRHAPTPAEAKT
ALVANPWQLGNVAAMLEDAARPEWLEPEFGVVRDGLYYLTEQQAQAILDLRLQKLTGLEH
EKLLDEYKELLDQIAELLRILGSADRLMEVIREELELVREQFGDKRREIT

>d1daaa_ e.17.1.1 (A:) D-amino acid aminotransferase {Bacillus sp., strain YM-1}

GYTLWNDQIVKDEEVKIDKEDRGYQFGDGVYEVVKVYNGEMFTVNEHIDRLYASAEKIR
ITIPYTKDKFHQLLHELVEKNELNTGHIYFQVTRGTSPRAHQFPENTVKPVIIGYTKENPRP
LENLEKGVKATFVEDIRWLRCDIKSLNLLGAVLAKQEAHEKGCYEAILHRNNTVTEGSSS
NVFGIKDGILYTHPANMILKGITRDVVIACANEINMPVKEIPFTTHEALKMDELFTSTTS
EITPVIEIDGKLIRDGKVGEWTRKQLKQFETKIP

>d1ilka_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Escherichia coli}

KADYIWFNGEMVRWEDAKVHVMSHALHYGTSVFEGIRCYDSHKGPVFRHREHMQRRL
HDSAKIYRFPVSQSIDELMEACRDVIRKNNLTSAYIRPLIFVGDVGMGVNPPAGYSTDVIIA
AFPWGAYLGAEALEQGIDAMVSSWNRAAPNTIPTAAKAGGNYLSSLLVGSEARRHGYQE
GIALDVNGYISEGAGENLFEVKDGVLFPTTSSALPGITRDALIKLAKELGIEVREQVLSRE
SLYLADEVFMSGTAAEITPVRSDGIQVGEGRCPVTKRIQQAFFGLFTGETEDKWGWLD
QVNQ

>d1ekfa_ e.17.1.1 (A:) Branched-chain amino acid aminotransferase {Human (Homo sapiens),
mitochondrial}

ASSSFKAADLQLEMTQKPHKKPGPGPEPLVFGKTFTDHMLMVEWNDKGWGQPRIQPFQN
LTLHPASSSLHYSLQLFEGMKAFAKGDQVRLFRPWLNMDRMLRSAMRLCLPSFDKLEL
LECIRRLIEVDKDWVPDAAGTSLYVRPVLIGNEPSLGSQPRRALLFVILCPVGAYFPGGSV
TPVSLLADPAFIRAWVGGVGNKLGNYGPTVLVQQEALKRGCEQVLWLYGPDHQLTEV
GTMNIFVYWTHEDGVLELVTPPLNGVILPGVVRQSLDMAQTWGEFRVVERTITMKQLL
RALEEGRVREVFSGTACQVCPVHRILYKDRNLHIPTMENGPELILRFQKELKEIQYGIRA
HEWMFPV

>d1et0a_ e.17.1.1 (A:) Aminodeoxychorismate lyase {Escherichia coli}

MFLINGHKQESLAVSDRATQFGDGCFTTARVIDGKVSLLSAHIQRLQDACQRLMISCDFWP
QLEQEMKTLAAEQNGVLKVVISRSGSGRGYSTLNSGPATRILSVTAYPAHYDRLRNEGIT
LALSPVRLGRNPHLAGIKHLNRLEQVLIRSHLEQTNADALVLDSEGWWTECCAANLFWR
KGNVVYTPRLDQAGVNGIMRQFCIRLLAQSSYQLVEVQASLEESLQADEMVICNALMPV
MPVCACGDVSFSSATLYEYLAPLCE

>d1frfl_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfovibrio
fructosovorans}

TPQSTFTGPIVDPITRIEGHLRIMVEVENGKVKDAWSSSQLFRGLEIILKGRDPRDAQHFT
QRACGVCTYVHALASSRCVDDAVKVSIPANARMMRNLMASQYLHDHLVHFYHLHALD
WVDVTAALKADPNKAAKLAASIDTARTGNSEKALKAVQDKLKAFVESGQLGIFTNAYFL
GGHKAYYLPPEVNLIAAHYLEALHMQVKAASAMAILGGKNPHTQFTTVVGGCSNYQGLT

KDPLANYLALSKEVCQFVNECYIPDLLAVAGFYKDWGGIGGTSNYLAFGEFATDDSSPEK
HLATSQFPSGVITGRDLGKVDNVDLGAIEDVKYSWYAPGGDGKHPYDGVTDPKYTKLD
DKDHYSWMKAPRYKGKAMEVGPLARTFIAYAKGQPDFKKVVDMLGKLSVPATALHST
LGRTAARGIETAIVCANMEKWIKEMADSGAKDNTLCAKWEMPEESKGVGLADAPRGSLS
HWIRIKGKKIDNFQLVVPSTWNLGPRGPQGDKSPVEEALIGTPIADPKRPVEILRTVHA FDP
CIACGVH

>d1cc11_ e.18.1.1 (L:) Nickel-iron hydrogenase, large subunit {Desulfomicrobium
baculatum}

VKISIDPLTRVEGHLKIEVEVKDGKVVDKCSGGMFRGFEQILRGRDPRDSSQIVQRICGV
CPTAHCTASVMAQDDAFGVKVTNNGRITRNLI FGANYLQSHILHFYHLAALDYVKGP DVS
PFVPRYANADLLTDRIKDGA KADATNTYGLNQYLKALEIRRICHEMVAMFGGRMPHVQG
MVVGGATEIPTADKVAEY AARFKEVQKFVIEEYLPLIYTLGSVYTDLFETGIGWKNVIAFG
VFPEDDDYKTFL LKPGVYIDGKDEEFDSKLVKEYVGHSFFDHSAPGGLHYSVGETNPNPD
KPGAYSFVKAPRYKDKPCEVGPLARMWVQNPELSPVGQKLLKELYGIEAKKFRDLGDKA
FSIMGRHVLRAEETWLTAVAVEKW LKQVQPGAETYVKSEIPDAAEGTGFT EAPRGALLHY
LKIKDKKIENYQIVSATLWNANPRDDMGQRGPIEEALIGVVPDIKNPVNVGRLVRSYDPX
LGCAVH

>d1cc1s_ e.19.1.1 (S:) Nickel-iron hydrogenase, small subunit {Desulfomicrobium
baculatum}

KKAPVIWVQGGQCTGCSVSLNVAHPRIKEILLDVISLEFHPTVMASEGEMALAHMYEIA
EKFNNGNFFLLVEGAIPTAKEGRYCIVGETLDAKAHHHEVTMMELIRDLAPKSLATVAVGTC
SAYGGIPAAEGNVTGSKSVR DFFADEKIEKLLVNVPGCPPHPDWMVGTLVAAWSHVLNPT
EHPLPELDDDGRPLLFFGDNIHENC PYLDKYDNSEFAETFTKPGCKAELGCKGPSTYADCA
KRRWNNGINWCVENAVCIGC VEPDFPDGKSPFYVAE

>d1e3da_ e.19.1.1 (A:) Nickel-iron hydrogenase, small subunit {Desulfovibrio
desulfuricans}

SRPSVVYLHAAECTGCSEALLRTYQPFIDTLILDYHETIMAAAGEAAEEALQAAVN
GPDGFICLVEGAIPTGMDNKYGYIAGHTMYDICKNILPKAKAVVSIGTCACYGGIQA AKP
NPTAAKGINDCYADLG VKAINVPGCPPNPLNMVGTLVAFLKGQKIELDEVGRPVMFFGQS
VHDL CERRKHFDAGEFAPSFNSEEARKGWCLYDVGCKGPETYNNCPKVL FNETNWPVAA
GHPCIGCSEPNFWDDMT PFYQN

>d1lci_ e.23.1.1 (-) Luciferase {Firefly (Photinus pyralis)}

AKNIKKGPAPFYPLEDGTAGEQLHKAMKRYALVPGTIAFTDAHIEVNITYAEYFEMSVRLA
EAMKRYGLNTNHRIVVCS ENSLQFFMPVLGALFIGVAVAPANDIYNERELLNSMNISQPTV
VFVSKKGLQKILNVQKKLP IIQKIIIMDSKTDYQGFQSMYTFVTSHLPPGFNEYDFVPESFD
RDKTIALIMNSSGSTGLPKGVALPHRTACVRFSHARDPIFGNQIIPDTAILS VVPFHHGFGMF
TTLGYLICGFRVVL MYRFEEELFLRSLQDYKIQSALLVPTLFSFFAKSTLIDKYDLSNLHEIA
SGGAPLSKEVGEAVAKRFHLP GIRQGYGLTETTSAILITPEGDDKPGAVGKVVPF FEAKVV
DLDTGKTLGVNQRGELCVRGPMIMSGYVNNPEATNALIDKDGWLHSGDIAYWDEDEHFF
IVDRLKSLIKYKGYQVAPAELESILLQHPNIFDAGVAGLPDDDAGELPA AVVVLEHGKTMT
EKEIVDYVASQVTTAKKLRGGVV FVDEV PKGLTGKLDARKIREILIKAKK

>d1amua_ e.23.1.1 (A:) Phenylalanine activating domain of gramicidin synthetase 1 {Bacillus
brevis}

GTHEEEQYLFVNNTKAEYPRDKTIHQLFEEQVSKRPNNVAIVCENEQLTYHELNVKANQ

LARIFIEKGIGKDTLVGIMMEKSIDLFILAVLKAGGAYVPIDIEYPKERIQYILDDSQARM
LLTQKHLVHLIHNQFNGQVEIFEEDTIKIREGTNLHVPSKSTDLAYVIYTS GTTGNPKGTM
LEHKGISNLKVFFENSLNVTEKDRIQGFASISFDASVWEMFMALLTGASLYIILKDTINDFV
KFEQYINQKEITVITLPPTYVVHLDPERILSIQTLITAGSATSPSLVNKWKEKVITYINAYGPT
ETTICATTWVATKETIGHSVPIGAPIQNTQIYIVDENLQLKSVGEAGELCIGGEGLARGYWK
RPELTSQKFVDNPFVPGKLYKTGDQARWLS DGNIEYLGRIDNQVKIRGHRVELEEVEESIL
LKHMYISETAVSVHKDHQEQPYLCAYFVSEKHIPLEQLRQFSSEELPTYMIPSYFIQLDKMP
LTSNGKIDRKQLPEPD LTF

>d1ad2__ e.24.1.1 (-) Ribosomal protein L1 {*Thermus thermophilus*}

KRYRALLEKVDPNKIYTIDEAAHLVKELATAKFDETVEVHAKLGIDPRRS DQNVRGTVSL
PHGLGKQVRVLAIAKGEKIKEAEEAGADYVGGEEIIQKILDGWMDFD AVVATPDVMGAV
GSKLGRILGPRGLLPNPKAGTVGFNIGEIIREIKAGRIEFRNDKTGAIHAPVGKACFPPEKL
ADNIRAFIRALEAHKPEGAKGTFLRSVYVTTT MGPSVRINPHS

>d1cjsa_ e.24.1.1 (A:) Ribosomal protein L1 {*Archaeon Methanococcus jannaschii*}

MDREALLQAVKEARELAKPRNFTQSFEFIATLKEIDMRKPENRIKTEVVLP HGRGKEAKIA
VIGTGDLAKQAEELGLTVIRKEEIEELGKNKRKLRKIAKAH DFFIAQADLMPLIGRYMGVI
LGPRGKMPKVPANANIKPLVERLKKTVVINTRDKPYFQVLVGNEKMTDEQIVDNIEAVL
NVVAKKYEKGLYHIKDAYVKLTMGPAVKVKK

>d1a87__ f.1.1.1 (-) Colicin N {*Escherichia coli*}

SAKVGEITITPDNSKPGRYISSNPEYSLLAKLIDAESIKGTEVYTFHTRKGQYVKVTVPSDN
IDKMRVDYVNWKGPKYNNKLVRKFVSQFLLFRKEEKEKNEKEALLKASELVSGMGDKL
GEYLGVKYKNVAKEVANDIKNFHGRNIRSYNEAMASLNKVLANPKMKVNKSDKDAIVN
AWKQVNAKDMANKIGNLGKAFKVADLAIKVEKIREKSIEGYNTGNWG PLLLEVESWIIIG
GVVAGVAISLFGAVLSFLPISGLAVTALGVIGIMTISYLS SFIDANRVSNINNISSVIR

>d1cii_1 f.1.1.1 (451-624) Colicin Ia {*Escherichia coli*}

DAINFTEFLKSVSEKYGAKAEQLAREMAGQAKGKKIRNV EEAALKTYEKYRADINKKIN
AKDRAAIAAALESVKLS DISSNLNRFSRGLGYAGKFTSLADWITEFGKAVRTENWRPLFV
KTETIIAGNAATALVALVFSILTGSALGIIGYGLLMAVTGALIDESLVEKANKFW

>d1dlc_3 f.1.3.1 (61-289) delta-Endotoxin (insectocide), N-terminal domain {*Bacillus thuringiensis*
tenebrionis, CRYIIIA (BT13)}

TTKDVIQKGISVVGDLLGVVGFPFGGALVSFYTNFLNTIWPSED PWKAFMEQVEALMDQ
KIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFRN
SMPSFAISGYEVLFTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEYT
DHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR

>d1ciy_3 f.1.3.1 (33-255) delta-Endotoxin (insectocide), N-terminal domain {*Bacillus thuringiensis*,
CRYIA (A)}

YTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQA
ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT TAIPLLAVQNYQVPLL
SVYVQAANLHLSVLRDVS VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLER
VWGPDSRDWVRYNQFRRELT LTVLDIVALFSNYDSRRY

>d1i5pa3 f.1.3.1 (A:1-263) delta-Endotoxin (insectocide), N-terminal domain {*Bacillus*
thuringiensis subsp. *kurstaki*, CRY2AA}

MNNVLNSGRTTICDAYNVVAHDPFSFEHKSLDTIQKEWMEWKRTDHS LYVAPVVGTVSSF
LLKKVGS LIGKRILSELWGIIFPSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELIGLQA

NIREFNQQVDNFLNPTQNPVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANM
HLSFIRDVILNADEWGISAATLRTYRDYLRNYTRDYSNYCINTYQTAFRGLNTRLHDMLEF
RTYMFLNVFEYVSIWSLFK

>d1lxl_ f.1.4.1 (-) Apoptosis regulator Bcl-xL {Human (Homo sapiens)}

MSMAMSQSNRELVVDFLSYKLSQKGYWSQFSDVEENRTEAPEGTESEMETPSAINGNPS
WHLADSPAVNGATGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLSQLHITPG
TAYQSFEQVVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAWMATYLN
HLEPWIQENGWDTFVELYGNNAAESRKGQERLEHHHHHH

>d2bida_ f.1.4.1 (A:) Proapoptotic molecule Bid {Human (Homo sapiens)}

GSMDCEVNNGSSLRDECITNLLVFGFLQSCSDNSFRRELDALGHELPVLAPQWEGYDELQ
TDGNRSSHSRLGRIEADSESQEDIIRNIARHLAQVGDSMDRSIPPGLVNGLALQLRNTSRSE
EDRNRDLATALEQLLQAYPRDMEKEKTMLVLALLAKKVASHTPSLLRDVFHTTVNFINQ
NLRTYVRSLARNGMD

>d1f16a_ f.1.4.1 (A:) Proapoptotic molecule Bax {Human (Homo sapiens)}

MDGSGEQPRGGGPTSSEQIMKTGALLQGFQDRAGRMGGEAPELALDPVPQDASTKKL
SECLKRIGDELDSNMELQRMIAAVDTPREVFFRVAADMFSNGFNWGRVVALFYFASK
LVLKALCTKVPILRTIMGWTLDFLRERLLGWIQDQGGWDGLLSYFGTPTWQTVTIFVAG
VLTASLTIWKKMG

>d1c3wa_ f.2.1.1 (A:) Bacteriorhodopsin {Halobacterium salinarum}

TGRPEWIWLALGTALMGLGTLYFLVKGMGVSDPDAKKFYAITTLVPAIAFTMYLSMLLGY
GLTMVPFGGEQNPIYWARYADWLFTTPLLDDALLVDADQGTILALVGADGIMIGTGLV
GALTKVYSYRFVWWAISTAAMLYILYVLFFGFSMRPEVASTFKVLRNVTVLWSAYPVV
WLIGSEGAGIVPLNIETLLFMVLDVSAKVGFGILLRSRAIFG

>d1e12a_ f.2.1.1 (A:) Halorhodopsin {Halobacterium salinarum}

RENALLSSSLWVNVALAGIAILVFVYMGRITRPGRPRLIWGATLMIPLVSISSYLGLLSGLTV
GMIEMPAGHALAGEMVRSQWGRYLTWALSTPMILLALGLLADVDLGSFLT VIAADIGMC
VTGLAAAMTTTSALLFRWAFYAISCAFFVVLSALVTDWAASASSAGTAEIFDTRLRVTLVVL
WLGYPVWAVGVEGLALVQSVGATSWAYSVLDVFAKYVF AFILLRWVANNERTVAV

>d1h68a_ f.2.1.1 (A:) Sensory rhodopsin II {Natronobacterium pharaonis}

VGLTTFLFWLGAIGMLVGTLAFAWAGRDAGSGERRYVYTLVGISGIAAVAYVVMALGVGW
VPVAERTVFAPRYIDWILTTP LIVYFLGLLAGLDSREFGIVITLNTVVMLAGFAGAMVPGIE
RYALFGMGAVAFLGLVYYLVGPMTESASQRSSGKSLYVRLRNLT VILWAIYPFIWLLGPPG
VALLTPTVDVALIVYLDLVTKVGFGFIALDAAATL

>d1hzxa_ f.2.1.1 (A:) Rhodopsin {Cow (Bos taurus)}

MNGTEGPNFYVPFSNKTGVVRSPFEAPQYYLAEPWQFSMLAAYMFLIMLGFPINFLTLY
VTVQHKKLRTPLNYILLNLAVADLFMVFGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGG
EIALWSLVVLAIERVYVVKPMSNFRFGENHAIMGVAFTWVMALACAAPPLVGWSRYIPE
GMQCSCGIDYYTPHEETNNESFVIYMFVVFHFIPLIVIFFCYGQLVFTVKEAAAQQQESATT
QKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKTSAYYNPVIY
IMMNKQFRNCMVTTLCCGKNPLGDDEASTTVSKTETSQVAPA

>d1dxrh2 f.2.1.2 (H:1-36) Photosynthetic reaction centre, L-, M- and H-chains
{Rhodospseudomonas viridis}

MYHGALAQHLDAQLVWYAQWLVIWTVVLLYLRRD

>d1dxrm1 f.2.1.2 (M:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodospseudomonas

viridis}

ADYQTIYTQIQARGPHITVSGEWDNDRVGKPFYSYWLKGIGDAQIGPIYLGASGIAAF
GSTAILILFNMAAEVHFDPLQFFRQFFWLGLYPPKAQYGMGIPPLHDGGWWLMAGLFMT
LSLGSWWIRVYSRARALGLGTHIAWNFAAAIFFVLCIGCIHPTLVGSWSEGVPGIWP
HIDWLTAFSIRYGNFYPCPWHGFSIGFAYGCGLLFAAHGATILAVARFGGDREIEQITDRGTAVE
RAALFWRWTIGFNATIESVHRWGWFFSLMVMVSASVGILLTGTTFVDNWYLWCVKHGAA
PDYPAYLPATPDASLPGAPK

>d1qov11 f.2.1.2 (L:) Photosynthetic reaction centre, L-, M- and H-chains {Rhodobacter
sphaeroides}

ALLSFERKYRVPGGTLVGGNLFDFWVGPFYVGFFGVATFFFAALGIILIAWSAVLQGTWNP
QLISVYPPALEYGLGGAPLAKGGLWQIITICATGAFVSWALREVEICRKLIGYHIPFAFAFA
ILAYLTLVLFRPVMGAWGYAFPYGIWTHLDWVSNTGYTYGNFHYNPAHMIAISFFFTNA
LALALHGALVLSAANPEKGKEMRTPDHEDTFFRDLVGYSIGTLGIHRLGLLLSLSAVFFSA
LCMIITGTIWFQWVDWWQWWVKLPWWANIPGGING

>d1eysh2 f.2.1.2 (H:7-43) Photosynthetic reaction centre, L-, M- and H-chains
{Thermochromatium tepidum}

HYIDAAQITIWAFLFFFGLIYLRREDKREGYPLDS

>d1ocrb2 f.2.1.3 (B:1-90) Cytochrome c oxidase {Cow (Bos taurus)}

MAYPMQLGFQDATSPIMEELLHFHDHTLMIVFLISSLVLYIISLMLTTKLTHSTMDAQEVE
TIWTILPAIILIALPSLRILYMMDEI

>d1ocrd1 f.2.1.3 (D:) Cytochrome c oxidase {Cow (Bos taurus)}

SVVKSEDYALPSYVDRRDYPLPDVAHVKNLSASQKALKEKEKASWSSLSIDEKVELYRLK
FKESFAEMNRSTNEWKTTVGAAMFFIGFTALLLIWEKHYYVYGPIPHTFEEEEWVAKQTKR
MLDMKVAPIQGFSAKWDYDKNEWKK

>d1ocrg1 f.2.1.3 (G:) Cytochrome c oxidase {Cow (Bos taurus)}

ASAAKGDHGGTGARTWRFLTFGLALPSVALCTLNSWLHSGHRERPAFIPYHHLRIRTKPFS
WGDGNHTFFHNPRVNPLPTGYEK

>d1ocri1 f.2.1.3 (I:) Cytochrome c oxidase {Cow (Bos taurus)}

STALAKPQMRGLLARLRHFHIVGAFMVSLGFATFYKFAVAEKRRKKAYADFYRNYDSMKD
FEEMRKAGIFQSAK

>d1ocrj1 f.2.1.3 (J:) Cytochrome c oxidase {Cow (Bos taurus)}

FENRVAEKQKLFQEDNGLPVHLKGGATDNILYRVMTLCLGGTLYSLYCLGWASFPHK

>d1ocr11 f.2.1.3 (L:) Cytochrome c oxidase {Cow (Bos taurus)}

SHYEEGPGKNIPFSVENKWRLAMMTLFFGSGFAAPFFIVRHQLLKK

>d1ocrm1 f.2.1.3 (M:) Cytochrome c oxidase {Cow (Bos taurus)}

ITAKPAKTPTSPKEQAIGLSVTFLSFLLPAGWVLYHLDNYKKS

>d1ar1a1 f.2.1.3 (A:) Cytochrome c oxidase {Paracoccus denitrificans}

GFFTRWFMSTNHKDIGILYLF TAGIVGLISVCFTVYMRMELQHPPGVQYMCLEGARLIADA
SAECTPNGHLWNVMITYHGVLMFFVVIPALFGGFGNYFMPLHIGAPDMAFPRLNNLSY
WMYVCGVALGVASLLAPGGNDQMGSVGWVLYPPLSTTEAGYSMDLAIFAVHVS GASSI
LGAINIITTF LNM RAPGMTLFKVPLFAWSVFITAWLILLSLPVLAGAITMLLMDRNFGTQFF
DPAGGGDPVLYQHILWFFGHPEVYIIILPGFGIISHVISTFAKKPIFGYLPMLVLA MA AIGILGF
VVAHHMYTAGMSLTQQAYFMLATMTIAVPTGIKVFSWIATMWGGSIEFKTPMLWAFGF
LFLFTVGGVTGVVLSQAPLDRVYHDTYYYVVAHFHYVMSLGA VFGIFAGVYYWIGKMSGR

QYPEWAGQLHFWMMFIGSNLIFFPQHFLGRQGMPPRRYIDYPVEFAYWNNISSIGAYISFAS
FLFFIGIVFYTLFAGKRVNVPNYWNEHADTLEWTLPSPPPEHTFET

>d1ar1b2 f.2.1.3 (B:1-107) Cytochrome c oxidase {Paracoccus denitrificans}

QDVLGDLVPVIGKPVNGGMNFQPASSPLAHDQQWLDHFVLYIITAVTIFVCLLLLICIVRFNR
RANPVPARFTHNTPIEVIWTLVPVLILVAIGAFSLPILFRSQEMP

>d1qlec1 f.2.1.3 (C:) Cytochrome c oxidase {Paracoccus denitrificans}

AHVKNHDYQILPPSIWPFPGAIGAFVMLTGAVAWMKGITFFGLPVEGPWMFLIGLVGVLY
VMFGWWADVNEGETGEHTPVVRIGLQYGFILFIMSEVMFFVAWFVAFIKNALYPMGPD
SPIKDGVPPEGIVTFDPWHLPLINTLILLLSGVAVTWAHHAFVLEGDRKTTINGLIVAVILG
VCFTGLQAYEYSHAAFGADTVYAGAFYMATGFHGAHVIIGTIFLVCLIRLLKGQMTQK
QHVGFEAAAWYWHFVDVWVWLFVVIYIWGR

>d1ehka1 f.2.1.3 (A:) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

AYPEKKATLYFLVLGFLALIVGSLFGPFQALNYGNVDAYPLLKRLLPFVQSYYQGLTLHG
V LNAIVFTQLFAQAIMVYLPARELNMRPNMGLMWLSWWMAFIGLVVAALPLLANEATVLY
TFYPPLKGHWAFFYLGASVFLSTWVSIYIVLDLWRRWKAANPGKVTPLVTYMAVFWL
MWFLASLGLVLEAVLFLLPWSFGLVEGVDPLVARTLFWWTGHPIVYFWLLPAYAIIYTILP
KQAGGKLVS DPMARLAFLFLLLSTPVGFHHQFADPGIDPTWKMIHSLTLFVAVPSLMTA
FTVAASLEFAGRLRGGRGLFGWIRALPWDNPAFVAPVLGLLGFIPGGAGGIVNASFTLDYV
VHNTAWVPGHFHLQVASLVTLTAMGSLYWLLPNLTGKPISDAQRRGLAVVWLWFLGMM
IMAVGLHWAGLLNVPRRAYIAQVPDAYPHAAPMVFNVLGIVLLVALLLFIYGLFSVLLS
RERKPELAEAPLPAEVISGPEDRRLVLAMDRIGFWFAVAAILVVLAYGPTLVQLFGHLNPV
PGWRLW

>d1ehkb2 f.2.1.3 (B:3-40) Cytochrome c oxidase {Thermus thermophilus, ba3 type}

DEHKAHKAILAYEKGWLAFLSLAMLFVFIALIAYTLATH

>d1fta1 f.2.1.3 (A:) Ubiquinol oxidase {Escherichia coli}

VDHKRLGIMYIIVAIVMLLRGFADAIMMRSQQALASAGEAGFLPPHHYDQIFTAHGVIMIF
FVAMPFVIGLMNLVPLQIGARDVAFPLNLSFWFTTVVGVILNVSLGVGEFAQTGWLA
YPLSGIEYSPGVGVWDYWIWSLQLSGIGTTLTGINFVTILKMRAPGMTMFKMPVFTWASL
CANVLIASFILTVTVALLTLDRYLGTHFFTNDMGGNMMMYINLIWAWGHPEVYILILPVF
GVFSEIAATFSRKRLFGYTSLVWATVCITVLSFIVWLHHFFTMGAGANVNAAFFGITTMIIAIP
TGVKIFNWLFTMYQGRIVFHSAMLWTIGFIVTFSVGGMTGVLLAVPGADVLHNSLFLIA
HFHNVIIGGVVFGCFAGMTYWWPKAFGFKLNETWGKRAFWFWIIGFFVAFMPLYALGFM
GMTRRLSQQIDPQFHTMLMIAASGAVLIALGILCLVIQMYVSIRDRDQNRDLTGDPWGGR
TLEWATSSPPPFYNF

>d1ftb2 f.2.1.3 (B:27-117) Ubiquinol oxidase {Escherichia coli}

SALLDPKGQIGLEQRSILTAFLGLMLIVVIPAILMAVGFAWKYRASNKDAKYSNWSHSNK
VEAVVWTVPIIIIFLAVLTWKTTHALEPS

>d1ftc1 f.2.1.3 (C:) Ubiquinol oxidase {Escherichia coli}

HDAGGTKIFGFWIYLMSDCILFSILFATYAVLVNGTAGGPTGKDIFELPFVLVETFLLLFSSIT
YGMAAIAMYKNNKSQVISWLALTWLFAGAGFIGMEIYEFHHLIVNGMGPDRSGFLSAFFAL
VGTHGLHVTSGLIWMAVLMVQIARRGLTSTNRTRIMCLSLFWHFLDVVVICVFTVVYLM
GA

>d1c0va_ f.2.1.4 (A:) Subunit C {Escherichia coli}

MENLNMDLLYMAAAVMMGLAAIGAAIGIGILGGKFLEGAARQPDLIPLLRTQFFIVMGLV

DAIPMIAVGLGLYVMFAVA

>d1c17m_ f.2.1.4 (M:) Subunit A {Escherichia coli}

HGKSKLIAPLALTIFVWVFLMNLMDLLPIDLLPYIAEHVLGLPALRVVPSADVNVTLSMAL
GVFILILFYSIKMKGIGGFTKELTLQPFNHWAFIPVNLILEGVSLLSKPVSLGLRLFGNMYAG
ELIFILIAGLLPWWSQWILNVPWAIHFILIIITLQAFIFMVLTIYLS

>d1h6ia_ f.2.1.5 (A:) Aquaporin-1 {Human (Homo sapiens)}

LFWRVVAEFLATTFLVFISIGSALGFKYPVGNNQTAVQDNVKVSLAFGLSIATLAQSVGHI
SGAHLNPAVTLGLLLSCQISIFRALMYIIAQCVGAIVATAILSGITSSLTGNSLGRNDLADGV
NSGQGLGIEIIGTLQLVLCVLATTDRRRRDLGGSAPLAIGLSVALGHLLAIDYTGCGINPAR
SFGSAVITHNFSNHWFVWVGPFIGGALAVLIYDFILAP

>d1fx8a_ f.2.1.5 (A:) Glycerol uptake facilitator protein GlpF {Escherichia coli}

TLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISVIWGLGVAMAIYLTAGVSGAH
LNPAVTIALWLFACFDKRKVIPFIVSQVAGAFCAAALVYGLYYNLFFDFEQTHHIVRGSVES
VDLAGTFSTYPNPHINFVQAFVEMVITAILMGLILALTDDGNGVPRGPLAPLLIGLLIAVIG
ASMGPLTGAMNPARDFGPKVFAWLAGWGNVAFTGGRDIPYFLVPLFGPIVGAIVGAFAY
RKLIGRHL

>d1f6ga_ f.2.1.11 (A:) Potassium channel protein {Streptomyces lividans}

MPPMLSGLLARLVKLLLGRHGSALHWAAAGAATVLLVIVLLAGSYLAVLAERGAPGAQLI
TYPALWWSVETATTVGYGDLYPVTWLGRCVAVVVMVAGITSFGLVTAALATWFGVREQ
ERRGHFVRHSEKAAEEAYTRTTRALHERFDRLERMLDDNRR

>d1kkda_ f.2.1.11 (A:) Small conductance potassium channel {Rat (Rattus norvegicus)}

RKLELTKAIEKHVHNFMMDTQLTKRVKNAAANVLRETWLIYKNTKLVKKIDHAKVRKHQ
RKFLQAIHQRLRSVKMEQRKLNDQANTLVDLAKTQ

>d1msla_ f.2.1.11 (A:) Gated mechanosensitive channel {Mycobacterium tuberculosis}

ARGNIVDLAVAVVIGTAFTALVTKFTDSIITPLINRIGVNAQSDVGILRIGIGGGQTIDLVLL
SAAINFFLIAFAVYFLVLPYNTLRKKGEVEQPGDTQVVLTEIR

>d1be3e2 f.2.1.8 (E:1-69) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

SHTDIKVPDFSDYRRPEVLDSTKSSKESSEARKGFSYLVATTTTVGVAYAANKNVVSQFVSS
MSASADVL

>d1be3f1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

AVSASSRWLEGIRKWYYNAAGFNKLGLMRDDTIHENDDVKEAIRRLPENLYDDRVFRIKR
ALDLSMRQQILPKEQWTKYEEDKSYLEPYLKEVIRERKEREWAKK

>d1be3g1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

GRQFGHLTRVRHVITYSLSPFEQRAFPHYFSKGIPNVLRTRACILRVAPPFVAFYLVYTWG
TQEFESKRKNPAAYENDR

>d1qcrk1 f.2.1.8 (K:) Cytochrome bc1 transmembrane subunits {Cow (Bos taurus)}

MLTRFLGPRYRQLARNWVPTAQLWGAVGAVGLVSATDSRLILDWV

>d1bccd3 f.2.1.8 (D:196-241) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

PEHDHRKRMGLKMLLMMGLLVPLVYYMKRHKWSVLKSRKLAYRPPK

>d1bcc1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

LVDPLTTVREQCEQLEKCVKARERLELCDERVSSRSQTEEDCTEELDFDLHARDHCVAHK
LFNSLK

>d1bccj1 f.2.1.8 (J:) Cytochrome bc1 transmembrane subunits {Chicken (Gallus gallus)}

TLTARLYSLLFRRTSTFALTIVVGALLFERAFDQGADAIYEHINEGKLWKHIKHKYENK

>d1ezvc1 f.2.1.8 (C:) Cytochrome bc1 transmembrane subunits {Baker's yeast (*Saccharomyces cerevisiae*)}

MAFRKSNVYLSLVNSYIIDSPQPSSINYWWNMGSLLGLCLVIQIVTGIFMAMHYSSNIELAF
SSVEHIMRDVHNGYILRYLHANGASFFFMVMFMHMAKGLYYGSYRSPRVTLWNVGVIIIF
TLTIATAFLGYCCVYGQMSHWGATVITNLFSAIPFVGNDIVSWLWGGFSVSNPTIQRFFAL
HYLVPFIIAAMVIMHLMALHHGSSNPLGITGNLDRIPMHSYFIFKDLVTVFLFMLILALFVF
YSPNTLGHDPNYIPGNPLVTPASIVPEWYLLPFYAILRSIPDKLLGVITMFAAILVLLVLPFTD
RSVVRGNTFKVLSKFFFFIFVFNFVLLGQIGACHVEVPYVLMGQIATFIYFAYFLIIVPVISTI
ENVLFYIGRVNK

>d1ezve2 f.2.1.8 (E:31-86) Cytochrome bc1 transmembrane subunits {Baker's yeast (*Saccharomyces cerevisiae*)}

KSTYRTPNFDDVLKENNDADKGRSYAYFMVGAMGLLSSAGAKSTVETFISSMTATA

>d1ezvf1 f.2.1.8 (F:) Cytochrome bc1 transmembrane subunits {Baker's yeast (*Saccharomyces cerevisiae*)}

QSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRRRLPE
DESYARAYRIIRAHQTELTHHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIEVS
K

>d1ezvg1 f.2.1.8 (G:) Cytochrome bc1 transmembrane subunits {Baker's yeast (*Saccharomyces cerevisiae*)}

GPPSGKTYMGWWGHMGGPKQKGITSYAVSPYAQKPLQGIFHNAVFNFSRRFKSQFLYVLI
PAGIYWYWKNNGNEYNEFLYSKAGREELERVNV

>d1ezvh1 f.2.1.8 (H:) Cytochrome bc1 transmembrane subunits {Baker's yeast (*Saccharomyces cerevisiae*)}

VTDQLEDLREHFKNTEEGKALVHHYEECAERVKIQQQQPGYADLEHKEDCVEEFFHLQH
YLDTATAPRLFDKLLK

>d1ezvi1 f.2.1.8 (I:) Cytochrome bc1 transmembrane subunits {Baker's yeast (*Saccharomyces cerevisiae*)}

SSLYKTFFKRNAVFGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAA

>d1fumc_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {*Escherichia coli*}

TTKRKPYPVPMSTSTWWKKLPFYRFYMLREGTAVPAVWFSIELIFGLFALKNGPEAWAGFV
DFLQNPVIVIINLITLAAALLHTKTWFELAPKAANIIVKDEKMGPEPIIKSLWAVTVVATIVIL
FVALYW

>d1fumd_ f.2.1.9 (D:) Fumarate reductase respiratory complex transmembrane subunits {*Escherichia coli*}

INPNPKRSDEPVFWGLFGAGGMWSAIIAPVMILLVGILLPLGLFPGDALSYERVLAFAQSFI
GRVFLFLMIVLPLWCGLHRMHAMHDLKIHVPAGKWVIFYGLAAILTVVTLIGVVTI

>d1qlac_ f.2.1.9 (C:) Fumarate reductase respiratory complex transmembrane subunits {*Wolinella succinogenes*}

MTNESILESYSGVTPERKKSRMPAKLDWWQSATGLFLGLFMIGHMFFVSTILLGDNVML
WVTKKFELDFIFEGGKPIVVSFLAAFVFAVFAHAFLAMRKFPINYRQYLTFTKTHKDLMRH
GDTTLWWIQAMTGAMFFLGSVHLYIMMTQPQTIGPVSSSFRMVSEWMWPLYLVLLFAV
ELHGSVGLYRLAVKWGWFDGETPDKTRANLKKLKTLMFAFLIVLGLLTFGAYVKKGLEQ
TDPNIDYKYFDYKRTH

>d1jb0a_ f.2.1.12 (A:) Photosystem I {Synechococcus elongatus}
RVVVDNDPVPTSFEKWAKPGHFDRTLARGPQTTTWIWNLHALAHDFDTHSTSDLEDISRKI
FSAHFGHLAVVFIWLSGMYFHGAKFSNYEAWLADPTGIKPSAQVVWPIVGGQILNGDVG
GGFHGIQITSGLFQLWRASGITNEFQLYCTAIGGLVMAGLMLFAGWGFHYHKRAPKLEWFQ
NVESMLNHHLAGLLGLGSLAWAGHQIHVSLPINKLLDAGVAAKDIPLPHEFILNPSLMAEL
YPKVDWGGFFSGVIPFFTFNWAAYSDFLTFNGGLNPVTGGLWLSDTAHHHLAIAVLFIAGH
MYRTNWGIGHSLKEILEAHKGPFTGAGHKGLYEVLTTSWHAQLAINLAMMGSLSIIVAQH
MYAMPPYPYLATDYPTQLSLFTHHMWIGGLVVGGAAGHGAIFMVRDYPAMNQNNVLD
RVLRRDAIISHLNWVCIFLGFHSFGLYVHNDTMRAFGRPQDMFSDTGILQPVFAQWVQ
NLHTLAPGGTAPNAAATASVAFGGDVVAVGGKVAMMPIVLGTADFMVHHIHAFTIHVTVL
ILLKGVLFARSSRLIPDKANLGRFPCDGPGRGGTCQVSGWDHVFLGLFWMYNCISVVIF
HFSWKMQSDVWGTVPDGTVSHITGGNFAQSAITINGWLRDFLWAQASQVIGSYGSALS
AYGLLFLGAHFIWAFSLMFLFSGRGYWQELIESIVWAHNKLKVAPAIQPRALSIIQGRAVGV
AHYLLGGIATTWAFFLARIISVG

>d1jb0f_ f.2.1.12 (F:) Photosystem I {Synechococcus elongatus}
DVAGLVPCKDSPAFQKRAAAVNNTADPASGQKRFRERYSQALCGEDGLPHLVVDGRLSRA
GDFLIPSVLFLYIAGWIGWVGRAYLIAVRNSGEANEKEIHDVPLAIKCMLTGFAWPLAALK
ELASGELTAKDNEITVSPR

>d1jb0i_ f.2.1.12 (I:) Photosystem I {Synechococcus elongatus}
MMGSYAASFLPWIFPVVCWLMPTVVMGLLFLYIEGEA

>d1jb0k_ f.2.1.12 (K:) Photosystem I {Synechococcus elongatus}
ILCNLFAIALGRYAIQSRGKGPGLPIALPALFEGFGLPELLATTSFGHLLAAGVVSGL

>d1jb0l_ f.2.1.12 (L:) Photosystem I {Synechococcus elongatus}
LVKPYNGDPFVGHLSPTISDSGLVKTFIGNLPAYRQGLSPILRGLEVGMAGHYFLIGPWVK
LGPLRDSVDANLGGSLISGIALILVATACLAAYGLVSFQKGGSSSDPLKTSEGWSQFTAGFFV
GAMGSAFVAFFLLENFLVVDGIMTGLFN

>d1kzua_ f.3.1.1 (A:) Light-harvesting complex subunits {Purple bacterium (Rhodospseudomonas acidophila)}
MNQGGKIWTVVNPAIGIPALLGSVTVIAILVHLAILSHTTWFPAYWQGGV

>d1lgha_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodospirillum molischianum}

SNPKDDYKIWLVINPSTWLPVIWIVATVVAIAVHAHVLAAPGFNWIALGAAKSAK

>d1lghb_ f.3.1.1 (B:) Light-harvesting complex subunits {Rhodospirillum molischianum}

RSLSGLTEEEAIAVHDQFKTTFSAFIILAAVAHVLVVWVKPWF

>d1jo5a_ f.3.1.1 (A:) Light-harvesting complex subunits {Rhodobacter sphaeroides}
ADKSDLGYTGLTDEQAQELHSVYMSGLWLFSAVAIAHLAVYIWRPWF

>d1g90a_ f.4.1.1 (A:) Outer membrane protein A (OMPA) transmembrane domain {Escherichia coli}

APKDNTWYTGAKLGFSQYHDTGFINNNGPTHENQLGAGAFGGYQVNPYVGFEMGYDFL
GRMPYKGSVENGAYKAQGVQLTAKLGYPITDDLDIYTRLGGMVFRADTKSNVYGKNHD
TGVSPVFAGGVEYAITPEIATRLEYQFTNNIGDAHTIGTRPDNGMLSLGVSYRFGQGEAA

>d1qj8a_ f.4.1.1 (A:) Outer membrane protein X (OMPX) {Escherichia coli}
ATSTVTGGYAQSDAQGQMNMKGGFNLKYRYEEDNSPLGVIGSFTYTEKSRTASSGDYNK

NQYYGITAGPAYRINDWASIYGVVGVGYGKFQTTEYPTYKNDTSDYGFSYGAGLQFNPM
ENVALDFSYEQSRIRSVDTVGTWIAGVGYRF

>d2por__ f.4.3.1 (-) Porin {Rhodobacter capsulatus}

EVKLSGDARMGVMYNGDDWNFSSRSRVLFTMSGTTDSGLEFGASFKAHESVGAETGED
GTVFLSGAFGKIEMGDALGASEALFGDLYEVGYTDLDDRGGNDIPYLTGDERLTAEDNPV
LLYTSAGAFSVAASMSDGKVGETSEDDAQEMAVAAAYTFGNYSVGLGYEKIDSPDTAL
MADMEQLELAAIAKFGATNVKAYYADGELDRDFARAVFDLTPVAAAATAVDHKAYGLSV
DSTFGATTVGGYVQVLIDITDDVTYYGLGASYDLGGGASIVGGIADNDLPNSDMVADL
GVKFKF

>d3prn__ f.4.3.1 (-) Porin {Rhodopseudomonas blastica, strain DSM2131}

MISLNGYGRFGLQYVEDRGVGLLEDTHISSRLRINIVGTTETDQGVTFGAKLRMQWDDGDA
FAGTAGNAAQFWTSYNGVTVS VGNVDTAFDSVALTYDSEMGYEWSSFGDAQSSFFAYNS
KYDASGALDNYNGIAVTYSISGVNLYLSYVDPDQTVDSSLVTEEFGIAADWSNDMISLAA
AYTTDAGGIVDNDIAFVGAAYKFNDAGTVGLNWDNGLSTAGDQVTLYGNYAFGATTV
RAYVSDIDRAGADTAYGIGADYQFAEGVKVSGSVQSGFANETVADVGVRFDF

>d1osma_ f.4.3.1 (A:) Porin {Klebsiella pneumoniae}

AEIYNKDGKLDLYGKIDGLHYFSDDKDVDGDQTYMRLGVKGETQINDQLTGYGQWEY
NVQANNTSSSDQAWTRLAFAGLKFAGDAGSFDYGRNYGVVYDVTSWTDVLPEFGGDTY
GSDNFLQSRANGVATYRNSDFFGLVDGLNFALQYQGKNGSVSGEGATNNGRGALKQNGD
GFGTSVTYDIFDGISAGFAYANSKRDDQNQLLLGEGDHAETYTGGLKYDANNIYLATQY
TQTYNATRAGSLGFANKAQNFVAAQYQFDFGLRPSVAYLQSKGKDLNGYGDQDILKYV
DVGATYYFNKNMSTYVDYKINLLDDNSFTRSAGISTDDVVALGLVYQF

>d1e54a_ f.4.3.1 (A:) Porin {Comamonas acidovorans}

ESSVTLFGIVDTNVAYVNKDAAGDSRYGLGTSGASTSRLGLRGTEDLGGGLKAGFWLEG
EIFGDDGNASGFNFKRRSTVSLSGNFGEVRLGRDLVPTSQKLTSYDLFSATGIGPFMGFRN
WAAGQGADDNGIRANNLISYYTPNFGGFNAGFGYAFDEKQTIGTADSVGRYIGGYVAYD
NGPLSASLGLAQQKTAVGGLATDRDEITLGASYNFVAKLSGLLQQTKFKRDIGGDIKTNS
YMLGASAPVGGVGEVKLQYALYDQKAIDSKAHQITLGYVHNLSKRTALYGNLAFLKNKD
ASTLGLQAKGVYAGGVQAGESQTGVQVGIRHAF

>d1af6a_ f.4.3.2 (A:) Maltoporin (also LamB protein) {Escherichia coli}

VDFHGYARSGIGWTGSGGEQQCFQTTGAQSKYRLGNECETYAELKLGQEVWKEGDKSF
YFDTNVAYSVAQQNDWEATDPAFREANVQGNLIEWLPGSTIWAGKRFYQRHVDHIMIDF
YYWDISGPGAGLENIDVGFGKLSLAATRSSEAGGSSSFASNNIYDYTNETANDVFDVRLA
QMEINPGGTLELGVYDGRANLRDNYRLVDGASKDGWLFTAHTQSVLKGFNKFVQYA
TDSMTSQGKGLSQSGVAFDNEKFAYNINNNGHMLRILDHGAISMGDNDMMYVGMY
QDINWDNDNGTKWWTVGIRPMYKWTPI MSTVMEIGYDNVESQRTGDKNNQYKITLAQQ
WQAGDSIWSRPAIRVFATYAKWDEKWGYDYTG NADNNANFGKAVPADFN GGSFGRGDS
DEWTFGAQMEIWW

>d1a0tp_ f.4.3.2 (P:) Sucrose-specific porin {Enterobacterium (Salmonella typhimurium)}

SGFEFHGYARSGVIMNDSGASTKSGAYITPAGETGGAIGRLGNQADTYVEMNLEHKQTLT
NGATTRFKVMVADGQTSYNDWTASTSDLNVRQAFVELGNLPTFAGPFKGSTLWAGKRFD
RDNFDIHWIDSDVVFLAGTGGGIYDVKWNDGLRSNFSLYGRNFGDIDDSSNSVQNYILTM
NHFAGPLQMMVSGLRAKDNDRKDSNGNLAKGDAANTGVHALLGLHNSDFYGLRDS
SKTALLYGHGLGAEVKIGSDGALRPGADTWRIASYGTTPLSENWSVAPAMLAQRSKDR

YADGDSYQWATFNLRLIQAINQNALAYEGSYQYMDLKPEGYNDRQAVNGSFYKLTFAPT
FKVGSIGDFFSRPEIRFYTSWMDWSKKLNNYASDDALGSDGFNSGGEWSFGVQMETWF
>d1by5a_ f.4.3.3 (A:) Ferric hydroxamate uptake receptor FhuA {Escherichia coli}
QESAWGPAATIAARQSATGKTDTPIQKVPQSSISVVTAEEEMALHQPKSVKEALSYPGVSV
GTRGASNTYDHLIIRGFAAEGSQNNYLNGLKLQGNFYNDAAVIDPYMLERAIEIMRGPVSV
LYGKSSPGGLLMVSKRPTTEPLKEVQFKAGTDSLFTGTGDFSDSLDDDDGVYSYRLTGLA
RSANAQQKGSEEQRYAIAPAFTWRPDDKTNFTFLSYFQNEPETGYYGWLPKEGTVEPLPN
GKRLPTDFNEGAKNNTYSRNEKMGVGSFDFHEFNDTFTVRQNLRAENKTSQNSVYGYG
VCSDPANAYSKQCAALAPADKGHYLARKYVVDDEKLQNFVSDTQLQSKFATGDIDHTLL
TGVDfMRMRNDINAWFGYDDSVPLLNLYNPVNTDFDFNAKDPANSGPYRILNKQKQGTGV
YVQDQAQWDKVLVTLGGRYDWADQESLNRVAGTTDKRDDKQFTWRGGVNYLFDNGVT
PYFSYSESFEPSSQVGKDNIFAPSKGKQYEVGVKYPEDRPIVVTGAVYNLTCTNNLMA
DPEGSFFSVEGGEIRARGVEIEAKRPLSASVNVVGSYTYTDAEYTTDTTYKGNTPAQVPK
HMASLWADYTFDGLPSGLTLGTGGRYTGSSYGDPANSFKVGSYTVVDALVRYDLARVG
MAGSNVALHVNNLFDREYVASCFTYGCFWGAERQVVATATFRF

>d1fepa_ f.4.3.3 (A:) Ferric enterobactin receptor FepA {Escherichia coli}
DDTIVVTAAEQNLQAPGVSTITADEIRKNPVARVSKIIRTMPGVNLTGNSTSGQRGNNRQI
DIRGMGPENTLILIDGKPVSSRNSVRQGWGERDTRGDTSWVPEMERIEVLRGPAAARY
GNGAAGGVVNIITKKGSGEWHGSWDAYFNAPEHKEEGATKRTNFSLTGPLGDEFSEFRLYG
NLDKTQADAWDINQGHQSARAGTYATTLPAGREGVINKDINGVVRWDFAPLQSLELEAG
YSRQGNLYAGDTQNTNSDSYTRSKYGDENRLYRQNYALTWNGGWDNGVTTSNWVQY
EHTRNSRIPEGLAGGTEGKFNEKATQDFVDIDLDDVMLHSEVNLPIDFLVNQTLTLGTEW
NQQRMKDLSSTQALTGTNTGGAIDGVSTTDRSPYSKAEIFSLFAENNMELTDSTIVTPGL
RFDHHSIVGNNWSPALNISQGLGDDFTLKMGIARAYKAPSLYQTNPNYILYSKGQGCYAS
AGGCYLQGNDDLKAETSINKEIGLEFKRDGWLAVGTWFRNDYRNKIEAGYVAVGQNAV
GTDLYQWDNVPKAVVEGLEGLSNVPVSETVMWTNNITYMLKSENKTTGDRLSIPEYTLN
STLSWQAREDLSMQTTFTWYGKQPKKYNKYGQPAVGPETKEISPYISIVGLSATWDVTK
NVSLTGVDNLFDKRLWRAGNAQTTGDLAGANYIAGAGAYTYNEPGRTWYMSVNTHF

>d7ahla_ f.6.1.1 (A:) Alpha-hemolysin {Staphylococcus aureus}
ADSDINIKTGTTDGSNTTVKTDGLVTDYDKENGMHKKVFYSFIDDKNHNKLLVIRTKGTI
AGQYRVYSEEGANKSGLAWPSAFKVQLQLPDNEVAQISDYPRNSIDTKEYMSTLTYGFN
GNVTGDDTGKIGGLIGANVSIGHTLKYYVQPDFKTILESPTDKKVGWKVIFNNMVNQNWG
PYDRDSWNPVYGNQLFMKTRNGSMKAADNFLDPNKASSLLSSGFSPDFATVITMDRKAS
KQQTNIIDVIYERVRDDYQLHWTSTNWKGTNTKDKWTDRSSERYKIDWEKEEMTN

>d1pvl_ f.6.1.1 (-) Leucocidin K component LukF-PV {Staphylococcus aureus}
AQHITPVSEKKVDDKITLYKTTATSDSKLKISQILTFNFIKDKSYDKDTLILKAAGNIYSGY
TKPNPKDTISSQFYWGSKYNISINSDSNDSVNVVDYAPKNQNEEFQVQQTVGYSGGDINI
SNGLSGGGNGSKSFSETINYKQESYRTSLDKRTNFKKIGWDVEAHKIMNNGWGPYGRDS
YHSTYGNEMFLGSRQSNLNAGQNFLEYHKMPVLSRGNFNPEFIGVLSRKQNAAKKSKIT
VTYQREMDRYTNFWNQLHWIGNNYKDENRATHTSIYEVDWENHTVKLIDTQSKEKNPM
S

>g6rlx.1 g.1.1.1 (B:,A:) Relaxin {Human (Homo sapiens)}

SWMEEVIKLCGRELVRAQIAICGMSTWXELYSALANKCCHVGCTKRSLARFC

>d3lria_ g.1.1.1 (A:) Insulin-like growth factor {Human (Homo sapiens)}

MFPAMPLSSLFVNGPRTLTCGAELVDALQFVCGDRGFYFNKPTGYGSSSSRRACQTGIVDEC
 CFRSCDLRRLEMYCAPLKPAKSA
 >g1bom.1 g.1.1.1 (B:,A:) Bombyxin-II {Silkworm (Bombyx mori)}
 EQPQAVHTYCGRHLARTLADLCWEAGVDXGIVDECCLRPCSVDVLLSYC
 >d1agg__ g.3.6.2 (-) omega-Agatoxin IV, IVa, IVb {Funnel web spider (Agelenopsis aperta)}
 EDNCIAEDYGKCTWGGTKCCRGRPCRCSMIGTNCECTPRLIMEGLSFA
 >d1qdp__ g.3.6.2 (-) Robustoxin {Funnel-web spider (Atrax robustus)}
 CAKKRNWCGKNEDCCCPMKCIYAWYNQQGSCQTTITGLFKKC
 >d1i25a__ g.3.6.2 (A:) Huwentoxin-II {Chinese bird spider (Selenocosmia huwena)}
 LFECSFSCEIEKEGDKPCKKKKCKGGWKCKFNMCKVKV
 >d1jzaa__ g.3.7.1 (A:) Scorpion toxin {Centruroides sculpturatus ewing, variant 2}
 KEGYLVNKSTGCKYGLKLGGENEGCDKECKAKNQGGSYGYCYAFACWCEGLPESTPTY
 PLPNKSCS
 >d1bcg__ g.3.7.1 (-) Scorpion toxin {Scorpion (Buthotus judaicus), BJXTR-IT}
 MKKNGYPLDRNGKTTECSGVNAIAPHYCNSECTKVYYAESGYCCWGACYCFGLEDDKPI
 GPMKDITKKYCDVQI
 >d1bmr__ g.3.7.1 (-) LQH III alpha-like toxin, LQH {Hebraei scorpion (Leiurus quinquestriatus hebraeus)}
 VRDGYIAQPENCYVYHCFPGSSGCDTLCKEKGGTSGHCGFKVGHGLACWCNALPDNVGII
 VEGEKCHS
 >d1cmr__ g.3.7.2 (-) Charybdotoxin {Scorpion (Leiurus quinquestriatus hebraeus)}
 CTTSKECWSVCQRLHNTSKGWCDHRGCICES
 >d1chl__ g.3.7.2 (-) Chlorotoxin {Scorpion (Leiurus quinquestriatus), venom}
 MCMPCFTTDHQMARCDDCCGGKGRGKCYGPQCLCR
 >d1c55a__ g.3.7.2 (A:) Butantoxin {Brazilian scorpion (Tityus serrulatus)}
 WCSTCLDLACGASRECYDPCFKAFGRAHGKCMNNKCRCYT
 >d1pnh__ g.3.7.2 (-) Toxin analog {Scorpion (Androctonus mauretanicus mauretanicus)}
 TVCNLRRCQLSCRSLLGKLCIGVKCECVKH
 >d1gpt__ g.3.7.5 (-) gamma-Thionin {Barley (Hordeum vulgare)}
 RICRRRSAGFKGPCVSNKNCAQVCMQEGWGGNCDGPLRRCKCMRRC
 >d1ayj__ g.3.7.5 (-) Antifungal protein 1 (RS-AFP1) {Radish (Raphanus sativus)}
 EKLCEPSGTWSGVCNNACKNQCNLEKARHGSCNYVFPAHKCICYFPC
 >d1brz__ g.3.7.5 (-) Brazzein {J'oublie (Pentadiplandra brazzeana)}
 EDKCKKVYENYPVSKCQLANQCNYDCKLDKHARSGEFCYDEKRNLCICDYCEY
 >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)}
 DLCPGTMECKPMCEKTTINNEYNYRCWTTNRCQKMCPSTCGKRACTENNECCHPECLGS
 CSAPDNDTACVACRHYYYAGVCVPACPPNTYRFEGWRCVDRDFCANILSAESSDSEGFVI
 HDGECMQECPSGFIRNGSQSMYCIPCEGPCP
 >d1lpa2 g.3.10.1 (A:45-90) (Pro)colipase {Pig (Sus scrofa)}

ENSECSAFTLYGVYYKPCERGLTCEGDKSLVGSITNTNFGICHNV
 >d1pco_1 g.3.10.1 (1-44) (Pro)colipase {Pig (Sus scrofa)}
 VPDPRGIIINLDEGELCLNSAQCKSNCCQHDTILSLSRCALKAR
 >d1imt_1 g.3.10.1 (1-36) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}
 AVITGACERDLQCGKGTCCAVSLWIKSVRVCTPVGT
 >d1imt_2 g.3.10.1 (37-80) Intestinal toxin 1 {Black mamba (Dendroaspis polylepis polylepis)}
 SGEDCHPASHKIPFSGQRMHHTCPCAPNLACVQTSPKKFKCLSK
 >d1pfxl2 g.3.11.1 (L:87-146) Factor IX (IXa) {Pig (Sus scrofa)}
 TCNIKNGRCKQFCKTGADSKVLCSTTG YRLAPDQKSCKPAVPFPCGRVSVSHSPTTLTR
 >d1danl2 g.3.11.1 (L:87-142) Coagulation factor VIIa {Human (Homo sapiens)}
 DQLICVNENGGCEQYCS DHTGTRKSCRCHEGYLLADGVSTPTVEYPCGKIPILE
 >d1f7ea_ g.3.11.1 (A:) Coagulation factor VIIa {Human (Homo sapiens)}
 SDGDQCASSPCQNGGSCKDQLQSYICFCLPAFEGRNCE THKDDGSA
 >d1glsa2 g.3.11.1 (A:119-158) E-selectin, EGF-domain {Human (Homo sapiens)}
 TASCQDMSCSKQGE CLETIGNYTCSCYPGFYGP ECEYVRD
 >d1autl1 g.3.11.1 (L:49-96) Activated protein c (autoprothrombin IIa) {Human (Homo sapiens)}
 QCLVLPLEHPCASLCCGHGTCIDGIGSFSCDCRS GWEGRFCQREV SFL
 >d1cvua2 g.3.11.1 (A:33-73) Prostaglandin H2 synthase-1, EGF-like module {Mouse (Mus musculus)}
 ANPCCSNPCQNRGECMSTGFDQYKCDCTRTGFYGENCTTPE
 >d3egf_ g.3.11.1 (-) Epidermal growth factor, EGF {Mouse (Mus musculus)}
 NSYPGCPSSYDGYCLNGGVC MHIESLDSYTCNCVIGYSGDRCQTRDLRWWELR
 >d3tgf_ g.3.11.1 (-) Transforming growth factor alpha {Human (Homo sapiens)}
 VVSHFNDCPDSHTQFCFHGTCRFLVQEDKPACVCHSGYVGARCEHADLLA
 >d1lurk_1 g.3.11.1 (6-49) Plasminogen activator (urokinase-type) {Human (Homo sapiens)}
 QVPSNCDCLNGGTCVSNKYFSNIHWCNCPKKFGGQHCEIDKSKT
 >d1hae_ g.3.11.1 (-) Heregulin-alpha, EGF-like domain {Human (Homo sapiens)}
 SHLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTENVPMKVQNQEK
 AEELY
 >d1zaq_ g.3.11.1 (-) Thrombomodulin, different EGF-like domains {Human (Homo sapiens)}
 EPVDPCFRANCEYQCQPLNQTSYLCVCAEGFAPIPH EPHRCQMF
 >d1lap_ g.3.11.1 (-) Complement protease C1R {Human (Homo sapiens)}
 AVDLDECASRSKSGEEDPQPQCQHLCHNYVGGYFCSCRPGYELQEDRHSCQAE
 >d1hz8a1 g.3.11.1 (A:1-41) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}
 GTNECLDNNGGCSHVCNDLKIGYECLCPDGFQLVAQRRCED
 >d1ijqa2 g.3.11.1 (A:643-692) Low density lipoprotein (LDL) receptor, different EGF domains {Human (Homo sapiens)}
 VNWCERTTSLNNGGCQYLCLPAPQINPHSPKFTCACPDGM LLARDMR SCLT
 >d1klo_1 g.3.11.2 (11-65) Laminin gamma1 chain {Mouse (Mus musculus)}
 CPCPGGSSCAIVPKTKEVVCTHCPTGTAGKRCEL CDDGYFGDPLGSNGPVRLCRP
 >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)}
CACNPYGTVQQSSCNPVTVGQCQCLPHVSGRDCGTCDPGYYNLQSGQGGER

>d1b9wa1 g.3.11.4 (A:1-45) Merozoite surface protein 1 (MSP-1) {Plasmodium cynomolgi}
MSSEHRCIDTNVPENAACYRYLDGTEEWRCCLLYFKEDAGKCVPA

>d1cjea2 g.3.11.4 (A:46-96) Merozoite surface protein 1 (MSP-1) {Plasmodium falciparum}
NPTCNENNGGCDADAKCTEEDSGSNGKKITCECTKPDSYPLFDGIFCSSN

>d1df9c_ g.3.13.1 (C:) Bowman-Birk inhibitor, BBI {Mung bean (Vigna radiata)}
SHDEPSESSEPCDSCDCTKSIPPQCHCANIRLNSCHSACKSCICTRSMPPGKCRCLDTDDFC
YKPCESMDKD

>d1c2aa1 g.3.13.1 (A:4-64) Bowman-Birk inhibitor, BBI {Barley (Hordeum vulgare)}
KRPWKCCDEAVCTRSIPPICTCMDEVFECPKTCKSCGPSMGDPSRRICQDQYVGDPGPICR

>d1ejab_ g.3.15.1 (B:) Bdellastasin {Medicinal leech (Hirudo medicinalis)}
TTPCGPVTCSGAQMCEVDKCVCSDLHCKVKCEHGFKKDDNGCEYACICADAPQ

>d1skz_1 g.3.15.1 (7-58) Factor Xa inhibitor antistasin {Mexican leech (Haementeria officinalis)}
GCEEAGCPGEGSACNIITDRCTCSGVRCRVHCPHGFQRSRYGCEFCRLEPM

>d1hrti_ g.3.15.2 (I:) Hirudin {Leech (Hirudo medicinalis)}
VVYTDCTESGQNLCLCEGSNVCGQGKNCILGSDGEKNQCVTGEGTPKPQSHNDGDFEEIP
EEYLQ

>d1e0fi_ g.3.15.2 (I:) Haemadin {Indian leech (Haemadipsa sylvestris)}
IRFGMGKVPCPDGEVGYTCDGCEKICLYGQSCNDGQCSGDPKPSSEFEFEIDEEEEK

>d1fas_ g.7.1.1 (-) Fasciculin {Green mamba (Dendroaspis angusticeps)}
TMCYSHTTTSRAILTNCGENSCYRKSRRHPPKMVLGRGCGCPPGDDYLEVKCCTSPDKC
NY

>d1hc9a_ g.7.1.1 (A:) Bungarotoxin {Many-banded krait (Bungarus multicinctus), Alpha-bungarotoxin}
IVCHTTATSPISAVTCPPGENLCYRKMWCDVFCSSRGKVVELGCAATCPSKKPYEEVTCCS
TDKCNPHPKQRP

>d1f94a_ g.7.1.1 (A:) Bucandin {Malayan krait (Bungarus candidus)}
MECYRCGVSGHLKITCSAEETFCYKWLNKISNERWLGCATCTEIDTWNVYNKCCTTN
LCNT

>d1jgka_ g.7.1.1 (A:) Candoxin {Malayan krait (Bungarus candidus)}
MKCKICNFDTCRAGELKVCASGEKYCFKESWREARGTRIERGCAATCPKGSVYGLYVLC
CTTDDCN

>d1erh_ g.7.1.3 (-) CD59 {Human (Homo sapiens)}
LQCYNCPNPTADCKTAVNCSSDFDAKLITKAGLQVYNKCWKFEHCNFDVTTRLRENEL
TYYCCKKDLN

>d1btea_ g.7.1.3 (A:) Type II activin receptor {Mouse (Mus musculus)}
ETQECLFFNANWERDRTNQTGVEPCYGDKDKRRHCFATWKNISGSIEIVKQGCWLDDINC
YDRTDICIEKKDSPEVYFCCCEGNMCNEKFSYFPEME

>d1es7b_ g.7.1.3 (B:) BMP receptor Ia ectodomain {Human (Homo sapiens)}
TLPFLKCYCSGHCPDDAINNTCITNGHCFIIEEDDQGETTLASGCMKYEGSDFQCKDSPK
AQLRRTIECCRTNLCNQYLQPTLPP

>d1ktzb_ g.7.1.3 (B:) TGF-beta type II receptor extracellular domain {Human (Homo sapiens)}

PQLCKFCDVRFSTCDNQKSCMSNCSITSICEKPQEVCAVWRKNDENITLETVCHDPKLPY
 HDFILEDAASPKCIMKEKKKPGETFFMCSCSSDECNDNIIFSEY
 >d1adz__ g.8.1.1 (-) Tissue factor pathway inhibitor {Human (Homo sapiens)}
 DYKDDDDKLKPDFCFLEEDPGICRGYITRYFYNNQTKQCERFKYGGCLGNMNNFETLEE
 CKNICEDGPNGF
 >d1irha_ g.8.1.1 (A:) Tissue factor pathway inhibitor {Human (Homo sapiens)}
 EFHGPSWCLTPADRGLCRANENRFYYNSVIGKCRPFKYSGCGGNENNFTSKQECLRACKK
 G
 >d1bunb_ g.8.1.1 (B:) beta2-bungarotoxin, neurotoxin chain {Many-banded krait
 (elapid) (Bungarus multicinctus)}
 RKRHPDCDKPPDTKICQTVVRAFYKPSAKRCVQFRYGGCNGNGNHFKSDHLCRCECLE
 YR
 >d1bf0__ g.8.1.1 (-) Calcicludine (cac) {Green mamba (Dendroaspis angusticeps)}
 WQPPWYCKEPVRIGSCKKQFSSFYFKWTAKKCLPFLFSGCGGNANRFQTIGECRKKCLGK
 >d1toer1 g.8.1.2 (R:1A-56) Ornithodorin {Soft tick (Ornithodoros moubata)}
 SLNVLCCNNPHTADCNNDAQVDRYFREGTTCLMSPACTSEGYASQHECQQACFVGGED
 >d1toer2 g.8.1.2 (R:57-119) Ornithodorin {Soft tick (Ornithodoros moubata)}
 HSSEMHSSCLGDPPTSCAEGTDITYYDSSTCKVLAASCPGENTFESEVECQVACGAPI
 EG
 >d1d0da_ g.8.1.2 (A:) Anticoagulant protein, factor Xa inhibitor {Soft tick (Ornithodoros moubata)}
 YNRLCIKPRDWIDECDSENGGERAYFRNGKGGCDSFWICPEDHTGADYYSSYRDCFNACI
 >d1fd3a_ g.9.1.1 (A:) Beta-defensin, BD {Human (Homo sapiens), HBD2}
 GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKKP
 >d1ewsa_ g.9.1.1 (A:) Alpha-defensin rk-1 {Rabbit (Oryctolagus cuniculus)}
 MPCSCKKYCDPWEVIDGSCGLFNSKYICCREK
 >d1b8wa_ g.9.1.1 (A:) Defensin-like peptide, DLP {Duckbilled platypus (Ornithorhynchus
 anatinus), DLP-1}
 FVQHRPRDCESINGVCRHKDTVNCREIFLADCYNDGQKCCRK
 >d1d6ba_ g.9.1.1 (A:) Defensin-like peptide, DLP {Duckbilled platypus (Ornithorhynchus
 anatinus), DLP-2}
 IMFFEMQACWSHSGVCRDKSERNCKPMAWTYCENRNQKCCEY
 >d2bds__ g.9.1.1 (-) BDs-I defensin {Sea anemone (Anemonia sulcata)}
 AAPCFCSGKPGRGDLWILRGTCPGGYGYTSNCYKWPNICCYPH
 >d1sh1__ g.9.1.1 (-) Sea anemone neurotoxin-1 {Sea anemone (Stichodactyla
 helianthus)}
 AACKCDDEGPDIRTAPLTGTVDLGSCNAGWEKCASYTYIIADCCRKKK
 >d1ahl__ g.9.1.1 (-) Anthopleurin-A {Giant green sea anemone (Anthopleura
 xanthogrammica)}
 GVSCLCDSGSPVRGNTLSGTLWLPSGCPGWHNCKAHGPTIGWCKKQ
 >d1d2la_ g.12.1.1 (A:) Ligand-binding domain of low-density lipoprotein receptor
 {Human (Homo sapiens)}
 GSPPQCQPGEFACANSRCIQERWKCDGDNDCLDNSDEAPALCHQH
 >d1ldl__ g.12.1.1 (-) Ligand-binding domain of low-density lipoprotein receptor
 {Human (Homo sapiens)}

AVGDR CERNEFQCQDGK CISYKWVCDGSAECQDGSDESQETCLSVT
 >d1k7ba_ g.12.1.1 (A:) soluble Tva ectodomain, sTva47 {Quail (Coturnix coturnix)}
 SCPPGQFRCSEPPGAHGECYPQDWLCDGHPDCDDGRDEWGCG
 >d1ejga_ g.13.1.1 (A:) Crambin {Abyssinian cabbage (Crambe abyssinica)}
 TTCCPSIVARSNFNVCR LPGTPEALCATYTGCIIPGATCPGDYAN
 >d1bhp__ g.13.1.1 (-) beta-Purothionin {Wheat (Triticum aestivum)}
 KSCCKSTLGRNCYNLCRARGAQKLCANVCRC KLTSG LSCP KDFPK
 >d1pmla_ g.14.1.1 (A:) Plasminogen kringles {Human (Homo sapiens)}
 SDCYFGNGSAYRGTHSLTESGASCLPWN SMILIGKVYTAQNPSAQALGLGKHNYCRNPD
 GDAKPWCHVLKNRRLTWEYCDVPSCST
 >d2pfl_1 g.14.1.1 (66-156) Prothrombin kringle domain {Cow (Bos taurus)}
 CAEGVGMNYRGNVSVTRSGIECQLWRSRYPHKPEINSTTHPGADLRENFCRNP DGSITGP
 WCYTTSP TLRREECSVPVCGQDRVTVEVIPR
 >d1a0ha1 g.14.1.1 (A:164-270) Meizothrombin kringle domain {Cow (Bos taurus)}
 SPLLET CVPDRGREYRGRLAVTTHGSRCLAWSSEQA KALSKDQDFNP AVPLAENFCRNP D
 GDEEGAWCYVADQPGDFEYCDLNYCEEPVDGDLGDR LGEDPDPDAAIEG
 >d1tbr1 g.15.1.1 (R:1-51) Rhodniin {Bug (Rhodnius prolixus)}
 EGGEPCACPHALHRVCGSDGETYSNPCTLNCAKFNGKPELVKVH DGPCEPD
 >d1tbr2 g.15.1.1 (R:52-103) Rhodniin {Bug (Rhodnius prolixus)}
 EDEDVCQEC DGDEYKPVCGSDDITYDNNCRLECASISSSPGV ELKH EGP CRT
 >d1nuba3 g.15.1.1 (A:78-135) Domain of BM-40/SPARC/osteonectin {Human (Homo sapiens)}
 CQDPTSCPAPIGEFEKVC SNDNKTFDSSCHFFATKCTLEGTKKG HKLHLDYIGPCKYI
 >d2bus__ g.15.1.1 (-) Seminal plasma inhibitor IIa {Cow (Bos taurus)}
 EGAQVDCAEFKDPKVYCTRESNPHCGSNGETYGNKCAFC KAVMKSGGKINLKH RGKC
 >d1pce__ g.15.1.1 (-) PEC-60 peptide {Pig (Sus scrofa)}
 EKQVFSRMPICEHMTESPD CSRIYDPVCGTDGVTY ESECKLCLARIENKQDIQIVKDGE C
 >d1pdga_ g.17.1.1 (A:) Platelet-derived growth factor BB {Human (Homo sapiens)}
 EPAMIAECKTRTEVF EISRRLIDRTNANFLVWPPC VEVQRCSGCCNNRN VQCRPTQVQLRP
 VQVRKIEIVRKKPIFKKATVTLEDHLACKCETVAA
 >d1fzva_ g.17.1.1 (A:) Placenta growth factor-1, PLGF-1 {Human (Homo sapiens)}
 SSEVEVVPFQEVWGRSYCRALERLVDV VSEYPSEVEHMFSPSCV SLLRCTGCCGDENLHC
 VPVETANVTMQLLKIRSGDRPSYVELTFSQHVRCECRPLR
 >d1tgj__ g.17.1.2 (-) TGF-beta3 {Human (Homo sapiens)}
 ALDTNYCFRNLEENCCVRPLYIDFRQDLGWK WVHEPKGYANFCSGPCPYLRSADTTHS
 TVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK SCKCS
 >d1bmp__ g.17.1.2 (-) Bone morphogenetic protein-7 (BMP-7) {Human (Homo sapiens)}
 QACKKHELYVSFRDLGWQDWIIAPEGYA AYYCEGECAFLNSYMNATNHAI VQTLVHFIN
 PETVPKPCCAPTQLNAISVLYFDDSSNVILKKYRNMVVRACGCH
 >d1agqa_ g.17.1.2 (A:) Glial cell-derived neurotrophic factor, GDNF {Rat (Rattus norvegicus)}
 NRGCVLTAIHLNVTDLGLGYETKEELIFRYCSGSCEAAETMYDKILKNLSR SRRLTSDKVG
 QACCRPVAFDDDL SFLDDSLVYHILRKHS AKRCGCI
 >d1hcna_ g.17.1.4 (A:) Glycoprotein hormones alpha chain (Gonadotropin A,
 Follicle-stimulating hormone) {Human (Homo sapiens)}
 QDCPECTLQENPFFSQPGAPILQCMGCCFSRAYPTPLRSKKTMLVQKNVTSESTCCVAKSY

NRVTVMGGFKVENHTACHCSTCY

>d1hcnb_ g.17.1.4 (B:) Gonadotropin B chain {Human (Homo sapiens)}

KEPLRPRCRPINATLAVEKEGCPVCITVNTTICAGYCPTMTRVLQGVLPALPQVVCNYRDV
RFESIRLPGCPRGVNPVVSVAVALSCQCALCRRSTTDCGGPKDHPLTCD

>d1fl7b_ g.17.1.4 (B:) Follicle stimulating hormone, follitropin, beta chain {Human (Homo sapiens)}

CELTNITIAIEKEECRFCISINTAWCAGYCYTRDLVYKDPARPKIQKTCTFKELVYETVRVPG
CAHHADSLYTYPVATQCHCGKCDSDSTDCTVRGLGPSYCSFGEM

>d1hcc_ g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}

EGLPCKSPPEISHGVVAHMSDSYQYGEEVYKCFEGFGIDGPAIAKCLGEKWSHPPSCI

>d1hfi_ g.18.1.1 (-) Factor H, 15th and 16th modules {Human (Homo sapiens)}

EKIPCSQPPQIEHGTINSSRSSQESYAHGTKLSYTCEGGFRISEENETTCYMGKWSSPPQCE

>d1g40a1 g.18.1.1 (A:1-64) Complement control protein {Vaccinia virus}

CCTIPSRPINMKFKNSVETDANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTFLN
QCIK

>d1g40a3 g.18.1.1 (A:127-184) Complement control protein {Vaccinia virus}

VKCQSPPSISNGRHNGYEDFYTDGSVVTYSCNSGYSLIGNSGVLCSGGEWSDPPTCQI

>d1g40a4 g.18.1.1 (A:185-243) Complement control protein {Vaccinia virus}

VKCPHPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPCV

>d1ckla1 g.18.1.1 (A:1-62) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}

CEEPPTFEAMELIGKPKPYEIGERVDYKCKKGYFYIPPLATHTICDRNHTWLPVSDDACY
R

>d1ckla2 g.18.1.1 (A:63-126) CD46 (membrane cofactor protein, MCP) {Human (Homo sapiens)}

ETCPYIRDPLNGQAVPANGTYEFGYQMHFICNEGYYLIGEEILYCEKGSVAIWSGKPPICE
KV

>d1clza5 g.18.1.1 (A:244-326) beta2-glycoprotein I {Human (Homo sapiens)}

SCKLPVKKATVVYQGERVKIQEKFKNGMLHGDKVSFFCKNKEKKCSYTEDAQCIDGTIE
VPKCFKEHSSLAFWKTDASDVKPC

>d1quba1 g.18.1.1 (A:1-62) beta2-glycoprotein I {Human (Homo sapiens)}

GRTCPKPDDLPFSTVVPLKTFYEPGEEITYSCKPGYVSRGGMRKFICPLTGLWPINTLKCTP

>d1quba2 g.18.1.1 (A:63-120) beta2-glycoprotein I {Human (Homo sapiens)}

RVCPPFAGILENGAVRYTTFEYPNTISFSCNTGFYLNAGADSAKCTEEGKWSPELPVCAP

>d1quba3 g.18.1.1 (A:121-183) beta2-glycoprotein I {Human (Homo sapiens)}

IICPPPSIPTFATLRVYKPSAGNNSLYRDTAVFECLPQHAMFGNDTITCTTHGNWTKLPECRE

>d1quba4 g.18.1.1 (A:184-243) beta2-glycoprotein I {Human (Homo sapiens)}

VKCPFPSRPDNGFVNYPKPTLYYKDKATFGCHDGYSLDGPEEIECTKLGNWSAMPSCA

>d1ghqb1 g.18.1.1 (B:1-66) Complement receptor 2, cr2 {Human (Homo sapiens)}

AISCGSPPIILNGRISYYSTPIAVGTVIRYSCSGTFRLIGEKSLLCITKDKVDGTWDPAPKCE
YF

>d1ghqb2 g.18.1.1 (B:67-129) Complement receptor 2, cr2 {Human (Homo sapiens)}

NKYSSCEPIVPGGYKIRGSTPYRHGDSVTFACKTNFSMNGNKSVMWCQANNMWGPTRLP
TCVS

>d1elva2 g.18.1.1 (A:342-409) Complement C1S protease domain {Human (Homo sapiens)}

LDCGIPESIEENGKVEDPESTLFGSVIRYTCEEPYYYMENGGGGEYHCAGNGSWVNEVLGP

ELPKCVPV

>d1atb__ g.22.1.1 (-) Ascaris trypsin inhibitor, ATI {Pig roundworm (*Ascaris Lumbricoides*), variant suum}

EAEKCTKPNEQWTKCGGCEGTCAQKIVPCTRECKPPRCECIASAGFVRDAQGNCIKFEDC
PK

>d1coua_ g.22.1.1 (A:) Anticoagulant protein {Dog hookworm (*Ancylostoma caninum*)}

KATMQCGENEKYDSCGSKECDKKCKYDGVVEEDDEEPNVPCLVRVCHQDCVCEEFGFYR
NKDDKCVSAEDCELDNMDFIYPGTRNP

>d1exta1 g.24.1.1 (A:13-71) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}
SVC PQGKYIHPQNNSICCTKCHKGTLYNDCPGPGQDTDCRECESGSFTASENHLRHCL

>d1exta2 g.24.1.1 (A:72-115) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}
SCSKCRKEMGQVEISSCTVDRDTVCGCRKNQYRHYWSENLFQCF

>d1exta3 g.24.1.1 (A:116-172) Tumor necrosis factor (TNF) receptor {Human (*Homo sapiens*)}
NCSLCLNGTVHLSCQEKQNTVCTCHAGFFLRENECVSCSNCKKSLECTKLCLPQIEN

>d1d4va1 g.24.1.1 (A:69-114) Death receptor-5 (dr5) fragment {Human (*Homo sapiens*)}
PQQKRSSPSEGLCPPGHHISEDGRDCISCKYQGQDYSTHWNDLLFCL

>d1jmab1 g.24.1.1 (B:4-59) Cellular receptor HveA {Human (*Homo sapiens*)}
CKEDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYYIAHLNGLSKCLQCQ

>d1e88a3 g.27.1.1 (A:1-41) Fibronectin {Human (*Homo sapiens*)}
YGHCVTD SGVVYSVGMQWLKTQGNKQMLCTCLGNGVSCQET

>d1fbr_2 g.27.1.1 (47-93) Fibronectin {Human (*Homo sapiens*)}
NRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNRGGEWK CERHTS

>d1qgba1 g.27.1.1 (A:17-60) Fibronectin {Human (*Homo sapiens*)}
SKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFN CESKP

>d1qgba2 g.27.1.1 (A:61-109) Fibronectin {Human (*Homo sapiens*)}
EAEETCFDKYTGNTRYRVGDTYERPKDSMIWDCTCIGAGRGRISCTIANR

>d1tpg_2 g.27.1.1 (1-50) Tissue-type plasminogen activator, t-PA {Human (*Homo sapiens*)}
SYQVICRDEKTQMIYQQHQSWLRPVLRNVRVEYCWNSGRAQCHSVPVKS

>d1isua_ g.35.1.1 (A:) HIPI (high potential iron protein) {*Rhodocyclus tenuis*}
GTNAAMRKAFNYQDTAKNGKKCSGCAQFVPGASPTAAGGCKVIPGDNQIAPGGYCDAFI
VKK

>d1js2a_ g.35.1.1 (A:) HIPI (high potential iron protein) {*Allochro matium vinosum*,
(formerly *Chromatium vinosum*)}

MEFMSAPANAVAADDAATAIALKYNQDATKSERVAAARPGLPPEEQHCANCQFMQADAAG
ATDEWKGCQLFPGKLINVNGWSASWTLKAG

>d2hipa_ g.35.1.1 (A:) HIPI (high potential iron protein) {*Ectothiorhodospira*
halophila}

EPRAEDGHAHDYVNEAADASGHPRYQEGQLCENCAFWGEAVQDGWGRCTHPDFDEVL
VKAEGWCSVYAPAS

>d1hpi__ g.35.1.1 (-) HIPI (high potential iron protein) {*Ectothiorhodospira*
vacuolata}

MERLSEDDPAAQALEYRHDASSVQHPAYEEGQTCLNCLLYTDASAQDWGPCSVFPGKLV
SANGWCTAWVAR

>d1f2ig1 g.37.1.1 (G:1093-1131) ZIF268 {Mouse (*Mus musculus*)}
 NLLNYVVPKMRPYACPVESCDRRFSRSEDLTRHIRIHTG

>d1bhi__ g.37.1.1 (-) Transactivation domain of cre-bp1/atf-2 {Human (*Homo sapiens*)}
 MSDDKPFLCTAPGCGQRFTNEDHLAVHKHKHEMTLKFG

>d1tf3a3 g.37.1.1 (A:71-101) Transcription factor IIIA, TFIIIA {*Xenopus laevis*}
 KNFTCDSDGCDLRFTTKANMKKHFNRFHNIK

>d1tf6a4 g.37.1.1 (A:101-131) Transcription factor IIIA, TFIIIA {*Xenopus laevis*}
 KICVYVCHFENCGKAFKKHNQLKVHQFSHTQ

>d1yuja_ g.37.1.1 (A:) GAGA factor {*Drosophila melanogaster*}
 PKAKRAKHPPGTEKPRSRSQSEQPATCPICYAVIRQSRNLRRHLELRHFAKPGV

>d1fu9a_ g.37.1.2 (A:) U-shaped transcription factor, different fingers {Fruit fly (*Drosophila melanogaster*)}
 GSAAEVMKKYCSTCDISFNYVKTYLAHKQFYCKNKP

>d1fv5a_ g.37.1.2 (A:) U-shaped transcription factor, different fingers {Fruit fly (*Drosophila melanogaster*)}
 GSLKPARFMCLPCGIAFSSPSTLEAHQAYYCSHRI

>d1aw6__ g.38.1.1 (-) Gal4 {Baker's yeast (*Saccharomyces cerevisiae*)}
 MKLLSSIEQACDICRLKKLKCSKEKPKCAKCLKNNWECRYSPK

>d1pyia1 g.38.1.1 (A:30-71) PPR1 {Baker's yeast (*Saccharomyces cerevisiae*)}
 SRTACKRCRLKKIKCDQEFPSCKRCAKLEVPCVSLDPATGKD

>d1zmec1 g.38.1.1 (C:31-66) PUT3 {Baker's yeast (*Saccharomyces cerevisiae*)}
 SVACLSCRKRHIKCPGGNPCQKCVTSNAICEYLEPS

>d2hapc1 g.38.1.1 (C:55-97) Hap1 (Cyp1) {Baker's yeast (*Saccharomyces cerevisiae*)}
 RKRNRIPRLCTICRKRKVKCDKLRPHCQOCTKTGVAHLCHYME

>d2alca_ g.38.1.1 (A:) Ethanol regulon transcriptional activator ALCR DNA-binding domain {*Aspergillus nidulans* and *Emericella nidulans*}
 GSMADTRRRQNHSCDPCRKGKRRCDAPENRNEANENGWVSCSNCKRWNKDCTFNWLS
 SQRSKNSS

>d2nllb_ g.39.1.2 (B:) Thyroid hormone receptor (TR-beta) DNA-binding domain {Human (*Homo sapiens*)}
 DELCVVCGDKATGYHYRCITCEGCKGFFRRTIQKNLHPSYSCKYEGKCVIDKVTRNQCQE
 CRFKKCIYVGMATDLVLDDSKRLAKRKLIEENREKRRREELEK

>d1glua_ g.39.1.2 (A:) Glucocorticoid receptor DNA-binding domain {Rat (*Rattus norvegicus*)}
 MKPARPCLVCSDEASGCHYGVLTCGSKVFFKRAVEGQHNYLCAGRNDICIIDKIRRNCP
 ACRYRKCLQAGMNLEARKTKK

>d1b8ta2 g.39.1.3 (A:36-100) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (*Gallus gallus*)}
 LCMVCKKNLDSTTVAVHGDEIYCKSCYGGKYGPKGKGKGMGAGTLSTDKGESLGIKYEE
 GQSHRP

>d1b8ta3 g.39.1.3 (A:101-143) Cysteine-rich (intestinal) protein, CRP, CRIP {Chicken (*Gallus gallus*)}
 TNPNASRMAQKVGGSDGCPRCGQAVYAAEKVIGAGKSWHKSCF

>d1tfi__ g.41.3.1 (-) Transcriptional factor SII, C-terminal domain {Human (*Homo sapiens*)}
 KTGGTQTDLFTCGKCKKKNCTYTTQVQTRSADPMTTFFVCNECGNRWKFC

>d1pft__ g.41.3.1 (-) Transcription initiation factor TFIIIB, N-terminal domain {Archaeon Pyrococcus furiosus}
MVNKQKVCACESAELIYDPERGEIVCAKCGYVIEENIIDMGPEWRAFDA

>d1dl6a_ g.41.3.1 (A:) Transcription initiation factor TFIIIB, N-terminal domain {Human (Homo sapiens)}
ASTSRLDALPRVTCPNHPDAILVEDYRAGDMICPECGLVVGDRVIDVGSEWRTFSNDK

>d1yua_1 g.41.3.3 (1-65) Prokariotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}
MNGEVAPPKEDPVPLPELPCEKSDAYFVLRDGAAGVFLAANTFPKSRETRAPLVEELYRFR
DRLP

>d1yua_2 g.41.3.3 (66-122) Prokariotic DNA topoisomerase I, a C-terminal fragment {Escherichia coli}
EKLRYLADAPQQDPEGNKT MVRF SRKTKQQYVSSEKDGKATGWSAFYVDGKWVEGKK

>d1qeva_ g.41.5.1 (A:) Rubredoxin {Archaeon Pyrococcus furiosus}
AKWVLKITGYIYDEDAGDPDNGISPGTKFEELPDDWVAPITGAPKSEFEKLED

>d1dx8a_ g.41.5.1 (A:) Rubredoxin {Guillardia theta}
MEIDEGKYECEACGYIYEPEKGDKFAGIPPGTPFVDLSDSFMCPACRSPKNQFKSIKKVIAG
FAENQKYG

>d1qyp__ g.41.9.1 (-) RBP9 subunit of RNA polymerase II {Archaeon Thermococcus celer}
GSHMEQDLKTLPTTKITCPKCGNDTAYWWEMQTRAGDEPSTIFYKCTKCGHTWRSYE

>d1i50i1 g.41.9.1 (I:1-49) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}
MTTFRFCRDCNNMLYPREDKENNRLLFECRTCSYVEEAGSPLVYRHELI

>d1i50i2 g.41.9.1 (I:50-122) RBP9 subunit of RNA polymerase II {Baker's yeast (Saccharomyces cerevisiae)}
TNIGETAGVVQDIGSDPTLPRSDRECPKCHSRENVFFQSQQRRKDTSMVLFFVCLSCSHIFT
SDQKNKRTQFS

>d1fbva4 g.44.1.1 (A:356-434) CBL {Human (Homo sapiens)}
TPQDHIKVTQEYELYCEMGSTFQLCKICAENDKDVKIEPCGHLMCTSCLT SWQESEGQG
CPFCRCEIKGTEPIVVDPF

>d1rmd_2 g.44.1.1 (1-86) V(D)J recombination activating protein 1 (RAG1), dimerization domain {Mouse (Mus musculus)}
NCSKIHLSTKLLAVDFPAHFVKSISCQICEHILADPVETSCKHLFCRICILRCLKVMGSYCPS
CRYPCFPTDLESPVKSFLNILNS

>d1lhc__ g.44.1.1 (-) Immediate early protein, IEEHV {Equine herpes virus type 1}
MATVAERCPILEDPSNYSMALPCLHAFYVCITRWIRQNPTCPLCKVPVESVVHTIESDSE
FGDQLI

>d1bor__ g.44.1.1 (-) Acute promyelocytic leukaemia proto-oncoprotein PML {Human (Homo sapiens)}
EEEFQFLRCQQCQAEAKCPKLLPCLHTLCSGCLEASGMQCPICQAPWPLGADTPAL

>d1g25a_ g.44.1.1 (A:) TFIIH Mat1 subunit {Human (Homo sapiens)}
MDDQGCPRCKTTKYRNPSLKL MNVCGHTLCESCVDLLFVRGAGNCPECGTPLRKS NFR
VQLFED

>d1e4ua_ g.44.1.1 (A:) Not-4 N-terminal RING finger domain {Human (Homo sapiens)}

MSRSPDAKEDPVECPLCMEPLEIDINFFPCTCGYQICRFCWHIRTDENGLCPACRKPYPE
DPAVYKPLSQEELQRI

>d1jm7a_ g.44.1.1 (A:) brca1 RING domain {Human (Homo sapiens)}

MDLSALRVEEVQNVINAMQKILECPICLELIKEPVSTKCDHIFCKFCMLKLLNQKKGPSQC
PLCKNDITKRSQESTRFSQLEELLKIICAFQLDTGLEYN

>d1jm7b_ g.44.1.1 (B:) bard1 RING domain {Human (Homo sapiens)}

MEPDGRGAWAHSRAALDRLEKLLRCSRCTNILREPVCCLGGCEHIFCSNCVSDCIGTGCPV
CYTPAWIQDLKINRQLDSMIQLCSKLRNLLHDNELSD

>d4mt2_ g.46.1.1 (-) Metallothionein {Rat (Rattus rattus)}

MDPNCSCATDGSCSCAGSCKCKQCKCTSCCKSCCSCCPVGCAKCSQGCICKEASDKCSC
CA

>d1qjka_ g.46.1.1 (A:) Metallothionein {Purple sea urchin (Strongylocentrotus
purpuratus)}

PDVKCVCTEGKECACFGQDCCVTGECCKDGTCCGI

>d1faq_ g.49.1.1 (-) RAF-1 {Human (Homo sapiens)}

LTTHNFARKTFLKLAFCDICQKFLNGFRCQTCGYKFHEHCSTKVPTMCVDW

>d1tbo_ g.49.1.1 (-) Protein kinase c-gamma {Rat (Rattus rattus)}

QTDDPRNKHKFRLLHSYSSPTFCDHCGSLLYGLVHQGMKSCCEMNVRRCVRSVPSLCG
VDHTERR

>d1kbea_ g.49.1.1 (A:) Kinase suppressor of Ras, Ksr {Mouse (Mus musculus)}

GSVTHRFSTKSWLSQVCNVCQKSMIFGVKCKHCRLKCHNKCTKEAPACR

>d1dvpa2 g.50.1.1 (A:149-220) Hrs {Fruit fly (Drosophila melanogaster)}

MFTADTAPNWADGRVCHRCRVEFTFTNRKHHCRNCGQVFCGQCTAKQCPLPKYGIEKEV
RVCDGCFAALQRG

>d1zbdb_ g.50.1.1 (B:) Effector domain of rabphilin-3a {Rat (Rattus norvegicus)}

EELTDEEKEIINRVIARAEMETMEQERIGRLVDRLETMRKNVAGDGVNRCILCGEQLGM
LGSASVVCEDCKKNVCTKCGVETSNNRPHPVWLCKICLEQREVWKRSGAWFFKGFPKQ
VLPQPM

>d1adt_2 g.51.1.1 (266-385) First Zn-domain of early E2A DNA-binding protein, ADDBP {Human
adenovirus type 5}

TGCALWLHRC AEIEGELKCLHGSIMINKEHVIEMDVTSENGQRALKEQSSKAKIVKNRWG
RNVVQISNTDARCCVHDAACPANQFSGKSCGMFFSEGAQAQVAFKQIKAFMQALYPNAQ
T

>d1adt_3 g.51.1.1 (386-529) Second Zn-domain of early E2A DNA-binding protein, ADDBP
{Human adenovirus type 5}

GHGHLLMPLRCECNSKPGHAPFLGRQLPKLTPFALSNAEDLDADLISDKSVLASVHHPALI
VFQCCNPVYRNSRAQGGGPNCDFKISAPDLLNALVMVRSLWSENFTELPRMVVPQFKWS
TKHQYRNVSLPVAHSDARQNPFD

>d1f9xa_ g.52.1.1 (A:) BIR domains of XIAP {Human (Homo sapiens)}

MSDAVSSDRNFPNSTNLPRNPSMADYEARIFTFGTWIYSVNKEQLARAGFYALGEGDKVK
CFHCGGLTDWKPSDPWEQHAKWYPGCKYLLEQKGQEYINNIHLTHSLEECLVRTT

>d1i3oe_ g.52.1.1 (E:) BIR domains of XIAP {Human (Homo sapiens)}

FALDRPSETHADYLLRTGQVVDISDTIYPRNPAMYSEEARKLSFQNWPDYAHLPRELASA
GLYYTGIGDQVQCFCACGGKLNWEPGDRAWSEHRRHFPNCFVLGRNLNI

>d1e31a_g.52.1.1 (A:) Anti-apoptotic protein survivin {Human (Homo sapiens)}

TLPPAWQPFLKDHRISTFKNWPFLEGCACTPERMAEAGFIHCPTENEPDLAQCFKCFKELE
GWEPDDDPIEEHKKHSSGCAFLSVKKQFEELTLGEFLKLDREERAKNKIAKETNNKKKEFE
ETAKKVRRAIEQLAA